dask Documentation

Release 0.19.3

Dask Development Team

Oct 06, 2018

Getting Started

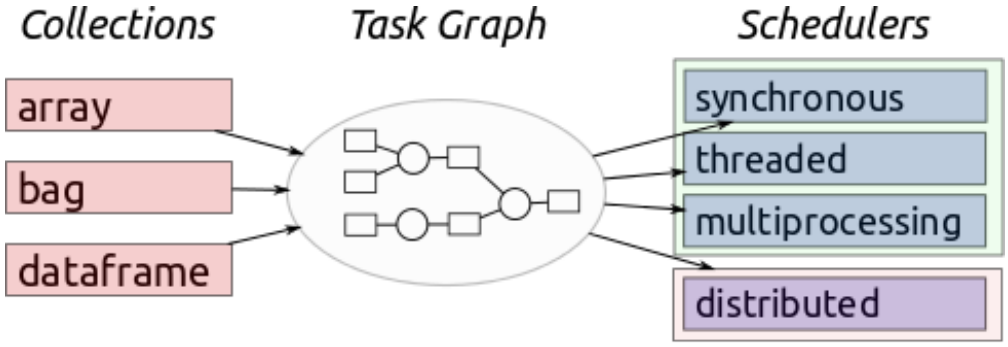
Dask is a flexible library for parallel computing in Python.

Dask is composed of two parts:

1. **Dynamic task scheduling** optimized for computation. This is similar to *Airflow, Luigi, Celery, or Make*, but optimized for interactive computational workloads.
2. **"Big Data" collections** like parallel arrays, dataframes, and lists that extend common interfaces like *NumPy, Pandas, or Python iterators* to larger-than-memory or distributed environments. These parallel collections run on top of dynamic task schedulers.

Dask emphasizes the following virtues:

- **Familiar**: Provides parallelized NumPy array and Pandas DataFrame objects
- **Flexible**: Provides a task scheduling interface for more custom workloads and integration with other projects.
- **Native**: Enables distributed computing in pure Python with access to the PyData stack.
- **Fast**: Operates with low overhead, low latency, and minimal serialization necessary for fast numerical algorithms
- **Scales up**: Runs resiliently on clusters with 1000s of cores
- **Scales down**: Trivial to set up and run on a laptop in a single process
- **Responsive**: Designed with interactive computing in mind, it provides rapid feedback and diagnostics to aid humans



See the dask.distributed documentation (separate website) for more technical information on Dask's distributed scheduler.

CHAPTER 1

Familiar user interface

Dask DataFrame mimics Pandas - *documentation*

```
import pandas as pd                          import dask.dataframe as dd
df = pd.read_csv('2015-01-01.csv')           df = dd.read_csv('2015-*-*.csv')
df.groupby(df.user_id).value.mean()          df.groupby(df.user_id).value.mean().compute()
```

Dask Array mimics NumPy - *documentation*

```
import numpy as np                           import dask.array as da
f = h5py.File('myfile.hdf5')                 f = h5py.File('myfile.hdf5')
x = np.array(f['/small-data'])               x = da.from_array(f['/big-data'],
                                                               chunks=(1000, 1000))
x - x.mean(axis=1)                           x - x.mean(axis=1).compute()
```

Dask Bag mimics iterators, Toolz, and PySpark - *documentation*

```
import dask.bag as db
b = db.read_text('2015-*-*.json.gz').map(json.loads)
b.pluck('name').frequencies().topk(10, lambda pair: pair[1]).compute()
```

Dask Delayed mimics for loops and wraps custom code - *documentation*

```
from dask import delayed
L = []
for fn in filenames:                    # Use for loops to build up computation
    data = delayed(load)(fn)            # Delay execution of function
    L.append(delayed(process)(data))    # Build connections between variables

result = delayed(summarize)(L)
result.compute()
```

The **concurrent.futures** interface provides general submission of custom tasks: - *documentation*

```
from dask.distributed import Client
client = Client('scheduler:port')

futures = []
for fn in filenames:
    future = client.submit(load, fn)
    futures.append(future)

summary = client.submit(summarize, futures)
summary.result()
```

CHAPTER 2

Scales from laptops to clusters

Dask is convenient on a laptop. It *installs* trivially with `conda` or `pip` and extends the size of convenient datasets from "fits in memory" to "fits on disk".

Dask can scale to a cluster of 100s of machines. It is resilient, elastic, data local, and low latency. For more information, see the documentation about the distributed scheduler.

This ease of transition between single-machine to moderate cluster enables users to both start simple and grow when necessary.

CHAPTER 3

Complex Algorithms

Dask represents parallel computations with *task graphs*. These directed acyclic graphs may have arbitrary structure, which enables both developers and users the freedom to build sophisticated algorithms and to handle messy situations not easily managed by the `map/filter/groupby` paradigm common in most data engineering frameworks.

We originally needed this complexity to build complex algorithms for n-dimensional arrays but have found it to be equally valuable when dealing with messy situations in everyday problems.

CHAPTER 4

Index

Getting Started

4.1 Install Dask

You can install dask with `conda`, with `pip`, or by installing from source.

4.1.1 Conda

Dask is installed by default in Anaconda.

You can update Dask using the conda command:

```
conda install dask
```

This installs Dask and **all** common dependencies, including Pandas and NumPy.

Dask packages are maintained both on the default channel and on conda-forge.

Optionally, you can obtain a minimal Dask installation using the following command:

```
conda install dask-core
```

This will install a minimal set of dependencies required to run Dask similar to (but not exactly the same as) `pip install dask` below.

4.1.2 Pip

You can install everything required for most common uses of Dask (arrays, dataframes, ...) This installs both Dask and dependencies like NumPy, Pandas, and so on that are necessary for different workloads. This is often the right choice for Dask users:

```
pip install "dask[complete]"    # Install everything
```

You can also install only the Dask library. Modules like `dask.array`, `dask.dataframe`, or `dask.distributed` won't work until you also install NumPy, Pandas, or Tornado, respectively. This is common for downstream library maintainers:

```
pip install dask                # Install only core parts of dask
```

We also maintain other dependency sets for different subsets of functionality:

```
pip install "dask[array]"       # Install requirements for dask array
pip install "dask[bag]"         # Install requirements for dask bag
pip install "dask[dataframe]"   # Install requirements for dask dataframe
pip install "dask[distributed]" # Install requirements for distributed dask
```

We have these options so that users of the lightweight core Dask scheduler aren't required to download the more exotic dependencies of the collections (Numpy, Pandas, Tornado, etc.).

4.1.3 Install from Source

To install Dask from source, clone the repository from github:

```
git clone https://github.com/dask/dask.git
cd dask
python setup.py install
```

or use `pip` locally if you want to install all dependencies as well:

```
pip install -e ".[complete]"
```

You can view the list of all dependencies within the `extras_require` field of `setup.py`.

4.1.4 Anaconda

Dask is included by default in the Anaconda distribution.

4.1.5 Test

Test Dask with `py.test`:

```
cd dask
py.test dask
```

Please be aware that installing Dask naively may not install all requirements by default. Please read the `pip` section above which discusses requirements. You may choose to install the `dask[complete]` version which includes all dependencies for all collections. Alternatively, you may choose to test only certain submodules depending on the libraries within your environment. For example, to test only Dask core and Dask array we would run tests as follows:

```
py.test dask/tests dask/array/tests
```

4.2 Setup

This page describes various ways to set up Dask on different hardware, either locally on your own machine or on a distributed cluster. If you are just getting started, then this page is unnecessary. Dask does not require any setup if you only want to use it on a single computer.

Dask has two families of task schedulers:

1. **Single machine scheduler**: This scheduler provides basic features on a local process or thread pool. This scheduler was made first and is the default. It is simple and cheap to use. It can only be used on a single machine and does not scale.
2. **Distributed scheduler**: This scheduler is more sophisticated. It offers more features, but also requires a bit more effort to set up. It can run locally or distributed across a cluster.

If you import Dask, set up a computation, and then call `compute`, then you will use the single-machine scheduler by default. To use the `dask.distributed` scheduler you must set up a `Client`

```
import dask.dataframe as dd
df = dd.read_csv(...)
df.x.sum().compute()  # This uses the single-machine scheduler by default
```

```
from dask.distributed import Client
client = Client(...)  # Connect to distributed cluster and override default
df.x.sum().compute()  # This now runs on the distributed system
```

Note that the newer `dask.distributed` scheduler is often preferable, even on single workstations. It contains many diagnostics and features not found in the older single-machine scheduler. The following pages explain in more detail how to set up Dask on a variety of local and distributed hardware.

- **Single Machine:**
  - *Default Scheduler*: The no-setup default. Uses local threads or processes for larger-than-memory processing
  - *dask.distributed*: The sophistication of the newer system on a single machine. This provides more advanced features while still requiring almost no setup.
- **Distributed computing:**
  - *Manual Setup*: The command line interface to set up `dask-scheduler` and `dask-worker` processes. Useful for IT or anyone building a deployment solution.
  - *SSH*: Use SSH to set up Dask across an un-managed cluster.
  - *High Performance Computers*: How to run Dask on traditional HPC environments using tools like MPI, or job schedulers like SLURM, SGE, TORQUE, LSF, and so on.
  - *Kubernetes*: Deploy Dask with the popular Kubernetes resource manager using either Helm or a native deployment.
  - YARN / Hadoop: Deploy Dask on YARN clusters, such as are found in traditional Hadoop installations.
  - *Python API (advanced)*: Create `Scheduler` and `Worker` objects from Python as part of a distributed Tornado TCP application. This page is useful for those building custom frameworks.

- *Docker* containers are available and may be useful in some of the solutions above.
- *Cloud* for current recommendations on how to deploy Dask and Jupyter on common cloud providers like Amazon, Google, or Microsoft Azure.

4.2.1 Single-Machine Scheduler

The default Dask scheduler provides parallelism on a single machine by using either threads or processes. It is the default choice used by Dask because it requires no setup. You don't need to make any choices or set anything up to use this scheduler. However, you do have a choice between threads and processes:

1. **Threads**: Use multiple threads in the same process. This option is good for numeric code that releases the GIL (like NumPy, Pandas, Scikit-Learn, Numba, ...) because data is free to share. This is the default scheduler for `dask.array`, `dask.dataframe`, and `dask.delayed`
2. **Processes**: Send data to separate processes for processing. This option is good when operating on pure Python objects like strings or JSON-like dictionary data that holds onto the GIL, but not very good when operating on numeric data like Pandas DataFrames or NumPy arrays. Using processes avoids GIL issues, but can also result in a lot of inter-process communication, which can be slow. This is the default scheduler for `dask.bag`, and it is sometimes useful with `dask.dataframe`

   Note that the `dask.distributed` scheduler is often a better choice when working with GIL-bound code. See *dask.distributed on a single machine*
3. **Single-threaded**: Execute computations in a single thread. This option provides no parallelism, but is useful when debugging or profiling. Turning your parallel execution into a sequential one can be a convenient option in many situations where you want to better understand what is going on

Selecting Threads, Processes, or Single Threaded

Currently, these options are available by selecting different `get` functions:

- `dask.threaded.get`: The threaded scheduler
- `dask.multiprocessing.get`: The multiprocessing scheduler
- `dask.local.get_sync`: The single-threaded scheduler

You can specify these functions in any of the following ways:

- When calling `.compute()`

```
x.compute(scheduler='threads')
```

- With a context manager

```
with dask.config.set(scheduler='threads'):
    x.compute()
    y.compute()
```

- As a global setting

```
dask.config.set(scheduler='threads')
```

Use the Distributed Scheduler

Dask's newer distributed scheduler also works well on a single machine and offers more features and diagnostics. See *this page* for more information.

4.2.2 Single Machine: dask.distributed

The `dask.distributed` scheduler works well on a single machine. It is sometimes preferred over the default scheduler for the following reasons:

1. It provides access to asynchronous API, notably *Futures*
2. It provides a diagnostic dashboard that can provide valuable insight on performance and progress
3. It handles data locality with more sophistication, and so can be more efficient than the multiprocessing scheduler on workloads that require multiple processes

You can create a `dask.distributed` scheduler by importing and creating a `Client` with no arguments. This overrides whatever default was previously set.

```
from dask.distributed import Client
client = Client()
```

You can navigate to http://localhost:8787/status to see the diagnostic dashboard if you have Bokeh installed.

Client

You can trivially set up a local cluster on your machine by instantiating a Dask Client with no arguments

```
from dask.distributed import Client
client = Client()
```

This sets up a scheduler in your local process and several processes running single-threaded Workers.

If you want to run workers in your same process, you can pass the `processes=False` keyword argument.

```
client = Client(processes=False)
```

This is sometimes preferable if you want to avoid inter-worker communication and your computations release the GIL. This is common when primarily using NumPy or Dask Array.

LocalCluster

The `Client()` call described above is shorthand for creating a LocalCluster and then passing that to your client.

```
from dask.distributed import Client, LocalCluster
cluster = LocalCluster()
client = Client(cluster)
```

This is equivalent, but somewhat more explicit. You may want to look at the keyword arguments available on `LocalCluster` to understand the options available to you on handling the mixture of threads and processes, like specifying explicit ports, and so on.

class distributed.deploy.local.**LocalCluster**(*n_workers=None*, *threads_per_worker=None*, *processes=True*, *loop=None*, *start=None*, *ip=None*, *scheduler_port=0*, *silence_logs=30*, *diagnostics_port=8787*, *services=None*, *worker_services=None*, *service_kwargs=None*, *asynchronous=False*, *security=None*, ***worker_kwargs*)

Create local Scheduler and Workers

This creates a "cluster" of a scheduler and workers running on the local machine.

Parameters

n_workers: int Number of workers to start

processes: bool Whether to use processes (True) or threads (False). Defaults to True

threads_per_worker: int Number of threads per each worker

scheduler_port: int Port of the scheduler. 8786 by default, use 0 to choose a random port

silence_logs: logging level Level of logs to print out to stdout. `logging.WARN` by default. Use a falsey value like False or None for no change.

ip: string IP address on which the scheduler will listen, defaults to only localhost

diagnostics_port: int Port on which the web will be provided. 8787 by default, use 0 to choose a random port, `None` to disable it, or an `(ip:port)` tuple to listen on a different IP address than the scheduler.

asynchronous: bool (False by default) Set to True if using this cluster within async/await functions or within Tornado gen.coroutines. This should remain False for normal use.

kwargs: dict Extra worker arguments, will be passed to the Worker constructor.

service_kwargs: Dict[str, Dict] Extra keywords to hand to the running services

security [Security]

Examples

```
>>> c = LocalCluster()  # Create a local cluster with as many workers as cores
>>> c
LocalCluster("127.0.0.1:8786", workers=8, ncores=8)
```

```
>>> c = Client(c)  # connect to local cluster
```

Add a new worker to the cluster

```
>>> w = c.start_worker(ncores=2)
```

Shut down the extra worker

```
>>> c.stop_worker(w)
```

Pass extra keyword arguments to Bokeh

```
>>> LocalCluster(service_kwargs={'bokeh': {'prefix': '/foo'}})
```

close(*timeout=20*)
Close the cluster

scale_down(*workers*)
Remove `workers` from the cluster

Given a list of worker addresses this function should remove those workers from the cluster. This may require tracking which jobs are associated to which worker address.

This can be implemented either as a function or as a Tornado coroutine.

scale_up(*n*, ***kwargs*)
Bring the total count of workers up to `n`

This function/coroutine should bring the total number of workers up to the number `n`.

This can be implemented either as a function or as a Tornado coroutine.

start_worker(***kwargs*)
Add a new worker to the running cluster

Parameters

port: int (optional) Port on which to serve the worker, defaults to 0 or random

ncores: int (optional) Number of threads to use. Defaults to number of logical cores

Returns

The created Worker or Nanny object. Can be discarded.

Examples

```
>>> c = LocalCluster()
>>> c.start_worker(ncores=2)
```

stop_worker(*w*)
Stop a running worker

Examples

```
>>> c = LocalCluster()
>>> w = c.start_worker(ncores=2)
>>> c.stop_worker(w)
```

4.2.3 Command Line

This is the most fundamental way to deploy Dask on multiple machines. In production environments, this process is often automated by some other resource manager. Hence, it is rare that people need to follow these instructions explicitly. Instead, these instructions are useful for IT professionals who may want to set up automated services to deploy Dask within their institution.

A `dask.distributed` network consists of one `dask-scheduler` process and several `dask-worker` processes that connect to that scheduler. These are normal Python processes that can be executed from the command line. We launch the `dask-scheduler` executable in one process and the `dask-worker` executable in several processes, possibly on different machines.

To accomplish this, launch `dask-scheduler` on one node:

```
$ dask-scheduler
Scheduler at:   tcp://192.0.0.100:8786
```

Then, launch `dask-worker` on the rest of the nodes, providing the address to the node that hosts `dask-scheduler`:

```
$ dask-worker tcp://192.0.0.100:8786
Start worker at:  tcp://192.0.0.1:12345
Registered to:    tcp://192.0.0.100:8786

$ dask-worker tcp://192.0.0.100:8786
Start worker at:  tcp://192.0.0.2:40483
Registered to:    tcp://192.0.0.100:8786

$ dask-worker tcp://192.0.0.100:8786
Start worker at:  tcp://192.0.0.3:27372
Registered to:    tcp://192.0.0.100:8786
```

The workers connect to the scheduler, which then sets up a long-running network connection back to the worker. The workers will learn the location of other workers from the scheduler.

Handling Ports

The scheduler and workers both need to accept TCP connections on an open port. By default, the scheduler binds to port `8786` and the worker binds to a random open port. If you are behind a firewall then you may have to open particular ports or tell Dask to listen on particular ports with the `--port` and `--worker-port` keywords.:

```
dask-scheduler --port 8000
dask-worker --bokeh-port 8000 --nanny-port 8001
```

Nanny Processes

Dask workers are run within a nanny process that monitors the worker process and restarts it if necessary.

Diagnostic Web Servers

Additionally, Dask schedulers and workers host interactive diagnostic web servers using Bokeh. These are optional, but generally useful to users. The diagnostic server on the scheduler is particularly valuable, and is served on port `8787` by default (configurable with the `--bokeh-port` keyword).

Note: For more information about relevant ports, please take a look at the help pages with `dask-scheduler --help` and `dask-worker --help`

Automated Tools

There are various mechanisms to deploy these executables on a cluster, ranging from manually SSH-ing into all of the machines to more automated systems like SGE/SLURM/Torque or Yarn/Mesos. Additionally, cluster SSH tools exist to send the same commands to many machines. We recommend searching online for "cluster ssh" or "cssh".

API

Warning: These may be out-dated. We recommend referring to the `--help` text of your installed version.

dask-scheduler

```
$ dask-scheduler --help
Usage: dask-scheduler [OPTIONS]

Options:
  --host TEXT             URI, IP or hostname of this server
  --port INTEGER          Serving port
  --interface TEXT        Preferred network interface like 'eth0' or 'ib0'
  --tls-ca-file PATH      CA cert(s) file for TLS (in PEM format)
  --tls-cert PATH         certificate file for TLS (in PEM format)
  --tls-key PATH          private key file for TLS (in PEM format)
  --bokeh-port INTEGER    Bokeh port for visual diagnostics
  --bokeh / --no-bokeh    Launch Bokeh Web UI  [default: True]
  --show / --no-show      Show web UI
  --bokeh-whitelist TEXT  IP addresses to whitelist for bokeh
  --bokeh-prefix TEXT     Prefix for the bokeh app
  --use-xheaders BOOLEAN  User xheaders in bokeh app for ssl termination in
                          header  [default: False]
  --pid-file TEXT         File to write the process PID
  --scheduler-file TEXT   File to write connection information. This may be a
                          good way to share connection information if your
                          cluster is on a shared network file system
  --local-directory TEXT  Directory to place scheduler files
  --preload TEXT          Module that should be loaded by each worker process
                          like "foo.bar" or "/path/to/foo.py"
  --help                  Show this message and exit
```

dask-worker

```
$ dask-worker --help
Usage: dask-worker [OPTIONS] [SCHEDULER]

Options:
  --tls-ca-file PATH            CA cert(s) file for TLS (in PEM format)
  --tls-cert PATH               certificate file for TLS (in PEM format)
  --tls-key PATH                private key file for TLS (in PEM format)
  --worker-port INTEGER         Serving computation port, defaults to random
  --nanny-port INTEGER          Serving nanny port, defaults to random
  --bokeh-port INTEGER          Bokeh port, defaults to 8789
  --bokeh / --no-bokeh          Launch Bokeh Web UI  [default: True]
  --listen-address TEXT         The address to which the worker binds.
                                Example: tcp://0.0.0.0:9000
  --contact-address TEXT        The address the worker advertises to the
                                scheduler for communication with it and other
                                workers. Example: tcp://127.0.0.1:9000
  --host TEXT                   Serving host. Should be an ip address that is
                                visible to the scheduler and other workers.
                                See --listen-address and --contact-address if
                                you need different listen and contact
                                addresses. See --interface
  --interface TEXT              Network interface like 'eth0' or 'ib0'
  --nthreads INTEGER            Number of threads per process
  --nprocs INTEGER              Number of worker processes.  Defaults to one
  --name TEXT                   A unique name for this worker like 'worker-1'
```

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```
  --memory-limit TEXT             Bytes of memory that the worker can use. This
                                  can be an integer (bytes), float (fraction of
                                  total system memory), string (like 5GB or
                                  5000M), 'auto', or zero for no memory
                                  management
  --reconnect / --no-reconnect    Reconnect to scheduler if disconnected
  --nanny / --no-nanny            Start workers in nanny process for management
  --pid-file TEXT                 File to write the process PID
  --local-directory TEXT          Directory to place worker files
  --resources TEXT                Resources for task constraints like "GPU=2
                                  MEM=10e9"
  --scheduler-file TEXT           Filename to JSON encoded scheduler information.
                                  Use with dask-scheduler --scheduler-file
  --death-timeout FLOAT           Seconds to wait for a scheduler before closing
  --bokeh-prefix TEXT             Prefix for the bokeh app
  --preload TEXT                  Module that should be loaded by each worker
                                  process like "foo.bar" or "/path/to/foo.py"
  --help                          Show this message and exit
```

4.2.4 SSH

The convenience script `dask-ssh` opens several SSH connections to your target computers and initializes the network accordingly. You can give it a list of hostnames or IP addresses:

```
$ dask-ssh 192.168.0.1 192.168.0.2 192.168.0.3 192.168.0.4
```

Or you can use normal UNIX grouping:

```
$ dask-ssh 192.168.0.{1,2,3,4}
```

Or you can specify a hostfile that includes a list of hosts:

```
$ cat hostfile.txt
192.168.0.1
192.168.0.2
192.168.0.3
192.168.0.4

$ dask-ssh --hostfile hostfile.txt
```

The `dask-ssh` utility depends on the `paramiko`:

```
pip install paramiko
```

CLI Options

Launch a distributed cluster over SSH. A `dask-scheduler` process will run on the first host specified in [HOSTNAMES] or in the hostfile (unless `--scheduler` is specified explicitly). One or more `dask-worker` processes will be run on each host in [HOSTNAMES] or in the hostfile. Use command line flags to adjust how many dask-worker process are run on each host (`--nprocs`) and how many cpus are used by each dask-worker process (`--nthreads`).

Options:

Note: This table may grow out of date, you should check `dask-ssh --help` to get an up-to-date listing of all options.

Option	TYPE	Description
–scheduler	TEXT	Specify scheduler node. Defaults to first address
–scheduler-port	INTEGER	Specify scheduler port number. Defaults to port 8786
–nthreads	INTEGER	Number of threads per worker process. Defaults to number of cores divided by the number of processes per host
–nprocs	INTEGER	Number of worker processes per host. Defaults to one
–hostfile	PATH	Textfile with hostnames/IP addresses
–ssh-username	TEXT	Username to use when establishing SSH connections
–ssh-port	INTEGER	Port to use for SSH connections
–ssh-private-key	TEXT	Private key file to use for SSH connections
–log-directory	PATH	Directory to use on all cluster nodes for the output of dask-scheduler and dask-worker commands
–remote-python	TEXT	Path to Python on remote nodes
–memory-limit	TEXT	Bytes of memory that the worker can use. This can be an integer (bytes), float(fraction of total system memory) string (like 5GB or 5000M), 'auto', or zero for no memory management
–worker-port	INTEGER	Serving computation port, defaults to random
–nanny-port	INTEGER	Serving nanny port, defaults to random
–nohost		Do not pass the hostname to the worker

4.2.5 High Performance Computers

Relevant Machines

This page includes instructions and guidelines when deploying Dask on high performance supercomputers commonly found in scientific and industry research labs. These systems commonly have the following attributes:

1. Some mechanism to launch MPI applications or use job schedulers like SLURM, SGE, TORQUE, LSF, DRMAA, PBS, or others
2. A shared network file system visible to all machines in the cluster

3. A high performance network interconnect, such as Infiniband
4. Little or no node-local storage

Where to start

Most of this page documents best practices to use Dask on an HPC cluster. This is technical and aimed both at users with some experience deploying Dask and also system administrators.

New users may instead prefer to start with one of the following projects which provide easy high-level access to Dask using resource managers that are commonly deployed on HPC systems:

1. dask-jobqueue for use with PBS, SLURM, and SGE resource managers
2. dask-drmaa for use with any DRMAA compliant resource manager

They provide interfaces that look like the following:

```
from dask_jobqueue import PBSCluster

cluster = PBSCluster(cores=36,
                     memory"100GB",
                     project='P48500028',
                     queue='premium',
                     walltime='02:00:00')

cluster.start_workers(100)  # Start 100 jobs that match the description above

from dask.distributed import Client
client = Client(cluster)    # Connect to that cluster
```

We recommend reading the dask-jobqueue documentation first to get a basic system running and then returning to this documentation for fine-tuning.

Using a Shared Network File System and a Job Scheduler

Note: This section is not necessary if you use a tool like dask-jobqueue.

Some clusters benefit from a shared Network File System (NFS), and can use this to communicate the scheduler location to the workers:

```
dask-scheduler --scheduler-file /path/to/scheduler.json  # writes address to file

dask-worker --scheduler-file /path/to/scheduler.json  # reads file for address
dask-worker --scheduler-file /path/to/scheduler.json  # reads file for address
```

```
>>> client = Client(scheduler_file='/path/to/scheduler.json')
```

This can be particularly useful when deploying `dask-scheduler` and `dask-worker` processes using a job scheduler like SGE/SLURM/Torque/etc. Here is an example using SGE's `qsub` command:

```
# Start a dask-scheduler somewhere and write the connection information to a file
qsub -b y /path/to/dask-scheduler --scheduler-file /home/$USER/scheduler.json
```

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```
# Start 100 dask-worker processes in an array job pointing to the same file
qsub -b y -t 1-100 /path/to/dask-worker --scheduler-file /home/$USER/scheduler.json
```

Note, the `--scheduler-file` option is *only* valuable if your scheduler and workers share a network file system.

Using MPI

Note: This section is not necessary if you use a tool like dask-jobqueue.

You can launch a Dask network using `mpirun` or `mpiexec` and the `dask-mpi` command line executable.

```
mpirun --np 4 dask-mpi --scheduler-file /home/$USER/scheduler.json
```

```
from dask.distributed import Client
client = Client(scheduler_file='/path/to/scheduler.json')
```

This depends on the mpi4py library. It only uses MPI to start the Dask cluster and not for inter-node communication. MPI implementations differ: the use of `mpirun --np 4` is specific to the `mpich` MPI implementation installed through conda and linked to mpi4py

```
conda install mpi4py
```

It is not necessary to use exactly this implementation, but you may want to verify that your `mpi4py` Python library is linked against the proper `mpirun/mpiexec` executable and that the flags used (like `--np 4`) are correct for your system. The system administrator of your cluster should be very familiar with these concerns and able to help.

Run `dask-mpi --help` to see more options for the `dask-mpi` command.

High Performance Network

Many HPC systems have both standard Ethernet networks as well as high-performance networks capable of increased bandwidth. You can instruct Dask to use the high-performance network interface by using the `--interface` keyword with the `dask-worker`, `dask-scheduler`, or `dask-mpi` commands or the `interface=` keyword with the dask-jobqueue `Cluster` objects:

```
mpirun --np 4 dask-mpi --scheduler-file /home/$USER/scheduler.json --interface ib0
```

In the code example above, we have assumed that your cluster has an Infiniband network interface called `ib0`. You can check this by asking your system administrator or by inspecting the output of `ifconfig`

```
$ ifconfig
lo          Link encap:Local Loopback                       # Localhost
                    inet addr:127.0.0.1  Mask:255.0.0.0
                    inet6 addr: ::1/128 Scope:Host
eth0        Link encap:Ethernet  HWaddr XX:XX:XX:XX:XX:XX    # Ethernet
                    inet addr:192.168.0.101
                    ...
ib0         Link encap:Infiniband                           # Fast InfiniBand
                    inet addr:172.42.0.101
```

https://stackoverflow.com/questions/43881157/how-do-i-use-an-infiniband-network-with-dask

No Local Storage

Users often exceed memory limits available to a specific Dask deployment. In normal operation, Dask spills excess data to disk. However, in HPC systems, the individual compute nodes often lack locally attached storage, preferring instead to store data in a robust high performance network storage solution. As a result, when a Dask cluster starts to exceed memory limits, its workers can start making many small writes to the remote network file system. This is both inefficient (small writes to a network file system are *much* slower than local storage for this use case) and potentially dangerous to the file system itself.

See this page for more information on Dask's memory policies. Consider changing the following values in your `~/.config/dask/distributed.yaml` file:

```
distributed:
  worker:
    memory:
      target: false  # don't spill to disk
      spill: false  # don't spill to disk
      pause: 0.80  # pause execution at 80% memory use
      terminate: 0.95  # restart the worker at 95% use
```

This stops Dask workers from spilling to disk, and instead relies entirely on mechanisms to stop them from processing when they reach memory limits.

As a reminder, you can set the memory limit for a worker using the `--memory-limit` keyword:

```
dask-mpi ... --memory-limit 10GB
```

Alternatively, if you *do* have local storage mounted on your compute nodes, you can point Dask workers to use a particular location in your filesystem using the `--local-directory` keyword:

```
dask-mpi ... --local-directory /scratch
```

Launch Many Small Jobs

HPC job schedulers are optimized for large monolithic jobs with many nodes that all need to run as a group at the same time. Dask jobs can be quite a bit more flexible: workers can come and go without strongly affecting the job. If we split our job into many smaller jobs, we can often get through the job scheduling queue much more quickly than a typical job. This is particularly valuable when we want to get started right away and interact with a Jupyter notebook session rather than waiting for hours for a suitable allocation block to become free.

So, to get a large cluster quickly, we recommend allocating a dask-scheduler process on one node with a modest wall time (the intended time of your session) and then allocating many small single-node dask-worker jobs with shorter wall times (perhaps 30 minutes) that can easily squeeze into extra space in the job scheduler. As you need more computation, you can add more of these single-node jobs or let them expire.

Use Dask to co-launch a Jupyter server

Dask can help you by launching other services alongside it. For example, you can run a Jupyter notebook server on the machine running the `dask-scheduler` process with the following commands

```
from dask.distributed import Client
client = Client(scheduler_file='scheduler.json')

import socket
host = client.run_on_scheduler(socket.gethostname)
```

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```
def start_jlab(dask_scheduler):
    import subprocess
    proc = subprocess.Popen(['/path/to/jupyter', 'lab', '--ip', host, '--no-browser'])
    dask_scheduler.jlab_proc = proc

client.run_on_scheduler(start_jlab)
```

4.2.6 Kubernetes

Kubernetes and Helm

It is easy to launch a Dask cluster and Jupyter notebook server on cloud resources using Kubernetes and Helm.

This is particularly useful when you want to deploy a fresh Python environment on Cloud services, like Amazon Web Services, Google Compute Engine, or Microsoft Azure.

If you already have Python environments running in a pre-existing Kubernetes cluster then you may prefer the *Kubernetes native* documentation, which is a bit lighter weight.

Launch Kubernetes Cluster

This document assumes that you have a Kubernetes cluster and Helm installed.

If this is not the case then you might consider setting up a Kubernetes cluster either on one of the common cloud providers like Google, Amazon, or Microsoft's. We recommend the first part of the documentation in the guide Zero to JupyterHub that focuses on Kubernetes and Helm. You do not need to follow all of these instructions. JupyterHub is not necessary to deploy Dask:

- Creating a Kubernetes Cluster
- Setting up Helm

Alternatively you may want to experiment with Kubernetes locally using Minikube.

Helm Install Dask

Dask maintains a Helm chart in the default stable channel at https://kubernetes-charts.storage.googleapis.com . This should be added to your helm installation by default. You can update the known channels to make sure you have up-to-date charts as follows:

```
helm repo update
```

Now you can launch Dask on your Kubernetes cluster using the Dask Helm chart:

```
helm install stable/dask
```

This deploys a `dask-scheduler`, several `dask-worker` processes, and also an optional Jupyter server.

Verify Deployment

This might make a minute to deploy. You can check on the status with `kubectl`:

```
kubectl get pods
kubectl get services

$ kubectl get pods
NAME                                    READY     STATUS              RESTARTS    AGE
bald-eel-jupyter-924045334-twtxd        0/1       ContainerCreating   0           1m
bald-eel-scheduler-3074430035-cn1dt     1/1       Running             0           1m
bald-eel-worker-3032746726-202jt        1/1       Running             0           1m
bald-eel-worker-3032746726-b8nqq        1/1       Running             0           1m
bald-eel-worker-3032746726-d0chx        0/1       ContainerCreating   0           1m

$ kubectl get services
NAME                 TYPE           CLUSTER-IP      EXTERNAL-IP      PORT(S)
 ↪            AGE
bald-eel-jupyter     LoadBalancer   10.11.247.201   35.226.183.149   80:30173/TCP
 ↪             2m
bald-eel-scheduler   LoadBalancer   10.11.245.241   35.202.201.129   8786:31166/TCP,
 ↪80:31626/TCP   2m
kubernetes           ClusterIP      10.11.240.1     <none>           443/TCP
48m
```

You can use the addresses under `EXTERNAL-IP` to connect to your now-running Jupyter and Dask systems.

Notice the name `bald-eel`. This is the name that Helm has given to your particular deployment of Dask. You could, for example, have multiple Dask-and-Jupyter clusters running at once and each would be given a different name. You will use this name to refer to your deployment in the future. You can list all active helm deployments with:

```
helm list

NAME            REVISION        UPDATED                         STATUS      CHART
 ↪      NAMESPACE
bald-eel        1               Wed Dec  6 11:19:54 2017        DEPLOYED    dask-0.1.
 ↪0      default
```

Connect to Dask and Jupyter

When we ran `kubectl get services` we saw some externally visible IPs

```
mrocklin@pangeo-181919:~$ kubectl get services
NAME                 TYPE           CLUSTER-IP      EXTERNAL-IP      PORT(S)
 ↪            AGE
bald-eel-jupyter     LoadBalancer   10.11.247.201   35.226.183.149   80:30173/TCP
 ↪             2m
bald-eel-scheduler   LoadBalancer   10.11.245.241   35.202.201.129   8786:31166/TCP,
 ↪80:31626/TCP   2m
kubernetes           ClusterIP      10.11.240.1     <none>           443/TCP
 ↪             48m
```

We can navigate to these from any web browser. One is the Dask diagnostic dashboard. The other is the Jupyter server. You can log into the Jupyter notebook server with the password, `dask`.

You can create a notebook and create a Dask client from there. The `DASK_SCHEDULER_ADDRESS` environment variable has been populated with the address of the Dask scheduler. This is available in Python in the `config` dictionary.

```
>>> from dask.distributed import Client, config
>>> config['scheduler-address']
'bald-eel-scheduler:8786'
```

Although you don't need to use this address, the Dask client will find this variable automatically.

```
from dask.distributed import Client, config
client = Client()
```

Configure Environment

By default the Helm deployment launches three workers using two cores each and a standard conda environment. We can customize this environment by creating a small yaml file that implements a subset of the values in the dask helm chart values.yaml file

For example we can increase the number of workers, and include extra conda and pip packages to install on the both the workers and Jupyter server (these two environments should be matched).

```
# config.yaml

worker:
  replicas: 8
  resources:
    limits:
      cpu: 2
      memory: 7.5G
    requests:
      cpu: 2
      memory: 7.5G
  env:
    - name: EXTRA_CONDA_PACKAGES
      value: numba xarray -c conda-forge
    - name: EXTRA_PIP_PACKAGES
      value: s3fs dask-ml --upgrade

# We want to keep the same packages on the worker and jupyter environments
jupyter:
  enabled: true
  env:
    - name: EXTRA_CONDA_PACKAGES
      value: numba xarray matplotlib -c conda-forge
    - name: EXTRA_PIP_PACKAGES
      value: s3fs dask-ml --upgrade
```

This config file overrides configuration for number and size of workers and the conda and pip packages installed on the worker and Jupyter containers. In general we will want to make sure that these two software environments match.

Update your deployment to use this configuration file. Note that *you will not use helm install* for this stage. That would create a *new* deployment on the same Kubernetes cluster. Instead you will upgrade your existing deployment by using the current name:

```
helm upgrade bald-eel stable/dask -f config.yaml
```

This will update those containers that need to be updated. It may take a minute or so.

As a reminder, you can list the names of deployments you have using `helm list`

Check status and logs

For standard issues you should be able to see worker status and logs using the Dask dashboard (in particular see the worker links from the `info/` page). However if your workers aren't starting you can check on the status of pods and their logs with the following commands

```
kubectl get pods
kubectl logs <PODNAME>
```

```
mrocklin@pangeo-181919:~$ kubectl get pods
NAME                                  READY     STATUS    RESTARTS   AGE
bald-eel-jupyter-3805078281-n1qk2     1/1       Running   0          18m
bald-eel-scheduler-3074430035-cn1dt   1/1       Running   0          58m
bald-eel-worker-1931881914-1q09p      1/1       Running   0          18m
bald-eel-worker-1931881914-856mm      1/1       Running   0          18m
bald-eel-worker-1931881914-9lgzb      1/1       Running   0          18m
bald-eel-worker-1931881914-bdn2c      1/1       Running   0          16m
bald-eel-worker-1931881914-jq70m      1/1       Running   0          17m
bald-eel-worker-1931881914-qsgj7      1/1       Running   0          18m
bald-eel-worker-1931881914-s2phd      1/1       Running   0          17m
bald-eel-worker-1931881914-srmmg      1/1       Running   0          17m

mrocklin@pangeo-181919:~$ kubectl logs bald-eel-worker-1931881914-856mm
EXTRA_CONDA_PACKAGES environment variable found.  Installing.
Fetching package metadata ...........
Solving package specifications: .
Package plan for installation in environment /opt/conda/envs/dask:
The following NEW packages will be INSTALLED:
    fasteners: 0.14.1-py36_2 conda-forge
    monotonic: 1.3-py36_0    conda-forge
    zarr:      2.1.4-py36_0  conda-forge
Proceed ([y]/n)?
monotonic-1.3- 100% |################################| Time: 0:00:00  11.16 MB/s
fasteners-0.14 100% |################################| Time: 0:00:00 576.56 kB/s
...
```

Delete Helm deployment

You can always delete a helm deployment using its name:

```
helm delete bald-eel --purge
```

Note that this does not destroy any clusters that you may have allocated on a Cloud service, you will need to delete those explicitly.

Avoid the Jupyter Server

Sometimes you do not need to run a Jupyter server alongside your Dask cluster.

```
jupyter:
  enabled: false
```

Kubernetes Native

See external documentation on Dask-Kubernetes for more information.

Kubernetes is a popular system for deploying distributed applications on clusters, particularly in the cloud. You can use Kubernetes to launch Dask workers in the following two ways:

1. **Helm**: You can launch a Dask scheduler, several workers, and an optional Jupyter Notebook server on a Kubernetes easily using Helm

```
helm repo update          # get latest helm charts
helm install stable/dask  # deploy standard dask chart
```

   This is a good choice if you want to do the following:

   (a) Run a managed Dask cluster for a long period of time

   (b) Also deploy a Jupyter server from which to run code

   (c) Share the same Dask cluster between many automated services

   (d) Try out Dask for the first time on a cloud-based system like Amazon, Google, or Microsoft Azure (see also our *Cloud documentation*)

   Note: For more information, see *Dask and Helm documentation*.

2. **Native**: You can quickly deploy Dask workers on Kubernetes from within a Python script or interactive session using Dask-Kubernetes

```
from dask_kubernetes import KubeCluster
cluster = KubeCluster.from_yaml('worker-template.yaml')
cluster.scale(20)  # add 20 workers
cluster.adapt()    # or create and destroy workers dynamically based on workload

from dask.distributed import Client
client = Client(cluster)
```

   This is a good choice if you want to do the following:

   (a) Dynamically create a personal and ephemeral deployment for interactive use

   (b) Allow many individuals the ability to launch their own custom dask deployments, rather than depend on a centralized system

   (c) Quickly adapt Dask cluster size to the current workload

   Note: For more information, see Dask-Kubernetes documentation.

You may also want to see the documentation on using *Dask with Docker containers* to help you manage your software environments on Kubernetes.

4.2.7 Python API (advanced)

In some rare cases experts may want to create `Scheduler` and `Worker` objects explicitly in Python manually. This is often necessary when making tools to automatically deploy Dask in custom settings.

However, often it is sufficient to rely on the *Dask command line interface*.

Scheduler

Start the Scheduler, provide the listening port (defaults to 8786) and Tornado IOLoop (defaults to `IOLoop.current()`)

```
from distributed import Scheduler
from tornado.ioloop import IOLoop
from threading import Thread

s = Scheduler()
s.start('tcp://:8786')   # Listen on TCP port 8786

loop = IOLoop.current()
loop.start()
```

Alternatively, you may want the IOLoop and scheduler to run in a separate thread. In that case you would replace the `loop.start()` call with the following:

```
t = Thread(target=loop.start, daemon=True)
t.start()
```

Worker

On other nodes start worker processes that point to the URL of the scheduler.

```
from distributed import Worker
from tornado.ioloop import IOLoop
from threading import Thread

w = Worker('tcp://127.0.0.1:8786')
w.start()  # choose randomly assigned port

loop = IOLoop.current()
loop.start()
```

Alternatively, replace `Worker` with `Nanny` if you want your workers to be managed in a separate process by a local nanny process. This allows workers to restart themselves in case of failure, provides some additional monitoring, and is useful when coordinating many workers that should live in different processes to avoid the GIL.

4.2.8 Cloud Deployments

To get started running Dask on common Cloud providers like Amazon, Google, or Microsoft we currently recommend deploying *Dask with Kubernetes and Helm*.

All three major cloud vendors now provide managed Kubernetes services. This allows us to reliably provide the same experience across all clouds, and ensures that solutions for any one provider remain up-to-date.

Data Access

You may want to install additional libraries in your Jupyter and worker images to access the object stores of each cloud

- s3fs for Amazon's S3
- gcsfs for Google's GCS
- adlfs for Microsoft's ADL

Historical Libraries

Dask previously maintained libraries for deploying Dask on Amazon's EC2. Due to sporadic interest, and churn both within the Dask library and EC2 itself, these were not well maintained. They have since been deprecated in favor of the *Kubernetes and Helm* solution.

4.2.9 Adaptive Deployments

Motivation

Most Dask deployments are static, with a single scheduler and a fixed number of workers. This results in predictable behavior, but is wasteful of resources in two situations:

1. The user may not be using the cluster, perhaps they are busy interpreting a recent result or plot, and so the workers sit idly, taking up valuable shared resources from other potential users
2. The user may be very active, and is limited by their original allocation.

Particularly efficient users may learn to manually add and remove workers during their session, but this is rare. Instead, we would like the size of a Dask cluster to match the computational needs at any given time. This is the goal of the *adaptive deployments* discussed in this document. These are particularly helpful for interactive workloads, which are characterized by long periods of inactivity interrupted with short bursts of heavy activity. Adaptive deployments can result in both faster analyses that give users much more power but with much less pressure on computational resources.

Adaptive

To make setting up adaptive deployments easy, some Dask deployment solutions offer an `.adapt()` method. Here is an example with dask_kubernetes.KubeCluster.

```
from dask_kubernetes import KubeCluster

cluster = KubeCluster()
cluster.adapt(minimum=0, maximum=100)  # scale between 0 and 100 workers
```

For more keyword options, see the Adaptive class below:

Adaptive(scheduler[, cluster, interval, ...])	Adaptively allocate workers based on scheduler load.

Dependence on a Resource Manager

The Dask scheduler does not know how to launch workers on its own, instead it relies on an external resource scheduler like Kubernetes above, or Yarn, SGE, SLURM, Mesos, or some other in-house system (see *setup documentation* for options). In order to use adaptive deployments you must provide some mechanism for the scheduler to launch new workers. Typically this is done by using one of the solutions listed in the *setup documentation*, or by subclassing from the Cluster superclass, and implementing that API

Cluster	Superclass for cluster objects

Scaling Heuristics

The Dask scheduler tracks a variety of information that is useful to correctly allocate the number of workers:

1. The historical runtime of every function and task that it has seen, and all of the functions that it is currently able to run for users
2. The amount of memory used and available on each worker
3. Which workers are idle or saturated for various reasons, like the presence of specialized hardware

From these it is able to determine a target number of workers by dividing the cumulative expected runtime of all pending tasks by the `target_duration` parameter (defaults to five seconds). This number of workers serves as a baseline request for the resource manager. This number can be altered for a variety of reasons:

1. If the cluster needs more memory then it will choose either the target number of workers, or twice the current number of workers, whichever is larger.
2. If the target is outside of the range of the minimum and maximum values then it is clipped to fit within that range.

Additionally, when scaling down Dask preferentially chooses those workers that are idle and have the least data in memory. It moves that data to other machines before retiring the worker. To avoid rapid cycling of the cluster up and down in size, we only retire a worker after a few cycles have gone by where it has consistently been a good idea to retire it (controlled by the `wait_count` and `interval` parameters.)

API

class distributed.deploy.**Adaptive**(*scheduler*, *cluster=None*, *interval='1s'*, *startup_cost='1s'*, *scale_factor=2*, *minimum=0*, *maximum=None*, *wait_count=3*, *target_duration='5s'*, *worker_key=<function Adaptive.<lambda>>*, ***kwargs*)

Adaptively allocate workers based on scheduler load. A superclass.

Contains logic to dynamically resize a Dask cluster based on current use. This class needs to be paired with a system that can create and destroy Dask workers using a cluster resource manager. Typically it is built into already existing solutions, rather than used directly by users. It is most commonly used from the `.adapt(...)` method of various Dask cluster classes.

Parameters

scheduler: distributed.Scheduler

cluster: object Must have scale_up and scale_down methods/coroutines

startup_cost [timedelta or str, default "1s"] Estimate of the number of seconds for nnFactor representing how costly it is to start an additional worker. Affects quickly to adapt to high tasks per worker loads

interval [timedelta or str, default "1000 ms"] Milliseconds between checks

wait_count: int, default 3 Number of consecutive times that a worker should be suggested for removal before we remove it.

scale_factor [int, default 2] Factor to scale by when it's determined additional workers are needed

target_duration: timedelta or str, default "5s" Amount of time we want a computation to take. This affects how aggressively we scale up.

worker_key: Callable[WorkerState] Function to group workers together when scaling down See Scheduler.workers_to_close for more information

minimum: int Minimum number of workers to keep around

maximum: int Maximum number of workers to keep around

****kwargs:** Extra parameters to pass to Scheduler.workers_to_close

Notes

Subclasses can override `Adaptive.should_scale_up()` and `Adaptive.workers_to_close()` to control when the cluster should be resized. The default implementation checks if there are too many tasks per worker or too little memory available (see `Adaptive.needs_cpu()` and `Adaptive.needs_memory()`).

`Adaptive.get_scale_up_kwargs()` method controls the arguments passed to the cluster's `scale_up` method.

Examples

This is commonly used from existing Dask classes, like KubeCluster

```
>>> from dask_kubernetes import KubeCluster
>>> cluster = KubeCluster()
>>> cluster.adapt(minimum=10, maximum=100)
```

Alternatively you can use it from your own Cluster class by subclassing from Dask's Cluster superclass

```
>>> from distributed.deploy import Cluster
>>> class MyCluster(Cluster):
...     def scale_up(self, n):
...         """ Bring worker count up to n """
...     def scale_down(self, workers):
...         """ Remove worker addresses from cluster """
```

```
>>> cluster = MyCluster()
>>> cluster.adapt(minimum=10, maximum=100)
```

class distributed.deploy.**Cluster**

Superclass for cluster objects

This expects a local Scheduler defined on the object. It provides common methods and an IPython widget display.

Clusters inheriting from this class should provide the following:

1. A local `Scheduler` object at `.scheduler`
2. scale_up and scale_down methods as defined below:

   def scale_up(self, n: int): ‘‘‘ Brings total worker count up to `n` ’’‘

   def scale_down(self, workers: List[str]): ‘‘‘ Close the workers with the given addresses ’’‘

This will provide a general `scale` method as well as an IPython widget for display.

See also:

LocalCluster a simple implementation with local workers

Examples

```
>>> from distributed.deploy import Cluster
>>> class MyCluster(cluster):
...     def scale_up(self, n):
...         ''' Bring the total worker count up to n '''
...         pass
...     def scale_down(self, workers):
...         ''' Close the workers with the given addresses '''
...         pass
```

```
>>> cluster = MyCluster()
>>> cluster.scale(5)                       # scale manually
>>> cluster.adapt(minimum=1, maximum=100)  # scale automatically
```

4.2.10 Docker Images

Example docker images are maintained at https://github.com/dask/dask-docker and https://hub.docker.com/r/daskdev/ .

Each image installs the full Dask conda package (including the distributed scheduler), Numpy, and Pandas on top of a Miniconda installation on top of a Debian image.

These images are large, around 1GB.

- **`daskdev/dask`: This a normal debian + miniconda image with the full Dask** conda package (including the distributed scheduler), Numpy, and Pandas. This image is about 1GB in size.
- `daskdev/dask-notebook`: This is based on the Jupyter base-notebook image and so is appropriate for use both normally as a Jupyter server, and also as part of a JupyterHub deployment. It also includes a matching Dask software environment described above. This image is about 2GB in size.

Example

Here is a simple example on the local host network

```
docker run -it --network host daskdev/dask dask-scheduler  # start scheduler

docker run -it --network host daskdev/dask dask-worker localhost:8786 # start worker
docker run -it --network host daskdev/dask dask-worker localhost:8786 # start worker
docker run -it --network host daskdev/dask dask-worker localhost:8786 # start worker

docker run -it --network host daskdev/dask-notebook  # start Jupyter server
```

Extensibility

Users can mildly customize the software environment by populating the environment variables `EXTRA_APT_PACKAGES`, `EXTRA_CONDA_PACKAGES`, and `EXTRA_PIP_PACKAGES`. If these environmet variables are set they will trigger calls to the following respectively:

```
apt-get install $EXTRA_APT_PACKAGES
conda install $EXTRA_CONDA_PACKAGES
pip install $EXTRA_PIP_PACKAGES
```

Note that using these can significantly delay the container from starting, especially when using `apt`, or `conda` (`pip` is relatively fast).

Remember that it is important for software versions to match between Dask workers and Dask clients. As a result it is often useful to include the same extra packages in both Jupyter and Worker images.

Source

Docker files are maintained at https://github.com/dask/dask-docker . This repository also includes a docker-compose configuration.

4.3 Use Cases

Dask is a versatile tool that supports a variety of workloads. This page contains brief and illustrative examples for how people use Dask in practice. This page emphasizes breadth and hopefully inspires readers to find new ways that Dask can serve them beyond their original intent.

4.3.1 Overview

Dask use cases can be roughly divided in the following two categories:

1. Large NumPy/Pandas/Lists with *dask.array*, *dask.dataframe*, *dask.bag* to analyze large datasets with familiar techniques. This is similar to Databases, Spark, or big array libraries.
2. Custom task scheduling. You submit a graph of functions that depend on each other for custom workloads. This is similar to Luigi, Airflow, Celery, or Makefiles.

Most people today approach Dask assuming it is a framework like Spark, designed for the first use case around large collections of uniformly shaped data. However, many of the more productive and novel use cases fall into the second category, using Dask to parallelize custom workflows.

Dask compute environments can be divided into the following two categories:

1. Single machine parallelism with threads or processes: The Dask single-machine scheduler leverages the full CPU power of a laptop or a large workstation and changes the space limitation from "fits in memory" to "fits on disk". This scheduler is simple to use and doesn't have the computational or conceptual overhead of most "big data" systems.
2. Distributed cluster parallelism on multiple nodes: The Dask distributed scheduler coordinates the actions of multiple machines on a cluster. It scales anywhere from a single machine to a thousand machines, but not significantly beyond.

The single machine scheduler is useful to more individuals (more people have personal laptops than have access to clusters) and probably accounts for 80+% of the use of Dask today. The distributed machine scheduler is useful to larger organizations like universities, research labs, or private companies.

Below we give specific examples of how people use Dask. We start with large NumPy/Pandas/List examples because they're somewhat more familiar to people looking at "big data" frameworks. We then follow with custom scheduling examples, which tend to be applicable more often, and are arguably a bit more interesting.

4.3.2 Collection Examples

Dask contains large parallel collections for n-dimensional arrays (similar to NumPy), dataframes (similar to Pandas), and lists (similar to PyToolz or PySpark).

On disk arrays

Scientists studying the earth have 10GB to 100GB of regularly gridded weather data on their laptop's hard drive stored as many individual HDF5 or NetCDF files. They use *dask.array* to treat this stack of HDF5 or NetCDF files as a single NumPy array (or a collection of NumPy arrays with the XArray project). They slice, perform reductions, perform seasonal averaging etc. all with straight Numpy syntax. These computations take a few minutes (reading 100GB from disk is somewhat slow) but previously infeasible computations become convenient from the comfort of a personal laptop.

It's not so much parallel computing that is valuable here but rather the ability to comfortably compute on larger-than-memory data without special hardware.

```
import h5py
dataset = h5py.File('myfile.hdf5')['/x']

import dask.array as da
x = da.from_array(dataset, chunks=dataset.chunks)

y = x[::10] - x.mean(axis=0)
y.compute()
```

Directory of CSV or tabular HDF files

Analysts studying time series data have a large directory of CSV, HDF, or otherwise formatted tabular files. They usually use Pandas for this kind of data but either the volume is too large or dealing with a large number of files is confusing. They use *dask.dataframe* to logically wrap all of these different files into one logical dataframe that is built on demand to save space. Most of their Pandas workflow is the same (Dask.dataframe is a subset of Pandas) so they switch from Pandas to Dask.dataframe and back easily without significantly changing their code.

```
import dask.dataframe as dd

df = dd.read_csv('data/2016-*.*.csv', parse_dates=['timestamp'])
df.groupby(df.timestamp.dt.hour).value.mean().compute()
```

Directory of CSV files on HDFS

The same analyst as above uses dask.dataframe with the dask.distributed scheduler to analyze terabytes of data on their institution's Hadoop cluster straight from Python. This uses either the hdfs3 or pyarrow Python libraries for HDFS management

This solution is particularly attractive because it stays within the Python ecosystem, and uses the speed and algorithm set of Pandas, a tool with which the analyst is already very comfortable.

```
from dask.distributed import Client
client = Client('cluster-address:8786')

import dask.dataframe as dd
df = dd.read_csv('hdfs://data/2016-*.*.csv', parse_dates=['timestamp'])
df.groupby(df.timestamp.dt.hour).value.mean().compute()
```

Directories of custom format files

The same analyst has a bunch of files of a custom format not supported by Dask.dataframe, or perhaps these files are in a directory structure that encodes important information about his data (such as the date or other metadata.) They use

dask.delayed to teach Dask.dataframe how to load the data and then pass into dask.dataframe for tabular algorithms.

- Example Notebook: https://gist.github.com/mrocklin/e7b7b3a65f2835cda813096332ec73ca

JSON data

Data Engineers with click stream data from a website or mechanical engineers with telemetry data from mechanical instruments have large volumes of data in JSON or some other semi-structured format. They use *dask.bag* to manipulate many Python objects in parallel either on their personal machine, where they stream the data through memory or across a cluster.

```
import dask.bag as db
import json

records = db.read_text('data/2015-*-*.json').map(json.loads)
records.filter(lambda d: d['name'] == 'Alice').pluck('id').frequencies()
```

4.3.3 Custom Examples

The large collections (array, dataframe, bag) are wonderful when they fit the application, for example if you want to perform a groupby on a directory of CSV data. However several parallel computing applications don't fit neatly into one of these higher level abstractions. Fortunately, Dask provides a wide variety of ways to parallelize more custom applications. These use the same machinery as the arrays and dataframes, but allow the user to develop custom algorithms specific to their problem.

Embarrassingly parallel computation

A programmer has a function that they want to run many times on different inputs. Their function and inputs might use arrays or dataframes internally, but conceptually their problem isn't a single large array or dataframe.

They want to run these functions in parallel on their laptop while they prototype but they also intend to eventually use an in-house cluster. They wrap their function in *dask.delayed* and let the appropriate dask scheduler parallelize and load balance the work.

```
def process(data):
    ...
    return ...
```

Normal Sequential Processing:

```
results = [process(x) for x in inputs]
```

Build Dask Computation:

```
from dask import compute, delayed
values = [delayed(process)(x) for x in inputs]
```

Multiple Threads:

```
import dask.threaded
results = compute(*values, scheduler='threads')
```

Multiple Processes:

```
import dask.multiprocessing
results = compute(*values, scheduler='processes')
```

Distributed Cluster:

```
from dask.distributed import Client
client = Client("cluster-address:8786")
results = compute(*values, scheduler='distributed')
```

Complex dependencies

A financial analyst has many models that depend on each other in a complex web of computations.

```
data = [load(fn) for fn in filenames]
reference = load_from_database(query)

A = [model_a(x, reference) for x in data]
B = [model_b(x, reference) for x in data]

roll_A = [roll(A[i], A[i + 1]) for i in range(len(A) - 1)]
roll_B = [roll(B[i], B[i + 1]) for i in range(len(B) - 1)]
compare = [compare_ab(a, b) for a, b in zip(A, B)]

results = summarize(compare, roll_A, roll_B)
```

These models are time consuming and need to be run on a variety of inputs and situations. The analyst has his code now as a collection of Python functions and is trying to figure out how to parallelize such a codebase. They use dask.delayed to wrap their function calls and capture the implicit parallelism.

```
from dask import compute, delayed

data = [delayed(load)(fn) for fn in filenames]
reference = delayed(load_from_database)(query)

A = [delayed(model_a)(x, reference) for x in data]
B = [delayed(model_b)(x, reference) for x in data]

roll_A = [delayed(roll)(A[i], A[i + 1]) for i in range(len(A) - 1)]
roll_B = [delayed(roll)(B[i], B[i + 1]) for i in range(len(B) - 1)]
compare = [delayed(compare_ab)(a, b) for a, b in zip(A, B)]

lazy_results = delayed(summarize)(compare, roll_A, roll_B)
```

They then depend on the dask schedulers to run this complex web of computations in parallel.

```
results = compute(lazy_results)
```

They appreciate how easy it was to transition from the experimental code to a scalable parallel version. This code is also easy enough for their teammates to understand easily and extend in the future.

Algorithm developer

A graduate student in machine learning is prototyping novel parallel algorithms. They are in a situation much like the financial analyst above except that they need to benchmark and profile their computation heavily under a variety of situations and scales. The *dask profiling tools* provide the feedback they need to understand their parallel performance,

including how long each task takes, how intense communication is, and their scheduling overhead. They scale their algorithm between 1 and 50 cores on single workstations and then scale out to a cluster running their computation at thousands of cores. They don't have access to an institutional cluster, so instead they use *dask on the cloud* to easily provision clusters of varying sizes.

Their algorithm is written the same in all cases, drastically reducing the cognitive load, and letting the readers of their work experiment with their system on their own machines, aiding reproducibility.

Scikit-Learn or Joblib User

A data scientist wants to scale their machine learning pipeline to run on their cluster to accelerate parameter searches. They already use the `sklearn` `njobs=` parameter to accelerate their computation on their local computer with Joblib. Now they wrap their `sklearn` code with a context manager to parallelize the exact same code across a cluster (also available with IPyParallel)

```
import distributed.joblib

with joblib.parallel_backend('distributed',
                             scheduler_host=('192.168.1.100', 8786)):
    result = GridSearchCV( ... )  # normal sklearn code
```

Academic Cluster Administrator

A system administrator for a university compute cluster wants to enable many researchers to use the available cluster resources, which are currently lying idle. The research faculty and graduate students lack experience with job schedulers and MPI, but are comfortable interacting with Python code through a Jupyter notebook.

Teaching the faculty and graduate students to parallelize software has proven time consuming. Instead the administrator sets up dask.distributed on a sandbox allocation of the cluster and broadly publishes the address of the scheduler, pointing researchers to the dask.distributed quickstart. Utilization of the cluster climbs steadily over the next week as researchers are more easily able to parallelize their computations without having to learn foreign interfaces. The administrator is happy because resources are being used without significant hand-holding.

As utilization increases the administrator has a new problem; the shared dask.distributed cluster is being overused. The administrator tracks use through Dask diagnostics to identify which users are taking most of the resources. They contact these users and teach them how to launch their own dask.distributed clusters using the traditional job scheduler on their cluster, making space for more new users in the sandbox allocation.

Financial Modeling Team

Similar to the case above, a team of modelers working at a financial institution run a complex network of computational models on top of each other. They started using *dask.delayed* individually, as suggested above, but realized that they often perform highly overlapping computations, such as always reading the same data.

Now they decide to use the same Dask cluster collaboratively to save on these costs. Because Dask intelligently hashes computations in a way similar to how Git works, they find that when two people submit similar computations the overlapping part of the computation runs only once.

Ever since working collaboratively on the same cluster they find that their frequently running jobs run much faster, because most of the work is already done by previous users. When they share scripts with colleagues they find that those repeated scripts complete immediately rather than taking several hours.

They are now able to iterate and share data as a team more effectively, decreasing their time to result and increasing their competitive edge.

As this becomes more heavily used on the company cluster they decide to set up an auto-scaling system. They use their dynamic job scheduler (perhaps SGE, LSF, Mesos, or Marathon) to run a single `dask-scheduler` 24/7 and then scale up and down the number of `dask-workers` running on the cluster based on computational load. This solution ends up being more responsive (and thus more heavily used) than their previous attempts to provide institution-wide access to parallel computing but because it responds to load it still acts as a good citizen in the cluster.

Streaming data engineering

A data engineer responsible for watching a data feed needs to scale out a continuous process. They combine dask.distributed with normal Python Queues to produce a rudimentary but effective stream processing system.

Because dask.distributed is elastic, they can scale up or scale down their cluster resources in response to demand.

4.4 Community

Dask is used and developed by individuals at a variety of institutions. It sits within the broader Python numeric ecosystem commonly referred to as PyData or SciPy.

4.4.1 Discussion

Conversation happens in the following places:

1. **Usage questions** are directed to Stack Overflow with the #dask tag. Dask developers monitor this tag and get e-mails whenever a question is asked.
2. **Bug reports and feature requests** are managed on the GitHub issue tracker
3. **Chat** occurs on at gitter.im/dask/dask for general conversation and gitter.im/dask/dev for developer conversation. Note that because gitter chat is not searchable by future users we discourage usage questions and bug reports on gitter and instead ask people to use Stack Overflow or GitHub.
4. **Weekly developer meeting** usually happens at Thursday 4pm UTC (11am in New York, 8am in Los Angeles, 12am in Beijing) at https://appear.in/dask-dev with meeting notes on a publicly viewable document Subscribe to this public calendar to receive updates if the meeting is rescheduled or canceled.

4.4.2 Asking for help

We welcome usage questions and bug reports from all users, even those who are new to using the project. There are a few things you can do to improve the likelihood of quickly getting a good answer.

1. **Ask questions in the right place**: We strongly prefer the use of StackOverflow or Github issues over Gitter chat. Github and StackOverflow are more easily searchable by future users and so is more efficient for everyone's time. Gitter chat is strictly reserved for developer and community discussion.

   If you have a general question about how something should work or want best practices then use Stack Overflow. If you think you have found a bug then use GitHub.
2. **Ask only in one place**: Please restrict yourself to posting your question in only one place (likely Stack Overflow or Github) and don't post in both.
3. **Create a minimal example**: It is ideal to create minimal, complete, verifiable examples. This significantly reduces the time that answerers spend understanding your situation and so results in higher quality answers more quickly.

See also this blogpost about crafting minimal bug reports. These have a much higher likelihood of being answered.

4.4.3 Paid support

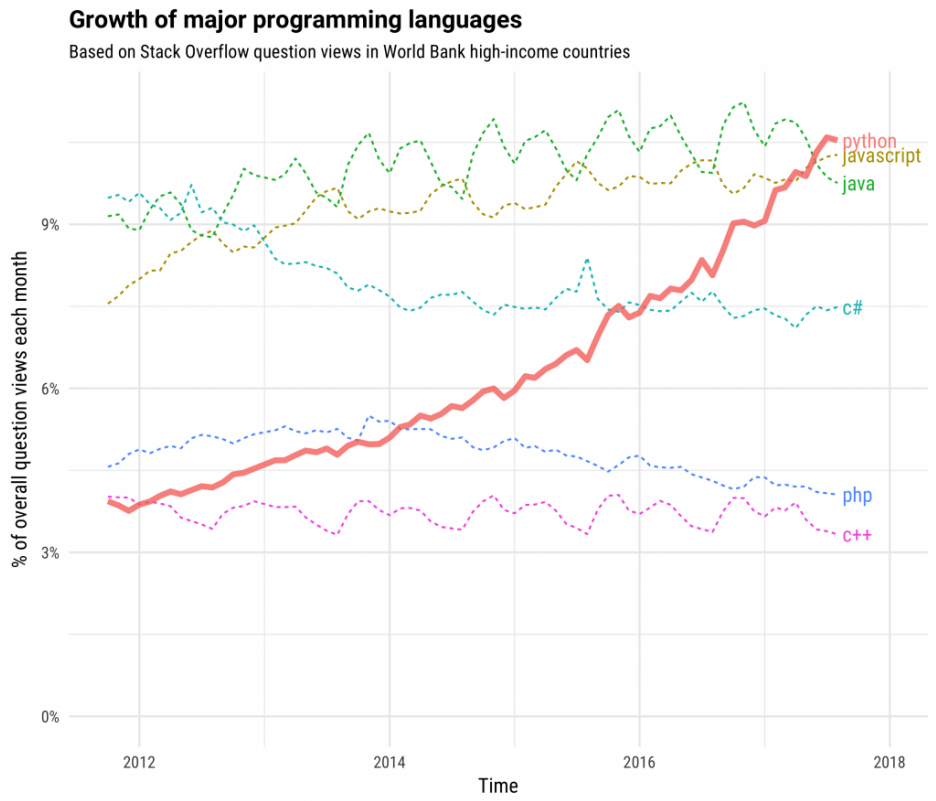
Dask is an open source project that originated at Anaconda Inc.. In addition to the previous options, Anaconda offers paid training and support: https://www.anaconda.com/support.

4.5 Why Dask?

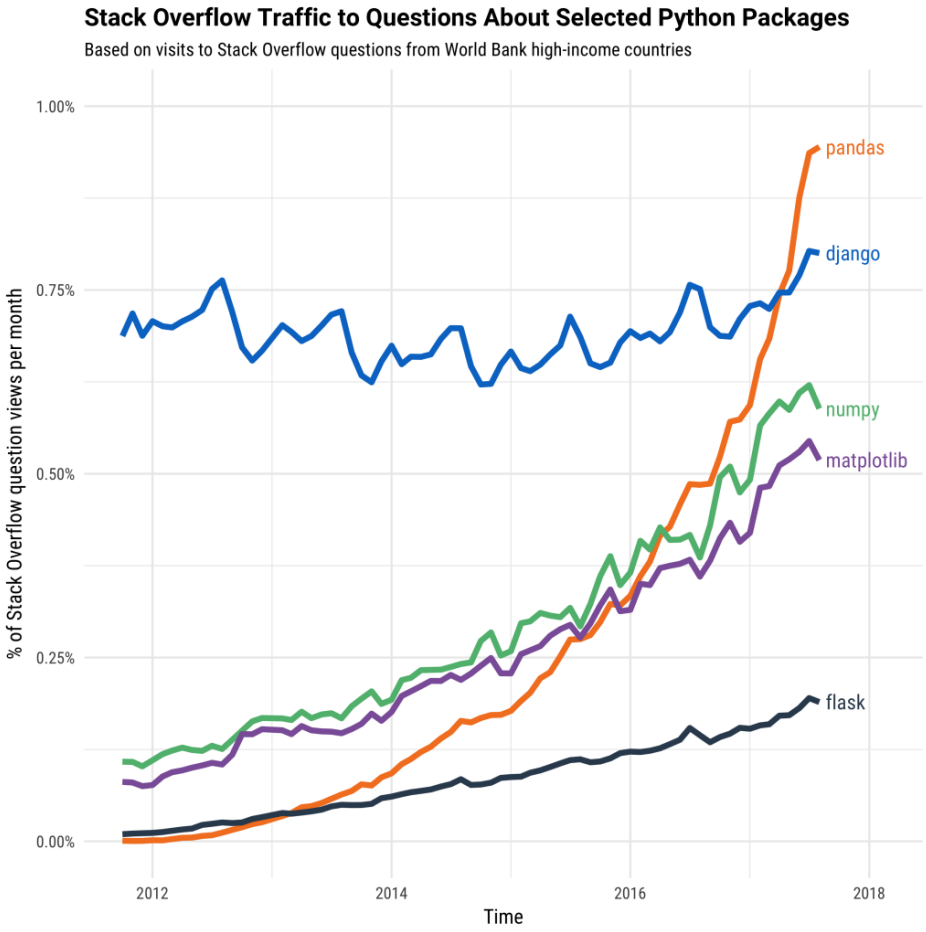
This document gives high-level motivation on why people choose to adopt Dask.

4.5.1 Python's role in Data Science

Python has grown to become the dominant language both in data analytics, and general programming:



This is fueled both by computational libraries like Numpy, Pandas, and Scikit-Learn and by a wealth of libraries for visualization, interactive notebooks, collaboration, and so forth.



However these packages were not designed to scale beyond a single machine. Dask was developed to scale these packages and the surrounding ecosystem. Dask works with the existing Python ecosystem to scale it to multi-core machines and distributed clusters.

Image credit to Stack Overflow blogposts #1 and #2

4.5.2 Familiar API

Analysts often use tools like Pandas, Scikit-Learn, Numpy, and the rest of the Python ecosystem to analyze data on their personal computer. They like these tools because they are efficient, intuitive, and widely trusted. However when they choose to apply their analyses to larger datasets they find that these tools were not designed to scale beyond a single machine, and so the analyst is forced to rewrite their computation using a more scalable tool, often in another language altogether. This rewrite process slows down discovery and causes frustration.

Dask provides ways to scale Pandas, Scikit-Learn, and Numpy workflows with minimal rewriting. Dask integrates well with these tools so that it copies most of their API and uses their data structures internally. Dask is co-developed with these libraries to ensure that they evolve consistently, minimizing friction caused from transitioning from workloads on a local laptop, to a multi-core workstation, to a distributed cluster. Analysts familiar with Pandas/Scikit-Learn/Numpy will be immediately familiar with their Dask equivalents, and have much of their intuition carry over to a scalable context.

4.5.3 Scales out to clusters

As datasets and computations scale faster than CPUs and RAM we need to find ways to scale our computations across multiple machines. This introduces many new concerns:

- How to have computers talk to each other over the network?
- How and when to move data between machines?
- How to recover from machine failures?
- How to deploy on an in-house cluster?
- How to deploy on the cloud?
- How to deploy on an HPC super-computer?
- How to provide an API to this system that users find intuitive?
- ...

While it is possible to build these systems in-house (and indeed, many exist) many organizations are increasingly depending on solutions developed within the open source community. These tend to be more robust, secure, and fully featured without being tended by in-house staff.

Dask solves these problems. It is routinely run on thousand-machine clusters to process hundreds of terabytes of data efficiently. It has utilities and documentation on how to deploy in-house, on the cloud, or on HPC super-computers. It supports encryption and authentication using TLS/SSL certificates. It is resilient and can handle the failure of worker nodes gracefully and is elastic and so can take advantage of new nodes added on-the-fly. Dask includes several user APIs that are used and smoothed over by thousands of researchers across the globe working in different domains.

4.5.4 Scales down to single computers

But a massive cluster is not always the right choice

Today's laptops and workstations are surprisingly powerful and, if used correctly, can often handle datasets and computations for which we previously depended on clusters. A modern laptop has a multi-core CPU, 32GB of RAM, and flash-based hard drives that can stream through data several times faster than HDDs or SSDs of even a year or two ago.

As a result analysts can often manipulate 100GB+ datasets on their laptop or 1TB+ datasets on a workstation without bothering with the cluster at all. They sometimes prefer this for the following reasons:

1. They can use their local software environment, rather than being constrained by what is available on the cluster
2. They can more easily work while in transit, at a coffee shop, or at home away from the VPN
3. Debugging errors and analyzing performance are generally much easier on a single machine without having to pore through logs
4. Generally their iteration cycles are faster
5. Their computations may be more efficient because all of the data is local and doesn't need to flow through the network or between separate processes

Dask can enable efficient parallel computations on single machines by leveraging their multi-core CPUs and streaming data efficiently from disk. Dask *can* run on a distributed cluster, but it doesn't have to. Dask allows you to swap out the cluster for single-machine schedulers which are surprisingly lightweight, require no setup, and can run entirely within the same process as the user's session.

To avoid excess memory use, Dask is good at finding ways to evaluate computations in a low-memory footprint when possible by pulling in chunks of data from disk, doing the necessary processing, and throwing away intermediate

values as quickly as possible. This lets analysts perform computations on moderately large datasets (100GB+) even on relatively low-power laptops. This requires no configuration and no setup, meaning that adding Dask to a single-machine computation adds very little cognitive overhead.

4.5.5 Integrates with the Python ecosystem

Python includes computational libraries like Numpy, Pandas, and Scikit-Learn, along with thousands of others in data access, plotting, statistics, image and signal processing, and more. These libraries work together seamlessly to produce a cohesive *ecosystem* of packages that co-evolve to meet the needs of analysts in many domains.

This ecosystem is tied together by common standards and protocols to which everyone adheres, which allows these packages to benefit each other in surprising and delightful ways.

Dask evolved from within this ecosystem. It abides by these standards and protocols and actively engages in community efforts to push forward new ones. This enables the rest of the ecosystem to benefit from parallel and distributed computing with minimal coordination. Dask does not seek to disrupt or displace the existing ecosystem, but rather to complement and benefit it from within.

As a result, Dask development is pushed forward by developer communities from Pandas, Numpy, Scikit-Learn, Scikit-Image, Jupyter, and others. This engagement from the broader community growth helps users to trust the project and helps to ensure that the Python ecosystem will continue to evolve in a smooth and sustainable manner.

4.5.6 Supports complex applications

Some parallel computations are simple and just apply the same routine onto many inputs without any kind of coordination. These are simple to parallelize with any system.

Somewhat more complex computations can be expressed with the map-shuffle-reduce pattern popularized by Hadoop and Spark. This is often sufficient to do most data cleaning tasks, database-style queries, and some lightweight machine learning algorithms.

However, more complex parallel computations exist which do not fit into these paradigms and so are difficult to perform with traditional big-data technologies. These include more advanced algorithms for statistics or machine learning, time series or local operations, or bespoke parallelism often found within the systems of large enterprises.

Many companies and institutions today have problems which are clearly parallelizable, but not clearly transformable into a big dataframe computation. Today these companies tend to solve their problems either by writing custom code with low-level systems like MPI, ZeroMQ, or sockets and complex queuing systems, or by shoving their problem into a standard big-data technology like MapReduce or Spark, and hoping for the best.

Dask helps to resolve these situations by exposing low-level APIs to its internal task scheduler which is capable of executing very advanced computations. This gives engineers within the institution the ability to build their own parallel computing system using the same engine that powers Dask's arrays, dataframes, and machine learning algorithms, but now with the institution's own custom logic. This allows in-house engineers to keep complex business logic in-house while still relying on Dask to handle network communication, load balancing, resilience, diagnostics, etc..

4.5.7 Responsive feedback

Because everything happens remotely, interactive parallel computing can be frustrating for users. They don't have a good sense of how computations are progressing, what might be going wrong, or what parts of their code should they focus on for performance. The added distance between a user and their computation can drastically affect how quickly they are able to identify and resolve bugs and performance problems, which can drastically increase their time to solution.

Dask keeps users informed and content with a suite of helpful diagnostic and investigative tools including the following:

1. A *real-time and responsive dashboard* that shows current progress, communication costs, memory use, and more, updated every 100ms
2. A statistical profiler installed on every worker that polls each thread every 10ms to determine which lines in your code are taking up the most time across your entire computation.
3. An embedded IPython kernel in every worker and the scheduler, allowing users to directly investigate the state of their computation with a pop-up terminal
4. The ability to reraise errors locally, so that they can use the traditional debugging tools to which they are accustomed, even when the error happens remotely

Collections

Dask collections are the main interaction point for users. They look like NumPy and Pandas but generate dask graphs internally. If you are a dask *user* then you should start here.

- *Array*
- *Bag*
- *Dataframe*
- *Delayed*
- *Futures*

4.6 User Interfaces

Dask supports several user interfaces:

- **High Level**
  - *Arrays*: parallel Numpy
  - *Bags*: parallel lists
  - *Dataframes*: parallel Pandas
  - Machine Learning : parallel Scikit-Learn
  - Others from external projects, like XArray
- **Low Level**
  - *Delayed*: parallel function evaluation
  - *Futures*: real-time parallel function evaluation

Each of these user interfaces employs the same underlying parallel computing machinery, and so has the same scaling, diagnostics, resilience, and so on, but each provides a different set of parallel algorithms and programming style.

This document helps you to decide which user interface best suits your needs, and gives some general information that applies to all of the interfaces. The pages linked to above give more information about each interface in greater depth.

4.6.1 High Level Collections

Many people who start using Dask are explicitly looking for a scalable version of Numpy, Pandas, or Scikit-Learn. For these situations the starting point within Dask is usually fairly clear. If you want scalable Numpy, they start with Dask array; if you want scalable Pandas, they start with Dask dataframe, and so on.

These high-level interfaces copy the standard interface with slight variation. These interfaces automatically parallelize over larger datasets for you for a large subset of the API from the original project.

```
# Arrays
import dask.array as da
x = da.random.uniform(low=0, high=10, size=(10000, 10000),  # normal Numpy code
                      chunks=(1000, 1000))  # break into chunks of size 1000x1000

y = x + x.T - x.mean(axis=0)  # Use normal syntax for high level algorithms

# Dataframes
import dask.dataframe as dd
df = dd.read_csv('2018-*-*.csv', parse_dates='timestamp',  # normal Pandas code
                 blocksize=64000000)  # break text into 64MB chunks

s = df.groupby('name').balance.mean()  # Use normal syntax for high level algorithms

# Bags / lists
import dask.bag as db
b = db.read_text('*.json').map(json.loads)
total = (b.filter(lambda d: d['name'] == 'Alice')
          .map(lambda d: d['balance'])
          .sum())
```

It is important to remember that while APIs may be similar some differences do exist. Additionally, the performance of some algorithms may differ from their in-memory counterparts due to the advantages and disadvantages of parallel programming. Some thought and attention is still required when using Dask.

4.6.2 Low Level Interfaces

Often when parallelizing existing code bases or building custom algorithms you run into code that is parallelizable, but isn't just a big dataframe or array. Consider the for-loopy code below:

```
results = []
for a in A:
    for b in B:
        if a < b:
            c = f(a, b)
        else:
            c = g(a, b)
        results.append(c)
```

There is potential parallelism in this code (the many calls to `f` and `g` can be done in parallel), but it's not clear how to rewrite it into a big array or dataframe so that it can use a higher-level API. Even if you could rewrite it into one of these paradigms, it's not clear that this would be a good idea. Much of the meaning would likely be lost in translation, and this process would become much more difficult for more complex systems.

Instead, Dask's lower-level APIs let you write parallel code one function call at a time within the context of your existing for loops. A common solution here is to use *Dask delayed* to wrap individual function calls into a lazily constructed task graph:

```
import dask

lazy_results = []
for a in A:
    for b in B:
        if a < b:
            c = dask.delayed(f)(a, b)  # add lazy task
        else:
            c = dask.delayed(g)(a, b)  # add lazy task
        lazy_results.append(c)

results = dask.compute(*lazy_results)  # compute all in parallel
```

4.6.3 Combining High and Low Level

It is common to combine high and low level interfaces. For example you might use Dask array/bag/dataframe to load in data and do initial pre-processing, then switch to Dask delayed for a custom algorithm that is specific to your domain, then switch back to Dask array/dataframe to clean up and store results. Understanding both sets of user interfaces and how to switch between them can be a productive combination.

```
# Convert to a list of delayed Pandas dataframes
delayed_values = df.to_delayed()

# Manipulate delayed values arbitrarily as you like

# Convert many delayed Pandas dataframes back to a single Dask dataframe
df = dd.from_delayed(delayed_values)
```

4.6.4 Laziness and Computing

Most Dask user interfaces are *lazy* meaning that they do not evaluate until you explicitly ask for a result using the `compute` method:

```
# This array syntax doesn't cause computation
y = x + x.T - x.mean(axis=0)

# Trigger computation by explicitly calling the compute method
y = y.compute()
```

If you have multiple results that you want to compute at the same time, use the `dask.compute` function. This can share intermediate results and so be more efficient:

```
# compute multiple results at the same time with the compute function
min, max = dask.compute(y.min(), y.max())
```

Note that the `compute()` function returns in-memory results. It converts Dask dataframes to Pandas dataframes, Dask arrays to Numpy arrays, and Dask bags to lists. *You should only call compute on results that will fit comfortably in memory*. If your result does not fit in memory then you might consider writing it to disk instead.

```
# Write larger results out to disk rather than store them in memory
my_dask_dataframe.to_parquet('myfile.parquet')
my_dask_array.to_hdf5('myfile.hdf5')
my_dask_bag.to_textfiles('myfile.*.txt')
```

4.6.5 Persist into Distributed Memory

Alternatively, if you are on a cluster then you may want to trigger a computation and store the results in distributed memory. In this case you do not want to call `compute`, which would create a single Pandas, Numpy, or List result, but instead you want to call `persist`, which returns a new Dask object that points to actively computing, or already computed results spread around your cluster's memory.

```
# Compute returns an in-memory non-Dask object
y = y.compute()

# Persist returns an in-memory Dask object that uses distributed storage if available
y = y.persist()
```

This is common to see after data loading an preprocessing steps, but before rapid iteration, exploration, or complex algorithms. For example we might read in a lot of data, filter down to a more manageable subset, and then persist data into memory so that we can iterate quickly.

```
import dask.dataframe as dd
df = dd.read_parquet('...')
df = df[df.name == 'Alice']  # select important subset of data
df = df.persist()  # trigger computation in the background

# These are all relatively fast now that the relevant data is in memory
df.groupby(df.id).balance.sum().compute()    # explore data quickly
df.groupby(df.id).balance.mean().compute()   # explore data quickly
df.id.nunique()                              # explore data quickly
```

4.6.6 Lazy vs Immediate

As mentioned above, most Dask workloads are lazy, that is they don't start any work, until you explicitly trigger them with a call to `compute()`. However sometimes you *do* want to submit work as quickly as possible, track it over time, submit new work or cancel work depending on partial results, and so on. This can be useful when tracking or responding to real-time events, handling streaming data, or when building complex and adaptive algorithms.

For these situations people typically turn to the *futures interface* which is a low-level interface like Dask delayed, but operates immediately rather than lazily.

Here is the same example with Dask delayed and Dask futures to illustrate the difference.

Delayed: Lazy

```
@dask.delayed
def inc(x):
    return x + 1

@dask.delayed
def add(x, y):
    return x + y

a = inc(1)       # no work has happened yet
b = inc(2)       # no work has happened yet
c = add(a, b)    # no work has happened yet

c = c.compute()  # This triggers all of the above computations
```

Futures: Immediate

```
from dask.distributed import Client
client = Client()

def inc(x):
    return x + 1

def add(x, y):
    return x + y

a = client.submit(inc, 1)      # work starts immediately
b = client.submit(inc, 2)      # work starts immediately
c = client.submit(add, a, b)   # work starts immediately

c = c.result()                 # block until work finishes, then gather result
```

You can also trigger work with the high-level collections using the `persist` function. This will cause work to happen in the background when using the distributed scheduler.

4.6.7 Combining Interfaces

There are established ways to combine the interfaces above:

1. The high-level interfaces (array, bag, dataframe) have a `to_delayed` method that can convert to a sequence (or grid) of Dask delayed objects

   ```
   delayeds = df.to_delayed()
   ```

2. The high-level interfaces (array, bag, dataframe) have a `from_delayed` method that can convert from either Delayed *or* Future objects

   ```
   df = dd.from_delayed(delayeds)
   df = dd.from_delayed(futures)
   ```

3. The `Client.compute` method converts Delayed objects into Futures.

   ```
   futures = client.compute(delayeds)
   ```

4. The `dask.distributed.futures_of` function gathers futures from persisted collections

   ```
   from dask.distributed import futures_of

   df = df.persist()  # start computation in the background
   futures = futures_of(df)
   ```

4. The Dask.delayed object converts Futures into delayed objects.

   ```
   delayed_value = dask.delayed(future)
   ```

The approaches above should suffice to convert any interface into any other. We often see some anti-patterns that do not work as well:

1. Calling low-level APIs (delayed or futures) on high-level objects (like Dask arrays or dataframes) This downgrades those objects to their Numpy or Pandas equivalents, which may not be desired. Often people are looking for APIs like `dask.array.map_blocks` or `dask.dataframe.map_partitions` instead.

2. Calling `compute()` on Future objects. Often people want the `.result()` method instead.
3. Calling Numpy/Pandas functions on high-level Dask objects or high-level Dask functions on Numpy/Pandas objects

4.6.8 Conclusion

Most people who use Dask start with only one of the interfaces above but eventually learn how to use a few interfaces together. This helps them leverage the sophisticated algorithms in the high-level interfaces while also working around tricky problems with the low-level interfaces.

For more information, see the documentation for the particular user interfaces below:

- **High Level**
  - *Arrays*: parallel Numpy
  - *Bags*: parallel lists
  - *Dataframes*: parallel Pandas
  - Machine Learning : parallel Scikit-Learn
  - Others from external projects, like XArray
- **Low Level**
  - *Delayed*: parallel function evaluation
  - *Futures*: real-time parallel function evaluation

4.7 Array

4.7.1 API

Top level user functions:

`all`(a[, axis, out, keepdims])	Test whether all array elements along a given axis evaluate to True.
`allclose`(a, b[, rtol, atol, equal_nan])	Returns True if two arrays are element-wise equal within a tolerance.
`angle`(x[, deg])	Return the angle of the complex argument.
`any`(a[, axis, out, keepdims])	Test whether any array element along a given axis evaluates to True.
`apply_along_axis`(func1d, axis, arr, *args, ...)	Apply a function to 1-D slices along the given axis.
`apply_over_axes`(func, a, axes)	Apply a function repeatedly over multiple axes.
`arange`(*args, **kwargs)	Return evenly spaced values from *start* to *stop* with step size *step*.
`arccos`(x[, out])	Trigonometric inverse cosine, element-wise.
`arccosh`(x[, out])	Inverse hyperbolic cosine, element-wise.
`arcsin`(x[, out])	Inverse sine, element-wise.
`arcsinh`(x[, out])	Inverse hyperbolic sine element-wise.
`arctan`(x[, out])	Trigonometric inverse tangent, element-wise.
`arctan2`(x1, x2[, out])	Element-wise arc tangent of `x1/x2` choosing the quadrant correctly.

Continued on next page

Table 3 – continued from previous page

arctanh(x[, out])	Inverse hyperbolic tangent element-wise.
argmax(a[, axis, out])	Returns the indices of the maximum values along an axis.
argmin(a[, axis, out])	Returns the indices of the minimum values along an axis.
argtopk(a, k[, axis, split_every])	Extract the indices of the k largest elements from a on the given axis, and return them sorted from largest to smallest.
argwhere(a)	Find the indices of array elements that are non-zero, grouped by element.
around(a[, decimals, out])	Evenly round to the given number of decimals.
array(object[, dtype, copy, order, subok, ndmin])	Create an array.
asanyarray(a)	Convert the input to a dask array.
asarray(a)	Convert the input to a dask array.
atleast_1d(*arys)	Convert inputs to arrays with at least one dimension.
atleast_2d(*arys)	View inputs as arrays with at least two dimensions.
atleast_3d(*arys)	View inputs as arrays with at least three dimensions.
average(a[, axis, weights, returned])	Compute the weighted average along the specified axis.
bincount(x[, weights, minlength])	Count number of occurrences of each value in array of non-negative ints.
bitwise_and(x1, x2[, out])	Compute the bit-wise AND of two arrays element-wise.
bitwise_not(x[, out])	Compute bit-wise inversion, or bit-wise NOT, element-wise.
bitwise_or(x1, x2[, out])	Compute the bit-wise OR of two arrays element-wise.
bitwise_xor(x1, x2[, out])	Compute the bit-wise XOR of two arrays element-wise.
block(arrays[, allow_unknown_chunksizes])	Assemble an nd-array from nested lists of blocks.
broadcast_arrays(*args, **kwargs)	Broadcast any number of arrays against each other.
broadcast_to(x, shape[, chunks])	Broadcast an array to a new shape.
coarsen(reduction, x, axes[, trim_excess])	Coarsen array by applying reduction to fixed size neighborhoods
ceil(x[, out])	Return the ceiling of the input, element-wise.
choose(a, choices[, out, mode])	Construct an array from an index array and a set of arrays to choose from.
clip(*args, **kwargs)	Clip (limit) the values in an array.
compress(condition, a[, axis, out])	Return selected slices of an array along given axis.
concatenate(seq[, axis, ...])	Concatenate arrays along an existing axis
conj(x[, out])	Return the complex conjugate, element-wise.
copysign(x1, x2[, out])	Change the sign of x1 to that of x2, element-wise.
corrcoef(x[, y, rowvar, bias, ddof])	Return Pearson product-moment correlation coefficients.
cos(x[, out])	Cosine element-wise.
cosh(x[, out])	Hyperbolic cosine, element-wise.
count_nonzero(a)	Counts the number of non-zero values in the array a.
cov(m[, y, rowvar, bias, ddof, fweights, ...])	Estimate a covariance matrix, given data and weights.
cumprod(a[, axis, dtype, out])	Return the cumulative product of elements along a given axis.
cumsum(a[, axis, dtype, out])	Return the cumulative sum of the elements along a given axis.
deg2rad(x[, out])	Convert angles from degrees to radians.
degrees(x[, out])	Convert angles from radians to degrees.
diag(v[, k])	Extract a diagonal or construct a diagonal array.

Continued on next page

Table 3 – continued from previous page

diff(a[, n, axis])	Calculate the n-th discrete difference along given axis.
digitize(x, bins[, right])	Return the indices of the bins to which each value in input array belongs.
dot(a, b[, out])	Dot product of two arrays.
dstack(tup)	Stack arrays in sequence depth wise (along third axis).
ediff1d(ary[, to_end, to_begin])	The differences between consecutive elements of an array.
einsum(subscripts, *operands[, out, dtype, ...])	Evaluates the Einstein summation convention on the operands.
empty(*args, **kwargs)	Blocked variant of empty
empty_like(a[, dtype, chunks])	Return a new array with the same shape and type as a given array.
exp(x[, out])	Calculate the exponential of all elements in the input array.
expm1(x[, out])	Calculate `exp(x) - 1` for all elements in the array.
eye(N, chunks[, M, k, dtype])	Return a 2-D Array with ones on the diagonal and zeros elsewhere.
fabs(x[, out])	Compute the absolute values element-wise.
fix(*args, **kwargs)	Round to nearest integer towards zero.
flatnonzero(a)	Return indices that are non-zero in the flattened version of a.
flip(m, axis)	Reverse element order along axis.
flipud(m)	Flip array in the up/down direction.
fliplr(m)	Flip array in the left/right direction.
floor(x[, out])	Return the floor of the input, element-wise.
fmax(x1, x2[, out])	Element-wise maximum of array elements.
fmin(x1, x2[, out])	Element-wise minimum of array elements.
fmod(x1, x2[, out])	Return the element-wise remainder of division.
frexp(x[, out1, out2])	Decompose the elements of x into mantissa and twos exponent.
fromfunction(function, shape, **kwargs)	Construct an array by executing a function over each coordinate.
frompyfunc(func, nin, nout)	Takes an arbitrary Python function and returns a Numpy ufunc.
full(*args, **kwargs)	Blocked variant of full
full_like(a, fill_value[, dtype, chunks])	Return a full array with the same shape and type as a given array.
gradient(f, *varargs, **kwargs)	Return the gradient of an N-dimensional array.
histogram(a[, bins, range, normed, weights, ...])	Blocked variant of `numpy.histogram()`.
hstack(tup)	Stack arrays in sequence horizontally (column wise).
hypot(x1, x2[, out])	Given the "legs" of a right triangle, return its hypotenuse.
imag(*args, **kwargs)	Return the imaginary part of the elements of the array.
indices(dimensions[, dtype, chunks])	Implements NumPy's `indices` for Dask Arrays.
insert(arr, obj, values[, axis])	Insert values along the given axis before the given indices.
isclose(a, b[, rtol, atol, equal_nan])	Returns a boolean array where two arrays are element-wise equal within a tolerance.
iscomplex(*args, **kwargs)	Returns a bool array, where True if input element is complex.

Continued on next page

Table 3 – continued from previous page

isfinite(x[, out])	Test element-wise for finiteness (not infinity or not Not a Number).
isin(element, test_elements[, ...])	
isinf(x[, out])	Test element-wise for positive or negative infinity.
isneginf(*args, **kwargs)	Test element-wise for negative infinity, return result as bool array.
isnan(x[, out])	Test element-wise for NaN and return result as a boolean array.
isnull(values)	pandas.isnull for dask arrays
isposinf(*args, **kwargs)	Test element-wise for positive infinity, return result as bool array.
isreal(*args, **kwargs)	Returns a bool array, where True if input element is real.
ldexp(x1, x2[, out])	Returns x1 * 2**x2, element-wise.
linspace(start, stop[, num, endpoint, ...])	Return *num* evenly spaced values over the closed interval [*start*, *stop*].
log(x[, out])	Natural logarithm, element-wise.
log10(x[, out])	Return the base 10 logarithm of the input array, element-wise.
log1p(x[, out])	Return the natural logarithm of one plus the input array, element-wise.
log2(x[, out])	Base-2 logarithm of *x*.
logaddexp(x1, x2[, out])	Logarithm of the sum of exponentiations of the inputs.
logaddexp2(x1, x2[, out])	Logarithm of the sum of exponentiations of the inputs in base-2.
logical_and(x1, x2[, out])	Compute the truth value of x1 AND x2 element-wise.
logical_not(x[, out])	Compute the truth value of NOT x element-wise.
logical_or(x1, x2[, out])	Compute the truth value of x1 OR x2 element-wise.
logical_xor(x1, x2[, out])	Compute the truth value of x1 XOR x2, element-wise.
map_blocks(func, *args, **kwargs)	Map a function across all blocks of a dask array.
map_overlap(x, func, depth[, boundary, trim])	Map a function over blocks of the array with some overlap
matmul(a, b[, out])	Matrix product of two arrays.
max(a[, axis, out, keepdims])	Return the maximum of an array or maximum along an axis.
maximum(x1, x2[, out])	Element-wise maximum of array elements.
mean(a[, axis, dtype, out, keepdims])	Compute the arithmetic mean along the specified axis.
meshgrid(*xi, **kwargs)	Return coordinate matrices from coordinate vectors.
min(a[, axis, out, keepdims])	Return the minimum of an array or minimum along an axis.
minimum(x1, x2[, out])	Element-wise minimum of array elements.
modf(x[, out1, out2])	Return the fractional and integral parts of an array, element-wise.
moment(a, order[, axis, dtype, keepdims, ...])	
nanargmax(x, axis, **kwargs)	
nanargmin(x, axis, **kwargs)	
nancumprod(a[, axis, dtype, out])	Return the cumulative product of array elements over a given axis treating Not a Numbers (NaNs) as one.
nancumsum(a[, axis, dtype, out])	Return the cumulative sum of array elements over a given axis treating Not a Numbers (NaNs) as zero.
nanmax(a[, axis, out, keepdims])	Return the maximum of an array or maximum along an axis, ignoring any NaNs.

Continued on next page

Table 3 – continued from previous page

nanmean(a[, axis, dtype, out, keepdims])	Compute the arithmetic mean along the specified axis, ignoring NaNs.
nanmin(a[, axis, out, keepdims])	Return minimum of an array or minimum along an axis, ignoring any NaNs.
nanprod(a[, axis, dtype, out, keepdims])	Return the product of array elements over a given axis treating Not a Numbers (NaNs) as zero.
nanstd(a[, axis, dtype, out, ddof, keepdims])	Compute the standard deviation along the specified axis, while ignoring NaNs.
nansum(a[, axis, dtype, out, keepdims])	Return the sum of array elements over a given axis treating Not a Numbers (NaNs) as zero.
nanvar(a[, axis, dtype, out, ddof, keepdims])	Compute the variance along the specified axis, while ignoring NaNs.
nan_to_num(*args, **kwargs)	Replace nan with zero and inf with finite numbers.
nextafter(x1, x2[, out])	Return the next floating-point value after x1 towards x2, element-wise.
nonzero(a)	Return the indices of the elements that are non-zero.
notnull(values)	pandas.notnull for dask arrays
ones(*args, **kwargs)	Blocked variant of ones
ones_like(a[, dtype, chunks])	Return an array of ones with the same shape and type as a given array.
outer(a, b[, out])	Compute the outer product of two vectors.
pad(array, pad_width, mode, **kwargs)	Pads an array.
percentile(a, q[, interpolation])	Approximate percentile of 1-D array
PerformanceWarning	A warning given when bad chunking may cause poor performance
piecewise(x, condlist, funclist, *args, **kw)	Evaluate a piecewise-defined function.
prod(a[, axis, dtype, out, keepdims])	Return the product of array elements over a given axis.
ptp(a[, axis, out])	Range of values (maximum - minimum) along an axis.
rad2deg(x[, out])	Convert angles from radians to degrees.
radians(x[, out])	Convert angles from degrees to radians.
ravel(a[, order])	Return a contiguous flattened array.
real(*args, **kwargs)	Return the real part of the elements of the array.
rechunk(x, chunks[, threshold, block_size_limit])	Convert blocks in dask array x for new chunks.
repeat(a, repeats[, axis])	Repeat elements of an array.
reshape(x, shape)	Reshape array to new shape
result_type(*arrays_and_dtypes)	Returns the type that results from applying the NumPy type promotion rules to the arguments.
rint(x[, out])	Round elements of the array to the nearest integer.
roll(a, shift[, axis])	Roll array elements along a given axis.
round(a[, decimals, out])	Round an array to the given number of decimals.
sign(x[, out])	Returns an element-wise indication of the sign of a number.
signbit(x[, out])	Returns element-wise True where signbit is set (less than zero).
sin(x[, out])	Trigonometric sine, element-wise.
sinh(x[, out])	Hyperbolic sine, element-wise.
sqrt(x[, out])	Return the positive square-root of an array, element-wise.
square(x[, out])	Return the element-wise square of the input.
squeeze(a[, axis])	Remove single-dimensional entries from the shape of an array.

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Table 3 – continued from previous page

stack(seq[, axis])	Stack arrays along a new axis
std(a[, axis, dtype, out, ddof, keepdims])	Compute the standard deviation along the specified axis.
sum(a[, axis, dtype, out, keepdims])	Sum of array elements over a given axis.
take(a, indices[, axis, out, mode])	Take elements from an array along an axis.
tan(x[, out])	Compute tangent element-wise.
tanh(x[, out])	Compute hyperbolic tangent element-wise.
tensordot(a, b[, axes])	Compute tensor dot product along specified axes for arrays >= 1-D.
tile(A, reps)	Construct an array by repeating A the number of times given by reps.
topk(a, k[, axis, split_every])	Extract the k largest elements from a on the given axis, and return them sorted from largest to smallest.
transpose(a[, axes])	Permute the dimensions of an array.
tril(m[, k])	Lower triangle of an array with elements above the *k*-th diagonal zeroed.
triu(m[, k])	Upper triangle of an array with elements above the *k*-th diagonal zeroed.
trunc(x[, out])	Return the truncated value of the input, element-wise.
unique(ar[, return_index, return_inverse, ...])	Find the unique elements of an array.
unravel_index(indices, dims[, order])	Converts a flat index or array of flat indices into a tuple of coordinate arrays.
var(a[, axis, dtype, out, ddof, keepdims])	Compute the variance along the specified axis.
vdot(a, b)	Return the dot product of two vectors.
vstack(tup)	Stack arrays in sequence vertically (row wise).
where(condition, [x, y])	Return elements, either from *x* or *y*, depending on *condition*.
zeros(*args, **kwargs)	Blocked variant of zeros
zeros_like(a[, dtype, chunks])	Return an array of zeros with the same shape and type as a given array.

Fast Fourier Transforms

fft.fft_wrap(fft_func[, kind, dtype])	Wrap 1D, 2D, and ND real and complex FFT functions
fft.fft(a[, n, axis])	Wrapping of numpy.fft.fftpack.fft
fft.fft2(a[, s, axes])	Wrapping of numpy.fft.fftpack.fft2
fft.fftn(a[, s, axes])	Wrapping of numpy.fft.fftpack.fftn
fft.ifft(a[, n, axis])	Wrapping of numpy.fft.fftpack.ifft
fft.ifft2(a[, s, axes])	Wrapping of numpy.fft.fftpack.ifft2
fft.ifftn(a[, s, axes])	Wrapping of numpy.fft.fftpack.ifftn
fft.rfft(a[, n, axis])	Wrapping of numpy.fft.fftpack.rfft
fft.rfft2(a[, s, axes])	Wrapping of numpy.fft.fftpack.rfft2
fft.rfftn(a[, s, axes])	Wrapping of numpy.fft.fftpack.rfftn
fft.irfft(a[, n, axis])	Wrapping of numpy.fft.fftpack.irfft
fft.irfft2(a[, s, axes])	Wrapping of numpy.fft.fftpack.irfft2
fft.irfftn(a[, s, axes])	Wrapping of numpy.fft.fftpack.irfftn
fft.hfft(a[, n, axis])	Wrapping of numpy.fft.fftpack.hfft
fft.ihfft(a[, n, axis])	Wrapping of numpy.fft.fftpack.ihfft
fft.fftfreq(n[, d])	Return the Discrete Fourier Transform sample frequencies.

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fft.rfftfreq(n[, d])	Return the Discrete Fourier Transform sample frequencies (for usage with rfft, irfft).
fft.fftshift(x[, axes])	Shift the zero-frequency component to the center of the spectrum.
fft.ifftshift(x[, axes])	The inverse of *fftshift*.

Linear Algebra

linalg.cholesky(a[, lower])	Returns the Cholesky decomposition, $A = LL^*$ or $A = U^*U$ of a Hermitian positive-definite matrix A.
linalg.inv(a)	Compute the inverse of a matrix with LU decomposition and forward / backward substitutions.
linalg.lstsq(a, b)	Return the least-squares solution to a linear matrix equation using QR decomposition.
linalg.lu(a)	Compute the lu decomposition of a matrix.
linalg.norm(x[, ord, axis, keepdims])	Matrix or vector norm.
linalg.qr(a)	Compute the qr factorization of a matrix.
linalg.solve(a, b[, sym_pos])	Solve the equation `a x = b` for `x`.
linalg.solve_triangular(a, b[, lower])	Solve the equation *a x = b* for *x*, assuming a is a triangular matrix.
linalg.svd(a)	Compute the singular value decomposition of a matrix.
linalg.svd_compressed(a, k[, n_power_iter, seed])	Randomly compressed rank-k thin Singular Value Decomposition.
linalg.sfqr(data[, name])	Direct Short-and-Fat QR
linalg.tsqr(data[, compute_svd, ...])	Direct Tall-and-Skinny QR algorithm

Masked Arrays

ma.filled
ma.fix_invalid
ma.getdata
ma.getmaskarray
ma.masked_array
ma.masked_equal
ma.masked_greater
ma.masked_greater_equal
ma.masked_inside
ma.masked_invalid
ma.masked_less
ma.masked_less_equal
ma.masked_not_equal
ma.masked_outside
ma.masked_values
ma.masked_where
ma.set_fill_value

Random

random.beta(a, b[, size])	Draw samples from a Beta distribution.
random.binomial(n, p[, size])	Draw samples from a binomial distribution.
random.chisquare(df[, size])	Draw samples from a chi-square distribution.
random.choice(a[, size, replace, p])	Generates a random sample from a given 1-D array
random.exponential([scale, size])	Draw samples from an exponential distribution.
random.f(dfnum, dfden[, size])	Draw samples from an F distribution.
random.gamma(shape[, scale, size])	Draw samples from a Gamma distribution.
random.geometric(p[, size])	Draw samples from the geometric distribution.
random.gumbel([loc, scale, size])	Draw samples from a Gumbel distribution.
random.hypergeometric(ngood, nbad, nsample)	Draw samples from a Hypergeometric distribution.
random.laplace([loc, scale, size])	Draw samples from the Laplace or double exponential distribution with specified location (or mean) and scale (decay).
random.logistic([loc, scale, size])	Draw samples from a logistic distribution.
random.lognormal([mean, sigma, size])	Draw samples from a log-normal distribution.
random.logseries(p[, size])	Draw samples from a logarithmic series distribution.
random.negative_binomial(n, p[, size])	Draw samples from a negative binomial distribution.
random.noncentral_chisquare(df, nonc[, size])	Draw samples from a noncentral chi-square distribution.
random.noncentral_f(dfnum, dfden, nonc[, size])	Draw samples from the noncentral F distribution.
random.normal([loc, scale, size])	Draw random samples from a normal (Gaussian) distribution.
random.pareto(a[, size])	Draw samples from a Pareto II or Lomax distribution with specified shape.
random.poisson([lam, size])	Draw samples from a Poisson distribution.
random.power(a[, size])	Draws samples in [0, 1] from a power distribution with positive exponent a - 1.
random.random([size])	Return random floats in the half-open interval [0.0, 1.0).
random.random_sample([size])	Return random floats in the half-open interval [0.0, 1.0).
random.rayleigh([scale, size])	Draw samples from a Rayleigh distribution.
random.standard_cauchy([size])	Draw samples from a standard Cauchy distribution with mode = 0.
random.standard_exponential([size])	Draw samples from the standard exponential distribution.
random.standard_gamma(shape[, size])	Draw samples from a standard Gamma distribution.
random.standard_normal([size])	Draw samples from a standard Normal distribution (mean=0, stdev=1).
random.standard_t(df[, size])	Draw samples from a standard Student's t distribution with *df* degrees of freedom.
random.triangular(left, mode, right[, size])	Draw samples from the triangular distribution.
random.uniform([low, high, size])	Draw samples from a uniform distribution.
random.vonmises(mu, kappa[, size])	Draw samples from a von Mises distribution.
random.wald(mean, scale[, size])	Draw samples from a Wald, or inverse Gaussian, distribution.
random.weibull(a[, size])	Draw samples from a Weibull distribution.
random.zipf(a[, size])	Standard distributions

Stats

stats.ttest_ind(a, b[, axis, equal_var])	Calculates the T-test for the means of TWO INDEPENDENT samples of scores.
stats.ttest_1samp(a, popmean[, axis, nan_policy])	Calculates the T-test for the mean of ONE group of scores.
stats.ttest_rel(a, b[, axis, nan_policy])	Calculates the T-test on TWO RELATED samples of scores, a and b.
stats.chisquare(f_obs[, f_exp, ddof, axis])	Calculates a one-way chi square test.
stats.power_divergence(f_obs[, f_exp, ddof, ...])	Cressie-Read power divergence statistic and goodness of fit test.
stats.skew(a[, axis, bias, nan_policy])	Computes the skewness of a data set.
stats.skewtest(a[, axis, nan_policy])	Tests whether the skew is different from the normal distribution.
stats.kurtosis(a[, axis, fisher, bias, ...])	Computes the kurtosis (Fisher or Pearson) of a dataset.
stats.kurtosistest(a[, axis, nan_policy])	Tests whether a dataset has normal kurtosis
stats.normaltest(a[, axis, nan_policy])	Tests whether a sample differs from a normal distribution.
stats.f_oneway(*args)	Performs a 1-way ANOVA.
stats.moment(a[, moment, axis, nan_policy])	Calculates the nth moment about the mean for a sample.

Image Support

image.imread(filename[, imread, preprocess])	Read a stack of images into a dask array

Slightly Overlapping Computations

overlap.overlap(x, depth, boundary)	Share boundaries between neighboring blocks
overlap.map_overlap(x, func, depth[, ...])	Map a function over blocks of the array with some overlap
overlap.trim_internal(x, axes[, boundary])	Trim sides from each block
overlap.trim_overlap(x, depth[, boundary])	Trim sides from each block.

Create and Store Arrays

from_array(x, chunks[, name, lock, asarray, ...])	Create dask array from something that looks like an array
from_delayed(value, shape, dtype[, name])	Create a dask array from a dask delayed value
from_npy_stack(dirname[, mmap_mode])	Load dask array from stack of npy files
from_zarr(url[, component, storage_options, ...])	Load array from the zarr storage format
store(sources, targets[, lock, regions, ...])	Store dask arrays in array-like objects, overwrite data in target
to_hdf5(filename, *args, **kwargs)	Store arrays in HDF5 file
to_zarr(arr, url[, component, ...])	Save array to the zarr storage format
to_npy_stack(dirname, x[, axis])	Write dask array to a stack of .npy files

Generalized Ufuncs

apply_gufunc(func, signature, *args, **kwargs)	Apply a generalized ufunc or similar python function to arrays.
as_gufunc([signature])	Decorator for `dask.array.gufunc`.
gufunc(pyfunc, **kwargs)	Binds *pyfunc* into `dask.array.apply_gufunc` when called.

Internal functions

atop(func, out_ind, *args, **kwargs)	Tensor operation: Generalized inner and outer products
normalize_chunks(chunks[, shape, limit, ...])	Normalize chunks to tuple of tuples
top(func, output, out_indices, ...)	Tensor operation

Other functions

`dask.array.`**`from_array`**(*x*, *chunks*, *name=None*, *lock=False*, *asarray=True*, *fancy=True*, *getitem=None*)

Create dask array from something that looks like an array

Input must have a `.shape` and support numpy-style slicing.

Parameters

x [array_like]

chunks [int, tuple] How to chunk the array. Must be one of the following forms: - A blocksize like 1000. - A blockshape like (1000, 1000). - Explicit sizes of all blocks along all dimensions like

((1000, 1000, 500), (400, 400)).

-1 as a blocksize indicates the size of the corresponding dimension.

name [str, optional] The key name to use for the array. Defaults to a hash of `x`. By default, hash uses python's standard sha1. This behaviour can be changed by installing cityhash, xxhash or murmurhash. If installed, a large-factor speedup can be obtained in the tokenisation step. Use `name=False` to generate a random name instead of hashing (fast)

lock [bool or Lock, optional] If `x` doesn't support concurrent reads then provide a lock here, or pass in True to have dask.array create one for you.

asarray [bool, optional] If True (default), then chunks will be converted to instances of `ndarray`. Set to False to pass passed chunks through unchanged.

fancy [bool, optional] If `x` doesn't support fancy indexing (e.g. indexing with lists or arrays) then set to False. Default is True.

Examples

```
>>> x = h5py.File('...')['/data/path']
>>> a = da.from_array(x, chunks=(1000, 1000))
```

If your underlying datastore does not support concurrent reads then include the `lock=True` keyword argument or `lock=mylock` if you want multiple arrays to coordinate around the same lock.

```
>>> a = da.from_array(x, chunks=(1000, 1000), lock=True)
```

dask.array.**from_delayed**(*value*, *shape*, *dtype*, *name=None*)
Create a dask array from a dask delayed value

This routine is useful for constructing dask arrays in an ad-hoc fashion using dask delayed, particularly when combined with stack and concatenate.

The dask array will consist of a single chunk.

Examples

```
>>> from dask import delayed
>>> value = delayed(np.ones)(5)
>>> array = from_delayed(value, (5,), float)
>>> array
dask.array<from-value, shape=(5,), dtype=float64, chunksize=(5,)>
>>> array.compute()
array([1., 1., 1., 1., 1.])
```

dask.array.**store**(*sources*, *targets*, *lock=True*, *regions=None*, *compute=True*, *return_stored=False*, ***kwargs*)
Store dask arrays in array-like objects, overwrite data in target

This stores dask arrays into object that supports numpy-style setitem indexing. It stores values chunk by chunk so that it does not have to fill up memory. For best performance you can align the block size of the storage target with the block size of your array.

If your data fits in memory then you may prefer calling `np.array(myarray)` instead.

Parameters

sources: Array or iterable of Arrays

targets: array-like or Delayed or iterable of array-likes and/or Delayeds These should support setitem syntax `target[10:20] = ...`

lock: boolean or threading.Lock, optional Whether or not to lock the data stores while storing. Pass True (lock each file individually), False (don't lock) or a particular `threading.Lock` object to be shared among all writes.

regions: tuple of slices or iterable of tuple of slices Each `region` tuple in `regions` should be such that `target[region].shape = source.shape` for the corresponding source and target in sources and targets, respectively.

compute: boolean, optional If true compute immediately, return `dask.delayed.Delayed` otherwise

return_stored: boolean, optional Optionally return the stored result (default False).

Examples

```
>>> x = ...
```

```
>>> import h5py
>>> f = h5py.File('myfile.hdf5')
>>> dset = f.create_dataset('/data', shape=x.shape,
...                                  chunks=x.chunks,
...                                  dtype='f8')
```

```
>>> store(x, dset)
```

Alternatively store many arrays at the same time

```
>>> store([x, y, z], [dset1, dset2, dset3])
```

dask.array.**coarsen**(*reduction*, *x*, *axes*, *trim_excess=False*)

Coarsen array by applying reduction to fixed size neighborhoods

Parameters

reduction: function Function like np.sum, np.mean, etc...

x: np.ndarray Array to be coarsened

axes: dict Mapping of axis to coarsening factor

Examples

```
>>> x = np.array([1, 2, 3, 4, 5, 6])
>>> coarsen(np.sum, x, {0: 2})
array([ 3,  7, 11])
>>> coarsen(np.max, x, {0: 3})
array([3, 6])
```

Provide dictionary of scale per dimension

```
>>> x = np.arange(24).reshape((4, 6))
>>> x
array([[ 0,  1,  2,  3,  4,  5],
       [ 6,  7,  8,  9, 10, 11],
       [12, 13, 14, 15, 16, 17],
       [18, 19, 20, 21, 22, 23]])
```

```
>>> coarsen(np.min, x, {0: 2, 1: 3})
array([[ 0,  3],
       [12, 15]])
```

You must avoid excess elements explicitly

```
>>> x = np.array([1, 2, 3, 4, 5, 6, 7, 8])
>>> coarsen(np.min, x, {0: 3}, trim_excess=True)
array([1, 4])
```

dask.array.**stack**(*seq*, *axis=0*)

Stack arrays along a new axis

Given a sequence of dask arrays, form a new dask array by stacking them along a new dimension (axis=0 by default)

See also:

concatenate

Examples

Create slices

```
>>> import dask.array as da
>>> import numpy as np
```

```
>>> data = [from_array(np.ones((4, 4)), chunks=(2, 2))
...          for i in range(3)]
```

```
>>> x = da.stack(data, axis=0)
>>> x.shape
(3, 4, 4)
```

```
>>> da.stack(data, axis=1).shape
(4, 3, 4)
```

```
>>> da.stack(data, axis=-1).shape
(4, 4, 3)
```

Result is a new dask Array

dask.array.**concatenate**(*seq*, *axis=0*, *allow_unknown_chunksizes=False*)

Concatenate arrays along an existing axis

Given a sequence of dask Arrays form a new dask Array by stacking them along an existing dimension (axis=0 by default)

Parameters

seq: list of dask.arrays

axis: int Dimension along which to align all of the arrays

allow_unknown_chunksizes: bool Allow unknown chunksizes, such as come from converting from dask dataframes. Dask.array is unable to verify that chunks line up. If data comes from differently aligned sources then this can cause unexpected results.

See also:

stack

Examples

Create slices

```
>>> import dask.array as da
>>> import numpy as np
```

```
>>> data = [from_array(np.ones((4, 4)), chunks=(2, 2))
...          for i in range(3)]
```

```
>>> x = da.concatenate(data, axis=0)
>>> x.shape
(12, 4)
```

```
>>> da.concatenate(data, axis=1).shape
(4, 12)
```

Result is a new dask Array

dask.array.**all**(*a*, *axis=None*, *out=None*, *keepdims=False*)

Test whether all array elements along a given axis evaluate to True.

Parameters

a [array_like] Input array or object that can be converted to an array.

axis [None or int or tuple of ints, optional] Axis or axes along which a logical AND reduction is performed. The default (*axis = None*) is to perform a logical AND over all the dimensions of the input array. *axis* may be negative, in which case it counts from the last to the first axis.

New in version 1.7.0.

If this is a tuple of ints, a reduction is performed on multiple axes, instead of a single axis or all the axes as before.

out [ndarray, optional] Alternate output array in which to place the result. It must have the same shape as the expected output and its type is preserved (e.g., if `dtype(out)` is float, the result will consist of 0.0's and 1.0's). See *doc.ufuncs* (Section "Output arguments") for more details.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

Returns

all [ndarray, bool] A new boolean or array is returned unless *out* is specified, in which case a reference to *out* is returned.

See also:

ndarray.all equivalent method

any Test whether any element along a given axis evaluates to True.

Notes

Not a Number (NaN), positive infinity and negative infinity evaluate to *True* because these are not equal to zero.

Examples

```
>>> np.all([[True,False],[True,True]])
False
```

```
>>> np.all([[True,False],[True,True]], axis=0)
array([ True, False], dtype=bool)
```

```
>>> np.all([-1, 4, 5])
True
```

```
>>> np.all([1.0, np.nan])
True
```

```
>>> o=np.array([False])
>>> z=np.all([-1, 4, 5], out=o)
>>> id(z), id(o), z
(28293632, 28293632, array([ True], dtype=bool))
```

dask.array.**allclose**(*a*, *b*, *rtol=1e-05*, *atol=1e-08*, *equal_nan=False*)

Returns True if two arrays are element-wise equal within a tolerance.

The tolerance values are positive, typically very small numbers. The relative difference (*rtol* * abs(*b*)) and the absolute difference *atol* are added together to compare against the absolute difference between *a* and *b*.

If either array contains one or more NaNs, False is returned. Infs are treated as equal if they are in the same place and of the same sign in both arrays.

Parameters

a, b [array_like] Input arrays to compare.

rtol [float] The relative tolerance parameter (see Notes).

atol [float] The absolute tolerance parameter (see Notes).

equal_nan [bool] Whether to compare NaN's as equal. If True, NaN's in *a* will be considered equal to NaN's in *b* in the output array.

New in version 1.10.0.

Returns

allclose [bool] Returns True if the two arrays are equal within the given tolerance; False otherwise.

See also:

isclose, *all*, *any*

Notes

If the following equation is element-wise True, then allclose returns True.

absolute(*a* - *b*) <= (*atol* + *rtol* * absolute(*b*))

The above equation is not symmetric in *a* and *b*, so that *allclose(a, b)* might be different from *allclose(b, a)* in some rare cases.

Examples

```
>>> np.allclose([1e10,1e-7], [1.00001e10,1e-8])
False
>>> np.allclose([1e10,1e-8], [1.00001e10,1e-9])
True
>>> np.allclose([1e10,1e-8], [1.0001e10,1e-9])
False
>>> np.allclose([1.0, np.nan], [1.0, np.nan])
False
>>> np.allclose([1.0, np.nan], [1.0, np.nan], equal_nan=True)
True
```

dask.array.**angle**(*x*, *deg=0*)

Return the angle of the complex argument.

Parameters

z [array_like] A complex number or sequence of complex numbers.

deg [bool, optional] Return angle in degrees if True, radians if False (default).

Returns

angle [ndarray or scalar] The counterclockwise angle from the positive real axis on the complex plane, with dtype as numpy.float64.

See also:

arctan2, absolute

Examples

```
>>> np.angle([1.0, 1.0j, 1+1j])               # in radians
array([ 0.        ,  1.57079633,  0.78539816])
>>> np.angle(1+1j, deg=True)                  # in degrees
45.0
```

dask.array.**any**(*a*, *axis=None*, *out=None*, *keepdims=False*)

Test whether any array element along a given axis evaluates to True.

Returns single boolean unless *axis* is not None

Parameters

a [array_like] Input array or object that can be converted to an array.

axis [None or int or tuple of ints, optional] Axis or axes along which a logical OR reduction is performed. The default (*axis = None*) is to perform a logical OR over all the dimensions of the input array. *axis* may be negative, in which case it counts from the last to the first axis.

New in version 1.7.0.

If this is a tuple of ints, a reduction is performed on multiple axes, instead of a single axis or all the axes as before.

out [ndarray, optional] Alternate output array in which to place the result. It must have the same shape as the expected output and its type is preserved (e.g., if it is of type float, then it will remain so, returning 1.0 for True and 0.0 for False, regardless of the type of *a*). See *doc.ufuncs* (Section "Output arguments") for details.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

Returns

any [bool or ndarray] A new boolean or *ndarray* is returned unless *out* is specified, in which case a reference to *out* is returned.

See also:

ndarray.any equivalent method

all Test whether all elements along a given axis evaluate to True.

Notes

Not a Number (NaN), positive infinity and negative infinity evaluate to *True* because these are not equal to zero.

Examples

```
>>> np.any([[True, False], [True, True]])
True
```

```
>>> np.any([[True, False], [False, False]], axis=0)
array([ True, False], dtype=bool)
```

```
>>> np.any([-1, 0, 5])
True
```

```
>>> np.any(np.nan)
True
```

```
>>> o=np.array([False])
>>> z=np.any([-1, 4, 5], out=o)
>>> z, o
(array([ True], dtype=bool), array([ True], dtype=bool))
>>> # Check now that z is a reference to o
>>> z is o
True
>>> id(z), id(o) # identity of z and o
(191614240, 191614240)
```

dask.array.**apply_along_axis**(*func1d*, *axis*, *arr*, **args*, ***kwargs*)

Apply a function to 1-D slices along the given axis.

Execute *func1d(a, *args)* where *func1d* operates on 1-D arrays and *a* is a 1-D slice of *arr* along *axis*.

Parameters

func1d [function] This function should accept 1-D arrays. It is applied to 1-D slices of *arr* along the specified axis.

axis [integer] Axis along which *arr* is sliced.

arr [ndarray] Input array.

args [any] Additional arguments to *func1d*.

kwargs: any Additional named arguments to *func1d*.

New in version 1.9.0.

Returns

apply_along_axis [ndarray] The output array. The shape of *outarr* is identical to the shape of *arr*, except along the *axis* dimension, where the length of *outarr* is equal to the size of the return value of *func1d*. If *func1d* returns a scalar *outarr* will have one fewer dimensions than *arr*.

See also:

apply_over_axes Apply a function repeatedly over multiple axes.

Examples

```
>>> def my_func(a):
...     """Average first and last element of a 1-D array"""
...     return (a[0] + a[-1]) * 0.5
>>> b = np.array([[1,2,3], [4,5,6], [7,8,9]])
>>> np.apply_along_axis(my_func, 0, b)
array([ 4.,  5.,  6.])
>>> np.apply_along_axis(my_func, 1, b)
array([ 2.,  5.,  8.])
```

For a function that doesn't return a scalar, the number of dimensions in *outarr* is the same as *arr*.

```
>>> b = np.array([[8,1,7], [4,3,9], [5,2,6]])
>>> np.apply_along_axis(sorted, 1, b)
array([[1, 7, 8],
       [3, 4, 9],
       [2, 5, 6]])
```

dask.array.**apply_over_axes**(*func*, *a*, *axes*)

Apply a function repeatedly over multiple axes.

func is called as *res = func(a, axis)*, where *axis* is the first element of *axes*. The result *res* of the function call must have either the same dimensions as *a* or one less dimension. If *res* has one less dimension than *a*, a dimension is inserted before *axis*. The call to *func* is then repeated for each axis in *axes*, with *res* as the first argument.

Parameters

func [function] This function must take two arguments, *func(a, axis)*.

a [array_like] Input array.

axes [array_like] Axes over which *func* is applied; the elements must be integers.

Returns

apply_over_axis [ndarray] The output array. The number of dimensions is the same as *a*, but the shape can be different. This depends on whether *func* changes the shape of its output with respect to its input.

See also:

apply_along_axis Apply a function to 1-D slices of an array along the given axis.

Notes

This function is equivalent to tuple axis arguments to reorderable ufuncs with keepdims=True. Tuple axis arguments to ufuncs have been availabe since version 1.7.0.

Examples

```
>>> a = np.arange(24).reshape(2,3,4)
>>> a
array([[[ 0,  1,  2,  3],
        [ 4,  5,  6,  7],
        [ 8,  9, 10, 11]],
```

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```
       [[12, 13, 14, 15],
        [16, 17, 18, 19],
        [20, 21, 22, 23]]])
```

Sum over axes 0 and 2. The result has same number of dimensions as the original array:

```
>>> np.apply_over_axes(np.sum, a, [0,2])
array([[[ 60],
        [ 92],
        [124]]])
```

Tuple axis arguments to ufuncs are equivalent:

```
>>> np.sum(a, axis=(0,2), keepdims=True)
array([[[ 60],
        [ 92],
        [124]]])
```

dask.array.**arange**(**args*, ***kwargs*)

Return evenly spaced values from *start* to *stop* with step size *step*.

The values are half-open [start, stop), so including start and excluding stop. This is basically the same as python's range function but for dask arrays.

When using a non-integer step, such as 0.1, the results will often not be consistent. It is better to use linspace for these cases.

Parameters

start [int, optional] The starting value of the sequence. The default is 0.

stop [int] The end of the interval, this value is excluded from the interval.

step [int, optional] The spacing between the values. The default is 1 when not specified. The last value of the sequence.

chunks [int] The number of samples on each block. Note that the last block will have fewer samples if `len(array) % chunks != 0`.

dtype [numpy.dtype] Output dtype. Omit to infer it from start, stop, step

Returns

samples [dask array]

See also:

dask.array.linspace

dask.array.**arccos**(*x*[, *out*])

Trigonometric inverse cosine, element-wise.

The inverse of *cos* so that, if `y = cos(x)`, then `x = arccos(y)`.

Parameters

x [array_like] *x*-coordinate on the unit circle. For real arguments, the domain is [-1, 1].

out [ndarray, optional] Array of the same shape as *a*, to store results in. See *doc.ufuncs* (Section "Output arguments") for more details.

Returns

angle [ndarray] The angle of the ray intersecting the unit circle at the given *x*-coordinate in radians [0, pi]. If *x* is a scalar then a scalar is returned, otherwise an array of the same shape as *x* is returned.

See also:

cos, *arctan*, *arcsin*, emath.arccos

Notes

arccos is a multivalued function: for each *x* there are infinitely many numbers *z* such that *cos(z) = x*. The convention is to return the angle *z* whose real part lies in *[0, pi]*.

For real-valued input data types, *arccos* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields nan and sets the *invalid* floating point error flag.

For complex-valued input, *arccos* is a complex analytic function that has branch cuts *[-inf, -1]* and *[1, inf]* and is continuous from above on the former and from below on the latter.

The inverse *cos* is also known as *acos* or cos^-1.

References

M. Abramowitz and I.A. Stegun, "Handbook of Mathematical Functions", 10th printing, 1964, pp. 79. http://www.math.sfu.ca/~cbm/aands/

Examples

We expect the arccos of 1 to be 0, and of -1 to be pi:

```
>>> np.arccos([1, -1])
array([ 0.        ,  3.14159265])
```

Plot arccos:

```
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-1, 1, num=100)
>>> plt.plot(x, np.arccos(x))
>>> plt.axis('tight')
>>> plt.show()
```

dask.array.**arccosh**(*x*[, *out*])

Inverse hyperbolic cosine, element-wise.

Parameters

x [array_like] Input array.

out [ndarray, optional] Array of the same shape as *x*, to store results in. See *doc.ufuncs* (Section "Output arguments") for details.

Returns

arccosh [ndarray] Array of the same shape as *x*.

See also:

cosh, *arcsinh*, *sinh*, *arctanh*, *tanh*

Notes

arccosh is a multivalued function: for each *x* there are infinitely many numbers *z* such that *cosh(z) = x*. The convention is to return the *z* whose imaginary part lies in *[-pi, pi]* and the real part in `[0, inf]`.

For real-valued input data types, *arccosh* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *arccosh* is a complex analytical function that has a branch cut *[-inf, 1]* and is continuous from above on it.

References

[1], *[2]*

Examples

```
>>> np.arccosh([np.e, 10.0])
array([ 1.65745445,  2.99322285])
>>> np.arccosh(1)
0.0
```

dask.array.**arcsin**(*x*[, *out*])

Inverse sine, element-wise.

Parameters

x [array_like] *y*-coordinate on the unit circle.

out [ndarray, optional] Array of the same shape as *x*, in which to store the results. See *doc.ufuncs* (Section "Output arguments") for more details.

Returns

angle [ndarray] The inverse sine of each element in *x*, in radians and in the closed interval `[-pi/2, pi/2]`. If *x* is a scalar, a scalar is returned, otherwise an array.

See also:

sin, *cos*, *arccos*, *tan*, *arctan*, *arctan2*, `emath.arcsin`

Notes

arcsin is a multivalued function: for each *x* there are infinitely many numbers *z* such that $sin(z) = x$. The convention is to return the angle *z* whose real part lies in [-pi/2, pi/2].

For real-valued input data types, *arcsin* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *arcsin* is a complex analytic function that has, by convention, the branch cuts [-inf, -1] and [1, inf] and is continuous from above on the former and from below on the latter.

The inverse sine is also known as *asin* or sin^{-1}.

References

Abramowitz, M. and Stegun, I. A., *Handbook of Mathematical Functions*, 10th printing, New York: Dover, 1964, pp. 79ff. http://www.math.sfu.ca/~cbm/aands/

Examples

```
>>> np.arcsin(1)     # pi/2
1.5707963267948966
>>> np.arcsin(-1)    # -pi/2
-1.5707963267948966
>>> np.arcsin(0)
0.0
```

dask.array.**arcsinh**(*x*[, *out*])

Inverse hyperbolic sine element-wise.

Parameters

x [array_like] Input array.

out [ndarray, optional] Array into which the output is placed. Its type is preserved and it must be of the right shape to hold the output. See *doc.ufuncs*.

Returns

out [ndarray] Array of of the same shape as *x*.

Notes

arcsinh is a multivalued function: for each *x* there are infinitely many numbers *z* such that *sinh(z) = x*. The convention is to return the *z* whose imaginary part lies in *[-pi/2, pi/2]*.

For real-valued input data types, *arcsinh* always returns real output. For each value that cannot be expressed as a real number or infinity, it returns `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *arccos* is a complex analytical function that has branch cuts *[1j, infj]* and *[-1j, -infj]* and is continuous from the right on the former and from the left on the latter.

The inverse hyperbolic sine is also known as *asinh* or `sinh^-1`.

References

[1], *[2]*

Examples

```
>>> np.arcsinh(np.array([np.e, 10.0]))
array([ 1.72538256,  2.99822295])
```

dask.array.**arctan**(*x*[, *out*])

Trigonometric inverse tangent, element-wise.

The inverse of tan, so that if `y = tan(x)` then `x = arctan(y)`.

Parameters

x [array_like] Input values. *arctan* is applied to each element of *x*.

Returns

out [ndarray] Out has the same shape as *x*. Its real part is in `[-pi/2, pi/2]` (`arctan(+/-inf)` returns `+/-pi/2`). It is a scalar if *x* is a scalar.

See also:

arctan2 The "four quadrant" arctan of the angle formed by (*x*, *y*) and the positive *x*-axis.

angle Argument of complex values.

Notes

arctan is a multi-valued function: for each *x* there are infinitely many numbers *z* such that tan(*z*) = *x*. The convention is to return the angle *z* whose real part lies in [-pi/2, pi/2].

For real-valued input data types, *arctan* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *arctan* is a complex analytic function that has [*1j, infj*] and [*-1j, -infj*] as branch cuts, and is continuous from the left on the former and from the right on the latter.

The inverse tangent is also known as *atan* or tan^{-1}.

References

Abramowitz, M. and Stegun, I. A., *Handbook of Mathematical Functions*, 10th printing, New York: Dover, 1964, pp. 79. http://www.math.sfu.ca/~cbm/aands/

Examples

We expect the arctan of 0 to be 0, and of 1 to be pi/4:

```
>>> np.arctan([0, 1])
array([ 0.        ,  0.78539816])
```

```
>>> np.pi/4
0.7853981633974483
```

Plot arctan:

```
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-10, 10)
>>> plt.plot(x, np.arctan(x))
>>> plt.axis('tight')
>>> plt.show()
```

`dask.array.`**arctan2**(*x1*, *x2*[, *out*])

Element-wise arc tangent of `x1/x2` choosing the quadrant correctly.

The quadrant (i.e., branch) is chosen so that `arctan2(x1, x2)` is the signed angle in radians between the ray ending at the origin and passing through the point (1,0), and the ray ending at the origin and passing through

the point (*x2*, *x1*). (Note the role reversal: the "*y*-coordinate" is the first function parameter, the "*x*-coordinate" is the second.) By IEEE convention, this function is defined for *x2* = +/-0 and for either or both of *x1* and *x2* = +/-inf (see Notes for specific values).

This function is not defined for complex-valued arguments; for the so-called argument of complex values, use *angle*.

Parameters

x1 [array_like, real-valued] *y*-coordinates.

x2 [array_like, real-valued] *x*-coordinates. *x2* must be broadcastable to match the shape of *x1* or vice versa.

Returns

angle [ndarray] Array of angles in radians, in the range `[-pi, pi]`.

See also:

arctan, *tan*, *angle*

Notes

arctan2 is identical to the *atan2* function of the underlying C library. The following special values are defined in the C standard: *[1]*

x1	*x2*	*arctan2(x1,x2)*
+/- 0	+0	+/- 0
+/- 0	-0	+/- pi
> 0	+/-inf	+0 / +pi
< 0	+/-inf	-0 / -pi
+/-inf	+inf	+/- (pi/4)
+/-inf	-inf	+/- (3*pi/4)

Note that +0 and -0 are distinct floating point numbers, as are +inf and -inf.

References

[1]

Examples

Consider four points in different quadrants:

```
>>> x = np.array([-1, +1, +1, -1])
>>> y = np.array([-1, -1, +1, +1])
>>> np.arctan2(y, x) * 180 / np.pi
array([-135.,  -45.,   45.,  135.])
```

Note the order of the parameters. *arctan2* is defined also when *x2* = 0 and at several other special points, obtaining values in the range `[-pi, pi]`:

```
>>> np.arctan2([1., -1.], [0., 0.])
array([ 1.57079633, -1.57079633])
>>> np.arctan2([0., 0., np.inf], [+0., -0., np.inf])
array([ 0.        ,  3.14159265,  0.78539816])
```

dask.array.**arctanh**(*x*[, *out*])

Inverse hyperbolic tangent element-wise.

Parameters

x [array_like] Input array.

Returns

out [ndarray] Array of the same shape as *x*.

See also:

`emath.arctanh`

Notes

arctanh is a multivalued function: for each *x* there are infinitely many numbers *z* such that *tanh(z) = x*. The convention is to return the *z* whose imaginary part lies in *[-pi/2, pi/2]*.

For real-valued input data types, *arctanh* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *arctanh* is a complex analytical function that has branch cuts *[-1, -inf]* and *[1, inf]* and is continuous from above on the former and from below on the latter.

The inverse hyperbolic tangent is also known as *atanh* or `tanh^-1`.

References

[1], *[2]*

Examples

```
>>> np.arctanh([0, -0.5])
array([ 0.        , -0.54930614])
```

dask.array.**argmax**(*a*, *axis=None*, *out=None*)

Returns the indices of the maximum values along an axis.

Parameters

a [array_like] Input array.

axis [int, optional] By default, the index is into the flattened array, otherwise along the specified axis.

out [array, optional] If provided, the result will be inserted into this array. It should be of the appropriate shape and dtype.

Returns

index_array [ndarray of ints] Array of indices into the array. It has the same shape as *a.shape* with the dimension along *axis* removed.

See also:

`ndarray.argmax`, *argmin*

amax The maximum value along a given axis.

unravel_index Convert a flat index into an index tuple.

Notes

In case of multiple occurrences of the maximum values, the indices corresponding to the first occurrence are returned.

Examples

```
>>> a = np.arange(6).reshape(2,3)
>>> a
array([[0, 1, 2],
       [3, 4, 5]])
>>> np.argmax(a)
5
>>> np.argmax(a, axis=0)
array([1, 1, 1])
>>> np.argmax(a, axis=1)
array([2, 2])
```

```
>>> b = np.arange(6)
>>> b[1] = 5
>>> b
array([0, 5, 2, 3, 4, 5])
>>> np.argmax(b) # Only the first occurrence is returned.
1
```

`dask.array.`**`argmin`**(*a*, *axis=None*, *out=None*)

Returns the indices of the minimum values along an axis.

Parameters

a [array_like] Input array.

axis [int, optional] By default, the index is into the flattened array, otherwise along the specified axis.

out [array, optional] If provided, the result will be inserted into this array. It should be of the appropriate shape and dtype.

Returns

index_array [ndarray of ints] Array of indices into the array. It has the same shape as *a.shape* with the dimension along *axis* removed.

See also:

`ndarray.argmin`, *argmax*

amin The minimum value along a given axis.

unravel_index Convert a flat index into an index tuple.

Notes

In case of multiple occurrences of the minimum values, the indices corresponding to the first occurrence are returned.

Examples

```
>>> a = np.arange(6).reshape(2,3)
>>> a
array([[0, 1, 2],
       [3, 4, 5]])
>>> np.argmin(a)
0
>>> np.argmin(a, axis=0)
array([0, 0, 0])
>>> np.argmin(a, axis=1)
array([0, 0])
```

```
>>> b = np.arange(6)
>>> b[4] = 0
>>> b
array([0, 1, 2, 3, 0, 5])
>>> np.argmin(b) # Only the first occurrence is returned.
0
```

dask.array.**argtopk**(*a*, *k*, *axis=-1*, *split_every=None*)

Extract the indices of the k largest elements from a on the given axis, and return them sorted from largest to smallest. If k is negative, extract the indices of the -k smallest elements instead, and return them sorted from smallest to largest.

This performs best when `k` is much smaller than the chunk size. All results will be returned in a single chunk along the given axis.

Parameters

x: Array Data being sorted

k: int

axis: int, optional

split_every: int >=2, optional See *topk()*. The performance considerations for topk also apply here.

Returns

Selection of np.intp indices of x with size abs(k) along the given axis.

Examples

```
>>> import dask.array as da
>>> x = np.array([5, 1, 3, 6])
>>> d = da.from_array(x, chunks=2)
```

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```
>>> d.argtopk(2).compute()
array([3, 0])
>>> d.argtopk(-2).compute()
array([1, 2])
```

dask.array.**argwhere**(*a*)

Find the indices of array elements that are non-zero, grouped by element.

Parameters

a [array_like] Input data.

Returns

index_array [ndarray] Indices of elements that are non-zero. Indices are grouped by element.

See also:

where, *nonzero*

Notes

`np.argwhere(a)` is the same as `np.transpose(np.nonzero(a))`.

The output of `argwhere` is not suitable for indexing arrays. For this purpose use `where(a)` instead.

Examples

```
>>> x = np.arange(6).reshape(2,3)
>>> x
array([[0, 1, 2],
       [3, 4, 5]])
>>> np.argwhere(x>1)
array([[0, 2],
       [1, 0],
       [1, 1],
       [1, 2]])
```

dask.array.**around**(*a*, *decimals=0*, *out=None*)

Evenly round to the given number of decimals.

Parameters

a [array_like] Input data.

decimals [int, optional] Number of decimal places to round to (default: 0). If decimals is negative, it specifies the number of positions to the left of the decimal point.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary. See *doc.ufuncs* (Section "Output arguments") for details.

Returns

rounded_array [ndarray] An array of the same type as *a*, containing the rounded values. Unless *out* was specified, a new array is created. A reference to the result is returned.

The real and imaginary parts of complex numbers are rounded separately. The result of rounding a float is a float.

See also:

ndarray.round equivalent method

ceil, *fix*, *floor*, *rint*, *trunc*

Notes

For values exactly halfway between rounded decimal values, Numpy rounds to the nearest even value. Thus 1.5 and 2.5 round to 2.0, -0.5 and 0.5 round to 0.0, etc. Results may also be surprising due to the inexact representation of decimal fractions in the IEEE floating point standard *[1]* and errors introduced when scaling by powers of ten.

References

[1], *[2]*

Examples

```
>>> np.around([0.37, 1.64])
array([ 0.,  2.])
>>> np.around([0.37, 1.64], decimals=1)
array([ 0.4,  1.6])
>>> np.around([.5, 1.5, 2.5, 3.5, 4.5]) # rounds to nearest even value
array([ 0.,  2.,  2.,  4.,  4.])
>>> np.around([1,2,3,11], decimals=1) # ndarray of ints is returned
array([ 1,  2,  3, 11])
>>> np.around([1,2,3,11], decimals=-1)
array([ 0,  0,  0, 10])
```

dask.array.**array**(*object*, *dtype=None*, *copy=True*, *order=None*, *subok=False*, *ndmin=0*)

Create an array.

Parameters

object [array_like] An array, any object exposing the array interface, an object whose __array__ method returns an array, or any (nested) sequence.

dtype [data-type, optional] The desired data-type for the array. If not given, then the type will be determined as the minimum type required to hold the objects in the sequence. This argument can only be used to 'upcast' the array. For downcasting, use the .astype(t) method.

copy [bool, optional] If true (default), then the object is copied. Otherwise, a copy will only be made if __array__ returns a copy, if obj is a nested sequence, or if a copy is needed to satisfy any of the other requirements (*dtype*, *order*, etc.).

order [{'C', 'F', 'A'}, optional] Specify the order of the array. If order is 'C', then the array will be in C-contiguous order (last-index varies the fastest). If order is 'F', then the returned array will be in Fortran-contiguous order (first-index varies the fastest). If order is 'A' (default), then the returned array may be in any order (either C-, Fortran-contiguous, or even discontiguous), unless a copy is required, in which case it will be C-contiguous.

subok [bool, optional] If True, then sub-classes will be passed-through, otherwise the returned array will be forced to be a base-class array (default).

ndmin [int, optional] Specifies the minimum number of dimensions that the resulting array should have. Ones will be pre-pended to the shape as needed to meet this requirement.

Returns

out [ndarray] An array object satisfying the specified requirements.

See also:

empty, *empty_like*, *zeros*, *zeros_like*, *ones*, *ones_like*, fill

Examples

```
>>> np.array([1, 2, 3])
array([1, 2, 3])
```

Upcasting:

```
>>> np.array([1, 2, 3.0])
array([ 1.,  2.,  3.])
```

More than one dimension:

```
>>> np.array([[1, 2], [3, 4]])
array([[1, 2],
       [3, 4]])
```

Minimum dimensions 2:

```
>>> np.array([1, 2, 3], ndmin=2)
array([[1, 2, 3]])
```

Type provided:

```
>>> np.array([1, 2, 3], dtype=complex)
array([ 1.+0.j,  2.+0.j,  3.+0.j])
```

Data-type consisting of more than one element:

```
>>> x = np.array([(1,2),(3,4)],dtype=[('a','<i4'),('b','<i4')])
>>> x['a']
array([1, 3])
```

Creating an array from sub-classes:

```
>>> np.array(np.mat('1 2; 3 4'))
array([[1, 2],
       [3, 4]])
```

```
>>> np.array(np.mat('1 2; 3 4'), subok=True)
matrix([[1, 2],
        [3, 4]])
```

dask.array.**asanyarray**(*a*)

Convert the input to a dask array.

Subclasses of np.ndarray will be passed through as chunks unchanged.

Parameters

a [array-like] Input data, in any form that can be converted to a dask array.

Returns

out [dask array] Dask array interpretation of a.

Examples

```
>>> import dask.array as da
>>> import numpy as np
>>> x = np.arange(3)
>>> da.asanyarray(x)
dask.array<array, shape=(3,), dtype=int64, chunksize=(3,)>
```

```
>>> y = [[1, 2, 3], [4, 5, 6]]
>>> da.asanyarray(y)
dask.array<array, shape=(2, 3), dtype=int64, chunksize=(2, 3)>
```

dask.array.**asarray**(*a*)

Convert the input to a dask array.

Parameters

a [array-like] Input data, in any form that can be converted to a dask array.

Returns

out [dask array] Dask array interpretation of a.

Examples

```
>>> import dask.array as da
>>> import numpy as np
>>> x = np.arange(3)
>>> da.asarray(x)
dask.array<array, shape=(3,), dtype=int64, chunksize=(3,)>
```

```
>>> y = [[1, 2, 3], [4, 5, 6]]
>>> da.asarray(y)
dask.array<array, shape=(2, 3), dtype=int64, chunksize=(2, 3)>
```

dask.array.**atleast_1d**(**arys*)

Convert inputs to arrays with at least one dimension.

Scalar inputs are converted to 1-dimensional arrays, whilst higher-dimensional inputs are preserved.

Parameters

arys1, arys2, ... [array_like] One or more input arrays.

Returns

ret [ndarray] An array, or sequence of arrays, each with `a.ndim >= 1`. Copies are made only if necessary.

See also:

atleast_2d, *atleast_3d*

Examples

```
>>> np.atleast_1d(1.0)
array([ 1.])
```

```
>>> x = np.arange(9.0).reshape(3,3)
>>> np.atleast_1d(x)
array([[ 0.,  1.,  2.],
       [ 3.,  4.,  5.],
       [ 6.,  7.,  8.]])
>>> np.atleast_1d(x) is x
True
```

```
>>> np.atleast_1d(1, [3, 4])
[array([1]), array([3, 4])]
```

dask.array.**atleast_2d**(**arys*)

View inputs as arrays with at least two dimensions.

Parameters

arys1, arys2, ... [array_like] One or more array-like sequences. Non-array inputs are converted to arrays. Arrays that already have two or more dimensions are preserved.

Returns

res, res2, ... [ndarray] An array, or tuple of arrays, each with `a.ndim >= 2`. Copies are avoided where possible, and views with two or more dimensions are returned.

See also:

atleast_1d, *atleast_3d*

Examples

```
>>> np.atleast_2d(3.0)
array([[ 3.]])
```

```
>>> x = np.arange(3.0)
>>> np.atleast_2d(x)
array([[ 0.,  1.,  2.]])
>>> np.atleast_2d(x).base is x
True
```

```
>>> np.atleast_2d(1, [1, 2], [[1, 2]])
[array([[1]]), array([[1, 2]]), array([[1, 2]])]
```

dask.array.**atleast_3d**(**arys*)

View inputs as arrays with at least three dimensions.

Parameters

arys1, arys2, ... [array_like] One or more array-like sequences. Non-array inputs are converted to arrays. Arrays that already have three or more dimensions are preserved.

Returns

res1, res2, ... [ndarray] An array, or tuple of arrays, each with `a.ndim >= 3`. Copies are avoided where possible, and views with three or more dimensions are returned. For example, a 1-D array of shape `(N,)` becomes a view of shape `(1, N, 1)`, and a 2-D array of shape `(M, N)` becomes a view of shape `(M, N, 1)`.

See also:

atleast_1d, *atleast_2d*

Examples

```
>>> np.atleast_3d(3.0)
array([[[ 3.]]])
```

```
>>> x = np.arange(3.0)
>>> np.atleast_3d(x).shape
(1, 3, 1)
```

```
>>> x = np.arange(12.0).reshape(4,3)
>>> np.atleast_3d(x).shape
(4, 3, 1)
>>> np.atleast_3d(x).base is x
True
```

```
>>> for arr in np.atleast_3d([1, 2], [[1, 2]], [[[1, 2]]]):
...     print(arr, arr.shape)
...
[[[1]
  [2]]] (1, 2, 1)
[[[1]
  [2]]] (1, 2, 1)
[[[1 2]]] (1, 1, 2)
```

`dask.array.`**`average`**(*a*, *axis=None*, *weights=None*, *returned=False*)

Compute the weighted average along the specified axis.

Parameters

a [array_like] Array containing data to be averaged. If *a* is not an array, a conversion is attempted.

axis [int, optional] Axis along which to average *a*. If *None*, averaging is done over the flattened array.

weights [array_like, optional] An array of weights associated with the values in *a*. Each value in *a* contributes to the average according to its associated weight. The weights array can either be 1-D (in which case its length must be the size of *a* along the given axis) or of the same shape as *a*. If *weights=None*, then all data in *a* are assumed to have a weight equal to one.

returned [bool, optional] Default is *False*. If *True*, the tuple (*average*, *sum_of_weights*) is returned, otherwise only the average is returned. If *weights=None*, *sum_of_weights* is equivalent to the number of elements over which the average is taken.

Returns

average, [sum_of_weights] [array_type or double] Return the average along the specified axis. When returned is *True*, return a tuple with the average as the first element and the sum of the weights as the second element. The return type is *Float* if *a* is of integer type, otherwise it is of the same type as *a*. *sum_of_weights* is of the same type as *average*.

Raises

ZeroDivisionError When all weights along axis are zero. See *numpy.ma.average* for a version robust to this type of error.

TypeError When the length of 1D *weights* is not the same as the shape of *a* along axis.

See also:

mean

ma.average average for masked arrays – useful if your data contains "missing" values

Examples

```
>>> data = range(1,5)
>>> data
[1, 2, 3, 4]
>>> np.average(data)
2.5
>>> np.average(range(1,11), weights=range(10,0,-1))
4.0
```

```
>>> data = np.arange(6).reshape((3,2))
>>> data
array([[0, 1],
       [2, 3],
       [4, 5]])
>>> np.average(data, axis=1, weights=[1./4, 3./4])
array([ 0.75,  2.75,  4.75])
>>> np.average(data, weights=[1./4, 3./4])
Traceback (most recent call last):
...
TypeError: Axis must be specified when shapes of a and weights differ.
```

dask.array.**bincount**(*x*, *weights=None*, *minlength=None*)

Count number of occurrences of each value in array of non-negative ints.

The number of bins (of size 1) is one larger than the largest value in *x*. If *minlength* is specified, there will be at least this number of bins in the output array (though it will be longer if necessary, depending on the contents of *x*). Each bin gives the number of occurrences of its index value in *x*. If *weights* is specified the input array is weighted by it, i.e. if a value `n` is found at position `i`, `out[n] += weight[i]` instead of `out[n] += 1`.

Parameters

x [array_like, 1 dimension, nonnegative ints] Input array.

weights [array_like, optional] Weights, array of the same shape as *x*.

minlength [int, optional] A minimum number of bins for the output array.

New in version 1.6.0.

Returns

out [ndarray of ints] The result of binning the input array. The length of *out* is equal to `np.amax(x)+1`.

Raises

ValueError If the input is not 1-dimensional, or contains elements with negative values, or if *minlength* is non-positive.

TypeError If the type of the input is float or complex.

See also:

histogram, *digitize*, *unique*

Examples

```
>>> np.bincount(np.arange(5))
array([1, 1, 1, 1, 1])
>>> np.bincount(np.array([0, 1, 1, 3, 2, 1, 7]))
array([1, 3, 1, 1, 0, 0, 0, 1])
```

```
>>> x = np.array([0, 1, 1, 3, 2, 1, 7, 23])
>>> np.bincount(x).size == np.amax(x)+1
True
```

The input array needs to be of integer dtype, otherwise a TypeError is raised:

```
>>> np.bincount(np.arange(5, dtype=np.float))
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
TypeError: array cannot be safely cast to required type
```

A possible use of `bincount` is to perform sums over variable-size chunks of an array, using the `weights` keyword.

```
>>> w = np.array([0.3, 0.5, 0.2, 0.7, 1., -0.6]) # weights
>>> x = np.array([0, 1, 1, 2, 2, 2])
>>> np.bincount(x,  weights=w)
array([ 0.3,  0.7,  1.1])
```

`dask.array.`**`bitwise_and`**(*x1*, *x2*[, *out*])

Compute the bit-wise AND of two arrays element-wise.

Computes the bit-wise AND of the underlying binary representation of the integers in the input arrays. This ufunc implements the C/Python operator `&`.

Parameters

x1, x2 [array_like] Only integer and boolean types are handled.

Returns

out [array_like] Result.

See also:

logical_and, *bitwise_or*, *bitwise_xor*

`binary_repr` Return the binary representation of the input number as a string.

Examples

The number 13 is represented by `00001101`. Likewise, 17 is represented by `00010001`. The bit-wise AND of 13 and 17 is therefore `000000001`, or 1:

```
>>> np.bitwise_and(13, 17)
1
```

```
>>> np.bitwise_and(14, 13)
12
>>> np.binary_repr(12)
'1100'
>>> np.bitwise_and([14,3], 13)
array([12,  1])
```

```
>>> np.bitwise_and([11,7], [4,25])
array([0, 1])
>>> np.bitwise_and(np.array([2,5,255]), np.array([3,14,16]))
array([ 2,  4, 16])
>>> np.bitwise_and([True, True], [False, True])
array([False,  True], dtype=bool)
```

`dask.array.`**`bitwise_not`**(*x*[, *out*])

Compute bit-wise inversion, or bit-wise NOT, element-wise.

Computes the bit-wise NOT of the underlying binary representation of the integers in the input arrays. This ufunc implements the C/Python operator ~.

For signed integer inputs, the two's complement is returned. In a two's-complement system negative numbers are represented by the two's complement of the absolute value. This is the most common method of representing signed integers on computers *[1]*. A N-bit two's-complement system can represent every integer in the range -2^{N-1} to $+2^{N-1}-1$.

Parameters

x1 [array_like] Only integer and boolean types are handled.

Returns

out [array_like] Result.

See also:

bitwise_and, *bitwise_or*, *bitwise_xor*, *logical_not*

`binary_repr` Return the binary representation of the input number as a string.

Notes

bitwise_not is an alias for *invert*:

```
>>> np.bitwise_not is np.invert
True
```

References

[1]

Examples

We've seen that 13 is represented by `00001101`. The invert or bit-wise NOT of 13 is then:

```
>>> np.invert(np.array([13], dtype=uint8))
array([242], dtype=uint8)
>>> np.binary_repr(x, width=8)
'00001101'
>>> np.binary_repr(242, width=8)
'11110010'
```

The result depends on the bit-width:

```
>>> np.invert(np.array([13], dtype=uint16))
array([65522], dtype=uint16)
>>> np.binary_repr(x, width=16)
'0000000000001101'
>>> np.binary_repr(65522, width=16)
'1111111111110010'
```

When using signed integer types the result is the two's complement of the result for the unsigned type:

```
>>> np.invert(np.array([13], dtype=int8))
array([-14], dtype=int8)
>>> np.binary_repr(-14, width=8)
'11110010'
```

Booleans are accepted as well:

```
>>> np.invert(array([True, False]))
array([False,  True], dtype=bool)
```

`dask.array.`**`bitwise_or`**(*x1*, *x2*[, *out*])

Compute the bit-wise OR of two arrays element-wise.

Computes the bit-wise OR of the underlying binary representation of the integers in the input arrays. This ufunc implements the C/Python operator `|`.

Parameters

x1, x2 [array_like] Only integer and boolean types are handled.

out [ndarray, optional] Array into which the output is placed. Its type is preserved and it must be of the right shape to hold the output. See doc.ufuncs.

Returns

out [array_like] Result.

See also:

logical_or, *bitwise_and*, *bitwise_xor*

binary_repr Return the binary representation of the input number as a string.

Examples

The number 13 has the binaray representation `00001101`. Likewise, 16 is represented by `00010000`. The bit-wise OR of 13 and 16 is then `000111011`, or 29:

```
>>> np.bitwise_or(13, 16)
29
>>> np.binary_repr(29)
'11101'
```

```
>>> np.bitwise_or(32, 2)
34
>>> np.bitwise_or([33, 4], 1)
array([33,  5])
>>> np.bitwise_or([33, 4], [1, 2])
array([33,  6])
```

```
>>> np.bitwise_or(np.array([2, 5, 255]), np.array([4, 4, 4]))
array([  6,   5, 255])
>>> np.array([2, 5, 255]) | np.array([4, 4, 4])
array([  6,   5, 255])
>>> np.bitwise_or(np.array([2, 5, 255, 2147483647L], dtype=np.int32),
...               np.array([4, 4, 4, 2147483647L], dtype=np.int32))
array([         6,          5,        255, 2147483647])
>>> np.bitwise_or([True, True], [False, True])
array([ True,  True], dtype=bool)
```

dask.array.**bitwise_xor**(*x1*, *x2*[, *out*])

Compute the bit-wise XOR of two arrays element-wise.

Computes the bit-wise XOR of the underlying binary representation of the integers in the input arrays. This ufunc implements the C/Python operator ^.

Parameters

x1, x2 [array_like] Only integer and boolean types are handled.

Returns

out [array_like] Result.

See also:

logical_xor, *bitwise_and*, *bitwise_or*

binary_repr Return the binary representation of the input number as a string.

Examples

The number 13 is represented by `00001101`. Likewise, 17 is represented by `00010001`. The bit-wise XOR of 13 and 17 is therefore `00011100`, or 28:

```
>>> np.bitwise_xor(13, 17)
28
>>> np.binary_repr(28)
'11100'
```

```
>>> np.bitwise_xor(31, 5)
26
>>> np.bitwise_xor([31,3], 5)
array([26,  6])
```

```
>>> np.bitwise_xor([31,3], [5,6])
array([26,  5])
>>> np.bitwise_xor([True, True], [False, True])
array([ True, False], dtype=bool)
```

dask.array.**block**(*arrays*, *allow_unknown_chunksizes=False*)

Assemble an nd-array from nested lists of blocks.

Blocks in the innermost lists are concatenated along the last dimension (-1), then these are concatenated along the second-last dimension (-2), and so on until the outermost list is reached

Blocks can be of any dimension, but will not be broadcasted using the normal rules. Instead, leading axes of size 1 are inserted, to make `block.ndim` the same for all blocks. This is primarily useful for working with scalars, and means that code like `block([v, 1])` is valid, where `v.ndim == 1`.

When the nested list is two levels deep, this allows block matrices to be constructed from their components.

Parameters

arrays [nested list of array_like or scalars (but not tuples)] If passed a single ndarray or scalar (a nested list of depth 0), this is returned unmodified (and not copied).

Elements shapes must match along the appropriate axes (without broadcasting), but leading 1s will be prepended to the shape as necessary to make the dimensions match.

allow_unknown_chunksizes: bool Allow unknown chunksizes, such as come from converting from dask dataframes. Dask.array is unable to verify that chunks line up. If data comes from differently aligned sources then this can cause unexpected results.

Returns

block_array [ndarray] The array assembled from the given blocks.

The dimensionality of the output is equal to the greatest of: * the dimensionality of all the inputs * the depth to which the input list is nested

Raises

ValueError

- If list depths are mismatched - for instance, `[[a, b], c]` is illegal, and should be spelt `[[a, b], [c]]`
- If lists are empty - for instance, `[[a, b], []]`

See also:

concatenate Join a sequence of arrays together.

stack Stack arrays in sequence along a new dimension.

hstack Stack arrays in sequence horizontally (column wise).

vstack Stack arrays in sequence vertically (row wise).

dstack Stack arrays in sequence depth wise (along third dimension).

vsplit Split array into a list of multiple sub-arrays vertically.

Notes

When called with only scalars, `block` is equivalent to an ndarray call. So `block([[1, 2], [3, 4]])` is equivalent to `array([[1, 2], [3, 4]])`.

This function does not enforce that the blocks lie on a fixed grid. `block([[a, b], [c, d]])` is not restricted to arrays of the form:

```
AAAbb
AAAbb
cccDD
```

But is also allowed to produce, for some `a, b, c, d`:

```
AAAbb
AAAbb
cDDDD
```

Since concatenation happens along the last axis first, *block* is _not_ capable of producing the following directly:

```
AAAbb
cccbb
cccDD
```

Matlab's "square bracket stacking", `[A, B, ...; p, q, ...]`, is equivalent to `block([[A, B, ...], [p, q, ...]])`.

`dask.array.`**`broadcast_arrays`**(**args*, ***kwargs*)

Broadcast any number of arrays against each other.

Parameters

'*args' [array_likes] The arrays to broadcast.

subok [bool, optional] If True, then sub-classes will be passed-through, otherwise the returned arrays will be forced to be a base-class array (default).

Returns

broadcasted [list of arrays] These arrays are views on the original arrays. They are typically not contiguous. Furthermore, more than one element of a broadcasted array may refer to a single memory location. If you need to write to the arrays, make copies first.

Examples

```
>>> x = np.array([[1,2,3]])
>>> y = np.array([[1],[2],[3]])
>>> np.broadcast_arrays(x, y)
[array([[1, 2, 3],
       [1, 2, 3],
       [1, 2, 3]]), array([[1, 1, 1],
       [2, 2, 2],
       [3, 3, 3]])]
```

Here is a useful idiom for getting contiguous copies instead of non-contiguous views.

```
>>> [np.array(a) for a in np.broadcast_arrays(x, y)]
[array([[1, 2, 3],
       [1, 2, 3],
       [1, 2, 3]]), array([[1, 1, 1],
       [2, 2, 2],
       [3, 3, 3]])]
```

dask.array.**broadcast_to**(*x*, *shape*, *chunks=None*)
Broadcast an array to a new shape.

Parameters

x [array_like] The array to broadcast.

shape [tuple] The shape of the desired array.

chunks [tuple, optional] If provided, then the result will use these chunks instead of the same chunks as the source array. Setting chunks explicitly as part of broadcast_to is more efficient than rechunking afterwards. Chunks are only allowed to differ from the original shape along dimensions that are new on the result or have size 1 the input array.

Returns

broadcast [dask array]

See also:

numpy.broadcast_to()

dask.array.**coarsen**(*reduction*, *x*, *axes*, *trim_excess=False*)
Coarsen array by applying reduction to fixed size neighborhoods

Parameters

reduction: function Function like np.sum, np.mean, etc...

x: np.ndarray Array to be coarsened

axes: dict Mapping of axis to coarsening factor

Examples

```
>>> x = np.array([1, 2, 3, 4, 5, 6])
>>> coarsen(np.sum, x, {0: 2})
array([ 3,  7, 11])
>>> coarsen(np.max, x, {0: 3})
array([3, 6])
```

Provide dictionary of scale per dimension

```
>>> x = np.arange(24).reshape((4, 6))
>>> x
array([[ 0,  1,  2,  3,  4,  5],
       [ 6,  7,  8,  9, 10, 11],
       [12, 13, 14, 15, 16, 17],
       [18, 19, 20, 21, 22, 23]])
```

```
>>> coarsen(np.min, x, {0: 2, 1: 3})
array([[ 0,  3],
       [12, 15]])
```

You must avoid excess elements explicitly

```
>>> x = np.array([1, 2, 3, 4, 5, 6, 7, 8])
>>> coarsen(np.min, x, {0: 3}, trim_excess=True)
array([1, 4])
```

dask.array.**ceil**(*x*[, *out*])

Return the ceiling of the input, element-wise.

The ceil of the scalar *x* is the smallest integer *i*, such that *i* >= *x*. It is often denoted as $\lceil x \rceil$.

Parameters

x [array_like] Input data.

Returns

y [ndarray or scalar] The ceiling of each element in *x*, with *float* dtype.

See also:

floor, *trunc*, *rint*

Examples

```
>>> a = np.array([-1.7, -1.5, -0.2, 0.2, 1.5, 1.7, 2.0])
>>> np.ceil(a)
array([-1., -1., -0.,  1.,  2.,  2.,  2.])
```

dask.array.**choose**(*a*, *choices*, *out=None*, *mode='raise'*)

Construct an array from an index array and a set of arrays to choose from.

First of all, if confused or uncertain, definitely look at the Examples - in its full generality, this function is less simple than it might seem from the following code description (below ndi = *numpy.lib.index_tricks*):

`np.choose(a,c) == np.array([c[a[I]][I] for I in ndi.ndindex(a.shape)])`.

But this omits some subtleties. Here is a fully general summary:

Given an "index" array (*a*) of integers and a sequence of *n* arrays (*choices*), *a* and each choice array are first broadcast, as necessary, to arrays of a common shape; calling these *Ba* and *Bchoices[i], i = 0,...,n-1* we have that, necessarily, `Ba.shape == Bchoices[i].shape` for each *i*. Then, a new array with shape `Ba.shape` is created as follows:

- if `mode=raise` (the default), then, first of all, each element of *a* (and thus *Ba*) must be in the range *[0, n-1]*; now, suppose that *i* (in that range) is the value at the *(j0, j1, ..., jm)* position in *Ba* - then the value at the same position in the new array is the value in *Bchoices[i]* at that same position;
- if `mode=wrap`, values in *a* (and thus *Ba*) may be any (signed) integer; modular arithmetic is used to map integers outside the range *[0, n-1]* back into that range; and then the new array is constructed as above;
- if `mode=clip`, values in *a* (and thus *Ba*) may be any (signed) integer; negative integers are mapped to 0; values greater than *n-1* are mapped to *n-1*; and then the new array is constructed as above.

Parameters

a [int array] This array must contain integers in *[0, n-1]*, where *n* is the number of choices, unless `mode=wrap` or `mode=clip`, in which cases any integers are permissible.

choices [sequence of arrays] Choice arrays. *a* and all of the choices must be broadcastable to the same shape. If *choices* is itself an array (not recommended), then its outermost dimension (i.e., the one corresponding to `choices.shape[0]`) is taken as defining the "sequence".

out [array, optional] If provided, the result will be inserted into this array. It should be of the appropriate shape and dtype.

mode [{'raise' (default), 'wrap', 'clip'}, optional] Specifies how indices outside *[0, n-1]* will be treated:

- 'raise' : an exception is raised
- 'wrap' : value becomes value mod *n*
- 'clip' : values < 0 are mapped to 0, values > n-1 are mapped to n-1

Returns

merged_array [array] The merged result.

Raises

ValueError: shape mismatch If *a* and each choice array are not all broadcastable to the same shape.

See also:

`ndarray.choose` equivalent method

Notes

To reduce the chance of misinterpretation, even though the following "abuse" is nominally supported, *choices* should neither be, nor be thought of as, a single array, i.e., the outermost sequence-like container should be either a list or a tuple.

Examples

```
>>> choices = [[0, 1, 2, 3], [10, 11, 12, 13],
...   [20, 21, 22, 23], [30, 31, 32, 33]]
>>> np.choose([2, 3, 1, 0], choices
... # the first element of the result will be the first element of the
... # third (2+1) "array" in choices, namely, 20; the second element
... # will be the second element of the fourth (3+1) choice array, i.e.,
... # 31, etc.
... )
array([20, 31, 12,  3])
>>> np.choose([2, 4, 1, 0], choices, mode='clip') # 4 goes to 3 (4-1)
array([20, 31, 12,  3])
>>> # because there are 4 choice arrays
>>> np.choose([2, 4, 1, 0], choices, mode='wrap') # 4 goes to (4 mod 4)
array([20,  1, 12,  3])
>>> # i.e., 0
```

A couple examples illustrating how choose broadcasts:

```
>>> a = [[1, 0, 1], [0, 1, 0], [1, 0, 1]]
>>> choices = [-10, 10]
>>> np.choose(a, choices)
array([[ 10, -10,  10],
       [-10,  10, -10],
       [ 10, -10,  10]])
```

```
>>> # With thanks to Anne Archibald
>>> a = np.array([0, 1]).reshape((2,1,1))
>>> c1 = np.array([1, 2, 3]).reshape((1,3,1))
>>> c2 = np.array([-1, -2, -3, -4, -5]).reshape((1,1,5))
```

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```
>>> np.choose(a, (c1, c2)) # result is 2x3x5, res[0,:,:]=c1, res[1,:,:]=c2
array([[[ 1,  1,  1,  1,  1],
        [ 2,  2,  2,  2,  2],
        [ 3,  3,  3,  3,  3]],
       [[-1, -2, -3, -4, -5],
        [-1, -2, -3, -4, -5],
        [-1, -2, -3, -4, -5]]])
```

dask.array.**clip**(**args*, ***kwargs*)

Clip (limit) the values in an array.

Given an interval, values outside the interval are clipped to the interval edges. For example, if an interval of `[0, 1]` is specified, values smaller than 0 become 0, and values larger than 1 become 1.

Parameters

a [array_like] Array containing elements to clip.

a_min [scalar or array_like] Minimum value.

a_max [scalar or array_like] Maximum value. If *a_min* or *a_max* are array_like, then they will be broadcasted to the shape of *a*.

out [ndarray, optional] The results will be placed in this array. It may be the input array for in-place clipping. *out* must be of the right shape to hold the output. Its type is preserved.

Returns

clipped_array [ndarray] An array with the elements of *a*, but where values < *a_min* are replaced with *a_min*, and those > *a_max* with *a_max*.

See also:

numpy.doc.ufuncs Section "Output arguments"

Examples

```
>>> a = np.arange(10)
>>> np.clip(a, 1, 8)
array([1, 1, 2, 3, 4, 5, 6, 7, 8, 8])
>>> a
array([0, 1, 2, 3, 4, 5, 6, 7, 8, 9])
>>> np.clip(a, 3, 6, out=a)
array([3, 3, 3, 3, 4, 5, 6, 6, 6, 6])
>>> a = np.arange(10)
>>> a
array([0, 1, 2, 3, 4, 5, 6, 7, 8, 9])
>>> np.clip(a, [3,4,1,1,1,4,4,4,4,4], 8)
array([3, 4, 2, 3, 4, 5, 6, 7, 8, 8])
```

dask.array.**compress**(*condition*, *a*, *axis=None*, *out=None*)

Return selected slices of an array along given axis.

When working along a given axis, a slice along that axis is returned in *output* for each index where *condition* evaluates to True. When working on a 1-D array, *compress* is equivalent to *extract*.

Parameters

condition [1-D array of bools] Array that selects which entries to return. If len(condition) is less than the size of *a* along the given axis, then output is truncated to the length of the condition array.

a [array_like] Array from which to extract a part.

axis [int, optional] Axis along which to take slices. If None (default), work on the flattened array.

out [ndarray, optional] Output array. Its type is preserved and it must be of the right shape to hold the output.

Returns

compressed_array [ndarray] A copy of *a* without the slices along axis for which *condition* is false.

See also:

take, *choose*, *diag*, `diagonal`, `select`

`ndarray.compress` Equivalent method in ndarray

`np.extract` Equivalent method when working on 1-D arrays

`numpy.doc.ufuncs` Section "Output arguments"

Examples

```
>>> a = np.array([[1, 2], [3, 4], [5, 6]])
>>> a
array([[1, 2],
       [3, 4],
       [5, 6]])
>>> np.compress([0, 1], a, axis=0)
array([[3, 4]])
>>> np.compress([False, True, True], a, axis=0)
array([[3, 4],
       [5, 6]])
>>> np.compress([False, True], a, axis=1)
array([[2],
       [4],
       [6]])
```

Working on the flattened array does not return slices along an axis but selects elements.

```
>>> np.compress([False, True], a)
array([2])
```

`dask.array.`**`concatenate`**(*seq*, *axis=0*, *allow_unknown_chunksizes=False*)

Concatenate arrays along an existing axis

Given a sequence of dask Arrays form a new dask Array by stacking them along an existing dimension (axis=0 by default)

Parameters

seq: list of dask.arrays

axis: int Dimension along which to align all of the arrays

allow_unknown_chunksizes: bool Allow unknown chunksizes, such as come from converting from dask dataframes. Dask.array is unable to verify that chunks line up. If data comes from differently aligned sources then this can cause unexpected results.

See also:

stack

Examples

Create slices

```
>>> import dask.array as da
>>> import numpy as np
```

```
>>> data = [from_array(np.ones((4, 4)), chunks=(2, 2))
...          for i in range(3)]
```

```
>>> x = da.concatenate(data, axis=0)
>>> x.shape
(12, 4)
```

```
>>> da.concatenate(data, axis=1).shape
(4, 12)
```

Result is a new dask Array

dask.array.**conj**(*x*[, *out*])

Return the complex conjugate, element-wise.

The complex conjugate of a complex number is obtained by changing the sign of its imaginary part.

Parameters

x [array_like] Input value.

Returns

y [ndarray] The complex conjugate of *x*, with same dtype as *y*.

Examples

```
>>> np.conjugate(1+2j)
(1-2j)
```

```
>>> x = np.eye(2) + 1j * np.eye(2)
>>> np.conjugate(x)
array([[ 1.-1.j,  0.-0.j],
       [ 0.-0.j,  1.-1.j]])
```

dask.array.**copysign**(*x1*, *x2*[, *out*])

Change the sign of x1 to that of x2, element-wise.

If both arguments are arrays or sequences, they have to be of the same length. If *x2* is a scalar, its sign will be copied to all elements of *x1*.

Parameters

x1 [array_like] Values to change the sign of.

x2 [array_like] The sign of *x2* is copied to *x1*.

out [ndarray, optional] Array into which the output is placed. Its type is preserved and it must be of the right shape to hold the output. See doc.ufuncs.

Returns

out [array_like] The values of *x1* with the sign of *x2*.

Examples

```
>>> np.copysign(1.3, -1)
-1.3
>>> 1/np.copysign(0, 1)
inf
>>> 1/np.copysign(0, -1)
-inf
```

```
>>> np.copysign([-1, 0, 1], -1.1)
array([-1., -0., -1.])
>>> np.copysign([-1, 0, 1], np.arange(3)-1)
array([-1.,  0.,  1.])
```

dask.array.**corrcoef**(*x*, *y=None*, *rowvar=1*, *bias=<class 'numpy._NoValue'>*, *ddof=<class 'numpy._NoValue'>*)

Return Pearson product-moment correlation coefficients.

Please refer to the documentation for *cov* for more detail. The relationship between the correlation coefficient matrix, *R*, and the covariance matrix, *C*, is

$$R_{ij} = \frac{C_{ij}}{\sqrt{C_{ii} * C_{jj}}}$$

The values of *R* are between -1 and 1, inclusive.

Parameters

x [array_like] A 1-D or 2-D array containing multiple variables and observations. Each row of *x* represents a variable, and each column a single observation of all those variables. Also see *rowvar* below.

y [array_like, optional] An additional set of variables and observations. *y* has the same shape as *x*.

rowvar [int, optional] If *rowvar* is non-zero (default), then each row represents a variable, with observations in the columns. Otherwise, the relationship is transposed: each column represents a variable, while the rows contain observations.

bias [_NoValue, optional] Has no effect, do not use.

Deprecated since version 1.10.0.

ddof [_NoValue, optional] Has no effect, do not use.

Deprecated since version 1.10.0.

Returns

R [ndarray] The correlation coefficient matrix of the variables.

See also:

cov Covariance matrix

Notes

Due to floating point rounding the resulting array may not be Hermitian, the diagonal elements may not be 1, and the elements may not satisfy the inequality abs(a) <= 1. The real and imaginary parts are clipped to the interval [-1, 1] in an attempt to improve on that situation but is not much help in the complex case.

This function accepts but discards arguments *bias* and *ddof*. This is for backwards compatibility with previous versions of this function. These arguments had no effect on the return values of the function and can be safely ignored in this and previous versions of numpy.

dask.array.**cos**(*x*[, *out*])
Cosine element-wise.

Parameters

x [array_like] Input array in radians.

out [ndarray, optional] Output array of same shape as *x*.

Returns

y [ndarray] The corresponding cosine values.

Raises

ValueError: invalid return array shape if *out* is provided and *out.shape* != *x.shape* (See Examples)

Notes

If *out* is provided, the function writes the result into it, and returns a reference to *out*. (See Examples)

References

M. Abramowitz and I. A. Stegun, Handbook of Mathematical Functions. New York, NY: Dover, 1972.

Examples

```
>>> np.cos(np.array([0, np.pi/2, np.pi]))
array([  1.00000000e+00,   6.12303177e-17,  -1.00000000e+00])
>>>
>>> # Example of providing the optional output parameter
>>> out2 = np.cos([0.1], out1)
>>> out2 is out1
True
>>>
>>> # Example of ValueError due to provision of shape mis-matched `out`
>>> np.cos(np.zeros((3,3)),np.zeros((2,2)))
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
ValueError: invalid return array shape
```

dask.array.**cosh**(*x*[, *out*])
Hyperbolic cosine, element-wise.

Equivalent to `1/2 * (np.exp(x) + np.exp(-x))` and `np.cos(1j*x)`.

Parameters

x [array_like] Input array.

Returns

out [ndarray] Output array of same shape as *x*.

Examples

```
>>> np.cosh(0)
1.0
```

The hyperbolic cosine describes the shape of a hanging cable:

```
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-4, 4, 1000)
>>> plt.plot(x, np.cosh(x))
>>> plt.show()
```

dask.array.**count_nonzero**(*a*)
Counts the number of non-zero values in the array `a`.

Parameters

a [array_like] The array for which to count non-zeros.

Returns

count [int or array of int] Number of non-zero values in the array.

See also:

nonzero Return the coordinates of all the non-zero values.

Examples

```
>>> np.count_nonzero(np.eye(4))
4
>>> np.count_nonzero([[0,1,7,0,0],[3,0,0,2,19]])
5
```

dask.array.**cov**(*m*, *y=None*, *rowvar=True*, *bias=False*, *ddof=None*, *fweights=None*, *aweights=None*)
Estimate a covariance matrix, given data and weights.

Covariance indicates the level to which two variables vary together. If we examine N-dimensional samples, $X = [x_1, x_2, ...x_N]^T$, then the covariance matrix element C_{ij} is the covariance of x_i and x_j. The element C_{ii} is the variance of x_i.

See the notes for an outline of the algorithm.

Parameters

m [array_like] A 1-D or 2-D array containing multiple variables and observations. Each row of *m* represents a variable, and each column a single observation of all those variables. Also see *rowvar* below.

y [array_like, optional] An additional set of variables and observations. *y* has the same form as that of *m*.

rowvar [bool, optional] If *rowvar* is True (default), then each row represents a variable, with observations in the columns. Otherwise, the relationship is transposed: each column represents a variable, while the rows contain observations.

bias [bool, optional] Default normalization (False) is by `(N - 1)`, where `N` is the number of observations given (unbiased estimate). If *bias* is True, then normalization is by `N`. These values can be overridden by using the keyword `ddof` in numpy versions >= 1.5.

ddof [int, optional] If not `None` the default value implied by *bias* is overridden. Note that `ddof=1` will return the unbiased estimate, even if both *fweights* and *aweights* are specified, and `ddof=0` will return the simple average. See the notes for the details. The default value is `None`.

New in version 1.5.

fweights [array_like, int, optional] 1-D array of integer freguency weights; the number of times each observation vector should be repeated.

New in version 1.10.

aweights [array_like, optional] 1-D array of observation vector weights. These relative weights are typically large for observations considered "important" and smaller for observations considered less "important". If `ddof=0` the array of weights can be used to assign probabilities to observation vectors.

New in version 1.10.

Returns

out [ndarray] The covariance matrix of the variables.

See also:

corrcoef Normalized covariance matrix

Notes

Assume that the observations are in the columns of the observation array *m* and let `f = fweights` and `a = aweights` for brevity. The steps to compute the weighted covariance are as follows:

```
>>> w = f * a
>>> v1 = np.sum(w)
>>> v2 = np.sum(w * a)
>>> m -= np.sum(m * w, axis=1, keepdims=True) / v1
>>> cov = np.dot(m * w, m.T) * v1 / (v1**2 - ddof * v2)
```

Note that when `a == 1`, the normalization factor `v1 / (v1**2 - ddof * v2)` goes over to `1 / (np.sum(f) - ddof)` as it should.

Examples

Consider two variables, x_0 and x_1, which correlate perfectly, but in opposite directions:

```
>>> x = np.array([[0, 2], [1, 1], [2, 0]]).T
>>> x
array([[0, 1, 2],
       [2, 1, 0]])
```

Note how x_0 increases while x_1 decreases. The covariance matrix shows this clearly:

```
>>> np.cov(x)
array([[ 1., -1.],
       [-1.,  1.]])
```

Note that element $C_{0,1}$, which shows the correlation between x_0 and x_1, is negative.

Further, note how *x* and *y* are combined:

```
>>> x = [-2.1, -1,  4.3]
>>> y = [3,  1.1,  0.12]
>>> X = np.vstack((x,y))
>>> print(np.cov(X))
[[ 11.71        -4.286     ]
 [ -4.286        2.14413333]]
>>> print(np.cov(x, y))
[[ 11.71        -4.286     ]
 [ -4.286        2.14413333]]
>>> print(np.cov(x))
11.71
```

dask.array.**cumprod**(*a*, *axis=None*, *dtype=None*, *out=None*)

Return the cumulative product of elements along a given axis.

Parameters

a [array_like] Input array.

axis [int, optional] Axis along which the cumulative product is computed. By default the input is flattened.

dtype [dtype, optional] Type of the returned array, as well as of the accumulator in which the elements are multiplied. If *dtype* is not specified, it defaults to the dtype of *a*, unless *a* has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used instead.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape and buffer length as the expected output but the type of the resulting values will be cast if necessary.

Returns

cumprod [ndarray] A new array holding the result is returned unless *out* is specified, in which case a reference to out is returned.

See also:

numpy.doc.ufuncs Section "Output arguments"

Notes

Arithmetic is modular when using integer types, and no error is raised on overflow.

Examples

```
>>> a = np.array([1,2,3])
>>> np.cumprod(a) # intermediate results 1, 1*2
...               # total product 1*2*3 = 6
array([1, 2, 6])
>>> a = np.array([[1, 2, 3], [4, 5, 6]])
>>> np.cumprod(a, dtype=float) # specify type of output
array([   1.,    2.,    6.,   24.,  120.,  720.])
```

The cumulative product for each column (i.e., over the rows) of *a*:

```
>>> np.cumprod(a, axis=0)
array([[ 1,  2,  3],
       [ 4, 10, 18]])
```

The cumulative product for each row (i.e. over the columns) of *a*:

```
>>> np.cumprod(a,axis=1)
array([[  1,   2,   6],
       [  4,  20, 120]])
```

dask.array.**cumsum**(*a*, *axis=None*, *dtype=None*, *out=None*)

Return the cumulative sum of the elements along a given axis.

Parameters

a [array_like] Input array.

axis [int, optional] Axis along which the cumulative sum is computed. The default (None) is to compute the cumsum over the flattened array.

dtype [dtype, optional] Type of the returned array and of the accumulator in which the elements are summed. If *dtype* is not specified, it defaults to the dtype of *a*, unless *a* has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape and buffer length as the expected output but the type will be cast if necessary. See *doc.ufuncs* (Section "Output arguments") for more details.

Returns

cumsum_along_axis [ndarray.] A new array holding the result is returned unless *out* is specified, in which case a reference to *out* is returned. The result has the same size as *a*, and the same shape as *a* if *axis* is not None or *a* is a 1-d array.

See also:

sum Sum array elements.

trapz Integration of array values using the composite trapezoidal rule.

diff Calculate the n-th discrete difference along given axis.

Notes

Arithmetic is modular when using integer types, and no error is raised on overflow.

Examples

```
>>> a = np.array([[1,2,3], [4,5,6]])
>>> a
array([[1, 2, 3],
       [4, 5, 6]])
>>> np.cumsum(a)
array([ 1,  3,  6, 10, 15, 21])
>>> np.cumsum(a, dtype=float)     # specifies type of output value(s)
array([  1.,   3.,   6.,  10.,  15.,  21.])
```

```
>>> np.cumsum(a,axis=0)      # sum over rows for each of the 3 columns
array([[1, 2, 3],
       [5, 7, 9]])
>>> np.cumsum(a,axis=1)      # sum over columns for each of the 2 rows
array([[ 1,  3,  6],
       [ 4,  9, 15]])
```

dask.array.**deg2rad**(*x*[, *out*])

Convert angles from degrees to radians.

Parameters

x [array_like] Angles in degrees.

Returns

y [ndarray] The corresponding angle in radians.

See also:

rad2deg Convert angles from radians to degrees.

unwrap Remove large jumps in angle by wrapping.

Notes

New in version 1.3.0.

`deg2rad(x)` is `x * pi / 180`.

Examples

```
>>> np.deg2rad(180)
3.1415926535897931
```

dask.array.**degrees**(*x*[, *out*])

Convert angles from radians to degrees.

Parameters

x [array_like] Input array in radians.

out [ndarray, optional] Output array of same shape as x.

Returns

y [ndarray of floats] The corresponding degree values; if *out* was supplied this is a reference to it.

See also:

rad2deg equivalent function

Examples

Convert a radian array to degrees

```
>>> rad = np.arange(12.)*np.pi/6
>>> np.degrees(rad)
array([   0.,   30.,   60.,   90.,  120.,  150.,  180.,  210.,  240.,
        270.,  300.,  330.])
```

```
>>> out = np.zeros((rad.shape))
>>> r = degrees(rad, out)
>>> np.all(r == out)
True
```

`dask.array.`**`diag`**(*v*, *k=0*)

Extract a diagonal or construct a diagonal array.

See the more detailed documentation for `numpy.diagonal` if you use this function to extract a diagonal and wish to write to the resulting array; whether it returns a copy or a view depends on what version of numpy you are using.

Parameters

v [array_like] If *v* is a 2-D array, return a copy of its *k*-th diagonal. If *v* is a 1-D array, return a 2-D array with *v* on the *k*-th diagonal.

k [int, optional] Diagonal in question. The default is 0. Use *k>0* for diagonals above the main diagonal, and *k<0* for diagonals below the main diagonal.

Returns

out [ndarray] The extracted diagonal or constructed diagonal array.

See also:

`diagonal` Return specified diagonals.

`diagflat` Create a 2-D array with the flattened input as a diagonal.

`trace` Sum along diagonals.

`triu` Upper triangle of an array.

`tril` Lower triangle of an array.

Examples

```
>>> x = np.arange(9).reshape((3,3))
>>> x
array([[0, 1, 2],
```

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```
       [3, 4, 5],
       [6, 7, 8]])
```

```
>>> np.diag(x)
array([0, 4, 8])
>>> np.diag(x, k=1)
array([1, 5])
>>> np.diag(x, k=-1)
array([3, 7])
```

```
>>> np.diag(np.diag(x))
array([[0, 0, 0],
       [0, 4, 0],
       [0, 0, 8]])
```

dask.array.**diff**(*a*, *n=1*, *axis=-1*)

Calculate the n-th discrete difference along given axis.

The first difference is given by `out[n] = a[n+1] - a[n]` along the given axis, higher differences are calculated by using *diff* recursively.

Parameters

a [array_like]

Input array

n [int, optional] The number of times values are differenced.

axis [int, optional] The axis along which the difference is taken, default is the last axis.

Returns

diff [ndarray] The n-th differences. The shape of the output is the same as *a* except along *axis* where the dimension is smaller by *n*.

.

Examples

```
>>> x = np.array([1, 2, 4, 7, 0])
>>> np.diff(x)
array([ 1,  2,  3, -7])
>>> np.diff(x, n=2)
array([  1,   1, -10])
```

```
>>> x = np.array([[1, 3, 6, 10], [0, 5, 6, 8]])
>>> np.diff(x)
array([[2, 3, 4],
       [5, 1, 2]])
>>> np.diff(x, axis=0)
array([[-1,  2,  0, -2]])
```

dask.array.**digitize**(*x*, *bins*, *right=False*)

Return the indices of the bins to which each value in input array belongs.

Each index `i` returned is such that `bins[i-1] <= x < bins[i]` if *bins* is monotonically increasing, or `bins[i-1] > x >= bins[i]` if *bins* is monotonically decreasing. If values in *x* are beyond the bounds of *bins*, 0 or `len(bins)` is returned as appropriate. If right is True, then the right bin is closed so that the index `i` is such that `bins[i-1] < x <= bins[i]` or bins[i-1] >= x > bins[i]‘‘ if *bins* is monotonically increasing or decreasing, respectively.

Parameters

x [array_like] Input array to be binned. Prior to Numpy 1.10.0, this array had to be 1-dimensional, but can now have any shape.

bins [array_like] Array of bins. It has to be 1-dimensional and monotonic.

right [bool, optional] Indicating whether the intervals include the right or the left bin edge. Default behavior is (right==False) indicating that the interval does not include the right edge. The left bin end is open in this case, i.e., bins[i-1] <= x < bins[i] is the default behavior for monotonically increasing bins.

Returns

out [ndarray of ints] Output array of indices, of same shape as *x*.

Raises

ValueError If *bins* is not monotonic.

TypeError If the type of the input is complex.

See also:

bincount, *histogram*, *unique*

Notes

If values in *x* are such that they fall outside the bin range, attempting to index *bins* with the indices that *digitize* returns will result in an IndexError.

New in version 1.10.0.

np.digitize is implemented in terms of *np.searchsorted*. This means that a binary search is used to bin the values, which scales much better for larger number of bins than the previous linear search. It also removes the requirement for the input array to be 1-dimensional.

Examples

```
>>> x = np.array([0.2, 6.4, 3.0, 1.6])
>>> bins = np.array([0.0, 1.0, 2.5, 4.0, 10.0])
>>> inds = np.digitize(x, bins)
>>> inds
array([1, 4, 3, 2])
>>> for n in range(x.size):
...   print(bins[inds[n]-1], "<=", x[n], "<", bins[inds[n]])
...
0.0 <= 0.2 < 1.0
4.0 <= 6.4 < 10.0
2.5 <= 3.0 < 4.0
1.0 <= 1.6 < 2.5
```

```
>>> x = np.array([1.2, 10.0, 12.4, 15.5, 20.])
>>> bins = np.array([0, 5, 10, 15, 20])
>>> np.digitize(x,bins,right=True)
array([1, 2, 3, 4, 4])
>>> np.digitize(x,bins,right=False)
array([1, 3, 3, 4, 5])
```

dask.array.**dot**(*a*, *b*, *out=None*)

Dot product of two arrays.

For 2-D arrays it is equivalent to matrix multiplication, and for 1-D arrays to inner product of vectors (without complex conjugation). For N dimensions it is a sum product over the last axis of *a* and the second-to-last of *b*:

```
dot(a, b)[i,j,k,m] = sum(a[i,j,:] * b[k,:,m])
```

Parameters

a [array_like] First argument.

b [array_like] Second argument.

out [ndarray, optional] Output argument. This must have the exact kind that would be returned if it was not used. In particular, it must have the right type, must be C-contiguous, and its dtype must be the dtype that would be returned for *dot(a,b)*. This is a performance feature. Therefore, if these conditions are not met, an exception is raised, instead of attempting to be flexible.

Returns

output [ndarray] Returns the dot product of *a* and *b*. If *a* and *b* are both scalars or both 1-D arrays then a scalar is returned; otherwise an array is returned. If *out* is given, then it is returned.

Raises

ValueError If the last dimension of *a* is not the same size as the second-to-last dimension of *b*.

See also:

vdot Complex-conjugating dot product.

tensordot Sum products over arbitrary axes.

einsum Einstein summation convention.

matmul '@' operator as method with out parameter.

Examples

```
>>> np.dot(3, 4)
12
```

Neither argument is complex-conjugated:

```
>>> np.dot([2j, 3j], [2j, 3j])
(-13+0j)
```

For 2-D arrays it is the matrix product:

```
>>> a = [[1, 0], [0, 1]]
>>> b = [[4, 1], [2, 2]]
>>> np.dot(a, b)
array([[4, 1],
       [2, 2]])
```

```
>>> a = np.arange(3*4*5*6).reshape((3,4,5,6))
>>> b = np.arange(3*4*5*6)[::-1].reshape((5,4,6,3))
>>> np.dot(a, b)[2,3,2,1,2,2]
499128
>>> sum(a[2,3,2,:] * b[1,2,:,2])
499128
```

dask.array.**dstack**(*tup*)

Stack arrays in sequence depth wise (along third axis).

Takes a sequence of arrays and stack them along the third axis to make a single array. Rebuilds arrays divided by *dsplit*. This is a simple way to stack 2D arrays (images) into a single 3D array for processing.

Parameters

tup [sequence of arrays] Arrays to stack. All of them must have the same shape along all but the third axis.

Returns

stacked [ndarray] The array formed by stacking the given arrays.

See also:

stack Join a sequence of arrays along a new axis.

vstack Stack along first axis.

hstack Stack along second axis.

concatenate Join a sequence of arrays along an existing axis.

dsplit Split array along third axis.

Notes

Equivalent to `np.concatenate(tup, axis=2)`.

Examples

```
>>> a = np.array((1,2,3))
>>> b = np.array((2,3,4))
>>> np.dstack((a,b))
array([[[1, 2],
        [2, 3],
        [3, 4]]])
```

```
>>> a = np.array([[1],[2],[3]])
>>> b = np.array([[2],[3],[4]])
>>> np.dstack((a,b))
```

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```
array([[[1, 2]],
       [[2, 3]],
       [[3, 4]]])
```

dask.array.**ediff1d**(*ary*, *to_end=None*, *to_begin=None*)

The differences between consecutive elements of an array.

Parameters

ary [array_like] If necessary, will be flattened before the differences are taken.

to_end [array_like, optional] Number(s) to append at the end of the returned differences.

to_begin [array_like, optional] Number(s) to prepend at the beginning of the returned differences.

Returns

ediff1d [ndarray] The differences. Loosely, this is `ary.flat[1:] - ary.flat[:-1]`.

See also:

diff, *gradient*

Notes

When applied to masked arrays, this function drops the mask information if the *to_begin* and/or *to_end* parameters are used.

Examples

```
>>> x = np.array([1, 2, 4, 7, 0])
>>> np.ediff1d(x)
array([ 1,  2,  3, -7])
```

```
>>> np.ediff1d(x, to_begin=-99, to_end=np.array([88, 99]))
array([-99,   1,   2,   3,  -7,  88,  99])
```

The returned array is always 1D.

```
>>> y = [[1, 2, 4], [1, 6, 24]]
>>> np.ediff1d(y)
array([ 1,  2, -3,  5, 18])
```

dask.array.**empty**(**args*, ***kwargs*)

Blocked variant of empty

Follows the signature of empty exactly except that it also requires a keyword argument chunks=(...)

Original signature follows below. empty(shape, dtype=float, order='C')

Return a new array of given shape and type, without initializing entries.

Parameters

shape [int or tuple of int] Shape of the empty array

dtype [data-type, optional] Desired output data-type.

order [{'C', 'F'}, optional] Whether to store multi-dimensional data in row-major (C-style) or column-major (Fortran-style) order in memory.

Returns

out [ndarray] Array of uninitialized (arbitrary) data of the given shape, dtype, and order. Object arrays will be initialized to None.

See also:

empty_like, *zeros*, *ones*

Notes

empty, unlike *zeros*, does not set the array values to zero, and may therefore be marginally faster. On the other hand, it requires the user to manually set all the values in the array, and should be used with caution.

Examples

```
>>> np.empty([2, 2])
array([[ -9.74499359e+001,   6.69583040e-309],
       [  2.13182611e-314,   3.06959433e-309]])         #random
```

```
>>> np.empty([2, 2], dtype=int)
array([[-1073741821, -1067949133],
       [  496041986,    19249760]])                     #random
```

dask.array.**empty_like**(*a*, *dtype=None*, *chunks=None*)

Return a new array with the same shape and type as a given array.

Parameters

a [array_like] The shape and data-type of *a* define these same attributes of the returned array.

dtype [data-type, optional] Overrides the data type of the result.

chunks [sequence of ints] The number of samples on each block. Note that the last block will have fewer samples if `len(array) % chunks != 0`.

Returns

out [ndarray] Array of uninitialized (arbitrary) data with the same shape and type as *a*.

See also:

ones_like Return an array of ones with shape and type of input.

zeros_like Return an array of zeros with shape and type of input.

empty Return a new uninitialized array.

ones Return a new array setting values to one.

zeros Return a new array setting values to zero.

Notes

This function does *not* initialize the returned array; to do that use *zeros_like* or *ones_like* instead. It may be marginally faster than the functions that do set the array values.

dask.array.**einsum**(*subscripts*, **operands*, *out=None*, *dtype=None*, *order='K'*, *casting='safe'*)

Evaluates the Einstein summation convention on the operands.

Using the Einstein summation convention, many common multi-dimensional array operations can be represented in a simple fashion. This function provides a way to compute such summations. The best way to understand this function is to try the examples below, which show how many common NumPy functions can be implemented as calls to *einsum*.

Parameters

subscripts [str] Specifies the subscripts for summation.

operands [list of array_like] These are the arrays for the operation.

out [ndarray, optional] If provided, the calculation is done into this array.

dtype [data-type, optional] If provided, forces the calculation to use the data type specified. Note that you may have to also give a more liberal *casting* parameter to allow the conversions.

order [{'C', 'F', 'A', 'K'}, optional] Controls the memory layout of the output. 'C' means it should be C contiguous. 'F' means it should be Fortran contiguous, 'A' means it should be 'F' if the inputs are all 'F', 'C' otherwise. 'K' means it should be as close to the layout as the inputs as is possible, including arbitrarily permuted axes. Default is 'K'.

casting [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Setting this to 'unsafe' is not recommended, as it can adversely affect accumulations.

- 'no' means the data types should not be cast at all.
- 'equiv' means only byte-order changes are allowed.
- 'safe' means only casts which can preserve values are allowed.
- 'same_kind' means only safe casts or casts within a kind, like float64 to float32, are allowed.
- 'unsafe' means any data conversions may be done.

Returns

output [ndarray] The calculation based on the Einstein summation convention.

See also:

dot, inner, *outer*, *tensordot*

Notes

New in version 1.6.0.

The subscripts string is a comma-separated list of subscript labels, where each label refers to a dimension of the corresponding operand. Repeated subscripts labels in one operand take the diagonal. For example, `np.einsum('ii', a)` is equivalent to `np.trace(a)`.

Whenever a label is repeated, it is summed, so `np.einsum('i,i', a, b)` is equivalent to `np.inner(a, b)`. If a label appears only once, it is not summed, so `np.einsum('i', a)` produces a view of `a` with no changes.

The order of labels in the output is by default alphabetical. This means that `np.einsum('ij', a)` doesn't affect a 2D array, while `np.einsum('ji', a)` takes its transpose.

The output can be controlled by specifying output subscript labels as well. This specifies the label order, and allows summing to be disallowed or forced when desired. The call `np.einsum('i->', a)` is like `np.sum(a, axis=-1)`, and `np.einsum('ii->i', a)` is like `np.diag(a)`. The difference is that *einsum* does not allow broadcasting by default.

To enable and control broadcasting, use an ellipsis. Default NumPy-style broadcasting is done by adding an ellipsis to the left of each term, like `np.einsum('...ii->...i', a)`. To take the trace along the first and last axes, you can do `np.einsum('i...i', a)`, or to do a matrix-matrix product with the left-most indices instead of rightmost, you can do `np.einsum('ij...,jk...->ik...', a, b)`.

When there is only one operand, no axes are summed, and no output parameter is provided, a view into the operand is returned instead of a new array. Thus, taking the diagonal as `np.einsum('ii->i', a)` produces a view.

An alternative way to provide the subscripts and operands is as `einsum(op0, sublist0, op1, sublist1, ..., [sublistout])`. The examples below have corresponding *einsum* calls with the two parameter methods.

New in version 1.10.0.

Views returned from einsum are now writeable whenever the input array is writeable. For example, `np.einsum('ijk...->kji...', a)` will now have the same effect as `np.swapaxes(a, 0, 2)` and `np.einsum('ii->i', a)` will return a writeable view of the diagonal of a 2D array.

Examples

```
>>> a = np.arange(25).reshape(5,5)
>>> b = np.arange(5)
>>> c = np.arange(6).reshape(2,3)
```

```
>>> np.einsum('ii', a)
60
>>> np.einsum(a, [0,0])
60
>>> np.trace(a)
60
```

```
>>> np.einsum('ii->i', a)
array([ 0,  6, 12, 18, 24])
>>> np.einsum(a, [0,0], [0])
array([ 0,  6, 12, 18, 24])
>>> np.diag(a)
array([ 0,  6, 12, 18, 24])
```

```
>>> np.einsum('ij,j', a, b)
array([ 30,  80, 130, 180, 230])
>>> np.einsum(a, [0,1], b, [1])
array([ 30,  80, 130, 180, 230])
>>> np.dot(a, b)
```

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```
array([ 30,  80, 130, 180, 230])
>>> np.einsum('...j,j', a, b)
array([ 30,  80, 130, 180, 230])
```

```
>>> np.einsum('ji', c)
array([[0, 3],
       [1, 4],
       [2, 5]])
>>> np.einsum(c, [1,0])
array([[0, 3],
       [1, 4],
       [2, 5]])
>>> c.T
array([[0, 3],
       [1, 4],
       [2, 5]])
```

```
>>> np.einsum('..., ...', 3, c)
array([[ 0,  3,  6],
       [ 9, 12, 15]])
>>> np.einsum(3, [Ellipsis], c, [Ellipsis])
array([[ 0,  3,  6],
       [ 9, 12, 15]])
>>> np.multiply(3, c)
array([[ 0,  3,  6],
       [ 9, 12, 15]])
```

```
>>> np.einsum('i,i', b, b)
30
>>> np.einsum(b, [0], b, [0])
30
>>> np.inner(b,b)
30
```

```
>>> np.einsum('i,j', np.arange(2)+1, b)
array([[0, 1, 2, 3, 4],
       [0, 2, 4, 6, 8]])
>>> np.einsum(np.arange(2)+1, [0], b, [1])
array([[0, 1, 2, 3, 4],
       [0, 2, 4, 6, 8]])
>>> np.outer(np.arange(2)+1, b)
array([[0, 1, 2, 3, 4],
       [0, 2, 4, 6, 8]])
```

```
>>> np.einsum('i...->...', a)
array([50, 55, 60, 65, 70])
>>> np.einsum(a, [0,Ellipsis], [Ellipsis])
array([50, 55, 60, 65, 70])
>>> np.sum(a, axis=0)
array([50, 55, 60, 65, 70])
```

```
>>> a = np.arange(60.).reshape(3,4,5)
>>> b = np.arange(24.).reshape(4,3,2)
>>> np.einsum('ijk,jil->kl', a, b)
```

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```
array([[ 4400.,  4730.],
       [ 4532.,  4874.],
       [ 4664.,  5018.],
       [ 4796.,  5162.],
       [ 4928.,  5306.]])
>>> np.einsum(a, [0,1,2], b, [1,0,3], [2,3])
array([[ 4400.,  4730.],
       [ 4532.,  4874.],
       [ 4664.,  5018.],
       [ 4796.,  5162.],
       [ 4928.,  5306.]])
>>> np.tensordot(a,b, axes=([1,0],[0,1]))
array([[ 4400.,  4730.],
       [ 4532.,  4874.],
       [ 4664.,  5018.],
       [ 4796.,  5162.],
       [ 4928.,  5306.]])
```

```
>>> a = np.arange(6).reshape((3,2))
>>> b = np.arange(12).reshape((4,3))
>>> np.einsum('ki,jk->ij', a, b)
array([[10, 28, 46, 64],
       [13, 40, 67, 94]])
>>> np.einsum('ki,...k->i...', a, b)
array([[10, 28, 46, 64],
       [13, 40, 67, 94]])
>>> np.einsum('k...,jk', a, b)
array([[10, 28, 46, 64],
       [13, 40, 67, 94]])
```

```
>>> # since version 1.10.0
>>> a = np.zeros((3, 3))
>>> np.einsum('ii->i', a)[:] = 1
>>> a
array([[ 1.,  0.,  0.],
       [ 0.,  1.,  0.],
       [ 0.,  0.,  1.]])
```

dask.array.**exp**(*x*[, *out*])

Calculate the exponential of all elements in the input array.

Parameters

x [array_like] Input values.

Returns

out [ndarray] Output array, element-wise exponential of *x*.

See also:

expm1 Calculate `exp(x) - 1` for all elements in the array.

exp2 Calculate `2**x` for all elements in the array.

Notes

The irrational number `e` is also known as Euler's number. It is approximately 2.718281, and is the base of the natural logarithm, `ln` (this means that, if $x = \ln y = \log_e y$, then $e^x = y$. For real input, `exp(x)` is always positive.

For complex arguments, `x = a + ib`, we can write $e^x = e^a e^{ib}$. The first term, e^a, is already known (it is the real argument, described above). The second term, e^{ib}, is $\cos b + i \sin b$, a function with magnitude 1 and a periodic phase.

References

[1], *[2]*

Examples

Plot the magnitude and phase of `exp(x)` in the complex plane:

```
>>> import matplotlib.pyplot as plt
```

```
>>> x = np.linspace(-2*np.pi, 2*np.pi, 100)
>>> xx = x + 1j * x[:, np.newaxis] # a + ib over complex plane
>>> out = np.exp(xx)
```

```
>>> plt.subplot(121)
>>> plt.imshow(np.abs(out),
...            extent=[-2*np.pi, 2*np.pi, -2*np.pi, 2*np.pi])
>>> plt.title('Magnitude of exp(x)')
```

```
>>> plt.subplot(122)
>>> plt.imshow(np.angle(out),
...            extent=[-2*np.pi, 2*np.pi, -2*np.pi, 2*np.pi])
>>> plt.title('Phase (angle) of exp(x)')
>>> plt.show()
```

`dask.array.`**`expm1`**(*x*[, *out*])

Calculate `exp(x) - 1` for all elements in the array.

Parameters

x [array_like] Input values.

Returns

out [ndarray] Element-wise exponential minus one: `out = exp(x) - 1`.

See also:

`log1p` `log(1 + x)`, the inverse of expm1.

Notes

This function provides greater precision than `exp(x) - 1` for small values of `x`.

Examples

The true value of `exp(1e-10) - 1` is `1.00000000005e-10` to about 32 significant digits. This example shows the superiority of expm1 in this case.

```
>>> np.expm1(1e-10)
1.00000000005e-10
>>> np.exp(1e-10) - 1
1.000000082740371e-10
```

`dask.array.`**`eye`**(*N*, *chunks*, *M=None*, *k=0*, *dtype=<class 'float'>*)

Return a 2-D Array with ones on the diagonal and zeros elsewhere.

Parameters

N [int] Number of rows in the output.

chunks: int chunk size of resulting blocks

M [int, optional] Number of columns in the output. If None, defaults to *N*.

k [int, optional] Index of the diagonal: 0 (the default) refers to the main diagonal, a positive value refers to an upper diagonal, and a negative value to a lower diagonal.

dtype [data-type, optional] Data-type of the returned array.

Returns

I [Array of shape (N,M)] An array where all elements are equal to zero, except for the *k*-th diagonal, whose values are equal to one.

`dask.array.`**`fabs`**(*x*[, *out*])

Compute the absolute values element-wise.

This function returns the absolute values (positive magnitude) of the data in *x*. Complex values are not handled, use *absolute* to find the absolute values of complex data.

Parameters

x [array_like] The array of numbers for which the absolute values are required. If *x* is a scalar, the result *y* will also be a scalar.

out [ndarray, optional] Array into which the output is placed. Its type is preserved and it must be of the right shape to hold the output. See doc.ufuncs.

Returns

y [ndarray or scalar] The absolute values of *x*, the returned values are always floats.

See also:

`absolute` Absolute values including *complex* types.

Examples

```
>>> np.fabs(-1)
1.0
>>> np.fabs([-1.2, 1.2])
array([ 1.2,  1.2])
```

dask.array.**fix**(*args*, ***kwargs*)

Round to nearest integer towards zero.

Round an array of floats element-wise to nearest integer towards zero. The rounded values are returned as floats.

Parameters

x [array_like] An array of floats to be rounded

y [ndarray, optional] Output array

Returns

out [ndarray of floats] The array of rounded numbers

See also:

trunc, *floor*, *ceil*

around Round to given number of decimals

Examples

```
>>> np.fix(3.14)
3.0
>>> np.fix(3)
3.0
>>> np.fix([2.1, 2.9, -2.1, -2.9])
array([ 2.,  2., -2., -2.])
```

dask.array.**flatnonzero**(*a*)

Return indices that are non-zero in the flattened version of a.

This is equivalent to a.ravel().nonzero()[0].

Parameters

a [ndarray] Input array.

Returns

res [ndarray] Output array, containing the indices of the elements of *a.ravel()* that are non-zero.

See also:

nonzero Return the indices of the non-zero elements of the input array.

ravel Return a 1-D array containing the elements of the input array.

Examples

```
>>> x = np.arange(-2, 3)
>>> x
array([-2, -1,  0,  1,  2])
>>> np.flatnonzero(x)
array([0, 1, 3, 4])
```

Use the indices of the non-zero elements as an index array to extract these elements:

```
>>> x.ravel()[np.flatnonzero(x)]
array([-2, -1,  1,  2])
```

dask.array.**flip**(*m*, *axis*)

Reverse element order along axis.

Parameters

axis [int] Axis to reverse element order of.

Returns

reversed array [ndarray]

dask.array.**flipud**(*m*)

Flip array in the up/down direction.

Flip the entries in each column in the up/down direction. Rows are preserved, but appear in a different order than before.

Parameters

m [array_like] Input array.

Returns

out [array_like] A view of *m* with the rows reversed. Since a view is returned, this operation is $\mathcal{O}(1)$.

See also:

fliplr Flip array in the left/right direction.

rot90 Rotate array counterclockwise.

Notes

Equivalent to `A[::-1,...]`. Does not require the array to be two-dimensional.

Examples

```
>>> A = np.diag([1.0, 2, 3])
>>> A
array([[ 1.,  0.,  0.],
       [ 0.,  2.,  0.],
       [ 0.,  0.,  3.]])
>>> np.flipud(A)
array([[ 0.,  0.,  3.],
       [ 0.,  2.,  0.],
       [ 1.,  0.,  0.]])
```

```
>>> A = np.random.randn(2,3,5)
>>> np.all(np.flipud(A)==A[::-1,...])
True
```

```
>>> np.flipud([1,2])
array([2, 1])
```

dask.array.**fliplr**(*m*)

Flip array in the left/right direction.

Flip the entries in each row in the left/right direction. Columns are preserved, but appear in a different order than before.

Parameters

m [array_like] Input array, must be at least 2-D.

Returns

f [ndarray] A view of *m* with the columns reversed. Since a view is returned, this operation is $\mathcal{O}(1)$.

See also:

flipud Flip array in the up/down direction.

rot90 Rot90 array counterclockwise.

Notes

Equivalent to A[:,::-1]. Requires the array to be at least 2-D.

Examples

```
>>> A = np.diag([1.,2.,3.])
>>> A
array([[ 1.,  0.,  0.],
       [ 0.,  2.,  0.],
       [ 0.,  0.,  3.]])
>>> np.fliplr(A)
array([[ 0.,  0.,  1.],
       [ 0.,  2.,  0.],
       [ 3.,  0.,  0.]])
```

```
>>> A = np.random.randn(2,3,5)
>>> np.all(np.fliplr(A)==A[:,::-1,...])
True
```

dask.array.**floor**(*x*[, *out*])

Return the floor of the input, element-wise.

The floor of the scalar *x* is the largest integer *i*, such that *i* <= *x*. It is often denoted as $\lfloor x \rfloor$.

Parameters

x [array_like] Input data.

Returns

y [ndarray or scalar] The floor of each element in *x*.

See also:

ceil, *trunc*, *rint*

Notes

Some spreadsheet programs calculate the "floor-towards-zero", in other words `floor(-2.5) == -2`. NumPy instead uses the definition of *floor* where *floor(-2.5) == -3*.

Examples

```
>>> a = np.array([-1.7, -1.5, -0.2, 0.2, 1.5, 1.7, 2.0])
>>> np.floor(a)
array([-2., -2., -1.,  0.,  1.,  1.,  2.])
```

dask.array.**fmax**(*x1*, *x2*[, *out*])

Element-wise maximum of array elements.

Compare two arrays and returns a new array containing the element-wise maxima. If one of the elements being compared is a NaN, then the non-nan element is returned. If both elements are NaNs then the first is returned. The latter distinction is important for complex NaNs, which are defined as at least one of the real or imaginary parts being a NaN. The net effect is that NaNs are ignored when possible.

Parameters

x1, x2 [array_like] The arrays holding the elements to be compared. They must have the same shape.

Returns

y [ndarray or scalar] The maximum of *x1* and *x2*, element-wise. Returns scalar if both *x1* and *x2* are scalars.

See also:

fmin Element-wise minimum of two arrays, ignores NaNs.

maximum Element-wise maximum of two arrays, propagates NaNs.

amax The maximum value of an array along a given axis, propagates NaNs.

nanmax The maximum value of an array along a given axis, ignores NaNs.

minimum, amin, *nanmin*

Notes

New in version 1.3.0.

The fmax is equivalent to `np.where(x1 >= x2, x1, x2)` when neither x1 nor x2 are NaNs, but it is faster and does proper broadcasting.

Examples

```
>>> np.fmax([2, 3, 4], [1, 5, 2])
array([ 2.,  5.,  4.])
```

```
>>> np.fmax(np.eye(2), [0.5, 2])
array([[ 1. ,  2. ],
       [ 0.5,  2. ]])
```

```
>>> np.fmax([np.nan, 0, np.nan],[0, np.nan, np.nan])
array([  0.,   0.,  NaN])
```

dask.array.**fmin**(*x1*, *x2*[, *out*])

Element-wise minimum of array elements.

Compare two arrays and returns a new array containing the element-wise minima. If one of the elements being compared is a NaN, then the non-nan element is returned. If both elements are NaNs then the first is returned. The latter distinction is important for complex NaNs, which are defined as at least one of the real or imaginary parts being a NaN. The net effect is that NaNs are ignored when possible.

Parameters

x1, x2 [array_like] The arrays holding the elements to be compared. They must have the same shape.

Returns

y [ndarray or scalar] The minimum of *x1* and *x2*, element-wise. Returns scalar if both *x1* and *x2* are scalars.

See also:

fmax Element-wise maximum of two arrays, ignores NaNs.

minimum Element-wise minimum of two arrays, propagates NaNs.

amin The minimum value of an array along a given axis, propagates NaNs.

nanmin The minimum value of an array along a given axis, ignores NaNs.

maximum, amax, *nanmax*

Notes

New in version 1.3.0.

The fmin is equivalent to `np.where(x1 <= x2, x1, x2)` when neither x1 nor x2 are NaNs, but it is faster and does proper broadcasting.

Examples

```
>>> np.fmin([2, 3, 4], [1, 5, 2])
array([2, 5, 4])
```

```
>>> np.fmin(np.eye(2), [0.5, 2])
array([[ 1. ,  2. ],
       [ 0.5,  2. ]])
```

```
>>> np.fmin([np.nan, 0, np.nan],[0, np.nan, np.nan])
array([  0.,   0.,  NaN])
```

dask.array.**fmod**(*x1*, *x2*[, *out*])

Return the element-wise remainder of division.

This is the NumPy implementation of the C library function fmod, the remainder has the same sign as the dividend *x1*. It is equivalent to the Matlab(TM) `rem` function and should not be confused with the Python modulus operator `x1 % x2`.

Parameters

x1 [array_like] Dividend.

x2 [array_like] Divisor.

Returns

y [array_like] The remainder of the division of *x1* by *x2*.

See also:

remainder Equivalent to the Python `%` operator.

divide

Notes

The result of the modulo operation for negative dividend and divisors is bound by conventions. For *fmod*, the sign of result is the sign of the dividend, while for *remainder* the sign of the result is the sign of the divisor. The *fmod* function is equivalent to the Matlab(TM) `rem` function.

Examples

```
>>> np.fmod([-3, -2, -1, 1, 2, 3], 2)
array([-1,  0, -1,  1,  0,  1])
>>> np.remainder([-3, -2, -1, 1, 2, 3], 2)
array([1, 0, 1, 1, 0, 1])
```

```
>>> np.fmod([5, 3], [2, 2.])
array([ 1.,  1.])
>>> a = np.arange(-3, 3).reshape(3, 2)
>>> a
array([[-3, -2],
       [-1,  0],
       [ 1,  2]])
>>> np.fmod(a, [2,2])
array([[-1,  0],
       [-1,  0],
       [ 1,  0]])
```

dask.array.**frexp**(*x*[, *out1*, *out2*])

Decompose the elements of x into mantissa and twos exponent.

Returns (*mantissa*, *exponent*), where *x = mantissa * 2**exponent‘*. The mantissa is lies in the open interval(-1, 1), while the twos exponent is a signed integer.

Parameters

x [array_like] Array of numbers to be decomposed.

out1 [ndarray, optional] Output array for the mantissa. Must have the same shape as *x*.

out2 [ndarray, optional] Output array for the exponent. Must have the same shape as *x*.

Returns

(mantissa, exponent) [tuple of ndarrays, (float, int)] *mantissa* is a float array with values between -1 and 1. *exponent* is an int array which represents the exponent of 2.

See also:

ldexp Compute `y = x1 * 2**x2`, the inverse of *frexp*.

Notes

Complex dtypes are not supported, they will raise a TypeError.

Examples

```
>>> x = np.arange(9)
>>> y1, y2 = np.frexp(x)
>>> y1
array([ 0.   ,  0.5  ,  0.5  ,  0.75 ,  0.5  ,  0.625,  0.75 ,  0.875,
        0.5  ])
>>> y2
array([0, 1, 2, 2, 3, 3, 3, 3, 4])
>>> y1 * 2**y2
array([ 0.,  1.,  2.,  3.,  4.,  5.,  6.,  7.,  8.])
```

`dask.array.`**`fromfunction`**(*function*, *shape*, ***kwargs*)

Construct an array by executing a function over each coordinate.

The resulting array therefore has a value `fn(x, y, z)` at coordinate `(x, y, z)`.

Parameters

function [callable] The function is called with N parameters, where N is the rank of *shape*. Each parameter represents the coordinates of the array varying along a specific axis. For example, if *shape* were `(2, 2)`, then the parameters in turn be (0, 0), (0, 1), (1, 0), (1, 1).

shape [(N,) tuple of ints] Shape of the output array, which also determines the shape of the coordinate arrays passed to *function*.

dtype [data-type, optional] Data-type of the coordinate arrays passed to *function*. By default, *dtype* is float.

Returns

fromfunction [any] The result of the call to *function* is passed back directly. Therefore the shape of *fromfunction* is completely determined by *function*. If *function* returns a scalar value, the shape of *fromfunction* would match the *shape* parameter.

See also:

indices, *meshgrid*

Notes

Keywords other than *dtype* are passed to *function*.

Examples

```
>>> np.fromfunction(lambda i, j: i == j, (3, 3), dtype=int)
array([[ True, False, False],
       [False,  True, False],
       [False, False,  True]], dtype=bool)
```

```
>>> np.fromfunction(lambda i, j: i + j, (3, 3), dtype=int)
array([[0, 1, 2],
       [1, 2, 3],
       [2, 3, 4]])
```

`dask.array.`**`frompyfunc`**(*func*, *nin*, *nout*)

Takes an arbitrary Python function and returns a Numpy ufunc.

Can be used, for example, to add broadcasting to a built-in Python function (see Examples section).

Parameters

func [Python function object] An arbitrary Python function.

nin [int] The number of input arguments.

nout [int] The number of objects returned by *func*.

Returns

out [ufunc] Returns a Numpy universal function (`ufunc`) object.

Notes

The returned ufunc always returns PyObject arrays.

Examples

Use frompyfunc to add broadcasting to the Python function `oct`:

```
>>> oct_array = np.frompyfunc(oct, 1, 1)
>>> oct_array(np.array((10, 30, 100)))
array([012, 036, 0144], dtype=object)
>>> np.array((oct(10), oct(30), oct(100))) # for comparison
array(['012', '036', '0144'],
      dtype='|S4')
```

`dask.array.`**`full`**(**args*, ***kwargs*)

Blocked variant of full

Follows the signature of full exactly except that it also requires a keyword argument chunks=(...)

Original signature follows below.

Return a new array of given shape and type, filled with *fill_value*.

Parameters

shape [int or sequence of ints] Shape of the new array, e.g., `(2, 3)` or `2`.

fill_value [scalar] Fill value.

dtype [data-type, optional] The desired data-type for the array, e.g., *np.int8*. Default is *float*, but will change to *np.array(fill_value).dtype* in a future release.

order [{'C', 'F'}, optional] Whether to store multidimensional data in C- or Fortran-contiguous (row- or column-wise) order in memory.

Returns

out [ndarray] Array of *fill_value* with the given shape, dtype, and order.

See also:

zeros_like Return an array of zeros with shape and type of input.

ones_like Return an array of ones with shape and type of input.

empty_like Return an empty array with shape and type of input.

full_like Fill an array with shape and type of input.

zeros Return a new array setting values to zero.

ones Return a new array setting values to one.

empty Return a new uninitialized array.

Examples

```
>>> np.full((2, 2), np.inf)
array([[ inf,  inf],
       [ inf,  inf]])
>>> np.full((2, 2), 10, dtype=np.int)
array([[10, 10],
       [10, 10]])
```

`dask.array.`**`full_like`**(*a*, *fill_value*, *dtype=None*, *chunks=None*)

Return a full array with the same shape and type as a given array.

Parameters

a [array_like] The shape and data-type of *a* define these same attributes of the returned array.

fill_value [scalar] Fill value.

dtype [data-type, optional] Overrides the data type of the result.

chunks [sequence of ints] The number of samples on each block. Note that the last block will have fewer samples if `len(array) % chunks != 0`.

Returns

out [ndarray] Array of *fill_value* with the same shape and type as *a*.

See also:

zeros_like Return an array of zeros with shape and type of input.

ones_like Return an array of ones with shape and type of input.

empty_like Return an empty array with shape and type of input.

zeros Return a new array setting values to zero.

ones Return a new array setting values to one.

empty Return a new uninitialized array.

full Fill a new array.

dask.array.**gradient**(*f*, **varargs*, ***kwargs*)
Return the gradient of an N-dimensional array.

The gradient is computed using second order accurate central differences in the interior and either first differences or second order accurate one-sides (forward or backwards) differences at the boundaries. The returned gradient hence has the same shape as the input array.

Parameters

f [array_like] An N-dimensional array containing samples of a scalar function.

varargs [scalar or list of scalar, optional] N scalars specifying the sample distances for each dimension, i.e. *dx*, *dy*, *dz*, ... Default distance: 1. single scalar specifies sample distance for all dimensions. if *axis* is given, the number of varargs must equal the number of axes.

edge_order [{1, 2}, optional] Gradient is calculated using N^{th} order accurate differences at the boundaries. Default: 1.

New in version 1.9.1.

axis [None or int or tuple of ints, optional] Gradient is calculated only along the given axis or axes The default (axis = None) is to calculate the gradient for all the axes of the input array. axis may be negative, in which case it counts from the last to the first axis.

New in version 1.11.0.

Returns

gradient [list of ndarray] Each element of *list* has the same shape as *f* giving the derivative of *f* with respect to each dimension.

Examples

```
>>> x = np.array([1, 2, 4, 7, 11, 16], dtype=np.float)
>>> np.gradient(x)
array([ 1. ,  1.5,  2.5,  3.5,  4.5,  5. ])
>>> np.gradient(x, 2)
array([ 0.5 ,  0.75,  1.25,  1.75,  2.25,  2.5 ])
```

For two dimensional arrays, the return will be two arrays ordered by axis. In this example the first array stands for the gradient in rows and the second one in columns direction:

```
>>> np.gradient(np.array([[1, 2, 6], [3, 4, 5]], dtype=np.float))
[array([[ 2.,  2., -1.],
        [ 2.,  2., -1.]]), array([[ 1. ,  2.5,  4. ],
        [ 1. ,  1. ,  1. ]])]
```

```
>>> x = np.array([0, 1, 2, 3, 4])
>>> dx = np.gradient(x)
>>> y = x**2
```

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```
>>> np.gradient(y, dx, edge_order=2)
array([-0.,  2.,  4.,  6.,  8.])
```

The axis keyword can be used to specify a subset of axes of which the gradient is calculated >>> np.gradient(np.array([[1, 2, 6], [3, 4, 5]], dtype=np.float), axis=0) array([[2., 2., -1.],

[2., 2., -1.]])

dask.array.**histogram**(*a*, *bins=None*, *range=None*, *normed=False*, *weights=None*, *density=None*)
Blocked variant of numpy.histogram().

Follows the signature of numpy.histogram() exactly with the following exceptions:

- Either an iterable specifying the bins or the number of bins and a range argument is required as computing min and max over blocked arrays is an expensive operation that must be performed explicitly.
- weights must be a dask.array.Array with the same block structure as a.

Examples

Using number of bins and range:

```
>>> import dask.array as da
>>> import numpy as np
>>> x = da.from_array(np.arange(10000), chunks=10)
>>> h, bins = da.histogram(x, bins=10, range=[0, 10000])
>>> bins
array([    0.,  1000.,  2000.,  3000.,  4000.,  5000.,  6000.,  7000.,
        8000.,  9000., 10000.])
>>> h.compute()
array([1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000])
```

Explicitly specifying the bins:

```
>>> h, bins = da.histogram(x, bins=np.array([0, 5000, 10000]))
>>> bins
array([    0,  5000, 10000])
>>> h.compute()
array([5000, 5000])
```

dask.array.**hstack**(*tup*)
Stack arrays in sequence horizontally (column wise).

Take a sequence of arrays and stack them horizontally to make a single array. Rebuild arrays divided by *hsplit*.

Parameters

tup [sequence of ndarrays] All arrays must have the same shape along all but the second axis.

Returns

stacked [ndarray] The array formed by stacking the given arrays.

See also:

stack Join a sequence of arrays along a new axis.

vstack Stack arrays in sequence vertically (row wise).

dstack Stack arrays in sequence depth wise (along third axis).

concatenate Join a sequence of arrays along an existing axis.

hsplit Split array along second axis.

Notes

Equivalent to `np.concatenate(tup, axis=1)`

Examples

```
>>> a = np.array((1,2,3))
>>> b = np.array((2,3,4))
>>> np.hstack((a,b))
array([1, 2, 3, 2, 3, 4])
>>> a = np.array([[1],[2],[3]])
>>> b = np.array([[2],[3],[4]])
>>> np.hstack((a,b))
array([[1, 2],
       [2, 3],
       [3, 4]])
```

`dask.array.`**hypot**(*x1*, *x2*[, *out*])

Given the "legs" of a right triangle, return its hypotenuse.

Equivalent to `sqrt(x1**2 + x2**2)`, element-wise. If *x1* or *x2* is scalar_like (i.e., unambiguously castable to a scalar type), it is broadcast for use with each element of the other argument. (See Examples)

Parameters

x1, x2 [array_like] Leg of the triangle(s).

out [ndarray, optional] Array into which the output is placed. Its type is preserved and it must be of the right shape to hold the output. See doc.ufuncs.

Returns

z [ndarray] The hypotenuse of the triangle(s).

Examples

```
>>> np.hypot(3*np.ones((3, 3)), 4*np.ones((3, 3)))
array([[ 5.,  5.,  5.],
       [ 5.,  5.,  5.],
       [ 5.,  5.,  5.]])
```

Example showing broadcast of scalar_like argument:

```
>>> np.hypot(3*np.ones((3, 3)), [4])
array([[ 5.,  5.,  5.],
       [ 5.,  5.,  5.],
       [ 5.,  5.,  5.]])
```

`dask.array.`**imag**(**args*, ***kwargs*)

Return the imaginary part of the elements of the array.

Parameters

val [array_like] Input array.

Returns

out [ndarray] Output array. If *val* is real, the type of *val* is used for the output. If *val* has complex elements, the returned type is float.

See also:

real, *angle*, real_if_close

Examples

```
>>> a = np.array([1+2j, 3+4j, 5+6j])
>>> a.imag
array([ 2.,  4.,  6.])
>>> a.imag = np.array([8, 10, 12])
>>> a
array([ 1. +8.j,  3.+10.j,  5.+12.j])
```

dask.array.**indices**(*dimensions*, *dtype=<class 'int'>*, *chunks=None*)

Implements NumPy's indices for Dask Arrays.

Generates a grid of indices covering the dimensions provided.

The final array has the shape (len(dimensions), *dimensions). The chunks are used to specify the chunking for axis 1 up to len(dimensions). The 0th axis always has chunks of length 1.

Parameters

dimensions [sequence of ints] The shape of the index grid.

dtype [dtype, optional] Type to use for the array. Default is int.

chunks [sequence of ints] The number of samples on each block. Note that the last block will have fewer samples if len(array) % chunks != 0.

Returns

grid [dask array]

dask.array.**insert**(*arr*, *obj*, *values*, *axis=None*)

Insert values along the given axis before the given indices.

Parameters

arr [array_like] Input array.

obj [int, slice or sequence of ints] Object that defines the index or indices before which *values* is inserted.

New in version 1.8.0.

Support for multiple insertions when *obj* is a single scalar or a sequence with one element (similar to calling insert multiple times).

values [array_like] Values to insert into *arr*. If the type of *values* is different from that of *arr*, *values* is converted to the type of *arr*. *values* should be shaped so that arr[...,obj,...] = values is legal.

axis [int, optional] Axis along which to insert *values*. If *axis* is None then *arr* is flattened first.

Returns

out [ndarray] A copy of *arr* with *values* inserted. Note that *insert* does not occur in-place: a new array is returned. If *axis* is None, *out* is a flattened array.

See also:

append Append elements at the end of an array.

concatenate Join a sequence of arrays along an existing axis.

delete Delete elements from an array.

Notes

Note that for higher dimensional inserts *obj=0* behaves very different from *obj=[0]* just like *arr[:,0,:] = values* is different from *arr[:,[0],:] = values*.

Examples

```
>>> a = np.array([[1, 1], [2, 2], [3, 3]])
>>> a
array([[1, 1],
       [2, 2],
       [3, 3]])
>>> np.insert(a, 1, 5)
array([1, 5, 1, 2, 2, 3, 3])
>>> np.insert(a, 1, 5, axis=1)
array([[1, 5, 1],
       [2, 5, 2],
       [3, 5, 3]])
```

Difference between sequence and scalars:

```
>>> np.insert(a, [1], [[1],[2],[3]], axis=1)
array([[1, 1, 1],
       [2, 2, 2],
       [3, 3, 3]])
>>> np.array_equal(np.insert(a, 1, [1, 2, 3], axis=1),
...                np.insert(a, [1], [[1],[2],[3]], axis=1))
True
```

```
>>> b = a.flatten()
>>> b
array([1, 1, 2, 2, 3, 3])
>>> np.insert(b, [2, 2], [5, 6])
array([1, 1, 5, 6, 2, 2, 3, 3])
```

```
>>> np.insert(b, slice(2, 4), [5, 6])
array([1, 1, 5, 2, 6, 2, 3, 3])
```

```
>>> np.insert(b, [2, 2], [7.13, False]) # type casting
array([1, 1, 7, 0, 2, 2, 3, 3])
```

```
>>> x = np.arange(8).reshape(2, 4)
>>> idx = (1, 3)
>>> np.insert(x, idx, 999, axis=1)
array([[  0, 999,   1,   2, 999,   3],
       [  4, 999,   5,   6, 999,   7]])
```

dask.array.**isclose**(*a*, *b*, *rtol=1e-05*, *atol=1e-08*, *equal_nan=False*)

Returns a boolean array where two arrays are element-wise equal within a tolerance.

The tolerance values are positive, typically very small numbers. The relative difference (*rtol* * abs(*b*)) and the absolute difference *atol* are added together to compare against the absolute difference between *a* and *b*.

Parameters

a, b [array_like] Input arrays to compare.

rtol [float] The relative tolerance parameter (see Notes).

atol [float] The absolute tolerance parameter (see Notes).

equal_nan [bool] Whether to compare NaN's as equal. If True, NaN's in *a* will be considered equal to NaN's in *b* in the output array.

Returns

y [array_like] Returns a boolean array of where *a* and *b* are equal within the given tolerance. If both *a* and *b* are scalars, returns a single boolean value.

See also:

allclose

Notes

New in version 1.7.0.

For finite values, isclose uses the following equation to test whether two floating point values are equivalent.

absolute(*a* - *b*) <= (*atol* + *rtol* * absolute(*b*))

The above equation is not symmetric in *a* and *b*, so that *isclose(a, b)* might be different from *isclose(b, a)* in some rare cases.

Examples

```
>>> np.isclose([1e10,1e-7], [1.00001e10,1e-8])
array([True, False])
>>> np.isclose([1e10,1e-8], [1.00001e10,1e-9])
array([True, True])
>>> np.isclose([1e10,1e-8], [1.0001e10,1e-9])
array([False, True])
>>> np.isclose([1.0, np.nan], [1.0, np.nan])
array([True, False])
>>> np.isclose([1.0, np.nan], [1.0, np.nan], equal_nan=True)
array([True, True])
```

dask.array.**iscomplex**(**args*, ***kwargs*)

Returns a bool array, where True if input element is complex.

What is tested is whether the input has a non-zero imaginary part, not if the input type is complex.

Parameters

x [array_like] Input array.

Returns

out [ndarray of bools] Output array.

See also:

isreal

iscomplexobj Return True if x is a complex type or an array of complex numbers.

Examples

```
>>> np.iscomplex([1+1j, 1+0j, 4.5, 3, 2, 2j])
array([ True, False, False, False, False,  True], dtype=bool)
```

dask.array.**isfinite**(*x*[, *out*])

Test element-wise for finiteness (not infinity or not Not a Number).

The result is returned as a boolean array.

Parameters

x [array_like] Input values.

out [ndarray, optional] Array into which the output is placed. Its type is preserved and it must be of the right shape to hold the output. See *doc.ufuncs*.

Returns

y [ndarray, bool] For scalar input, the result is a new boolean with value True if the input is finite; otherwise the value is False (input is either positive infinity, negative infinity or Not a Number).

For array input, the result is a boolean array with the same dimensions as the input and the values are True if the corresponding element of the input is finite; otherwise the values are False (element is either positive infinity, negative infinity or Not a Number).

See also:

isinf, *isneginf*, *isposinf*, *isnan*

Notes

Not a Number, positive infinity and negative infinity are considered to be non-finite.

Numpy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754). This means that Not a Number is not equivalent to infinity. Also that positive infinity is not equivalent to negative infinity. But infinity is equivalent to positive infinity. Errors result if the second argument is also supplied when *x* is a scalar input, or if first and second arguments have different shapes.

Examples

```
>>> np.isfinite(1)
True
>>> np.isfinite(0)
True
>>> np.isfinite(np.nan)
False
>>> np.isfinite(np.inf)
False
>>> np.isfinite(np.NINF)
False
>>> np.isfinite([np.log(-1.),1.,np.log(0)])
array([False,  True, False], dtype=bool)
```

```
>>> x = np.array([-np.inf, 0., np.inf])
>>> y = np.array([2, 2, 2])
>>> np.isfinite(x, y)
array([0, 1, 0])
>>> y
array([0, 1, 0])
```

dask.array.**isin**(*element*, *test_elements*, *assume_unique=False*, *invert=False*)

dask.array.**isinf**(*x*[, *out*])

Test element-wise for positive or negative infinity.

Returns a boolean array of the same shape as *x*, True where `x == +/-inf`, otherwise False.

Parameters

x [array_like] Input values

out [array_like, optional] An array with the same shape as *x* to store the result.

Returns

y [bool (scalar) or boolean ndarray] For scalar input, the result is a new boolean with value True if the input is positive or negative infinity; otherwise the value is False.

For array input, the result is a boolean array with the same shape as the input and the values are True where the corresponding element of the input is positive or negative infinity; elsewhere the values are False. If a second argument was supplied the result is stored there. If the type of that array is a numeric type the result is represented as zeros and ones, if the type is boolean then as False and True, respectively. The return value *y* is then a reference to that array.

See also:

isneginf, *isposinf*, *isnan*, *isfinite*

Notes

Numpy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754).

Errors result if the second argument is supplied when the first argument is a scalar, or if the first and second arguments have different shapes.

Examples

```
>>> np.isinf(np.inf)
True
>>> np.isinf(np.nan)
False
>>> np.isinf(np.NINF)
True
>>> np.isinf([np.inf, -np.inf, 1.0, np.nan])
array([ True,  True, False, False], dtype=bool)
```

```
>>> x = np.array([-np.inf, 0., np.inf])
>>> y = np.array([2, 2, 2])
>>> np.isinf(x, y)
array([1, 0, 1])
>>> y
array([1, 0, 1])
```

dask.array.**isneginf**(**args*, ***kwargs*)

Test element-wise for negative infinity, return result as bool array.

Parameters

x [array_like] The input array.

y [array_like, optional] A boolean array with the same shape and type as *x* to store the result.

Returns

y [ndarray] A boolean array with the same dimensions as the input. If second argument is not supplied then a numpy boolean array is returned with values True where the corresponding element of the input is negative infinity and values False where the element of the input is not negative infinity.

If a second argument is supplied the result is stored there. If the type of that array is a numeric type the result is represented as zeros and ones, if the type is boolean then as False and True. The return value *y* is then a reference to that array.

See also:

isinf, *isposinf*, *isnan*, *isfinite*

Notes

Numpy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754).

Errors result if the second argument is also supplied when x is a scalar input, or if first and second arguments have different shapes.

Examples

```
>>> np.isneginf(np.NINF)
array(True, dtype=bool)
>>> np.isneginf(np.inf)
array(False, dtype=bool)
>>> np.isneginf(np.PINF)
```

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```
array(False, dtype=bool)
>>> np.isneginf([-np.inf, 0., np.inf])
array([ True, False, False], dtype=bool)
```

```
>>> x = np.array([-np.inf, 0., np.inf])
>>> y = np.array([2, 2, 2])
>>> np.isneginf(x, y)
array([1, 0, 0])
>>> y
array([1, 0, 0])
```

dask.array.**isnan**(*x*[, *out*])

Test element-wise for NaN and return result as a boolean array.

Parameters

x [array_like] Input array.

Returns

y [ndarray or bool] For scalar input, the result is a new boolean with value True if the input is NaN; otherwise the value is False.

For array input, the result is a boolean array of the same dimensions as the input and the values are True if the corresponding element of the input is NaN; otherwise the values are False.

See also:

isinf, *isneginf*, *isposinf*, *isfinite*

Notes

Numpy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754). This means that Not a Number is not equivalent to infinity.

Examples

```
>>> np.isnan(np.nan)
True
>>> np.isnan(np.inf)
False
>>> np.isnan([np.log(-1.),1.,np.log(0)])
array([ True, False, False], dtype=bool)
```

dask.array.**isnull**(*values*)

pandas.isnull for dask arrays

dask.array.**isposinf**(**args*, ***kwargs*)

Test element-wise for positive infinity, return result as bool array.

Parameters

x [array_like] The input array.

y [array_like, optional] A boolean array with the same shape as *x* to store the result.

Returns

y [ndarray] A boolean array with the same dimensions as the input. If second argument is not supplied then a boolean array is returned with values True where the corresponding element of the input is positive infinity and values False where the element of the input is not positive infinity.

If a second argument is supplied the result is stored there. If the type of that array is a numeric type the result is represented as zeros and ones, if the type is boolean then as False and True. The return value *y* is then a reference to that array.

See also:

isinf, *isneginf*, *isfinite*, *isnan*

Notes

Numpy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754).

Errors result if the second argument is also supplied when *x* is a scalar input, or if first and second arguments have different shapes.

Examples

```
>>> np.isposinf(np.PINF)
array(True, dtype=bool)
>>> np.isposinf(np.inf)
array(True, dtype=bool)
>>> np.isposinf(np.NINF)
array(False, dtype=bool)
>>> np.isposinf([-np.inf, 0., np.inf])
array([False, False,  True], dtype=bool)
```

```
>>> x = np.array([-np.inf, 0., np.inf])
>>> y = np.array([2, 2, 2])
>>> np.isposinf(x, y)
array([0, 0, 1])
>>> y
array([0, 0, 1])
```

dask.array.**isreal**(**args*, ***kwargs*)

Returns a bool array, where True if input element is real.

If element has complex type with zero complex part, the return value for that element is True.

Parameters

x [array_like] Input array.

Returns

out [ndarray, bool] Boolean array of same shape as *x*.

See also:

iscomplex

isrealobj Return True if x is not a complex type.

Examples

```
>>> np.isreal([1+1j, 1+0j, 4.5, 3, 2, 2j])
array([False,  True,  True,  True,  True, False], dtype=bool)
```

dask.array.**ldexp**(*x1*, *x2*[, *out*])

Returns x1 * 2**x2, element-wise.

The mantissas *x1* and twos exponents *x2* are used to construct floating point numbers `x1 * 2**x2`.

Parameters

x1 [array_like] Array of multipliers.

x2 [array_like, int] Array of twos exponents.

out [ndarray, optional] Output array for the result.

Returns

y [ndarray or scalar] The result of `x1 * 2**x2`.

See also:

frexp Return (y1, y2) from `x = y1 * 2**y2`, inverse to *ldexp*.

Notes

Complex dtypes are not supported, they will raise a TypeError.

ldexp is useful as the inverse of *frexp*, if used by itself it is more clear to simply use the expression `x1 * 2**x2`.

Examples

```
>>> np.ldexp(5, np.arange(4))
array([  5.,  10.,  20.,  40.], dtype=float32)
```

```
>>> x = np.arange(6)
>>> np.ldexp(*np.frexp(x))
array([ 0.,  1.,  2.,  3.,  4.,  5.])
```

dask.array.**linspace**(*start*, *stop*, *num=50*, *endpoint=True*, *retstep=False*, *chunks=None*, *dtype=None*)

Return *num* evenly spaced values over the closed interval [*start*, *stop*].

Parameters

start [scalar] The starting value of the sequence.

stop [scalar] The last value of the sequence.

num [int, optional] Number of samples to include in the returned dask array, including the endpoints. Default is 50.

endpoint [bool, optional] If True, `stop` is the last sample. Otherwise, it is not included. Default is True.

retstep [bool, optional] If True, return (samples, step), where step is the spacing between samples. Default is False.

chunks [int] The number of samples on each block. Note that the last block will have fewer samples if *num % blocksize != 0*

dtype [dtype, optional] The type of the output array. Default is given by `numpy.dtype(float)`.

Returns

samples [dask array]

step [float, optional] Only returned if `retstep` is True. Size of spacing between samples.

See also:

dask.array.arange

`dask.array.log`(*x*[, *out*])

Natural logarithm, element-wise.

The natural logarithm *log* is the inverse of the exponential function, so that *log(exp(x)) = x*. The natural logarithm is logarithm in base *e*.

Parameters

x [array_like] Input value.

Returns

y [ndarray] The natural logarithm of *x*, element-wise.

See also:

log10, *log2*, *log1p*, `emath.log`

Notes

Logarithm is a multivalued function: for each *x* there is an infinite number of *z* such that *exp(z) = x*. The convention is to return the *z* whose imaginary part lies in *[-pi, pi]*.

For real-valued input data types, *log* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *log* is a complex analytical function that has a branch cut *[-inf, 0]* and is continuous from above on it. *log* handles the floating-point negative zero as an infinitesimal negative number, conforming to the C99 standard.

References

[1], *[2]*

Examples

```
>>> np.log([1, np.e, np.e**2, 0])
array([  0.,   1.,   2., -Inf])
```

`dask.array.log10`(*x*[, *out*])

Return the base 10 logarithm of the input array, element-wise.

Parameters

x [array_like] Input values.

Returns

y [ndarray] The logarithm to the base 10 of *x*, element-wise. NaNs are returned where x is negative.

See also:

`emath.log10`

Notes

Logarithm is a multivalued function: for each *x* there is an infinite number of *z* such that *10**z = x*. The convention is to return the *z* whose imaginary part lies in *[-pi, pi]*.

For real-valued input data types, *log10* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *log10* is a complex analytical function that has a branch cut *[-inf, 0]* and is continuous from above on it. *log10* handles the floating-point negative zero as an infinitesimal negative number, conforming to the C99 standard.

References

[1], *[2]*

Examples

```
>>> np.log10([1e-15, -3.])
array([-15.,  NaN])
```

`dask.array.`**`log1p`**(*x*[, *out*])

Return the natural logarithm of one plus the input array, element-wise.

Calculates `log(1 + x)`.

Parameters

x [array_like] Input values.

Returns

y [ndarray] Natural logarithm of *1 + x*, element-wise.

See also:

expm1 `exp(x) - 1`, the inverse of *log1p*.

Notes

For real-valued input, *log1p* is accurate also for *x* so small that *1 + x == 1* in floating-point accuracy.

Logarithm is a multivalued function: for each *x* there is an infinite number of *z* such that *exp(z) = 1 + x*. The convention is to return the *z* whose imaginary part lies in *[-pi, pi]*.

For real-valued input data types, *log1p* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *log1p* is a complex analytical function that has a branch cut *[-inf, -1]* and is continuous from above on it. *log1p* handles the floating-point negative zero as an infinitesimal negative number, conforming to the C99 standard.

References

[1], *[2]*

Examples

```
>>> np.log1p(1e-99)
1e-99
>>> np.log(1 + 1e-99)
0.0
```

`dask.array.log2`(*x*[, *out*])

Base-2 logarithm of *x*.

Parameters

x [array_like] Input values.

Returns

y [ndarray] Base-2 logarithm of *x*.

See also:

log, *log10*, *log1p*, `emath.log2`

Notes

New in version 1.3.0.

Logarithm is a multivalued function: for each *x* there is an infinite number of *z* such that *2**z = x*. The convention is to return the *z* whose imaginary part lies in *[-pi, pi]*.

For real-valued input data types, *log2* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *log2* is a complex analytical function that has a branch cut *[-inf, 0]* and is continuous from above on it. *log2* handles the floating-point negative zero as an infinitesimal negative number, conforming to the C99 standard.

Examples

```
>>> x = np.array([0, 1, 2, 2**4])
>>> np.log2(x)
array([-Inf,   0.,   1.,   4.])
```

```
>>> xi = np.array([0+1.j, 1, 2+0.j, 4.j])
>>> np.log2(xi)
array([ 0.+2.26618007j,  0.+0.j        ,  1.+0.j        ,  2.+2.26618007j])
```

dask.array.**logaddexp**(*x1*, *x2*[, *out*])

Logarithm of the sum of exponentiations of the inputs.

Calculates `log(exp(x1) + exp(x2))`. This function is useful in statistics where the calculated probabilities of events may be so small as to exceed the range of normal floating point numbers. In such cases the logarithm of the calculated probability is stored. This function allows adding probabilities stored in such a fashion.

Parameters

x1, x2 [array_like] Input values.

Returns

result [ndarray] Logarithm of `exp(x1) + exp(x2)`.

See also:

logaddexp2 Logarithm of the sum of exponentiations of inputs in base 2.

Notes

New in version 1.3.0.

Examples

```
>>> prob1 = np.log(1e-50)
>>> prob2 = np.log(2.5e-50)
>>> prob12 = np.logaddexp(prob1, prob2)
>>> prob12
-113.87649168120691
>>> np.exp(prob12)
3.5000000000000057e-50
```

dask.array.**logaddexp2**(*x1*, *x2*[, *out*])

Logarithm of the sum of exponentiations of the inputs in base-2.

Calculates `log2(2**x1 + 2**x2)`. This function is useful in machine learning when the calculated probabilities of events may be so small as to exceed the range of normal floating point numbers. In such cases the base-2 logarithm of the calculated probability can be used instead. This function allows adding probabilities stored in such a fashion.

Parameters

x1, x2 [array_like] Input values.

out [ndarray, optional] Array to store results in.

Returns

result [ndarray] Base-2 logarithm of `2**x1 + 2**x2`.

See also:

logaddexp Logarithm of the sum of exponentiations of the inputs.

Notes

New in version 1.3.0.

Examples

```
>>> prob1 = np.log2(1e-50)
>>> prob2 = np.log2(2.5e-50)
>>> prob12 = np.logaddexp2(prob1, prob2)
>>> prob1, prob2, prob12
(-166.09640474436813, -164.77447664948076, -164.28904982231052)
>>> 2**prob12
3.4999999999999914e-50
```

dask.array.**logical_and**(*x1*, *x2*[, *out*])

Compute the truth value of x1 AND x2 element-wise.

Parameters

x1, x2 [array_like] Input arrays. *x1* and *x2* must be of the same shape.

Returns

y [ndarray or bool] Boolean result with the same shape as *x1* and *x2* of the logical AND operation on corresponding elements of *x1* and *x2*.

See also:

logical_or, *logical_not*, *logical_xor*, *bitwise_and*

Examples

```
>>> np.logical_and(True, False)
False
>>> np.logical_and([True, False], [False, False])
array([False, False], dtype=bool)
```

```
>>> x = np.arange(5)
>>> np.logical_and(x>1, x<4)
array([False, False,  True,  True, False], dtype=bool)
```

dask.array.**logical_not**(*x*[, *out*])

Compute the truth value of NOT x element-wise.

Parameters

x [array_like] Logical NOT is applied to the elements of *x*.

Returns

y [bool or ndarray of bool] Boolean result with the same shape as *x* of the NOT operation on elements of *x*.

See also:

logical_and, *logical_or*, *logical_xor*

Examples

```
>>> np.logical_not(3)
False
>>> np.logical_not([True, False, 0, 1])
array([False,  True,  True, False], dtype=bool)
```

```
>>> x = np.arange(5)
>>> np.logical_not(x<3)
array([False, False, False,  True,  True], dtype=bool)
```

dask.array.**logical_or**(*x1*, *x2*[, *out*])

Compute the truth value of x1 OR x2 element-wise.

Parameters

x1, x2 [array_like] Logical OR is applied to the elements of *x1* and *x2*. They have to be of the same shape.

Returns

y [ndarray or bool] Boolean result with the same shape as *x1* and *x2* of the logical OR operation on elements of *x1* and *x2*.

See also:

logical_and, *logical_not*, *logical_xor*, *bitwise_or*

Examples

```
>>> np.logical_or(True, False)
True
>>> np.logical_or([True, False], [False, False])
array([ True, False], dtype=bool)
```

```
>>> x = np.arange(5)
>>> np.logical_or(x < 1, x > 3)
array([ True, False, False, False,  True], dtype=bool)
```

dask.array.**logical_xor**(*x1*, *x2*[, *out*])

Compute the truth value of x1 XOR x2, element-wise.

Parameters

x1, x2 [array_like] Logical XOR is applied to the elements of *x1* and *x2*. They must be broadcastable to the same shape.

Returns

y [bool or ndarray of bool] Boolean result of the logical XOR operation applied to the elements of *x1* and *x2*; the shape is determined by whether or not broadcasting of one or both arrays was required.

See also:

logical_and, *logical_or*, *logical_not*, *bitwise_xor*

Examples

```
>>> np.logical_xor(True, False)
True
>>> np.logical_xor([True, True, False, False], [True, False, True, False])
array([False,  True,  True, False], dtype=bool)
```

```
>>> x = np.arange(5)
>>> np.logical_xor(x < 1, x > 3)
array([ True, False, False, False,  True], dtype=bool)
```

Simple example showing support of broadcasting

```
>>> np.logical_xor(0, np.eye(2))
array([[ True, False],
       [False,  True]], dtype=bool)
```

dask.array.**matmul**(*a*, *b*, *out=None*)

Matrix product of two arrays.

The behavior depends on the arguments in the following way.

- If both arguments are 2-D they are multiplied like conventional matrices.
- If either argument is N-D, N > 2, it is treated as a stack of matrices residing in the last two indexes and broadcast accordingly.
- If the first argument is 1-D, it is promoted to a matrix by prepending a 1 to its dimensions. After matrix multiplication the prepended 1 is removed.
- If the second argument is 1-D, it is promoted to a matrix by appending a 1 to its dimensions. After matrix multiplication the appended 1 is removed.

Multiplication by a scalar is not allowed, use `*` instead. Note that multiplying a stack of matrices with a vector will result in a stack of vectors, but matmul will not recognize it as such.

`matmul` differs from `dot` in two important ways.

- Multiplication by scalars is not allowed.
- Stacks of matrices are broadcast together as if the matrices were elements.

Warning: This function is preliminary and included in Numpy 1.10 for testing and documentation. Its semantics will not change, but the number and order of the optional arguments will.

New in version 1.10.0.

Parameters

a [array_like] First argument.

b [array_like] Second argument.

out [ndarray, optional] Output argument. This must have the exact kind that would be returned if it was not used. In particular, it must have the right type, must be C-contiguous, and its dtype must be the dtype that would be returned for *dot(a,b)*. This is a performance feature. Therefore, if these conditions are not met, an exception is raised, instead of attempting to be flexible.

Returns

output [ndarray] Returns the dot product of *a* and *b*. If *a* and *b* are both 1-D arrays then a scalar is returned; otherwise an array is returned. If *out* is given, then it is returned.

Raises

ValueError If the last dimension of *a* is not the same size as the second-to-last dimension of *b*.

If scalar value is passed.

See also:

vdot Complex-conjugating dot product.

tensordot Sum products over arbitrary axes.

einsum Einstein summation convention.

dot alternative matrix product with different broadcasting rules.

Notes

The matmul function implements the semantics of the @ operator introduced in Python 3.5 following PEP465.

Examples

For 2-D arrays it is the matrix product:

```
>>> a = [[1, 0], [0, 1]]
>>> b = [[4, 1], [2, 2]]
>>> np.matmul(a, b)
array([[4, 1],
       [2, 2]])
```

For 2-D mixed with 1-D, the result is the usual.

```
>>> a = [[1, 0], [0, 1]]
>>> b = [1, 2]
>>> np.matmul(a, b)
array([1, 2])
>>> np.matmul(b, a)
array([1, 2])
```

Broadcasting is conventional for stacks of arrays

```
>>> a = np.arange(2*2*4).reshape((2,2,4))
>>> b = np.arange(2*2*4).reshape((2,4,2))
>>> np.matmul(a,b).shape
(2, 2, 2)
>>> np.matmul(a,b)[0,1,1]
98
>>> sum(a[0,1,:] * b[0,:,1])
98
```

Vector, vector returns the scalar inner product, but neither argument is complex-conjugated:

```
>>> np.matmul([2j, 3j], [2j, 3j])
(-13+0j)
```

Scalar multiplication raises an error.

```
>>> np.matmul([1,2], 3)
Traceback (most recent call last):
...
ValueError: Scalar operands are not allowed, use '*' instead
```

dask.array.**max**(*a*, *axis=None*, *out=None*, *keepdims=False*)

Return the maximum of an array or maximum along an axis.

Parameters

a [array_like] Input data.

axis [None or int or tuple of ints, optional] Axis or axes along which to operate. By default, flattened input is used.

If this is a tuple of ints, the maximum is selected over multiple axes, instead of a single axis or all the axes as before.

out [ndarray, optional] Alternative output array in which to place the result. Must be of the same shape and buffer length as the expected output. See *doc.ufuncs* (Section "Output arguments") for more details.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

Returns

amax [ndarray or scalar] Maximum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is an array of dimension `a.ndim - 1`.

See also:

amin The minimum value of an array along a given axis, propagating any NaNs.

nanmax The maximum value of an array along a given axis, ignoring any NaNs.

maximum Element-wise maximum of two arrays, propagating any NaNs.

fmax Element-wise maximum of two arrays, ignoring any NaNs.

argmax Return the indices of the maximum values.

nanmin, *minimum*, *fmin*

Notes

NaN values are propagated, that is if at least one item is NaN, the corresponding max value will be NaN as well. To ignore NaN values (MATLAB behavior), please use nanmax.

Don't use *amax* for element-wise comparison of 2 arrays; when `a.shape[0]` is 2, `maximum(a[0], a[1])` is faster than `amax(a, axis=0)`.

Examples

```
>>> a = np.arange(4).reshape((2,2))
>>> a
array([[0, 1],
       [2, 3]])
>>> np.amax(a)           # Maximum of the flattened array
3
>>> np.amax(a, axis=0)   # Maxima along the first axis
array([2, 3])
>>> np.amax(a, axis=1)   # Maxima along the second axis
array([1, 3])
```

```
>>> b = np.arange(5, dtype=np.float)
>>> b[2] = np.NaN
>>> np.amax(b)
nan
>>> np.nanmax(b)
4.0
```

dask.array.**maximum**(*x1*, *x2*[, *out*])

Element-wise maximum of array elements.

Compare two arrays and returns a new array containing the element-wise maxima. If one of the elements being compared is a NaN, then that element is returned. If both elements are NaNs then the first is returned. The latter distinction is important for complex NaNs, which are defined as at least one of the real or imaginary parts being a NaN. The net effect is that NaNs are propagated.

Parameters

x1, x2 [array_like] The arrays holding the elements to be compared. They must have the same shape, or shapes that can be broadcast to a single shape.

Returns

y [ndarray or scalar] The maximum of *x1* and *x2*, element-wise. Returns scalar if both *x1* and *x2* are scalars.

See also:

minimum Element-wise minimum of two arrays, propagates NaNs.

fmax Element-wise maximum of two arrays, ignores NaNs.

amax The maximum value of an array along a given axis, propagates NaNs.

nanmax The maximum value of an array along a given axis, ignores NaNs.

fmin, amin, *nanmin*

Notes

The maximum is equivalent to `np.where(x1 >= x2, x1, x2)` when neither x1 nor x2 are nans, but it is faster and does proper broadcasting.

Examples

```
>>> np.maximum([2, 3, 4], [1, 5, 2])
array([2, 5, 4])
```

```
>>> np.maximum(np.eye(2), [0.5, 2]) # broadcasting
array([[ 1. ,  2. ],
       [ 0.5,  2. ]])
```

```
>>> np.maximum([np.nan, 0, np.nan], [0, np.nan, np.nan])
array([ NaN,  NaN,  NaN])
>>> np.maximum(np.Inf, 1)
inf
```

dask.array.**mean**(*a*, *axis=None*, *dtype=None*, *out=None*, *keepdims=False*)

Compute the arithmetic mean along the specified axis.

Returns the average of the array elements. The average is taken over the flattened array by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

Parameters

a [array_like] Array containing numbers whose mean is desired. If *a* is not an array, a conversion is attempted.

axis [None or int or tuple of ints, optional] Axis or axes along which the means are computed. The default is to compute the mean of the flattened array.

If this is a tuple of ints, a mean is performed over multiple axes, instead of a single axis or all the axes as before.

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is *float64*; for floating point inputs, it is the same as the input dtype.

out [ndarray, optional] Alternate output array in which to place the result. The default is `None`; if provided, it must have the same shape as the expected output, but the type will be cast if necessary. See *doc.ufuncs* for details.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

Returns

m [ndarray, see dtype parameter above] If *out=None*, returns a new array containing the mean values, otherwise a reference to the output array is returned.

See also:

average Weighted average

std, *var*, *nanmean*, *nanstd*, *nanvar*

Notes

The arithmetic mean is the sum of the elements along the axis divided by the number of elements.

Note that for floating-point input, the mean is computed using the same precision the input has. Depending on the input data, this can cause the results to be inaccurate, especially for *float32* (see example below). Specifying a higher-precision accumulator using the *dtype* keyword can alleviate this issue.

Examples

```
>>> a = np.array([[1, 2], [3, 4]])
>>> np.mean(a)
2.5
>>> np.mean(a, axis=0)
array([ 2.,  3.])
>>> np.mean(a, axis=1)
array([ 1.5,  3.5])
```

In single precision, *mean* can be inaccurate:

```
>>> a = np.zeros((2, 512*512), dtype=np.float32)
>>> a[0, :] = 1.0
>>> a[1, :] = 0.1
>>> np.mean(a)
0.546875
```

Computing the mean in float64 is more accurate:

```
>>> np.mean(a, dtype=np.float64)
0.55000000074505806
```

dask.array.**meshgrid**(**xi*, ***kwargs*)

Return coordinate matrices from coordinate vectors.

Make N-D coordinate arrays for vectorized evaluations of N-D scalar/vector fields over N-D grids, given one-dimensional coordinate arrays x1, x2,..., xn.

Changed in version 1.9: 1-D and 0-D cases are allowed.

Parameters

x1, x2,..., xn [array_like] 1-D arrays representing the coordinates of a grid.

indexing [{'xy', 'ij'}, optional] Cartesian ('xy', default) or matrix ('ij') indexing of output. See Notes for more details.

New in version 1.7.0.

sparse [bool, optional] If True a sparse grid is returned in order to conserve memory. Default is False.

New in version 1.7.0.

copy [bool, optional] If False, a view into the original arrays are returned in order to conserve memory. Default is True. Please note that `sparse=False, copy=False` will likely return non-contiguous arrays. Furthermore, more than one element of a broadcast array may refer to a single memory location. If you need to write to the arrays, make copies first.

New in version 1.7.0.

Returns

X1, X2,..., XN [ndarray] For vectors *x1*, *x2*,..., 'xn' with lengths `Ni=len(xi)` , return `(N1, N2, N3,...Nn)` shaped arrays if indexing='ij' or `(N2, N1, N3,...Nn)` shaped arrays if indexing='xy' with the elements of *xi* repeated to fill the matrix along the first dimension for *x1*, the second for *x2* and so on.

See also:

index_tricks.mgrid Construct a multi-dimensional "meshgrid" using indexing notation.

index_tricks.ogrid Construct an open multi-dimensional "meshgrid" using indexing notation.

Notes

This function supports both indexing conventions through the indexing keyword argument. Giving the string 'ij' returns a meshgrid with matrix indexing, while 'xy' returns a meshgrid with Cartesian indexing. In the 2-D case with inputs of length M and N, the outputs are of shape (N, M) for 'xy' indexing and (M, N) for 'ij' indexing. In the 3-D case with inputs of length M, N and P, outputs are of shape (N, M, P) for 'xy' indexing and (M, N, P) for 'ij' indexing. The difference is illustrated by the following code snippet:

```
xv, yv = meshgrid(x, y, sparse=False, indexing='ij')
for i in range(nx):
    for j in range(ny):
        # treat xv[i,j], yv[i,j]

xv, yv = meshgrid(x, y, sparse=False, indexing='xy')
for i in range(nx):
    for j in range(ny):
        # treat xv[j,i], yv[j,i]
```

In the 1-D and 0-D case, the indexing and sparse keywords have no effect.

Examples

```
>>> nx, ny = (3, 2)
>>> x = np.linspace(0, 1, nx)
>>> y = np.linspace(0, 1, ny)
>>> xv, yv = meshgrid(x, y)
>>> xv
array([[ 0. ,  0.5,  1. ],
       [ 0. ,  0.5,  1. ]])
>>> yv
array([[ 0.,  0.,  0.],
       [ 1.,  1.,  1.]])
>>> xv, yv = meshgrid(x, y, sparse=True)  # make sparse output arrays
>>> xv
array([[ 0. ,  0.5,  1. ]])
>>> yv
array([[ 0.],
       [ 1.]])
```

meshgrid is very useful to evaluate functions on a grid.

```
>>> x = np.arange(-5, 5, 0.1)
>>> y = np.arange(-5, 5, 0.1)
>>> xx, yy = meshgrid(x, y, sparse=True)
>>> z = np.sin(xx**2 + yy**2) / (xx**2 + yy**2)
>>> h = plt.contourf(x,y,z)
```

dask.array.**min**(*a*, *axis=None*, *out=None*, *keepdims=False*)

Return the minimum of an array or minimum along an axis.

Parameters

a [array_like] Input data.

axis [None or int or tuple of ints, optional] Axis or axes along which to operate. By default, flattened input is used.

If this is a tuple of ints, the minimum is selected over multiple axes, instead of a single axis or all the axes as before.

out [ndarray, optional] Alternative output array in which to place the result. Must be of the same shape and buffer length as the expected output. See *doc.ufuncs* (Section "Output arguments") for more details.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

Returns

amin [ndarray or scalar] Minimum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is an array of dimension `a.ndim - 1`.

See also:

amax The maximum value of an array along a given axis, propagating any NaNs.

nanmin The minimum value of an array along a given axis, ignoring any NaNs.

minimum Element-wise minimum of two arrays, propagating any NaNs.

fmin Element-wise minimum of two arrays, ignoring any NaNs.

argmin Return the indices of the minimum values.

nanmax, *maximum*, *fmax*

Notes

NaN values are propagated, that is if at least one item is NaN, the corresponding min value will be NaN as well. To ignore NaN values (MATLAB behavior), please use nanmin.

Don't use *amin* for element-wise comparison of 2 arrays; when `a.shape[0]` is 2, `minimum(a[0], a[1])` is faster than `amin(a, axis=0)`.

Examples

```
>>> a = np.arange(4).reshape((2,2))
>>> a
array([[0, 1],
       [2, 3]])
>>> np.amin(a)           # Minimum of the flattened array
0
>>> np.amin(a, axis=0)   # Minima along the first axis
array([0, 1])
>>> np.amin(a, axis=1)   # Minima along the second axis
array([0, 2])
```

```
>>> b = np.arange(5, dtype=np.float)
>>> b[2] = np.NaN
>>> np.amin(b)
nan
>>> np.nanmin(b)
0.0
```

dask.array.**minimum**(*x1*, *x2*[, *out*])

Element-wise minimum of array elements.

Compare two arrays and returns a new array containing the element-wise minima. If one of the elements being compared is a NaN, then that element is returned. If both elements are NaNs then the first is returned. The latter distinction is important for complex NaNs, which are defined as at least one of the real or imaginary parts being a NaN. The net effect is that NaNs are propagated.

Parameters

x1, x2 [array_like] The arrays holding the elements to be compared. They must have the same shape, or shapes that can be broadcast to a single shape.

Returns

y [ndarray or scalar] The minimum of *x1* and *x2*, element-wise. Returns scalar if both *x1* and *x2* are scalars.

See also:

maximum Element-wise maximum of two arrays, propagates NaNs.

fmin Element-wise minimum of two arrays, ignores NaNs.

amin The minimum value of an array along a given axis, propagates NaNs.

nanmin The minimum value of an array along a given axis, ignores NaNs.

fmax, amax, *nanmax*

Notes

The minimum is equivalent to `np.where(x1 <= x2, x1, x2)` when neither x1 nor x2 are NaNs, but it is faster and does proper broadcasting.

Examples

```
>>> np.minimum([2, 3, 4], [1, 5, 2])
array([1, 3, 2])
```

```
>>> np.minimum(np.eye(2), [0.5, 2]) # broadcasting
array([[ 0.5,  0. ],
       [ 0. ,  1. ]])
```

```
>>> np.minimum([np.nan, 0, np.nan],[0, np.nan, np.nan])
array([ NaN,  NaN,  NaN])
>>> np.minimum(-np.Inf, 1)
-inf
```

dask.array.**modf**(*x*[, *out1*, *out2*])
Return the fractional and integral parts of an array, element-wise.

The fractional and integral parts are negative if the given number is negative.

Parameters

x [array_like] Input array.

Returns

y1 [ndarray] Fractional part of *x*.

y2 [ndarray] Integral part of *x*.

Notes

For integer input the return values are floats.

Examples

```
>>> np.modf([0, 3.5])
(array([ 0. ,  0.5]), array([ 0.,  3.]))
>>> np.modf(-0.5)
(-0.5, -0)
```

dask.array.**moment**(*a*, *order*, *axis=None*, *dtype=None*, *keepdims=False*, *ddof=0*, *split_every=None*, *out=None*)

dask.array.**nanargmax**(*x*, *axis*, ***kwargs*)

dask.array.**nanargmin**(*x*, *axis*, ***kwargs*)

dask.array.**nancumprod**(*a*, *axis=None*, *dtype=None*, *out=None*)
Return the cumulative product of array elements over a given axis treating Not a Numbers (NaNs) as one. The cumulative product does not change when NaNs are encountered and leading NaNs are replaced by ones.

Ones are returned for slices that are all-NaN or empty.

New in version 1.12.0.

Parameters

a [array_like] Input array.

axis [int, optional] Axis along which the cumulative product is computed. By default the input is flattened.

dtype [dtype, optional] Type of the returned array, as well as of the accumulator in which the elements are multiplied. If *dtype* is not specified, it defaults to the dtype of *a*, unless *a* has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used instead.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape and buffer length as the expected output but the type of the resulting values will be cast if necessary.

Returns

nancumprod [ndarray] A new array holding the result is returned unless *out* is specified, in which case it is returned.

See also:

numpy.cumprod() Cumulative product across array propagating NaNs.

isnan Show which elements are NaN.

Examples

```
>>> nancumprod(1)
array([1])
>>> nancumprod([1])
array([1])
>>> nancumprod([1, np.nan])
array([ 1.,  1.])
>>> a = np.array([[1, 2], [3, np.nan]])
>>> nancumprod(a)
array([ 1.,  2.,  6.,  6.])
>>> nancumprod(a, axis=0)
array([[ 1.,  2.],
       [ 3.,  2.]])
>>> nancumprod(a, axis=1)
array([[ 1.,  2.],
       [ 3.,  3.]])
```

dask.array.**nancumsum**(*a*, *axis=None*, *dtype=None*, *out=None*)

Return the cumulative sum of array elements over a given axis treating Not a Numbers (NaNs) as zero. The cumulative sum does not change when NaNs are encountered and leading NaNs are replaced by zeros.

Zeros are returned for slices that are all-NaN or empty.

New in version 1.12.0.

Parameters

a [array_like] Input array.

axis [int, optional] Axis along which the cumulative sum is computed. The default (None) is to compute the cumsum over the flattened array.

dtype [dtype, optional] Type of the returned array and of the accumulator in which the elements are summed. If *dtype* is not specified, it defaults to the dtype of *a*, unless *a* has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape and buffer length as the expected output but the type will be cast if necessary. See *doc.ufuncs* (Section "Output arguments") for more details.

Returns

nancumsum [ndarray.] A new array holding the result is returned unless *out* is specified, in which it is returned. The result has the same size as *a*, and the same shape as *a* if *axis* is not None or *a* is a 1-d array.

See also:

numpy.cumsum() Cumulative sum across array propagating NaNs.

isnan Show which elements are NaN.

Examples

```
>>> nancumsum(1)
array([1])
>>> nancumsum([1])
array([1])
>>> nancumsum([1, np.nan])
array([ 1.,  1.])
>>> a = np.array([[1, 2], [3, np.nan]])
>>> nancumsum(a)
array([ 1.,  3.,  6.,  6.])
>>> nancumsum(a, axis=0)
array([[ 1.,  2.],
       [ 4.,  2.]])
>>> nancumsum(a, axis=1)
array([[ 1.,  3.],
       [ 3.,  3.]])
```

dask.array.**nanmax**(*a*, *axis=None*, *out=None*, *keepdims=False*)

Return the maximum of an array or maximum along an axis, ignoring any NaNs. When all-NaN slices are encountered a RuntimeWarning is raised and NaN is returned for that slice.

Parameters

a [array_like] Array containing numbers whose maximum is desired. If *a* is not an array, a conversion is attempted.

axis [int, optional] Axis along which the maximum is computed. The default is to compute the maximum of the flattened array.

out [ndarray, optional] Alternate output array in which to place the result. The default is None; if provided, it must have the same shape as the expected output, but the type will be cast if necessary. See *doc.ufuncs* for details.

New in version 1.8.0.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *a*.

New in version 1.8.0.

Returns

nanmax [ndarray] An array with the same shape as *a*, with the specified axis removed. If *a* is a 0-d array, or if axis is None, an ndarray scalar is returned. The same dtype as *a* is returned.

See also:

nanmin The minimum value of an array along a given axis, ignoring any NaNs.

amax The maximum value of an array along a given axis, propagating any NaNs.

fmax Element-wise maximum of two arrays, ignoring any NaNs.

maximum Element-wise maximum of two arrays, propagating any NaNs.

isnan Shows which elements are Not a Number (NaN).

isfinite Shows which elements are neither NaN nor infinity.

amin, *fmin*, *minimum*

Notes

Numpy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754). This means that Not a Number is not equivalent to infinity. Positive infinity is treated as a very large number and negative infinity is treated as a very small (i.e. negative) number.

If the input has a integer type the function is equivalent to np.max.

Examples

```
>>> a = np.array([[1, 2], [3, np.nan]])
>>> np.nanmax(a)
3.0
>>> np.nanmax(a, axis=0)
array([ 3.,  2.])
>>> np.nanmax(a, axis=1)
array([ 2.,  3.])
```

When positive infinity and negative infinity are present:

```
>>> np.nanmax([1, 2, np.nan, np.NINF])
2.0
>>> np.nanmax([1, 2, np.nan, np.inf])
inf
```

dask.array.**nanmean**(*a*, *axis=None*, *dtype=None*, *out=None*, *keepdims=False*)
Compute the arithmetic mean along the specified axis, ignoring NaNs.

Returns the average of the array elements. The average is taken over the flattened array by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

For all-NaN slices, NaN is returned and a *RuntimeWarning* is raised.

New in version 1.8.0.

Parameters

a [array_like] Array containing numbers whose mean is desired. If *a* is not an array, a conversion is attempted.

axis [int, optional] Axis along which the means are computed. The default is to compute the mean of the flattened array.

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is *float64*; for inexact inputs, it is the same as the input dtype.

out [ndarray, optional] Alternate output array in which to place the result. The default is `None`; if provided, it must have the same shape as the expected output, but the type will be cast if necessary. See *doc.ufuncs* for details.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

Returns

m [ndarray, see dtype parameter above] If *out=None*, returns a new array containing the mean values, otherwise a reference to the output array is returned. Nan is returned for slices that contain only NaNs.

See also:

average Weighted average

mean Arithmetic mean taken while not ignoring NaNs

var, *nanvar*

Notes

The arithmetic mean is the sum of the non-NaN elements along the axis divided by the number of non-NaN elements.

Note that for floating-point input, the mean is computed using the same precision the input has. Depending on the input data, this can cause the results to be inaccurate, especially for *float32*. Specifying a higher-precision accumulator using the *dtype* keyword can alleviate this issue.

Examples

```
>>> a = np.array([[1, np.nan], [3, 4]])
>>> np.nanmean(a)
2.6666666666666665
>>> np.nanmean(a, axis=0)
array([ 2.,  4.])
>>> np.nanmean(a, axis=1)
array([ 1.,  3.5])
```

`dask.array.`**`nanmin`**(*a*, *axis=None*, *out=None*, *keepdims=False*)

Return minimum of an array or minimum along an axis, ignoring any NaNs. When all-NaN slices are encountered a `RuntimeWarning` is raised and Nan is returned for that slice.

Parameters

a [array_like] Array containing numbers whose minimum is desired. If *a* is not an array, a conversion is attempted.

axis [int, optional] Axis along which the minimum is computed. The default is to compute the minimum of the flattened array.

out [ndarray, optional] Alternate output array in which to place the result. The default is `None`; if provided, it must have the same shape as the expected output, but the type will be cast if necessary. See *doc.ufuncs* for details.

New in version 1.8.0.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *a*.

New in version 1.8.0.

Returns

nanmin [ndarray] An array with the same shape as *a*, with the specified axis removed. If *a* is a 0-d array, or if axis is None, an ndarray scalar is returned. The same dtype as *a* is returned.

See also:

nanmax The maximum value of an array along a given axis, ignoring any NaNs.

amin The minimum value of an array along a given axis, propagating any NaNs.

fmin Element-wise minimum of two arrays, ignoring any NaNs.

minimum Element-wise minimum of two arrays, propagating any NaNs.

isnan Shows which elements are Not a Number (NaN).

isfinite Shows which elements are neither NaN nor infinity.

amax, *fmax*, *maximum*

Notes

Numpy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754). This means that Not a Number is not equivalent to infinity. Positive infinity is treated as a very large number and negative infinity is treated as a very small (i.e. negative) number.

If the input has a integer type the function is equivalent to np.min.

Examples

```
>>> a = np.array([[1, 2], [3, np.nan]])
>>> np.nanmin(a)
1.0
>>> np.nanmin(a, axis=0)
array([ 1.,  2.])
>>> np.nanmin(a, axis=1)
array([ 1.,  3.])
```

When positive infinity and negative infinity are present:

```
>>> np.nanmin([1, 2, np.nan, np.inf])
1.0
>>> np.nanmin([1, 2, np.nan, np.NINF])
-inf
```

dask.array.**nanprod**(*a*, *axis=None*, *dtype=None*, *out=None*, *keepdims=0*)

Return the product of array elements over a given axis treating Not a Numbers (NaNs) as zero.

One is returned for slices that are all-NaN or empty.

New in version 1.10.0.

Parameters

a [array_like] Array containing numbers whose sum is desired. If *a* is not an array, a conversion is attempted.

axis [int, optional] Axis along which the product is computed. The default is to compute the product of the flattened array.

dtype [data-type, optional] The type of the returned array and of the accumulator in which the elements are summed. By default, the dtype of *a* is used. An exception is when *a* has an integer type with less precision than the platform (u)intp. In that case, the default will be either (u)int32 or (u)int64 depending on whether the platform is 32 or 64 bits. For inexact inputs, dtype must be inexact.

out [ndarray, optional] Alternate output array in which to place the result. The default is `None`. If provided, it must have the same shape as the expected output, but the type will be cast if necessary. See *doc.ufuncs* for details. The casting of NaN to integer can yield unexpected results.

keepdims [bool, optional] If True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

Returns

y [ndarray or numpy scalar]

See also:

`numpy.prod` Product across array propagating NaNs.

`isnan` Show which elements are NaN.

Notes

Numpy integer arithmetic is modular. If the size of a product exceeds the size of an integer accumulator, its value will wrap around and the result will be incorrect. Specifying `dtype=double` can alleviate that problem.

Examples

```
>>> np.nanprod(1)
1
>>> np.nanprod([1])
1
>>> np.nanprod([1, np.nan])
1.0
>>> a = np.array([[1, 2], [3, np.nan]])
>>> np.nanprod(a)
6.0
>>> np.nanprod(a, axis=0)
array([ 3.,  2.])
```

`dask.array.`**`nanstd`**(*a*, *axis=None*, *dtype=None*, *out=None*, *ddof=0*, *keepdims=False*)

Compute the standard deviation along the specified axis, while ignoring NaNs.

Returns the standard deviation, a measure of the spread of a distribution, of the non-NaN array elements. The standard deviation is computed for the flattened array by default, otherwise over the specified axis.

For all-NaN slices or slices with zero degrees of freedom, NaN is returned and a *RuntimeWarning* is raised.

New in version 1.8.0.

Parameters

a [array_like] Calculate the standard deviation of the non-NaN values.

axis [int, optional] Axis along which the standard deviation is computed. The default is to compute the standard deviation of the flattened array.

dtype [dtype, optional] Type to use in computing the standard deviation. For arrays of integer type the default is float64, for arrays of float types it is the same as the array type.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape as the expected output but the type (of the calculated values) will be cast if necessary.

ddof [int, optional] Means Delta Degrees of Freedom. The divisor used in calculations is `N - ddof`, where `N` represents the number of non-NaN elements. By default *ddof* is zero.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

Returns

standard_deviation [ndarray, see dtype parameter above.] If *out* is None, return a new array containing the standard deviation, otherwise return a reference to the output array. If ddof is >= the number of non-NaN elements in a slice or the slice contains only NaNs, then the result for that slice is NaN.

See also:

var, *mean*, *std*, *nanvar*, *nanmean*

numpy.doc.ufuncs Section "Output arguments"

Notes

The standard deviation is the square root of the average of the squared deviations from the mean: `std = sqrt(mean(abs(x - x.mean())**2))`.

The average squared deviation is normally calculated as `x.sum() / N`, where `N = len(x)`. If, however, *ddof* is specified, the divisor `N - ddof` is used instead. In standard statistical practice, `ddof=1` provides an unbiased estimator of the variance of the infinite population. `ddof=0` provides a maximum likelihood estimate of the variance for normally distributed variables. The standard deviation computed in this function is the square root of the estimated variance, so even with `ddof=1`, it will not be an unbiased estimate of the standard deviation per se.

Note that, for complex numbers, *std* takes the absolute value before squaring, so that the result is always real and nonnegative.

For floating-point input, the *std* is computed using the same precision the input has. Depending on the input data, this can cause the results to be inaccurate, especially for float32 (see example below). Specifying a higher-accuracy accumulator using the *dtype* keyword can alleviate this issue.

Examples

```
>>> a = np.array([[1, np.nan], [3, 4]])
>>> np.nanstd(a)
1.247219128924647
>>> np.nanstd(a, axis=0)
array([ 1.,  0.])
>>> np.nanstd(a, axis=1)
array([ 0.,  0.5])
```

dask.array.**nansum**(*a*, *axis=None*, *dtype=None*, *out=None*, *keepdims=0*)

Return the sum of array elements over a given axis treating Not a Numbers (NaNs) as zero.

In Numpy versions <= 1.8 Nan is returned for slices that are all-NaN or empty. In later versions zero is returned.

Parameters

a [array_like] Array containing numbers whose sum is desired. If *a* is not an array, a conversion is attempted.

axis [int, optional] Axis along which the sum is computed. The default is to compute the sum of the flattened array.

dtype [data-type, optional] The type of the returned array and of the accumulator in which the elements are summed. By default, the dtype of *a* is used. An exception is when *a* has an integer type with less precision than the platform (u)intp. In that case, the default will be either (u)int32 or (u)int64 depending on whether the platform is 32 or 64 bits. For inexact inputs, dtype must be inexact.

New in version 1.8.0.

out [ndarray, optional] Alternate output array in which to place the result. The default is `None`. If provided, it must have the same shape as the expected output, but the type will be cast if necessary. See *doc.ufuncs* for details. The casting of NaN to integer can yield unexpected results.

New in version 1.8.0.

keepdims [bool, optional] If True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

New in version 1.8.0.

Returns

y [ndarray or numpy scalar]

See also:

`numpy.sum` Sum across array propagating NaNs.

`isnan` Show which elements are NaN.

`isfinite` Show which elements are not NaN or +/-inf.

Notes

If both positive and negative infinity are present, the sum will be Not A Number (NaN).

Numpy integer arithmetic is modular. If the size of a sum exceeds the size of an integer accumulator, its value will wrap around and the result will be incorrect. Specifying `dtype=double` can alleviate that problem.

Examples

```
>>> np.nansum(1)
1
>>> np.nansum([1])
1
>>> np.nansum([1, np.nan])
1.0
>>> a = np.array([[1, 1], [1, np.nan]])
>>> np.nansum(a)
3.0
>>> np.nansum(a, axis=0)
```

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```
array([ 2.,  1.])
>>> np.nansum([1, np.nan, np.inf])
inf
>>> np.nansum([1, np.nan, np.NINF])
-inf
>>> np.nansum([1, np.nan, np.inf, -np.inf]) # both +/- infinity present
nan
```

dask.array.**nanvar**(*a*, *axis=None*, *dtype=None*, *out=None*, *ddof=0*, *keepdims=False*)

Compute the variance along the specified axis, while ignoring NaNs.

Returns the variance of the array elements, a measure of the spread of a distribution. The variance is computed for the flattened array by default, otherwise over the specified axis.

For all-NaN slices or slices with zero degrees of freedom, NaN is returned and a *RuntimeWarning* is raised.

New in version 1.8.0.

Parameters

a [array_like] Array containing numbers whose variance is desired. If *a* is not an array, a conversion is attempted.

axis [int, optional] Axis along which the variance is computed. The default is to compute the variance of the flattened array.

dtype [data-type, optional] Type to use in computing the variance. For arrays of integer type the default is *float32*; for arrays of float types it is the same as the array type.

out [ndarray, optional] Alternate output array in which to place the result. It must have the same shape as the expected output, but the type is cast if necessary.

ddof [int, optional] "Delta Degrees of Freedom": the divisor used in the calculation is `N - ddof`, where `N` represents the number of non-NaN elements. By default *ddof* is zero.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

Returns

variance [ndarray, see dtype parameter above] If *out* is None, return a new array containing the variance, otherwise return a reference to the output array. If ddof is >= the number of non-NaN elements in a slice or the slice contains only NaNs, then the result for that slice is NaN.

See also:

std Standard deviation

mean Average

var Variance while not ignoring NaNs

nanstd, *nanmean*

numpy.doc.ufuncs Section "Output arguments"

Notes

The variance is the average of the squared deviations from the mean, i.e., `var = mean(abs(x - x.mean())**2)`.

The mean is normally calculated as `x.sum() / N`, where `N = len(x)`. If, however, *ddof* is specified, the divisor `N - ddof` is used instead. In standard statistical practice, `ddof=1` provides an unbiased estimator of the variance of a hypothetical infinite population. `ddof=0` provides a maximum likelihood estimate of the variance for normally distributed variables.

Note that for complex numbers, the absolute value is taken before squaring, so that the result is always real and nonnegative.

For floating-point input, the variance is computed using the same precision the input has. Depending on the input data, this can cause the results to be inaccurate, especially for *float32* (see example below). Specifying a higher-accuracy accumulator using the `dtype` keyword can alleviate this issue.

Examples

```
>>> a = np.array([[1, np.nan], [3, 4]])
>>> np.var(a)
1.5555555555555554
>>> np.nanvar(a, axis=0)
array([ 1.,  0.])
>>> np.nanvar(a, axis=1)
array([ 0.,  0.25])
```

dask.array.**nan_to_num**(**args*, ***kwargs*)

Replace nan with zero and inf with finite numbers.

Returns an array or scalar replacing Not a Number (NaN) with zero, (positive) infinity with a very large number and negative infinity with a very small (or negative) number.

Parameters

x [array_like] Input data.

Returns

out [ndarray] New Array with the same shape as *x* and dtype of the element in *x* with the greatest precision. If *x* is inexact, then NaN is replaced by zero, and infinity (-infinity) is replaced by the largest (smallest or most negative) floating point value that fits in the output dtype. If *x* is not inexact, then a copy of *x* is returned.

See also:

isinf Shows which elements are negative or negative infinity.

isneginf Shows which elements are negative infinity.

isposinf Shows which elements are positive infinity.

isnan Shows which elements are Not a Number (NaN).

isfinite Shows which elements are finite (not NaN, not infinity)

Notes

Numpy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754). This means that Not a Number is not equivalent to infinity.

Examples

```
>>> np.set_printoptions(precision=8)
>>> x = np.array([np.inf, -np.inf, np.nan, -128, 128])
>>> np.nan_to_num(x)
array([  1.79769313e+308,  -1.79769313e+308,   0.00000000e+000,
        -1.28000000e+002,   1.28000000e+002])
```

dask.array.**nextafter**(*x1*, *x2*[, *out*])

Return the next floating-point value after x1 towards x2, element-wise.

Parameters

x1 [array_like] Values to find the next representable value of.

x2 [array_like] The direction where to look for the next representable value of *x1*.

out [ndarray, optional] Array into which the output is placed. Its type is preserved and it must be of the right shape to hold the output. See *doc.ufuncs*.

Returns

out [array_like] The next representable values of *x1* in the direction of *x2*.

Examples

```
>>> eps = np.finfo(np.float64).eps
>>> np.nextafter(1, 2) == eps + 1
True
>>> np.nextafter([1, 2], [2, 1]) == [eps + 1, 2 - eps]
array([ True,  True], dtype=bool)
```

dask.array.**nonzero**(*a*)

Return the indices of the elements that are non-zero.

Returns a tuple of arrays, one for each dimension of *a*, containing the indices of the non-zero elements in that dimension. The values in *a* are always tested and returned in row-major, C-style order. The corresponding non-zero values can be obtained with:

```
a[nonzero(a)]
```

To group the indices by element, rather than dimension, use:

```
transpose(nonzero(a))
```

The result of this is always a 2-D array, with a row for each non-zero element.

Parameters

a [array_like] Input array.

Returns

tuple_of_arrays [tuple] Indices of elements that are non-zero.

See also:

flatnonzero Return indices that are non-zero in the flattened version of the input array.

ndarray.nonzero Equivalent ndarray method.

count_nonzero Counts the number of non-zero elements in the input array.

Examples

```
>>> x = np.eye(3)
>>> x
array([[ 1.,  0.,  0.],
       [ 0.,  1.,  0.],
       [ 0.,  0.,  1.]])
>>> np.nonzero(x)
(array([0, 1, 2]), array([0, 1, 2]))
```

```
>>> x[np.nonzero(x)]
array([ 1.,  1.,  1.])
>>> np.transpose(np.nonzero(x))
array([[0, 0],
       [1, 1],
       [2, 2]])
```

A common use for `nonzero` is to find the indices of an array, where a condition is True. Given an array *a*, the condition *a* > 3 is a boolean array and since False is interpreted as 0, np.nonzero(a > 3) yields the indices of the *a* where the condition is true.

```
>>> a = np.array([[1,2,3],[4,5,6],[7,8,9]])
>>> a > 3
array([[False, False, False],
       [ True,  True,  True],
       [ True,  True,  True]], dtype=bool)
>>> np.nonzero(a > 3)
(array([1, 1, 1, 2, 2, 2]), array([0, 1, 2, 0, 1, 2]))
```

The `nonzero` method of the boolean array can also be called.

```
>>> (a > 3).nonzero()
(array([1, 1, 1, 2, 2, 2]), array([0, 1, 2, 0, 1, 2]))
```

`dask.array.`**`notnull`**(*values*)
pandas.notnull for dask arrays

`dask.array.`**`ones`**(**args*, ***kwargs*)
Blocked variant of ones

Follows the signature of ones exactly except that it also requires a keyword argument chunks=(...)

Original signature follows below.

Return a new array of given shape and type, filled with ones.

Parameters

shape [int or sequence of ints] Shape of the new array, e.g., `(2, 3)` or `2`.

dtype [data-type, optional] The desired data-type for the array, e.g., *numpy.int8*. Default is *numpy.float64*.

order [{'C', 'F'}, optional] Whether to store multidimensional data in C- or Fortran-contiguous (row- or column-wise) order in memory.

Returns

out [ndarray] Array of ones with the given shape, dtype, and order.

See also:

zeros, *ones_like*

Examples

```
>>> np.ones(5)
array([ 1.,  1.,  1.,  1.,  1.])
```

```
>>> np.ones((5,), dtype=np.int)
array([1, 1, 1, 1, 1])
```

```
>>> np.ones((2, 1))
array([[ 1.],
       [ 1.]])
```

```
>>> s = (2,2)
>>> np.ones(s)
array([[ 1.,  1.],
       [ 1.,  1.]])
```

dask.array.**ones_like**(*a*, *dtype=None*, *chunks=None*)

Return an array of ones with the same shape and type as a given array.

Parameters

a [array_like] The shape and data-type of *a* define these same attributes of the returned array.

dtype [data-type, optional] Overrides the data type of the result.

chunks [sequence of ints] The number of samples on each block. Note that the last block will have fewer samples if `len(array) % chunks != 0`.

Returns

out [ndarray] Array of ones with the same shape and type as *a*.

See also:

zeros_like Return an array of zeros with shape and type of input.

empty_like Return an empty array with shape and type of input.

zeros Return a new array setting values to zero.

ones Return a new array setting values to one.

empty Return a new uninitialized array.

dask.array.**outer**(*a*, *b*, *out=None*)

Compute the outer product of two vectors.

Given two vectors, `a = [a0, a1, ..., aM]` and `b = [b0, b1, ..., bN]`, the outer product *[1]* is:

```
[[a0*b0  a0*b1 ... a0*bN ]
 [a1*b0    .
 [ ...          .
 [aM*b0            aM*bN ]]
```

Parameters

a [(M,) array_like] First input vector. Input is flattened if not already 1-dimensional.

b [(N,) array_like] Second input vector. Input is flattened if not already 1-dimensional.

out [(M, N) ndarray, optional] A location where the result is stored

New in version 1.9.0.

Returns

out [(M, N) ndarray] `out[i, j] = a[i] * b[j]`

See also:

`inner`, *einsum*

References

[1]

Examples

Make a (*very* coarse) grid for computing a Mandelbrot set:

```
>>> rl = np.outer(np.ones((5,)), np.linspace(-2, 2, 5))
>>> rl
array([[-2., -1.,  0.,  1.,  2.],
       [-2., -1.,  0.,  1.,  2.],
       [-2., -1.,  0.,  1.,  2.],
       [-2., -1.,  0.,  1.,  2.],
       [-2., -1.,  0.,  1.,  2.]])
>>> im = np.outer(1j*np.linspace(2, -2, 5), np.ones((5,)))
>>> im
array([[ 0.+2.j,  0.+2.j,  0.+2.j,  0.+2.j,  0.+2.j],
       [ 0.+1.j,  0.+1.j,  0.+1.j,  0.+1.j,  0.+1.j],
       [ 0.+0.j,  0.+0.j,  0.+0.j,  0.+0.j,  0.+0.j],
       [ 0.-1.j,  0.-1.j,  0.-1.j,  0.-1.j,  0.-1.j],
       [ 0.-2.j,  0.-2.j,  0.-2.j,  0.-2.j,  0.-2.j]])
>>> grid = rl + im
>>> grid
array([[-2.+2.j, -1.+2.j,  0.+2.j,  1.+2.j,  2.+2.j],
       [-2.+1.j, -1.+1.j,  0.+1.j,  1.+1.j,  2.+1.j],
       [-2.+0.j, -1.+0.j,  0.+0.j,  1.+0.j,  2.+0.j],
       [-2.-1.j, -1.-1.j,  0.-1.j,  1.-1.j,  2.-1.j],
       [-2.-2.j, -1.-2.j,  0.-2.j,  1.-2.j,  2.-2.j]])
```

An example using a "vector" of letters:

```
>>> x = np.array(['a', 'b', 'c'], dtype=object)
>>> np.outer(x, [1, 2, 3])
array([[a, aa, aaa],
       [b, bb, bbb],
       [c, cc, ccc]], dtype=object)
```

dask.array.**pad**(*array*, *pad_width*, *mode*, ***kwargs*)

Pads an array.

Parameters

array [array_like of rank N] Input array

pad_width [{sequence, array_like, int}] Number of values padded to the edges of each axis. ((before_1, after_1), … (before_N, after_N)) unique pad widths for each axis. ((before, after),) yields same before and after pad for each axis. (pad,) or int is a shortcut for before = after = pad width for all axes.

mode [str or function] One of the following string values or a user supplied function.

'constant' Pads with a constant value.

'edge' Pads with the edge values of array.

'linear_ramp' Pads with the linear ramp between end_value and the array edge value.

'maximum' Pads with the maximum value of all or part of the vector along each axis.

'mean' Pads with the mean value of all or part of the vector along each axis.

'median' Pads with the median value of all or part of the vector along each axis.

'minimum' Pads with the minimum value of all or part of the vector along each axis.

'reflect' Pads with the reflection of the vector mirrored on the first and last values of the vector along each axis.

'symmetric' Pads with the reflection of the vector mirrored along the edge of the array.

'wrap' Pads with the wrap of the vector along the axis. The first values are used to pad the end and the end values are used to pad the beginning.

<function> Padding function, see Notes.

stat_length [sequence or int, optional] Used in 'maximum', 'mean', 'median', and 'minimum'. Number of values at edge of each axis used to calculate the statistic value.

((before_1, after_1), … (before_N, after_N)) unique statistic lengths for each axis.

((before, after),) yields same before and after statistic lengths for each axis.

(stat_length,) or int is a shortcut for before = after = statistic length for all axes.

Default is `None`, to use the entire axis.

constant_values [sequence or int, optional] Used in 'constant'. The values to set the padded values for each axis.

((before_1, after_1), … (before_N, after_N)) unique pad constants for each axis.

((before, after),) yields same before and after constants for each axis.

(constant,) or int is a shortcut for before = after = constant for all axes.

Default is 0.

end_values [sequence or int, optional] Used in 'linear_ramp'. The values used for the ending value of the linear_ramp and that will form the edge of the padded array.

((before_1, after_1), ... (before_N, after_N)) unique end values for each axis.

((before, after),) yields same before and after end values for each axis.

(constant,) or int is a shortcut for before = after = end value for all axes.

Default is 0.

reflect_type [{'even', 'odd'}, optional] Used in 'reflect', and 'symmetric'. The 'even' style is the default with an unaltered reflection around the edge value. For the 'odd' style, the extented part of the array is created by subtracting the reflected values from two times the edge value.

Returns

pad [ndarray] Padded array of rank equal to *array* with shape increased according to *pad_width*.

Notes

New in version 1.7.0.

For an array with rank greater than 1, some of the padding of later axes is calculated from padding of previous axes. This is easiest to think about with a rank 2 array where the corners of the padded array are calculated by using padded values from the first axis.

The padding function, if used, should return a rank 1 array equal in length to the vector argument with padded values replaced. It has the following signature:

```
padding_func(vector, iaxis_pad_width, iaxis, **kwargs)
```

where

vector [ndarray] A rank 1 array already padded with zeros. Padded values are vector[:pad_tuple[0]] and vector[-pad_tuple[1]:].

iaxis_pad_width [tuple] A 2-tuple of ints, iaxis_pad_width[0] represents the number of values padded at the beginning of vector where iaxis_pad_width[1] represents the number of values padded at the end of vector.

iaxis [int] The axis currently being calculated.

kwargs [misc] Any keyword arguments the function requires.

Examples

```
>>> a = [1, 2, 3, 4, 5]
>>> np.lib.pad(a, (2,3), 'constant', constant_values=(4, 6))
array([4, 4, 1, 2, 3, 4, 5, 6, 6, 6])
```

```
>>> np.lib.pad(a, (2, 3), 'edge')
array([1, 1, 1, 2, 3, 4, 5, 5, 5, 5])
```

```
>>> np.lib.pad(a, (2, 3), 'linear_ramp', end_values=(5, -4))
array([ 5,  3,  1,  2,  3,  4,  5,  2, -1, -4])
```

```
>>> np.lib.pad(a, (2,), 'maximum')
array([5, 5, 1, 2, 3, 4, 5, 5, 5])
```

```
>>> np.lib.pad(a, (2,), 'mean')
array([3, 3, 1, 2, 3, 4, 5, 3, 3])
```

```
>>> np.lib.pad(a, (2,), 'median')
array([3, 3, 1, 2, 3, 4, 5, 3, 3])
```

```
>>> a = [[1, 2], [3, 4]]
>>> np.lib.pad(a, ((3, 2), (2, 3)), 'minimum')
array([[1, 1, 1, 2, 1, 1, 1],
       [1, 1, 1, 2, 1, 1, 1],
       [1, 1, 1, 2, 1, 1, 1],
       [1, 1, 1, 2, 1, 1, 1],
       [3, 3, 3, 4, 3, 3, 3],
       [1, 1, 1, 2, 1, 1, 1],
       [1, 1, 1, 2, 1, 1, 1]])
```

```
>>> a = [1, 2, 3, 4, 5]
>>> np.lib.pad(a, (2, 3), 'reflect')
array([3, 2, 1, 2, 3, 4, 5, 4, 3, 2])
```

```
>>> np.lib.pad(a, (2, 3), 'reflect', reflect_type='odd')
array([-1,  0,  1,  2,  3,  4,  5,  6,  7,  8])
```

```
>>> np.lib.pad(a, (2, 3), 'symmetric')
array([2, 1, 1, 2, 3, 4, 5, 5, 4, 3])
```

```
>>> np.lib.pad(a, (2, 3), 'symmetric', reflect_type='odd')
array([0, 1, 1, 2, 3, 4, 5, 5, 6, 7])
```

```
>>> np.lib.pad(a, (2, 3), 'wrap')
array([4, 5, 1, 2, 3, 4, 5, 1, 2, 3])
```

```
>>> def padwithtens(vector, pad_width, iaxis, kwargs):
...     vector[:pad_width[0]] = 10
...     vector[-pad_width[1]:] = 10
...     return vector
```

```
>>> a = np.arange(6)
>>> a = a.reshape((2, 3))
```

```
>>> np.lib.pad(a, 2, padwithtens)
array([[10, 10, 10, 10, 10, 10, 10],
       [10, 10, 10, 10, 10, 10, 10],
       [10, 10,  0,  1,  2, 10, 10],
       [10, 10,  3,  4,  5, 10, 10],
       [10, 10, 10, 10, 10, 10, 10],
       [10, 10, 10, 10, 10, 10, 10]])
```

dask.array.**percentile**(*a*, *q*, *interpolation='linear'*)

Approximate percentile of 1-D array

See numpy.percentile() for more information

dask.array.**piecewise**(*x*, *condlist*, *funclist*, **args*, ***kw*)

Evaluate a piecewise-defined function.

Given a set of conditions and corresponding functions, evaluate each function on the input data wherever its condition is true.

Parameters

x [ndarray] The input domain.

condlist [list of bool arrays] Each boolean array corresponds to a function in *funclist*. Wherever *condlist[i]* is True, *funclist[i](x)* is used as the output value.

Each boolean array in *condlist* selects a piece of *x*, and should therefore be of the same shape as *x*.

The length of *condlist* must correspond to that of *funclist*. If one extra function is given, i.e. if `len(funclist) - len(condlist) == 1`, then that extra function is the default value, used wherever all conditions are false.

funclist [list of callables, f(x,*args,**kw), or scalars] Each function is evaluated over *x* wherever its corresponding condition is True. It should take an array as input and give an array or a scalar value as output. If, instead of a callable, a scalar is provided then a constant function (`lambda x: scalar`) is assumed.

args [tuple, optional] Any further arguments given to *piecewise* are passed to the functions upon execution, i.e., if called `piecewise(..., ..., 1, 'a')`, then each function is called as `f(x, 1, 'a')`.

kw [dict, optional] Keyword arguments used in calling *piecewise* are passed to the functions upon execution, i.e., if called `piecewise(..., ..., lambda=1)`, then each function is called as `f(x, lambda=1)`.

Returns

out [ndarray] The output is the same shape and type as x and is found by calling the functions in *funclist* on the appropriate portions of *x*, as defined by the boolean arrays in *condlist*. Portions not covered by any condition have a default value of 0.

See also:

choose, select, *where*

Notes

This is similar to choose or select, except that functions are evaluated on elements of *x* that satisfy the corresponding condition from *condlist*.

The result is:

```
      |--
      |funclist[0](x[condlist[0]])
out = |funclist[1](x[condlist[1]])
      |...
      |funclist[n2](x[condlist[n2]])
      |--
```

Examples

Define the sigma function, which is -1 for `x < 0` and +1 for `x >= 0`.

```
>>> x = np.linspace(-2.5, 2.5, 6)
>>> np.piecewise(x, [x < 0, x >= 0], [-1, 1])
array([-1., -1., -1.,  1.,  1.,  1.])
```

Define the absolute value, which is `-x` for `x <0` and `x` for `x >= 0`.

```
>>> np.piecewise(x, [x < 0, x >= 0], [lambda x: -x, lambda x: x])
array([ 2.5,  1.5,  0.5,  0.5,  1.5,  2.5])
```

`dask.array.`**`prod`**(*a*, *axis=None*, *dtype=None*, *out=None*, *keepdims=False*)

Return the product of array elements over a given axis.

Parameters

a [array_like] Input data.

axis [None or int or tuple of ints, optional] Axis or axes along which a product is performed. The default, axis=None, will calculate the product of all the elements in the input array. If axis is negative it counts from the last to the first axis.

New in version 1.7.0.

If axis is a tuple of ints, a product is performed on all of the axes specified in the tuple instead of a single axis or all the axes as before.

dtype [dtype, optional] The type of the returned array, as well as of the accumulator in which the elements are multiplied. The dtype of *a* is used by default unless *a* has an integer dtype of less precision than the default platform integer. In that case, if *a* is signed then the platform integer is used while if *a* is unsigned then an unsigned integer of the same precision as the platform integer is used.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array.

Returns

product_along_axis [ndarray, see *dtype* parameter above.] An array shaped as *a* but with the specified axis removed. Returns a reference to *out* if specified.

See also:

`ndarray.prod` equivalent method

`numpy.doc.ufuncs` Section "Output arguments"

Notes

Arithmetic is modular when using integer types, and no error is raised on overflow. That means that, on a 32-bit platform:

```
>>> x = np.array([536870910, 536870910, 536870910, 536870910])
>>> np.prod(x) #random
16
```

The product of an empty array is the neutral element 1:

```
>>> np.prod([])
1.0
```

Examples

By default, calculate the product of all elements:

```
>>> np.prod([1.,2.])
2.0
```

Even when the input array is two-dimensional:

```
>>> np.prod([[1.,2.],[3.,4.]])
24.0
```

But we can also specify the axis over which to multiply:

```
>>> np.prod([[1.,2.],[3.,4.]], axis=1)
array([  2.,  12.])
```

If the type of *x* is unsigned, then the output type is the unsigned platform integer:

```
>>> x = np.array([1, 2, 3], dtype=np.uint8)
>>> np.prod(x).dtype == np.uint
True
```

If *x* is of a signed integer type, then the output type is the default platform integer:

```
>>> x = np.array([1, 2, 3], dtype=np.int8)
>>> np.prod(x).dtype == np.int
True
```

dask.array.**ptp**(*a*, *axis=None*, *out=None*)

Range of values (maximum - minimum) along an axis.

The name of the function comes from the acronym for 'peak to peak'.

Parameters

a [array_like] Input values.

axis [int, optional] Axis along which to find the peaks. By default, flatten the array.

out [array_like] Alternative output array in which to place the result. It must have the same shape and buffer length as the expected output, but the type of the output values will be cast if necessary.

Returns

ptp [ndarray] A new array holding the result, unless *out* was specified, in which case a reference to *out* is returned.

Examples

```
>>> x = np.arange(4).reshape((2,2))
>>> x
array([[0, 1],
       [2, 3]])
```

```
>>> np.ptp(x, axis=0)
array([2, 2])
```

```
>>> np.ptp(x, axis=1)
array([1, 1])
```

dask.array.**rad2deg**(*x*[, *out*])

Convert angles from radians to degrees.

Parameters

x [array_like] Angle in radians.

out [ndarray, optional] Array into which the output is placed. Its type is preserved and it must be of the right shape to hold the output. See doc.ufuncs.

Returns

y [ndarray] The corresponding angle in degrees.

See also:

deg2rad Convert angles from degrees to radians.

unwrap Remove large jumps in angle by wrapping.

Notes

New in version 1.3.0.

rad2deg(x) is `180 * x / pi`.

Examples

```
>>> np.rad2deg(np.pi/2)
90.0
```

dask.array.**radians**(*x*[, *out*])

Convert angles from degrees to radians.

Parameters

x [array_like] Input array in degrees.

out [ndarray, optional] Output array of same shape as *x*.

Returns

y [ndarray] The corresponding radian values.

See also:

deg2rad equivalent function

Examples

Convert a degree array to radians

```
>>> deg = np.arange(12.) * 30.
>>> np.radians(deg)
array([ 0.        ,  0.52359878,  1.04719755,  1.57079633,  2.0943951 ,
        2.61799388,  3.14159265,  3.66519143,  4.1887902 ,  4.71238898,
        5.23598776,  5.75958653])
```

```
>>> out = np.zeros((deg.shape))
>>> ret = np.radians(deg, out)
>>> ret is out
True
```

dask.array.**ravel**(*a*, *order='C'*)

Return a contiguous flattened array.

A 1-D array, containing the elements of the input, is returned. A copy is made only if needed.

As of NumPy 1.10, the returned array will have the same type as the input array. (for example, a masked array will be returned for a masked array input)

Parameters

a [array_like] Input array. The elements in *a* are read in the order specified by *order*, and packed as a 1-D array.

order [{'C','F', 'A', 'K'}, optional] The elements of *a* are read using this index order. 'C' means to index the elements in row-major, C-style order, with the last axis index changing fastest, back to the first axis index changing slowest. 'F' means to index the elements in column-major, Fortran-style order, with the first index changing fastest, and the last index changing slowest. Note that the 'C' and 'F' options take no account of the memory layout of the underlying array, and only refer to the order of axis indexing. 'A' means to read the elements in Fortran-like index order if *a* is Fortran *contiguous* in memory, C-like order otherwise. 'K' means to read the elements in the order they occur in memory, except for reversing the data when strides are negative. By default, 'C' index order is used.

Returns

y [array_like] If *a* is a matrix, y is a 1-D ndarray, otherwise y is an array of the same subtype as *a*. The shape of the returned array is `(a.size,)`. Matrices are special cased for backward compatibility.

See also:

ndarray.flat 1-D iterator over an array.

ndarray.flatten 1-D array copy of the elements of an array in row-major order.

ndarray.reshape Change the shape of an array without changing its data.

Notes

In row-major, C-style order, in two dimensions, the row index varies the slowest, and the column index the quickest. This can be generalized to multiple dimensions, where row-major order implies that the index along

the first axis varies slowest, and the index along the last quickest. The opposite holds for column-major, Fortran-style index ordering.

When a view is desired in as many cases as possible, `arr.reshape(-1)` may be preferable.

Examples

It is equivalent to `reshape(-1, order=order)`.

```
>>> x = np.array([[1, 2, 3], [4, 5, 6]])
>>> print(np.ravel(x))
[1 2 3 4 5 6]
```

```
>>> print(x.reshape(-1))
[1 2 3 4 5 6]
```

```
>>> print(np.ravel(x, order='F'))
[1 4 2 5 3 6]
```

When `order` is 'A', it will preserve the array's 'C' or 'F' ordering:

```
>>> print(np.ravel(x.T))
[1 4 2 5 3 6]
>>> print(np.ravel(x.T, order='A'))
[1 2 3 4 5 6]
```

When `order` is 'K', it will preserve orderings that are neither 'C' nor 'F', but won't reverse axes:

```
>>> a = np.arange(3)[::-1]; a
array([2, 1, 0])
>>> a.ravel(order='C')
array([2, 1, 0])
>>> a.ravel(order='K')
array([2, 1, 0])
```

```
>>> a = np.arange(12).reshape(2,3,2).swapaxes(1,2); a
array([[[ 0,  2,  4],
        [ 1,  3,  5]],
       [[ 6,  8, 10],
        [ 7,  9, 11]]])
>>> a.ravel(order='C')
array([ 0,  2,  4,  1,  3,  5,  6,  8, 10,  7,  9, 11])
>>> a.ravel(order='K')
array([ 0,  1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11])
```

`dask.array.`**`real`**`(*args, **kwargs)`

Return the real part of the elements of the array.

Parameters

val [array_like] Input array.

Returns

out [ndarray] Output array. If *val* is real, the type of *val* is used for the output. If *val* has complex elements, the returned type is float.

See also:

`real_if_close`, *imag*, *angle*

Examples

```
>>> a = np.array([1+2j, 3+4j, 5+6j])
>>> a.real
array([ 1.,  3.,  5.])
>>> a.real = 9
>>> a
array([ 9.+2.j,  9.+4.j,  9.+6.j])
>>> a.real = np.array([9, 8, 7])
>>> a
array([ 9.+2.j,  8.+4.j,  7.+6.j])
```

`dask.array.`**`rechunk`**(*x*, *chunks*, *threshold=None*, *block_size_limit=None*)

Convert blocks in dask array x for new chunks.

Parameters

x: dask array Array to be rechunked.

chunks: int, tuple or dict The new block dimensions to create. -1 indicates the full size of the corresponding dimension.

threshold: int The graph growth factor under which we don't bother introducing an intermediate step.

block_size_limit: int The maximum block size (in bytes) we want to produce Defaults to the configuration value `array.chunk-size`

Examples

```
>>> import dask.array as da
>>> x = da.ones((1000, 1000), chunks=(100, 100))
```

Specify uniform chunk sizes with a tuple

```
>>> y = x.rechunk((1000, 10))
```

Or chunk only specific dimensions with a dictionary

```
>>> y = x.rechunk({0: 1000})
```

Use the value `-1` to specify that you want a single chunk along a dimension or the value `"auto"` to specify that dask can freely rechunk a dimension to attain blocks of a uniform block size

```
>>> y = x.rechunk({0: -1, 1: 'auto'}, block_size_limit=1e8)
```

`dask.array.`**`repeat`**(*a*, *repeats*, *axis=None*)

Repeat elements of an array.

Parameters

a [array_like] Input array.

repeats [int or array of ints] The number of repetitions for each element. *repeats* is broadcasted to fit the shape of the given axis.

axis [int, optional] The axis along which to repeat values. By default, use the flattened input array, and return a flat output array.

Returns

repeated_array [ndarray] Output array which has the same shape as *a*, except along the given axis.

See also:

tile Tile an array.

Examples

```
>>> x = np.array([[1,2],[3,4]])
>>> np.repeat(x, 2)
array([1, 1, 2, 2, 3, 3, 4, 4])
>>> np.repeat(x, 3, axis=1)
array([[1, 1, 1, 2, 2, 2],
       [3, 3, 3, 4, 4, 4]])
>>> np.repeat(x, [1, 2], axis=0)
array([[1, 2],
       [3, 4],
       [3, 4]])
```

dask.array.**reshape**(*x*, *shape*)
Reshape array to new shape

This is a parallelized version of the `np.reshape` function with the following limitations:

1. It assumes that the array is stored in C-order
2. It only allows for reshapings that collapse or merge dimensions like `(1, 2, 3, 4) -> (1, 6, 4)` or `(64,) -> (4, 4, 4)`

When communication is necessary this algorithm depends on the logic within rechunk. It endeavors to keep chunk sizes roughly the same when possible.

See also:

dask.array.rechunk, `numpy.reshape`

dask.array.**result_type**(**arrays_and_dtypes*)
Returns the type that results from applying the NumPy type promotion rules to the arguments.

Type promotion in NumPy works similarly to the rules in languages like C++, with some slight differences. When both scalars and arrays are used, the array's type takes precedence and the actual value of the scalar is taken into account.

For example, calculating 3*a, where a is an array of 32-bit floats, intuitively should result in a 32-bit float output. If the 3 is a 32-bit integer, the NumPy rules indicate it can't convert losslessly into a 32-bit float, so a 64-bit float should be the result type. By examining the value of the constant, '3', we see that it fits in an 8-bit integer, which can be cast losslessly into the 32-bit float.

Parameters

arrays_and_dtypes [list of arrays and dtypes] The operands of some operation whose result type is needed.

Returns

out [dtype] The result type.

See also:

`dtype`, `promote_types`, `min_scalar_type`, `can_cast`

Notes

New in version 1.6.0.

The specific algorithm used is as follows.

Categories are determined by first checking which of boolean, integer (int/uint), or floating point (float/complex) the maximum kind of all the arrays and the scalars are.

If there are only scalars or the maximum category of the scalars is higher than the maximum category of the arrays, the data types are combined with `promote_types()` to produce the return value.

Otherwise, *min_scalar_type* is called on each array, and the resulting data types are all combined with `promote_types()` to produce the return value.

The set of int values is not a subset of the uint values for types with the same number of bits, something not reflected in `min_scalar_type()`, but handled as a special case in *result_type*.

Examples

```
>>> np.result_type(3, np.arange(7, dtype='i1'))
dtype('int8')
```

```
>>> np.result_type('i4', 'c8')
dtype('complex128')
```

```
>>> np.result_type(3.0, -2)
dtype('float64')
```

`dask.array.`**`rint`**(*x*[, *out*])

Round elements of the array to the nearest integer.

Parameters

x [array_like] Input array.

Returns

out [ndarray or scalar] Output array is same shape and type as *x*.

See also:

ceil, *floor*, *trunc*

Examples

```
>>> a = np.array([-1.7, -1.5, -0.2, 0.2, 1.5, 1.7, 2.0])
>>> np.rint(a)
array([-2., -2., -0.,  0.,  2.,  2.,  2.])
```

dask.array.**roll**(*a*, *shift*, *axis=None*)

Roll array elements along a given axis.

Elements that roll beyond the last position are re-introduced at the first.

Parameters

a [array_like] Input array.

shift [int] The number of places by which elements are shifted.

axis [int, optional] The axis along which elements are shifted. By default, the array is flattened before shifting, after which the original shape is restored.

Returns

res [ndarray] Output array, with the same shape as *a*.

See also:

rollaxis Roll the specified axis backwards, until it lies in a given position.

Examples

```
>>> x = np.arange(10)
>>> np.roll(x, 2)
array([8, 9, 0, 1, 2, 3, 4, 5, 6, 7])
```

```
>>> x2 = np.reshape(x, (2,5))
>>> x2
array([[0, 1, 2, 3, 4],
       [5, 6, 7, 8, 9]])
>>> np.roll(x2, 1)
array([[9, 0, 1, 2, 3],
       [4, 5, 6, 7, 8]])
>>> np.roll(x2, 1, axis=0)
array([[5, 6, 7, 8, 9],
       [0, 1, 2, 3, 4]])
>>> np.roll(x2, 1, axis=1)
array([[4, 0, 1, 2, 3],
       [9, 5, 6, 7, 8]])
```

dask.array.**round**(*a*, *decimals=0*, *out=None*)

Round an array to the given number of decimals.

Refer to *around* for full documentation.

See also:

around equivalent function

dask.array.**sign**(*x*[, *out*])

Returns an element-wise indication of the sign of a number.

The *sign* function returns `-1 if x < 0, 0 if x==0, 1 if x > 0`. nan is returned for nan inputs.

For complex inputs, the *sign* function returns `sign(x.real) + 0j if x.real != 0 else sign(x.imag) + 0j`.

complex(nan, 0) is returned for complex nan inputs.

Parameters

x [array_like] Input values.

Returns

y [ndarray] The sign of x.

Notes

There is more than one definition of sign in common use for complex numbers. The definition used here is equivalent to $x/\sqrt{x*x}$ which is different from a common alternative, $x/|x|$.

Examples

```
>>> np.sign([-5., 4.5])
array([-1.,  1.])
>>> np.sign(0)
0
>>> np.sign(5-2j)
(1+0j)
```

dask.array.**signbit**(*x*[, *out*])

Returns element-wise True where signbit is set (less than zero).

Parameters

x [array_like] The input value(s).

out [ndarray, optional] Array into which the output is placed. Its type is preserved and it must be of the right shape to hold the output. See *doc.ufuncs*.

Returns

result [ndarray of bool] Output array, or reference to *out* if that was supplied.

Examples

```
>>> np.signbit(-1.2)
True
>>> np.signbit(np.array([1, -2.3, 2.1]))
array([False,  True, False], dtype=bool)
```

dask.array.**sin**(*x*[, *out*])

Trigonometric sine, element-wise.

Parameters

x [array_like] Angle, in radians (2π rad equals 360 degrees).

Returns

y [array_like] The sine of each element of x.

See also:

arcsin, *sinh*, *cos*

Notes

The sine is one of the fundamental functions of trigonometry (the mathematical study of triangles). Consider a circle of radius 1 centered on the origin. A ray comes in from the $+x$ axis, makes an angle at the origin (measured counter-clockwise from that axis), and departs from the origin. The y coordinate of the outgoing ray's intersection with the unit circle is the sine of that angle. It ranges from -1 for $x = 3\pi/2$ to +1 for $\pi/2$. The function has zeroes where the angle is a multiple of π. Sines of angles between π and 2π are negative. The numerous properties of the sine and related functions are included in any standard trigonometry text.

Examples

Print sine of one angle:

```
>>> np.sin(np.pi/2.)
1.0
```

Print sines of an array of angles given in degrees:

```
>>> np.sin(np.array((0., 30., 45., 60., 90.)) * np.pi / 180. )
array([ 0.        ,  0.5       ,  0.70710678,  0.8660254 ,  1.        ])
```

Plot the sine function:

```
>>> import matplotlib.pylab as plt
>>> x = np.linspace(-np.pi, np.pi, 201)
>>> plt.plot(x, np.sin(x))
>>> plt.xlabel('Angle [rad]')
>>> plt.ylabel('sin(x)')
>>> plt.axis('tight')
>>> plt.show()
```

`dask.array.`**`sinh`**(*x*[, *out*])

Hyperbolic sine, element-wise.

Equivalent to `1/2 * (np.exp(x) - np.exp(-x))` or `-1j * np.sin(1j*x)`.

Parameters

x [array_like] Input array.

out [ndarray, optional] Output array of same shape as *x*.

Returns

y [ndarray] The corresponding hyperbolic sine values.

Raises

ValueError: invalid return array shape if *out* is provided and *out.shape* != *x.shape* (See Examples)

Notes

If *out* is provided, the function writes the result into it, and returns a reference to *out*. (See Examples)

References

M. Abramowitz and I. A. Stegun, Handbook of Mathematical Functions. New York, NY: Dover, 1972, pg. 83.

Examples

```
>>> np.sinh(0)
0.0
>>> np.sinh(np.pi*1j/2)
1j
>>> np.sinh(np.pi*1j) # (exact value is 0)
1.2246063538223773e-016j
>>> # Discrepancy due to vagaries of floating point arithmetic.
```

```
>>> # Example of providing the optional output parameter
>>> out2 = np.sinh([0.1], out1)
>>> out2 is out1
True
```

```
>>> # Example of ValueError due to provision of shape mis-matched `out`
>>> np.sinh(np.zeros((3,3)),np.zeros((2,2)))
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
ValueError: invalid return array shape
```

`dask.array.`**`sqrt`**(*x*[, *out*])

Return the positive square-root of an array, element-wise.

Parameters

x [array_like] The values whose square-roots are required.

out [ndarray, optional] Alternate array object in which to put the result; if provided, it must have the same shape as *x*

Returns

y [ndarray] An array of the same shape as *x*, containing the positive square-root of each element in *x*. If any element in *x* is complex, a complex array is returned (and the square-roots of negative reals are calculated). If all of the elements in *x* are real, so is *y*, with negative elements returning `nan`. If *out* was provided, *y* is a reference to it.

See also:

`lib.scimath.sqrt` A version which returns complex numbers when given negative reals.

Notes

sqrt has–consistent with common convention–as its branch cut the real "interval" [-*inf*, 0), and is continuous from above on it. A branch cut is a curve in the complex plane across which a given complex function fails to be continuous.

Examples

```
>>> np.sqrt([1,4,9])
array([ 1.,  2.,  3.])
```

```
>>> np.sqrt([4, -1, -3+4J])
array([ 2.+0.j,  0.+1.j,  1.+2.j])
```

```
>>> np.sqrt([4, -1, numpy.inf])
array([  2.,  NaN,  Inf])
```

dask.array.**square**(*x*[, *out*])

Return the element-wise square of the input.

Parameters

x [array_like] Input data.

Returns

out [ndarray] Element-wise *x*x*, of the same shape and dtype as *x*. Returns scalar if *x* is a scalar.

See also:

numpy.linalg.matrix_power, *sqrt*, power

Examples

```
>>> np.square([-1j, 1])
array([-1.-0.j,  1.+0.j])
```

dask.array.**squeeze**(*a*, *axis=None*)

Remove single-dimensional entries from the shape of an array.

Parameters

a [array_like] Input data.

axis [None or int or tuple of ints, optional] New in version 1.7.0.

Selects a subset of the single-dimensional entries in the shape. If an axis is selected with shape entry greater than one, an error is raised.

Returns

squeezed [ndarray] The input array, but with all or a subset of the dimensions of length 1 removed. This is always *a* itself or a view into *a*.

Examples

```
>>> x = np.array([[[0], [1], [2]]])
>>> x.shape
(1, 3, 1)
>>> np.squeeze(x).shape
(3,)
>>> np.squeeze(x, axis=(2,)).shape
(1, 3)
```

dask.array.**stack**(*seq*, *axis=0*)
Stack arrays along a new axis

Given a sequence of dask arrays, form a new dask array by stacking them along a new dimension (axis=0 by default)

See also:

concatenate

Examples

Create slices

```
>>> import dask.array as da
>>> import numpy as np
```

```
>>> data = [from_array(np.ones((4, 4)), chunks=(2, 2))
...          for i in range(3)]
```

```
>>> x = da.stack(data, axis=0)
>>> x.shape
(3, 4, 4)
```

```
>>> da.stack(data, axis=1).shape
(4, 3, 4)
```

```
>>> da.stack(data, axis=-1).shape
(4, 4, 3)
```

Result is a new dask Array

dask.array.**std**(*a*, *axis=None*, *dtype=None*, *out=None*, *ddof=0*, *keepdims=False*)
Compute the standard deviation along the specified axis.

Returns the standard deviation, a measure of the spread of a distribution, of the array elements. The standard deviation is computed for the flattened array by default, otherwise over the specified axis.

Parameters

a [array_like] Calculate the standard deviation of these values.

axis [None or int or tuple of ints, optional] Axis or axes along which the standard deviation is computed. The default is to compute the standard deviation of the flattened array.

If this is a tuple of ints, a standard deviation is performed over multiple axes, instead of a single axis or all the axes as before.

dtype [dtype, optional] Type to use in computing the standard deviation. For arrays of integer type the default is float64, for arrays of float types it is the same as the array type.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape as the expected output but the type (of the calculated values) will be cast if necessary.

ddof [int, optional] Means Delta Degrees of Freedom. The divisor used in calculations is `N - ddof`, where `N` represents the number of elements. By default *ddof* is zero.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

Returns

standard_deviation [ndarray, see dtype parameter above.] If *out* is None, return a new array containing the standard deviation, otherwise return a reference to the output array.

See also:

var, *mean*, *nanmean*, *nanstd*, *nanvar*

numpy.doc.ufuncs Section "Output arguments"

Notes

The standard deviation is the square root of the average of the squared deviations from the mean, i.e., `std = sqrt(mean(abs(x - x.mean())**2))`.

The average squared deviation is normally calculated as `x.sum() / N`, where `N = len(x)`. If, however, *ddof* is specified, the divisor `N - ddof` is used instead. In standard statistical practice, `ddof=1` provides an unbiased estimator of the variance of the infinite population. `ddof=0` provides a maximum likelihood estimate of the variance for normally distributed variables. The standard deviation computed in this function is the square root of the estimated variance, so even with `ddof=1`, it will not be an unbiased estimate of the standard deviation per se.

Note that, for complex numbers, *std* takes the absolute value before squaring, so that the result is always real and nonnegative.

For floating-point input, the *std* is computed using the same precision the input has. Depending on the input data, this can cause the results to be inaccurate, especially for float32 (see example below). Specifying a higher-accuracy accumulator using the *dtype* keyword can alleviate this issue.

Examples

```
>>> a = np.array([[1, 2], [3, 4]])
>>> np.std(a)
1.1180339887498949
>>> np.std(a, axis=0)
array([ 1.,  1.])
>>> np.std(a, axis=1)
array([ 0.5,  0.5])
```

In single precision, std() can be inaccurate:

```
>>> a = np.zeros((2, 512*512), dtype=np.float32)
>>> a[0, :] = 1.0
>>> a[1, :] = 0.1
>>> np.std(a)
0.45000005
```

Computing the standard deviation in float64 is more accurate:

```
>>> np.std(a, dtype=np.float64)
0.44999999925494177
```

dask.array.**sum**(*a*, *axis=None*, *dtype=None*, *out=None*, *keepdims=False*)

Sum of array elements over a given axis.

Parameters

a [array_like] Elements to sum.

axis [None or int or tuple of ints, optional] Axis or axes along which a sum is performed. The default, axis=None, will sum all of the elements of the input array. If axis is negative it counts from the last to the first axis.

New in version 1.7.0.

If axis is a tuple of ints, a sum is performed on all of the axes specified in the tuple instead of a single axis or all the axes as before.

dtype [dtype, optional] The type of the returned array and of the accumulator in which the elements are summed. The dtype of *a* is used by default unless *a* has an integer dtype of less precision than the default platform integer. In that case, if *a* is signed then the platform integer is used while if *a* is unsigned then an unsigned integer of the same precision as the platform integer is used.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array.

Returns

sum_along_axis [ndarray] An array with the same shape as *a*, with the specified axis removed. If *a* is a 0-d array, or if *axis* is None, a scalar is returned. If an output array is specified, a reference to *out* is returned.

See also:

ndarray.sum Equivalent method.

cumsum Cumulative sum of array elements.

trapz Integration of array values using the composite trapezoidal rule.

mean, *average*

Notes

Arithmetic is modular when using integer types, and no error is raised on overflow.

The sum of an empty array is the neutral element 0:

```
>>> np.sum([])
0.0
```

Examples

```
>>> np.sum([0.5, 1.5])
2.0
>>> np.sum([0.5, 0.7, 0.2, 1.5], dtype=np.int32)
1
>>> np.sum([[0, 1], [0, 5]])
6
>>> np.sum([[0, 1], [0, 5]], axis=0)
array([0, 6])
>>> np.sum([[0, 1], [0, 5]], axis=1)
array([1, 5])
```

If the accumulator is too small, overflow occurs:

```
>>> np.ones(128, dtype=np.int8).sum(dtype=np.int8)
-128
```

dask.array.**take**(*a*, *indices*, *axis=None*, *out=None*, *mode='raise'*)

Take elements from an array along an axis.

This function does the same thing as "fancy" indexing (indexing arrays using arrays); however, it can be easier to use if you need elements along a given axis.

Parameters

a [array_like] The source array.

indices [array_like] The indices of the values to extract.

New in version 1.8.0.

Also allow scalars for indices.

axis [int, optional] The axis over which to select values. By default, the flattened input array is used.

out [ndarray, optional] If provided, the result will be placed in this array. It should be of the appropriate shape and dtype.

mode [{'raise', 'wrap', 'clip'}, optional] Specifies how out-of-bounds indices will behave.

- 'raise' – raise an error (default)
- 'wrap' – wrap around
- 'clip' – clip to the range

'clip' mode means that all indices that are too large are replaced by the index that addresses the last element along that axis. Note that this disables indexing with negative numbers.

Returns

subarray [ndarray] The returned array has the same type as *a*.

See also:

compress Take elements using a boolean mask

ndarray.take equivalent method

Examples

```
>>> a = [4, 3, 5, 7, 6, 8]
>>> indices = [0, 1, 4]
>>> np.take(a, indices)
array([4, 3, 6])
```

In this example if *a* is an ndarray, "fancy" indexing can be used.

```
>>> a = np.array(a)
>>> a[indices]
array([4, 3, 6])
```

If *indices* is not one dimensional, the output also has these dimensions.

```
>>> np.take(a, [[0, 1], [2, 3]])
array([[4, 3],
       [5, 7]])
```

`dask.array.tan`(*x*[, *out*])
Compute tangent element-wise.

Equivalent to `np.sin(x)/np.cos(x)` element-wise.

Parameters

x [array_like] Input array.

out [ndarray, optional] Output array of same shape as *x*.

Returns

y [ndarray] The corresponding tangent values.

Raises

ValueError: invalid return array shape if *out* is provided and *out.shape* != *x.shape* (See Examples)

Notes

If *out* is provided, the function writes the result into it, and returns a reference to *out*. (See Examples)

References

M. Abramowitz and I. A. Stegun, Handbook of Mathematical Functions. New York, NY: Dover, 1972.

Examples

```
>>> from math import pi
>>> np.tan(np.array([-pi,pi/2,pi]))
array([  1.22460635e-16,   1.63317787e+16,  -1.22460635e-16])
>>>
>>> # Example of providing the optional output parameter illustrating
>>> # that what is returned is a reference to said parameter
```

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```
>>> out2 = np.cos([0.1], out1)
>>> out2 is out1
True
>>>
>>> # Example of ValueError due to provision of shape mis-matched `out`
>>> np.cos(np.zeros((3,3)),np.zeros((2,2)))
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
ValueError: invalid return array shape
```

dask.array.**tanh**(*x*[, *out*])

Compute hyperbolic tangent element-wise.

Equivalent to `np.sinh(x)/np.cosh(x)` or `-1j * np.tan(1j*x)`.

Parameters

x [array_like] Input array.

out [ndarray, optional] Output array of same shape as *x*.

Returns

y [ndarray] The corresponding hyperbolic tangent values.

Raises

ValueError: invalid return array shape if *out* is provided and *out.shape* != *x.shape* (See Examples)

Notes

If *out* is provided, the function writes the result into it, and returns a reference to *out*. (See Examples)

References

[1], *[2]*

Examples

```
>>> np.tanh((0, np.pi*1j, np.pi*1j/2))
array([ 0. +0.00000000e+00j,  0. -1.22460635e-16j,  0. +1.63317787e+16j])
```

```
>>> # Example of providing the optional output parameter illustrating
>>> # that what is returned is a reference to said parameter
>>> out2 = np.tanh([0.1], out1)
>>> out2 is out1
True
```

```
>>> # Example of ValueError due to provision of shape mis-matched `out`
>>> np.tanh(np.zeros((3,3)),np.zeros((2,2)))
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
ValueError: invalid return array shape
```

dask.array.**tensordot**(*a*, *b*, *axes=2*)

Compute tensor dot product along specified axes for arrays >= 1-D.

Given two tensors (arrays of dimension greater than or equal to one), *a* and *b*, and an array_like object containing two array_like objects, `(a_axes, b_axes)`, sum the products of *a*'s and *b*'s elements (components) over the axes specified by `a_axes` and `b_axes`. The third argument can be a single non-negative integer_like scalar, `N`; if it is such, then the last `N` dimensions of *a* and the first `N` dimensions of *b* are summed over.

Parameters

a, b [array_like, len(shape) >= 1] Tensors to "dot".

axes [int or (2,) array_like]

- integer_like If an int N, sum over the last N axes of *a* and the first N axes of *b* in order. The sizes of the corresponding axes must match.
- (2,) array_like Or, a list of axes to be summed over, first sequence applying to *a*, second to *b*. Both elements array_like must be of the same length.

See also:

dot, *einsum*

Notes

Three common use cases are: `axes = 0` : tensor product $aotimes b$ `axes = 1` : tensor dot product $acdot b$ `axes = 2` : (default) tensor double contraction $a:b$

When *axes* is integer_like, the sequence for evaluation will be: first the -Nth axis in *a* and 0th axis in *b*, and the -1th axis in *a* and Nth axis in *b* last.

When there is more than one axis to sum over - and they are not the last (first) axes of *a* (*b*) - the argument *axes* should consist of two sequences of the same length, with the first axis to sum over given first in both sequences, the second axis second, and so forth.

Examples

A "traditional" example:

```
>>> a = np.arange(60.).reshape(3,4,5)
>>> b = np.arange(24.).reshape(4,3,2)
>>> c = np.tensordot(a,b, axes=([1,0],[0,1]))
>>> c.shape
(5, 2)
>>> c
array([[ 4400.,  4730.],
       [ 4532.,  4874.],
       [ 4664.,  5018.],
       [ 4796.,  5162.],
       [ 4928.,  5306.]])
>>> # A slower but equivalent way of computing the same...
>>> d = np.zeros((5,2))
>>> for i in range(5):
...   for j in range(2):
...     for k in range(3):
...       for n in range(4):
```

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```
...             d[i,j] += a[k,n,i] * b[n,k,j]
>>> c == d
array([[ True,  True],
       [ True,  True],
       [ True,  True],
       [ True,  True],
       [ True,  True]], dtype=bool)
```

An extended example taking advantage of the overloading of + and *:

```
>>> a = np.array(range(1, 9))
>>> a.shape = (2, 2, 2)
>>> A = np.array(('a', 'b', 'c', 'd'), dtype=object)
>>> A.shape = (2, 2)
>>> a; A
array([[[1, 2],
        [3, 4]],
       [[5, 6],
        [7, 8]]])
array([[a, b],
       [c, d]], dtype=object)
```

```
>>> np.tensordot(a, A) # third argument default is 2 for double-contraction
array([abbcccdddd, aaaaabbbbbbccccccdddddddd], dtype=object)
```

```
>>> np.tensordot(a, A, 1)
array([[[acc, bdd],
        [aaacccc, bbbdddd]],
       [[aaaaacccccc, bbbbbddddddd],
        [aaaaaaaccccccc, bbbbbbbddddddddd]]], dtype=object)
```

```
>>> np.tensordot(a, A, 0) # tensor product (result too long to incl.)
array([[[[[a, b],
          [c, d]],
          ...
```

```
>>> np.tensordot(a, A, (0, 1))
array([[[abbbbb, cddddd],
        [aabbbbbb, ccdddddd]],
       [[aaabbbbbbb, cccddddddd],
        [aaaabbbbbbbb, ccccddddddddd]]], dtype=object)
```

```
>>> np.tensordot(a, A, (2, 1))
array([[[abb, cdd],
        [aaabbbb, cccdddd]],
       [[aaaaabbbbbb, ccccccddddddd],
        [aaaaaaabbbbbbbbb, cccccccddddddddd]]], dtype=object)
```

```
>>> np.tensordot(a, A, ((0, 1), (0, 1)))
array([abbbcccccddddddd, aabbbbccccccddddddddd], dtype=object)
```

```
>>> np.tensordot(a, A, ((2, 1), (1, 0)))
array([acccbbdddd, aaaaacccccccbbbbbbddddddddd], dtype=object)
```

dask.array.**tile**(*A*, *reps*)

Construct an array by repeating A the number of times given by reps.

If *reps* has length d, the result will have dimension of max(d, A.ndim).

If A.ndim < d, *A* is promoted to be d-dimensional by prepending new axes. So a shape (3,) array is promoted to (1, 3) for 2-D replication, or shape (1, 1, 3) for 3-D replication. If this is not the desired behavior, promote *A* to d-dimensions manually before calling this function.

If A.ndim > d, *reps* is promoted to *A*.ndim by pre-pending 1's to it. Thus for an *A* of shape (2, 3, 4, 5), a *reps* of (2, 2) is treated as (1, 1, 2, 2).

Note : Although tile may be used for broadcasting, it is strongly recommended to use numpy's broadcasting operations and functions.

Parameters

A [array_like] The input array.

reps [array_like] The number of repetitions of *A* along each axis.

Returns

c [ndarray] The tiled output array.

See also:

repeat Repeat elements of an array.

broadcast_to Broadcast an array to a new shape

Examples

```
>>> a = np.array([0, 1, 2])
>>> np.tile(a, 2)
array([0, 1, 2, 0, 1, 2])
>>> np.tile(a, (2, 2))
array([[0, 1, 2, 0, 1, 2],
       [0, 1, 2, 0, 1, 2]])
>>> np.tile(a, (2, 1, 2))
array([[[0, 1, 2, 0, 1, 2]],
       [[0, 1, 2, 0, 1, 2]]])
```

```
>>> b = np.array([[1, 2], [3, 4]])
>>> np.tile(b, 2)
array([[1, 2, 1, 2],
       [3, 4, 3, 4]])
>>> np.tile(b, (2, 1))
array([[1, 2],
       [3, 4],
       [1, 2],
       [3, 4]])
```

```
>>> c = np.array([1,2,3,4])
>>> np.tile(c,(4,1))
array([[1, 2, 3, 4],
       [1, 2, 3, 4],
       [1, 2, 3, 4],
       [1, 2, 3, 4]])
```

dask.array.**topk**(*a*, *k*, *axis=-1*, *split_every=None*)

Extract the k largest elements from a on the given axis, and return them sorted from largest to smallest. If k is negative, extract the -k smallest elements instead, and return them sorted from smallest to largest.

This performs best when `k` is much smaller than the chunk size. All results will be returned in a single chunk along the given axis.

Parameters

x: Array Data being sorted

k: int

axis: int, optional

split_every: int >=2, optional See `reduce()`. This parameter becomes very important when k is on the same order of magnitude of the chunk size or more, as it prevents getting the whole or a significant portion of the input array in memory all at once, with a negative impact on network transfer too when running on distributed.

Returns

Selection of x with size abs(k) along the given axis.

Examples

```
>>> import dask.array as da
>>> x = np.array([5, 1, 3, 6])
>>> d = da.from_array(x, chunks=2)
>>> d.topk(2).compute()
array([6, 5])
>>> d.topk(-2).compute()
array([1, 3])
```

dask.array.**transpose**(*a*, *axes=None*)

Permute the dimensions of an array.

Parameters

a [array_like] Input array.

axes [list of ints, optional] By default, reverse the dimensions, otherwise permute the axes according to the values given.

Returns

p [ndarray] *a* with its axes permuted. A view is returned whenever possible.

See also:

`moveaxis`, `argsort`

Notes

Use *transpose(a, argsort(axes))* to invert the transposition of tensors when using the *axes* keyword argument.

Transposing a 1-D array returns an unchanged view of the original array.

Examples

```
>>> x = np.arange(4).reshape((2,2))
>>> x
array([[0, 1],
       [2, 3]])
```

```
>>> np.transpose(x)
array([[0, 2],
       [1, 3]])
```

```
>>> x = np.ones((1, 2, 3))
>>> np.transpose(x, (1, 0, 2)).shape
(2, 1, 3)
```

dask.array.**tril**(*m*, *k=0*)

Lower triangle of an array with elements above the *k*-th diagonal zeroed.

Parameters

m [array_like, shape (M, M)] Input array.

k [int, optional] Diagonal above which to zero elements. *k = 0* (the default) is the main diagonal, *k < 0* is below it and *k > 0* is above.

Returns

tril [ndarray, shape (M, M)] Lower triangle of *m*, of same shape and data-type as *m*.

See also:

triu upper triangle of an array

dask.array.**triu**(*m*, *k=0*)

Upper triangle of an array with elements above the *k*-th diagonal zeroed.

Parameters

m [array_like, shape (M, N)] Input array.

k [int, optional] Diagonal above which to zero elements. *k = 0* (the default) is the main diagonal, *k < 0* is below it and *k > 0* is above.

Returns

triu [ndarray, shape (M, N)] Upper triangle of *m*, of same shape and data-type as *m*.

See also:

tril lower triangle of an array

dask.array.**trunc**(*x*[, *out*])

Return the truncated value of the input, element-wise.

The truncated value of the scalar *x* is the nearest integer *i* which is closer to zero than *x* is. In short, the fractional part of the signed number *x* is discarded.

Parameters

x [array_like] Input data.

Returns

y [ndarray or scalar] The truncated value of each element in *x*.

See also:

ceil, *floor*, *rint*

Notes

New in version 1.3.0.

Examples

```
>>> a = np.array([-1.7, -1.5, -0.2, 0.2, 1.5, 1.7, 2.0])
>>> np.trunc(a)
array([-1., -1., -0.,  0.,  1.,  1.,  2.])
```

dask.array.**unique**(*ar*, *return_index=False*, *return_inverse=False*, *return_counts=False*)

Find the unique elements of an array.

Returns the sorted unique elements of an array. There are three optional outputs in addition to the unique elements: the indices of the input array that give the unique values, the indices of the unique array that reconstruct the input array, and the number of times each unique value comes up in the input array.

Parameters

ar [array_like] Input array. This will be flattened if it is not already 1-D.

return_index [bool, optional] If True, also return the indices of *ar* that result in the unique array.

return_inverse [bool, optional] If True, also return the indices of the unique array that can be used to reconstruct *ar*.

return_counts [bool, optional] If True, also return the number of times each unique value comes up in *ar*.

New in version 1.9.0.

Returns

unique [ndarray] The sorted unique values.

unique_indices [ndarray, optional] The indices of the first occurrences of the unique values in the (flattened) original array. Only provided if *return_index* is True.

unique_inverse [ndarray, optional] The indices to reconstruct the (flattened) original array from the unique array. Only provided if *return_inverse* is True.

unique_counts [ndarray, optional] The number of times each of the unique values comes up in the original array. Only provided if *return_counts* is True.

New in version 1.9.0.

See also:

numpy.lib.arraysetops Module with a number of other functions for performing set operations on arrays.

Examples

```
>>> np.unique([1, 1, 2, 2, 3, 3])
array([1, 2, 3])
>>> a = np.array([[1, 1], [2, 3]])
>>> np.unique(a)
array([1, 2, 3])
```

Return the indices of the original array that give the unique values:

```
>>> a = np.array(['a', 'b', 'b', 'c', 'a'])
>>> u, indices = np.unique(a, return_index=True)
>>> u
array(['a', 'b', 'c'],
      dtype='|S1')
>>> indices
array([0, 1, 3])
>>> a[indices]
array(['a', 'b', 'c'],
      dtype='|S1')
```

Reconstruct the input array from the unique values:

```
>>> a = np.array([1, 2, 6, 4, 2, 3, 2])
>>> u, indices = np.unique(a, return_inverse=True)
>>> u
array([1, 2, 3, 4, 6])
>>> indices
array([0, 1, 4, 3, 1, 2, 1])
>>> u[indices]
array([1, 2, 6, 4, 2, 3, 2])
```

`dask.array.`**`unravel_index`**(*indices*, *dims*, *order='C'*)

Converts a flat index or array of flat indices into a tuple of coordinate arrays.

Parameters

indices [array_like] An integer array whose elements are indices into the flattened version of an array of dimensions `dims`. Before version 1.6.0, this function accepted just one index value.

dims [tuple of ints] The shape of the array to use for unraveling `indices`.

order [{'C', 'F'}, optional] Determines whether the indices should be viewed as indexing in row-major (C-style) or column-major (Fortran-style) order.

New in version 1.6.0.

Returns

unraveled_coords [tuple of ndarray] Each array in the tuple has the same shape as the `indices` array.

See also:

`ravel_multi_index`

Examples

```
>>> np.unravel_index([22, 41, 37], (7,6))
(array([3, 6, 6]), array([4, 5, 1]))
>>> np.unravel_index([31, 41, 13], (7,6), order='F')
(array([3, 6, 6]), array([4, 5, 1]))
```

```
>>> np.unravel_index(1621, (6,7,8,9))
(3, 1, 4, 1)
```

dask.array.**var**(*a*, *axis=None*, *dtype=None*, *out=None*, *ddof=0*, *keepdims=False*)

Compute the variance along the specified axis.

Returns the variance of the array elements, a measure of the spread of a distribution. The variance is computed for the flattened array by default, otherwise over the specified axis.

Parameters

a [array_like] Array containing numbers whose variance is desired. If *a* is not an array, a conversion is attempted.

axis [None or int or tuple of ints, optional] Axis or axes along which the variance is computed. The default is to compute the variance of the flattened array.

If this is a tuple of ints, a variance is performed over multiple axes, instead of a single axis or all the axes as before.

dtype [data-type, optional] Type to use in computing the variance. For arrays of integer type the default is *float32*; for arrays of float types it is the same as the array type.

out [ndarray, optional] Alternate output array in which to place the result. It must have the same shape as the expected output, but the type is cast if necessary.

ddof [int, optional] "Delta Degrees of Freedom": the divisor used in the calculation is `N - ddof`, where `N` represents the number of elements. By default *ddof* is zero.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

Returns

variance [ndarray, see dtype parameter above] If `out=None`, returns a new array containing the variance; otherwise, a reference to the output array is returned.

See also:

std, *mean*, *nanmean*, *nanstd*, *nanvar*

numpy.doc.ufuncs Section "Output arguments"

Notes

The variance is the average of the squared deviations from the mean, i.e., `var = mean(abs(x - x.mean())**2)`.

The mean is normally calculated as `x.sum() / N`, where `N = len(x)`. If, however, *ddof* is specified, the divisor `N - ddof` is used instead. In standard statistical practice, `ddof=1` provides an unbiased estimator of the variance of a hypothetical infinite population. `ddof=0` provides a maximum likelihood estimate of the variance for normally distributed variables.

Note that for complex numbers, the absolute value is taken before squaring, so that the result is always real and nonnegative.

For floating-point input, the variance is computed using the same precision the input has. Depending on the input data, this can cause the results to be inaccurate, especially for *float32* (see example below). Specifying a higher-accuracy accumulator using the `dtype` keyword can alleviate this issue.

Examples

```
>>> a = np.array([[1, 2], [3, 4]])
>>> np.var(a)
1.25
>>> np.var(a, axis=0)
array([ 1.,  1.])
>>> np.var(a, axis=1)
array([ 0.25,  0.25])
```

In single precision, var() can be inaccurate:

```
>>> a = np.zeros((2, 512*512), dtype=np.float32)
>>> a[0, :] = 1.0
>>> a[1, :] = 0.1
>>> np.var(a)
0.20250003
```

Computing the variance in float64 is more accurate:

```
>>> np.var(a, dtype=np.float64)
0.20249999932944759
>>> ((1-0.55)**2 + (0.1-0.55)**2)/2
0.2025
```

`dask.array.`**vdot**(*a*, *b*)

Return the dot product of two vectors.

The vdot(*a*, *b*) function handles complex numbers differently than dot(*a*, *b*). If the first argument is complex the complex conjugate of the first argument is used for the calculation of the dot product.

Note that *vdot* handles multidimensional arrays differently than *dot*: it does *not* perform a matrix product, but flattens input arguments to 1-D vectors first. Consequently, it should only be used for vectors.

Parameters

a [array_like] If *a* is complex the complex conjugate is taken before calculation of the dot product.

b [array_like] Second argument to the dot product.

Returns

output [ndarray] Dot product of *a* and *b*. Can be an int, float, or complex depending on the types of *a* and *b*.

See also:

dot Return the dot product without using the complex conjugate of the first argument.

Examples

```
>>> a = np.array([1+2j,3+4j])
>>> b = np.array([5+6j,7+8j])
>>> np.vdot(a, b)
(70-8j)
>>> np.vdot(b, a)
(70+8j)
```

Note that higher-dimensional arrays are flattened!

```
>>> a = np.array([[1, 4], [5, 6]])
>>> b = np.array([[4, 1], [2, 2]])
>>> np.vdot(a, b)
30
>>> np.vdot(b, a)
30
>>> 1*4 + 4*1 + 5*2 + 6*2
30
```

dask.array.**vstack**(*tup*)

Stack arrays in sequence vertically (row wise).

Take a sequence of arrays and stack them vertically to make a single array. Rebuild arrays divided by *vsplit*.

Parameters

tup [sequence of ndarrays] Tuple containing arrays to be stacked. The arrays must have the same shape along all but the first axis.

Returns

stacked [ndarray] The array formed by stacking the given arrays.

See also:

stack Join a sequence of arrays along a new axis.

hstack Stack arrays in sequence horizontally (column wise).

dstack Stack arrays in sequence depth wise (along third dimension).

concatenate Join a sequence of arrays along an existing axis.

vsplit Split array into a list of multiple sub-arrays vertically.

Notes

Equivalent to `np.concatenate(tup, axis=0)` if *tup* contains arrays that are at least 2-dimensional.

Examples

```
>>> a = np.array([1, 2, 3])
>>> b = np.array([2, 3, 4])
>>> np.vstack((a,b))
array([[1, 2, 3],
       [2, 3, 4]])
```

```
>>> a = np.array([[1], [2], [3]])
>>> b = np.array([[2], [3], [4]])
>>> np.vstack((a,b))
array([[1],
       [2],
       [3],
       [2],
       [3],
       [4]])
```

dask.array.**where**(*condition*[, *x*, *y*])

Return elements, either from *x* or *y*, depending on *condition*.

If only *condition* is given, return `condition.nonzero()`.

Parameters

condition [array_like, bool] When True, yield *x*, otherwise yield *y*.

x, y [array_like, optional] Values from which to choose. *x* and *y* need to have the same shape as *condition*.

Returns

out [ndarray or tuple of ndarrays] If both *x* and *y* are specified, the output array contains elements of *x* where *condition* is True, and elements from *y* elsewhere.

If only *condition* is given, return the tuple `condition.nonzero()`, the indices where *condition* is True.

See also:

nonzero, *choose*

Notes

If *x* and *y* are given and input arrays are 1-D, *where* is equivalent to:

```
[xv if c else yv for (c,xv,yv) in zip(condition,x,y)]
```

Examples

```
>>> np.where([[True, False], [True, True]],
...          [[1, 2], [3, 4]],
...          [[9, 8], [7, 6]])
array([[1, 8],
       [3, 4]])
```

```
>>> np.where([[0, 1], [1, 0]])
(array([0, 1]), array([1, 0]))
```

```
>>> x = np.arange(9.).reshape(3, 3)
>>> np.where( x > 5 )
(array([2, 2, 2]), array([0, 1, 2]))
>>> x[np.where( x > 3.0 )]               # Note: result is 1D.
array([ 4.,  5.,  6.,  7.,  8.])
```

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```
>>> np.where(x < 5, x, -1)               # Note: broadcasting.
array([[ 0.,  1.,  2.],
       [ 3.,  4., -1.],
       [-1., -1., -1.]])
```

Find the indices of elements of *x* that are in *goodvalues*.

```
>>> goodvalues = [3, 4, 7]
>>> ix = np.in1d(x.ravel(), goodvalues).reshape(x.shape)
>>> ix
array([[False, False, False],
       [ True,  True, False],
       [False,  True, False]], dtype=bool)
>>> np.where(ix)
(array([1, 1, 2]), array([0, 1, 1]))
```

dask.array.**zeros**(**args*, ***kwargs*)

Blocked variant of zeros

Follows the signature of zeros exactly except that it also requires a keyword argument chunks=(...)

Original signature follows below. zeros(shape, dtype=float, order='C')

Return a new array of given shape and type, filled with zeros.

Parameters

shape [int or sequence of ints] Shape of the new array, e.g., `(2, 3)` or `2`.

dtype [data-type, optional] The desired data-type for the array, e.g., *numpy.int8*. Default is *numpy.float64*.

order [{'C', 'F'}, optional] Whether to store multidimensional data in C- or Fortran-contiguous (row- or column-wise) order in memory.

Returns

out [ndarray] Array of zeros with the given shape, dtype, and order.

See also:

zeros_like Return an array of zeros with shape and type of input.

ones_like Return an array of ones with shape and type of input.

empty_like Return an empty array with shape and type of input.

ones Return a new array setting values to one.

empty Return a new uninitialized array.

Examples

```
>>> np.zeros(5)
array([ 0.,  0.,  0.,  0.,  0.])
```

```
>>> np.zeros((5,), dtype=np.int)
array([0, 0, 0, 0, 0])
```

```
>>> np.zeros((2, 1))
array([[ 0.],
       [ 0.]])
```

```
>>> s = (2,2)
>>> np.zeros(s)
array([[ 0.,  0.],
       [ 0.,  0.]])
```

```
>>> np.zeros((2,), dtype=[('x', 'i4'), ('y', 'i4')]) # custom dtype
array([(0, 0), (0, 0)],
      dtype=[('x', '<i4'), ('y', '<i4')])
```

dask.array.**zeros_like**(*a*, *dtype=None*, *chunks=None*)

Return an array of zeros with the same shape and type as a given array.

Parameters

a [array_like] The shape and data-type of *a* define these same attributes of the returned array.

dtype [data-type, optional] Overrides the data type of the result.

chunks [sequence of ints] The number of samples on each block. Note that the last block will have fewer samples if `len(array) % chunks != 0`.

Returns

out [ndarray] Array of zeros with the same shape and type as *a*.

See also:

ones_like Return an array of ones with shape and type of input.

empty_like Return an empty array with shape and type of input.

zeros Return a new array setting values to zero.

ones Return a new array setting values to one.

empty Return a new uninitialized array.

dask.array.linalg.**cholesky**(*a*, *lower=False*)

Returns the Cholesky decomposition, $A = LL^*$ or $A = U^*U$ of a Hermitian positive-definite matrix A.

Parameters

a [(M, M) array_like] Matrix to be decomposed

lower [bool, optional] Whether to compute the upper or lower triangular Cholesky factorization. Default is upper-triangular.

Returns

c [(M, M) Array] Upper- or lower-triangular Cholesky factor of *a*.

dask.array.linalg.**inv**(*a*)

Compute the inverse of a matrix with LU decomposition and forward / backward substitutions.

Parameters

a [array_like] Square matrix to be inverted.

Returns

ainv [Array] Inverse of the matrix *a*.

dask.array.linalg.**lstsq**(*a*, *b*)

Return the least-squares solution to a linear matrix equation using QR decomposition.

Solves the equation *a x* = *b* by computing a vector *x* that minimizes the Euclidean 2-norm || *b* - *a x* ||^2. The equation may be under-, well-, or over- determined (i.e., the number of linearly independent rows of *a* can be less than, equal to, or greater than its number of linearly independent columns). If *a* is square and of full rank, then *x* (but for round-off error) is the "exact" solution of the equation.

Parameters

a [(M, N) array_like] "Coefficient" matrix.

b [(M,) array_like] Ordinate or "dependent variable" values.

Returns

x [(N,) Array] Least-squares solution. If *b* is two-dimensional, the solutions are in the *K* columns of *x*.

residuals [(1,) Array] Sums of residuals; squared Euclidean 2-norm for each column in `b - a*x`.

rank [Array] Rank of matrix *a*.

s [(min(M, N),) Array] Singular values of *a*.

dask.array.linalg.**lu**(*a*)

Compute the lu decomposition of a matrix.

Returns

p: Array, permutation matrix

l: Array, lower triangular matrix with unit diagonal.

u: Array, upper triangular matrix

Examples

```
>>> p, l, u = da.linalg.lu(x)
```

dask.array.linalg.**norm**(*x*, *ord=None*, *axis=None*, *keepdims=False*)

Matrix or vector norm.

This function is able to return one of eight different matrix norms, or one of an infinite number of vector norms (described below), depending on the value of the `ord` parameter.

Parameters

x [array_like] Input array. If *axis* is None, *x* must be 1-D or 2-D.

ord [{non-zero int, inf, -inf, 'fro', 'nuc'}, optional] Order of the norm (see table under `Notes`). inf means numpy's *inf* object.

axis [{int, 2-tuple of ints, None}, optional] If *axis* is an integer, it specifies the axis of *x* along which to compute the vector norms. If *axis* is a 2-tuple, it specifies the axes that hold 2-D matrices, and the matrix norms of these matrices are computed. If *axis* is None then either a vector norm (when *x* is 1-D) or a matrix norm (when *x* is 2-D) is returned.

keepdims [bool, optional] If this is set to True, the axes which are normed over are left in the result as dimensions with size one. With this option the result will broadcast correctly against the original *x*.

New in version 1.10.0.

Returns

n [float or ndarray] Norm of the matrix or vector(s).

Notes

For values of `ord <= 0`, the result is, strictly speaking, not a mathematical 'norm', but it may still be useful for various numerical purposes.

The following norms can be calculated:

ord	norm for matrices	norm for vectors
None	Frobenius norm	2-norm
'fro'	Frobenius norm	–
'nuc'	nuclear norm	–
inf	max(sum(abs(x), axis=1))	max(abs(x))
-inf	min(sum(abs(x), axis=1))	min(abs(x))
0	–	sum(x != 0)
1	max(sum(abs(x), axis=0))	as below
-1	min(sum(abs(x), axis=0))	as below
2	2-norm (largest sing. value)	as below
-2	smallest singular value	as below
other	–	sum(abs(x)**ord)**(1./ord)

The Frobenius norm is given by *[1]*:

$||A||_F = [\sum_{i,j} abs(a_{i,j})^2]^{1/2}$

The nuclear norm is the sum of the singular values.

References

[1]

Examples

```
>>> from numpy import linalg as LA
>>> a = np.arange(9) - 4
>>> a
array([-4, -3, -2, -1,  0,  1,  2,  3,  4])
>>> b = a.reshape((3, 3))
>>> b
array([[-4, -3, -2],
       [-1,  0,  1],
       [ 2,  3,  4]])
```

```
>>> LA.norm(a)
7.745966692414834
>>> LA.norm(b)
7.745966692414834
>>> LA.norm(b, 'fro')
7.745966692414834
>>> LA.norm(a, np.inf)
4.0
>>> LA.norm(b, np.inf)
9.0
>>> LA.norm(a, -np.inf)
0.0
>>> LA.norm(b, -np.inf)
2.0
```

```
>>> LA.norm(a, 1)
20.0
>>> LA.norm(b, 1)
7.0
>>> LA.norm(a, -1)
-4.6566128774142013e-010
>>> LA.norm(b, -1)
6.0
>>> LA.norm(a, 2)
7.745966692414834
>>> LA.norm(b, 2)
7.3484692283495345
```

```
>>> LA.norm(a, -2)
nan
>>> LA.norm(b, -2)
1.8570331885190563e-016
>>> LA.norm(a, 3)
5.8480354764257312
>>> LA.norm(a, -3)
nan
```

Using the *axis* argument to compute vector norms:

```
>>> c = np.array([[ 1, 2, 3],
...               [-1, 1, 4]])
>>> LA.norm(c, axis=0)
array([ 1.41421356,  2.23606798,  5.        ])
>>> LA.norm(c, axis=1)
array([ 3.74165739,  4.24264069])
>>> LA.norm(c, ord=1, axis=1)
array([ 6.,  6.])
```

Using the *axis* argument to compute matrix norms:

```
>>> m = np.arange(8).reshape(2,2,2)
>>> LA.norm(m, axis=(1,2))
array([  3.74165739,  11.22497216])
>>> LA.norm(m[0, :, :]), LA.norm(m[1, :, :])
(3.7416573867739413, 11.224972160321824)
```

dask.array.linalg.**qr**(*a*)

Compute the qr factorization of a matrix.

Returns

q: Array, orthonormal

r: Array, upper-triangular

See also:

np.linalg.qr Equivalent NumPy Operation

dask.array.linalg.tsqr Implementation for tall-and-skinny arrays

dask.array.linalg.sfqr Implementation for short-and-fat arrays

Examples

```
>>> q, r = da.linalg.qr(x)
```

dask.array.linalg.**solve**(*a*, *b*, *sym_pos=False*)

Solve the equation `a x = b` for `x`. By default, use LU decomposition and forward / backward substitutions. When `sym_pos` is `True`, use Cholesky decomposition.

Parameters

a [(M, M) array_like] A square matrix.

b [(M,) or (M, N) array_like] Right-hand side matrix in `a x = b`.

sym_pos [bool] Assume a is symmetric and positive definite. If `True`, use Cholesky decomposition.

Returns

x [(M,) or (M, N) Array] Solution to the system `a x = b`. Shape of the return matches the shape of *b*.

dask.array.linalg.**solve_triangular**(*a*, *b*, *lower=False*)

Solve the equation *a x = b* for *x*, assuming a is a triangular matrix.

Parameters

a [(M, M) array_like] A triangular matrix

b [(M,) or (M, N) array_like] Right-hand side matrix in *a x = b*

lower [bool, optional] Use only data contained in the lower triangle of *a*. Default is to use upper triangle.

Returns

x [(M,) or (M, N) array] Solution to the system *a x = b*. Shape of return matches *b*.

dask.array.linalg.**svd**(*a*)

Compute the singular value decomposition of a matrix.

Returns

u: Array, unitary / orthogonal

s: Array, singular values in decreasing order (largest first)

v: Array, unitary / orthogonal

See also:

np.linalg.svd Equivalent NumPy Operation

dask.array.linalg.tsqr Implementation for tall-and-skinny arrays

Examples

```
>>> u, s, v = da.linalg.svd(x)
```

dask.array.linalg.**svd_compressed**(*a*, *k*, *n_power_iter=0*, *seed=None*)

Randomly compressed rank-k thin Singular Value Decomposition.

This computes the approximate singular value decomposition of a large array. This algorithm is generally faster than the normal algorithm but does not provide exact results. One can balance between performance and accuracy with input parameters (see below).

Parameters

a: Array Input array

k: int Rank of the desired thin SVD decomposition.

n_power_iter: int Number of power iterations, useful when the singular values decay slowly. Error decreases exponentially as n_power_iter increases. In practice, set n_power_iter <= 4.

Returns

u: Array, unitary / orthogonal

s: Array, singular values in decreasing order (largest first)

v: Array, unitary / orthogonal

References

N. Halko, P. G. Martinsson, and J. A. Tropp. Finding structure with randomness: Probabilistic algorithms for constructing approximate matrix decompositions. SIAM Rev., Survey and Review section, Vol. 53, num. 2, pp. 217-288, June 2011 http://arxiv.org/abs/0909.4061

Examples

```
>>> u, s, vt = svd_compressed(x, 20)
```

dask.array.linalg.**tsqr**(*data*, *compute_svd=False*, *_max_vchunk_size=None*)

Direct Tall-and-Skinny QR algorithm

As presented in:

> A. Benson, D. Gleich, and J. Demmel. Direct QR factorizations for tall-and-skinny matrices in MapReduce architectures. IEEE International Conference on Big Data, 2013. http://arxiv.org/abs/1301.1071

This algorithm is used to compute both the QR decomposition and the Singular Value Decomposition. It requires that the input array have a single column of blocks, each of which fit in memory.

Parameters

data: Array

compute_svd: bool Whether to compute the SVD rather than the QR decomposition

_max_vchunk_size: Integer Used internally in recursion to set the maximum row dimension of chunks in subsequent recursive calls.

See also:

dask.array.linalg.qr, *dask.array.linalg.svd*, dask.array.linalg.sfqr

Notes

With k blocks of size (m, n), this algorithm has memory use that scales as k * m * n.

The implementation here is the recursive variant due to the ultimate need for one "single core" QR decomposition. In the non-recursive version of the algorithm, given k blocks, after k m * n QR decompositions, there will be a "single core" QR decomposition that will have to work with a (k * n, n) matrix.

Here, recursion is applied as necessary to ensure that k * n is not larger than m (if m / n >= 2). In particular, this is done to ensure that single core computations do not have to work on blocks larger than (m, n).

Where blocks are irregular, the above logic is applied with the "height" of the "tallest" block used in place of m.

Consider use of the rechunk method to control this behavior. Blocks that are as tall as possible are recommended.

dask.array.overlap.**overlap**(*x*, *depth*, *boundary*)
Share boundaries between neighboring blocks

Parameters

x: da.Array A dask array

depth: dict The size of the shared boundary per axis

boundary: dict The boundary condition on each axis. Options are 'reflect', 'periodic', 'nearest', 'none', or an array value. Such a value will fill the boundary with that value.

The depth input informs how many cells to overlap between neighboring

blocks "{0: 2, 2: 5}" means share two cells in 0 axis, 5 cells in 2 axis.

Axes missing from this input will not be overlapped.

Examples

```
>>> import numpy as np
>>> import dask.array as da
```

```
>>> x = np.arange(64).reshape((8, 8))
>>> d = da.from_array(x, chunks=(4, 4))
>>> d.chunks
((4, 4), (4, 4))
```

```
>>> g = da.overlap.overlap(d, depth={0: 2, 1: 1},
...                        boundary={0: 100, 1: 'reflect'})
>>> g.chunks
((8, 8), (6, 6))
```

```
>>> np.array(g)
array([[100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100],
       [100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100],
       [  0,   0,   1,   2,   3,   4,   3,   4,   5,   6,   7,   7],
       [  8,   8,   9,  10,  11,  12,  11,  12,  13,  14,  15,  15],
       [ 16,  16,  17,  18,  19,  20,  19,  20,  21,  22,  23,  23],
       [ 24,  24,  25,  26,  27,  28,  27,  28,  29,  30,  31,  31],
       [ 32,  32,  33,  34,  35,  36,  35,  36,  37,  38,  39,  39],
       [ 40,  40,  41,  42,  43,  44,  43,  44,  45,  46,  47,  47],
       [ 16,  16,  17,  18,  19,  20,  19,  20,  21,  22,  23,  23],
       [ 24,  24,  25,  26,  27,  28,  27,  28,  29,  30,  31,  31],
       [ 32,  32,  33,  34,  35,  36,  35,  36,  37,  38,  39,  39],
       [ 40,  40,  41,  42,  43,  44,  43,  44,  45,  46,  47,  47],
       [ 48,  48,  49,  50,  51,  52,  51,  52,  53,  54,  55,  55],
       [ 56,  56,  57,  58,  59,  60,  59,  60,  61,  62,  63,  63],
       [100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100],
       [100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100]])
```

dask.array.overlap.**map_overlap**(*x*, *func*, *depth*, *boundary=None*, *trim=True*, ***kwargs*)

Map a function over blocks of the array with some overlap

We share neighboring zones between blocks of the array, then map a function, then trim away the neighboring strips.

Parameters

func: function The function to apply to each extended block

depth: int, tuple, or dict The number of elements that each block should share with its neighbors If a tuple or dict then this can be different per axis

boundary: str, tuple, dict How to handle the boundaries. Values include 'reflect', 'periodic', 'nearest', 'none', or any constant value like 0 or np.nan

trim: bool Whether or not to trim `depth` elements from each block after calling the map function. Set this to False if your mapping function already does this for you

****kwargs:** Other keyword arguments valid in `map_blocks`

Examples

```
>>> import numpy as np
>>> import dask.array as da
```

```
>>> x = np.array([1, 1, 2, 3, 3, 3, 2, 1, 1])
>>> x = da.from_array(x, chunks=5)
>>> def derivative(x):
...     return x - np.roll(x, 1)
```

```
>>> y = x.map_overlap(derivative, depth=1, boundary=0)
>>> y.compute()
array([ 1,  0,  1,  1,  0,  0, -1, -1,  0])
```

```
>>> x = np.arange(16).reshape((4, 4))
>>> d = da.from_array(x, chunks=(2, 2))
>>> d.map_overlap(lambda x: x + x.size, depth=1).compute()
```

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```
array([[16, 17, 18, 19],
       [20, 21, 22, 23],
       [24, 25, 26, 27],
       [28, 29, 30, 31]])
```

```
>>> func = lambda x: x + x.size
>>> depth = {0: 1, 1: 1}
>>> boundary = {0: 'reflect', 1: 'none'}
>>> d.map_overlap(func, depth, boundary).compute()
array([[12,  13,  14,  15],
       [16,  17,  18,  19],
       [20,  21,  22,  23],
       [24,  25,  26,  27]])
```

dask.array.**from_array**(*x*, *chunks*, *name=None*, *lock=False*, *asarray=True*, *fancy=True*, *getitem=None*)

Create dask array from something that looks like an array

Input must have a `.shape` and support numpy-style slicing.

Parameters

x [array_like]

chunks [int, tuple] How to chunk the array. Must be one of the following forms: - A blocksize like 1000. - A blockshape like (1000, 1000). - Explicit sizes of all blocks along all dimensions like

((1000, 1000, 500), (400, 400)).

-1 as a blocksize indicates the size of the corresponding dimension.

name [str, optional] The key name to use for the array. Defaults to a hash of `x`. By default, hash uses python's standard sha1. This behaviour can be changed by installing cityhash, xxhash or murmurhash. If installed, a large-factor speedup can be obtained in the tokenisation step. Use `name=False` to generate a random name instead of hashing (fast)

lock [bool or Lock, optional] If `x` doesn't support concurrent reads then provide a lock here, or pass in True to have dask.array create one for you.

asarray [bool, optional] If True (default), then chunks will be converted to instances of `ndarray`. Set to False to pass passed chunks through unchanged.

fancy [bool, optional] If `x` doesn't support fancy indexing (e.g. indexing with lists or arrays) then set to False. Default is True.

Examples

```
>>> x = h5py.File('...')['/data/path']
>>> a = da.from_array(x, chunks=(1000, 1000))
```

If your underlying datastore does not support concurrent reads then include the `lock=True` keyword argument or `lock=mylock` if you want multiple arrays to coordinate around the same lock.

```
>>> a = da.from_array(x, chunks=(1000, 1000), lock=True)
```

dask.array.**from_delayed**(*value*, *shape*, *dtype*, *name=None*)

Create a dask array from a dask delayed value

This routine is useful for constructing dask arrays in an ad-hoc fashion using dask delayed, particularly when combined with stack and concatenate.

The dask array will consist of a single chunk.

Examples

```
>>> from dask import delayed
>>> value = delayed(np.ones)(5)
>>> array = from_delayed(value, (5,), float)
>>> array
dask.array<from-value, shape=(5,), dtype=float64, chunksize=(5,)>
>>> array.compute()
array([1., 1., 1., 1., 1.])
```

dask.array.**from_npy_stack**(*dirname*, *mmap_mode='r'*)
Load dask array from stack of npy files

See `da.to_npy_stack` for docstring

Parameters

dirname: string Directory of .npy files

mmap_mode: (None or 'r') Read data in memory map mode

dask.array.**from_zarr**(*url*, *component=None*, *storage_options=None*, *chunks=None*, ***kwargs*)
Load array from the zarr storage format

See https://zarr.readthedocs.io for details about the format.

Parameters

url: Zarr Array or str or MutableMapping Location of the data. A URL can include a protocol specifier like s3:// for remote data. Can also be any MutableMapping instance, which should be serializable if used in multiple processes.

component: str or None If the location is a zarr group rather than an array, this is the subcomponent that should be loaded, something like `'foo/bar'`.

storage_options: dict Any additional parameters for the storage backend (ignored for local paths)

chunks: tuple of ints or tuples of ints Passed to `da.from_array`, allows setting the chunks on initialisation, if the chunking scheme in the on-disc dataset is not optimal for the calculations to follow.

kwargs: passed to ''zarr.Array''.

dask.array.**store**(*sources*, *targets*, *lock=True*, *regions=None*, *compute=True*, *return_stored=False*, ***kwargs*)
Store dask arrays in array-like objects, overwrite data in target

This stores dask arrays into object that supports numpy-style setitem indexing. It stores values chunk by chunk so that it does not have to fill up memory. For best performance you can align the block size of the storage target with the block size of your array.

If your data fits in memory then you may prefer calling `np.array(myarray)` instead.

Parameters

sources: Array or iterable of Arrays

targets: array-like or Delayed or iterable of array-likes and/or Delayeds These should support setitem syntax `target[10:20] = ...`

lock: boolean or threading.Lock, optional Whether or not to lock the data stores while storing. Pass True (lock each file individually), False (don't lock) or a particular `threading.Lock` object to be shared among all writes.

regions: tuple of slices or iterable of tuple of slices Each `region` tuple in `regions` should be such that `target[region].shape = source.shape` for the corresponding source and target in sources and targets, respectively.

compute: boolean, optional If true compute immediately, return `dask.delayed.Delayed` otherwise

return_stored: boolean, optional Optionally return the stored result (default False).

Examples

```
>>> x = ...
```

```
>>> import h5py
>>> f = h5py.File('myfile.hdf5')
>>> dset = f.create_dataset('/data', shape=x.shape,
...                                  chunks=x.chunks,
...                                  dtype='f8')
```

```
>>> store(x, dset)
```

Alternatively store many arrays at the same time

```
>>> store([x, y, z], [dset1, dset2, dset3])
```

`dask.array.`**`to_hdf5`**(*filename*, **args*, ***kwargs*)

Store arrays in HDF5 file

This saves several dask arrays into several datapaths in an HDF5 file. It creates the necessary datasets and handles clean file opening/closing.

```
>>> da.to_hdf5('myfile.hdf5', '/x', x)
```

or

```
>>> da.to_hdf5('myfile.hdf5', {'/x': x, '/y': y})
```

Optionally provide arguments as though to `h5py.File.create_dataset`

```
>>> da.to_hdf5('myfile.hdf5', '/x', x, compression='lzf', shuffle=True)
```

This can also be used as a method on a single Array

```
>>> x.to_hdf5('myfile.hdf5', '/x')
```

See also:

`da.store`, `h5py.File.create_dataset`

dask.array.**to_zarr**(*arr*, *url*, *component=None*, *storage_options=None*, *overwrite=False*, *compute=True*, *return_stored=False*, ***kwargs*)

Save array to the zarr storage format

See https://zarr.readthedocs.io for details about the format.

Parameters

arr: dask.array Data to store

url: Zarr Array or str or MutableMapping Location of the data. A URL can include a protocol specifier like s3:// for remote data. Can also be any MutableMapping instance, which should be serializable if used in multiple processes.

component: str or None If the location is a zarr group rather than an array, this is the subcomponent that should be created/over-written.

storage_options: dict Any additional parameters for the storage backend (ignored for local paths)

overwrite: bool If given array already exists, overwrite=False will cause an error, where overwrite=True will replace the existing data.

compute, return_stored: see ‘‘store()‘‘

kwargs: passed to the ‘‘zarr.create()‘‘ function, e.g., compression options

dask.array.**to_npy_stack**(*dirname*, *x*, *axis=0*)

Write dask array to a stack of .npy files

This partitions the dask.array along one axis and stores each block along that axis as a single .npy file in the specified directory

See also:

from_npy_stack

Examples

```
>>> x = da.ones((5, 10, 10), chunks=(2, 4, 4))
>>> da.to_npy_stack('data/', x, axis=0)
```

$ tree data/ data/ |– 0.npy |– 1.npy |– 2.npy |– info

The `.npy` files store numpy arrays for `x[0:2], x[2:4], and x[4:5]` respectively, as is specified by the chunk size along the zeroth axis. The info file stores the dtype, chunks, and axis information of the array.

You can load these stacks with the `da.from_npy_stack` function.

```
>>> y = da.from_npy_stack('data/')
```

dask.array.fft.**fft_wrap**(*fft_func*, *kind=None*, *dtype=None*)

Wrap 1D, 2D, and ND real and complex FFT functions

Takes a function that behaves like `numpy.fft` functions and a specified kind to match it to that are named after the functions in the `numpy.fft` API.

Supported kinds include:

- fft
- fft2

- fftn
- ifft
- ifft2
- ifftn
- rfft
- rfft2
- rfftn
- irfft
- irfft2
- irfftn
- hfft
- ihfft

Examples

```
>>> parallel_fft = fft_wrap(np.fft.fft)
>>> parallel_ifft = fft_wrap(np.fft.ifft)
```

dask.array.fft.**fft**(*a*, *n=None*, *axis=None*)

Wrapping of numpy.fft.fftpack.fft

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.fft docstring follows below:

Compute the one-dimensional discrete Fourier Transform.

This function computes the one-dimensional *n*-point discrete Fourier Transform (DFT) with the efficient Fast Fourier Transform (FFT) algorithm [CT].

Parameters

a [array_like] Input array, can be complex.

n [int, optional] Length of the transformed axis of the output. If *n* is smaller than the length of the input, the input is cropped. If it is larger, the input is padded with zeros. If *n* is not given, the length of the input along the axis specified by *axis* is used.

axis [int, optional] Axis over which to compute the FFT. If not given, the last axis is used.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified.

Raises

IndexError if *axes* is larger than the last axis of *a*.

See also:

numpy.fft for definition of the DFT and conventions used.

ifft The inverse of *fft*.

fft2 The two-dimensional FFT.

fftn The *n*-dimensional FFT.

rfftn The *n*-dimensional FFT of real input.

fftfreq Frequency bins for given FFT parameters.

Notes

FFT (Fast Fourier Transform) refers to a way the discrete Fourier Transform (DFT) can be calculated efficiently, by using symmetries in the calculated terms. The symmetry is highest when *n* is a power of 2, and the transform is therefore most efficient for these sizes.

The DFT is defined, with the conventions used in this implementation, in the documentation for the *numpy.fft* module.

References

[CT]

Examples

```
>>> np.fft.fft(np.exp(2j * np.pi * np.arange(8) / 8))
array([ -3.44505240e-16 +1.14383329e-17j,
          8.00000000e+00 -5.71092652e-15j,
          2.33482938e-16 +1.22460635e-16j,
          1.64863782e-15 +1.77635684e-15j,
          9.95839695e-17 +2.33482938e-16j,
          0.00000000e+00 +1.66837030e-15j,
          1.14383329e-17 +1.22460635e-16j,
          -1.64863782e-15 +1.77635684e-15j])
```

```
>>> import matplotlib.pyplot as plt
>>> t = np.arange(256)
>>> sp = np.fft.fft(np.sin(t))
>>> freq = np.fft.fftfreq(t.shape[-1])
>>> plt.plot(freq, sp.real, freq, sp.imag)
[<matplotlib.lines.Line2D object at 0x...>, <matplotlib.lines.Line2D object at 0x.
↪..>]
>>> plt.show()
```

In this example, real input has an FFT which is Hermitian, i.e., symmetric in the real part and anti-symmetric in the imaginary part, as described in the *numpy.fft* documentation.

dask.array.fft.**fft2**(*a*, *s=None*, *axes=None*)

Wrapping of numpy.fft.fftpack.fft2

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.fft2 docstring follows below:

Compute the 2-dimensional discrete Fourier Transform

This function computes the *n*-dimensional discrete Fourier Transform over any axes in an *M*-dimensional array by means of the Fast Fourier Transform (FFT). By default, the transform is computed over the last two axes of the input array, i.e., a 2-dimensional FFT.

Parameters

a [array_like] Input array, can be complex

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (*s[0]* refers to axis 0, *s[1]* to axis 1, etc.). This corresponds to *n* for *fft(x, n)*. Along each axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last two axes are used. A repeated index in *axes* means the transform over that axis is performed multiple times. A one-element sequence means that a one-dimensional FFT is performed.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or the last two axes if *axes* is not given.

Raises

ValueError If *s* and *axes* have different length, or *axes* not given and `len(s) != 2`.

IndexError If an element of *axes* is larger than than the number of axes of *a*.

See also:

`numpy.fft` Overall view of discrete Fourier transforms, with definitions and conventions used.

`ifft2` The inverse two-dimensional FFT.

`fft` The one-dimensional FFT.

`fftn` The *n*-dimensional FFT.

`fftshift` Shifts zero-frequency terms to the center of the array. For two-dimensional input, swaps first and third quadrants, and second and fourth quadrants.

Notes

fft2 is just *fftn* with a different default for *axes*.

The output, analogously to *fft*, contains the term for zero frequency in the low-order corner of the transformed axes, the positive frequency terms in the first half of these axes, the term for the Nyquist frequency in the middle of the axes and the negative frequency terms in the second half of the axes, in order of decreasingly negative frequency.

See *fftn* for details and a plotting example, and *numpy.fft* for definitions and conventions used.

Examples

```
>>> a = np.mgrid[:5, :5][0]
>>> np.fft.fft2(a)
array([[ 50.0 +0.j        ,   0.0 +0.j        ,   0.0 +0.j        ,
          0.0 +0.j        ,   0.0 +0.j        ],
       [-12.5+17.20477401j,   0.0 +0.j        ,   0.0 +0.j        ,
          0.0 +0.j        ,   0.0 +0.j        ],
       [-12.5 +4.0614962j ,   0.0 +0.j        ,   0.0 +0.j        ,
          0.0 +0.j        ,   0.0 +0.j        ],
       [-12.5 -4.0614962j ,   0.0 +0.j        ,   0.0 +0.j        ,
            0.0 +0.j        ,   0.0 +0.j        ],
       [-12.5-17.20477401j,   0.0 +0.j        ,   0.0 +0.j        ,
          0.0 +0.j        ,   0.0 +0.j        ]])
```

`dask.array.fft.`**`fftn`**(*a*, *s=None*, *axes=None*)

Wrapping of numpy.fft.fftpack.fftn

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.fftn docstring follows below:

Compute the N-dimensional discrete Fourier Transform.

This function computes the *N*-dimensional discrete Fourier Transform over any number of axes in an *M*-dimensional array by means of the Fast Fourier Transform (FFT).

Parameters

a [array_like] Input array, can be complex.

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (*s[0]* refers to axis 0, *s[1]* to axis 1, etc.). This corresponds to *n* for *fft(x, n)*. Along any axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified. Repeated indices in *axes* means that the transform over that axis is performed multiple times.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* and *a*, as explained in the parameters section above.

Raises

ValueError If *s* and *axes* have different length.

IndexError If an element of *axes* is larger than than the number of axes of *a*.

See also:

`numpy.fft` Overall view of discrete Fourier transforms, with definitions and conventions used.

`ifftn` The inverse of *fftn*, the inverse *n*-dimensional FFT.

`fft` The one-dimensional FFT, with definitions and conventions used.

rfftn The *n*-dimensional FFT of real input.

fft2 The two-dimensional FFT.

fftshift Shifts zero-frequency terms to centre of array

Notes

The output, analogously to *fft*, contains the term for zero frequency in the low-order corner of all axes, the positive frequency terms in the first half of all axes, the term for the Nyquist frequency in the middle of all axes and the negative frequency terms in the second half of all axes, in order of decreasingly negative frequency.

See *numpy.fft* for details, definitions and conventions used.

Examples

```
>>> a = np.mgrid[:3, :3, :3][0]
>>> np.fft.fftn(a, axes=(1, 2))
array([[[  0.+0.j,   0.+0.j,   0.+0.j],
        [  0.+0.j,   0.+0.j,   0.+0.j],
        [  0.+0.j,   0.+0.j,   0.+0.j]],
       [[  9.+0.j,   0.+0.j,   0.+0.j],
        [  0.+0.j,   0.+0.j,   0.+0.j],
        [  0.+0.j,   0.+0.j,   0.+0.j]],
       [[ 18.+0.j,   0.+0.j,   0.+0.j],
        [  0.+0.j,   0.+0.j,   0.+0.j],
        [  0.+0.j,   0.+0.j,   0.+0.j]]])
>>> np.fft.fftn(a, (2, 2), axes=(0, 1))
array([[[ 2.+0.j,  2.+0.j,  2.+0.j],
        [ 0.+0.j,  0.+0.j,  0.+0.j]],
       [[-2.+0.j, -2.+0.j, -2.+0.j],
        [ 0.+0.j,  0.+0.j,  0.+0.j]]])
```

```
>>> import matplotlib.pyplot as plt
>>> [X, Y] = np.meshgrid(2 * np.pi * np.arange(200) / 12,
...                      2 * np.pi * np.arange(200) / 34)
>>> S = np.sin(X) + np.cos(Y) + np.random.uniform(0, 1, X.shape)
>>> FS = np.fft.fftn(S)
>>> plt.imshow(np.log(np.abs(np.fft.fftshift(FS))**2))
<matplotlib.image.AxesImage object at 0x...>
>>> plt.show()
```

dask.array.fft.**ifft**(*a*, *n=None*, *axis=None*)

Wrapping of numpy.fft.fftpack.ifft

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.ifft docstring follows below:

Compute the one-dimensional inverse discrete Fourier Transform.

This function computes the inverse of the one-dimensional *n*-point discrete Fourier transform computed by *fft*. In other words, `ifft(fft(a)) == a` to within numerical accuracy. For a general description of the algorithm and definitions, see *numpy.fft*.

The input should be ordered in the same way as is returned by *fft*, i.e.,

- `a[0]` should contain the zero frequency term,
- `a[1:n//2]` should contain the positive-frequency terms,
- `a[n//2 + 1:]` should contain the negative-frequency terms, in increasing order starting from the most negative frequency.

For an even number of input points, `A[n//2]` represents the sum of the values at the positive and negative Nyquist frequencies, as the two are aliased together. See *numpy.fft* for details.

Parameters

a [array_like] Input array, can be complex.

n [int, optional] Length of the transformed axis of the output. If *n* is smaller than the length of the input, the input is cropped. If it is larger, the input is padded with zeros. If *n* is not given, the length of the input along the axis specified by *axis* is used. See notes about padding issues.

axis [int, optional] Axis over which to compute the inverse DFT. If not given, the last axis is used.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified.

Raises

IndexError If *axes* is larger than the last axis of *a*.

See also:

numpy.fft An introduction, with definitions and general explanations.

fft The one-dimensional (forward) FFT, of which *ifft* is the inverse

ifft2 The two-dimensional inverse FFT.

ifftn The n-dimensional inverse FFT.

Notes

If the input parameter *n* is larger than the size of the input, the input is padded by appending zeros at the end. Even though this is the common approach, it might lead to surprising results. If a different padding is desired, it must be performed before calling *ifft*.

Examples

```
>>> np.fft.ifft([0, 4, 0, 0])
array([ 1.+0.j,  0.+1.j, -1.+0.j,  0.-1.j])
```

Create and plot a band-limited signal with random phases:

```
>>> import matplotlib.pyplot as plt
>>> t = np.arange(400)
>>> n = np.zeros((400,), dtype=complex)
>>> n[40:60] = np.exp(1j*np.random.uniform(0, 2*np.pi, (20,)))
>>> s = np.fft.ifft(n)
>>> plt.plot(t, s.real, 'b-', t, s.imag, 'r--')
...
>>> plt.legend(('real', 'imaginary'))
...
>>> plt.show()
```

dask.array.fft.**ifft2**(*a*, *s=None*, *axes=None*)

Wrapping of numpy.fft.fftpack.ifft2

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.ifft2 docstring follows below:

Compute the 2-dimensional inverse discrete Fourier Transform.

This function computes the inverse of the 2-dimensional discrete Fourier Transform over any number of axes in an M-dimensional array by means of the Fast Fourier Transform (FFT). In other words, `ifft2(fft2(a)) == a` to within numerical accuracy. By default, the inverse transform is computed over the last two axes of the input array.

The input, analogously to *ifft*, should be ordered in the same way as is returned by *fft2*, i.e. it should have the term for zero frequency in the low-order corner of the two axes, the positive frequency terms in the first half of these axes, the term for the Nyquist frequency in the middle of the axes and the negative frequency terms in the second half of both axes, in order of decreasingly negative frequency.

Parameters

a [array_like] Input array, can be complex.

s [sequence of ints, optional] Shape (length of each axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). This corresponds to *n* for `ifft(x, n)`. Along each axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used. See notes for issue on *ifft* zero padding.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last two axes are used. A repeated index in *axes* means the transform over that axis is performed multiple times. A one-element sequence means that a one-dimensional FFT is performed.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or the last two axes if *axes* is not given.

Raises

ValueError If *s* and *axes* have different length, or *axes* not given and `len(s) != 2`.

IndexError If an element of *axes* is larger than than the number of axes of *a*.

See also:

`numpy.fft` Overall view of discrete Fourier transforms, with definitions and conventions used.

fft2 The forward 2-dimensional FFT, of which *ifft2* is the inverse.

ifftn The inverse of the *n*-dimensional FFT.

fft The one-dimensional FFT.

ifft The one-dimensional inverse FFT.

Notes

ifft2 is just *ifftn* with a different default for *axes*.

See *ifftn* for details and a plotting example, and *numpy.fft* for definition and conventions used.

Zero-padding, analogously with *ifft*, is performed by appending zeros to the input along the specified dimension. Although this is the common approach, it might lead to surprising results. If another form of zero padding is desired, it must be performed before *ifft2* is called.

Examples

```
>>> a = 4 * np.eye(4)
>>> np.fft.ifft2(a)
array([[ 1.+0.j,  0.+0.j,  0.+0.j,  0.+0.j],
       [ 0.+0.j,  0.+0.j,  0.+0.j,  1.+0.j],
       [ 0.+0.j,  0.+0.j,  1.+0.j,  0.+0.j],
       [ 0.+0.j,  1.+0.j,  0.+0.j,  0.+0.j]])
```

dask.array.fft.**ifftn**(*a*, *s=None*, *axes=None*)

Wrapping of numpy.fft.fftpack.ifftn

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.ifftn docstring follows below:

Compute the N-dimensional inverse discrete Fourier Transform.

This function computes the inverse of the N-dimensional discrete Fourier Transform over any number of axes in an M-dimensional array by means of the Fast Fourier Transform (FFT). In other words, `ifftn(fftn(a)) == a` to within numerical accuracy. For a description of the definitions and conventions used, see *numpy.fft*.

The input, analogously to *ifft*, should be ordered in the same way as is returned by *fftn*, i.e. it should have the term for zero frequency in all axes in the low-order corner, the positive frequency terms in the first half of all axes, the term for the Nyquist frequency in the middle of all axes and the negative frequency terms in the second half of all axes, in order of decreasingly negative frequency.

Parameters

a [array_like] Input array, can be complex.

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). This corresponds to `n` for `ifft(x, n)`. Along any axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used. See notes for issue on *ifft* zero padding.

axes [sequence of ints, optional] Axes over which to compute the IFFT. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified. Repeated indices in *axes* means that the inverse transform over that axis is performed multiple times.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* or *a*, as explained in the parameters section above.

Raises

ValueError If *s* and *axes* have different length.

IndexError If an element of *axes* is larger than than the number of axes of *a*.

See also:

numpy.fft Overall view of discrete Fourier transforms, with definitions and conventions used.

fftn The forward *n*-dimensional FFT, of which *ifftn* is the inverse.

ifft The one-dimensional inverse FFT.

ifft2 The two-dimensional inverse FFT.

ifftshift Undoes *fftshift*, shifts zero-frequency terms to beginning of array.

Notes

See *numpy.fft* for definitions and conventions used.

Zero-padding, analogously with *ifft*, is performed by appending zeros to the input along the specified dimension. Although this is the common approach, it might lead to surprising results. If another form of zero padding is desired, it must be performed before *ifftn* is called.

Examples

```
>>> a = np.eye(4)
>>> np.fft.ifftn(np.fft.fftn(a, axes=(0,)), axes=(1,))
array([[ 1.+0.j,  0.+0.j,  0.+0.j,  0.+0.j],
       [ 0.+0.j,  1.+0.j,  0.+0.j,  0.+0.j],
       [ 0.+0.j,  0.+0.j,  1.+0.j,  0.+0.j],
       [ 0.+0.j,  0.+0.j,  0.+0.j,  1.+0.j]])
```

Create and plot an image with band-limited frequency content:

```
>>> import matplotlib.pyplot as plt
>>> n = np.zeros((200,200), dtype=complex)
>>> n[60:80, 20:40] = np.exp(1j*np.random.uniform(0, 2*np.pi, (20, 20)))
>>> im = np.fft.ifftn(n).real
>>> plt.imshow(im)
<matplotlib.image.AxesImage object at 0x...>
>>> plt.show()
```

dask.array.fft.**rfft**(*a*, *n=None*, *axis=None*)

Wrapping of numpy.fft.fftpack.rfft

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.rfft docstring follows below:

Compute the one-dimensional discrete Fourier Transform for real input.

This function computes the one-dimensional *n*-point discrete Fourier Transform (DFT) of a real-valued array by means of an efficient algorithm called the Fast Fourier Transform (FFT).

Parameters

a [array_like] Input array

n [int, optional] Number of points along transformation axis in the input to use. If *n* is smaller than the length of the input, the input is cropped. If it is larger, the input is padded with zeros. If *n* is not given, the length of the input along the axis specified by *axis* is used.

axis [int, optional] Axis over which to compute the FFT. If not given, the last axis is used.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified. If *n* is even, the length of the transformed axis is `(n/2)+1`. If *n* is odd, the length is `(n+1)/2`.

Raises

IndexError If *axis* is larger than the last axis of *a*.

See also:

`numpy.fft` For definition of the DFT and conventions used.

`irfft` The inverse of *rfft*.

`fft` The one-dimensional FFT of general (complex) input.

`fftn` The *n*-dimensional FFT.

`rfftn` The *n*-dimensional FFT of real input.

Notes

When the DFT is computed for purely real input, the output is Hermitian-symmetric, i.e. the negative frequency terms are just the complex conjugates of the corresponding positive-frequency terms, and the negative-frequency terms are therefore redundant. This function does not compute the negative frequency terms, and the length of the transformed axis of the output is therefore `n//2 + 1`.

When `A = rfft(a)` and fs is the sampling frequency, `A[0]` contains the zero-frequency term 0*fs, which is real due to Hermitian symmetry.

If *n* is even, `A[-1]` contains the term representing both positive and negative Nyquist frequency (+fs/2 and -fs/2), and must also be purely real. If *n* is odd, there is no term at fs/2; `A[-1]` contains the largest positive frequency (fs/2*(n-1)/n), and is complex in the general case.

If the input *a* contains an imaginary part, it is silently discarded.

Examples

```
>>> np.fft.fft([0, 1, 0, 0])
array([ 1.+0.j,  0.-1.j, -1.+0.j,  0.+1.j])
>>> np.fft.rfft([0, 1, 0, 0])
array([ 1.+0.j,  0.-1.j, -1.+0.j])
```

Notice how the final element of the *fft* output is the complex conjugate of the second element, for real input. For *rfft*, this symmetry is exploited to compute only the non-negative frequency terms.

dask.array.fft.**rfft2**(*a*, *s=None*, *axes=None*)

Wrapping of numpy.fft.fftpack.rfft2

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.rfft2 docstring follows below:

Compute the 2-dimensional FFT of a real array.

Parameters

a [array] Input array, taken to be real.

s [sequence of ints, optional] Shape of the FFT.

axes [sequence of ints, optional] Axes over which to compute the FFT.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [ndarray] The result of the real 2-D FFT.

See also:

rfftn Compute the N-dimensional discrete Fourier Transform for real input.

Notes

This is really just *rfftn* with different default behavior. For more details see *rfftn*.

dask.array.fft.**rfftn**(*a*, *s=None*, *axes=None*)

Wrapping of numpy.fft.fftpack.rfftn

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.rfftn docstring follows below:

Compute the N-dimensional discrete Fourier Transform for real input.

This function computes the N-dimensional discrete Fourier Transform over any number of axes in an M-dimensional real array by means of the Fast Fourier Transform (FFT). By default, all axes are transformed, with the real transform performed over the last axis, while the remaining transforms are complex.

Parameters

a [array_like] Input array, taken to be real.

s [sequence of ints, optional] Shape (length along each transformed axis) to use from the input. (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). The final element of *s* corresponds to *n* for `rfft(x, n)`, while for the remaining axes, it corresponds to *n* for `fft(x, n)`. Along any axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* and *a*, as explained in the parameters section above. The length of the last axis transformed will be `s[-1]//2+1`, while the remaining transformed axes will have lengths according to *s*, or unchanged from the input.

Raises

ValueError If *s* and *axes* have different length.

IndexError If an element of *axes* is larger than than the number of axes of *a*.

See also:

irfftn The inverse of *rfftn*, i.e. the inverse of the n-dimensional FFT of real input.

fft The one-dimensional FFT, with definitions and conventions used.

rfft The one-dimensional FFT of real input.

fftn The n-dimensional FFT.

rfft2 The two-dimensional FFT of real input.

Notes

The transform for real input is performed over the last transformation axis, as by *rfft*, then the transform over the remaining axes is performed as by *fftn*. The order of the output is as for *rfft* for the final transformation axis, and as for *fftn* for the remaining transformation axes.

See *fft* for details, definitions and conventions used.

Examples

```
>>> a = np.ones((2, 2, 2))
>>> np.fft.rfftn(a)
array([[[ 8.+0.j,  0.+0.j],
        [ 0.+0.j,  0.+0.j]],
       [[ 0.+0.j,  0.+0.j],
        [ 0.+0.j,  0.+0.j]]])
```

```
>>> np.fft.rfftn(a, axes=(2, 0))
array([[[ 4.+0.j,  0.+0.j],
        [ 4.+0.j,  0.+0.j]],
       [[ 0.+0.j,  0.+0.j],
        [ 0.+0.j,  0.+0.j]]])
```

dask.array.fft.**irfft**(*a*, *n=None*, *axis=None*)

Wrapping of numpy.fft.fftpack.irfft

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.irfft docstring follows below:

Compute the inverse of the n-point DFT for real input.

This function computes the inverse of the one-dimensional *n*-point discrete Fourier Transform of real input computed by *rfft*. In other words, `irfft(rfft(a), len(a)) == a` to within numerical accuracy. (See Notes below for why `len(a)` is necessary here.)

The input is expected to be in the form returned by *rfft*, i.e. the real zero-frequency term followed by the complex positive frequency terms in order of increasing frequency. Since the discrete Fourier Transform of real input is Hermitian-symmetric, the negative frequency terms are taken to be the complex conjugates of the corresponding positive frequency terms.

Parameters

a [array_like] The input array.

n [int, optional] Length of the transformed axis of the output. For *n* output points, `n//2+1` input points are necessary. If the input is longer than this, it is cropped. If it is shorter than this, it is padded with zeros. If *n* is not given, it is determined from the length of the input along the axis specified by *axis*.

axis [int, optional] Axis over which to compute the inverse FFT. If not given, the last axis is used.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified. The length of the transformed axis is *n*, or, if *n* is not given, `2*(m-1)` where `m` is the length of the transformed axis of the input. To get an odd number of output points, *n* must be specified.

Raises

IndexError If *axis* is larger than the last axis of *a*.

See also:

numpy.fft For definition of the DFT and conventions used.

rfft The one-dimensional FFT of real input, of which *irfft* is inverse.

fft The one-dimensional FFT.

irfft2 The inverse of the two-dimensional FFT of real input.

irfftn The inverse of the *n*-dimensional FFT of real input.

Notes

Returns the real valued *n*-point inverse discrete Fourier transform of *a*, where *a* contains the non-negative frequency terms of a Hermitian-symmetric sequence. *n* is the length of the result, not the input.

If you specify an *n* such that *a* must be zero-padded or truncated, the extra/removed values will be added/removed at high frequencies. One can thus resample a series to *m* points via Fourier interpolation by: `a_resamp = irfft(rfft(a), m)`.

Examples

```
>>> np.fft.ifft([1, -1j, -1, 1j])
array([ 0.+0.j,  1.+0.j,  0.+0.j,  0.+0.j])
>>> np.fft.irfft([1, -1j, -1])
array([ 0.,  1.,  0.,  0.])
```

Notice how the last term in the input to the ordinary *ifft* is the complex conjugate of the second term, and the output has zero imaginary part everywhere. When calling *irfft*, the negative frequencies are not specified, and the output array is purely real.

`dask.array.fft.`**`irfft2`**(*a*, *s=None*, *axes=None*)
Wrapping of numpy.fft.fftpack.irfft2

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.irfft2 docstring follows below:

Compute the 2-dimensional inverse FFT of a real array.

Parameters

a [array_like] The input array

s [sequence of ints, optional] Shape of the inverse FFT.

axes [sequence of ints, optional] The axes over which to compute the inverse fft. Default is the last two axes.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [ndarray] The result of the inverse real 2-D FFT.

See also:

irfftn Compute the inverse of the N-dimensional FFT of real input.

Notes

This is really *irfftn* with different defaults. For more details see *irfftn*.

`dask.array.fft.`**`irfftn`**(*a*, *s=None*, *axes=None*)
Wrapping of numpy.fft.fftpack.irfftn

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.irfftn docstring follows below:

Compute the inverse of the N-dimensional FFT of real input.

This function computes the inverse of the N-dimensional discrete Fourier Transform for real input over any number of axes in an M-dimensional array by means of the Fast Fourier Transform (FFT). In other words, `irfftn(rfftn(a), a.shape) == a` to within numerical accuracy. (The `a.shape` is necessary like `len(a)` is for *irfft*, and for the same reason.)

The input should be ordered in the same way as is returned by *rfftn*, i.e. as for *irfft* for the final transformation axis, and as for *ifftn* along all the other axes.

Parameters

a [array_like] Input array.

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). *s* is also the number of input points used along this axis, except for the last axis, where `s[-1]//2+1` points of the input are used. Along any axis, if the shape indicated by *s* is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. If *s* is not given, the shape of the input along the axes specified by *axes* is used.

axes [sequence of ints, optional] Axes over which to compute the inverse FFT. If not given, the last *len(s)* axes are used, or all axes if *s* is also not specified. Repeated indices in *axes* means that the inverse transform over that axis is performed multiple times.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* or *a*, as explained in the parameters section above. The length of each transformed axis is as given by the corresponding element of *s*, or the length of the input in every axis except for the last one if *s* is not given. In the final transformed axis the length of the output when *s* is not given is `2*(m-1)` where `m` is the length of the final transformed axis of the input. To get an odd number of output points in the final axis, *s* must be specified.

Raises

ValueError If *s* and *axes* have different length.

IndexError If an element of *axes* is larger than than the number of axes of *a*.

See also:

rfftn The forward n-dimensional FFT of real input, of which *ifftn* is the inverse.

fft The one-dimensional FFT, with definitions and conventions used.

irfft The inverse of the one-dimensional FFT of real input.

irfft2 The inverse of the two-dimensional FFT of real input.

Notes

See *fft* for definitions and conventions used.

See *rfft* for definitions and conventions used for real input.

Examples

```
>>> a = np.zeros((3, 2, 2))
>>> a[0, 0, 0] = 3 * 2 * 2
>>> np.fft.irfftn(a)
array([[[ 1.,  1.],
        [ 1.,  1.]],
       [[ 1.,  1.],
        [ 1.,  1.]],
       [[ 1.,  1.],
        [ 1.,  1.]]])
```

dask.array.fft.**hfft**(*a*, *n=None*, *axis=None*)

Wrapping of numpy.fft.fftpack.hfft

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.hfft docstring follows below:

Compute the FFT of a signal which has Hermitian symmetry (real spectrum).

Parameters

a [array_like] The input array.

n [int, optional] Length of the transformed axis of the output. For *n* output points, `n//2+1` input points are necessary. If the input is longer than this, it is cropped. If it is shorter than this, it is padded with zeros. If *n* is not given, it is determined from the length of the input along the axis specified by *axis*.

axis [int, optional] Axis over which to compute the FFT. If not given, the last axis is used.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified. The length of the transformed axis is *n*, or, if *n* is not given, `2*(m-1)` where `m` is the length of the transformed axis of the input. To get an odd number of output points, *n* must be specified.

Raises

IndexError If *axis* is larger than the last axis of *a*.

See also:

rfft Compute the one-dimensional FFT for real input.

ihfft The inverse of *hfft*.

Notes

hfft/*ihfft* are a pair analogous to *rfft*/*irfft*, but for the opposite case: here the signal has Hermitian symmetry in the time domain and is real in the frequency domain. So here it's *hfft* for which you must supply the length of the result if it is to be odd: `ihfft(hfft(a), len(a)) == a`, within numerical accuracy.

Examples

```
>>> signal = np.array([1, 2, 3, 4, 3, 2])
>>> np.fft.fft(signal)
array([ 15.+0.j,  -4.+0.j,   0.+0.j,  -1.-0.j,   0.+0.j,  -4.+0.j])
>>> np.fft.hfft(signal[:4]) # Input first half of signal
array([ 15.,  -4.,   0.,  -1.,   0.,  -4.])
>>> np.fft.hfft(signal, 6)  # Input entire signal and truncate
array([ 15.,  -4.,   0.,  -1.,   0.,  -4.])
```

```
>>> signal = np.array([[1, 1.j], [-1.j, 2]])
>>> np.conj(signal.T) - signal   # check Hermitian symmetry
array([[ 0.-0.j,  0.+0.j],
       [ 0.+0.j,  0.-0.j]])
>>> freq_spectrum = np.fft.hfft(signal)
>>> freq_spectrum
array([[ 1.,  1.],
       [ 2., -2.]])
```

dask.array.fft.**ihfft**(*a*, *n=None*, *axis=None*)

Wrapping of numpy.fft.fftpack.ihfft

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftpack.ihfft docstring follows below:

Compute the inverse FFT of a signal which has Hermitian symmetry.

Parameters

a [array_like] Input array.

n [int, optional] Length of the inverse FFT. Number of points along transformation axis in the input to use. If *n* is smaller than the length of the input, the input is cropped. If it is larger, the input is padded with zeros. If *n* is not given, the length of the input along the axis specified by *axis* is used.

axis [int, optional] Axis over which to compute the inverse FFT. If not given, the last axis is used.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified. If *n* is even, the length of the transformed axis is `(n/2)+1`. If *n* is odd, the length is `(n+1)/2`.

See also:

hfft, *irfft*

Notes

hfft/*ihfft* are a pair analogous to *rfft*/*irfft*, but for the opposite case: here the signal has Hermitian symmetry in the time domain and is real in the frequency domain. So here it's *hfft* for which you must supply the length of the result if it is to be odd: `ihfft(hfft(a), len(a)) == a`, within numerical accuracy.

Examples

```
>>> spectrum = np.array([ 15, -4, 0, -1, 0, -4])
>>> np.fft.ifft(spectrum)
array([ 1.+0.j,  2.-0.j,  3.+0.j,  4.+0.j,  3.+0.j,  2.-0.j])
>>> np.fft.ihfft(spectrum)
array([ 1.-0.j,  2.-0.j,  3.-0.j,  4.-0.j])
```

dask.array.fft.**fftfreq**(*n*, *d=1.0*)

Return the Discrete Fourier Transform sample frequencies.

The returned float array *f* contains the frequency bin centers in cycles per unit of the sample spacing (with zero at the start). For instance, if the sample spacing is in seconds, then the frequency unit is cycles/second.

Given a window length *n* and a sample spacing *d*:

```
f = [0, 1, ...,   n/2-1,     -n/2, ..., -1] / (d*n)   if n is even
f = [0, 1, ..., (n-1)/2, -(n-1)/2, ..., -1] / (d*n)   if n is odd
```

Parameters

n [int] Window length.

d [scalar, optional] Sample spacing (inverse of the sampling rate). Defaults to 1.

Returns

f [ndarray] Array of length *n* containing the sample frequencies.

Examples

```
>>> signal = np.array([-2, 8, 6, 4, 1, 0, 3, 5], dtype=float)
>>> fourier = np.fft.fft(signal)
>>> n = signal.size
>>> timestep = 0.1
>>> freq = np.fft.fftfreq(n, d=timestep)
>>> freq
array([ 0.  ,  1.25,  2.5 ,  3.75, -5.  , -3.75, -2.5 , -1.25])
```

dask.array.fft.**rfftfreq**(*n*, *d=1.0*)

Return the Discrete Fourier Transform sample frequencies (for usage with rfft, irfft).

The returned float array *f* contains the frequency bin centers in cycles per unit of the sample spacing (with zero at the start). For instance, if the sample spacing is in seconds, then the frequency unit is cycles/second.

Given a window length *n* and a sample spacing *d*:

```
f = [0, 1, ...,     n/2-1,     n/2] / (d*n)   if n is even
f = [0, 1, ..., (n-1)/2-1, (n-1)/2] / (d*n)   if n is odd
```

Unlike *fftfreq* (but like *scipy.fftpack.rfftfreq*) the Nyquist frequency component is considered to be positive.

Parameters

n [int] Window length.

d [scalar, optional] Sample spacing (inverse of the sampling rate). Defaults to 1.

Returns

f [ndarray] Array of length `n//2 + 1` containing the sample frequencies.

Examples

```
>>> signal = np.array([-2, 8, 6, 4, 1, 0, 3, 5, -3, 4], dtype=float)
>>> fourier = np.fft.rfft(signal)
>>> n = signal.size
>>> sample_rate = 100
>>> freq = np.fft.fftfreq(n, d=1./sample_rate)
>>> freq
array([  0.,  10.,  20.,  30.,  40., -50., -40., -30., -20., -10.])
>>> freq = np.fft.rfftfreq(n, d=1./sample_rate)
>>> freq
array([  0.,  10.,  20.,  30.,  40.,  50.])
```

`dask.array.fft.`**`fftshift`**(*x*, *axes=None*)

Shift the zero-frequency component to the center of the spectrum.

This function swaps half-spaces for all axes listed (defaults to all). Note that `y[0]` is the Nyquist component only if `len(x)` is even.

Parameters

x [array_like] Input array.

axes [int or shape tuple, optional] Axes over which to shift. Default is None, which shifts all axes.

Returns

y [ndarray] The shifted array.

See also:

`ifftshift` The inverse of *fftshift*.

Examples

```
>>> freqs = np.fft.fftfreq(10, 0.1)
>>> freqs
array([ 0.,  1.,  2.,  3.,  4., -5., -4., -3., -2., -1.])
>>> np.fft.fftshift(freqs)
array([-5., -4., -3., -2., -1.,  0.,  1.,  2.,  3.,  4.])
```

Shift the zero-frequency component only along the second axis:

```
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)
>>> freqs
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
>>> np.fft.fftshift(freqs, axes=(1,))
array([[ 2.,  0.,  1.],
       [-4.,  3.,  4.],
       [-1., -3., -2.]])
```

dask.array.fft.**ifftshift**(*x*, *axes=None*)

The inverse of *fftshift*. Although identical for even-length *x*, the functions differ by one sample for odd-length *x*.

Parameters

x [array_like] Input array.

axes [int or shape tuple, optional] Axes over which to calculate. Defaults to None, which shifts all axes.

Returns

y [ndarray] The shifted array.

See also:

fftshift Shift zero-frequency component to the center of the spectrum.

Examples

```
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)
>>> freqs
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
>>> np.fft.ifftshift(np.fft.fftshift(freqs))
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
```

dask.array.random.**beta**(*a*, *b*, *size=None*)

Draw samples from a Beta distribution.

The Beta distribution is a special case of the Dirichlet distribution, and is related to the Gamma distribution. It has the probability distribution function

$$f(x; a, b) = \frac{1}{B(\alpha, \beta)} x^{\alpha-1}(1-x)^{\beta-1},$$

where the normalisation, B, is the beta function,

$$B(\alpha, \beta) = \int_0^1 t^{\alpha-1}(1-t)^{\beta-1} dt.$$

It is often seen in Bayesian inference and order statistics.

Parameters

a [float] Alpha, non-negative.

b [float] Beta, non-negative.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

out [ndarray] Array of the given shape, containing values drawn from a Beta distribution.

dask.array.random.**binomial**(*n*, *p*, *size=None*)

Draw samples from a binomial distribution.

Samples are drawn from a binomial distribution with specified parameters, n trials and p probability of success where n an integer >= 0 and p is in the interval [0,1]. (n may be input as a float, but it is truncated to an integer in use)

Parameters

n [float (but truncated to an integer)] parameter, >= 0.

p [float] parameter, >= 0 and <=1.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] where the values are all integers in [0, n].

See also:

scipy.stats.distributions.binom probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the binomial distribution is

$$P(N) = \binom{n}{N} p^N (1-p)^{n-N},$$

where n is the number of trials, p is the probability of success, and N is the number of successes.

When estimating the standard error of a proportion in a population by using a random sample, the normal distribution works well unless the product p*n <=5, where p = population proportion estimate, and n = number of samples, in which case the binomial distribution is used instead. For example, a sample of 15 people shows 4 who are left handed, and 11 who are right handed. Then p = 4/15 = 27%. 0.27*15 = 4, so the binomial distribution should be used in this case.

References

[1], *[2]*, *[3]*, *[4]*, *[5]*

Examples

Draw samples from the distribution:

```
>>> n, p = 10, .5  # number of trials, probability of each trial
>>> s = np.random.binomial(n, p, 1000)
# result of flipping a coin 10 times, tested 1000 times.
```

A real world example. A company drills 9 wild-cat oil exploration wells, each with an estimated probability of success of 0.1. All nine wells fail. What is the probability of that happening?

Let's do 20,000 trials of the model, and count the number that generate zero positive results.

```
>>> sum(np.random.binomial(9, 0.1, 20000) == 0)/20000.
# answer = 0.38885, or 38%.
```

dask.array.random.**chisquare**(*df*, *size=None*)

Draw samples from a chi-square distribution.

When *df* independent random variables, each with standard normal distributions (mean 0, variance 1), are squared and summed, the resulting distribution is chi-square (see Notes). This distribution is often used in hypothesis testing.

Parameters

df [int] Number of degrees of freedom.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

output [ndarray] Samples drawn from the distribution, packed in a *size*-shaped array.

Raises

ValueError When *df* <= 0 or when an inappropriate *size* (e.g. `size=-1`) is given.

Notes

The variable obtained by summing the squares of *df* independent, standard normally distributed random variables:

$$Q = \sum_{i=0}^{\mathtt{df}} X_i^2$$

is chi-square distributed, denoted

$$Q \sim \chi_k^2.$$

The probability density function of the chi-squared distribution is

$$p(x) = \frac{(1/2)^{k/2}}{\Gamma(k/2)} x^{k/2-1} e^{-x/2},$$

where Γ is the gamma function,

$$\Gamma(x) = \int_0^{-\infty} t^{x-1} e^{-t} dt.$$

References

[1]

Examples

```
>>> np.random.chisquare(2,4)
array([ 1.89920014,  9.00867716,  3.13710533,  5.62318272])
```

dask.array.random.**exponential**(*scale=1.0*, *size=None*)

Draw samples from an exponential distribution.

Its probability density function is

$$f(x; \frac{1}{\beta}) = \frac{1}{\beta} \exp(-\frac{x}{\beta}),$$

for `x > 0` and 0 elsewhere. β is the scale parameter, which is the inverse of the rate parameter $\lambda = 1/\beta$. The rate parameter is an alternative, widely used parameterization of the exponential distribution *[3]*.

The exponential distribution is a continuous analogue of the geometric distribution. It describes many common situations, such as the size of raindrops measured over many rainstorms *[1]*, or the time between page requests to Wikipedia *[2]*.

Parameters

scale [float] The scale parameter, $\beta = 1/\lambda$.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

References

[1], *[2]*, *[3]*

dask.array.random.**f**(*dfnum*, *dfden*, *size=None*)

Draw samples from an F distribution.

Samples are drawn from an F distribution with specified parameters, *dfnum* (degrees of freedom in numerator) and *dfden* (degrees of freedom in denominator), where both parameters should be greater than zero.

The random variate of the F distribution (also known as the Fisher distribution) is a continuous probability distribution that arises in ANOVA tests, and is the ratio of two chi-square variates.

Parameters

dfnum [float] Degrees of freedom in numerator. Should be greater than zero.

dfden [float] Degrees of freedom in denominator. Should be greater than zero.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] Samples from the Fisher distribution.

See also:

scipy.stats.distributions.f probability density function, distribution or cumulative density function, etc.

Notes

The F statistic is used to compare in-group variances to between-group variances. Calculating the distribution depends on the sampling, and so it is a function of the respective degrees of freedom in the problem. The variable *dfnum* is the number of samples minus one, the between-groups degrees of freedom, while *dfden* is the within-groups degrees of freedom, the sum of the number of samples in each group minus the number of groups.

References

[1], *[2]*

Examples

An example from Glantz[1], pp 47-40:

Two groups, children of diabetics (25 people) and children from people without diabetes (25 controls). Fasting blood glucose was measured, case group had a mean value of 86.1, controls had a mean value of 82.2. Standard deviations were 2.09 and 2.49 respectively. Are these data consistent with the null hypothesis that the parents diabetic status does not affect their children's blood glucose levels? Calculating the F statistic from the data gives a value of 36.01.

Draw samples from the distribution:

```
>>> dfnum = 1. # between group degrees of freedom
>>> dfden = 48. # within groups degrees of freedom
>>> s = np.random.f(dfnum, dfden, 1000)
```

The lower bound for the top 1% of the samples is :

```
>>> sort(s)[-10]
7.61988120985
```

So there is about a 1% chance that the F statistic will exceed 7.62, the measured value is 36, so the null hypothesis is rejected at the 1% level.

`dask.array.random.`**`gamma`**(*shape*, *scale=1.0*, *size=None*)

Draw samples from a Gamma distribution.

Samples are drawn from a Gamma distribution with specified parameters, *shape* (sometimes designated "k") and *scale* (sometimes designated "theta"), where both parameters are > 0.

Parameters

shape [scalar > 0] The shape of the gamma distribution.

scale [scalar > 0, optional] The scale of the gamma distribution. Default is equal to 1.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

out [ndarray, float] Returns one sample unless *size* parameter is specified.

See also:

`scipy.stats.distributions.gamma` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Gamma distribution is

$$p(x) = x^{k-1}\frac{e^{-x/\theta}}{\theta^k \Gamma(k)},$$

where k is the shape and θ the scale, and Γ is the Gamma function.

The Gamma distribution is often used to model the times to failure of electronic components, and arises naturally in processes for which the waiting times between Poisson distributed events are relevant.

References

[1], *[2]*

Examples

Draw samples from the distribution:

```
>>> shape, scale = 2., 2. # mean and dispersion
>>> s = np.random.gamma(shape, scale, 1000)
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> import scipy.special as sps
>>> count, bins, ignored = plt.hist(s, 50, normed=True)
>>> y = bins**(shape-1)*(np.exp(-bins/scale) /
...                      (sps.gamma(shape)*scale**shape))
>>> plt.plot(bins, y, linewidth=2, color='r')
>>> plt.show()
```

dask.array.random.**geometric**(*p*, *size=None*)
Draw samples from the geometric distribution.

Bernoulli trials are experiments with one of two outcomes: success or failure (an example of such an experiment is flipping a coin). The geometric distribution models the number of trials that must be run in order to achieve success. It is therefore supported on the positive integers, `k = 1, 2, ...`.

The probability mass function of the geometric distribution is

$$f(k) = (1-p)^{k-1}p$$

where p is the probability of success of an individual trial.

Parameters

p [float] The probability of success of an individual trial.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

out [ndarray] Samples from the geometric distribution, shaped according to *size*.

Examples

Draw ten thousand values from the geometric distribution, with the probability of an individual success equal to 0.35:

```
>>> z = np.random.geometric(p=0.35, size=10000)
```

How many trials succeeded after a single run?

```
>>> (z == 1).sum() / 10000.
0.34889999999999999 #random
```

dask.array.random.**gumbel**(*loc=0.0*, *scale=1.0*, *size=None*)

Draw samples from a Gumbel distribution.

Draw samples from a Gumbel distribution with specified location and scale. For more information on the Gumbel distribution, see Notes and References below.

Parameters

loc [float] The location of the mode of the distribution.

scale [float] The scale parameter of the distribution.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar]

See also:

`scipy.stats.gumbel_l`, `scipy.stats.gumbel_r`, `scipy.stats.genextreme`, *weibull*

Notes

The Gumbel (or Smallest Extreme Value (SEV) or the Smallest Extreme Value Type I) distribution is one of a class of Generalized Extreme Value (GEV) distributions used in modeling extreme value problems. The Gumbel is a special case of the Extreme Value Type I distribution for maximums from distributions with "exponential-like" tails.

The probability density for the Gumbel distribution is

$$p(x) = \frac{e^{-(x-\mu)/\beta}}{\beta} e^{-e^{-(x-\mu)/\beta}},$$

where μ is the mode, a location parameter, and β is the scale parameter.

The Gumbel (named for German mathematician Emil Julius Gumbel) was used very early in the hydrology literature, for modeling the occurrence of flood events. It is also used for modeling maximum wind speed and rainfall rates. It is a "fat-tailed" distribution - the probability of an event in the tail of the distribution is larger than if one used a Gaussian, hence the surprisingly frequent occurrence of 100-year floods. Floods were initially modeled as a Gaussian process, which underestimated the frequency of extreme events.

It is one of a class of extreme value distributions, the Generalized Extreme Value (GEV) distributions, which also includes the Weibull and Frechet.

The function has a mean of $\mu + 0.57721\beta$ and a variance of $\frac{\pi^2}{6}\beta^2$.

References

[1], *[2]*

Examples

Draw samples from the distribution:

```
>>> mu, beta = 0, 0.1 # location and scale
>>> s = np.random.gumbel(mu, beta, 1000)
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> count, bins, ignored = plt.hist(s, 30, normed=True)
>>> plt.plot(bins, (1/beta)*np.exp(-(bins - mu)/beta)
...          * np.exp( -np.exp( -(bins - mu) /beta) ),
...          linewidth=2, color='r')
>>> plt.show()
```

Show how an extreme value distribution can arise from a Gaussian process and compare to a Gaussian:

```
>>> means = []
>>> maxima = []
>>> for i in range(0,1000) :
...    a = np.random.normal(mu, beta, 1000)
...    means.append(a.mean())
...    maxima.append(a.max())
>>> count, bins, ignored = plt.hist(maxima, 30, normed=True)
>>> beta = np.std(maxima) * np.sqrt(6) / np.pi
>>> mu = np.mean(maxima) - 0.57721*beta
>>> plt.plot(bins, (1/beta)*np.exp(-(bins - mu)/beta)
...          * np.exp(-np.exp(-(bins - mu)/beta)),
...          linewidth=2, color='r')
>>> plt.plot(bins, 1/(beta * np.sqrt(2 * np.pi))
...          * np.exp(-(bins - mu)**2 / (2 * beta**2)),
...          linewidth=2, color='g')
>>> plt.show()
```

dask.array.random.**hypergeometric**(*ngood*, *nbad*, *nsample*, *size=None*)

Draw samples from a Hypergeometric distribution.

Samples are drawn from a hypergeometric distribution with specified parameters, ngood (ways to make a good selection), nbad (ways to make a bad selection), and nsample = number of items sampled, which is less than or equal to the sum ngood + nbad.

Parameters

ngood [int or array_like] Number of ways to make a good selection. Must be nonnegative.

nbad [int or array_like] Number of ways to make a bad selection. Must be nonnegative.

nsample [int or array_like] Number of items sampled. Must be at least 1 and at most `ngood + nbad`.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] The values are all integers in [0, n].

See also:

scipy.stats.distributions.hypergeom probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Hypergeometric distribution is

$$P(x) = \frac{\binom{m}{n}\binom{N-m}{n-x}}{\binom{N}{n}},$$

where $0 \leq x \leq m$ and $n + m - N \leq x \leq n$

for P(x) the probability of x successes, n = ngood, m = nbad, and N = number of samples.

Consider an urn with black and white marbles in it, ngood of them black and nbad are white. If you draw nsample balls without replacement, then the hypergeometric distribution describes the distribution of black balls in the drawn sample.

Note that this distribution is very similar to the binomial distribution, except that in this case, samples are drawn without replacement, whereas in the Binomial case samples are drawn with replacement (or the sample space is infinite). As the sample space becomes large, this distribution approaches the binomial.

References

[1], *[2]*, *[3]*

Examples

Draw samples from the distribution:

```
>>> ngood, nbad, nsamp = 100, 2, 10
# number of good, number of bad, and number of samples
>>> s = np.random.hypergeometric(ngood, nbad, nsamp, 1000)
>>> hist(s)
#   note that it is very unlikely to grab both bad items
```

Suppose you have an urn with 15 white and 15 black marbles. If you pull 15 marbles at random, how likely is it that 12 or more of them are one color?

```
>>> s = np.random.hypergeometric(15, 15, 15, 100000)
>>> sum(s>=12)/100000. + sum(s<=3)/100000.
#   answer = 0.003 ... pretty unlikely!
```

dask.array.random.**laplace**(*loc=0.0*, *scale=1.0*, *size=None*)

Draw samples from the Laplace or double exponential distribution with specified location (or mean) and scale (decay).

The Laplace distribution is similar to the Gaussian/normal distribution, but is sharper at the peak and has fatter tails. It represents the difference between two independent, identically distributed exponential random variables.

Parameters

loc [float, optional] The position, μ, of the distribution peak.

scale [float, optional] λ, the exponential decay.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or float]

Notes

It has the probability density function

$$f(x; \mu, \lambda) = \frac{1}{2\lambda} \exp\left(-\frac{|x-\mu|}{\lambda}\right).$$

The first law of Laplace, from 1774, states that the frequency of an error can be expressed as an exponential function of the absolute magnitude of the error, which leads to the Laplace distribution. For many problems in economics and health sciences, this distribution seems to model the data better than the standard Gaussian distribution.

References

[1], *[2]*, *[3]*, *[4]*

Examples

Draw samples from the distribution

```
>>> loc, scale = 0., 1.
>>> s = np.random.laplace(loc, scale, 1000)
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> count, bins, ignored = plt.hist(s, 30, normed=True)
>>> x = np.arange(-8., 8., .01)
>>> pdf = np.exp(-abs(x-loc)/scale)/(2.*scale)
>>> plt.plot(x, pdf)
```

Plot Gaussian for comparison:

```
>>> g = (1/(scale * np.sqrt(2 * np.pi)) *
...      np.exp(-(x - loc)**2 / (2 * scale**2)))
>>> plt.plot(x,g)
```

`dask.array.random.`**`logistic`**(*loc=0.0*, *scale=1.0*, *size=None*)

Draw samples from a logistic distribution.

Samples are drawn from a logistic distribution with specified parameters, loc (location or mean, also median), and scale (>0).

Parameters

loc [float]

scale [float > 0.]

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] where the values are all integers in [0, n].

See also:

`scipy.stats.distributions.logistic` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Logistic distribution is

$$P(x) = P(x) = \frac{e^{-(x-\mu)/s}}{s(1+e^{-(x-\mu)/s})^2},$$

where μ = location and s = scale.

The Logistic distribution is used in Extreme Value problems where it can act as a mixture of Gumbel distributions, in Epidemiology, and by the World Chess Federation (FIDE) where it is used in the Elo ranking system, assuming the performance of each player is a logistically distributed random variable.

References

[1], *[2]*, *[3]*

Examples

Draw samples from the distribution:

```
>>> loc, scale = 10, 1
>>> s = np.random.logistic(loc, scale, 10000)
>>> count, bins, ignored = plt.hist(s, bins=50)
```

plot against distribution

```
>>> def logist(x, loc, scale):
...     return exp((loc-x)/scale)/(scale*(1+exp((loc-x)/scale))**2)
>>> plt.plot(bins, logist(bins, loc, scale)*count.max()/\
... logist(bins, loc, scale).max())
>>> plt.show()
```

`dask.array.random.`**`lognormal`**(*mean=0.0*, *sigma=1.0*, *size=None*)

Draw samples from a log-normal distribution.

Draw samples from a log-normal distribution with specified mean, standard deviation, and array shape. Note that the mean and standard deviation are not the values for the distribution itself, but of the underlying normal distribution it is derived from.

Parameters

mean [float]

Mean value of the underlying normal distribution

sigma [float, > 0.] Standard deviation of the underlying normal distribution

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or float] The desired samples. An array of the same shape as *size* if given, if *size* is None a float is returned.

See also:

`scipy.stats.lognorm` probability density function, distribution, cumulative density function, etc.

Notes

A variable *x* has a log-normal distribution if *log(x)* is normally distributed. The probability density function for the log-normal distribution is:

$$p(x) = \frac{1}{\sigma x \sqrt{2\pi}} e^{(-\frac{(ln(x)-\mu)^2}{2\sigma^2})}$$

where μ is the mean and σ is the standard deviation of the normally distributed logarithm of the variable. A log-normal distribution results if a random variable is the *product* of a large number of independent, identically-distributed variables in the same way that a normal distribution results if the variable is the *sum* of a large number of independent, identically-distributed variables.

```
>>> # Generate a thousand samples: each is the product of 100 random
>>> # values, drawn from a normal distribution.
        >>> b = []
        >>> for i in range(1000):
        ...     a = 10. + np.random.random(100)
        ...     b.append(np.product(a))
```

```
>>> b = np.array(b) / np.min(b) # scale values to be positive
>>> count, bins, ignored = plt.hist(b, 100, normed=True, align='mid')
>>> sigma = np.std(np.log(b))
>>> mu = np.mean(np.log(b))
```

```
>>> x = np.linspace(min(bins), max(bins), 10000)
>>> pdf = (np.exp(-(np.log(x) - mu)**2 / (2 * sigma**2))
...        / (x * sigma * np.sqrt(2 * np.pi)))
```

```
>>> plt.plot(x, pdf, color='r', linewidth=2)
>>> plt.show()
```

`dask.array.random.`**`logseries`**(*p*, *size=None*)

Draw samples from a logarithmic series distribution.

Samples are drawn from a log series distribution with specified shape parameter, $0 < p < 1$.

Parameters

loc [float]

scale [float > 0.]

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] where the values are all integers in [0, n].

See also:

`scipy.stats.distributions.logser` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Log Series distribution is

$$P(k) = \frac{-p^k}{k \ln(1-p)},$$

where p = probability.

The log series distribution is frequently used to represent species richness and occurrence, first proposed by Fisher, Corbet, and Williams in 1943 [2]. It may also be used to model the numbers of occupants seen in cars [3].

References

[1], *[2]*, *[3]*, *[4]*

Examples

Draw samples from the distribution:

```
>>> a = .6
>>> s = np.random.logseries(a, 10000)
>>> count, bins, ignored = plt.hist(s)
```

plot against distribution

```
>>> def logseries(k, p):
...     return -p**k/(k*log(1-p))
>>> plt.plot(bins, logseries(bins, a)*count.max()/
             logseries(bins, a).max(), 'r')
>>> plt.show()
```

`dask.array.random.`**`negative_binomial`**(*n*, *p*, *size=None*)

Draw samples from a negative binomial distribution.

Samples are drawn from a negative binomial distribution with specified parameters, *n* trials and *p* probability of success where *n* is an integer > 0 and *p* is in the interval [0, 1].

Parameters

n [int] Parameter, > 0.

p [float] Parameter, >= 0 and <=1.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [int or ndarray of ints] Drawn samples.

Notes

The probability density for the negative binomial distribution is

$$P(N;n,p) = \binom{N+n-1}{n-1} p^n (1-p)^N,$$

where $n-1$ is the number of successes, p is the probability of success, and $N+n-1$ is the number of trials. The negative binomial distribution gives the probability of n-1 successes and N failures in N+n-1 trials, and success on the (N+n)th trial.

If one throws a die repeatedly until the third time a "1" appears, then the probability distribution of the number of non-"1"s that appear before the third "1" is a negative binomial distribution.

References

[1], *[2]*

Examples

Draw samples from the distribution:

A real world example. A company drills wild-cat oil exploration wells, each with an estimated probability of success of 0.1. What is the probability of having one success for each successive well, that is what is the probability of a single success after drilling 5 wells, after 6 wells, etc.?

```
>>> s = np.random.negative_binomial(1, 0.1, 100000)
>>> for i in range(1, 11):
...    probability = sum(s<i) / 100000.
...    print i, "wells drilled, probability of one success =", probability
```

`dask.array.random.`**`noncentral_chisquare`**(*df*, *nonc*, *size=None*)

Draw samples from a noncentral chi-square distribution.

The noncentral χ^2 distribution is a generalisation of the χ^2 distribution.

Parameters

df [int] Degrees of freedom, should be > 0 as of Numpy 1.10, should be > 1 for earlier versions.

nonc [float] Non-centrality, should be non-negative.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Notes

The probability density function for the noncentral Chi-square distribution is

$$P(x;df,nonc) = \sum_{i=0}^{\infty} \frac{e^{-nonc/2}(nonc/2)^i}{i!} \P_{Y_{df+2i}}(x),$$

where Y_q is the Chi-square with q degrees of freedom.

In Delhi (2007), it is noted that the noncentral chi-square is useful in bombing and coverage problems, the probability of killing the point target given by the noncentral chi-squared distribution.

References

[1], *[2]*

Examples

Draw values from the distribution and plot the histogram

```
>>> import matplotlib.pyplot as plt
>>> values = plt.hist(np.random.noncentral_chisquare(3, 20, 100000),
...                   bins=200, normed=True)
>>> plt.show()
```

Draw values from a noncentral chisquare with very small noncentrality, and compare to a chisquare.

```
>>> plt.figure()
>>> values = plt.hist(np.random.noncentral_chisquare(3, .0000001, 100000),
...                   bins=np.arange(0., 25, .1), normed=True)
>>> values2 = plt.hist(np.random.chisquare(3, 100000),
...                    bins=np.arange(0., 25, .1), normed=True)
>>> plt.plot(values[1][0:-1], values[0]-values2[0], 'ob')
>>> plt.show()
```

Demonstrate how large values of non-centrality lead to a more symmetric distribution.

```
>>> plt.figure()
>>> values = plt.hist(np.random.noncentral_chisquare(3, 20, 100000),
...                   bins=200, normed=True)
>>> plt.show()
```

dask.array.random.**noncentral_f**(*dfnum*, *dfden*, *nonc*, *size=None*)

Draw samples from the noncentral F distribution.

Samples are drawn from an F distribution with specified parameters, *dfnum* (degrees of freedom in numerator) and *dfden* (degrees of freedom in denominator), where both parameters > 1. *nonc* is the non-centrality parameter.

Parameters

dfnum [int] Parameter, should be > 1.

dfden [int] Parameter, should be > 1.

nonc [float] Parameter, should be >= 0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [scalar or ndarray] Drawn samples.

Notes

When calculating the power of an experiment (power = probability of rejecting the null hypothesis when a specific alternative is true) the non-central F statistic becomes important. When the null hypothesis is true, the F statistic follows a central F distribution. When the null hypothesis is not true, then it follows a non-central F statistic.

References

[1], *[2]*

Examples

In a study, testing for a specific alternative to the null hypothesis requires use of the Noncentral F distribution. We need to calculate the area in the tail of the distribution that exceeds the value of the F distribution for the null hypothesis. We'll plot the two probability distributions for comparison.

```
>>> dfnum = 3 # between group deg of freedom
>>> dfden = 20 # within groups degrees of freedom
>>> nonc = 3.0
>>> nc_vals = np.random.noncentral_f(dfnum, dfden, nonc, 1000000)
>>> NF = np.histogram(nc_vals, bins=50, normed=True)
>>> c_vals = np.random.f(dfnum, dfden, 1000000)
>>> F = np.histogram(c_vals, bins=50, normed=True)
>>> plt.plot(F[1][1:], F[0])
>>> plt.plot(NF[1][1:], NF[0])
>>> plt.show()
```

dask.array.random.**normal**(*loc=0.0*, *scale=1.0*, *size=None*)

Draw random samples from a normal (Gaussian) distribution.

The probability density function of the normal distribution, first derived by De Moivre and 200 years later by both Gauss and Laplace independently *[2]*, is often called the bell curve because of its characteristic shape (see the example below).

The normal distributions occurs often in nature. For example, it describes the commonly occurring distribution of samples influenced by a large number of tiny, random disturbances, each with its own unique distribution *[2]*.

Parameters

loc [float] Mean ("centre") of the distribution.

scale [float] Standard deviation (spread or "width") of the distribution.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

See also:

scipy.stats.distributions.norm probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Gaussian distribution is

$$p(x) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x-\mu)^2}{2\sigma^2}},$$

where μ is the mean and σ the standard deviation. The square of the standard deviation, σ^2, is called the variance.

The function has its peak at the mean, and its "spread" increases with the standard deviation (the function reaches 0.607 times its maximum at $x + \sigma$ and $x - \sigma$ *[2]*). This implies that *numpy.random.normal* is more likely to return samples lying close to the mean, rather than those far away.

References

[1], *[2]*

Examples

Draw samples from the distribution:

```
>>> mu, sigma = 0, 0.1 # mean and standard deviation
>>> s = np.random.normal(mu, sigma, 1000)
```

Verify the mean and the variance:

```
>>> abs(mu - np.mean(s)) < 0.01
True
```

```
>>> abs(sigma - np.std(s, ddof=1)) < 0.01
True
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> count, bins, ignored = plt.hist(s, 30, normed=True)
>>> plt.plot(bins, 1/(sigma * np.sqrt(2 * np.pi)) *
...                np.exp( - (bins - mu)**2 / (2 * sigma**2) ),
...          linewidth=2, color='r')
>>> plt.show()
```

dask.array.random.**pareto**(*a*, *size=None*)

Draw samples from a Pareto II or Lomax distribution with specified shape.

The Lomax or Pareto II distribution is a shifted Pareto distribution. The classical Pareto distribution can be obtained from the Lomax distribution by adding 1 and multiplying by the scale parameter `m` (see Notes). The smallest value of the Lomax distribution is zero while for the classical Pareto distribution it is `mu`, where the standard Pareto distribution has location `mu = 1`. Lomax can also be considered as a simplified version of the Generalized Pareto distribution (available in SciPy), with the scale set to one and the location set to zero.

The Pareto distribution must be greater than zero, and is unbounded above. It is also known as the "80-20 rule". In this distribution, 80 percent of the weights are in the lowest 20 percent of the range, while the other 20 percent fill the remaining 80 percent of the range.

Parameters

shape [float, > 0.] Shape of the distribution.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

See also:

`scipy.stats.distributions.lomax.pdf` probability density function, distribution or cumulative density function, etc.

`scipy.stats.distributions.genpareto.pdf` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Pareto distribution is

$$p(x) = \frac{am^a}{x^{a+1}}$$

where a is the shape and m the scale.

The Pareto distribution, named after the Italian economist Vilfredo Pareto, is a power law probability distribution useful in many real world problems. Outside the field of economics it is generally referred to as the Bradford distribution. Pareto developed the distribution to describe the distribution of wealth in an economy. It has also found use in insurance, web page access statistics, oil field sizes, and many other problems, including the download frequency for projects in Sourceforge *[1]*. It is one of the so-called "fat-tailed" distributions.

References

[1], *[2]*, *[3]*, *[4]*

Examples

Draw samples from the distribution:

```
>>> a, m = 3., 2.  # shape and mode
>>> s = (np.random.pareto(a, 1000) + 1) * m
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> count, bins, _ = plt.hist(s, 100, normed=True)
>>> fit = a*m**a / bins**(a+1)
>>> plt.plot(bins, max(count)*fit/max(fit), linewidth=2, color='r')
>>> plt.show()
```

`dask.array.random.`**`poisson`**(*lam=1.0*, *size=None*)

Draw samples from a Poisson distribution.

The Poisson distribution is the limit of the binomial distribution for large N.

Parameters

lam [float or sequence of float] Expectation of interval, should be >= 0. A sequence of expectation intervals must be broadcastable over the requested size.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] The drawn samples, of shape *size*, if it was provided.

Notes

The Poisson distribution

$$f(k;\lambda) = \frac{\lambda^k e^{-\lambda}}{k!}$$

For events with an expected separation λ the Poisson distribution $f(k;\lambda)$ describes the probability of k events occurring within the observed interval λ.

Because the output is limited to the range of the C long type, a ValueError is raised when *lam* is within 10 sigma of the maximum representable value.

References

[1], *[2]*

Examples

Draw samples from the distribution:

```
>>> import numpy as np
>>> s = np.random.poisson(5, 10000)
```

Display histogram of the sample:

```
>>> import matplotlib.pyplot as plt
>>> count, bins, ignored = plt.hist(s, 14, normed=True)
>>> plt.show()
```

Draw each 100 values for lambda 100 and 500:

```
>>> s = np.random.poisson(lam=(100., 500.), size=(100, 2))
```

`dask.array.random.`**`power`**(*a*, *size=None*)

Draws samples in [0, 1] from a power distribution with positive exponent a - 1.

Also known as the power function distribution.

Parameters

a [float] parameter, > 0

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] The returned samples lie in [0, 1].

Raises

ValueError If a < 1.

Notes

The probability density function is

$$P(x; a) = ax^{a-1}, 0 \leq x \leq 1, a > 0.$$

The power function distribution is just the inverse of the Pareto distribution. It may also be seen as a special case of the Beta distribution.

It is used, for example, in modeling the over-reporting of insurance claims.

References

[1], *[2]*

Examples

Draw samples from the distribution:

```
>>> a = 5. # shape
>>> samples = 1000
>>> s = np.random.power(a, samples)
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> count, bins, ignored = plt.hist(s, bins=30)
>>> x = np.linspace(0, 1, 100)
>>> y = a*x**(a-1.)
>>> normed_y = samples*np.diff(bins)[0]*y
>>> plt.plot(x, normed_y)
>>> plt.show()
```

Compare the power function distribution to the inverse of the Pareto.

```
>>> from scipy import stats
>>> rvs = np.random.power(5, 1000000)
>>> rvsp = np.random.pareto(5, 1000000)
>>> xx = np.linspace(0,1,100)
>>> powpdf = stats.powerlaw.pdf(xx,5)
```

```
>>> plt.figure()
>>> plt.hist(rvs, bins=50, normed=True)
>>> plt.plot(xx,powpdf,'r-')
>>> plt.title('np.random.power(5)')
```

```
>>> plt.figure()
>>> plt.hist(1./(1.+rvsp), bins=50, normed=True)
>>> plt.plot(xx,powpdf,'r-')
>>> plt.title('inverse of 1 + np.random.pareto(5)')
```

```
>>> plt.figure()
>>> plt.hist(1./(1.+rvsp), bins=50, normed=True)
>>> plt.plot(xx,powpdf,'r-')
>>> plt.title('inverse of stats.pareto(5)')
```

dask.array.random.**random**(*size=None*)

Return random floats in the half-open interval [0.0, 1.0).

Results are from the "continuous uniform" distribution over the stated interval. To sample $Unif[a, b), b > a$ multiply the output of *random_sample* by *(b-a)* and add *a*:

```
(b - a) * random_sample() + a
```

Parameters

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

out [float or ndarray of floats] Array of random floats of shape *size* (unless `size=None`, in which case a single float is returned).

Examples

```
>>> np.random.random_sample()
0.47108547995356098
>>> type(np.random.random_sample())
<type 'float'>
>>> np.random.random_sample((5,))
array([ 0.30220482,  0.86820401,  0.1654503 ,  0.11659149,  0.54323428])
```

Three-by-two array of random numbers from [-5, 0):

```
>>> 5 * np.random.random_sample((3, 2)) - 5
array([[-3.99149989, -0.52338984],
       [-2.99091858, -0.79479508],
       [-1.23204345, -1.75224494]])
```

dask.array.random.**random_sample**(*size=None*)

Return random floats in the half-open interval [0.0, 1.0).

Results are from the "continuous uniform" distribution over the stated interval. To sample $Unif[a, b), b > a$ multiply the output of *random_sample* by *(b-a)* and add *a*:

```
(b - a) * random_sample() + a
```

Parameters

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

out [float or ndarray of floats] Array of random floats of shape *size* (unless `size=None`, in which case a single float is returned).

Examples

```
>>> np.random.random_sample()
0.47108547995356098
>>> type(np.random.random_sample())
<type 'float'>
>>> np.random.random_sample((5,))
array([ 0.30220482,  0.86820401,  0.1654503 ,  0.11659149,  0.54323428])
```

Three-by-two array of random numbers from [-5, 0):

```
>>> 5 * np.random.random_sample((3, 2)) - 5
array([[-3.99149989, -0.52338984],
       [-2.99091858, -0.79479508],
       [-1.23204345, -1.75224494]])
```

`dask.array.random.`**`rayleigh`**(*scale=1.0*, *size=None*)

Draw samples from a Rayleigh distribution.

The χ and Weibull distributions are generalizations of the Rayleigh.

Parameters

scale [scalar] Scale, also equals the mode. Should be >= 0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Notes

The probability density function for the Rayleigh distribution is

$$P(x; scale) = \frac{x}{scale^2} e^{\frac{-x^2}{2 \cdot scale^2}}$$

The Rayleigh distribution would arise, for example, if the East and North components of the wind velocity had identical zero-mean Gaussian distributions. Then the wind speed would have a Rayleigh distribution.

References

[1], *[2]*

Examples

Draw values from the distribution and plot the histogram

```
>>> values = hist(np.random.rayleigh(3, 100000), bins=200, normed=True)
```

Wave heights tend to follow a Rayleigh distribution. If the mean wave height is 1 meter, what fraction of waves are likely to be larger than 3 meters?

```
>>> meanvalue = 1
>>> modevalue = np.sqrt(2 / np.pi) * meanvalue
>>> s = np.random.rayleigh(modevalue, 1000000)
```

The percentage of waves larger than 3 meters is:

```
>>> 100.*sum(s>3)/1000000.
0.087300000000000003
```

dask.array.random.**standard_cauchy**(*size=None*)

Draw samples from a standard Cauchy distribution with mode = 0.

Also known as the Lorentz distribution.

Parameters

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] The drawn samples.

Notes

The probability density function for the full Cauchy distribution is

$$P(x; x_0, \gamma) = \frac{1}{\pi\gamma\left[1 + \left(\frac{x-x_0}{\gamma}\right)^2\right]}$$

and the Standard Cauchy distribution just sets $x_0 = 0$ and $\gamma = 1$

The Cauchy distribution arises in the solution to the driven harmonic oscillator problem, and also describes spectral line broadening. It also describes the distribution of values at which a line tilted at a random angle will cut the x axis.

When studying hypothesis tests that assume normality, seeing how the tests perform on data from a Cauchy distribution is a good indicator of their sensitivity to a heavy-tailed distribution, since the Cauchy looks very much like a Gaussian distribution, but with heavier tails.

References

[1], *[2]*, *[3]*

Examples

Draw samples and plot the distribution:

```
>>> s = np.random.standard_cauchy(1000000)
>>> s = s[(s>-25) & (s<25)]  # truncate distribution so it plots well
>>> plt.hist(s, bins=100)
>>> plt.show()
```

dask.array.random.**standard_exponential**(*size=None*)

Draw samples from the standard exponential distribution.

standard_exponential is identical to the exponential distribution with a scale parameter of 1.

Parameters

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

out [float or ndarray] Drawn samples.

Examples

Output a 3x8000 array:

```
>>> n = np.random.standard_exponential((3, 8000))
```

`dask.array.random.`**`standard_gamma`**(*shape*, *size=None*)

Draw samples from a standard Gamma distribution.

Samples are drawn from a Gamma distribution with specified parameters, shape (sometimes designated "k") and scale=1.

Parameters

shape [float] Parameter, should be > 0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] The drawn samples.

See also:

`scipy.stats.distributions.gamma` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Gamma distribution is

$$p(x) = x^{k-1}\frac{e^{-x/\theta}}{\theta^k\Gamma(k)},$$

where k is the shape and θ the scale, and Γ is the Gamma function.

The Gamma distribution is often used to model the times to failure of electronic components, and arises naturally in processes for which the waiting times between Poisson distributed events are relevant.

References

[1], *[2]*

Examples

Draw samples from the distribution:

```
>>> shape, scale = 2., 1. # mean and width
>>> s = np.random.standard_gamma(shape, 1000000)
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> import scipy.special as sps
>>> count, bins, ignored = plt.hist(s, 50, normed=True)
>>> y = bins**(shape-1) * ((np.exp(-bins/scale))/ \
...                       (sps.gamma(shape) * scale**shape))
>>> plt.plot(bins, y, linewidth=2, color='r')
>>> plt.show()
```

dask.array.random.**standard_normal**(*size=None*)

Draw samples from a standard Normal distribution (mean=0, stdev=1).

Parameters

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

out [float or ndarray] Drawn samples.

Examples

```
>>> s = np.random.standard_normal(8000)
>>> s
array([ 0.6888893 ,  0.78096262, -0.89086505, ...,  0.49876311, #random
       -0.38672696, -0.4685006 ])                               #random
>>> s.shape
(8000,)
>>> s = np.random.standard_normal(size=(3, 4, 2))
>>> s.shape
(3, 4, 2)
```

dask.array.random.**standard_t**(*df*, *size=None*)

Draw samples from a standard Student's t distribution with *df* degrees of freedom.

A special case of the hyperbolic distribution. As *df* gets large, the result resembles that of the standard normal distribution (*standard_normal*).

Parameters

df [int] Degrees of freedom, should be > 0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] Drawn samples.

Notes

The probability density function for the t distribution is

$$P(x, df) = \frac{\Gamma(\frac{df+1}{2})}{\sqrt{\pi df}\,\Gamma(\frac{df}{2})}\left(1 + \frac{x^2}{df}\right)^{-(df+1)/2}$$

The t test is based on an assumption that the data come from a Normal distribution. The t test provides a way to test whether the sample mean (that is the mean calculated from the data) is a good estimate of the true mean.

The derivation of the t-distribution was first published in 1908 by William Gisset while working for the Guinness Brewery in Dublin. Due to proprietary issues, he had to publish under a pseudonym, and so he used the name Student.

References

[1], *[2]*

Examples

From Dalgaard page 83 *[1]*, suppose the daily energy intake for 11 women in Kj is:

```
>>> intake = np.array([5260., 5470, 5640, 6180, 6390, 6515, 6805, 7515, \
...                    7515, 8230, 8770])
```

Does their energy intake deviate systematically from the recommended value of 7725 kJ?

We have 10 degrees of freedom, so is the sample mean within 95% of the recommended value?

```
>>> s = np.random.standard_t(10, size=100000)
>>> np.mean(intake)
6753.636363636364
>>> intake.std(ddof=1)
1142.1232221373727
```

Calculate the t statistic, setting the ddof parameter to the unbiased value so the divisor in the standard deviation will be degrees of freedom, N-1.

```
>>> t = (np.mean(intake)-7725)/(intake.std(ddof=1)/np.sqrt(len(intake)))
>>> import matplotlib.pyplot as plt
>>> h = plt.hist(s, bins=100, normed=True)
```

For a one-sided t-test, how far out in the distribution does the t statistic appear?

```
>>> np.sum(s<t) / float(len(s))
0.0090699999999999999  #random
```

So the p-value is about 0.009, which says the null hypothesis has a probability of about 99% of being true.

dask.array.random.**triangular**(*left*, *mode*, *right*, *size=None*)

Draw samples from the triangular distribution.

The triangular distribution is a continuous probability distribution with lower limit left, peak at mode, and upper limit right. Unlike the other distributions, these parameters directly define the shape of the pdf.

Parameters

left [scalar] Lower limit.

mode [scalar] The value where the peak of the distribution occurs. The value should fulfill the condition `left <= mode <= right`.

right [scalar] Upper limit, should be larger than *left*.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] The returned samples all lie in the interval [left, right].

Notes

The probability density function for the triangular distribution is

$$P(x;l,m,r) = \begin{cases} \frac{2(x-l)}{(r-l)(m-l)} & \text{for } l \leq x \leq m, \\ \frac{2(r-x)}{(r-l)(r-m)} & \text{for } m \leq x \leq r, \\ 0 & \text{otherwise.} \end{cases}$$

The triangular distribution is often used in ill-defined problems where the underlying distribution is not known, but some knowledge of the limits and mode exists. Often it is used in simulations.

References

[1]

Examples

Draw values from the distribution and plot the histogram:

```
>>> import matplotlib.pyplot as plt
>>> h = plt.hist(np.random.triangular(-3, 0, 8, 100000), bins=200,
...              normed=True)
>>> plt.show()
```

`dask.array.random.`**`uniform`**(*low=0.0*, *high=1.0*, *size=None*)

Draw samples from a uniform distribution.

Samples are uniformly distributed over the half-open interval `[low, high)` (includes low, but excludes high). In other words, any value within the given interval is equally likely to be drawn by *uniform*.

Parameters

low [float, optional] Lower boundary of the output interval. All values generated will be greater than or equal to low. The default value is 0.

high [float] Upper boundary of the output interval. All values generated will be less than high. The default value is 1.0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

out [ndarray] Drawn samples, with shape *size*.

See also:

randint Discrete uniform distribution, yielding integers.

random_integers Discrete uniform distribution over the closed interval `[low, high]`.

random_sample Floats uniformly distributed over `[0, 1)`.

random Alias for *random_sample*.

rand Convenience function that accepts dimensions as input, e.g., `rand(2,2)` would generate a 2-by-2 array of floats, uniformly distributed over `[0, 1)`.

Notes

The probability density function of the uniform distribution is

$$p(x) = \frac{1}{b - a}$$

anywhere within the interval `[a, b)`, and zero elsewhere.

Examples

Draw samples from the distribution:

```
>>> s = np.random.uniform(-1,0,1000)
```

All values are within the given interval:

```
>>> np.all(s >= -1)
True
>>> np.all(s < 0)
True
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> count, bins, ignored = plt.hist(s, 15, normed=True)
>>> plt.plot(bins, np.ones_like(bins), linewidth=2, color='r')
>>> plt.show()
```

`dask.array.random.`**vonmises**(*mu*, *kappa*, *size=None*)

Draw samples from a von Mises distribution.

Samples are drawn from a von Mises distribution with specified mode (mu) and dispersion (kappa), on the interval [-pi, pi].

The von Mises distribution (also known as the circular normal distribution) is a continuous probability distribution on the unit circle. It may be thought of as the circular analogue of the normal distribution.

Parameters

mu [float] Mode (“center”) of the distribution.

kappa [float] Dispersion of the distribution, has to be >=0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [scalar or ndarray] The returned samples, which are in the interval [-pi, pi].

See also:

`scipy.stats.distributions.vonmises` probability density function, distribution, or cumulative density function, etc.

Notes

The probability density for the von Mises distribution is

$$p(x) = \frac{e^{\kappa cos(x-\mu)}}{2\pi I_0(\kappa)},$$

where μ is the mode and κ the dispersion, and $I_0(\kappa)$ is the modified Bessel function of order 0.

The von Mises is named for Richard Edler von Mises, who was born in Austria-Hungary, in what is now the Ukraine. He fled to the United States in 1939 and became a professor at Harvard. He worked in probability theory, aerodynamics, fluid mechanics, and philosophy of science.

References

[1], *[2]*

Examples

Draw samples from the distribution:

```
>>> mu, kappa = 0.0, 4.0 # mean and dispersion
>>> s = np.random.vonmises(mu, kappa, 1000)
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> from scipy.special import i0
>>> plt.hist(s, 50, normed=True)
>>> x = np.linspace(-np.pi, np.pi, num=51)
>>> y = np.exp(kappa*np.cos(x-mu))/(2*np.pi*i0(kappa))
>>> plt.plot(x, y, linewidth=2, color='r')
>>> plt.show()
```

`dask.array.random.`**`wald`**(*mean*, *scale*, *size=None*)

Draw samples from a Wald, or inverse Gaussian, distribution.

As the scale approaches infinity, the distribution becomes more like a Gaussian. Some references claim that the Wald is an inverse Gaussian with mean equal to 1, but this is by no means universal.

The inverse Gaussian distribution was first studied in relationship to Brownian motion. In 1956 M.C.K. Tweedie used the name inverse Gaussian because there is an inverse relationship between the time to cover a unit distance and distance covered in unit time.

Parameters

mean [scalar] Distribution mean, should be > 0.

scale [scalar] Scale parameter, should be >= 0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] Drawn sample, all greater than zero.

Notes

The probability density function for the Wald distribution is

$$P(x; mean, scale) = \sqrt{\frac{scale}{2\pi x^3}} e^{\frac{-scale(x-mean)^2}{2 \cdot mean^2 x}}$$

As noted above the inverse Gaussian distribution first arise from attempts to model Brownian motion. It is also a competitor to the Weibull for use in reliability modeling and modeling stock returns and interest rate processes.

References

[1], *[2]*, *[3]*

Examples

Draw values from the distribution and plot the histogram:

```
>>> import matplotlib.pyplot as plt
>>> h = plt.hist(np.random.wald(3, 2, 100000), bins=200, normed=True)
>>> plt.show()
```

`dask.array.random.`**`weibull`**(*a*, *size=None*)

Draw samples from a Weibull distribution.

Draw samples from a 1-parameter Weibull distribution with the given shape parameter a.

$$X = (-ln(U))^{1/a}$$

Here, U is drawn from the uniform distribution over (0,1].

The more common 2-parameter Weibull, including a scale parameter λ is just $X = \lambda(-ln(U))^{1/a}$.

Parameters

a [float] Shape of the distribution.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray]

See also:

`scipy.stats.distributions.weibull_max`, `scipy.stats.distributions.weibull_min`, `scipy.stats.distributions.genextreme`, *gumbel*

Notes

The Weibull (or Type III asymptotic extreme value distribution for smallest values, SEV Type III, or Rosin-Rammler distribution) is one of a class of Generalized Extreme Value (GEV) distributions used in modeling extreme value problems. This class includes the Gumbel and Frechet distributions.

The probability density for the Weibull distribution is

$$p(x) = \frac{a}{\lambda}(\frac{x}{\lambda})^{a-1}e^{-(x/\lambda)^a},$$

where a is the shape and λ the scale.

The function has its peak (the mode) at $\lambda(\frac{a-1}{a})^{1/a}$.

When `a = 1`, the Weibull distribution reduces to the exponential distribution.

References

[1], *[2]*, *[3]*

Examples

Draw samples from the distribution:

```
>>> a = 5. # shape
>>> s = np.random.weibull(a, 1000)
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> x = np.arange(1,100.)/50.
>>> def weib(x,n,a):
...     return (a / n) * (x / n)**(a - 1) * np.exp(-(x / n)**a)
```

```
>>> count, bins, ignored = plt.hist(np.random.weibull(5.,1000))
>>> x = np.arange(1,100.)/50.
>>> scale = count.max()/weib(x, 1., 5.).max()
>>> plt.plot(x, weib(x, 1., 5.)*scale)
>>> plt.show()
```

`dask.array.random.`**`zipf`**(*a*, *size=None*)
Standard distributions

`dask.array.stats.`**`ttest_ind`**(*a*, *b*, *axis=0*, *equal_var=True*)
Calculates the T-test for the means of TWO INDEPENDENT samples of scores.

This is a two-sided test for the null hypothesis that 2 independent samples have identical average (expected) values. This test assumes that the populations have identical variances by default.

Parameters

a, b [array_like] The arrays must have the same shape, except in the dimension corresponding to *axis* (the first, by default).

axis [int or None, optional] Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

equal_var [bool, optional] If True (default), perform a standard independent 2 sample test that assumes equal population variances *[1]*. If False, perform Welch's t-test, which does not assume equal population variance *[2]*. .. versionadded:: 0.11.0

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

statistic [float or array] The calculated t-statistic.

pvalue [float or array] The two-tailed p-value.

Notes

We can use this test, if we observe two independent samples from the same or different population, e.g. exam scores of boys and girls or of two ethnic groups. The test measures whether the average (expected) value differs significantly across samples. If we observe a large p-value, for example larger than 0.05 or 0.1, then we cannot reject the null hypothesis of identical average scores. If the p-value is smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages.

References

[1], *[2]*

Examples

```
>>> from scipy import stats
>>> np.random.seed(12345678)
```

Test with sample with identical means:

```
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs2 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> stats.ttest_ind(rvs1,rvs2)
(0.26833823296239279, 0.78849443369564776)
>>> stats.ttest_ind(rvs1,rvs2, equal_var = False)
(0.26833823296239279, 0.78849452749500748)
```

ttest_ind underestimates p for unequal variances:

```
>>> rvs3 = stats.norm.rvs(loc=5, scale=20, size=500)
>>> stats.ttest_ind(rvs1, rvs3)
(-0.46580283298287162, 0.64145827413436174)
>>> stats.ttest_ind(rvs1, rvs3, equal_var = False)
(-0.46580283298287162, 0.64149646246569292)
```

When n1 != n2, the equal variance t-statistic is no longer equal to the unequal variance t-statistic:

```
>>> rvs4 = stats.norm.rvs(loc=5, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs4)
(-0.99882539442782481, 0.3182832709103896)
>>> stats.ttest_ind(rvs1, rvs4, equal_var = False)
(-0.69712570584654099, 0.48716927725402048)
```

T-test with different means, variance, and n:

```
>>> rvs5 = stats.norm.rvs(loc=8, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs5)
(-1.4679669854490653, 0.14263895620529152)
>>> stats.ttest_ind(rvs1, rvs5, equal_var = False)
(-0.94365973617132992, 0.34744170334794122)
```

dask.array.stats.**ttest_1samp**(*a*, *popmean*, *axis=0*, *nan_policy='propagate'*)

Calculates the T-test for the mean of ONE group of scores.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations *a* is equal to the given population mean, *popmean*.

Parameters

a [array_like] sample observation

popmean [float or array_like] expected value in null hypothesis, if array_like than it must have the same shape as *a* excluding the axis dimension

axis [int or None, optional] Axis along which to compute test. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

statistic [float or array] t-statistic

pvalue [float or array] two-tailed p-value

Examples

```
>>> from scipy import stats
```

```
>>> np.random.seed(7654567)  # fix seed to get the same result
>>> rvs = stats.norm.rvs(loc=5, scale=10, size=(50,2))
```

Test if mean of random sample is equal to true mean, and different mean. We reject the null hypothesis in the second case and don't reject it in the first case.

```
>>> stats.ttest_1samp(rvs,5.0)
(array([-0.68014479, -0.04323899]), array([ 0.49961383,  0.96568674]))
>>> stats.ttest_1samp(rvs,0.0)
(array([ 2.77025808,  4.11038784]), array([ 0.00789095,  0.00014999]))
```

Examples using axis and non-scalar dimension for population mean.

```
>>> stats.ttest_1samp(rvs,[5.0,0.0])
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs.T,[5.0,0.0],axis=1)
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs,[[5.0],[0.0]])
(array([[-0.68014479, -0.04323899],
       [ 2.77025808,  4.11038784]]), array([[  4.99613833e-01,   9.65686743e-01],
       [  7.89094663e-03,   1.49986458e-04]]))
```

dask.array.stats.**ttest_rel**(*a*, *b*, *axis=0*, *nan_policy='propagate'*)

Calculates the T-test on TWO RELATED samples of scores, a and b.

This is a two-sided test for the null hypothesis that 2 related or repeated samples have identical average (expected) values.

Parameters

a, b [array_like] The arrays must have the same shape.

axis [int or None, optional] Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

statistic [float or array] t-statistic

pvalue [float or array] two-tailed p-value

Notes

Examples for the use are scores of the same set of student in different exams, or repeated sampling from the same units. The test measures whether the average score differs significantly across samples (e.g. exams). If we observe a large p-value, for example greater than 0.05 or 0.1 then we cannot reject the null hypothesis of identical average scores. If the p-value is smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages. Small p-values are associated with large t-statistics.

References

http://en.wikipedia.org/wiki/T-test#Dependent_t-test

Examples

```
>>> from scipy import stats
>>> np.random.seed(12345678) # fix random seed to get same numbers
```

```
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs2 = (stats.norm.rvs(loc=5,scale=10,size=500) +
...         stats.norm.rvs(scale=0.2,size=500))
>>> stats.ttest_rel(rvs1,rvs2)
(0.24101764965300962, 0.80964043445811562)
>>> rvs3 = (stats.norm.rvs(loc=8,scale=10,size=500) +
...         stats.norm.rvs(scale=0.2,size=500))
>>> stats.ttest_rel(rvs1,rvs3)
(-3.9995108708727933, 7.3082402191726459e-005)
```

dask.array.stats.**chisquare**(*f_obs*, *f_exp=None*, *ddof=0*, *axis=0*)

Calculates a one-way chi square test.

The chi square test tests the null hypothesis that the categorical data has the given frequencies.

Parameters

f_obs [array_like] Observed frequencies in each category.

f_exp [array_like, optional] Expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof [int, optional] "Delta degrees of freedom": adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with `k - 1 - ddof` degrees of freedom, where *k* is the number of observed frequencies. The default value of *ddof* is 0.

axis [int or None, optional] The axis of the broadcast result of *f_obs* and *f_exp* along which to apply the test. If axis is None, all values in *f_obs* are treated as a single data set. Default is 0.

Returns

chisq [float or ndarray] The chi-squared test statistic. The value is a float if *axis* is None or *f_obs* and *f_exp* are 1-D.

p [float or ndarray] The p-value of the test. The value is a float if *ddof* and the return value *chisq* are scalars.

See also:

power_divergence, `mstats.chisquare`

Notes

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If p parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-p. If the parameters are estimated in a different way, then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distribution is not a chisquare, in which case this test is not appropriate.

References

[1], *[2]*

Examples

When just *f_obs* is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies.

```
>>> from scipy.stats import chisquare
>>> chisquare([16, 18, 16, 14, 12, 12])
(2.0, 0.84914503608460956)
```

With *f_exp* the expected frequencies can be given.

```
>>> chisquare([16, 18, 16, 14, 12, 12], f_exp=[16, 16, 16, 16, 16, 8])
(3.5, 0.62338762774958223)
```

When *f_obs* is 2-D, by default the test is applied to each column.

```
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T
>>> obs.shape
(6, 2)
>>> chisquare(obs)
(array([ 2.        ,  6.66666667]), array([ 0.84914504,  0.24663415]))
```

By setting `axis=None`, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```
>>> chisquare(obs, axis=None)
(23.31034482758621, 0.015975692534127565)
>>> chisquare(obs.ravel())
(23.31034482758621, 0.015975692534127565)
```

ddof is the change to make to the default degrees of freedom.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.73575888234288467)
```

The calculation of the p-values is done by broadcasting the chi-squared statistic with *ddof*.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([ 0.84914504,  0.73575888,  0.5724067 ]))
```

f_obs and *f_exp* are also broadcast. In the following, *f_obs* has shape (6,) and *f_exp* has shape (2, 6), so the result of broadcasting *f_obs* and *f_exp* has shape (2, 6). To compute the desired chi-squared statistics, we use `axis=1`:

```
>>> chisquare([16, 18, 16, 14, 12, 12],
...           f_exp=[[16, 16, 16, 16, 16, 8], [8, 20, 20, 16, 12, 12]],
...           axis=1)
(array([ 3.5 ,  9.25]), array([ 0.62338763,  0.09949846]))
```

`dask.array.stats.`**`power_divergence`**(*f_obs*, *f_exp=None*, *ddof=0*, *axis=0*, *lambda_=None*)

Cressie-Read power divergence statistic and goodness of fit test.

This function tests the null hypothesis that the categorical data has the given frequencies, using the Cressie-Read power divergence statistic.

Parameters

f_obs [array_like] Observed frequencies in each category.

f_exp [array_like, optional] Expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof [int, optional] "Delta degrees of freedom": adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with `k - 1 - ddof` degrees of freedom, where *k* is the number of observed frequencies. The default value of *ddof* is 0.

axis [int or None, optional] The axis of the broadcast result of *f_obs* and *f_exp* along which to apply the test. If axis is None, all values in *f_obs* are treated as a single data set. Default is 0.

lambda_ [float or str, optional] *lambda_* gives the power in the Cressie-Read power divergence statistic. The default is 1. For convenience, *lambda_* may be assigned one of the following strings, in which case the corresponding numerical value is used:

```
String               Value   Description
"pearson"              1     Pearson's chi-squared statistic.
                             In this case, the function is
                             equivalent to `stats.chisquare`.
"log-likelihood"       0     Log-likelihood ratio. Also known as
                             the G-test [R5ed189a69e5c-3]_.
"freeman-tukey"      -1/2    Freeman-Tukey statistic.
"mod-log-likelihood" -1      Modified log-likelihood ratio.
"neyman"             -2      Neyman's statistic.
"cressie-read"        2/3    The power recommended in␣
↪[R5ed189a69e5c-5]_.
```

Returns

statistic [float or ndarray] The Cressie-Read power divergence test statistic. The value is a float if *axis* is None or if‘ *f_obs* and *f_exp* are 1-D.

pvalue [float or ndarray] The p-value of the test. The value is a float if *ddof* and the return value *stat* are scalars.

See also:

chisquare

Notes

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5.

When *lambda_* is less than zero, the formula for the statistic involves dividing by *f_obs*, so a warning or error may be generated if any value in *f_obs* is 0.

Similarly, a warning or error may be generated if any value in *f_exp* is zero when *lambda_* >= 0.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If p parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-p. If the parameters are estimated in a different way, then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distribution is not a chisquare, in which case this test is not appropriate.

This function handles masked arrays. If an element of *f_obs* or *f_exp* is masked, then data at that position is ignored, and does not count towards the size of the data set.

New in version 0.13.0.

References

[1], *[2]*, *[3]*, *[4]*, *[5]*

Examples

(See *chisquare* for more examples.)

When just *f_obs* is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies. Here we perform a G-test (i.e. use the log-likelihood ratio statistic):

```
>>> from scipy.stats import power_divergence
>>> power_divergence([16, 18, 16, 14, 12, 12], lambda_='log-likelihood')
(2.006573162632538, 0.84823476779463769)
```

The expected frequencies can be given with the *f_exp* argument:

```
>>> power_divergence([16, 18, 16, 14, 12, 12],
...                  f_exp=[16, 16, 16, 16, 16, 8],
...                  lambda_='log-likelihood')
(3.3281031458963746, 0.6495419288047497)
```

When *f_obs* is 2-D, by default the test is applied to each column.

```
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T
>>> obs.shape
(6, 2)
>>> power_divergence(obs, lambda_="log-likelihood")
(array([ 2.00657316,  6.77634498]), array([ 0.84823477,  0.23781225]))
```

By setting `axis=None`, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```
>>> power_divergence(obs, axis=None)
(23.31034482758621, 0.015975692534127565)
>>> power_divergence(obs.ravel())
(23.31034482758621, 0.015975692534127565)
```

ddof is the change to make to the default degrees of freedom.

```
>>> power_divergence([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.7357588823428847)
```

The calculation of the p-values is done by broadcasting the test statistic with *ddof*.

```
>>> power_divergence([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([ 0.84914504,  0.73575888,  0.5724067 ]))
```

f_obs and *f_exp* are also broadcast. In the following, *f_obs* has shape (6,) and *f_exp* has shape (2, 6), so the result of broadcasting *f_obs* and *f_exp* has shape (2, 6). To compute the desired chi-squared statistics, we must use `axis=1`:

```
>>> power_divergence([16, 18, 16, 14, 12, 12],
...                  f_exp=[[16, 16, 16, 16, 16, 8],
...                         [8, 20, 20, 16, 12, 12]],
...                  axis=1)
(array([ 3.5 ,  9.25]), array([ 0.62338763,  0.09949846]))
```

`dask.array.stats.`**`skew`**(*a*, *axis=0*, *bias=True*, *nan_policy='propagate'*)

Computes the skewness of a data set.

For normally distributed data, the skewness should be about 0. A skewness value > 0 means that there is more weight in the left tail of the distribution. The function *skewtest* can be used to determine if the skewness value is close enough to 0, statistically speaking.

Parameters

a [ndarray] data

axis [int or None, optional] Axis along which skewness is calculated. Default is 0. If None, compute over the whole array *a*.

bias [bool, optional] If False, then the calculations are corrected for statistical bias.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

skewness [ndarray] The skewness of values along an axis, returning 0 where all values are equal.

References

[1]

dask.array.stats.**skewtest**(*a*, *axis=0*, *nan_policy='propagate'*)
Tests whether the skew is different from the normal distribution.

This function tests the null hypothesis that the skewness of the population that the sample was drawn from is the same as that of a corresponding normal distribution.

Parameters

a [array] The data to be tested

axis [int or None, optional] Axis along which statistics are calculated. Default is 0. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

statistic [float] The computed z-score for this test.

pvalue [float] a 2-sided p-value for the hypothesis test

Notes

The sample size must be at least 8.

dask.array.stats.**kurtosis**(*a*, *axis=0*, *fisher=True*, *bias=True*, *nan_policy='propagate'*)
Computes the kurtosis (Fisher or Pearson) of a dataset.

Kurtosis is the fourth central moment divided by the square of the variance. If Fisher's definition is used, then 3.0 is subtracted from the result to give 0.0 for a normal distribution.

If bias is False then the kurtosis is calculated using k statistics to eliminate bias coming from biased moment estimators

Use *kurtosistest* to see if result is close enough to normal.

Parameters

a [array] data for which the kurtosis is calculated

axis [int or None, optional] Axis along which the kurtosis is calculated. Default is 0. If None, compute over the whole array *a*.

fisher [bool, optional] If True, Fisher's definition is used (normal ==> 0.0). If False, Pearson's definition is used (normal ==> 3.0).

bias [bool, optional] If False, then the calculations are corrected for statistical bias.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

kurtosis [array] The kurtosis of values along an axis. If all values are equal, return -3 for Fisher's definition and 0 for Pearson's definition.

References

[1]

dask.array.stats.**kurtosistest**(*a*, *axis=0*, *nan_policy='propagate'*)
Tests whether a dataset has normal kurtosis

This function tests the null hypothesis that the kurtosis of the population from which the sample was drawn is that of the normal distribution: `kurtosis = 3(n-1)/(n+1)`.

Parameters

a [array] array of the sample data

axis [int or None, optional] Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

statistic [float] The computed z-score for this test.

pvalue [float] The 2-sided p-value for the hypothesis test

Notes

Valid only for n>20. The Z-score is set to 0 for bad entries.

dask.array.stats.**normaltest**(*a*, *axis=0*, *nan_policy='propagate'*)
Tests whether a sample differs from a normal distribution.

This function tests the null hypothesis that a sample comes from a normal distribution. It is based on D'Agostino and Pearson's *[1]*, *[2]* test that combines skew and kurtosis to produce an omnibus test of normality.

Parameters

a [array_like] The array containing the data to be tested.

axis [int or None, optional] Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

statistic [float or array] `s^2 + k^2`, where `s` is the z-score returned by *skewtest* and `k` is the z-score returned by *kurtosistest*.

pvalue [float or array] A 2-sided chi squared probability for the hypothesis test.

References

[1], *[2]*

`dask.array.stats.f_oneway(*args)`

Performs a 1-way ANOVA.

The one-way ANOVA tests the null hypothesis that two or more groups have the same population mean. The test is applied to samples from two or more groups, possibly with differing sizes.

Parameters

sample1, sample2, ... [array_like] The sample measurements for each group.

Returns

statistic [float] The computed F-value of the test.

pvalue [float] The associated p-value from the F-distribution.

Notes

The ANOVA test has important assumptions that must be satisfied in order for the associated p-value to be valid.

1. The samples are independent.
2. Each sample is from a normally distributed population.
3. The population standard deviations of the groups are all equal. This property is known as homoscedasticity.

If these assumptions are not true for a given set of data, it may still be possible to use the Kruskal-Wallis H-test (*scipy.stats.kruskal*) although with some loss of power.

The algorithm is from Heiman[2], pp.394-7.

References

[1], *[2]*, *[3]*

Examples

```
>>> import scipy.stats as stats
```

[3] Here are some data on a shell measurement (the length of the anterior adductor muscle scar, standardized by dividing by length) in the mussel Mytilus trossulus from five locations: Tillamook, Oregon; Newport, Oregon; Petersburg, Alaska; Magadan, Russia; and Tvarminne, Finland, taken from a much larger data set used in McDonald et al. (1991).

```
>>> tillamook = [0.0571, 0.0813, 0.0831, 0.0976, 0.0817, 0.0859, 0.0735,
...              0.0659, 0.0923, 0.0836]
>>> newport = [0.0873, 0.0662, 0.0672, 0.0819, 0.0749, 0.0649, 0.0835,
...            0.0725]
>>> petersburg = [0.0974, 0.1352, 0.0817, 0.1016, 0.0968, 0.1064, 0.105]
>>> magadan = [0.1033, 0.0915, 0.0781, 0.0685, 0.0677, 0.0697, 0.0764,
...            0.0689]
>>> tvarminne = [0.0703, 0.1026, 0.0956, 0.0973, 0.1039, 0.1045]
>>> stats.f_oneway(tillamook, newport, petersburg, magadan, tvarminne)
(7.1210194716424473, 0.00028122423145345439)
```

dask.array.stats.**moment**(*a*, *moment=1*, *axis=0*, *nan_policy='propagate'*)

Calculates the nth moment about the mean for a sample.

A moment is a specific quantitative measure of the shape of a set of points. It is often used to calculate coefficients of skewness and kurtosis due to its close relationship with them.

Parameters

a [array_like] data

moment [int or array_like of ints, optional] order of central moment that is returned. Default is 1.

axis [int or None, optional] Axis along which the central moment is computed. Default is 0. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

n-th central moment [ndarray or float] The appropriate moment along the given axis or over all values if axis is None. The denominator for the moment calculation is the number of observations, no degrees of freedom correction is done.

See also:

kurtosis, *skew*, describe

Notes

The k-th central moment of a data sample is:

$$m_k = \frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^k$$

Where n is the number of samples and x-bar is the mean. This function uses exponentiation by squares *[1]* for efficiency.

References

[1]

dask.array.image.**imread**(*filename*, *imread=None*, *preprocess=None*)

Read a stack of images into a dask array

Parameters

filename: string A globstring like 'myfile.*.png'

imread: function (optional) Optionally provide custom imread function. Function should expect a filename and produce a numpy array. Defaults to `skimage.io.imread`.

preprocess: function (optional) Optionally provide custom function to preprocess the image. Function should expect a numpy array for a single image.

Returns

Dask array of all images stacked along the first dimension. All images

will be treated as individual chunks

Examples

```
>>> from dask.array.image import imread
>>> im = imread('2015-*-*.png')
>>> im.shape
(365, 1000, 1000, 3)
```

`dask.array.gufunc.`**`apply_gufunc`**(*func*, *signature*, **args*, ***kwargs*)

Apply a generalized ufunc or similar python function to arrays.

`signature` determines if the function consumes or produces core dimensions. The remaining dimensions in given input arrays (`*args`) are considered loop dimensions and are required to broadcast naturally against each other.

In other terms, this function is like np.vectorize, but for the blocks of dask arrays. If the function itself shall also be vectorized use `vectorize=True` for convenience.

Parameters

func [callable] Function to call like `func(*args, **kwargs)` on input arrays (`*args`) that returns an array or tuple of arrays. If multiple arguments with non-matching dimensions are supplied, this function is expected to vectorize (broadcast) over axes of positional arguments in the style of NumPy universal functions *[1]* (if this is not the case, set `vectorize=True`). If this function returns multiple outputs, `output_core_dims` has to be set as well.

signature: string Specifies what core dimensions are consumed and produced by `func`. According to the specification of numpy.gufunc signature *[2]*

***args** [numeric] Input arrays or scalars to the callable function.

output_dtypes [Optional, dtype or list of dtypes, keyword only] Valid numpy dtype specification or list thereof. If not given, a call of `func` with a small set of data is performed in order to try to automatically determine the output dtypes.

output_sizes [dict, optional, keyword only] Optional mapping from dimension names to sizes for outputs. Only used if new core dimensions (not found on inputs) appear on outputs.

vectorize: bool, keyword only If set to `True`, `np.vectorize` is applied to `func` for convenience. Defaults to `False`.

allow_rechunk: Optional, bool, keyword only Allows rechunking, otherwise chunk sizes need to match and core dimensions are to consist only of one chunk. Warning: enabling this can increase memory usage significantly. Defaults to `False`.

****kwargs** [dict] Extra keyword arguments to pass to *func*

Returns

Single dask.array.Array or tuple of dask.array.Array

References

[1], *[2]*

Examples

```
>>> import dask.array as da
>>> import numpy as np
>>> def stats(x):
...     return np.mean(x, axis=-1), np.std(x, axis=-1)
>>> a = da.random.normal(size=(10,20,30), chunks=(5, 10, 30))
>>> mean, std = da.apply_gufunc(stats, "(i)->(),()", a, output_dtypes=2*(a.dtype,
↪))
>>> mean.compute().shape
(10, 20)
```

```
>>> def outer_product(x, y):
...     return np.einsum("i,j->ij", x, y)
>>> a = da.random.normal(size=(   20,30), chunks=(10, 30))
>>> b = da.random.normal(size=(10, 1,40), chunks=(5, 1, 40))
>>> c = da.apply_gufunc(outer_product, "(i),(j)->(i,j)", a, b, output_dtypes=a.
↪dtype, vectorize=True)
>>> c.compute().shape
(10, 20, 30, 40)
```

dask.array.gufunc.**as_gufunc**(*signature=None*, ***kwargs*)

Decorator for dask.array.gufunc.

Parameters

signature [String] Specifies what core dimensions are consumed and produced by func. According to the specification of numpy.gufunc signature *[2]*

output_dtypes [dtype or list of dtypes, keyword only] dtype or list of output dtypes.

output_sizes [dict, optional, keyword only] Optional mapping from dimension names to sizes for outputs. Only used if new core dimensions (not found on inputs) appear on outputs.

vectorize: bool, keyword only If set to True, np.vectorize is applied to func for convenience. Defaults to False.

allow_rechunk: Optional, bool, keyword only Allows rechunking, otherwise chunk sizes need to match and core dimensions are to consist only of one chunk. Warning: enabling this can increase memory usage significantly. Defaults to False.

Returns

Decorator for 'pyfunc' that itself returns a 'gufunc'.

References

[1], *[2]*

Examples

```
>>> import dask.array as da
>>> import numpy as np
>>> a = da.random.normal(size=(10,20,30), chunks=(5, 10, 30))
>>> @da.as_gufunc("(i)->(),()", output_dtypes=(float, float))
... def stats(x):
...     return np.mean(x, axis=-1), np.std(x, axis=-1)
>>> mean, std = stats(a)
>>> mean.compute().shape
(10, 20)
```

```
>>> a = da.random.normal(size=(   20,30), chunks=(10, 30))
>>> b = da.random.normal(size=(10, 1,40), chunks=(5, 1, 40))
>>> @da.as_gufunc("(i),(j)->(i,j)", output_dtypes=float, vectorize=True)
... def outer_product(x, y):
...     return np.einsum("i,j->ij", x, y)
>>> c = outer_product(a, b)
>>> c.compute().shape
(10, 20, 30, 40)
```

dask.array.gufunc.**gufunc**(*pyfunc*, ***kwargs*)

Binds *pyfunc* into `dask.array.apply_gufunc` when called.

Parameters

pyfunc [callable] Function to call like `func(*args, **kwargs)` on input arrays (`*args`) that returns an array or tuple of arrays. If multiple arguments with non-matching dimensions are supplied, this function is expected to vectorize (broadcast) over axes of positional arguments in the style of NumPy universal functions *[1]* (if this is not the case, set `vectorize=True`). If this function returns multiple outputs, `output_core_dims` has to be set as well.

signature [String, keyword only] Specifies what core dimensions are consumed and produced by `func`. According to the specification of numpy.gufunc signature *[2]*

output_dtypes [dtype or list of dtypes, keyword only] dtype or list of output dtypes.

output_sizes [dict, optional, keyword only] Optional mapping from dimension names to sizes for outputs. Only used if new core dimensions (not found on inputs) appear on outputs.

vectorize: bool, keyword only If set to `True`, `np.vectorize` is applied to `func` for convenience. Defaults to `False`.

allow_rechunk: Optional, bool, keyword only Allows rechunking, otherwise chunk sizes need to match and core dimensions are to consist only of one chunk. Warning: enabling this can increase memory usage significantly. Defaults to `False`.

Returns

Wrapped function

References

[1], *[2]*

Examples

```
>>> import dask.array as da
>>> import numpy as np
>>> a = da.random.normal(size=(10,20,30), chunks=(5, 10, 30))
>>> def stats(x):
...     return np.mean(x, axis=-1), np.std(x, axis=-1)
>>> gustats = da.gufunc(stats, signature="(i)->(),()", output_dtypes=(float,␣
↪float))
>>> mean, std = gustats(a)
>>> mean.compute().shape
(10, 20)
```

```
>>> a = da.random.normal(size=(   20,30), chunks=(10, 30))
>>> b = da.random.normal(size=(10, 1,40), chunks=(5, 1, 40))
>>> def outer_product(x, y):
...     return np.einsum("i,j->ij", x, y)
>>> guouter_product = da.gufunc(outer_product, signature="(i),(j)->(i,j)", output_
↪dtypes=float, vectorize=True)
>>> c = guouter_product(a, b)
>>> c.compute().shape
(10, 20, 30, 40)
```

dask.array.core.**map_blocks**(*func*, **args*, ***kwargs*)

Map a function across all blocks of a dask array.

Parameters

func [callable] Function to apply to every block in the array.

args [dask arrays or other objects]

dtype [np.dtype, optional] The `dtype` of the output array. It is recommended to provide this. If not provided, will be inferred by applying the function to a small set of fake data.

chunks [tuple, optional] Chunk shape of resulting blocks if the function does not preserve shape. If not provided, the resulting array is assumed to have the same block structure as the first input array.

drop_axis [number or iterable, optional] Dimensions lost by the function.

new_axis [number or iterable, optional] New dimensions created by the function. Note that these are applied after `drop_axis` (if present).

token [string, optional] The key prefix to use for the output array. If not provided, will be determined from the function name.

name [string, optional] The key name to use for the output array. Note that this fully specifies the output key name, and must be unique. If not provided, will be determined by a hash of the arguments.

****kwargs :** Other keyword arguments to pass to function. Values must be constants (not dask.arrays)

Examples

```
>>> import dask.array as da
>>> x = da.arange(6, chunks=3)
```

```
>>> x.map_blocks(lambda x: x * 2).compute()
array([ 0,  2,  4,  6,  8, 10])
```

The `da.map_blocks` function can also accept multiple arrays.

```
>>> d = da.arange(5, chunks=2)
>>> e = da.arange(5, chunks=2)
```

```
>>> f = map_blocks(lambda a, b: a + b**2, d, e)
>>> f.compute()
array([ 0,  2,  6, 12, 20])
```

If the function changes shape of the blocks then you must provide chunks explicitly.

```
>>> y = x.map_blocks(lambda x: x[::2], chunks=((2, 2),))
```

You have a bit of freedom in specifying chunks. If all of the output chunk sizes are the same, you can provide just that chunk size as a single tuple.

```
>>> a = da.arange(18, chunks=(6,))
>>> b = a.map_blocks(lambda x: x[:3], chunks=(3,))
```

If the function changes the dimension of the blocks you must specify the created or destroyed dimensions.

```
>>> b = a.map_blocks(lambda x: x[None, :, None], chunks=(1, 6, 1),
...                  new_axis=[0, 2])
```

Map_blocks aligns blocks by block positions without regard to shape. In the following example we have two arrays with the same number of blocks but with different shape and chunk sizes.

```
>>> x = da.arange(1000, chunks=(100,))
>>> y = da.arange(100, chunks=(10,))
```

The relevant attribute to match is numblocks.

```
>>> x.numblocks
(10,)
>>> y.numblocks
(10,)
```

If these match (up to broadcasting rules) then we can map arbitrary functions across blocks

```
>>> def func(a, b):
...     return np.array([a.max(), b.max()])
```

```
>>> da.map_blocks(func, x, y, chunks=(2,), dtype='i8')
dask.array<func, shape=(20,), dtype=int64, chunksize=(2,)>
```

```
>>> _.compute()
array([ 99,   9, 199,  19, 299,  29, 399,  39, 499,  49, 599,  59, 699,
        69, 799,  79, 899,  89, 999,  99])
```

Your block function get information about where it is in the array by accepting a special `block_info` keyword argument.

```
>>> def func(block, block_info=None):
...     pass
```

This will receive the following information:

```
>>> block_info
{0: {'shape': (1000,),
     'num-chunks': (10,),
     'chunk-location': (4,),
     'array-location': [(400, 500)]}}
```

For each argument and keyword arguments that are dask arrays (the positions of which are the first index), you will receive the shape of the full array, the number of chunks of the full array in each dimension, the chunk location (for example the fourth chunk over in the first dimension), and the array location (for example the slice corresponding to `40:50`).

You may specify the key name prefix of the resulting task in the graph with the optional `token` keyword argument.

```
>>> x.map_blocks(lambda x: x + 1, name='increment')
dask.array<increment, shape=(100,), dtype=int64, chunksize=(10,)>
```

`dask.array.core.`**`atop`**(*func*, *out_ind*, **args*, ***kwargs*)

Tensor operation: Generalized inner and outer products

A broad class of blocked algorithms and patterns can be specified with a concise multi-index notation. The `atop` function applies an in-memory function across multiple blocks of multiple inputs in a variety of ways. Many dask.array operations are special cases of atop including elementwise, broadcasting, reductions, tensordot, and transpose.

Parameters

func [callable] Function to apply to individual tuples of blocks

out_ind [iterable] Block pattern of the output, something like 'ijk' or (1, 2, 3)

***args** [sequence of Array, index pairs] Sequence like (x, 'ij', y, 'jk', z, 'i')

****kwargs** [dict] Extra keyword arguments to pass to function

dtype [np.dtype] Datatype of resulting array.

concatenate [bool, keyword only] If true concatenate arrays along dummy indices, else provide lists

adjust_chunks [dict] Dictionary mapping index to function to be applied to chunk sizes

new_axes [dict, keyword only] New indexes and their dimension lengths

See also:

top, `contains`

Examples

2D embarrassingly parallel operation from two arrays, x, and y.

```
>>> z = atop(operator.add, 'ij', x, 'ij', y, 'ij', dtype='f8')  # z = x + y
```

Outer product multiplying x by y, two 1-d vectors

```
>>> z = atop(operator.mul, 'ij', x, 'i', y, 'j', dtype='f8')
```

z = x.T

```
>>> z = atop(np.transpose, 'ji', x, 'ij', dtype=x.dtype)
```

The transpose case above is illustrative because it does same transposition both on each in-memory block by calling `np.transpose` and on the order of the blocks themselves, by switching the order of the index `ij -> ji`.

We can compose these same patterns with more variables and more complex in-memory functions

z = X + Y.T

```
>>> z = atop(lambda x, y: x + y.T, 'ij', x, 'ij', y, 'ji', dtype='f8')
```

Any index, like `i` missing from the output index is interpreted as a contraction (note that this differs from Einstein convention; repeated indices do not imply contraction.) In the case of a contraction the passed function should expect an iterable of blocks on any array that holds that index. To receive arrays concatenated along contracted dimensions instead pass `concatenate=True`.

Inner product multiplying x by y, two 1-d vectors

```
>>> def sequence_dot(x_blocks, y_blocks):
...     result = 0
...     for x, y in zip(x_blocks, y_blocks):
...         result += x.dot(y)
...     return result
```

```
>>> z = atop(sequence_dot, '', x, 'i', y, 'i', dtype='f8')
```

Add new single-chunk dimensions with the `new_axes=` keyword, including the length of the new dimension. New dimensions will always be in a single chunk.

```
>>> def f(x):
...     return x[:, None] * np.ones((1, 5))
```

```
>>> z = atop(f, 'az', x, 'a', new_axes={'z': 5}, dtype=x.dtype)
```

If the applied function changes the size of each chunk you can specify this with a `adjust_chunks={...}` dictionary holding a function for each index that modifies the dimension size in that index.

```
>>> def double(x):
...     return np.concatenate([x, x])
```

```
>>> y = atop(double, 'ij', x, 'ij',
...          adjust_chunks={'i': lambda n: 2 * n}, dtype=x.dtype)
```

Include literals by indexing with None

```
>>> y = atop(add, 'ij', x, 'ij', 1234, None, dtype=x.dtype)
```

dask.array.core.**normalize_chunks**(*chunks*, *shape=None*, *limit=None*, *dtype=None*, *previous_chunks=None*)

Normalize chunks to tuple of tuples

This takes in a variety of input types and information and produces a full tuple-of-tuples result for chunks, suitable to be passed to Array or rechunk or any other operation that creates a Dask array.

Parameters

chunks: tuple, int, dict, or string The chunks to be normalized. See examples below for more details

shape: Tuple[int] The shape of the array

limit: int (optional) The maximum block size to target in bytes, if freedom is given to choose

dtype: np.dtype

previous_chunks: Tuple[Tuple[int]] optional Chunks from a previous array that we should use for inspiration when rechunking auto dimensions. If not provided but auto-chunking exists then auto-dimensions will prefer square-like chunk shapes.

Examples

Specify uniform chunk sizes

```
>>> normalize_chunks((2, 2), shape=(5, 6))
((2, 2, 1), (2, 2, 2))
```

Also passes through fully explicit tuple-of-tuples

```
>>> normalize_chunks(((2, 2, 1), (2, 2, 2)), shape=(5, 6))
((2, 2, 1), (2, 2, 2))
```

Cleans up lists to tuples

```
>>> normalize_chunks([[2, 2], [3, 3]])
((2, 2), (3, 3))
```

Expands integer inputs 10 -> (10, 10)

```
>>> normalize_chunks(10, shape=(30, 5))
((10, 10, 10), (5,))
```

Expands dict inputs

```
>>> normalize_chunks({0: 2, 1: 3}, shape=(6, 6))
((2, 2, 2), (3, 3))
```

The value -1 gets mapped to full size

```
>>> normalize_chunks((5, -1), shape=(10, 10))
((5, 5), (10,))
```

Use the value “auto” to automatically determine chunk sizes along certain dimensions. This uses the `limit=` and `dtype=` keywords to determine how large to make the chunks. The term “auto” can be used anywhere an integer can be used. See array chunking documentation for more information.

```
>>> normalize_chunks(("auto",), shape=(20,), limit=5, dtype='uint8')
((5, 5, 5, 5),)
```

Respects null dimensions

```
>>> normalize_chunks((), shape=(0, 0))
((0,), (0,))
```

dask.array.core.**top**(*func*, *output*, *out_indices*, **arrind_pairs*, ***kwargs*)

Tensor operation

Applies a function, `func`, across blocks from many different input dasks. We arrange the pattern with which those blocks interact with sets of matching indices. E.g.:

```
top(func, 'z', 'i', 'x', 'i', 'y', 'i')
```

yield an embarrassingly parallel communication pattern and is read as

$$ z_i = func(x_i, y_i) $$

More complex patterns may emerge, including multiple indices:

```
top(func, 'z', 'ij', 'x', 'ij', 'y', 'ji')

$$ z_{ij} = func(x_{ij}, y_{ji}) $$
```

Indices missing in the output but present in the inputs results in many inputs being sent to one function (see examples).

See also:

atop

Examples

Simple embarrassing map operation

```
>>> inc = lambda x: x + 1
>>> top(inc, 'z', 'ij', 'x', 'ij', numblocks={'x': (2, 2)})
{('z', 0, 0): (inc, ('x', 0, 0)),
 ('z', 0, 1): (inc, ('x', 0, 1)),
 ('z', 1, 0): (inc, ('x', 1, 0)),
 ('z', 1, 1): (inc, ('x', 1, 1))}
```

Simple operation on two datasets

```
>>> add = lambda x, y: x + y
>>> top(add, 'z', 'ij', 'x', 'ij', 'y', 'ij', numblocks={'x': (2, 2),
...                                                      'y': (2, 2)})
{('z', 0, 0): (add, ('x', 0, 0), ('y', 0, 0)),
 ('z', 0, 1): (add, ('x', 0, 1), ('y', 0, 1)),
 ('z', 1, 0): (add, ('x', 1, 0), ('y', 1, 0)),
 ('z', 1, 1): (add, ('x', 1, 1), ('y', 1, 1))}
```

Operation that flips one of the datasets

```
>>> addT = lambda x, y: x + y.T  # Transpose each chunk
>>> #                                        z_ij ~ x_ij y_ji
>>> #                 ..         ..         .. notice swap
>>> top(addT, 'z', 'ij', 'x', 'ij', 'y', 'ji', numblocks={'x': (2, 2),
...                                                       'y': (2, 2)})
{('z', 0, 0): (add, ('x', 0, 0), ('y', 0, 0)),
 ('z', 0, 1): (add, ('x', 0, 1), ('y', 1, 0)),
 ('z', 1, 0): (add, ('x', 1, 0), ('y', 0, 1)),
 ('z', 1, 1): (add, ('x', 1, 1), ('y', 1, 1))}
```

Dot product with contraction over `j` index. Yields list arguments

```
>>> top(dotmany, 'z', 'ik', 'x', 'ij', 'y', 'jk', numblocks={'x': (2, 2),
...                                                         'y': (2, 2)})
{('z', 0, 0): (dotmany, [('x', 0, 0), ('x', 0, 1)],
                        [('y', 0, 0), ('y', 1, 0)]),
 ('z', 0, 1): (dotmany, [('x', 0, 0), ('x', 0, 1)],
                        [('y', 0, 1), ('y', 1, 1)]),
 ('z', 1, 0): (dotmany, [('x', 1, 0), ('x', 1, 1)],
                        [('y', 0, 0), ('y', 1, 0)]),
 ('z', 1, 1): (dotmany, [('x', 1, 0), ('x', 1, 1)],
                        [('y', 0, 1), ('y', 1, 1)])}
```

Pass `concatenate=True` to concatenate arrays ahead of time

```
>>> top(f, 'z', 'i', 'x', 'ij', 'y', 'ij', concatenate=True,
...     numblocks={'x': (2, 2), 'y': (2, 2,)})
{('z', 0): (f, (concatenate_axes, [('x', 0, 0), ('x', 0, 1)], (1,)),
               (concatenate_axes, [('y', 0, 0), ('y', 0, 1)], (1,)))
 ('z', 1): (f, (concatenate_axes, [('x', 1, 0), ('x', 1, 1)], (1,)),
               (concatenate_axes, [('y', 1, 0), ('y', 1, 1)], (1,)))}
```

Supports Broadcasting rules

```
>>> top(add, 'z', 'ij', 'x', 'ij', 'y', 'ij', numblocks={'x': (1, 2),
...                                                      'y': (2, 2)})
{('z', 0, 0): (add, ('x', 0, 0), ('y', 0, 0)),
 ('z', 0, 1): (add, ('x', 0, 1), ('y', 0, 1)),
 ('z', 1, 0): (add, ('x', 0, 0), ('y', 1, 0)),
 ('z', 1, 1): (add, ('x', 0, 1), ('y', 1, 1))}
```

Support keyword arguments with apply

```
>>> def f(a, b=0): return a + b
>>> top(f, 'z', 'i', 'x', 'i', numblocks={'x': (2,)}, b=10)
{('z', 0): (apply, f, [('x', 0)], {'b': 10}),
 ('z', 1): (apply, f, [('x', 1)], {'b': 10})}
```

Include literals by indexing with `None`

```
>>> top(add, 'z', 'i', 'x', 'i', 100, None,  numblocks={'x': (2,)})
{('z', 0): (add, ('x', 0), 100),
 ('z', 1): (add, ('x', 1), 100)}
```

Array Methods

class dask.array.**Array**
Parallel Dask Array

A parallel nd-array comprised of many numpy arrays arranged in a grid.

This constructor is for advanced uses only. For normal use see the `da.from_array` function.

Parameters

dask [dict] Task dependency graph

name [string] Name of array in dask

shape [tuple of ints] Shape of the entire array

chunks: iterable of tuples block sizes along each dimension

See also:

dask.array.from_array

all(*axis=None*, *out=None*, *keepdims=False*)
Returns True if all elements evaluate to True.

Refer to *numpy.all* for full documentation.

See also:

numpy.all equivalent function

any(*axis=None*, *out=None*, *keepdims=False*)
Returns True if any of the elements of *a* evaluate to True.

Refer to *numpy.any* for full documentation.

See also:

numpy.any equivalent function

argmax(*axis=None*, *out=None*)
Return indices of the maximum values along the given axis.

Refer to *numpy.argmax* for full documentation.

See also:

numpy.argmax equivalent function

argmin(*axis=None*, *out=None*)
Return indices of the minimum values along the given axis of *a*.

Refer to *numpy.argmin* for detailed documentation.

See also:

numpy.argmin equivalent function

argtopk(*k*, *axis=-1*, *split_every=None*)
The indices of the top k elements of an array.

See `da.argtopk` for docstring

astype(*dtype*, ***kwargs*)
Copy of the array, cast to a specified type.

Parameters

dtype [str or dtype] Typecode or data-type to which the array is cast.

casting [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to 'unsafe' for backwards compatibility.

- 'no' means the data types should not be cast at all.
- 'equiv' means only byte-order changes are allowed.
- 'safe' means only casts which can preserve values are allowed.
- **'same_kind' means only safe casts or casts within a kind,** like float64 to float32, are allowed.
- 'unsafe' means any data conversions may be done.

copy [bool, optional] By default, astype always returns a newly allocated array. If this is set to False and the *dtype* requirement is satisfied, the input array is returned instead of a copy.

blocks
Slice an array by blocks

This allows blockwise slicing of a Dask array. You can perform normal Numpy-style slicing but now rather than slice elements of the array you slice along blocks so, for example, `x.blocks[0, ::2]` produces a new dask array with every other block in the first row of blocks.

You can index blocks in any way that could index a numpy array of shape equal to the number of blocks in each dimension, (available as array.numblocks). The dimension of the output array will be the same as the dimension of this array, even if integer indices are passed. This does not support slicing with `np.newaxis` or multiple lists.

Returns

A Dask array

Examples

```
>>> import dask.array as da
>>> x = da.arange(10, chunks=2)
>>> x.blocks[0].compute()
array([0, 1])
>>> x.blocks[:3].compute()
array([0, 1, 2, 3, 4, 5])
>>> x.blocks[::2].compute()
array([0, 1, 4, 5, 8, 9])
>>> x.blocks[[-1, 0]].compute()
array([8, 9, 0, 1])
```

choose(*choices*, *out=None*, *mode='raise'*)
Use an index array to construct a new array from a set of choices.

Refer to *numpy.choose* for full documentation.

See also:

numpy.choose equivalent function

clip(*min=None*, *max=None*, *out=None*)
Return an array whose values are limited to `[min, max]`. One of max or min must be given.

Refer to *numpy.clip* for full documentation.

See also:

numpy.clip equivalent function

copy()
Copy array. This is a no-op for dask.arrays, which are immutable

cumprod(*axis*, *dtype=None*, *out=None*)
See da.cumprod for docstring

cumsum(*axis*, *dtype=None*, *out=None*)
See da.cumsum for docstring

dot(*b*, *out=None*)
Dot product of two arrays.

Refer to *numpy.dot* for full documentation.

See also:

numpy.dot equivalent function

Examples

```
>>> a = np.eye(2)
>>> b = np.ones((2, 2)) * 2
>>> a.dot(b)
array([[ 2.,  2.],
       [ 2.,  2.]])
```

This array method can be conveniently chained:

```
>>> a.dot(b).dot(b)
array([[ 8.,  8.],
       [ 8.,  8.]])
```

flatten([*order*])
Return a flattened array.

Refer to *numpy.ravel* for full documentation.

See also:

numpy.ravel equivalent function

ndarray.flat a flat iterator on the array.

itemsize
Length of one array element in bytes

map_blocks(**args*, ***kwargs*)
Map a function across all blocks of a dask array.

Parameters

func [callable] Function to apply to every block in the array.

args [dask arrays or other objects]

dtype [np.dtype, optional] The `dtype` of the output array. It is recommended to provide this. If not provided, will be inferred by applying the function to a small set of fake data.

chunks [tuple, optional] Chunk shape of resulting blocks if the function does not preserve shape. If not provided, the resulting array is assumed to have the same block structure as the first input array.

drop_axis [number or iterable, optional] Dimensions lost by the function.

new_axis [number or iterable, optional] New dimensions created by the function. Note that these are applied after `drop_axis` (if present).

token [string, optional] The key prefix to use for the output array. If not provided, will be determined from the function name.

name [string, optional] The key name to use for the output array. Note that this fully specifies the output key name, and must be unique. If not provided, will be determined by a hash of the arguments.

****kwargs :** Other keyword arguments to pass to function. Values must be constants (not dask.arrays)

Examples

```
>>> import dask.array as da
>>> x = da.arange(6, chunks=3)
```

```
>>> x.map_blocks(lambda x: x * 2).compute()
array([ 0,  2,  4,  6,  8, 10])
```

The `da.map_blocks` function can also accept multiple arrays.

```
>>> d = da.arange(5, chunks=2)
>>> e = da.arange(5, chunks=2)
```

```
>>> f = map_blocks(lambda a, b: a + b**2, d, e)
>>> f.compute()
array([ 0,  2,  6, 12, 20])
```

If the function changes shape of the blocks then you must provide chunks explicitly.

```
>>> y = x.map_blocks(lambda x: x[::2], chunks=((2, 2),))
```

You have a bit of freedom in specifying chunks. If all of the output chunk sizes are the same, you can provide just that chunk size as a single tuple.

```
>>> a = da.arange(18, chunks=(6,))
>>> b = a.map_blocks(lambda x: x[:3], chunks=(3,))
```

If the function changes the dimension of the blocks you must specify the created or destroyed dimensions.

```
>>> b = a.map_blocks(lambda x: x[None, :, None], chunks=(1, 6, 1),
...                  new_axis=[0, 2])
```

Map_blocks aligns blocks by block positions without regard to shape. In the following example we have two arrays with the same number of blocks but with different shape and chunk sizes.

```
>>> x = da.arange(1000, chunks=(100,))
>>> y = da.arange(100, chunks=(10,))
```

The relevant attribute to match is numblocks.

```
>>> x.numblocks
(10,)
>>> y.numblocks
(10,)
```

If these match (up to broadcasting rules) then we can map arbitrary functions across blocks

```
>>> def func(a, b):
...     return np.array([a.max(), b.max()])
```

```
>>> da.map_blocks(func, x, y, chunks=(2,), dtype='i8')
dask.array<func, shape=(20,), dtype=int64, chunksize=(2,)>
```

```
>>> _.compute()
array([ 99,   9, 199,  19, 299,  29, 399,  39, 499,  49, 599,  59, 699,
        69, 799,  79, 899,  89, 999,  99])
```

Your block function get information about where it is in the array by accepting a special `block_info` keyword argument.

```
>>> def func(block, block_info=None):
...     pass
```

This will receive the following information:

```
>>> block_info
{0: {'shape': (1000,),
     'num-chunks': (10,),
     'chunk-location': (4,),
     'array-location': [(400, 500)]}}
```

For each argument and keyword arguments that are dask arrays (the positions of which are the first index), you will receive the shape of the full array, the number of chunks of the full array in each dimension, the chunk location (for example the fourth chunk over in the first dimension), and the array location (for example the slice corresponding to `40:50`).

You may specify the key name prefix of the resulting task in the graph with the optional `token` keyword argument.

```
>>> x.map_blocks(lambda x: x + 1, name='increment')
dask.array<increment, shape=(100,), dtype=int64, chunksize=(10,)>
```

map_overlap (*func*, *depth*, *boundary=None*, *trim=True*, ***kwargs*)

Map a function over blocks of the array with some overlap

We share neighboring zones between blocks of the array, then map a function, then trim away the neighboring strips.

Parameters

func: function The function to apply to each extended block

depth: int, tuple, or dict The number of elements that each block should share with its neighbors If a tuple or dict then this can be different per axis

boundary: str, tuple, dict How to handle the boundaries. Values include 'reflect', 'periodic', 'nearest', 'none', or any constant value like 0 or np.nan

trim: bool Whether or not to trim `depth` elements from each block after calling the map function. Set this to False if your mapping function already does this for you

****kwargs:** Other keyword arguments valid in `map_blocks`

Examples

```
>>> x = np.array([1, 1, 2, 3, 3, 3, 2, 1, 1])
>>> x = from_array(x, chunks=5)
>>> def derivative(x):
...     return x - np.roll(x, 1)
```

```
>>> y = x.map_overlap(derivative, depth=1, boundary=0)
>>> y.compute()
array([ 1,  0,  1,  1,  0,  0, -1, -1,  0])
```

```
>>> import dask.array as da
>>> x = np.arange(16).reshape((4, 4))
>>> d = da.from_array(x, chunks=(2, 2))
>>> d.map_overlap(lambda x: x + x.size, depth=1).compute()
array([[16, 17, 18, 19],
       [20, 21, 22, 23],
       [24, 25, 26, 27],
       [28, 29, 30, 31]])
```

```
>>> func = lambda x: x + x.size
>>> depth = {0: 1, 1: 1}
>>> boundary = {0: 'reflect', 1: 'none'}
>>> d.map_overlap(func, depth, boundary).compute()
array([[12,  13,  14,  15],
       [16,  17,  18,  19],
       [20,  21,  22,  23],
       [24,  25,  26,  27]])
```

max(*axis=None*, *out=None*)
Return the maximum along a given axis.

Refer to *numpy.amax* for full documentation.

See also:

numpy.amax equivalent function

mean(*axis=None*, *dtype=None*, *out=None*, *keepdims=False*)
Returns the average of the array elements along given axis.

Refer to *numpy.mean* for full documentation.

See also:

numpy.mean equivalent function

min(*axis=None*, *out=None*, *keepdims=False*)
Return the minimum along a given axis.

Refer to *numpy.amin* for full documentation.

See also:

numpy.amin equivalent function

moment(*order*, *axis=None*, *dtype=None*, *keepdims=False*, *ddof=0*, *split_every=None*, *out=None*)
Calculate the nth centralized moment.

Parameters

order [int] Order of the moment that is returned, must be >= 2.

axis [int, optional] Axis along which the central moment is computed. The default is to compute the moment of the flattened array.

dtype [data-type, optional] Type to use in computing the moment. For arrays of integer type the default is float64; for arrays of float types it is the same as the array type.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original array.

ddof [int, optional] "Delta Degrees of Freedom": the divisor used in the calculation is N - ddof, where N represents the number of elements. By default ddof is zero.

Returns

moment [ndarray]

References

Computation of Covariances and Arbitrary-Order Statistical Moments" (PDF), Technical Report SAND2008-6212, Sandia National Laboratories

[1]

nbytes
Number of bytes in array

nonzero()
Return the indices of the elements that are non-zero.

Refer to *numpy.nonzero* for full documentation.

See also:

numpy.nonzero equivalent function

prod(*axis=None*, *dtype=None*, *out=None*, *keepdims=False*)
Return the product of the array elements over the given axis

Refer to *numpy.prod* for full documentation.

See also:

numpy.prod equivalent function

ravel([*order*])
Return a flattened array.

Refer to *numpy.ravel* for full documentation.

See also:

numpy.ravel equivalent function

ndarray.flat a flat iterator on the array.

rechunk(*chunks*, *threshold=None*, *block_size_limit=None*)
See da.rechunk for docstring

repeat(*repeats*, *axis=None*)
Repeat elements of an array.

Refer to *numpy.repeat* for full documentation.

See also:

numpy.repeat equivalent function

reshape(*shape*, *order='C'*)
Returns an array containing the same data with a new shape.

Refer to *numpy.reshape* for full documentation.

See also:

numpy.reshape equivalent function

round(*decimals=0*, *out=None*)
Return *a* with each element rounded to the given number of decimals.

Refer to *numpy.around* for full documentation.

See also:

numpy.around equivalent function

size
Number of elements in array

squeeze(*axis=None*)
Remove single-dimensional entries from the shape of *a*.

Refer to *numpy.squeeze* for full documentation.

See also:

numpy.squeeze equivalent function

std(*axis=None*, *dtype=None*, *out=None*, *ddof=0*, *keepdims=False*)
Returns the standard deviation of the array elements along given axis.

Refer to *numpy.std* for full documentation.

See also:

numpy.std equivalent function

store(*targets*, *lock=True*, *regions=None*, *compute=True*, *return_stored=False*, ***kwargs*)
Store dask arrays in array-like objects, overwrite data in target

This stores dask arrays into object that supports numpy-style setitem indexing. It stores values chunk by chunk so that it does not have to fill up memory. For best performance you can align the block size of the storage target with the block size of your array.

If your data fits in memory then you may prefer calling `np.array(myarray)` instead.

Parameters

sources: Array or iterable of Arrays

targets: array-like or Delayed or iterable of array-likes and/or Delayeds These should support setitem syntax `target[10:20] = ...`

lock: boolean or threading.Lock, optional Whether or not to lock the data stores while storing. Pass True (lock each file individually), False (don't lock) or a particular `threading.Lock` object to be shared among all writes.

regions: tuple of slices or iterable of tuple of slices Each `region` tuple in `regions` should be such that `target[region].shape = source.shape` for the corresponding source and target in sources and targets, respectively.

compute: boolean, optional If true compute immediately, return `dask.delayed.Delayed` otherwise

return_stored: boolean, optional Optionally return the stored result (default False).

Examples

```
>>> x = ...
```

```
>>> import h5py
>>> f = h5py.File('myfile.hdf5')
>>> dset = f.create_dataset('/data', shape=x.shape,
...                                  chunks=x.chunks,
...                                  dtype='f8')
```

```
>>> store(x, dset)
```

Alternatively store many arrays at the same time

```
>>> store([x, y, z], [dset1, dset2, dset3])
```

sum(*axis=None*, *dtype=None*, *out=None*, *keepdims=False*)
Return the sum of the array elements over the given axis.

Refer to *numpy.sum* for full documentation.

See also:

numpy.sum equivalent function

swapaxes(*axis1*, *axis2*)
Return a view of the array with *axis1* and *axis2* interchanged.

Refer to *numpy.swapaxes* for full documentation.

See also:

`numpy.swapaxes` equivalent function

to_dask_dataframe(*columns=None*)
Convert dask Array to dask Dataframe

Parameters

columns: list or string list of column names if DataFrame, single string if Series

See also:

dask.dataframe.from_dask_array

to_delayed(*optimize_graph=True*)
Convert into an array of `dask.delayed` objects, one per chunk.

Parameters

optimize_graph [bool, optional] If True [default], the graph is optimized before converting into `dask.delayed` objects.

See also:

dask.array.from_delayed

to_hdf5(*filename*, *datapath*, ***kwargs*)
Store array in HDF5 file

```
>>> x.to_hdf5('myfile.hdf5', '/x')
```

Optionally provide arguments as though to `h5py.File.create_dataset`

```
>>> x.to_hdf5('myfile.hdf5', '/x', compression='lzf', shuffle=True)
```

See also:

`da.store`, `h5py.File.create_dataset`

to_zarr(**args*, ***kwargs*)
Save array to the zarr storage format

See https://zarr.readthedocs.io for details about the format.

See function `to_zarr()` for parameters.

topk(*k*, *axis=-1*, *split_every=None*)
The top k elements of an array.

See `da.topk` for docstring

transpose(**axes*)
Returns a view of the array with axes transposed.

For a 1-D array, this has no effect. (To change between column and row vectors, first cast the 1-D array into a matrix object.) For a 2-D array, this is the usual matrix transpose. For an n-D array, if axes are given, their order indicates how the axes are permuted (see Examples). If axes are not provided and `a.shape = (i[0], i[1], ... i[n-2], i[n-1])`, then `a.transpose().shape = (i[n-1], i[n-2], ... i[1], i[0])`.

Parameters

axes [None, tuple of ints, or *n* ints]

- None or no argument: reverses the order of the axes.

- tuple of ints: *i* in the *j*-th place in the tuple means *a*'s *i*-th axis becomes *a.transpose()*'s *j*-th axis.
- *n* ints: same as an n-tuple of the same ints (this form is intended simply as a "convenience" alternative to the tuple form)

Returns

out [ndarray] View of *a*, with axes suitably permuted.

See also:

ndarray.T Array property returning the array transposed.

Examples

```
>>> a = np.array([[1, 2], [3, 4]])
>>> a
array([[1, 2],
       [3, 4]])
>>> a.transpose()
array([[1, 3],
       [2, 4]])
>>> a.transpose((1, 0))
array([[1, 3],
       [2, 4]])
>>> a.transpose(1, 0)
array([[1, 3],
       [2, 4]])
```

var(*axis=None*, *dtype=None*, *out=None*, *ddof=0*, *keepdims=False*)

Returns the variance of the array elements, along given axis.

Refer to *numpy.var* for full documentation.

See also:

numpy.var equivalent function

view(*dtype*, *order='C'*)

Get a view of the array as a new data type

Parameters

dtype: The dtype by which to view the array

order: string 'C' or 'F' (Fortran) ordering

This reinterprets the bytes of the array under a new dtype. If that dtype does not have the same size as the original array then the shape will change.

Beware that both numpy and dask.array can behave oddly when taking shape-changing views of arrays under Fortran ordering. Under some versions of NumPy this function will fail when taking shape-changing views of Fortran ordered arrays if the first dimension has chunks of

size one.

vindex

Vectorized indexing with broadcasting.

This is equivalent to numpy's advanced indexing, using arrays that are broadcast against each other. This allows for pointwise indexing:

```
>>> x = np.array([[1, 2, 3], [4, 5, 6], [7, 8, 9]])
>>> x = from_array(x, chunks=2)
>>> x.vindex[[0, 1, 2], [0, 1, 2]].compute()
array([1, 5, 9])
```

Mixed basic/advanced indexing with slices/arrays is also supported. The order of dimensions in the result follows those proposed for ndarray.vindex [1]_: the subspace spanned by arrays is followed by all slices.

Note: `vindex` provides more general functionality than standard indexing, but it also has fewer optimizations and can be significantly slower.

_[1]: https://github.com/numpy/numpy/pull/6256

4.7.2 Chunks

Dask arrays are composed of many Numpy arrays. How these arrays are arranged can significantly affect performance. For example for a square array you might arrange your chunks along rows, along columns, or in a more square-like fashion. Different arrangements of Numpy arrays will be faster or slower for different algorithms.

Thinking about and controlling chunking is important to optimize advanced algorithms.

Specifying Chunk shapes

We always specify a `chunks` argument to tell dask.array how to break up the underlying array into chunks. We can specify `chunks` in a variety of ways

1. A uniform dimension size like `1000`, meaning chunks of size `1000` in each dimension
2. A uniform chunk shape like `(1000, 2000, 3000)`, meaning chunks of size `1000` in the first axis, `2000` in the second axis, and `3000` in the third.
3. Fully explicit sizes of all blocks along all dimensions, like `((1000, 1000, 500), (400, 400), (5, 5, 5, 5, 5))`
4. A dictionary specifying chunk size per dimension like `{0: 1000, 1: 2000, 2: 3000}`. This is just another way of writing the forms 2 and 3 above.

Your chunks input will be normalized and stored in the third and most explicit form. Note that `chunks` stands for "chunk shape" rather than "number of chunks" so specifying `chunks=1` means that you will have very many chunks, each with exactly one element.

For performance, a good choice of `chunks` follows the following rules:

1. A chunk should be small enough to fit comfortably in memory. We'll have many chunks in memory at once.
2. A chunk must be large enough so that computations on that chunk take significantly longer than the 1ms overhead per task that dask scheduling incurs. A task should take longer than 100ms.
3. Chunk sizes between 10MB-1GB are common, depending on the availability of RAM and the duration of computations

4. Chunks should align with the computation that you want to do.

   For example if you plan to frequently slice along a particular dimension then it's more efficient if your chunks are aligned so that you have to touch fewer chunks. If you want to add two arrays then its convenient if those arrays have matching chunks patterns.

5. Chunks should align with your storage, if applicable

   Array data formats are often chunked as well. When loading or saving data if it useful to have dask array chunks that are aligned with the chunking of your storage, often an even multiple times larger in each direction.

Unknown Chunks

Some arrays have unknown chunk sizes. This arises whenever the size of an array depends on lazy computations that we haven't yet performed like the following:

```
x = x[x > 100]  # don't know how many values are greater than 100 ahead of time
```

Operations like the above result in arrays with unknown shapes and also unknown chunk sizes. Unknown values within shape or chunks are designated using `np.nan` rather than an integer. These arrays support many but not all operations. In particular, operations like slicing are not possible and will result in an error.

```
>>> x.shape
(np.nan, np.nan)

>>> x[100]
ValueError: Array chunk sizes unknown
```

Chunks Examples

We show of how different inputs for `chunks=` cut up the following array:

```
1 2 3 4 5 6
7 8 9 0 1 2
3 4 5 6 7 8
9 0 1 2 3 4
5 6 7 8 9 0
1 2 3 4 5 6
```

We show how different `chunks=` arguments split the array into different blocks

chunks=3: Symmetric blocks of size 3:

```
1 2 3  4 5 6
7 8 9  0 1 2
3 4 5  6 7 8

9 0 1  2 3 4
5 6 7  8 9 0
1 2 3  4 5 6
```

chunks=2: Symmetric blocks of size 2:

```
1 2  3 4  5 6
7 8  9 0  1 2
```

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```
3 4  5 6  7 8
9 0  1 2  3 4

5 6  7 8  9 0
1 2  3 4  5 6
```

chunks=(3, 2): Asymmetric but repeated blocks of size `(3, 2)`:

```
1 2  3 4  5 6
7 8  9 0  1 2
3 4  5 6  7 8

9 0  1 2  3 4
5 6  7 8  9 0
1 2  3 4  5 6
```

chunks=(1, 6): Asymmetric but repeated blocks of size `(1, 6)`:

```
1 2 3 4 5 6

7 8 9 0 1 2

3 4 5 6 7 8

9 0 1 2 3 4

5 6 7 8 9 0

1 2 3 4 5 6
```

chunks=((2, 4), (3, 3)): Asymmetric and non-repeated blocks:

```
1 2 3  4 5 6
7 8 9  0 1 2

3 4 5  6 7 8
9 0 1  2 3 4
5 6 7  8 9 0
1 2 3  4 5 6
```

chunks=((2, 2, 1, 1), (3, 2, 1)): Asymmetric and non-repeated blocks:

```
1 2 3  4 5  6
7 8 9  0 1  2

3 4 5  6 7  8
9 0 1  2 3  4

5 6 7  8 9  0

1 2 3  4 5  6
```

Discussion

The latter examples are rarely provided by users on original data but arise from complex slicing and broadcasting operations. Generally people use the simplest form until they need more complex forms. The choice of chunks should align with the computations you want to do.

For example, if you plan to take out thin slices along the first dimension then you might want to make that dimension skinnier than the others. If you plan to do linear algebra then you might want more symmetric blocks.

Loading Chunked Data

Modern NDArray storage formats like HDF5, NetCDF, TIFF, and Zarr, allow arrays to be stored in chunks or tiles, so that blocks of data can be pulled out efficiently without having to seek through a linear data stream. It is best to align the chunks of your Dask array with the chunks of your underlying data store.

However, data stores often chunk more finely than is ideal for Dask array, so it is common to choose a chunking that is a multiple of your storage chunk size, otherwise you might incur high overhead.

For example if you are loading a data store that is chunked in blocks of `(100, 100)` then you might choose a chunking more like `(1000, 2000)` that is larger, but still evenly divisible by `(100, 100)`. Data storage technologies will be able to tell you how their data is chunked.

Rechunking

rechunk(x, chunks[, threshold, block_size_limit])	Convert blocks in dask array x for new chunks.

Sometimes you need to change the chunking layout of your data. For example perhaps it comes to you chunked row-wise, but you need to do an operation that is much faster if done across columns. You can change the chunking with the `rechunk` method.

```
x = x.rechunk((50, 1000))
```

Rechunking across axes can be expensive and incur a lot of communication, but Dask array has fairly efficient algorithms to accomplish this.

You can pass rechunk any valid chunking form:

```
x = x.rechunk(1000)
x = x.rechunk((50, 1000))
x = x.rechunk({0: 50, 1: 1000})
```

Automatic Chunking

Chunks also includes three special values:

1. `-1`: no chunking along this dimension
2. `None`: no change to the chunking along this dimension (useful for rechunk)
3. `"auto"`: allow the chunking in this dimension to accomodate ideal chunk sizes.

So for example one could rechunk a 3D array to have no chunking along the zeroth dimension, but still have sensible chunk sizes as follows:

```
x = x.rechunk({0: -1, 1: 'auto', 2: 'auto'})
```

Or one can allow *all* dimensions to be auto-scaled to get to a good chunk size:

```
x = x.rechunk('auto')
```

Automatic chunking expands or contracts all dimensions marked with `"auto"` to try to reach chunk sizes with a number of bytes equal to the config value `array.chunk-size`, which is set to 128MiB by default, but which you can change in your *configuration*.

```
>>> dask.config.get('array.chunk-size')
'128MiB'
```

Automatic rechunking tries to respect the median chunk shape of the auto-rescaled dimensions, but will modify this to accomodate the shape of the full array (can't have larger chunks than the array itself) and to find chunk shapes that nicely divide the shape.

These values can also be used when creating arrays with operations like `da.ones` or `da.from_array`

```
>>> da.ones((10000, 10000), chunks=(-1, 'auto'))
dask.array<wrapped, shape=(10000, 10000), dtype=float64, chunksize=(10000, 1250)>
```

4.7.3 Create Dask Arrays

You can load or store dask arrays from a variety of common sources like HDF5, and NetCDF, Zarr, or any format that supports Numpy-style slicing.

from_array(x, chunks[, name, lock, asarray, ...])	Create dask array from something that looks like an array
from_delayed(value, shape, dtype[, name])	Create a dask array from a dask delayed value
from_npy_stack(dirname[, mmap_mode])	Load dask array from stack of npy files
from_zarr(url[, component, storage_options, ...])	Load array from the zarr storage format
stack(seq[, axis])	Stack arrays along a new axis
concatenate(seq[, axis, ...])	Concatenate arrays along an existing axis

NumPy Slicing

from_array(x, chunks[, name, lock, asarray, ...])	Create dask array from something that looks like an array

Many storage formats have Python projects that expose storage using NumPy slicing syntax. These include HDF5, NetCDF, BColz, Zarr, GRIB, etc.. For example we can load a Dask array from an HDF5 file using h5py:

```
>>> import h5py
>>> f = h5py.File('myfile.hdf5') # HDF5 file
>>> d = f['/data/path']          # Pointer on on-disk array
>>> d.shape                      # d can be very large
(1000000, 1000000)

>>> x = d[:5, :5]                # We slice to get numpy arrays
```

Given an object like `d` above that has `dtype` and `shape` properties and that supports Numpy style slicing we can construct a lazy Dask array.

```
>>> import dask.array as da
>>> x = da.from_array(d, chunks=(1000, 1000))
```

This process is entirely lazy. Neither creating the h5py object nor wrapping it with `da.from_array` have loaded

any data.

Concatenation and Stacking

stack(seq[, axis])	Stack arrays along a new axis
concatenate(seq[, axis, ...])	Concatenate arrays along an existing axis

Often we store data in several different locations and want to stitch them together.

```
dask_arrays = []
for fn in filenames:
    f = h5py.File(fn)
    d = f['/data']
    array = da.from_array(d, chunks=(1000, 1000))
    dask_arrays.append(array)

x = da.concatenate(dask_arrays, axis=0)  # concatenate arrays along first axis
```

For more information see *concatenation and stacking* docs.

Using `dask.delayed`

from_delayed(value, shape, dtype[, name])	Create a dask array from a dask delayed value
stack(seq[, axis])	Stack arrays along a new axis
concatenate(seq[, axis, ...])	Concatenate arrays along an existing axis

Sometimes Numpy-style data resides in formats that do not support numpy-style slicing. We can still construct Dask arrays around this data if we have a Python function that can generate pieces of the full array if we use *dask.delayed*. Dask delayed lets us delay a single function call that would create a numpy array. We can then wrap this delayed object with `da.from_delayed`, providing a dtype and shape to produce a single-chunked Dask array. We can then use `stack` or `concatenate` from before to construct a larger lazy array.

As an example, consider loading a stack of images using `skimage.io.imread`:

```
import skimage.io
import dask.array as da
import dask

imread = dask.delayed(skimage.io.imread, pure=True)  # Lazy version of imread

filenames = sorted(glob.glob('*.jpg'))

lazy_images = [imread(path) for path in filenames]     # Lazily evaluate imread on␣
↪each path
sample = lazy_images[0].compute() # load the first image (assume rest are same shape/
↪dtype)

arrays = [da.from_delayed(lazy_image,           # Construct a small Dask array
                          dtype=sample.dtype,   # for every lazy value
                          shape=sample.shape)
          for lazy_image in lazy_images]

stack = da.stack(arrays, axis=0)                # Stack all small Dask arrays into one
```

See *documentation on using dask.delayed with collections*.

From Dask.dataframe

You can create dask arrays from dask dataframes using the `.values` attribute or the `.to_records()` method.

```
>>> x = df.values
>>> x = df.to_records()
```

However these arrays do not have known chunk sizes (dask.dataframe does not track the number of rows in each partition) and so some operations like slicing will not operate correctly.

If you have a function that converts a Pandas dataframe into a Numpy array then calling `map_partitions` with that function on a Dask dataframe will produce a Dask array.

```
>>> x = df.map_partitions(np.asarray)
```

Interactions with NumPy arrays

Dask.array operations will automatically convert NumPy arrays into single-chunk dask arrays

```
>>> x = da.sum(np.ones(5))
>>> x.compute()
5
```

When NumPy and Dask arrays interact the result will be a Dask array. Automatic rechunking rules will generally slice the NumPy array into the appropriate Dask chunk shape

```
>>> x = da.ones(10, chunks=(5,))
>>> y = np.ones(10)
>>> z = x + y
>>> z
dask.array<add, shape=(10,), dtype=float64, chunksize=(5,)>
```

These interactions work not just for NumPy arrays, but for any object that has shape and dtype attributes and implements NumPy slicing syntax.

Chunks

See *documentation on Array Chunks* for more information.

4.7.4 Store Dask Arrays

store(sources, targets[, lock, regions, ...])	Store dask arrays in array-like objects, overwrite data in target
to_hdf5(filename, *args, **kwargs)	Store arrays in HDF5 file
to_npy_stack(dirname, x[, axis])	Write dask array to a stack of .npy files
to_zarr(arr, url[, component, ...])	Save array to the zarr storage format
compute(*args, **kwargs)	Compute several dask collections at once.

In Memory

compute(*args, **kwargs)	Compute several dask collections at once.

If you have a small amount of data, you can call `np.array` or `.compute()` on your Dask array to turn in to a normal NumPy array:

```
>>> x = da.arange(6, chunks=3)
>>> y = x**2
>>> np.array(y)
array([0, 1, 4, 9, 16, 25])

>>> y.compute()
array([0, 1, 4, 9, 16, 25])
```

Numpy style slicing

store(sources, targets[, lock, regions, ...])	Store dask arrays in array-like objects, overwrite data in target

You can store dask arrays in any object that supports numpy-style slice assignment like `h5py.Dataset`:

```
>>> import h5py
>>> f = h5py.File('myfile.hdf5')
>>> d = f.require_dataset('/data', shape=x.shape, dtype=x.dtype)
>>> da.store(x, d)
```

You can store several arrays in one computation by passing lists of sources and destinations:

```
>>> da.store([array1, array2], [output1, output2])  # doctest: +SKIP
```

HDF5

to_hdf5(filename, *args, **kwargs)	Store arrays in HDF5 file

HDF5 is sufficiently common that there is a special function, `to_hdf5` to store data into HDF5 files using `h5py`:

```
>>> da.to_hdf5('myfile.hdf5', '/y', y)  # doctest: +SKIP
```

Store several arrays in one computation with the function `da.to_hdf5` by passing in a dict:

```
>>> da.to_hdf5('myfile.hdf5', {'/x': x, '/y': y})  # doctest: +SKIP
```

Zarr

The Zarr format is a chunk-wise binary array storage file format, with a good selection of encoding and compression options. Due to each chunk being stored in a separate file, it is ideal for parallel access in both reading and writing (for the latter, if the dask array chunks are alligned with the target). Furthermore, storage in *remote data services* such as S3 and GCS is supported.

For example, to save data to a local zarr dataset:

```
>>> arr.to_zarr('output.zarr')
```

or to save to a particular bucket on S3:

```
>>> arr.to_zarr('s3://mybucket/output.zarr', storage_option={'key': 'mykey',
                'secret': 'mysecret'})
```

or your own custom zarr Array:

```
>>> z = zarr.create((10,), dtype=float, store=zarr.ZipStore("output.zarr"))
>>> arr.to_zarr(z)
```

To retrieve those data, you would do `da.read_zarr` with exactly the same arguments. The chunking of the resultant dask.Array is defined by how the files were saved, unless otherwise specified.

4.7.5 Plugins

We can run arbitrary user-defined functions on dask.arrays whenever they are constructed. This allows us to build a variety of custom behaviors that improve debugging, user warning, etc.. You can register a list of functions to run on all dask.arrays to the global `array_plugins=` value:

```
>>> def f(x):
...     print(x.nbytes)

>>> with dask.config.set(array_plugins=[f]):
...     x = da.ones((10, 1), chunks=(5, 1))
...     y = x.dot(x.T)
80
80
800
800
```

If the plugin function returns None then the input Dask.array will be returned without change. If the plugin function returns something else then that value will be the result of the constructor.

Examples

Automatically compute

We may wish to turn some Dask.array code into normal NumPy code. This is useful for example to track down errors immediately that would otherwise be hidden by Dask's lazy semantics.

```
>>> with dask.config.set(array_plugins=[lambda x: x.compute()]):
...     x = da.arange(5, chunks=2)

>>> x  # this was automatically converted into a numpy array
array([0, 1, 2, 3, 4])
```

Warn on large chunks

We may wish to warn users if they are creating chunks that are too large

```
def warn_on_large_chunks(x):
    shapes = list(itertools.product(*x.chunks))
    nbytes = [x.dtype.itemsize * np.prod(shape) for shape in shapes]
    if any(nb > 1e9 for nb in nbytes):
        warnings.warn("Array contains very large chunks")

with dask.config.set(array_plugins=[warn_on_large_chunks]):
    ...
```

Combine

You can also combine these plugins into a list. They will run one after the other, chaining results through them.

```
with dask.config.set(array_plugins=[warn_on_large_chunks, lambda x: x.compute()]):
    ...
```

4.7.6 Overlapping Computations

Some array operations require communication of borders between neighboring blocks. Example operations include the following:

- Convolve a filter across an image
- Sliding sum/mean/max, ...
- Search for image motifs like a Gaussian blob that might span the border of a block
- Evaluate a partial derivative
- Play the game of Life

Dask array supports these operations by creating a new array where each block is slightly expanded by the borders of its neighbors. This costs an excess copy and the communication of many small chunks but allows localized functions to evaluate in an embarrassingly parallel manner.

The main API for these computations is the `map_overlap` method defined below:

map_overlap(x, func, depth[, boundary, trim])	Map a function over blocks of the array with some overlap

dask.array.**map_overlap**(*x*, *func*, *depth*, *boundary=None*, *trim=True*, ***kwargs*)

Map a function over blocks of the array with some overlap

We share neighboring zones between blocks of the array, then map a function, then trim away the neighboring strips.

Parameters

func: function The function to apply to each extended block

depth: int, tuple, or dict The number of elements that each block should share with its neighbors If a tuple or dict then this can be different per axis

boundary: str, tuple, dict How to handle the boundaries. Values include 'reflect', 'periodic', 'nearest', 'none', or any constant value like 0 or np.nan

trim: bool Whether or not to trim `depth` elements from each block after calling the map

function. Set this to False if your mapping function already does this for you

****kwargs:** Other keyword arguments valid in `map_blocks`

Examples

```
>>> import numpy as np
>>> import dask.array as da
```

```
>>> x = np.array([1, 1, 2, 3, 3, 3, 2, 1, 1])
>>> x = da.from_array(x, chunks=5)
>>> def derivative(x):
...     return x - np.roll(x, 1)
```

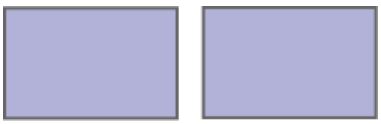
```
>>> y = x.map_overlap(derivative, depth=1, boundary=0)
>>> y.compute()
array([ 1,  0,  1,  1,  0,  0, -1, -1,  0])
```

```
>>> x = np.arange(16).reshape((4, 4))
>>> d = da.from_array(x, chunks=(2, 2))
>>> d.map_overlap(lambda x: x + x.size, depth=1).compute()
array([[16, 17, 18, 19],
       [20, 21, 22, 23],
       [24, 25, 26, 27],
       [28, 29, 30, 31]])
```

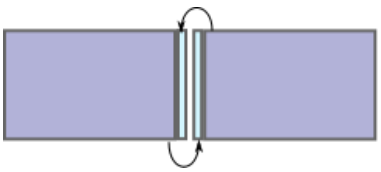
```
>>> func = lambda x: x + x.size
>>> depth = {0: 1, 1: 1}
>>> boundary = {0: 'reflect', 1: 'none'}
>>> d.map_overlap(func, depth, boundary).compute()
array([[12,  13,  14,  15],
       [16,  17,  18,  19],
       [20,  21,  22,  23],
       [24,  25,  26,  27]])
```

Explanation

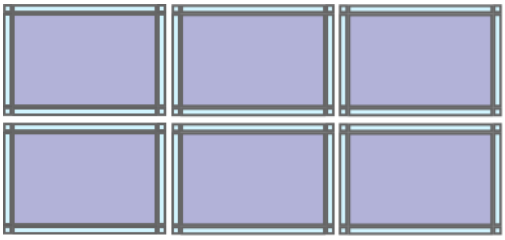
Consider two neighboring blocks in a Dask array.



We extend each block by trading thin nearby slices between arrays



We do this in all directions, including also diagonal interactions with the overlap function:



```
>>> import dask.array as da
>>> import numpy as np

>>> x = np.arange(64).reshape((8, 8))
>>> d = da.from_array(x, chunks=(4, 4))
>>> d.chunks
((4, 4), (4, 4))

>>> g = da.overlap.overlap(d, depth={0: 2, 1: 1},
...                        boundary={0: 100, 1: 'reflect'})
>>> g.chunks
((8, 8), (6, 6))

>>> np.array(g)
array([[100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100],
       [100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100],
       [  0,   0,   1,   2,   3,   4,   3,   4,   5,   6,   7,   7],
       [  8,   8,   9,  10,  11,  12,  11,  12,  13,  14,  15,  15],
       [ 16,  16,  17,  18,  19,  20,  19,  20,  21,  22,  23,  23],
       [ 24,  24,  25,  26,  27,  28,  27,  28,  29,  30,  31,  31],
       [ 32,  32,  33,  34,  35,  36,  35,  36,  37,  38,  39,  39],
       [ 40,  40,  41,  42,  43,  44,  43,  44,  45,  46,  47,  47],
       [ 16,  16,  17,  18,  19,  20,  19,  20,  21,  22,  23,  23],
       [ 24,  24,  25,  26,  27,  28,  27,  28,  29,  30,  31,  31],
       [ 32,  32,  33,  34,  35,  36,  35,  36,  37,  38,  39,  39],
       [ 40,  40,  41,  42,  43,  44,  43,  44,  45,  46,  47,  47],
       [ 48,  48,  49,  50,  51,  52,  51,  52,  53,  54,  55,  55],
       [ 56,  56,  57,  58,  59,  60,  59,  60,  61,  62,  63,  63],
       [100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100],
       [100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100]])
```

Boundaries

With respect to overlaping you can specify how to handle the boundaries. Current policies include the following:

- `periodic` - wrap borders around to the other side
- `reflect` - reflect each border outwards
- `any-constant` - pad the border with this value

So an example boundary kind argument might look like the following

```
{0: 'periodic',
 1: 'reflect',
 2: np.nan}
```

Alternatively, you can use *`dask.array.pad()`* for other types of paddings.

Map a function across blocks

Overlapping goes hand-in-hand with mapping a function across blocks. This function can now use the additional information copied over from the neighbors that is not stored locally in each block

```
>>> from scipy.ndimage.filters import gaussian_filter
>>> def func(block):
...     return gaussian_filter(block, sigma=1)

>>> filt = g.map_blocks(func)
```

While in this case we used a SciPy function, any arbitrary function could have been used instead. This is a good interaction point with Numba.

If your function does not preserve the shape of the block then you will need to provide a `chunks` keyword argument. If your block size is regular, then this argument can take a block shape of, for example, `(1000, 1000)`. In case of irregular block sizes, it must be a tuple with the full chunks shape like `((1000, 700, 1000), (200, 300))`.

```
>>> g.map_blocks(myfunc, chunks=(5, 5))
```

If your function needs to know the location of the block on which it operates, you can give your function a keyword argument `block_id`

```
def func(block, block_id=None):
    ...
```

This extra keyword argument will be given a tuple that provides the block location like `(0, 0)` for the upper right block or `(0, 1)` for the block just to the right of that block.

Trim Excess

After mapping a blocked function, you may want to trim off the borders from each block by the same amount by which they were expanded. The function `trim_internal` is useful here and takes the same `depth` argument given to `overlap`.

```
>>> x.chunks
((10, 10, 10, 10), (10, 10, 10, 10))

>>> y = da.overlap.trim_internal(x, {0: 2, 1: 1})
>>> y.chunks
((6, 6, 6, 6), (8, 8, 8, 8))
```

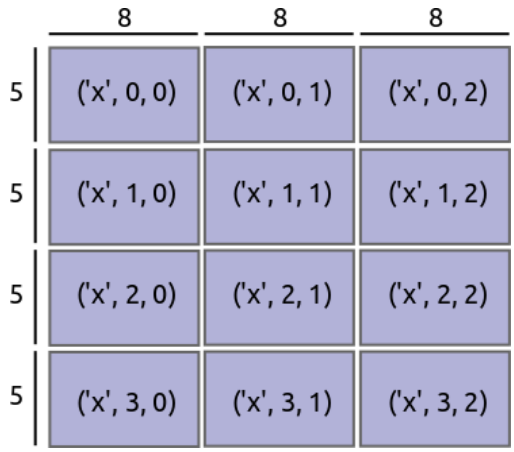
Full Workflow

And so, a pretty typical overlaping workflow includes `overlap`, `map_blocks` and `trim_internal`

```
>>> x = ...
>>> g = da.overlap.overlap(x, depth={0: 2, 1: 2},
...                        boundary={0: 'periodic', 1: 'periodic'})
>>> g2 = g.map_blocks(myfunc)
>>> result = da.overlap.trim_internal(g2, {0: 2, 1: 2})
```

4.7.7 Internal Design

Overview



Dask arrays define a large array with a grid of blocks of smaller arrays. These arrays may be concrete, or functions that produce arrays. We define a Dask array with the following components

- A Dask graph with a special set of keys designating blocks such as `('x', 0, 0), ('x', 0, 1), ...` (See *Dask graph documentation* for more details.)
- A sequence of chunk sizes along each dimension called `chunks`, for example `((5, 5, 5, 5), (8, 8, 8))`
- A name to identify which keys in the dask graph refer to this array, like `'x'`
- A NumPy dtype

Example

```
>>> import dask.array as da
>>> x = da.arange(0, 15, chunks=(5,))

>>> x.name
'arange-539766a'

>>> x.dask  # somewhat simplified
{('arange-539766a', 0): (np.arange, 0, 5),
 ('arange-539766a', 1): (np.arange, 5, 10),
 ('arange-539766a', 2): (np.arange, 10, 15)}

>>> x.chunks
((5, 5, 5),)

>>> x.dtype
dtype('int64')
```

Keys of the Dask graph

By special convention we refer to each block of the array with a tuple of the form `(name, i, j, k)` for `i, j, k` being the indices of the block, ranging from `0` to the number of blocks in that dimension. The dask graph must hold

key-value pairs referring to these keys. It likely also holds other key-value pairs required to eventually compute the desired values, for example

```
{
 ('x', 0, 0): (add, 1, ('y', 0, 0)),
 ('x', 0, 1): (add, 1, ('y', 0, 1)),
 ...
 ('y', 0, 0): (getitem, dataset, (slice(0, 1000), slice(0, 1000))),
 ('y', 0, 1): (getitem, dataset, (slice(0, 1000), slice(1000, 2000)))
 ...
}
```

The name of an `Array` object can be found in the `name` attribute. One can get a nested list of keys with the `.__dask_keys__()` method. One can flatten down this list with `dask.array.core.flatten()`; this is sometimes useful when building new dictionaries.

Chunks

We also store the size of each block along each axis. This is a tuple of tuples such that the length of the outer tuple is equal to the dimension and the lengths of the inner tuples are equal to the number of blocks along each dimension. In the example illustrated above this value is as follows:

```
chunks = ((5, 5, 5, 5), (8, 8, 8))
```

Note that these numbers do not necessarily need to be regular. We often create regularly sized grids but blocks change shape after complex slicing. Beware that some operations do expect certain symmetries in the block-shapes. For example matrix multiplication requires that blocks on each side have anti-symmetric shapes.

Some ways in which `chunks` reflects properties of our array

1. `len(x.chunks) == x.ndim`: The length of chunks is the number of dimensions
2. `tuple(map(sum, x.chunks)) == x.shape`: The sum of each internal chunk, is the length of that dimension.
3. The length of each internal chunk is the number of keys in that dimension. For instance, for `chunks == ((a, b), (d, e, f))` and name == `'x'` our array has tasks with the following keys:

   ```
   ('x', 0, 0), ('x', 0, 1), ('x', 0, 2)
   ('x', 1, 0), ('x', 1, 1), ('x', 1, 2)
   ```

Create an Array Object

So to create an `da.Array` object we need a dictionary with these special keys

```
dsk = {('x', 0, 0): ...}
```

a name specifying to which keys this array refers

```
name = 'x'
```

and a chunks tuple:

```
chunks = ((5, 5, 5, 5), (8, 8, 8))
```

Then one can construct an array:

```
x = da.Array(dsk, name, chunks)
```

So `dask.array` operations update dask graphs, update dtypes, and track chunk shapes.

Example - `eye` function

As an example lets build the `np.eye` function for `dask.array` to make the identity matrix

```
def eye(n, blocksize):
    chunks = ((blocksize,) * (n // blocksize),
              (blocksize,) * (n // blocksize))

    name = 'eye' + next(tokens)  # unique identifier

    dsk = {(name, i, j): (np.eye, blocksize)
                         if i == j else
                         (np.zeros, (blocksize, blocksize))
           for i in range(n // blocksize)
           for j in range(n // blocksize)}

    dtype = np.eye(0).dtype  # take dtype default from numpy

    return dask.array.Array(dsk, name, chunks, dtype)
```

4.7.8 Sparse Arrays

By swapping out in-memory numpy arrays with in-memory sparse arrays we can reuse the blocked algorithms of Dask.array to achieve parallel and distributed sparse arrays.

The blocked algorithms in Dask.array normally parallelize around in-memory numpy arrays. However, if another in-memory array library supports the NumPy interface then it too can take advantage of dask.array's parallel algorithms. In particular the sparse array library satisfies a subset of the NumPy API and works well with, and is tested against, Dask.array.

Example

Say we have a dask.array with mostly zeros

```
x = da.random.random((100000, 100000), chunks=(1000, 1000))
x[x < 0.95] = 0
```

We can convert each of these chunks of NumPy arrays into a sparse.COO array.

```
import sparse
s = x.map_blocks(sparse.COO)
```

Now our array is composed not of many NumPy arrays, but rather of many sparse arrays. Semantically this does not change anything. Operations that work will work identically (assuming that the behavior of `numpy` and `sparse` are identical) but performance characteristics and storage costs may change significantly

```
>>> s.sum(axis=0)[:100].compute()
<COO: shape=(100,), dtype=float64, nnz=100>
```

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```
>>> _.todense()
array([ 4803.06859272,  4913.94964525,  4877.13266438,  4860.7470773 ,
        4938.94446802,  4849.51326473,  4858.83977856,  4847.81468485,
        ... ])
```

Requirements

Any in-memory library that copies the NumPy ndarray interface should work here. The sparse library is a minimal example. In particular an in-memory library should implement at least the following operations:

1. Simple slicing with slices, lists, and elements (for slicing, rechunking, reshaping, etc).
2. A `concatenate` function matching the interface of `np.concatenate`. This must be registered in `dask.array.core.concatenate_lookup`.
3. All ufuncs must support the full ufunc interface, including `dtype=` and `out=` parameters (even if they don't function properly)
4. All reductions must support the full `axis=` and `keepdims=` keywords and behave like numpy in this respect
5. The array class should follow the `__array_priority__` protocol and be prepared to respond to other arrays of lower priority.
6. If `dot` support is desired, a `tensordot` function matching the interface of `np.tensordot` should be registered in `dask.array.core.tensordot_lookup`.

The implementation of other operations like reshape, transpose, etc. should follow standard NumPy conventions regarding shape and dtype. Not implementing these is fine; the parallel `dask.array` will err at runtime if these operations are attempted.

Mixed Arrays

Dask.array supports mixing different kinds of in-memory arrays. This relies on the in-memory arrays knowing how to interact with each other when necessary. When two arrays interact the functions from the array with the highest `__array_priority__` will take precedence (for example for concatenate, tensordot, etc.).

4.7.9 Stats

Dask Array implements a subset of the scipy.stats package.

Statistical Functions

You can calculate various measures of an array including skewnes, kurtosis, and arbitrary moments.

```
>>> from dask.array import stats
>>> x = da.random.beta(1, 1, size=(1000,), chunks=10)
>>> k, s, m = [stats.kurtosis(x), stats.skew(x), stats.moment(x, 5)]
>>> dask.compute(k, s, m)
(1.7612340817172787, -0.064073498030693302, -0.00054523780628304799)
```

Statistical Tests

You can perform basic statistical tests on dask arrays. Each of these tests return a `dask.delayed` wrapping one of the scipy `namedtuple` results.

```
>>> a = da.random.uniform(size=(50,), chunks=(25,))
>>> b = a + da.random.uniform(low=-0.15, high=0.15, size=(50,), chunks=(25,))
>>> result = ttest_rel(a, b)
>>> result.compute()
Ttest_relResult(statistic=-1.5102104380013242, pvalue=0.13741197274874514)
```

4.7.10 LinearOperator

Dask arrays implement the SciPy LinearOperator interface and so can be used with any SciPy algorithm depending on that interface.

Example

```
import dask.array as da
x = da.random.random(size=(10000, 10000), chunks=(1000, 1000))

from scipy.sparse.linalg.interface import MatrixLinearOperator
A = MatrixLinearOperator(x)

import numpy as np
b = np.random.random(10000)

from scipy.sparse.linalg import gmres
x = gmres(A, b)
```

Disclaimer: This is just a toy example and not necessarily the best way to solve this problem for this data.

4.7.11 Slicing

Dask array supports most of the NumPy slicing syntax. In particular it supports the following:

- Slicing by integers and slices `x[0, :5]`
- Slicing by lists/arrays of integers `x[[1, 2, 4]]`
- Slicing by lists/arrays of booleans `x[[False, True, True, False, True]]`
- Slicing one *Array* with a *Array* of bools `x[x > 0]`
- Slicing one *Array* with a zero or one-dimensional *Array* of ints `a[b.argtopk(5)]`

It does not currently support the following:

- Slicing with lists in multiple axes `x[[1, 2, 3], [3, 2, 1]]`

  This is straightforward to add though. If you have a use case then raise an issue. Also users interested in this should take a look at *vindex*.

- Slicing one *Array* with a multi-dimensional *Array* of ints

Efficiency

The normal dask schedulers are smart enough to compute only those blocks that are necessary to achieve the desired slicing. So large operations may be cheap if only a small output is desired.

In the example below we create a trillion element Dask array in million element blocks. We then operate on the entire array and finally slice out only a portion of the output.

```
>>> Trillion element array of ones, in 1000 by 1000 blocks
>>> x = da.ones((1000000, 1000000), chunks=(1000, 1000))

>>> da.exp(x)[:1500, :1500]
...
```

This only needs to compute the top-left four blocks to achieve the result. We are still slightly wasteful on those blocks where we need only partial results. We are also a bit wasteful in that we still need to manipulate the dask-graph with a million or so tasks in it. This can cause an interactive overhead of a second or two.

But generally, slicing works well.

4.7.12 Stack, Concatenate, and Block

Often we have many arrays stored on disk that we want to stack together and think of as one large array. This is common with geospatial data in which we might have many HDF5/NetCDF files on disk, one for every day, but we want to do operations that span multiple days.

To solve this problem we use the functions `da.stack`, `da.concatenate`, and `da.block`.

Stack

We stack many existing Dask arrays into a new array, creating a new dimension as we go.

```
>>> import dask.array as da

>>> arr0 = da.from_array(np.zeros((3, 4)), chunks=(1, 2))
>>> arr1 = da.from_array(np.ones((3, 4)), chunks=(1, 2))

>>> data = [arr0, arr1]

>>> x = da.stack(data, axis=0)
>>> x.shape
(2, 3, 4)

>>> da.stack(data, axis=1).shape
(3, 2, 4)

>>> da.stack(data, axis=-1).shape
(3, 4, 2)
```

This creates a new dimension with length equal to the number of slices

Concatenate

We concatenate existing arrays into a new array, extending them along an existing dimension

```
>>> import dask.array as da
>>> import numpy as np

>>> arr0 = da.from_array(np.zeros((3, 4)), chunks=(1, 2))
>>> arr1 = da.from_array(np.ones((3, 4)), chunks=(1, 2))

>>> data = [arr0, arr1]

>>> x = da.concatenate(data, axis=0)
>>> x.shape
(6, 4)

>>> da.concatenate(data, axis=1).shape
(3, 8)
```

Block

We can handle a larger variety of cases with `da.block` as it allows concatenation to be applied over multiple dimensions at once. This is useful if your chunks tile a space, for example if small squares tile a larger 2-D plane.

```
>>> import dask.array as da
>>> import numpy as np

>>> arr0 = da.from_array(np.zeros((3, 4)), chunks=(1, 2))
>>> arr1 = da.from_array(np.ones((3, 4)), chunks=(1, 2))

>>> data = [
...     [arr0, arr1],
...     [arr1, arr0]
... ]

>>> x = da.block(data)
>>> x.shape
(6, 8)
```

4.7.13 Generalized Ufuncs

EXPERIMENTAL FEATURE added to Version 0.18.0 and above - see *disclaimer*.

numpy provides the concept of generalized ufuncs. Generalized ufuncs are functions that distinguish the various dimensions of passed arrays in the two classes loop dimensions and core dimensions. To accomplish this, a signature is specified for numpy generalized ufuncs.

dask integrates interoperability with numpy's generalized ufuncs by adhering to respective ufunc protocol, as well as provides a wrapper to make a Python function a generalized ufunc.

Usage

NumPy generalized ufunc

Note: numpy generalized ufuncs are currently (v1.14.3 and below) stored in inside `np.linalg._umath_linalg` and might change in the future.

```
import dask.array as da
import numpy as np

x = da.random.normal(size=(3, 10, 10), chunks=(2, 10, 10))

w, v = np.linalg._umath_linalg.eig(x, output_dtypes=(float, float))
```

Wrap own Python function

`gufunc` can be used to make a Python function behave like a generalized ufunc:

```
x = da.random.normal(size=(10, 5), chunks=(2, 5))

def foo(x):
    return np.mean(x, axis=-1)

gufoo = da.gufunc(foo, signature="(i)->()", output_dtypes=float, vectorize=True)

y = gufoo(x)
```

Instead of `gufunc`, also the `as_gufunc` decorator can be used for convenience:

```
x = da.random.normal(size=(10, 5), chunks=(2, 5))

@da.as_gufunc(signature="(i)->()", output_dtypes=float, vectorize=True)
def gufoo(x):
    return np.mean(x, axis=-1)

y = gufoo(x)
```

Disclaimer

This experimental generalized ufunc integration is not complete:

- `gufunc` does not create a true generalized ufunc to be used with other input arrays, but dask. I.e. at the moment `gufunc` casts all input arguments to `dask.array.Array`.
- Inferring `output_dtypes` automatically is not implemented yet.

API

apply_gufunc(func, signature, *args, **kwargs)	Apply a generalized ufunc or similar python function to arrays.
as_gufunc([signature])	Decorator for `dask.array.gufunc`.
gufunc(pyfunc, **kwargs)	Binds *pyfunc* into `dask.array.apply_gufunc` when called.

Dask Array implements a subset of the NumPy ndarray interface using blocked algorithms, cutting up the large array into many small arrays. This lets us compute on arrays larger than memory using all of our cores. We coordinate these blocked algorithms using dask graphs.

4.7.14 Design

Dask arrays coordinate many NumPy arrays arranged into a grid. These NumPy arrays may live on disk or on other machines.

4.7.15 Common Uses

Dask array used in fields like atmospheric and oceanographic science, large scale imaging, genomics, numerical algorithms for optimization or statistics , and more.

4.7.16 Scope

Dask arrays supports most of the Numpy interface like the following:

- Arithmetic and scalar mathematics, `+, *, exp, log, ...`
- Reductions along axes, `sum(), mean(), std(), sum(axis=0), ...`
- Tensor contractions / dot products / matrix multiply, `tensordot`
- Axis reordering / transpose, `transpose`
- Slicing, `x[:100, 500:100:-2]`
- Fancy indexing along single axes with lists or numpy arrays, `x[:, [10, 1, 5]]`
- Array protocols like `__array__`, and `__array_ufunc__`
- Some linear algebra `svd, qr, solve, solve_triangular, lstsq`
- ...

However Dask array does not implement the entire numpy interface. Users expecting this will be disappointed. Notably, Dask array lacks the following features:

- Much of `np.linalg` has not been implemented. This has been done by a number of excellent BLAS/LAPACK implementations, and is the focus of numerous ongoing academic research projects.
- Arrays with unknown shapes do not support all operations
- Operations like `sort` which are notoriously difficult to do in parallel, and are of somewhat diminished value on very large data (you rarely actually need a full sort). Often we include parallel-friendly alternatives like `topk`.
- Dask array doesn't implement operations like `tolist` that would be very inefficient for larger datasets. Likewise it is very inefficient to iterate over a Dask array with for loops.
- Dask development is driven by immediate need, and so many lesser used functions have not been implemented. Community contributions are encouraged.

See *the dask.array API* for a more extensive list of functionality.

4.7.17 Execution

By default Dask array uses the threaded scheduler in order to avoid data transfer costs and because NumPy releases the GIL well. It is also quite effective on a cluster using the dask.distributed scheduler.

4.8 Bag

Dask.Bag parallelizes computations across a large collection of generic Python objects. It is particularly useful when dealing with large quantities of semi-structured data like JSON blobs or log files.

4.8.1 Overview

Dask.Bag implements operations like `map`, `filter`, `fold`, and `groupby` on collections of Python objects. It does this in parallel and in small memory using Python iterators. It is similar to a parallel version of PyToolz or a Pythonic version of the PySpark RDD.

Design

Dask bags coordinate many Python lists or Iterators, each of which forms a partition of a larger collection.

Common Uses

Dask bags are often used to parallelize simple computations on unstructured or semi-structured data like text data, log files, JSON records, or user defined Python objects.

Execution

Execution on bags provide two benefits:

1. Parallel: data is split up, allowing multiple cores or machines to execute in parallel.
2. Iterating: data processes lazily, allowing smooth execution of larger-than-memory data, even on a single machine within a single partition

Default scheduler

By default `dask.bag` uses `dask.multiprocessing` for computation. As a benefit Dask bypasses the GIL and uses multiple cores on Pure Python objects. As a drawback Dask.bag doesn't perform well on computations that include a great deal of inter-worker communication. For common operations this is rarely an issue as most Dask.bag workflows are embarrassingly parallel or result in reductions with little data moving between workers.

Shuffle

Some operations, like `groupby`, require substantial inter-worker communication. On a single machine, dask uses partd to perform efficient, parallel, spill-to-disk shuffles. When working in a cluster, dask uses a task based shuffle.

These shuffle operations are expensive and better handled by projects like `dask.dataframe`. It is best to use `dask.bag` to clean and process data, then transform it into an array or dataframe before embarking on the more complex operations that require shuffle steps.

Known Limitations

Bags provide very general computation (any Python function.) This generality comes at cost. Bags have the following known limitations:

1. By default they rely on the multiprocessing scheduler, which has its own set of known limitations (see shared)
2. Bags are immutable and so you can not change individual elements
3. Bag operations tend to be slower than array/dataframe computations in the same way that standard Python containers tend to be slower than NumPy arrays and Pandas dataframes.
4. `Bag.groupby` is slow. You should try to use `Bag.foldby` if possible. Using `Bag.foldby` requires more thought.

Name

Bag is the mathematical name for an unordered collection allowing repeats. It is a friendly synonym to multiset. A bag or a multiset is a generalization of the concept of a set that, unlike a set, allows multiple instances of the multiset's elements.

- `list`: *ordered* collection *with repeats*, `[1, 2, 3, 2]`
- `set`: *unordered* collection *without repeats*, `{1, 2, 3}`
- `bag`: *unordered* collection *with repeats*, `{1, 2, 2, 3}`

So a bag is like a list, but it doesn't guarantee an ordering among elements. There can be repeated elements but you can't ask for the ith element.

4.8.2 Create Dask Bags

There are several ways to create Dask.bags around your data:

db.from_sequence

You can create a bag from an existing Python iterable:

```
>>> import dask.bag as db
>>> b = db.from_sequence([1, 2, 3, 4, 5, 6])
```

You can control the number of partitions into which this data is binned:

```
>>> b = db.from_sequence([1, 2, 3, 4, 5, 6], npartitions=2)
```

This controls the granularity of the parallelism that you expose. By default dask will try to partition your data into about 100 partitions.

IMPORTANT: do not load your data into Python and then load that data into dask.bag. Instead, use dask.bag to load your data. This parallelizes the loading step and reduces inter-worker communication:

```
>>> b = db.from_sequence(['1.dat', '2.dat', ...]).map(load_from_filename)
```

db.read_text

Dask.bag can load data directly from textfiles. You can pass either a single filename, a list of filenames, or a globstring. The resulting bag will have one item per line, one file per partition:

```
>>> b = db.read_text('myfile.txt')
>>> b = db.read_text(['myfile.1.txt', 'myfile.2.txt', ...])
>>> b = db.read_text('myfile.*.txt')
```

This handles standard compression libraries like `gzip`, `bz2`, `xz`, or any easily installed compression library that has a File-like object. Compression will be inferred by filename extension, or by using the `compression='gzip'` keyword:

```
>>> b = db.read_text('myfile.*.txt.gz')
```

The resulting items in the bag are strings. If you have encoded data like line-delimited JSON then you may want to map a decoding or load function across the bag:

```
>>> import json
>>> b = db.read_text('myfile.*.json').map(json.loads)
```

Or do string munging tasks. For convenience there is a string namespace attached directly to bags with `.str.methodname`:

```
>>> b = db.read_text('myfile.*.csv').str.strip().str.split(',')
```

db.from_delayed

You can construct a dask bag from *dask.delayed* values using the `db.from_delayed` function. See *documentation on using dask.delayed with collections* for more information.

4.8.3 Store Dask Bags

In Memory

You can convert a dask bag to a list or Python iterable by calling `compute()` or by converting the object into a list

```
>>> result = b.compute()
or
>>> result = list(b)
```

To Textfiles

You can convert a dask bag into a sequence of files on disk by calling the `.to_textfiles()` method

`dask.bag.core.`**`to_textfiles`**(*b*, *path*, *name_function=None*, *compression='infer'*, *encoding='utf-8'*, *compute=True*, *storage_options=None*, *last_endline=False*, ***kwargs*)

Write dask Bag to disk, one filename per partition, one line per element.

Paths: This will create one file for each partition in your bag. You can specify the filenames in a variety of ways.

Use a globstring

```
>>> b.to_textfiles('/path/to/data/*.json.gz')
```

The * will be replaced by the increasing sequence 1, 2, ...

```
/path/to/data/0.json.gz
/path/to/data/1.json.gz
```

Use a globstring and a `name_function=` keyword argument. The name_function function should expect an integer and produce a string. Strings produced by name_function must preserve the order of their respective partition indices.

```
>>> from datetime import date, timedelta
>>> def name(i):
...     return str(date(2015, 1, 1) + i * timedelta(days=1))
```

```
>>> name(0)
'2015-01-01'
>>> name(15)
'2015-01-16'
```

```
>>> b.to_textfiles('/path/to/data/*.json.gz', name_function=name)
```

```
/path/to/data/2015-01-01.json.gz
/path/to/data/2015-01-02.json.gz
...
```

You can also provide an explicit list of paths.

```
>>> paths = ['/path/to/data/alice.json.gz', '/path/to/data/bob.json.gz', ...]
>>> b.to_textfiles(paths)
```

Compression: Filenames with extensions corresponding to known compression algorithms (gz, bz2) will be compressed accordingly.

Bag Contents: The bag calling `to_textfiles` must be a bag of text strings. For example, a bag of dictionaries could be written to JSON text files by mapping `json.dumps` on to the bag first, and then calling `to_textfiles`:

```
>>> b_dict.map(json.dumps).to_textfiles("/path/to/data/*.json")
```

Last endline: By default the last line does not end with a newline character. Pass `last_endline=True` to invert the default.

To DataFrames

You can convert a dask bag into a *dask dataframe* and use those storage solutions.

`Bag.`**`to_dataframe`**(*meta=None*, *columns=None*)

Create Dask Dataframe from a Dask Bag.

Bag should contain tuples, dict records, or scalars.

Index will not be particularly meaningful. Use `reindex` afterwards if necessary.

Parameters

meta [pd.DataFrame, dict, iterable, optional] An empty `pd.DataFrame` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. If not provided or a list, a single element from the first partition will be computed, triggering a potentially expensive call to `compute`. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

columns [sequence, optional] Column names to use. If the passed data do not have names associated with them, this argument provides names for the columns. Otherwise this argument indicates the order of the columns in the result (any names not found in the data will become all-NA columns). Note that if `meta` is provided, column names will be taken from there and this parameter is invalid.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence([{'name': 'Alice',   'balance': 100},
...                       {'name': 'Bob',     'balance': 200},
...                       {'name': 'Charlie', 'balance': 300}],
...                      npartitions=2)
>>> df = b.to_dataframe()
```

```
>>> df.compute()
   balance     name
0      100    Alice
1      200      Bob
0      300  Charlie
```

To Delayed Values

You can convert a dask bag into a list of *dask delayed values* and custom storage solutions from there.

`Bag.`**`to_delayed`**`(`*optimize_graph=True*`)`

Convert into a list of `dask.delayed` objects, one per partition.

Parameters

optimize_graph [bool, optional] If True [default], the graph is optimized before converting into `dask.delayed` objects.

See also:

`dask.bag.from_delayed`

4.8.4 API

Top level user functions:

`Bag`(dsk, name, npartitions)	Parallel collection of Python objects
`Bag.all`([split_every])	Are all elements truthy?
`Bag.any`([split_every])	Are any of the elements truthy?

Continued on next page

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Bag.compute(**kwargs)	Compute this dask collection
Bag.count([split_every])	Count the number of elements.
Bag.distinct()	Distinct elements of collection
Bag.filter(predicate)	Filter elements in collection by a predicate function.
Bag.flatten()	Concatenate nested lists into one long list.
Bag.fold(binop[, combine, initial, split_every])	Parallelizable reduction
Bag.foldby(key, binop[, initial, combine, ...])	Combined reduction and groupby.
Bag.frequencies([split_every, sort])	Count number of occurrences of each distinct element.
Bag.groupby(grouper[, method, npartitions, ...])	Group collection by key function
Bag.join(other, on_self[, on_other])	Joins collection with another collection.
Bag.map(func, *args, **kwargs)	Apply a function elementwise across one or more bags.
Bag.map_partitions(func, *args, **kwargs)	Apply a function to every partition across one or more bags.
Bag.max([split_every])	Maximum element
Bag.mean()	Arithmetic mean
Bag.min([split_every])	Minimum element
Bag.pluck(key[, default])	Select item from all tuples/dicts in collection.
Bag.product(other)	Cartesian product between two bags.
Bag.reduction(perpartition, aggregate[, ...])	Reduce collection with reduction operators.
Bag.random_sample(prob[, random_state])	Return elements from bag with probability of prob.
Bag.remove(predicate)	Remove elements in collection that match predicate.
Bag.repartition(npartitions)	Coalesce bag into fewer partitions.
Bag.starmap(func, **kwargs)	Apply a function using argument tuples from the given bag.
Bag.std([ddof])	Standard deviation
Bag.sum([split_every])	Sum all elements
Bag.take(k[, npartitions, compute, warn])	Take the first k elements.
Bag.to_dataframe([meta, columns])	Create Dask Dataframe from a Dask Bag.
Bag.to_delayed([optimize_graph])	Convert into a list of dask.delayed objects, one per partition.
Bag.to_textfiles(path[, name_function, ...])	Write dask Bag to disk, one filename per partition, one line per element.
Bag.topk(k[, key, split_every])	K largest elements in collection
Bag.var([ddof])	Variance
Bag.visualize([filename, format, optimize_graph])	Render the computation of this object's task graph using graphviz.

Create Bags

from_sequence(seq[, partition_size, npartitions])	Create a dask Bag from Python sequence.
from_delayed(values)	Create bag from many dask Delayed objects.
read_text(urlpath[, blocksize, compression, ...])	Read lines from text files
from_url(urls)	Create a dask Bag from a url.
range(n, npartitions)	Numbers from zero to n

Top-level functions

concat(bags)	Concatenate many bags together, unioning all elements.

Continued on next page

Table 27 – continued from previous page

map(func, *args, **kwargs)	Apply a function elementwise across one or more bags.
map_partitions(func, *args, **kwargs)	Apply a function to every partition across one or more bags.
zip(*bags)	Partition-wise bag zip

Turn Bags into other things

Bag.to_textfiles(path[, name_function, ...])	Write dask Bag to disk, one filename per partition, one line per element.
Bag.to_dataframe([meta, columns])	Create Dask Dataframe from a Dask Bag.
Bag.to_delayed([optimize_graph])	Convert into a list of `dask.delayed` objects, one per partition.

Bag methods

class dask.bag.**Bag**(*dsk*, *name*, *npartitions*)

Parallel collection of Python objects

Examples

Create Bag from sequence

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(5))
>>> list(b.filter(lambda x: x % 2 == 0).map(lambda x: x * 10))
[0, 20, 40]
```

Create Bag from filename or globstring of filenames

```
>>> b = db.read_text('/path/to/mydata.*.json.gz').map(json.loads)
```

Create manually (expert use)

```
>>> dsk = {('x', 0): (range, 5),
...        ('x', 1): (range, 5),
...        ('x', 2): (range, 5)}
>>> b = Bag(dsk, 'x', npartitions=3)
```

```
>>> sorted(b.map(lambda x: x * 10))
[0, 0, 0, 10, 10, 10, 20, 20, 20, 30, 30, 30, 40, 40, 40]
```

```
>>> int(b.fold(lambda x, y: x + y))
30
```

accumulate(*binop*, *initial='__no__default__'*)

Repeatedly apply binary function to a sequence, accumulating results.

This assumes that the bag is ordered. While this is typically the case not all Dask.bag functions preserve this property.

Examples

```
>>> from operator import add
>>> b = from_sequence([1, 2, 3, 4, 5], npartitions=2)
>>> b.accumulate(add).compute()
[1, 3, 6, 10, 15]
```

Accumulate also takes an optional argument that will be used as the first value.

```
>>> b.accumulate(add, initial=-1)
[-1, 0, 2, 5, 9, 14]
```

all(*split_every=None*)
Are all elements truthy?

any(*split_every=None*)
Are any of the elements truthy?

count(*split_every=None*)
Count the number of elements.

distinct()
Distinct elements of collection

Unordered without repeats.

```
>>> b = from_sequence(['Alice', 'Bob', 'Alice'])
>>> sorted(b.distinct())
['Alice', 'Bob']
```

filter(*predicate*)
Filter elements in collection by a predicate function.

```
>>> def iseven(x):
...     return x % 2 == 0
```

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(5))
>>> list(b.filter(iseven))
[0, 2, 4]
```

flatten()
Concatenate nested lists into one long list.

```
>>> b = from_sequence([[1], [2, 3]])
>>> list(b)
[[1], [2, 3]]
```

```
>>> list(b.flatten())
[1, 2, 3]
```

fold(*binop*, *combine=None*, *initial='__no__default__'*, *split_every=None*)
Parallelizable reduction

Fold is like the builtin function `reduce` except that it works in parallel. Fold takes two binary operator functions, one to reduce each partition of our dataset and another to combine results between partitions

1. `binop`: Binary operator to reduce within each partition

2. `combine`: Binary operator to combine results from binop

Sequentially this would look like the following:

```
>>> intermediates = [reduce(binop, part) for part in partitions]
>>> final = reduce(combine, intermediates)
```

If only one function is given then it is used for both functions `binop` and `combine` as in the following example to compute the sum:

```
>>> def add(x, y):
...     return x + y
```

```
>>> b = from_sequence(range(5))
>>> b.fold(add).compute()
10
```

In full form we provide both binary operators as well as their default arguments

```
>>> b.fold(binop=add, combine=add, initial=0).compute()
10
```

More complex binary operators are also doable

```
>>> def add_to_set(acc, x):
...     ''' Add new element x to set acc '''
...     return acc | set([x])
>>> b.fold(add_to_set, set.union, initial=set()).compute()
{1, 2, 3, 4, 5}
```

See also:

Bag.foldby

foldby(*key*, *binop*, *initial='__no__default__'*, *combine=None*, *combine_initial='__no__default__'*, *split_every=None*)

Combined reduction and groupby.

Foldby provides a combined groupby and reduce for efficient parallel split-apply-combine tasks.

The computation

```
>>> b.foldby(key, binop, init)
```

is equivalent to the following:

```
>>> def reduction(group):
...     return reduce(binop, group, init)
```

```
>>> b.groupby(key).map(lambda (k, v): (k, reduction(v)))
```

But uses minimal communication and so is *much* faster.

```
>>> b = from_sequence(range(10))
>>> iseven = lambda x: x % 2 == 0
>>> add = lambda x, y: x + y
>>> dict(b.foldby(iseven, add))
{True: 20, False: 25}
```

Key Function

The key function determines how to group the elements in your bag. In the common case where your bag holds dictionaries then the key function often gets out one of those elements.

```
>>> def key(x):
...     return x['name']
```

This case is so common that it is special cased, and if you provide a key that is not a callable function then dask.bag will turn it into one automatically. The following are equivalent:

```
>>> b.foldby(lambda x: x['name'], ...)
>>> b.foldby('name', ...)
```

Binops

It can be tricky to construct the right binary operators to perform analytic queries. The `foldby` method accepts two binary operators, `binop` and `combine`. Binary operators two inputs and output must have the same type.

Binop takes a running total and a new element and produces a new total:

```
>>> def binop(total, x):
...     return total + x['amount']
```

Combine takes two totals and combines them:

```
>>> def combine(total1, total2):
...     return total1 + total2
```

Each of these binary operators may have a default first value for total, before any other value is seen. For addition binary operators like above this is often `0` or the identity element for your operation.

split_every

Group partitions into groups of this size while performing reduction. Defaults to 8.

```
>>> b.foldby('name', binop, 0, combine, 0)
```

See also:

`toolz.reduceby`, `pyspark.combineByKey`

frequencies(*split_every=None*, *sort=False*)
Count number of occurrences of each distinct element.

```
>>> b = from_sequence(['Alice', 'Bob', 'Alice'])
>>> dict(b.frequencies())
{'Alice': 2, 'Bob', 1}
```

groupby(*grouper*, *method=None*, *npartitions=None*, *blocksize=1048576*, *max_branch=None*, *shuffle=None*)
Group collection by key function

This requires a full dataset read, serialization and shuffle. This is expensive. If possible you should use `foldby`.

Parameters

grouper: function Function on which to group elements

shuffle: str Either 'disk' for an on-disk shuffle or 'tasks' to use the task scheduling framework. Use 'disk' if you are on a single machine and 'tasks' if you are on a distributed cluster.

npartitions: int If using the disk-based shuffle, the number of output partitions

blocksize: int If using the disk-based shuffle, the size of shuffle blocks (bytes)

max_branch: int If using the task-based shuffle, the amount of splitting each partition undergoes. Increase this for fewer copies but more scheduler overhead.

See also:

Bag.foldby

Examples

```
>>> b = from_sequence(range(10))
>>> iseven = lambda x: x % 2 == 0
>>> dict(b.groupby(iseven))
{True: [0, 2, 4, 6, 8], False: [1, 3, 5, 7, 9]}
```

join(*other*, *on_self*, *on_other=None*)

Joins collection with another collection.

Other collection must be one of the following:

1. An iterable. We recommend tuples over lists for internal performance reasons.
2. A delayed object, pointing to a tuple. This is recommended if the other collection is sizable and you're using the distributed scheduler. Dask is able to pass around data wrapped in delayed objects with greater sophistication.
3. A Bag with a single partition

You might also consider Dask Dataframe, whose join operations are much more heavily optimized.

Parameters

other: Iterable, Delayed, Bag Other collection on which to join

on_self: callable Function to call on elements in this collection to determine a match

on_other: callable (defaults to on_self) Function to call on elements in the other collection to determine a match

Examples

```
>>> people = from_sequence(['Alice', 'Bob', 'Charlie'])
>>> fruit = ['Apple', 'Apricot', 'Banana']
>>> list(people.join(fruit, lambda x: x[0]))
[('Apple', 'Alice'), ('Apricot', 'Alice'), ('Banana', 'Bob')]
```

map(*func*, **args*, ***kwargs*)

Apply a function elementwise across one or more bags.

Note that all `Bag` arguments must be partitioned identically.

Parameters

func [callable]

***args, **kwargs** [Bag, Item, or object] Extra arguments and keyword arguments to pass to `func` *after* the calling bag instance. Non-Bag args/kwargs are broadcasted across all calls to `func`.

Notes

For calls with multiple *Bag* arguments, corresponding partitions should have the same length; if they do not, the call will error at compute time.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(5), npartitions=2)
>>> b2 = db.from_sequence(range(5, 10), npartitions=2)
```

Apply a function to all elements in a bag:

```
>>> b.map(lambda x: x + 1).compute()
[1, 2, 3, 4, 5]
```

Apply a function with arguments from multiple bags:

```
>>> from operator import add
>>> b.map(add, b2).compute()
[5, 7, 9, 11, 13]
```

Non-bag arguments are broadcast across all calls to the mapped function:

```
>>> b.map(add, 1).compute()
[1, 2, 3, 4, 5]
```

Keyword arguments are also supported, and have the same semantics as regular arguments:

```
>>> def myadd(x, y=0):
...     return x + y
>>> b.map(myadd, y=b2).compute()
[5, 7, 9, 11, 13]
>>> b.map(myadd, y=1).compute()
[1, 2, 3, 4, 5]
```

Both arguments and keyword arguments can also be instances of `dask.bag.Item`. Here we'll add the max value in the bag to each element:

```
>>> b.map(myadd, b.max()).compute()
[4, 5, 6, 7, 8]
```

map_partitions (*func*, **args*, ***kwargs*)

Apply a function to every partition across one or more bags.

Note that all `Bag` arguments must be partitioned identically.

Parameters

func [callable] The function to be called on every partition. This function should expect an `Iterator` or `Iterable` for every partition and should return an `Iterator` or `Iterable` in return.

***args, **kwargs** [Bag, Item, Delayed, or object] Arguments and keyword arguments to pass to `func`. Partitions from this bag will be the first argument, and these will be passed *after*.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(1, 101), npartitions=10)
>>> def div(nums, den=1):
...     return [num / den for num in nums]
```

Using a python object:

```
>>> hi = b.max().compute()
>>> hi
100
>>> b.map_partitions(div, den=hi).take(5)
(0.01, 0.02, 0.03, 0.04, 0.05)
```

Using an `Item`:

```
>>> b.map_partitions(div, den=b.max()).take(5)
(0.01, 0.02, 0.03, 0.04, 0.05)
```

Note that while both versions give the same output, the second forms a single graph, and then computes everything at once, and in some cases may be more efficient.

max(*split_every=None*)
Maximum element

mean()
Arithmetic mean

min(*split_every=None*)
Minimum element

pluck(*key*, *default='__no__default__'*)
Select item from all tuples/dicts in collection.

```
>>> b = from_sequence([{'name': 'Alice', 'credits': [1, 2, 3]},
...                    {'name': 'Bob',   'credits': [10, 20]}])
>>> list(b.pluck('name'))
['Alice', 'Bob']
>>> list(b.pluck('credits').pluck(0))
[1, 10]
```

product(*other*)
Cartesian product between two bags.

random_sample(*prob*, *random_state=None*)
Return elements from bag with probability of `prob`.

Parameters

prob [float] A float between 0 and 1, representing the probability that each element will be returned.

random_state [int or random.Random, optional] If an integer, will be used to seed a new `random.Random` object. If provided, results in deterministic sampling.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(5))
>>> list(b.random_sample(0.5, 42))
[1, 3]
>>> list(b.random_sample(0.5, 42))
[1, 3]
```

reduction(*perpartition*, *aggregate*, *split_every=None*, *out_type=<class 'dask.bag.core.Item'>*, *name=None*)

Reduce collection with reduction operators.

Parameters

perpartition: function reduction to apply to each partition

aggregate: function reduction to apply to the results of all partitions

split_every: int (optional) Group partitions into groups of this size while performing reduction Defaults to 8

out_type: {Bag, Item} The out type of the result, Item if a single element, Bag if a list of elements. Defaults to Item.

Examples

```
>>> b = from_sequence(range(10))
>>> b.reduction(sum, sum).compute()
45
```

remove(*predicate*)

Remove elements in collection that match predicate.

```
>>> def iseven(x):
...     return x % 2 == 0
```

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(5))
>>> list(b.remove(iseven))
[1, 3]
```

repartition(*npartitions*)

Coalesce bag into fewer partitions.

Examples

```
>>> b.repartition(5)  # set to have 5 partitions
```

starmap(*func*, ***kwargs*)

Apply a function using argument tuples from the given bag.

This is similar to `itertools.starmap`, except it also accepts keyword arguments. In pseudocode, this is could be written as:

```
>>> def starmap(func, bag, **kwargs):
...     return (func(*args, **kwargs) for args in bag)
```

Parameters

func [callable]

****kwargs** [Item, Delayed, or object, optional] Extra keyword arguments to pass to `func`. These can either be normal objects, `dask.bag.Item`, or `dask.delayed.Delayed`.

Examples

```
>>> import dask.bag as db
>>> data = [(1, 2), (3, 4), (5, 6), (7, 8), (9, 10)]
>>> b = db.from_sequence(data, npartitions=2)
```

Apply a function to each argument tuple:

```
>>> from operator import add
>>> b.starmap(add).compute()
[3, 7, 11, 15, 19]
```

Apply a function to each argument tuple, with additional keyword arguments:

```
>>> def myadd(x, y, z=0):
...     return x + y + z
>>> b.starmap(myadd, z=10).compute()
[13, 17, 21, 25, 29]
```

Keyword arguments can also be instances of `dask.bag.Item` or `dask.delayed.Delayed`:

```
>>> max_second = b.pluck(1).max()
>>> max_second.compute()
10
>>> b.starmap(myadd, z=max_second).compute()
[13, 17, 21, 25, 29]
```

std(*ddof=0*)
Standard deviation

str
String processing functions

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence(['Alice Smith', 'Bob Jones', 'Charlie Smith'])
>>> list(b.str.lower())
['alice smith', 'bob jones', 'charlie smith']
```

```
>>> list(b.str.match('*Smith'))
['Alice Smith', 'Charlie Smith']
```

```
>>> list(b.str.split(' '))
[['Alice', 'Smith'], ['Bob', 'Jones'], ['Charlie', 'Smith']]
```

sum(*split_every=None*)
Sum all elements

take(*k*, *npartitions=1*, *compute=True*, *warn=True*)
Take the first k elements.

Parameters

k [int] The number of elements to return

npartitions [int, optional] Elements are only taken from the first `npartitions`, with a default of 1. If there are fewer than `k` rows in the first `npartitions` a warning will be raised and any found rows returned. Pass -1 to use all partitions.

compute [bool, optional] Whether to compute the result, default is True.

warn [bool, optional] Whether to warn if the number of elements returned is less than requested, default is True.

>>> b = from_sequence(range(10))

>>> b.take(3) # doctest: +SKIP

(0, 1, 2)

to_dataframe(*meta=None*, *columns=None*)
Create Dask Dataframe from a Dask Bag.

Bag should contain tuples, dict records, or scalars.

Index will not be particularly meaningful. Use `reindex` afterwards if necessary.

Parameters

meta [pd.DataFrame, dict, iterable, optional] An empty `pd.DataFrame` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. If not provided or a list, a single element from the first partition will be computed, triggering a potentially expensive call to `compute`. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

columns [sequence, optional] Column names to use. If the passed data do not have names associated with them, this argument provides names for the columns. Otherwise this argument indicates the order of the columns in the result (any names not found in the data will become all-NA columns). Note that if `meta` is provided, column names will be taken from there and this parameter is invalid.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence([{'name': 'Alice',   'balance': 100},
...                       {'name': 'Bob',     'balance': 200},
...                       {'name': 'Charlie', 'balance': 300}],
...                      npartitions=2)
>>> df = b.to_dataframe()
```

```
>>> df.compute()
   balance     name
0      100    Alice
1      200      Bob
0      300  Charlie
```

to_delayed(*optimize_graph=True*)
Convert into a list of `dask.delayed` objects, one per partition.

Parameters

optimize_graph [bool, optional] If True [default], the graph is optimized before converting into `dask.delayed` objects.

See also:

dask.bag.from_delayed

to_textfiles(*path*, *name_function=None*, *compression='infer'*, *encoding='utf-8'*, *compute=True*, *storage_options=None*, *last_endline=False*, ***kwargs*)
Write dask Bag to disk, one filename per partition, one line per element.

Paths: This will create one file for each partition in your bag. You can specify the filenames in a variety of ways.

Use a globstring

```
>>> b.to_textfiles('/path/to/data/*.json.gz')
```

The * will be replaced by the increasing sequence 1, 2, ...

```
/path/to/data/0.json.gz
/path/to/data/1.json.gz
```

Use a globstring and a `name_function=` keyword argument. The name_function function should expect an integer and produce a string. Strings produced by name_function must preserve the order of their respective partition indices.

```
>>> from datetime import date, timedelta
>>> def name(i):
...     return str(date(2015, 1, 1) + i * timedelta(days=1))
```

```
>>> name(0)
'2015-01-01'
>>> name(15)
'2015-01-16'
```

```
>>> b.to_textfiles('/path/to/data/*.json.gz', name_function=name)
```

```
/path/to/data/2015-01-01.json.gz
/path/to/data/2015-01-02.json.gz
...
```

You can also provide an explicit list of paths.

```
>>> paths = ['/path/to/data/alice.json.gz', '/path/to/data/bob.json.gz', ...]
>>> b.to_textfiles(paths)
```

Compression: Filenames with extensions corresponding to known compression algorithms (gz, bz2) will be compressed accordingly.

Bag Contents: The bag calling `to_textfiles` must be a bag of text strings. For example, a bag of dictionaries could be written to JSON text files by mapping `json.dumps` on to the bag first, and then calling `to_textfiles`:

```
>>> b_dict.map(json.dumps).to_textfiles("/path/to/data/*.json")
```

Last endline: By default the last line does not end with a newline character. Pass `last_endline=True` to invert the default.

topk(*k*, *key=None*, *split_every=None*)
K largest elements in collection

Optionally ordered by some key function

```
>>> b = from_sequence([10, 3, 5, 7, 11, 4])
>>> list(b.topk(2))
[11, 10]
```

```
>>> list(b.topk(2, lambda x: -x))
[3, 4]
```

unzip(*n*)
Transform a bag of tuples to `n` bags of their elements.

Examples

```
>>> b = from_sequence([(i, i + 1, i + 2) for i in range(10)])
>>> first, second, third = b.unzip(3)
>>> isinstance(first, Bag)
True
>>> first.compute()
[0, 1, 2, 3, 4, 5, 6, 7, 8, 9]
```

Note that this is equivalent to:

```
>>> first, second, third = (b.pluck(i) for i in range(3))
```

var(*ddof=0*)
Variance

Other functions

dask.bag.**from_sequence**(*seq*, *partition_size=None*, *npartitions=None*)
Create a dask Bag from Python sequence.

This sequence should be relatively small in memory. Dask Bag works best when it handles loading your data itself. Commonly we load a sequence of filenames into a Bag and then use `.map` to open them.

Parameters

seq: Iterable A sequence of elements to put into the dask

partition_size: int (optional) The length of each partition

npartitions: int (optional) The number of desired partitions

It is best to provide either ‘‘partition_size‘‘ or ‘‘npartitions‘‘

(though not both.)

See also:

read_text Create bag from text files

Examples

```
>>> b = from_sequence(['Alice', 'Bob', 'Chuck'], partition_size=2)
```

dask.bag.**from_delayed**(*values*)

Create bag from many dask Delayed objects.

These objects will become the partitions of the resulting Bag. They should evaluate to a `list` or some other concrete sequence.

Parameters

values: list of delayed values An iterable of dask Delayed objects. Each evaluating to a list.

Returns

Bag

See also:

`dask.delayed`

Examples

```
>>> x, y, z = [delayed(load_sequence_from_file)(fn)
...               for fn in filenames]
>>> b = from_delayed([x, y, z])
```

dask.bag.**read_text**(*urlpath*, *blocksize=None*, *compression='infer'*, *encoding='utf-8'*, *errors='strict'*, *linedelimiter='\n'*, *collection=True*, *storage_options=None*, *files_per_partition=None*)

Read lines from text files

Parameters

urlpath [string or list] Absolute or relative filepath(s). Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol.

blocksize: None or int Size (in bytes) to cut up larger files. Streams by default.

compression: string Compression format like ‘gzip’ or ‘xz’. Defaults to ‘infer’

encoding: string

errors: string

linedelimiter: string

collection: bool, optional Return dask.bag if True, or list of delayed values if false

storage_options: dict Extra options that make sense to a particular storage connection, e.g. host, port, username, password, etc.

files_per_partition: None or int If set, group input files into partitions of the requested size, instead of one partition per file. Mutually exclusive with blocksize.

Returns

dask.bag.Bag if collection is True or list of Delayed lists otherwise

See also:

from_sequence Build bag from Python sequence

Examples

```
>>> b = read_text('myfiles.1.txt')
>>> b = read_text('myfiles.*.txt')
>>> b = read_text('myfiles.*.txt.gz')
>>> b = read_text('s3://bucket/myfiles.*.txt')
>>> b = read_text('s3://key:secret@bucket/myfiles.*.txt')
>>> b = read_text('hdfs://namenode.example.com/myfiles.*.txt')
```

Parallelize a large file by providing the number of uncompressed bytes to load into each partition.

```
>>> b = read_text('largefile.txt', blocksize=1e7)
```

dask.bag.**from_url**(*urls*)
Create a dask Bag from a url.

Examples

```
>>> a = from_url('http://raw.githubusercontent.com/dask/dask/master/README.rst')
>>> a.npartitions
1
```

```
>>> a.take(8)
(b'Dask\n',
 b'====\n',
 b'\n',
 b'|Build Status| |Coverage| |Doc Status| |Gitter| |Version Status|\n',
 b'\n',
 b'Dask is a flexible parallel computing library for analytics.  See\n',
 b'documentation_ for more information.\n',
 b'\n')
```

```
>>> b = from_url(['http://github.com', 'http://google.com'])
>>> b.npartitions
2
```

dask.bag.**range**(*n*, *npartitions*)
Numbers from zero to n

Examples

```
>>> import dask.bag as db
>>> b = db.range(5, npartitions=2)
>>> list(b)
[0, 1, 2, 3, 4]
```

dask.bag.**concat**(*bags*)

Concatenate many bags together, unioning all elements.

```
>>> import dask.bag as db
>>> a = db.from_sequence([1, 2, 3])
>>> b = db.from_sequence([4, 5, 6])
>>> c = db.concat([a, b])
```

```
>>> list(c)
[1, 2, 3, 4, 5, 6]
```

dask.bag.**map_partitions**(*func*, **args*, ***kwargs*)

Apply a function to every partition across one or more bags.

Note that all `Bag` arguments must be partitioned identically.

Parameters

func [callable]

***args, **kwargs** [Bag, Item, Delayed, or object] Arguments and keyword arguments to pass to `func`.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(1, 101), npartitions=10)
>>> def div(nums, den=1):
...     return [num / den for num in nums]
```

Using a python object:

```
>>> hi = b.max().compute()
>>> hi
100
>>> b.map_partitions(div, den=hi).take(5)
(0.01, 0.02, 0.03, 0.04, 0.05)
```

Using an `Item`:

```
>>> b.map_partitions(div, den=b.max()).take(5)
(0.01, 0.02, 0.03, 0.04, 0.05)
```

Note that while both versions give the same output, the second forms a single graph, and then computes everything at once, and in some cases may be more efficient.

dask.bag.**map**(*func*, **args*, ***kwargs*)

Apply a function elementwise across one or more bags.

Note that all `Bag` arguments must be partitioned identically.

Parameters

func [callable]

***args, **kwargs** [Bag, Item, Delayed, or object] Arguments and keyword arguments to pass to `func`. Non-Bag args/kwargs are broadcasted across all calls to `func`.

Notes

For calls with multiple *Bag* arguments, corresponding partitions should have the same length; if they do not, the call will error at compute time.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(5), npartitions=2)
>>> b2 = db.from_sequence(range(5, 10), npartitions=2)
```

Apply a function to all elements in a bag:

```
>>> db.map(lambda x: x + 1, b).compute()
[1, 2, 3, 4, 5]
```

Apply a function with arguments from multiple bags:

```
>>> from operator import add
>>> db.map(add, b, b2).compute()
[5, 7, 9, 11, 13]
```

Non-bag arguments are broadcast across all calls to the mapped function:

```
>>> db.map(add, b, 1).compute()
[1, 2, 3, 4, 5]
```

Keyword arguments are also supported, and have the same semantics as regular arguments:

```
>>> def myadd(x, y=0):
...     return x + y
>>> db.map(myadd, b, y=b2).compute()
[5, 7, 9, 11, 13]
>>> db.map(myadd, b, y=1).compute()
[1, 2, 3, 4, 5]
```

Both arguments and keyword arguments can also be instances of `dask.bag.Item` or `dask.delayed.Delayed`. Here we'll add the max value in the bag to each element:

```
>>> db.map(myadd, b, b.max()).compute()
[4, 5, 6, 7, 8]
```

`dask.bag.`**`zip`**`(*bags)`

Partition-wise bag zip

All passed bags must have the same number of partitions.

NOTE: corresponding partitions should have the same length; if they do not, the "extra" elements from the longer partition(s) will be dropped. If you have this case chances are that what you really need is a data alignment mechanism like pandas's, and not a missing value filler like zip_longest.

Examples

Correct usage:

```
>>> import dask.bag as db
>>> evens = db.from_sequence(range(0, 10, 2), partition_size=4)
>>> odds = db.from_sequence(range(1, 10, 2), partition_size=4)
>>> pairs = db.zip(evens, odds)
>>> list(pairs)
[(0, 1), (2, 3), (4, 5), (6, 7), (8, 9)]
```

Incorrect usage:

```
>>> numbers = db.range(20)
>>> fizz = numbers.filter(lambda n: n % 3 == 0)
>>> buzz = numbers.filter(lambda n: n % 5 == 0)
>>> fizzbuzz = db.zip(fizz, buzz)
>>> list(fizzbuzzz)
[(0, 0), (3, 5), (6, 10), (9, 15), (12, 20), (15, 25), (18, 30)]
```

When what you really wanted was more along the lines of the following:

```
>>> list(fizzbuzzz)
[(0, 0), (3, None), (None, 5), (6, None), (None 10), (9, None),
(12, None), (15, 15), (18, None), (None, 20), (None, 25), (None, 30)]
```

4.9 Dataframe

4.9.1 API

Dataframe

DataFrame(dsk, name, meta, divisions)	Parallel Pandas DataFrame
DataFrame.add(other[, axis, level, fill_value])	Addition of dataframe and other, element-wise (binary operator *add*).
DataFrame.append(other)	Append rows of *other* to the end of this frame, returning a new object.
DataFrame.apply(func[, axis, broadcast, ...])	Parallel version of pandas.DataFrame.apply
DataFrame.assign(**kwargs)	Assign new columns to a DataFrame, returning a new object (a copy) with the new columns added to the original ones.
DataFrame.astype(dtype)	Cast a pandas object to a specified dtype `dtype`.
DataFrame.categorize([columns, index, ...])	Convert columns of the DataFrame to category dtype.
`DataFrame.columns`	
DataFrame.compute(**kwargs)	Compute this dask collection
DataFrame.corr([method, min_periods, ...])	Compute pairwise correlation of columns, excluding NA/null values
DataFrame.count([axis, split_every])	Count non-NA cells for each column or row.
DataFrame.cov([min_periods, split_every])	Compute pairwise covariance of columns, excluding NA/null values.

Continued on next page

Table 29 – continued from previous page

DataFrame.cummax([axis, skipna, out])	Return cumulative maximum over a DataFrame or Series axis.
DataFrame.cummin([axis, skipna, out])	Return cumulative minimum over a DataFrame or Series axis.
DataFrame.cumprod([axis, skipna, dtype, out])	Return cumulative product over a DataFrame or Series axis.
DataFrame.cumsum([axis, skipna, dtype, out])	Return cumulative sum over a DataFrame or Series axis.
DataFrame.describe([split_every])	Generates descriptive statistics that summarize the central tendency, dispersion and shape of a dataset's distribution, excluding NaN values.
DataFrame.div(other[, axis, level, fill_value])	Floating division of dataframe and other, element-wise (binary operator *truediv*).
DataFrame.drop(labels[, axis, errors])	Drop specified labels from rows or columns.
DataFrame.drop_duplicates([split_every, ...])	Return DataFrame with duplicate rows removed, optionally only considering certain columns
DataFrame.dropna([how, subset])	Remove missing values.
DataFrame.dtypes	Return data types
DataFrame.fillna([value, method, limit, axis])	Fill NA/NaN values using the specified method
DataFrame.floordiv(other[, axis, level, ...])	Integer division of dataframe and other, element-wise (binary operator *floordiv*).
DataFrame.get_partition(n)	Get a dask DataFrame/Series representing the *nth* partition.
DataFrame.groupby([by])	Group series using mapper (dict or key function, apply given function to group, return result as series) or by a series of columns.
DataFrame.head([n, npartitions, compute])	First n rows of the dataset
DataFrame.iloc	Purely integer-location based indexing for selection by position.
DataFrame.index	Return dask Index instance
DataFrame.isna()	Detect missing values.
DataFrame.isnull()	Detect missing values.
DataFrame.iterrows()	Iterate over DataFrame rows as (index, Series) pairs.
DataFrame.itertuples()	Iterate over DataFrame rows as namedtuples, with index value as first element of the tuple.
DataFrame.join(other[, on, how, lsuffix, ...])	Join columns with other DataFrame either on index or on a key column.
DataFrame.known_divisions	Whether divisions are already known
DataFrame.loc	Purely label-location based indexer for selection by label.
DataFrame.map_partitions(func, *args, **kwargs)	Apply Python function on each DataFrame partition.
DataFrame.mask(cond[, other])	Return an object of same shape as self and whose corresponding entries are from self where *cond* is False and otherwise are from *other*.
DataFrame.max([axis, skipna, split_every, out])	This method returns the maximum of the values in the object.
DataFrame.mean([axis, skipna, split_every, ...])	Return the mean of the values for the requested axis
DataFrame.merge(right[, how, on, left_on, ...])	Merge DataFrame objects by performing a database-style join operation by columns or indexes.
DataFrame.min([axis, skipna, split_every, out])	This method returns the minimum of the values in the object.

Continued on next page

Table 29 – continued from previous page

DataFrame.mod(other[, axis, level, fill_value])	Modulo of dataframe and other, element-wise (binary operator *mod*).
DataFrame.mul(other[, axis, level, fill_value])	Multiplication of dataframe and other, element-wise (binary operator *mul*).
DataFrame.ndim	Return dimensionality
DataFrame.nlargest([n, columns, split_every])	Return the first *n* rows ordered by *columns* in descending order.
DataFrame.npartitions	Return number of partitions
DataFrame.pow(other[, axis, level, fill_value])	Exponential power of dataframe and other, element-wise (binary operator *pow*).
DataFrame.quantile([q, axis])	Approximate row-wise and precise column-wise quantiles of DataFrame
DataFrame.query(expr, **kwargs)	Filter dataframe with complex expression
DataFrame.radd(other[, axis, level, fill_value])	Addition of dataframe and other, element-wise (binary operator *radd*).
DataFrame.random_split(frac[, random_state])	Pseudorandomly split dataframe into different pieces row-wise
DataFrame.rdiv(other[, axis, level, fill_value])	Floating division of dataframe and other, element-wise (binary operator *rtruediv*).
DataFrame.rename([index, columns])	Alter axes labels.
DataFrame.repartition([divisions, ...])	Repartition dataframe along new divisions
DataFrame.reset_index([drop])	Reset the index to the default index.
DataFrame.rfloordiv(other[, axis, level, ...])	Integer division of dataframe and other, element-wise (binary operator *rfloordiv*).
DataFrame.rmod(other[, axis, level, fill_value])	Modulo of dataframe and other, element-wise (binary operator *rmod*).
DataFrame.rmul(other[, axis, level, fill_value])	Multiplication of dataframe and other, element-wise (binary operator *rmul*).
DataFrame.rpow(other[, axis, level, fill_value])	Exponential power of dataframe and other, element-wise (binary operator *rpow*).
DataFrame.rsub(other[, axis, level, fill_value])	Subtraction of dataframe and other, element-wise (binary operator *rsub*).
DataFrame.rtruediv(other[, axis, level, ...])	Floating division of dataframe and other, element-wise (binary operator *rtruediv*).
DataFrame.sample([n, frac, replace, ...])	Random sample of items
DataFrame.set_index(other[, drop, sorted, ...])	Set the DataFrame index (row labels) using an existing column
DataFrame.shape	Return a tuple representing the dimensionality of the DataFrame.
DataFrame.std([axis, skipna, ddof, ...])	Return sample standard deviation over requested axis.
DataFrame.sub(other[, axis, level, fill_value])	Subtraction of dataframe and other, element-wise (binary operator *sub*).
DataFrame.sum([axis, skipna, split_every, ...])	Return the sum of the values for the requested axis
DataFrame.tail([n, compute])	Last n rows of the dataset
DataFrame.to_bag([index])	Create Dask Bag from a Dask DataFrame
DataFrame.to_csv(filename, **kwargs)	Store Dask DataFrame to CSV files
DataFrame.to_dask_array([lengths])	Convert a dask DataFrame to a dask array.
DataFrame.to_delayed([optimize_graph])	Convert into a list of `dask.delayed` objects, one per partition.
DataFrame.to_hdf(path_or_buf, key[, mode, ...])	Store Dask Dataframe to Hierarchical Data Format (HDF) files

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Table 29 – continued from previous page

DataFrame.to_json(filename, *args, **kwargs)	See dd.to_json docstring for more information
DataFrame.to_records([index])	Create Dask Array from a Dask Dataframe
DataFrame.truediv(other[, axis, level, ...])	Floating division of dataframe and other, element-wise (binary operator *truediv*).
DataFrame.values	Return a dask.array of the values of this dataframe
DataFrame.var([axis, skipna, ddof, ...])	Return unbiased variance over requested axis.
DataFrame.visualize([filename, format, ...])	Render the computation of this object's task graph using graphviz.
DataFrame.where(cond[, other])	Return an object of same shape as self and whose corresponding entries are from self where *cond* is True and otherwise are from *other*.

Series

Series(dsk, name, meta, divisions)	Parallel Pandas Series
Series.add(other[, level, fill_value, axis])	Addition of series and other, element-wise (binary operator *add*).
Series.align(other[, join, axis, fill_value])	Align two objects on their axes with the specified join method for each axis Index
Series.all([axis, skipna, split_every, out])	Return whether all elements are True, potentially over an axis.
Series.any([axis, skipna, split_every, out])	Return whether any element is True over requested axis.
Series.append(other)	Concatenate two or more Series.
Series.apply(func[, convert_dtype, meta, args])	Parallel version of pandas.Series.apply
Series.astype(dtype)	Cast a pandas object to a specified dtype `dtype`.
Series.autocorr([lag, split_every])	Lag-N autocorrelation
Series.between(left, right[, inclusive])	Return boolean Series equivalent to left <= series <= right.
Series.bfill([axis, limit])	Synonym for *DataFrame.fillna(method='bfill')*
Series.cat	
Series.clear_divisions()	Forget division information
Series.clip([lower, upper, out])	Trim values at input threshold(s).
Series.clip_lower(threshold)	Return copy of the input with values below a threshold truncated.
Series.clip_upper(threshold)	Return copy of input with values above given value(s) truncated.
Series.compute(**kwargs)	Compute this dask collection
Series.copy()	Make a copy of the dataframe
Series.corr(other[, method, min_periods, ...])	Compute correlation with *other* Series, excluding missing values
Series.count([split_every])	Return number of non-NA/null observations in the Series
Series.cov(other[, min_periods, split_every])	Compute covariance with Series, excluding missing values
Series.cummax([axis, skipna, out])	Return cumulative maximum over a DataFrame or Series axis.
Series.cummin([axis, skipna, out])	Return cumulative minimum over a DataFrame or Series axis.

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Series.cumprod([axis, skipna, dtype, out])	Return cumulative product over a DataFrame or Series axis.
Series.cumsum([axis, skipna, dtype, out])	Return cumulative sum over a DataFrame or Series axis.
Series.describe([split_every])	Generates descriptive statistics that summarize the central tendency, dispersion and shape of a dataset's distribution, excluding NaN values.
Series.diff([periods, axis])	First discrete difference of element.
Series.div(other[, level, fill_value, axis])	Floating division of series and other, element-wise (binary operator *truediv*).
Series.drop_duplicates([split_every, split_out])	Return DataFrame with duplicate rows removed, optionally only considering certain columns
Series.dropna()	Return a new Series with missing values removed.
Series.dt	Namespace of datetime methods
Series.dtype	Return data type
Series.eq(other[, level, axis])	Equal to of series and other, element-wise (binary operator *eq*).
Series.ffill([axis, limit])	Synonym for DataFrame.fillna(method='ffill')
Series.fillna([value, method, limit, axis])	Fill NA/NaN values using the specified method
Series.first(offset)	Convenience method for subsetting initial periods of time series data based on a date offset.
Series.floordiv(other[, level, fill_value, axis])	Integer division of series and other, element-wise (binary operator *floordiv*).
Series.ge(other[, level, axis])	Greater than or equal to of series and other, element-wise (binary operator *ge*).
Series.get_partition(n)	Get a dask DataFrame/Series representing the *nth* partition.
Series.groupby([by])	Group series using mapper (dict or key function, apply given function to group, return result as series) or by a series of columns.
Series.gt(other[, level, axis])	Greater than of series and other, element-wise (binary operator *gt*).
Series.head([n, npartitions, compute])	First n rows of the dataset
Series.idxmax([axis, skipna, split_every])	Return index of first occurrence of maximum over requested axis.
Series.idxmin([axis, skipna, split_every])	Return index of first occurrence of minimum over requested axis.
Series.isin(values)	Check whether *values* are contained in Series.
Series.isna()	Detect missing values.
Series.isnull()	Detect missing values.
Series.iteritems()	Lazily iterate over (index, value) tuples
Series.known_divisions	Whether divisions are already known
Series.last(offset)	Convenience method for subsetting final periods of time series data based on a date offset.
Series.le(other[, level, axis])	Less than or equal to of series and other, element-wise (binary operator *le*).
Series.loc	Purely label-location based indexer for selection by label.
Series.lt(other[, level, axis])	Less than of series and other, element-wise (binary operator *lt*).

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Series.map(arg[, na_action, meta])	Map values of Series using input correspondence (a dict, Series, or function).
Series.map_overlap(func, before, after, ...)	Apply a function to each partition, sharing rows with adjacent partitions.
Series.map_partitions(func, *args, **kwargs)	Apply Python function on each DataFrame partition.
Series.mask(cond[, other])	Return an object of same shape as self and whose corresponding entries are from self where *cond* is False and otherwise are from *other*.
Series.max([axis, skipna, split_every, out])	This method returns the maximum of the values in the object.
Series.mean([axis, skipna, split_every, ...])	Return the mean of the values for the requested axis
Series.memory_usage([index, deep])	Return the memory usage of the Series.
Series.min([axis, skipna, split_every, out])	This method returns the minimum of the values in the object.
Series.mod(other[, level, fill_value, axis])	Modulo of series and other, element-wise (binary operator *mod*).
Series.mul(other[, level, fill_value, axis])	Multiplication of series and other, element-wise (binary operator *mul*).
Series.nbytes	Number of bytes
Series.ndim	Return dimensionality
Series.ne(other[, level, axis])	Not equal to of series and other, element-wise (binary operator *ne*).
Series.nlargest([n, split_every])	Return the largest *n* elements.
Series.notnull()	Detect existing (non-missing) values.
Series.nsmallest([n, split_every])	Return the smallest *n* elements.
Series.nunique([split_every])	Return number of unique elements in the object.
Series.nunique_approx([split_every])	Approximate number of unique rows.
Series.persist(**kwargs)	Persist this dask collection into memory
Series.pipe(func, *args, **kwargs)	Apply func(self, *args, **kwargs)
Series.pow(other[, level, fill_value, axis])	Exponential power of series and other, element-wise (binary operator *pow*).
Series.prod([axis, skipna, split_every, ...])	Return the product of the values for the requested axis
Series.quantile([q])	Approximate quantiles of Series
Series.radd(other[, level, fill_value, axis])	Addition of series and other, element-wise (binary operator *radd*).
Series.random_split(frac[, random_state])	Pseudorandomly split dataframe into different pieces row-wise
Series.rdiv(other[, level, fill_value, axis])	Floating division of series and other, element-wise (binary operator *rtruediv*).
Series.reduction(chunk[, aggregate, ...])	Generic row-wise reductions.
Series.repartition([divisions, npartitions, ...])	Repartition dataframe along new divisions
Series.rename([index, inplace, sorted_index])	Alter Series index labels or name
Series.resample(rule[, closed, label])	Convenience method for frequency conversion and resampling of time series.
Series.reset_index([drop])	Reset the index to the default index.
Series.rolling(window[, min_periods, freq, ...])	Provides rolling transformations.
Series.round([decimals])	Round each value in a Series to the given number of decimals.
Series.sample([n, frac, replace, random_state])	Random sample of items
Series.sem([axis, skipna, ddof, split_every])	Return unbiased standard error of the mean over requested axis.

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`Series.shape`	Return a tuple representing the dimensionality of a Series.
`Series.shift`([periods, freq, axis])	Shift index by desired number of periods with an optional time freq
`Series.size`	Size of the Series or DataFrame as a Delayed object.
`Series.std`([axis, skipna, ddof, ...])	Return sample standard deviation over requested axis.
`Series.str`	Namespace for string methods
`Series.sub`(other[, level, fill_value, axis])	Subtraction of series and other, element-wise (binary operator *sub*).
`Series.sum`([axis, skipna, split_every, ...])	Return the sum of the values for the requested axis
`Series.to_bag`([index])	Craeate a Dask Bag from a Series
`Series.to_csv`(filename, **kwargs)	Store Dask DataFrame to CSV files
`Series.to_dask_array`([lengths])	Convert a dask DataFrame to a dask array.
`Series.to_delayed`([optimize_graph])	Convert into a list of `dask.delayed` objects, one per partition.
`Series.to_frame`([name])	Convert Series to DataFrame
`Series.to_hdf`(path_or_buf, key[, mode, append])	Store Dask Dataframe to Hierarchical Data Format (HDF) files
`Series.to_parquet`(path, *args, **kwargs)	Store Dask.dataframe to Parquet files
`Series.to_string`([max_rows])	Render a string representation of the Series
`Series.to_timestamp`([freq, how, axis])	Cast to DatetimeIndex of timestamps, at *beginning* of period
`Series.truediv`(other[, level, fill_value, axis])	Floating division of series and other, element-wise (binary operator *truediv*).
`Series.unique`([split_every, split_out])	Return Series of unique values in the object.
`Series.value_counts`([split_every, split_out])	Returns object containing counts of unique values.
`Series.values`	Return a dask.array of the values of this dataframe
`Series.var`([axis, skipna, ddof, ...])	Return unbiased variance over requested axis.
`Series.visualize`([filename, format, ...])	Render the computation of this object's task graph using graphviz.
`Series.where`(cond[, other])	Return an object of same shape as self and whose corresponding entries are from self where *cond* is True and otherwise are from *other*.

Groupby Operations

`DataFrameGroupBy.aggregate`(arg[, ...])	Aggregate using one or more operations over the specified axis.
`DataFrameGroupBy.apply`(func, *args, **kwargs)	Parallel version of pandas GroupBy.apply
`DataFrameGroupBy.count`([split_every, split_out])	Compute count of group, excluding missing values
`DataFrameGroupBy.cumcount`([axis])	Number each item in each group from 0 to the length of that group - 1.
`DataFrameGroupBy.cumprod`([axis])	Cumulative product for each group
`DataFrameGroupBy.cumsum`([axis])	Cumulative sum for each group
`DataFrameGroupBy.get_group`(key)	Constructs NDFrame from group with provided name
`DataFrameGroupBy.max`([split_every, split_out])	Compute max of group values
`DataFrameGroupBy.mean`([split_every, split_out])	Compute mean of groups, excluding missing values
`DataFrameGroupBy.min`([split_every, split_out])	Compute min of group values

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DataFrameGroupBy.size([split_every, split_out])	Compute group sizes
DataFrameGroupBy.std([ddof, split_every, ...])	Compute standard deviation of groups, excluding missing values
DataFrameGroupBy.sum([split_every, split_out])	Compute sum of group values
DataFrameGroupBy.var([ddof, split_every, ...])	Compute variance of groups, excluding missing values
DataFrameGroupBy.first([split_every, split_out])	Compute first of group values
DataFrameGroupBy.last([split_every, split_out])	Compute last of group values

SeriesGroupBy.aggregate(arg[, split_every, ...])	Aggregate using one or more operations over the specified axis.
SeriesGroupBy.apply(func, *args, **kwargs)	Parallel version of pandas GroupBy.apply
SeriesGroupBy.count([split_every, split_out])	Compute count of group, excluding missing values
SeriesGroupBy.cumcount([axis])	Number each item in each group from 0 to the length of that group - 1.
SeriesGroupBy.cumprod([axis])	Cumulative product for each group
SeriesGroupBy.cumsum([axis])	Cumulative sum for each group
SeriesGroupBy.get_group(key)	Constructs NDFrame from group with provided name
SeriesGroupBy.max([split_every, split_out])	Compute max of group values
SeriesGroupBy.mean([split_every, split_out])	Compute mean of groups, excluding missing values
SeriesGroupBy.min([split_every, split_out])	Compute min of group values
SeriesGroupBy.nunique([split_every, split_out])	
SeriesGroupBy.size([split_every, split_out])	Compute group sizes
SeriesGroupBy.std([ddof, split_every, split_out])	Compute standard deviation of groups, excluding missing values
SeriesGroupBy.sum([split_every, split_out])	Compute sum of group values
SeriesGroupBy.var([ddof, split_every, split_out])	Compute variance of groups, excluding missing values
SeriesGroupBy.first([split_every, split_out])	Compute first of group values
SeriesGroupBy.last([split_every, split_out])	Compute last of group values

Rolling Operations

rolling.map_overlap(func, df, before, after, ...)	Apply a function to each partition, sharing rows with adjacent partitions.
Series.rolling(window[, min_periods, freq, ...])	Provides rolling transformations.
DataFrame.rolling(window[, min_periods, ...])	Provides rolling transformations.

Rolling.apply(func[, args, kwargs])	rolling function apply
Rolling.count()	The rolling count of any non-NaN observations inside the window.
Rolling.kurt()	Calculate unbiased rolling kurtosis.
Rolling.max()	rolling maximum
Rolling.mean()	Calculate the rolling mean of the values.
Rolling.median()	Calculate the rolling median.
Rolling.min()	Calculate the rolling minimum.
Rolling.quantile(quantile)	rolling quantile.
Rolling.skew()	Unbiased rolling skewness
Rolling.std([ddof])	Calculate rolling standard deviation.

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`Rolling.sum`()	Calculate rolling sum of given DataFrame or Series.
`Rolling.var`([ddof])	Calculate unbiased rolling variance.

Create DataFrames

read_csv(urlpath[, blocksize, collection, ...])	Read CSV files into a Dask.DataFrame
read_table(urlpath[, blocksize, collection, ...])	Read delimited files into a Dask.DataFrame
read_parquet(path[, columns, filters, ...])	Read ParquetFile into a Dask DataFrame
read_hdf(pattern, key[, start, stop, ...])	Read HDF files into a Dask DataFrame
read_json(url_path[, orient, lines, ...])	Create a dataframe from a set of JSON files
read_orc(path[, columns, storage_options])	Read dataframe from ORC file(s)
read_sql_table(table, uri, index_col[, ...])	Create dataframe from an SQL table.
from_array(x[, chunksize, columns])	Read any slicable array into a Dask Dataframe
from_bcolz(x[, chunksize, categorize, ...])	Read BColz CTable into a Dask Dataframe
from_dask_array(x[, columns, index])	Create a Dask DataFrame from a Dask Array.
from_delayed(dfs[, meta, divisions, prefix])	Create Dask DataFrame from many Dask Delayed objects
from_pandas(data[, npartitions, chunksize, ...])	Construct a Dask DataFrame from a Pandas DataFrame
dask.bag.core.Bag.to_dataframe([meta, columns])	Create Dask Dataframe from a Dask Bag.

Store DataFrames

to_csv(df, filename[, name_function, ...])	Store Dask DataFrame to CSV files
to_parquet(df, path[, engine, compression, ...])	Store Dask.dataframe to Parquet files
to_hdf(df, path, key[, mode, append, get, ...])	Store Dask Dataframe to Hierarchical Data Format (HDF) files
to_records(df)	Create Dask Array from a Dask Dataframe
to_bag(df[, index])	Create Dask Bag from a Dask DataFrame
to_json(df, url_path[, orient, lines, ...])	Write dataframe into JSON text files

Covert DataFrames

`to_dask_array`
`to_delayed`

DataFrame Methods

class `dask.dataframe.`**`DataFrame`**(*dsk*, *name*, *meta*, *divisions*)

Parallel Pandas DataFrame

Do not use this class directly. Instead use functions like `dd.read_csv`, `dd.read_parquet`, or `dd.from_pandas`.

Parameters

dsk: dict The dask graph to compute this DataFrame

name: str The key prefix that specifies which keys in the dask comprise this particular DataFrame

meta: pandas.DataFrame An empty `pandas.DataFrame` with names, dtypes, and index matching the expected output.

divisions: tuple of index values Values along which we partition our blocks on the index

abs()

Return a Series/DataFrame with absolute numeric value of each element.

This function only applies to elements that are all numeric.

Returns

abs Series/DataFrame containing the absolute value of each element.

See also:

numpy.absolute calculate the absolute value element-wise.

Notes

For `complex` inputs, `1.2 + 1j`, the absolute value is $\sqrt{a^2 + b^2}$.

Examples

Absolute numeric values in a Series.

```
>>> s = pd.Series([-1.10, 2, -3.33, 4])
>>> s.abs()
0    1.10
1    2.00
2    3.33
3    4.00
dtype: float64
```

Absolute numeric values in a Series with complex numbers.

```
>>> s = pd.Series([1.2 + 1j])
>>> s.abs()
0    1.56205
dtype: float64
```

Absolute numeric values in a Series with a Timedelta element.

```
>>> s = pd.Series([pd.Timedelta('1 days')])
>>> s.abs()
0   1 days
dtype: timedelta64[ns]
```

Select rows with data closest to certain value using argsort (from StackOverflow).

```
>>> df = pd.DataFrame({
...     'a': [4, 5, 6, 7],
...     'b': [10, 20, 30, 40],
...     'c': [100, 50, -30, -50]
... })
>>> df
     a    b    c
```

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```
0    4   10  100
1    5   20   50
2    6   30  -30
3    7   40  -50
>>> df.loc[(df.c - 43).abs().argsort()]
     a    b    c
1    5   20   50
0    4   10  100
2    6   30  -30
3    7   40  -50
```

add(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Addition of dataframe and other, element-wise (binary operator *add*).

Equivalent to `dataframe + other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.radd

Notes

Mismatched indices will be unioned together

Examples

```
>>> a = pd.DataFrame([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'],
...                  columns=['one'])
>>> a
   one
a  1.0
b  1.0
c  1.0
d  NaN
>>> b = pd.DataFrame(dict(one=[1, np.nan, 1, np.nan],
...                       two=[np.nan, 2, np.nan, 2]),
...                  index=['a', 'b', 'd', 'e'])
```

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```
>>> b
   one  two
a  1.0  NaN
b  NaN  2.0
d  1.0  NaN
e  NaN  2.0
>>> a.add(b, fill_value=0)
   one  two
a  2.0  NaN
b  1.0  2.0
c  1.0  NaN
d  1.0  NaN
e  NaN  2.0
```

align(*other*, *join='outer'*, *axis=None*, *fill_value=None*)

Align two objects on their axes with the specified join method for each axis Index

Parameters

other [DataFrame or Series]

join [{'outer', 'inner', 'left', 'right'}, default 'outer']

axis [allowed axis of the other object, default None] Align on index (0), columns (1), or both (None)

level [int or level name, default None] Broadcast across a level, matching Index values on the passed MultiIndex level

copy [boolean, default True] Always returns new objects. If copy=False and no reindexing is required then original objects are returned.

fill_value [scalar, default np.NaN] Value to use for missing values. Defaults to NaN, but can be any "compatible" value

method [str, default None]

limit [int, default None]

fill_axis [{0 or 'index', 1 or 'columns'}, default 0] Filling axis, method and limit

broadcast_axis [{0 or 'index', 1 or 'columns'}, default None] Broadcast values along this axis, if aligning two objects of different dimensions

Returns

(left, right) [(DataFrame, type of other)] Aligned objects

Notes

Dask doesn't support the following argument(s).

- level
- copy
- method
- limit
- fill_axis

- broadcast_axis

all(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)

Return whether all elements are True, potentially over an axis.

Returns True if all elements within a series or along a Dataframe axis are non-zero, not-empty or not-False.

Parameters

axis [{0 or 'index', 1 or 'columns', None}, default 0] Indicate which axis or axes should be reduced.

- 0 / 'index' : reduce the index, return a Series whose index is the original column labels.
- 1 / 'columns' : reduce the columns, return a Series whose index is the original index.
- None : reduce all axes, return a scalar.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

bool_only [boolean, default None] Include only boolean columns. If None, will attempt to use everything, then use only boolean data. Not implemented for Series.

****kwargs** [any, default None] Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

all [Series or DataFrame (if level specified)]

See also:

pandas.Series.all Return True if all elements are True

pandas.DataFrame.any Return True if one (or more) elements are True

Notes

Dask doesn't support the following argument(s).

- bool_only
- level

Examples

Series

```
>>> pd.Series([True, True]).all()
True
>>> pd.Series([True, False]).all()
False
```

DataFrames

Create a dataframe from a dictionary.

```
>>> df = pd.DataFrame({'col1': [True, True], 'col2': [True, False]})
>>> df
   col1   col2
0  True   True
1  True  False
```

Default behaviour checks if column-wise values all return True.

```
>>> df.all()
col1     True
col2    False
dtype: bool
```

Specify `axis='columns'` to check if row-wise values all return True.

```
>>> df.all(axis='columns')
0     True
1    False
dtype: bool
```

Or `axis=None` for whether every value is True.

```
>>> df.all(axis=None)
False
```

any(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)
Return whether any element is True over requested axis.

Unlike *DataFrame.all()*, this performs an *or* operation. If any of the values along the specified axis is True, this will return True.

Parameters

axis [{0 or 'index', 1 or 'columns', None}, default 0] Indicate which axis or axes should be reduced.

- 0 / 'index' : reduce the index, return a Series whose index is the original column labels.
- 1 / 'columns' : reduce the columns, return a Series whose index is the original index.
- None : reduce all axes, return a scalar.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

bool_only [boolean, default None] Include only boolean columns. If None, will attempt to use everything, then use only boolean data. Not implemented for Series.

****kwargs** [any, default None] Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

any [Series or DataFrame (if level specified)]

See also:

`pandas.DataFrame.all` Return whether all elements are True.

Notes

Dask doesn't support the following argument(s).

- bool_only
- level

Examples

Series

For Series input, the output is a scalar indicating whether any element is True.

```
>>> pd.Series([True, False]).any()
True
```

DataFrame

Whether each column contains at least one True element (the default).

```
>>> df = pd.DataFrame({"A": [1, 2], "B": [0, 2], "C": [0, 0]})
>>> df
   A  B  C
0  1  0  0
1  2  2  0
```

```
>>> df.any()
A     True
B     True
C    False
dtype: bool
```

Aggregating over the columns.

```
>>> df = pd.DataFrame({"A": [True, False], "B": [1, 2]})
>>> df
       A  B
0   True  1
1  False  2
```

```
>>> df.any(axis='columns')
0    True
1    True
dtype: bool
```

```
>>> df = pd.DataFrame({"A": [True, False], "B": [1, 0]})
>>> df
       A  B
0   True  1
1  False  0
```

```
>>> df.any(axis='columns')
0    True
1    False
dtype: bool
```

Aggregating over the entire DataFrame with `axis=None`.

```
>>> df.any(axis=None)
True
```

any for an empty DataFrame is an empty Series.

```
>>> pd.DataFrame([]).any()
Series([], dtype: bool)
```

append(*other*)

Append rows of *other* to the end of this frame, returning a new object. Columns not in this frame are added as new columns.

Parameters

other [DataFrame or Series/dict-like object, or list of these] The data to append.

ignore_index [boolean, default False] If True, do not use the index labels.

verify_integrity [boolean, default False] If True, raise ValueError on creating index with duplicates.

sort [boolean, default None] Sort columns if the columns of *self* and *other* are not aligned. The default sorting is deprecated and will change to not-sorting in a future version of pandas. Explicitly pass `sort=True` to silence the warning and sort. Explicitly pass `sort=False` to silence the warning and not sort.

New in version 0.23.0.

Returns

appended [DataFrame]

See also:

pandas.concat General function to concatenate DataFrame, Series or Panel objects

Notes

If a list of dict/series is passed and the keys are all contained in the DataFrame's index, the order of the columns in the resulting DataFrame will be unchanged.

Iteratively appending rows to a DataFrame can be more computationally intensive than a single concatenate. A better solution is to append those rows to a list and then concatenate the list with the original DataFrame all at once.

Examples

```
>>> df = pd.DataFrame([[1, 2], [3, 4]], columns=list('AB'))
>>> df
   A  B
0  1  2
1  3  4
>>> df2 = pd.DataFrame([[5, 6], [7, 8]], columns=list('AB'))
>>> df.append(df2)
   A  B
0  1  2
1  3  4
0  5  6
1  7  8
```

With *ignore_index* set to True:

```
>>> df.append(df2, ignore_index=True)
   A  B
0  1  2
1  3  4
2  5  6
3  7  8
```

The following, while not recommended methods for generating DataFrames, show two ways to generate a DataFrame from multiple data sources.

Less efficient:

```
>>> df = pd.DataFrame(columns=['A'])
>>> for i in range(5):
...     df = df.append({'A': i}, ignore_index=True)
>>> df
   A
0  0
1  1
2  2
3  3
4  4
```

More efficient:

```
>>> pd.concat([pd.DataFrame([i], columns=['A']) for i in range(5)],
...           ignore_index=True)
   A
0  0
1  1
2  2
3  3
4  4
```

apply(*func*, *axis=0*, *broadcast=None*, *raw=False*, *reduce=None*, *args=()*, *meta='__no_default__'*, ***kwds*)

Parallel version of pandas.DataFrame.apply

This mimics the pandas version except for the following:

1. Only `axis=1` is supported (and must be specified explicitly).
2. The user should provide output metadata via the *meta* keyword.

Parameters

func [function] Function to apply to each column/row

axis [{0 or 'index', 1 or 'columns'}, default 0]

- 0 or 'index': apply function to each column (NOT SUPPORTED)
- 1 or 'columns': apply function to each row

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

args [tuple] Positional arguments to pass to function in addition to the array/series

Additional keyword arguments will be passed as keywords to the function

Returns

applied [Series or DataFrame]

See also:

`dask.DataFrame.map_partitions`

Examples

```
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': [1, 2, 3, 4, 5],
...                    'y': [1., 2., 3., 4., 5.]})
>>> ddf = dd.from_pandas(df, npartitions=2)
```

Apply a function to row-wise passing in extra arguments in `args` and `kwargs`:

```
>>> def myadd(row, a, b=1):
...     return row.sum() + a + b
>>> res = ddf.apply(myadd, axis=1, args=(2,), b=1.5)
```

By default, dask tries to infer the output metadata by running your provided function on some fake data. This works well in many cases, but can sometimes be expensive, or even fail. To avoid this, you can manually specify the output metadata with the `meta` keyword. This can be specified in many forms, for more information see `dask.dataframe.utils.make_meta`.

Here we specify the output is a Series with name `'x'`, and dtype `float64`:

```
>>> res = ddf.apply(myadd, axis=1, args=(2,), b=1.5, meta=('x', 'f8'))
```

In the case where the metadata doesn't change, you can also pass in the object itself directly:

```
>>> res = ddf.apply(lambda row: row + 1, axis=1, meta=ddf)
```

applymap (*func*, *meta='__no_default__'*)
Apply a function to a Dataframe elementwise.

This method applies a function that accepts and returns a scalar to every element of a DataFrame.

Parameters

func [callable] Python function, returns a single value from a single value.

Returns

DataFrame Transformed DataFrame.

See also:

DataFrame.apply Apply a function along input axis of DataFrame

Examples

```
>>> df = pd.DataFrame([[1, 2.12], [3.356, 4.567]])
>>> df
       0      1
0  1.000  2.120
1  3.356  4.567
```

```
>>> df.applymap(lambda x: len(str(x)))
   0  1
0  3  4
1  5  5
```

Note that a vectorized version of *func* often exists, which will be much faster. You could square each number elementwise.

```
>>> df.applymap(lambda x: x**2)
           0          1
0   1.000000   4.494400
1  11.262736  20.857489
```

But it's better to avoid applymap in that case.

```
>>> df ** 2
           0          1
0   1.000000   4.494400
1  11.262736  20.857489
```

assign (***kwargs*)
Assign new columns to a DataFrame, returning a new object (a copy) with the new columns added to the original ones. Existing columns that are re-assigned will be overwritten.

Parameters

kwargs [keyword, value pairs] keywords are the column names. If the values are callable, they are computed on the DataFrame and assigned to the new columns. The callable must not change input DataFrame (though pandas doesn't check it). If the values are not callable, (e.g. a Series, scalar, or array), they are simply assigned.

Returns

df [DataFrame] A new DataFrame with the new columns in addition to all the existing columns.

Notes

Assigning multiple columns within the same `assign` is possible. For Python 3.6 and above, later items in '**kwargs' may refer to newly created or modified columns in 'df'; items are computed and assigned into 'df' in order. For Python 3.5 and below, the order of keyword arguments is not specified, you cannot refer to newly created or modified columns. All items are computed first, and then assigned in alphabetical order.

Changed in version 0.23.0: Keyword argument order is maintained for Python 3.6 and later.

Examples

```
>>> df = pd.DataFrame({'A': range(1, 11), 'B': np.random.randn(10)})
```

Where the value is a callable, evaluated on *df*:

```
>>> df.assign(ln_A = lambda x: np.log(x.A))
    A         B      ln_A
0   1  0.426905  0.000000
1   2 -0.780949  0.693147
2   3 -0.418711  1.098612
3   4 -0.269708  1.386294
4   5 -0.274002  1.609438
5   6 -0.500792  1.791759
6   7  1.649697  1.945910
7   8 -1.495604  2.079442
8   9  0.549296  2.197225
9  10 -0.758542  2.302585
```

Where the value already exists and is inserted:

```
>>> newcol = np.log(df['A'])
>>> df.assign(ln_A=newcol)
    A         B      ln_A
0   1  0.426905  0.000000
1   2 -0.780949  0.693147
2   3 -0.418711  1.098612
3   4 -0.269708  1.386294
4   5 -0.274002  1.609438
5   6 -0.500792  1.791759
6   7  1.649697  1.945910
7   8 -1.495604  2.079442
8   9  0.549296  2.197225
9  10 -0.758542  2.302585
```

Where the keyword arguments depend on each other

```
>>> df = pd.DataFrame({'A': [1, 2, 3]})
```

```
>>> df.assign(B=df.A, C=lambda x:x['A']+ x['B'])
    A  B  C
```

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```
0  1  1  2
1  2  2  4
2  3  3  6
```

astype (*dtype*)

Cast a pandas object to a specified dtype `dtype`.

Parameters

dtype [data type, or dict of column name -> data type] Use a numpy.dtype or Python type to cast entire pandas object to the same type. Alternatively, use {col: dtype, ...}, where col is a column label and dtype is a numpy.dtype or Python type to cast one or more of the DataFrame's columns to column-specific types.

copy [bool, default True.] Return a copy when `copy=True` (be very careful setting `copy=False` as changes to values then may propagate to other pandas objects).

errors [{'raise', 'ignore'}, default 'raise'.] Control raising of exceptions on invalid data for provided dtype.

- `raise` : allow exceptions to be raised
- `ignore` : suppress exceptions. On error return original object

New in version 0.20.0.

raise_on_error [raise on invalid input] Deprecated since version 0.20.0: Use `errors` instead

kwargs [keyword arguments to pass on to the constructor]

Returns

casted [type of caller]

See also:

pandas.to_datetime Convert argument to datetime.

pandas.to_timedelta Convert argument to timedelta.

pandas.to_numeric Convert argument to a numeric type.

numpy.ndarray.astype Cast a numpy array to a specified type.

Notes

Dask doesn't support the following argument(s).

- copy
- errors

Examples

```
>>> ser = pd.Series([1, 2], dtype='int32')
>>> ser
0    1
1    2
```

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```
dtype: int32
>>> ser.astype('int64')
0    1
1    2
dtype: int64
```

Convert to categorical type:

```
>>> ser.astype('category')
0    1
1    2
dtype: category
Categories (2, int64): [1, 2]
```

Convert to ordered categorical type with custom ordering:

```
>>> ser.astype('category', ordered=True, categories=[2, 1])
0    1
1    2
dtype: category
Categories (2, int64): [2 < 1]
```

Note that using `copy=False` and changing data on a new pandas object may propagate changes:

```
>>> s1 = pd.Series([1,2])
>>> s2 = s1.astype('int64', copy=False)
>>> s2[0] = 10
>>> s1  # note that s1[0] has changed too
0    10
1     2
dtype: int64
```

bfill (*axis=None*, *limit=None*)
Synonym for *DataFrame.fillna(method='bfill')*

Notes

Dask doesn't support the following argument(s).

- inplace
- downcast

categorize (*columns=None*, *index=None*, *split_every=None*, ***kwargs*)
Convert columns of the DataFrame to category dtype.

Parameters

columns [list, optional] A list of column names to convert to categoricals. By default any column with an object dtype is converted to a categorical, and any unknown categoricals are made known.

index [bool, optional] Whether to categorize the index. By default, object indices are converted to categorical, and unknown categorical indices are made known. Set True to always categorize the index, False to never.

split_every [int, optional] Group partitions into groups of this size while performing a tree-reduction. If set to False, no tree-reduction will be used. Default is 16.

kwargs Keyword arguments are passed on to compute.

clear_divisions()
Forget division information

clip(*lower=None*, *upper=None*, *out=None*)
Trim values at input threshold(s).

Assigns values outside boundary to boundary values. Thresholds can be singular values or array like, and in the latter case the clipping is performed element-wise in the specified axis.

Parameters

lower [float or array_like, default None] Minimum threshold value. All values below this threshold will be set to it.

upper [float or array_like, default None] Maximum threshold value. All values above this threshold will be set to it.

axis [int or string axis name, optional] Align object with lower and upper along the given axis.

inplace [boolean, default False] Whether to perform the operation in place on the data.

New in version 0.21.0.

***args, **kwargs** Additional keywords have no effect but might be accepted for compatibility with numpy.

Returns

Series or DataFrame Same type as calling object with the values outside the clip boundaries replaced

See also:

clip_lower Clip values below specified threshold(s).

clip_upper Clip values above specified threshold(s).

Notes

Dask doesn't support the following argument(s).

- axis
- inplace

Examples

```
>>> data = {'col_0': [9, -3, 0, -1, 5], 'col_1': [-2, -7, 6, 8, -5]}
>>> df = pd.DataFrame(data)
>>> df
   col_0  col_1
0      9     -2
1     -3     -7
2      0      6
3     -1      8
4      5     -5
```

Clips per column using lower and upper thresholds:

```
>>> df.clip(-4, 6)
   col_0  col_1
0      6     -2
1     -3     -4
2      0      6
3     -1      6
4      5     -4
```

Clips using specific lower and upper thresholds per column element:

```
>>> t = pd.Series([2, -4, -1, 6, 3])
>>> t
0    2
1   -4
2   -1
3    6
4    3
dtype: int64
```

```
>>> df.clip(t, t + 4, axis=0)
   col_0  col_1
0      6      2
1     -3     -4
2      0      3
3      6      8
4      5      3
```

clip_lower(*threshold*)

Return copy of the input with values below a threshold truncated.

Parameters

threshold [numeric or array-like] Minimum value allowed. All values below threshold will be set to this value.

- float : every value is compared to *threshold*.
- array-like : The shape of *threshold* should match the object it's compared to. When *self* is a Series, *threshold* should be the length. When *self* is a DataFrame, *threshold* should 2-D and the same shape as *self* for `axis=None`, or 1-D and the same length as the axis being compared.

axis [{0 or 'index', 1 or 'columns'}, default 0] Align *self* with *threshold* along the given axis.

inplace [boolean, default False] Whether to perform the operation in place on the data.

New in version 0.21.0.

Returns

clipped [same type as input]

See also:

Series.clip Return copy of input with values below and above thresholds truncated.

Series.clip_upper Return copy of input with values above threshold truncated.

Notes

Dask doesn't support the following argument(s).

- axis
- inplace

Examples

Series single threshold clipping:

```
>>> s = pd.Series([5, 6, 7, 8, 9])
>>> s.clip_lower(8)
0    8
1    8
2    8
3    8
4    9
dtype: int64
```

Series clipping element-wise using an array of thresholds. *threshold* should be the same length as the Series.

```
>>> elemwise_thresholds = [4, 8, 7, 2, 5]
>>> s.clip_lower(elemwise_thresholds)
0    5
1    8
2    7
3    8
4    9
dtype: int64
```

DataFrames can be compared to a scalar.

```
>>> df = pd.DataFrame({"A": [1, 3, 5], "B": [2, 4, 6]})
>>> df
   A  B
0  1  2
1  3  4
2  5  6
```

```
>>> df.clip_lower(3)
   A  B
0  3  3
1  3  4
2  5  6
```

Or to an array of values. By default, *threshold* should be the same shape as the DataFrame.

```
>>> df.clip_lower(np.array([[3, 4], [2, 2], [6, 2]]))
   A  B
0  3  4
1  3  4
2  6  6
```

Control how *threshold* is broadcast with *axis*. In this case *threshold* should be the same length as the axis specified by *axis*.

```
>>> df.clip_lower(np.array([3, 3, 5]), axis='index')
   A  B
0  3  3
1  3  4
2  5  6
```

```
>>> df.clip_lower(np.array([4, 5]), axis='columns')
   A  B
0  4  5
1  4  5
2  5  6
```

clip_upper(*threshold*)

Return copy of input with values above given value(s) truncated.

Parameters

threshold [float or array_like]

axis [int or string axis name, optional] Align object with threshold along the given axis.

inplace [boolean, default False] Whether to perform the operation in place on the data

New in version 0.21.0.

Returns

clipped [same type as input]

See also:

clip

Notes

Dask doesn't support the following argument(s).

- axis
- inplace

combine(*other*, *func*, *fill_value=None*, *overwrite=True*)

Add two DataFrame objects and do not propagate NaN values, so if for a (column, time) one frame is missing a value, it will default to the other frame's value (which might be NaN as well)

Parameters

other [DataFrame]

func [function] Function that takes two series as inputs and return a Series or a scalar

fill_value [scalar value]

overwrite [boolean, default True] If True then overwrite values for common keys in the calling frame

Returns

result [DataFrame]

See also:

DataFrame.combine_first Combine two DataFrame objects and default to non-null values in frame calling the method

Examples

```
>>> df1 = DataFrame({'A': [0, 0], 'B': [4, 4]})
>>> df2 = DataFrame({'A': [1, 1], 'B': [3, 3]})
>>> df1.combine(df2, lambda s1, s2: s1 if s1.sum() < s2.sum() else s2)
   A  B
0  0  3
1  0  3
```

combine_first(*other*)

Combine two DataFrame objects and default to non-null values in frame calling the method. Result index columns will be the union of the respective indexes and columns

Parameters

other [DataFrame]

Returns

combined [DataFrame]

See also:

DataFrame.combine Perform series-wise operation on two DataFrames using a given function

Examples

df1's values prioritized, use values from df2 to fill holes:

```
>>> df1 = pd.DataFrame([[1, np.nan]])
>>> df2 = pd.DataFrame([[3, 4]])
>>> df1.combine_first(df2)
   0    1
0  1  4.0
```

compute(***kwargs*)

Compute this dask collection

This turns a lazy Dask collection into its in-memory equivalent. For example a Dask.array turns into a `numpy.array()` and a Dask.dataframe turns into a Pandas dataframe. The entire dataset must fit into memory before calling this operation.

Parameters

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

optimize_graph [bool, optional] If True [default], the graph is optimized before computation. Otherwise the graph is run as is. This can be useful for debugging.

kwargs Extra keywords to forward to the scheduler function.

See also:

`dask.base.compute`

copy()
Make a copy of the dataframe

This is strictly a shallow copy of the underlying computational graph. It does not affect the underlying data

corr(*method='pearson'*, *min_periods=None*, *split_every=False*)
Compute pairwise correlation of columns, excluding NA/null values

Parameters

method [{'pearson', 'kendall', 'spearman'}]

- pearson : standard correlation coefficient
- kendall : Kendall Tau correlation coefficient
- spearman : Spearman rank correlation

min_periods [int, optional] Minimum number of observations required per pair of columns to have a valid result. Currently only available for pearson and spearman correlation

Returns

y [DataFrame]

count(*axis=None*, *split_every=False*)
Count non-NA cells for each column or row.

The values *None*, *NaN*, *NaT*, and optionally *numpy.inf* (depending on *pandas.options.mode.use_inf_as_na*) are considered NA.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] If 0 or 'index' counts are generated for each column. If 1 or 'columns' counts are generated for each **row**.

level [int or str, optional] If the axis is a *MultiIndex* (hierarchical), count along a particular *level*, collapsing into a *DataFrame*. A *str* specifies the level name.

numeric_only [boolean, default False] Include only *float*, *int* or *boolean* data.

Returns

Series or DataFrame For each column/row the number of non-NA/null entries. If *level* is specified returns a *DataFrame*.

See also:

Series.count number of non-NA elements in a Series

DataFrame.shape number of DataFrame rows and columns (including NA elements)

DataFrame.isna boolean same-sized DataFrame showing places of NA elements

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

Examples

Constructing DataFrame from a dictionary:

```
>>> df = pd.DataFrame({"Person":
...                    ["John", "Myla", None, "John", "Myla"],
...                    "Age": [24., np.nan, 21., 33, 26],
...                    "Single": [False, True, True, True, False]})
>>> df
   Person   Age  Single
0    John  24.0   False
1    Myla   NaN    True
2    None  21.0    True
3    John  33.0    True
4    Myla  26.0   False
```

Notice the uncounted NA values:

```
>>> df.count()
Person    4
Age       4
Single    5
dtype: int64
```

Counts for each **row**:

```
>>> df.count(axis='columns')
0    3
1    2
2    2
3    3
4    3
dtype: int64
```

Counts for one level of a *MultiIndex*:

```
>>> df.set_index(["Person", "Single"]).count(level="Person")
        Age
Person
John      2
Myla      1
```

cov(*min_periods=None*, *split_every=False*)

Compute pairwise covariance of columns, excluding NA/null values.

Compute the pairwise covariance among the series of a DataFrame. The returned data frame is the covariance matrix of the columns of the DataFrame.

Both NA and null values are automatically excluded from the calculation. (See the note below about bias from missing values.) A threshold can be set for the minimum number of observations for each value created. Comparisons with observations below this threshold will be returned as `NaN`.

This method is generally used for the analysis of time series data to understand the relationship between different measures across time.

Parameters

min_periods [int, optional] Minimum number of observations required per pair of columns to have a valid result.

Returns

DataFrame The covariance matrix of the series of the DataFrame.

See also:

`pandas.Series.cov` compute covariance with another Series

`pandas.core.window.EWM.cov` expoential weighted sample covariance

`pandas.core.window.Expanding.cov` expanding sample covariance

`pandas.core.window.Rolling.cov` rolling sample covariance

Notes

Returns the covariance matrix of the DataFrame's time series. The covariance is normalized by N-1.

For DataFrames that have Series that are missing data (assuming that data is missing at random) the returned covariance matrix will be an unbiased estimate of the variance and covariance between the member Series.

However, for many applications this estimate may not be acceptable because the estimate covariance matrix is not guaranteed to be positive semi-definite. This could lead to estimate correlations having absolute values which are greater than one, and/or a non-invertible covariance matrix. See Estimation of covariance matrices for more details.

Examples

```
>>> df = pd.DataFrame([(1, 2), (0, 3), (2, 0), (1, 1)],
...                   columns=['dogs', 'cats'])
>>> df.cov()
          dogs      cats
dogs  0.666667 -1.000000
cats -1.000000  1.666667
```

```
>>> np.random.seed(42)
>>> df = pd.DataFrame(np.random.randn(1000, 5),
...                   columns=['a', 'b', 'c', 'd', 'e'])
>>> df.cov()
          a         b         c         d         e
a  0.998438 -0.020161  0.059277 -0.008943  0.014144
b -0.020161  1.059352 -0.008543 -0.024738  0.009826
c  0.059277 -0.008543  1.010670 -0.001486 -0.000271
d -0.008943 -0.024738 -0.001486  0.921297 -0.013692
e  0.014144  0.009826 -0.000271 -0.013692  0.977795
```

Minimum number of periods

This method also supports an optional `min_periods` keyword that specifies the required minimum number of non-NA observations for each column pair in order to have a valid result:

```
>>> np.random.seed(42)
>>> df = pd.DataFrame(np.random.randn(20, 3),
...                   columns=['a', 'b', 'c'])
>>> df.loc[df.index[:5], 'a'] = np.nan
```

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```
>>> df.loc[df.index[5:10], 'b'] = np.nan
>>> df.cov(min_periods=12)
          a         b         c
a  0.316741       NaN -0.150812
b       NaN  1.248003  0.191417
c -0.150812  0.191417  0.895202
```

cummax(*axis=None*, *skipna=True*, *out=None*)

Return cumulative maximum over a DataFrame or Series axis.

Returns a DataFrame or Series of the same size containing the cumulative maximum.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cummax [Series or DataFrame]

See also:

pandas.core.window.Expanding.max Similar functionality but ignores `NaN` values.

DataFrame.max Return the maximum over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])
>>> s
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cummax()
0    2.0
1    NaN
```

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```
2    5.0
3    5.0
4    5.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cummax(skipna=False)
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the maximum in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cummax()
     A    B
0  2.0  1.0
1  3.0  NaN
2  3.0  1.0
```

To iterate over columns and find the maximum in each row, use `axis=1`

```
>>> df.cummax(axis=1)
     A    B
0  2.0  2.0
1  3.0  NaN
2  1.0  1.0
```

cummin (*axis=None*, *skipna=True*, *out=None*)

Return cumulative minimum over a DataFrame or Series axis.

Returns a DataFrame or Series of the same size containing the cumulative minimum.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cummin [Series or DataFrame]

See also:

`pandas.core.window.Expanding.min` Similar functionality but ignores `NaN` values.

DataFrame.min Return the minimum over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])
>>> s
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cummin()
0    2.0
1    NaN
2    2.0
3   -1.0
4   -1.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cummin(skipna=False)
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df
     A    B
```

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```
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the minimum in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cummin()
     A    B
0  2.0  1.0
1  2.0  NaN
2  1.0  0.0
```

To iterate over columns and find the minimum in each row, use `axis=1`

```
>>> df.cummin(axis=1)
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

cumprod(*axis=None*, *skipna=True*, *dtype=None*, *out=None*)

Return cumulative product over a DataFrame or Series axis.

Returns a DataFrame or Series of the same size containing the cumulative product.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cumprod [Series or DataFrame]

See also:

pandas.core.window.Expanding.prod Similar functionality but ignores `NaN` values.

DataFrame.prod Return the product over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])
>>> s
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cumprod()
0     2.0
1     NaN
2    10.0
3   -10.0
4    -0.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cumprod(skipna=False)
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the product in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cumprod()
     A    B
0  2.0  1.0
1  6.0  NaN
2  6.0  0.0
```

To iterate over columns and find the product in each row, use `axis=1`

```
>>> df.cumprod(axis=1)
     A    B
0  2.0  2.0
1  3.0  NaN
2  1.0  0.0
```

cumsum(*axis=None*, *skipna=True*, *dtype=None*, *out=None*)

Return cumulative sum over a DataFrame or Series axis.

Returns a DataFrame or Series of the same size containing the cumulative sum.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cumsum [Series or DataFrame]

See also:

pandas.core.window.Expanding.sum Similar functionality but ignores `NaN` values.

DataFrame.sum Return the sum over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])
>>> s
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cumsum()
0    2.0
1    NaN
2    7.0
3    6.0
4    6.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cumsum(skipna=False)
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the sum in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cumsum()
     A    B
0  2.0  1.0
1  5.0  NaN
2  6.0  1.0
```

To iterate over columns and find the sum in each row, use `axis=1`

```
>>> df.cumsum(axis=1)
     A    B
0  2.0  3.0
1  3.0  NaN
2  1.0  1.0
```

describe(*split_every=False*)

Generates descriptive statistics that summarize the central tendency, dispersion and shape of a dataset's distribution, excluding `NaN` values.

Analyzes both numeric and object series, as well as `DataFrame` column sets of mixed data types. The output will vary depending on what is provided. Refer to the notes below for more detail.

Parameters

percentiles [list-like of numbers, optional] The percentiles to include in the output. All should fall between 0 and 1. The default is `[.25, .5, .75]`, which returns the 25th, 50th, and 75th percentiles.

include ['all', list-like of dtypes or None (default), optional] A white list of data types to include in the result. Ignored for `Series`. Here are the options:

- 'all' : All columns of the input will be included in the output.
- A list-like of dtypes : Limits the results to the provided data types. To limit the result to numeric types submit `numpy.number`. To limit it instead to object columns submit the `numpy.object` data type. Strings can also be used in the

style of `select_dtypes` (e.g. `df.describe(include=['O'])`). To select pandas categorical columns, use `'category'`

- None (default) : The result will include all numeric columns.

exclude [list-like of dtypes or None (default), optional,] A black list of data types to omit from the result. Ignored for `Series`. Here are the options:

- A list-like of dtypes : Excludes the provided data types from the result. To exclude numeric types submit `numpy.number`. To exclude object columns submit the data type `numpy.object`. Strings can also be used in the style of `select_dtypes` (e.g. `df.describe(include=['O'])`). To exclude pandas categorical columns, use `'category'`
- None (default) : The result will exclude nothing.

Returns

summary: Series/DataFrame of summary statistics

See also:

`DataFrame.count`, *`DataFrame.max`*, *`DataFrame.min`*, *`DataFrame.mean`*, *`DataFrame.std`*, *`DataFrame.select_dtypes`*

Notes

For numeric data, the result's index will include `count`, `mean`, `std`, `min`, `max` as well as lower, `50` and upper percentiles. By default the lower percentile is `25` and the upper percentile is `75`. The `50` percentile is the same as the median.

For object data (e.g. strings or timestamps), the result's index will include `count`, `unique`, `top`, and `freq`. The `top` is the most common value. The `freq` is the most common value's frequency. Timestamps also include the `first` and `last` items.

If multiple object values have the highest count, then the `count` and `top` results will be arbitrarily chosen from among those with the highest count.

For mixed data types provided via a `DataFrame`, the default is to return only an analysis of numeric columns. If the dataframe consists only of object and categorical data without any numeric columns, the default is to return an analysis of both the object and categorical columns. If `include='all'` is provided as an option, the result will include a union of attributes of each type.

The *include* and *exclude* parameters can be used to limit which columns in a `DataFrame` are analyzed for the output. The parameters are ignored when analyzing a `Series`.

Examples

Describing a numeric `Series`.

```
>>> s = pd.Series([1, 2, 3])
>>> s.describe()
count    3.0
mean     2.0
std      1.0
min      1.0
25%      1.5
50%      2.0
```

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```
75%      2.5
max      3.0
```

Describing a categorical `Series`.

```
>>> s = pd.Series(['a', 'a', 'b', 'c'])
>>> s.describe()
count     4
unique    3
top       a
freq      2
dtype: object
```

Describing a timestamp `Series`.

```
>>> s = pd.Series([
...   np.datetime64("2000-01-01"),
...   np.datetime64("2010-01-01"),
...   np.datetime64("2010-01-01")
... ])
>>> s.describe()
count                      3
unique                     2
top       2010-01-01 00:00:00
freq                       2
first     2000-01-01 00:00:00
last      2010-01-01 00:00:00
dtype: object
```

Describing a `DataFrame`. By default only numeric fields are returned.

```
>>> df = pd.DataFrame({ 'object': ['a', 'b', 'c'],
...                     'numeric': [1, 2, 3],
...                     'categorical': pd.Categorical(['d','e','f'])
...                   })
>>> df.describe()
       numeric
count      3.0
mean       2.0
std        1.0
min        1.0
25%        1.5
50%        2.0
75%        2.5
max        3.0
```

Describing all columns of a `DataFrame` regardless of data type.

```
>>> df.describe(include='all')
        categorical  numeric object
count             3      3.0      3
unique            3      NaN      3
top               f      NaN      c
freq              1      NaN      1
mean            NaN      2.0    NaN
std             NaN      1.0    NaN
```

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```
min            NaN      1.0    NaN
25%            NaN      1.5    NaN
50%            NaN      2.0    NaN
75%            NaN      2.5    NaN
max            NaN      3.0    NaN
```

Describing a column from a `DataFrame` by accessing it as an attribute.

```
>>> df.numeric.describe()
count    3.0
mean     2.0
std      1.0
min      1.0
25%      1.5
50%      2.0
75%      2.5
max      3.0
Name: numeric, dtype: float64
```

Including only numeric columns in a `DataFrame` description.

```
>>> df.describe(include=[np.number])
       numeric
count      3.0
mean       2.0
std        1.0
min        1.0
25%        1.5
50%        2.0
75%        2.5
max        3.0
```

Including only string columns in a `DataFrame` description.

```
>>> df.describe(include=[np.object])
       object
count       3
unique      3
top         c
freq        1
```

Including only categorical columns from a `DataFrame` description.

```
>>> df.describe(include=['category'])
       categorical
count            3
unique           3
top              f
freq             1
```

Excluding numeric columns from a `DataFrame` description.

```
>>> df.describe(exclude=[np.number])
       categorical object
count            3      3
unique           3      3
```

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```
top              f      c
freq             1      1
```

Excluding object columns from a `DataFrame` description.

```
>>> df.describe(exclude=[np.object])
        categorical  numeric
count             3      3.0
unique            3      NaN
top               f      NaN
freq              1      NaN
mean            NaN      2.0
std             NaN      1.0
min             NaN      1.0
25%             NaN      1.5
50%             NaN      2.0
75%             NaN      2.5
max             NaN      3.0
```

diff (*periods=1*, *axis=0*)

First discrete difference of element.

Calculates the difference of a DataFrame element compared with another element in the DataFrame (default is the element in the same column of the previous row).

Parameters

periods [int, default 1] Periods to shift for calculating difference, accepts negative values.

axis [{0 or 'index', 1 or 'columns'}, default 0] Take difference over rows (0) or columns (1).

New in version 0.16.1..

Returns

diffed [DataFrame]

See also:

Series.diff First discrete difference for a Series.

DataFrame.pct_change Percent change over given number of periods.

DataFrame.shift Shift index by desired number of periods with an optional time freq.

Examples

Difference with previous row

```
>>> df = pd.DataFrame({'a': [1, 2, 3, 4, 5, 6],
...                    'b': [1, 1, 2, 3, 5, 8],
...                    'c': [1, 4, 9, 16, 25, 36]})
>>> df
   a  b   c
0  1  1   1
1  2  1   4
2  3  2   9
```

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```
3  4  3  16
4  5  5  25
5  6  8  36
```

```
>>> df.diff()
     a    b     c
0  NaN  NaN   NaN
1  1.0  0.0   3.0
2  1.0  1.0   5.0
3  1.0  1.0   7.0
4  1.0  2.0   9.0
5  1.0  3.0  11.0
```

Difference with previous column

```
>>> df.diff(axis=1)
    a    b     c
0 NaN  0.0   0.0
1 NaN -1.0   3.0
2 NaN -1.0   7.0
3 NaN -1.0  13.0
4 NaN  0.0  20.0
5 NaN  2.0  28.0
```

Difference with 3rd previous row

```
>>> df.diff(periods=3)
     a    b     c
0  NaN  NaN   NaN
1  NaN  NaN   NaN
2  NaN  NaN   NaN
3  3.0  2.0  15.0
4  3.0  4.0  21.0
5  3.0  6.0  27.0
```

Difference with following row

```
>>> df.diff(periods=-1)
     a    b     c
0 -1.0  0.0  -3.0
1 -1.0 -1.0  -5.0
2 -1.0 -1.0  -7.0
3 -1.0 -2.0  -9.0
4 -1.0 -3.0 -11.0
5  NaN  NaN   NaN
```

div(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Floating division of dataframe and other, element-wise (binary operator *truediv*).

Equivalent to `dataframe / other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.rtruediv

Notes

Mismatched indices will be unioned together

Examples

None

drop(*labels*, *axis=0*, *errors='raise'*)
Drop specified labels from rows or columns.

Remove rows or columns by specifying label names and corresponding axis, or by specifying directly index or column names. When using a multi-index, labels on different levels can be removed by specifying the level.

Parameters

labels [single label or list-like] Index or column labels to drop.

axis [{0 or 'index', 1 or 'columns'}, default 0] Whether to drop labels from the index (0 or 'index') or columns (1 or 'columns').

index, columns [single label or list-like] Alternative to specifying axis (`labels, axis=1` is equivalent to `columns=labels`).

New in version 0.21.0.

level [int or level name, optional] For MultiIndex, level from which the labels will be removed.

inplace [bool, default False] If True, do operation inplace and return None.

errors [{'ignore', 'raise'}, default 'raise'] If 'ignore', suppress error and only existing labels are dropped.

Returns

dropped [pandas.DataFrame]

Raises

KeyError If none of the labels are found in the selected axis

See also:

DataFrame.loc Label-location based indexer for selection by label.

DataFrame.dropna Return DataFrame with labels on given axis omitted where (all or any) data are missing

DataFrame.drop_duplicates Return DataFrame with duplicate rows removed, optionally only considering certain columns

Series.drop Return Series with specified index labels removed.

Notes

Dask doesn't support the following argument(s).

- index
- columns
- level
- inplace

Examples

```
>>> df = pd.DataFrame(np.arange(12).reshape(3,4),
...                   columns=['A', 'B', 'C', 'D'])
>>> df
   A  B   C   D
0  0  1   2   3
1  4  5   6   7
2  8  9  10  11
```

Drop columns

```
>>> df.drop(['B', 'C'], axis=1)
   A   D
0  0   3
1  4   7
2  8  11
```

```
>>> df.drop(columns=['B', 'C'])
   A   D
0  0   3
1  4   7
2  8  11
```

Drop a row by index

```
>>> df.drop([0, 1])
   A  B   C   D
2  8  9  10  11
```

Drop columns and/or rows of MultiIndex DataFrame

```
>>> midx = pd.MultiIndex(levels=[['lama', 'cow', 'falcon'],
...                              ['speed', 'weight', 'length']],
...                      labels=[[0, 0, 0, 1, 1, 1, 2, 2, 2],
...                              [0, 1, 2, 0, 1, 2, 0, 1, 2]])
```

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```
>>> df = pd.DataFrame(index=midx, columns=['big', 'small'],
...                   data=[[45, 30], [200, 100], [1.5, 1], [30, 20],
...                         [250, 150], [1.5, 0.8], [320, 250],
...                         [1, 0.8], [0.3,0.2]])
>>> df
                big     small
lama    speed   45.0    30.0
        weight  200.0   100.0
        length  1.5     1.0
cow     speed   30.0    20.0
        weight  250.0   150.0
        length  1.5     0.8
falcon  speed   320.0   250.0
        weight  1.0     0.8
        length  0.3     0.2
```

```
>>> df.drop(index='cow', columns='small')
                big
lama    speed   45.0
        weight  200.0
        length  1.5
falcon  speed   320.0
        weight  1.0
        length  0.3
```

```
>>> df.drop(index='length', level=1)
                big     small
lama    speed   45.0    30.0
        weight  200.0   100.0
cow     speed   30.0    20.0
        weight  250.0   150.0
falcon  speed   320.0   250.0
        weight  1.0     0.8
```

drop_duplicates(*split_every=None*, *split_out=1*, ***kwargs*)

Return DataFrame with duplicate rows removed, optionally only considering certain columns

Parameters

subset [column label or sequence of labels, optional] Only consider certain columns for identifying duplicates, by default use all of the columns

keep [{'first', 'last', False}, default 'first']

- `first` : Drop duplicates except for the first occurrence.
- `last` : Drop duplicates except for the last occurrence.
- False : Drop all duplicates.

inplace [boolean, default False] Whether to drop duplicates in place or to return a copy

Returns

deduplicated [DataFrame]

Notes

Dask doesn't support the following argument(s).

- subset
- keep
- inplace

dropna(*how='any'*, *subset=None*)
Remove missing values.

See the User Guide for more on which values are considered missing, and how to work with missing data.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] Determine if rows or columns which contain missing values are removed.

- 0, or 'index' : Drop rows which contain missing values.
- 1, or 'columns' : Drop columns which contain missing value.

Deprecated since version 0.23.0:: Pass tuple or list to drop on multiple

axes.

how [{'any', 'all'}, default 'any'] Determine if row or column is removed from DataFrame, when we have at least one NA or all NA.

- 'any' : If any NA values are present, drop that row or column.
- 'all' : If all values are NA, drop that row or column.

thresh [int, optional] Require that many non-NA values.

subset [array-like, optional] Labels along other axis to consider, e.g. if you are dropping rows these would be a list of columns to include.

inplace [bool, default False] If True, do operation inplace and return None.

Returns

DataFrame DataFrame with NA entries dropped from it.

See also:

DataFrame.isna Indicate missing values.

DataFrame.notna Indicate existing (non-missing) values.

DataFrame.fillna Replace missing values.

Series.dropna Drop missing values.

Index.dropna Drop missing indices.

Notes

Dask doesn't support the following argument(s).

- axis
- thresh

- inplace

Examples

```
>>> df = pd.DataFrame({"name": ['Alfred', 'Batman', 'Catwoman'],
...                    "toy": [np.nan, 'Batmobile', 'Bullwhip'],
...                    "born": [pd.NaT, pd.Timestamp("1940-04-25"),
...                             pd.NaT]})
>>> df
       name        toy       born
0    Alfred        NaN        NaT
1    Batman  Batmobile 1940-04-25
2  Catwoman   Bullwhip        NaT
```

Drop the rows where at least one element is missing.

```
>>> df.dropna()
     name        toy       born
1  Batman  Batmobile 1940-04-25
```

Drop the columns where at least one element is missing.

```
>>> df.dropna(axis='columns')
       name
0    Alfred
1    Batman
2  Catwoman
```

Drop the rows where all elements are missing.

```
>>> df.dropna(how='all')
       name        toy       born
0    Alfred        NaN        NaT
1    Batman  Batmobile 1940-04-25
2  Catwoman   Bullwhip        NaT
```

Keep only the rows with at least 2 non-NA values.

```
>>> df.dropna(thresh=2)
       name        toy       born
1    Batman  Batmobile 1940-04-25
2  Catwoman   Bullwhip        NaT
```

Define in which columns to look for missing values.

```
>>> df.dropna(subset=['name', 'born'])
       name        toy       born
1    Batman  Batmobile 1940-04-25
```

Keep the DataFrame with valid entries in the same variable.

```
>>> df.dropna(inplace=True)
>>> df
     name        toy       born
1  Batman  Batmobile 1940-04-25
```

dtypes
Return data types

eq(*other*, *axis='columns'*, *level=None*)
Wrapper for flexible comparison methods eq

eval(*expr*, *inplace=None*, ***kwargs*)
Evaluate a string describing operations on DataFrame columns.

Operates on columns only, not specific rows or elements. This allows *eval* to run arbitrary code, which can make you vulnerable to code injection if you pass user input to this function.

Parameters

expr [str] The expression string to evaluate.

inplace [bool, default False] If the expression contains an assignment, whether to perform the operation inplace and mutate the existing DataFrame. Otherwise, a new DataFrame is returned.

New in version 0.18.0..

kwargs [dict] See the documentation for `eval()` for complete details on the keyword arguments accepted by `query()`.

Returns

ndarray, scalar, or pandas object The result of the evaluation.

See also:

DataFrame.query Evaluates a boolean expression to query the columns of a frame.

DataFrame.assign Can evaluate an expression or function to create new values for a column.

pandas.eval Evaluate a Python expression as a string using various backends.

Notes

For more details see the API documentation for `eval()`. For detailed examples see enhancing performance with eval.

Examples

```
>>> df = pd.DataFrame({'A': range(1, 6), 'B': range(10, 0, -2)})
>>> df
   A   B
0  1  10
1  2   8
2  3   6
3  4   4
4  5   2
>>> df.eval('A + B')
0    11
1    10
2     9
3     8
4     7
dtype: int64
```

Assignment is allowed though by default the original DataFrame is not modified.

```
>>> df.eval('C = A + B')
   A   B   C
0  1  10  11
1  2   8  10
2  3   6   9
3  4   4   8
4  5   2   7
>>> df
   A   B
0  1  10
1  2   8
2  3   6
3  4   4
4  5   2
```

Use `inplace=True` to modify the original DataFrame.

```
>>> df.eval('C = A + B', inplace=True)
>>> df
   A   B   C
0  1  10  11
1  2   8  10
2  3   6   9
3  4   4   8
4  5   2   7
```

ffill (*axis=None*, *limit=None*)
Synonym for *DataFrame.fillna(method='ffill')*

Notes

Dask doesn't support the following argument(s).

- inplace
- downcast

fillna (*value=None*, *method=None*, *limit=None*, *axis=None*)
Fill NA/NaN values using the specified method

Parameters

value [scalar, dict, Series, or DataFrame] Value to use to fill holes (e.g. 0), alternately a dict/Series/DataFrame of values specifying which value to use for each index (for a Series) or column (for a DataFrame). (values not in the dict/Series/DataFrame will not be filled). This value cannot be a list.

method [{'backfill', 'bfill', 'pad', 'ffill', None}, default None] Method to use for filling holes in reindexed Series pad / ffill: propagate last valid observation forward to next valid backfill / bfill: use NEXT valid observation to fill gap

axis [{0 or 'index', 1 or 'columns'}]

inplace [boolean, default False] If True, fill in place. Note: this will modify any other views on this object, (e.g. a no-copy slice for a column in a DataFrame).

limit [int, default None] If method is specified, this is the maximum number of consecutive NaN values to forward/backward fill. In other words, if there is a gap with more

than this number of consecutive NaNs, it will only be partially filled. If method is not specified, this is the maximum number of entries along the entire axis where NaNs will be filled. Must be greater than 0 if not None.

downcast [dict, default is None] a dict of item->dtype of what to downcast if possible, or the string 'infer' which will try to downcast to an appropriate equal type (e.g. float64 to int64 if possible)

Returns

filled [DataFrame]

See also:

`interpolate` Fill NaN values using interpolation.

`reindex`, `asfreq`

Notes

Dask doesn't support the following argument(s).

- inplace
- downcast

Examples

```
>>> df = pd.DataFrame([[np.nan, 2, np.nan, 0],
...                    [3, 4, np.nan, 1],
...                    [np.nan, np.nan, np.nan, 5],
...                    [np.nan, 3, np.nan, 4]],
...                   columns=list('ABCD'))
>>> df
     A    B   C  D
0  NaN  2.0 NaN  0
1  3.0  4.0 NaN  1
2  NaN  NaN NaN  5
3  NaN  3.0 NaN  4
```

Replace all NaN elements with 0s.

```
>>> df.fillna(0)
    A   B   C   D
0   0.0 2.0 0.0 0
1   3.0 4.0 0.0 1
2   0.0 0.0 0.0 5
3   0.0 3.0 0.0 4
```

We can also propagate non-null values forward or backward.

```
>>> df.fillna(method='ffill')
    A   B   C   D
0   NaN 2.0 NaN 0
1   3.0 4.0 NaN 1
2   3.0 4.0 NaN 5
3   3.0 3.0 NaN 4
```

Replace all NaN elements in column 'A', 'B', 'C', and 'D', with 0, 1, 2, and 3 respectively.

```
>>> values = {'A': 0, 'B': 1, 'C': 2, 'D': 3}
>>> df.fillna(value=values)
    A   B   C   D
0   0.0 2.0 2.0 0
1   3.0 4.0 2.0 1
2   0.0 1.0 2.0 5
3   0.0 3.0 2.0 4
```

Only replace the first NaN element.

```
>>> df.fillna(value=values, limit=1)
    A   B   C   D
0   0.0 2.0 2.0 0
1   3.0 4.0 NaN 1
2   NaN 1.0 NaN 5
3   NaN 3.0 NaN 4
```

first (*offset*)

Convenience method for subsetting initial periods of time series data based on a date offset.

Parameters

offset [string, DateOffset, dateutil.relativedelta]

Returns

subset [type of caller]

Raises

TypeError If the index is not a `DatetimeIndex`

See also:

last Select final periods of time series based on a date offset

at_time Select values at a particular time of the day

between_time Select values between particular times of the day

Examples

```
>>> i = pd.date_range('2018-04-09', periods=4, freq='2D')
>>> ts = pd.DataFrame({'A': [1,2,3,4]}, index=i)
>>> ts
            A
2018-04-09  1
2018-04-11  2
2018-04-13  3
2018-04-15  4
```

Get the rows for the first 3 days:

```
>>> ts.first('3D')
            A
2018-04-09  1
2018-04-11  2
```

Notice the data for 3 first calender days were returned, not the first 3 days observed in the dataset, and therefore data for 2018-04-13 was not returned.

floordiv(*other*, *axis='columns'*, *level=None*, *fill_value=None*)
Integer division of dataframe and other, element-wise (binary operator *floordiv*).

Equivalent to `dataframe // other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.rfloordiv

Notes

Mismatched indices will be unioned together

Examples

None

ge(*other*, *axis='columns'*, *level=None*)
Wrapper for flexible comparison methods ge

get_dtype_counts()
Return counts of unique dtypes in this object.

Returns

dtype [Series] Series with the count of columns with each dtype.

See also:

dtypes Return the dtypes in this object.

Examples

```
>>> a = [['a', 1, 1.0], ['b', 2, 2.0], ['c', 3, 3.0]]
>>> df = pd.DataFrame(a, columns=['str', 'int', 'float'])
>>> df
  str  int  float
0   a    1    1.0
1   b    2    2.0
2   c    3    3.0
```

```
>>> df.get_dtype_counts()
float64    1
int64      1
object     1
dtype: int64
```

get_ftype_counts()

Return counts of unique ftypes in this object.

Deprecated since version 0.23.0.

This is useful for SparseDataFrame or for DataFrames containing sparse arrays.

Returns

dtype [Series] Series with the count of columns with each type and sparsity (dense/sparse)

See also:

ftypes Return ftypes (indication of sparse/dense and dtype) in this object.

Examples

```
>>> a = [['a', 1, 1.0], ['b', 2, 2.0], ['c', 3, 3.0]]
>>> df = pd.DataFrame(a, columns=['str', 'int', 'float'])
>>> df
  str  int  float
0   a    1    1.0
1   b    2    2.0
2   c    3    3.0
```

```
>>> df.get_ftype_counts()
float64:dense    1
int64:dense      1
object:dense     1
dtype: int64
```

get_partition(*n*)

Get a dask DataFrame/Series representing the *nth* partition.

groupby(*by=None*, ***kwargs*)

Group series using mapper (dict or key function, apply given function to group, return result as series) or by a series of columns.

Parameters

by [mapping, function, label, or list of labels] Used to determine the groups for the groupby. If `by` is a function, it's called on each value of the object's index. If a

dict or Series is passed, the Series or dict VALUES will be used to determine the groups (the Series' values are first aligned; see `.align()` method). If an ndarray is passed, the values are used as-is determine the groups. A label or list of labels may be passed to group by the columns in `self`. Notice that a tuple is interpreted a (single) key.

axis [int, default 0]

level [int, level name, or sequence of such, default None] If the axis is a MultiIndex (hierarchical), group by a particular level or levels

as_index [boolean, default True] For aggregated output, return object with group labels as the index. Only relevant for DataFrame input. as_index=False is effectively "SQL-style" grouped output

sort [boolean, default True] Sort group keys. Get better performance by turning this off. Note this does not influence the order of observations within each group. groupby preserves the order of rows within each group.

group_keys [boolean, default True] When calling apply, add group keys to index to identify pieces

squeeze [boolean, default False] reduce the dimensionality of the return type if possible, otherwise return a consistent type

observed [boolean, default False] This only applies if any of the groupers are Categoricals If True: only show observed values for categorical groupers. If False: show all values for categorical groupers.

New in version 0.23.0.

Returns

GroupBy object

See also:

resample Convenience method for frequency conversion and resampling of time series.

Notes

See the user guide for more.

Examples

DataFrame results

```
>>> data.groupby(func, axis=0).mean()
>>> data.groupby(['col1', 'col2'])['col3'].mean()
```

DataFrame with hierarchical index

```
>>> data.groupby(['col1', 'col2']).mean()
```

gt(*other*, *axis='columns'*, *level=None*)
Wrapper for flexible comparison methods gt

head(*n=5*, *npartitions=1*, *compute=True*)
First n rows of the dataset

Parameters

n [int, optional] The number of rows to return. Default is 5.

npartitions [int, optional] Elements are only taken from the first `npartitions`, with a default of 1. If there are fewer than `n` rows in the first `npartitions` a warning will be raised and any found rows returned. Pass -1 to use all partitions.

compute [bool, optional] Whether to compute the result, default is True.

idxmax(*axis=None*, *skipna=True*, *split_every=False*)

Return index of first occurrence of maximum over requested axis. NA/null values are excluded.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

Returns

idxmax [Series]

Raises

ValueError

- If the row/column is empty

See also:

Series.idxmax

Notes

This method is the DataFrame version of `ndarray.argmax`.

idxmin(*axis=None*, *skipna=True*, *split_every=False*)

Return index of first occurrence of minimum over requested axis. NA/null values are excluded.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

Returns

idxmin [Series]

Raises

ValueError

- If the row/column is empty

See also:

Series.idxmin

Notes

This method is the DataFrame version of `ndarray.argmin`.

iloc
Purely integer-location based indexing for selection by position.

Only indexing the column positions is supported. Trying to select row positions will raise a ValueError.

See *Indexing into Dask DataFrames* for more.

Examples

```
>>> df.iloc[:, [2, 0, 1]]
```

index
Return dask Index instance

info(*buf=None*, *verbose=False*, *memory_usage=False*)
Concise summary of a Dask DataFrame.

isin(*values*)
Return boolean DataFrame showing whether each element in the DataFrame is contained in values.

Parameters

values [iterable, Series, DataFrame or dictionary] The result will only be true at a location if all the labels match. If *values* is a Series, that's the index. If *values* is a dictionary, the keys must be the column names, which must match. If *values* is a DataFrame, then both the index and column labels must match.

Returns

DataFrame of booleans

Examples

When `values` is a list:

```
>>> df = pd.DataFrame({'A': [1, 2, 3], 'B': ['a', 'b', 'f']})
>>> df.isin([1, 3, 12, 'a'])
       A      B
0   True   True
1  False  False
2   True  False
```

When `values` is a dict:

```
>>> df = pd.DataFrame({'A': [1, 2, 3], 'B': [1, 4, 7]})
>>> df.isin({'A': [1, 3], 'B': [4, 7, 12]})
       A      B
0   True  False  # Note that B didn't match the 1 here.
1  False   True
2   True   True
```

When `values` is a Series or DataFrame:

```
>>> df = pd.DataFrame({'A': [1, 2, 3], 'B': ['a', 'b', 'f']})
>>> other = DataFrame({'A': [1, 3, 3, 2], 'B': ['e', 'f', 'f', 'e']})
>>> df.isin(other)
       A      B
0   True  False
1  False  False  # Column A in `other` has a 3, but not at index 1.
2   True   True
```

isna()

Detect missing values.

Return a boolean same-sized object indicating if the values are NA. NA values, such as None or `numpy.NaN`, gets mapped to True values. Everything else gets mapped to False values. Characters such as empty strings `''` or `numpy.inf` are not considered NA values (unless you set `pandas.options.mode.use_inf_as_na = True`).

Returns

DataFrame Mask of bool values for each element in DataFrame that indicates whether an element is not an NA value.

See also:

DataFrame.isnull alias of isna

DataFrame.notna boolean inverse of isna

DataFrame.dropna omit axes labels with missing values

isna top-level isna

Examples

Show which entries in a DataFrame are NA.

```
>>> df = pd.DataFrame({'age': [5, 6, np.NaN],
...                    'born': [pd.NaT, pd.Timestamp('1939-05-27'),
...                             pd.Timestamp('1940-04-25')],
...                    'name': ['Alfred', 'Batman', ''],
...                    'toy': [None, 'Batmobile', 'Joker']})
>>> df
   age       born    name        toy
0  5.0        NaT  Alfred       None
1  6.0 1939-05-27  Batman  Batmobile
2  NaN 1940-04-25              Joker
```

```
>>> df.isna()
     age   born   name    toy
0  False   True  False   True
1  False  False  False  False
2   True  False  False  False
```

Show which entries in a Series are NA.

```
>>> ser = pd.Series([5, 6, np.NaN])
>>> ser
0    5.0
```

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```
1    6.0
2    NaN
dtype: float64
```

```
>>> ser.isna()
0    False
1    False
2     True
dtype: bool
```

isnull()

Detect missing values.

Return a boolean same-sized object indicating if the values are NA. NA values, such as None or `numpy.NaN`, gets mapped to True values. Everything else gets mapped to False values. Characters such as empty strings `''` or `numpy.inf` are not considered NA values (unless you set `pandas.options.mode.use_inf_as_na = True`).

Returns

DataFrame Mask of bool values for each element in DataFrame that indicates whether an element is not an NA value.

See also:

DataFrame.isnull alias of isna

DataFrame.notna boolean inverse of isna

DataFrame.dropna omit axes labels with missing values

isna top-level isna

Examples

Show which entries in a DataFrame are NA.

```
>>> df = pd.DataFrame({'age': [5, 6, np.NaN],
...                    'born': [pd.NaT, pd.Timestamp('1939-05-27'),
...                             pd.Timestamp('1940-04-25')],
...                    'name': ['Alfred', 'Batman', ''],
...                    'toy': [None, 'Batmobile', 'Joker']})
>>> df
   age       born    name        toy
0  5.0        NaT  Alfred       None
1  6.0 1939-05-27  Batman  Batmobile
2  NaN 1940-04-25              Joker
```

```
>>> df.isna()
     age   born   name    toy
0  False   True  False   True
1  False  False  False  False
2   True  False  False  False
```

Show which entries in a Series are NA.

```
>>> ser = pd.Series([5, 6, np.NaN])
>>> ser
0    5.0
1    6.0
2    NaN
dtype: float64
```

```
>>> ser.isna()
0    False
1    False
2     True
dtype: bool
```

iterrows()

Iterate over DataFrame rows as (index, Series) pairs.

Returns

it [generator] A generator that iterates over the rows of the frame.

See also:

itertuples Iterate over DataFrame rows as namedtuples of the values.

iteritems Iterate over (column name, Series) pairs.

Notes

1. Because `iterrows` returns a Series for each row, it does **not** preserve dtypes across the rows (dtypes are preserved across columns for DataFrames). For example,

```
>>> df = pd.DataFrame([[1, 1.5]], columns=['int', 'float'])
>>> row = next(df.iterrows())[1]
>>> row
int      1.0
float    1.5
Name: 0, dtype: float64
>>> print(row['int'].dtype)
float64
>>> print(df['int'].dtype)
int64
```

   To preserve dtypes while iterating over the rows, it is better to use *`itertuples()`* which returns namedtuples of the values and which is generally faster than `iterrows`.

2. You should **never modify** something you are iterating over. This is not guaranteed to work in all cases. Depending on the data types, the iterator returns a copy and not a view, and writing to it will have no effect.

itertuples()

Iterate over DataFrame rows as namedtuples, with index value as first element of the tuple.

Parameters

index [boolean, default True] If True, return the index as the first element of the tuple.

name [string, default "Pandas"] The name of the returned namedtuples or None to return regular tuples.

See also:

iterrows Iterate over DataFrame rows as (index, Series) pairs.

iteritems Iterate over (column name, Series) pairs.

Notes

The column names will be renamed to positional names if they are invalid Python identifiers, repeated, or start with an underscore. With a large number of columns (>255), regular tuples are returned.

Examples

```
>>> df = pd.DataFrame({'col1': [1, 2], 'col2': [0.1, 0.2]},
                      index=['a', 'b'])
>>> df
   col1  col2
a     1   0.1
b     2   0.2
>>> for row in df.itertuples():
...     print(row)
...
Pandas(Index='a', col1=1, col2=0.10000000000000001)
Pandas(Index='b', col1=2, col2=0.20000000000000001)
```

join(*other*, *on=None*, *how='left'*, *lsuffix=''*, *rsuffix=''*, *npartitions=None*, *shuffle=None*)
Join columns with other DataFrame either on index or on a key column. Efficiently Join multiple DataFrame objects by index at once by passing a list.

Parameters

other [DataFrame, Series with name field set, or list of DataFrame] Index should be similar to one of the columns in this one. If a Series is passed, its name attribute must be set, and that will be used as the column name in the resulting joined DataFrame

on [name, tuple/list of names, or array-like] Column or index level name(s) in the caller to join on the index in *other*, otherwise joins index-on-index. If multiple values given, the *other* DataFrame must have a MultiIndex. Can pass an array as the join key if it is not already contained in the calling DataFrame. Like an Excel VLOOKUP operation

how [{'left', 'right', 'outer', 'inner'}, default: 'left'] How to handle the operation of the two objects.

- left: use calling frame's index (or column if on is specified)
- right: use other frame's index
- outer: form union of calling frame's index (or column if on is specified) with other frame's index, and sort it lexicographically
- inner: form intersection of calling frame's index (or column if on is specified) with other frame's index, preserving the order of the calling's one

lsuffix [string] Suffix to use from left frame's overlapping columns

rsuffix [string] Suffix to use from right frame's overlapping columns

sort [boolean, default False] Order result DataFrame lexicographically by the join key. If False, the order of the join key depends on the join type (how keyword)

Returns

joined [DataFrame]

See also:

DataFrame.merge For column(s)-on-columns(s) operations

Notes

on, lsuffix, and rsuffix options are not supported when passing a list of DataFrame objects

Support for specifying index levels as the *on* parameter was added in version 0.23.0

Examples

```
>>> caller = pd.DataFrame({'key': ['K0', 'K1', 'K2', 'K3', 'K4', 'K5'],
...                        'A': ['A0', 'A1', 'A2', 'A3', 'A4', 'A5']})
```

```
>>> caller
    A key
0  A0  K0
1  A1  K1
2  A2  K2
3  A3  K3
4  A4  K4
5  A5  K5
```

```
>>> other = pd.DataFrame({'key': ['K0', 'K1', 'K2'],
...                       'B': ['B0', 'B1', 'B2']})
```

```
>>> other
    B key
0  B0  K0
1  B1  K1
2  B2  K2
```

Join DataFrames using their indexes.

```
>>> caller.join(other, lsuffix='_caller', rsuffix='_other')
```

```
>>>     A key_caller    B key_other
    0  A0         K0   B0        K0
    1  A1         K1   B1        K1
    2  A2         K2   B2        K2
    3  A3         K3  NaN       NaN
    4  A4         K4  NaN       NaN
    5  A5         K5  NaN       NaN
```

If we want to join using the key columns, we need to set key to be the index in both caller and other. The joined DataFrame will have key as its index.

```
>>> caller.set_index('key').join(other.set_index('key'))
```

```
>>>      A    B
    key
    K0   A0   B0
    K1   A1   B1
    K2   A2   B2
    K3   A3  NaN
    K4   A4  NaN
    K5   A5  NaN
```

Another option to join using the key columns is to use the on parameter. DataFrame.join always uses other's index but we can use any column in the caller. This method preserves the original caller's index in the result.

```
>>> caller.join(other.set_index('key'), on='key')
```

```
>>>     A key    B
    0  A0  K0   B0
    1  A1  K1   B1
    2  A2  K2   B2
    3  A3  K3  NaN
    4  A4  K4  NaN
    5  A5  K5  NaN
```

known_divisions
Whether divisions are already known

last(*offset*)
Convenience method for subsetting final periods of time series data based on a date offset.

Parameters

offset [string, DateOffset, dateutil.relativedelta]

Returns

subset [type of caller]

Raises

TypeError If the index is not a `DatetimeIndex`

See also:

first Select initial periods of time series based on a date offset

at_time Select values at a particular time of the day

between_time Select values between particular times of the day

Examples

```
>>> i = pd.date_range('2018-04-09', periods=4, freq='2D')
>>> ts = pd.DataFrame({'A': [1,2,3,4]}, index=i)
>>> ts
            A
2018-04-09  1
2018-04-11  2
2018-04-13  3
2018-04-15  4
```

Get the rows for the last 3 days:

```
>>> ts.last('3D')
            A
2018-04-13  3
2018-04-15  4
```

Notice the data for 3 last calender days were returned, not the last 3 observed days in the dataset, and therefore data for 2018-04-11 was not returned.

le (*other*, *axis='columns'*, *level=None*)
Wrapper for flexible comparison methods le

loc
Purely label-location based indexer for selection by label.

```
>>> df.loc["b"]
>>> df.loc["b":"d"]
```

lt (*other*, *axis='columns'*, *level=None*)
Wrapper for flexible comparison methods lt

map_overlap (*func*, *before*, *after*, **args*, ***kwargs*)
Apply a function to each partition, sharing rows with adjacent partitions.

This can be useful for implementing windowing functions such as `df.rolling(...).mean()` or `df.diff()`.

Parameters

func [function] Function applied to each partition.

before [int] The number of rows to prepend to partition `i` from the end of partition `i - 1`.

after [int] The number of rows to append to partition `i` from the beginning of partition `i + 1`.

args, kwargs : Arguments and keywords to pass to the function. The partition will be the first argument, and these will be passed *after*.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Notes

Given positive integers `before` and `after`, and a function `func`, `map_overlap` does the following:

1. Prepend `before` rows to each partition `i` from the end of partition `i - 1`. The first partition has no rows prepended.
2. Append `after` rows to each partition `i` from the beginning of partition `i + 1`. The last partition has no rows appended.

3. Apply `func` to each partition, passing in any extra `args` and `kwargs` if provided.
4. Trim `before` rows from the beginning of all but the first partition.
5. Trim `after` rows from the end of all but the last partition.

Note that the index and divisions are assumed to remain unchanged.

Examples

Given a DataFrame, Series, or Index, such as:

```
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': [1, 2, 4, 7, 11],
...                    'y': [1., 2., 3., 4., 5.]})
>>> ddf = dd.from_pandas(df, npartitions=2)
```

A rolling sum with a trailing moving window of size 2 can be computed by overlapping 2 rows before each partition, and then mapping calls to `df.rolling(2).sum()`:

```
>>> ddf.compute()
    x    y
0   1  1.0
1   2  2.0
2   4  3.0
3   7  4.0
4  11  5.0
>>> ddf.map_overlap(lambda df: df.rolling(2).sum(), 2, 0).compute()
      x    y
0   NaN  NaN
1   3.0  3.0
2   6.0  5.0
3  11.0  7.0
4  18.0  9.0
```

The pandas `diff` method computes a discrete difference shifted by a number of periods (can be positive or negative). This can be implemented by mapping calls to `df.diff` to each partition after prepending/appending that many rows, depending on sign:

```
>>> def diff(df, periods=1):
...     before, after = (periods, 0) if periods > 0 else (0, -periods)
...     return df.map_overlap(lambda df, periods=1: df.diff(periods),
...                           periods, 0, periods=periods)
>>> diff(ddf, 1).compute()
     x    y
0  NaN  NaN
1  1.0  1.0
2  2.0  1.0
3  3.0  1.0
4  4.0  1.0
```

If you have a `DatetimeIndex`, you can use a `pd.Timedelta` for time- based windows.

```
>>> ts = pd.Series(range(10), index=pd.date_range('2017', periods=10))
>>> dts = dd.from_pandas(ts, npartitions=2)
>>> dts.map_overlap(lambda df: df.rolling('2D').sum(),
...                 pd.Timedelta('2D'), 0).compute()
```

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```
2017-01-01     0.0
2017-01-02     1.0
2017-01-03     3.0
2017-01-04     5.0
2017-01-05     7.0
2017-01-06     9.0
2017-01-07    11.0
2017-01-08    13.0
2017-01-09    15.0
2017-01-10    17.0
dtype: float64
```

map_partitions (*func*, **args*, ***kwargs*)

Apply Python function on each DataFrame partition.

Note that the index and divisions are assumed to remain unchanged.

Parameters

func [function] Function applied to each partition.

args, kwargs : Arguments and keywords to pass to the function. The partition will be the first argument, and these will be passed *after*. Arguments and keywords may contain `Scalar`, `Delayed` or regular python objects.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Examples

Given a DataFrame, Series, or Index, such as:

```
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': [1, 2, 3, 4, 5],
...                    'y': [1., 2., 3., 4., 5.]})
>>> ddf = dd.from_pandas(df, npartitions=2)
```

One can use `map_partitions` to apply a function on each partition. Extra arguments and keywords can optionally be provided, and will be passed to the function after the partition.

Here we apply a function with arguments and keywords to a DataFrame, resulting in a Series:

```
>>> def myadd(df, a, b=1):
...     return df.x + df.y + a + b
>>> res = ddf.map_partitions(myadd, 1, b=2)
>>> res.dtype
dtype('float64')
```

By default, dask tries to infer the output metadata by running your provided function on some fake data. This works well in many cases, but can sometimes be expensive, or even fail. To avoid this, you can

manually specify the output metadata with the `meta` keyword. This can be specified in many forms, for more information see `dask.dataframe.utils.make_meta`.

Here we specify the output is a Series with no name, and dtype `float64`:

```
>>> res = ddf.map_partitions(myadd, 1, b=2, meta=(None, 'f8'))
```

Here we map a function that takes in a DataFrame, and returns a DataFrame with a new column:

```
>>> res = ddf.map_partitions(lambda df: df.assign(z=df.x * df.y))
>>> res.dtypes
x      int64
y    float64
z    float64
dtype: object
```

As before, the output metadata can also be specified manually. This time we pass in a `dict`, as the output is a DataFrame:

```
>>> res = ddf.map_partitions(lambda df: df.assign(z=df.x * df.y),
...                          meta={'x': 'i8', 'y': 'f8', 'z': 'f8'})
```

In the case where the metadata doesn't change, you can also pass in the object itself directly:

```
>>> res = ddf.map_partitions(lambda df: df.head(), meta=df)
```

Also note that the index and divisions are assumed to remain unchanged. If the function you're mapping changes the index/divisions, you'll need to clear them afterwards:

```
>>> ddf.map_partitions(func).clear_divisions()
```

mask(*cond*, *other=nan*)

Return an object of same shape as self and whose corresponding entries are from self where *cond* is False and otherwise are from *other*.

Parameters

cond [boolean NDFrame, array-like, or callable] Where *cond* is False, keep the original value. Where True, replace with corresponding value from *other*. If *cond* is callable, it is computed on the NDFrame and should return boolean NDFrame or array. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as cond.

other [scalar, NDFrame, or callable] Entries where *cond* is True are replaced with corresponding value from *other*. If other is callable, it is computed on the NDFrame and should return scalar or NDFrame. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as other.

inplace [boolean, default False] Whether to perform the operation in place on the data

axis [alignment axis if needed, default None]

level [alignment level if needed, default None]

errors [str, {'raise', 'ignore'}, default 'raise']

- `raise` : allow exceptions to be raised
- `ignore` : suppress exceptions. On error return original object

Note that currently this parameter won't affect the results and will always coerce to a suitable dtype.

try_cast [boolean, default False] try to cast the result back to the input type (if possible),

raise_on_error [boolean, default True] Whether to raise on invalid data types (e.g. trying to where on strings)

Deprecated since version 0.21.0.

Returns

wh [same type as caller]

See also:

DataFrame.where()

Notes

The mask method is an application of the if-then idiom. For each element in the calling DataFrame, if `cond` is `False` the element is used; otherwise the corresponding element from the DataFrame `other` is used.

The signature for *DataFrame.where()* differs from `numpy.where()`. Roughly `df1.where(m, df2)` is equivalent to `np.where(m, df1, df2)`.

For further details and examples see the `mask` documentation in indexing.

Examples

```
>>> s = pd.Series(range(5))
>>> s.where(s > 0)
0    NaN
1    1.0
2    2.0
3    3.0
4    4.0
```

```
>>> s.mask(s > 0)
0    0.0
1    NaN
2    NaN
3    NaN
4    NaN
```

```
>>> s.where(s > 1, 10)
0    10.0
1    10.0
2    2.0
3    3.0
4    4.0
```

```
>>> df = pd.DataFrame(np.arange(10).reshape(-1, 2), columns=['A', 'B'])
>>> m = df % 3 == 0
>>> df.where(m, -df)
```

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```
   A  B
0  0 -1
1 -2  3
2 -4 -5
3  6 -7
4 -8  9
>>> df.where(m, -df) == np.where(m, df, -df)
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
>>> df.where(m, -df) == df.mask(~m, -df)
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
```

max(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)

This method returns the maximum of the values in the object. If you want the *index* of the maximum, use `idxmax`. This is the equivalent of the `numpy.ndarray` method `argmax`.

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values when computing the result.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

max [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

mean(*axis=None*, *skipna=True*, *split_every=False*, *dtype=None*, *out=None*)

Return the mean of the values for the requested axis

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values when computing the result.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

mean [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

memory_usage (*index=True*, *deep=False*)
Return the memory usage of each column in bytes.

The memory usage can optionally include the contribution of the index and elements of *object* dtype.

This value is displayed in *DataFrame.info* by default. This can be suppressed by setting `pandas.options.display.memory_usage` to False.

Parameters

index [bool, default True] Specifies whether to include the memory usage of the DataFrame's index in returned Series. If `index=True` the memory usage of the index the first item in the output.

deep [bool, default False] If True, introspect the data deeply by interrogating *object* dtypes for system-level memory consumption, and include it in the returned values.

Returns

sizes [Series] A Series whose index is the original column names and whose values is the memory usage of each column in bytes.

See also:

numpy.ndarray.nbytes Total bytes consumed by the elements of an ndarray.

Series.memory_usage Bytes consumed by a Series.

pandas.Categorical Memory-efficient array for string values with many repeated values.

DataFrame.info Concise summary of a DataFrame.

Examples

```
>>> dtypes = ['int64', 'float64', 'complex128', 'object', 'bool']
>>> data = dict([(t, np.ones(shape=5000).astype(t))
...              for t in dtypes])
>>> df = pd.DataFrame(data)
>>> df.head()
   int64  float64  complex128 object  bool
0      1      1.0      (1+0j)      1  True
```

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```
1       1       1.0       (1+0j)       1  True
2       1       1.0       (1+0j)       1  True
3       1       1.0       (1+0j)       1  True
4       1       1.0       (1+0j)       1  True
```

```
>>> df.memory_usage()
Index            80
int64         40000
float64       40000
complex128    80000
object        40000
bool           5000
dtype: int64
```

```
>>> df.memory_usage(index=False)
int64         40000
float64       40000
complex128    80000
object        40000
bool           5000
dtype: int64
```

The memory footprint of *object* dtype columns is ignored by default:

```
>>> df.memory_usage(deep=True)
Index            80
int64         40000
float64       40000
complex128    80000
object       160000
bool           5000
dtype: int64
```

Use a Categorical for efficient storage of an object-dtype column with many repeated values.

```
>>> df['object'].astype('category').memory_usage(deep=True)
5168
```

merge(*right*, *how='inner'*, *on=None*, *left_on=None*, *right_on=None*, *left_index=False*, *right_index=False*, *suffixes=('_x', '_y')*, *indicator=False*, *npartitions=None*, *shuffle=None*)

Merge DataFrame objects by performing a database-style join operation by columns or indexes.

If joining columns on columns, the DataFrame indexes *will be ignored*. Otherwise if joining indexes on indexes or indexes on a column or columns, the index will be passed on.

Parameters

right [DataFrame]

how [{'left', 'right', 'outer', 'inner'}, default 'inner']

- left: use only keys from left frame, similar to a SQL left outer join; preserve key order
- right: use only keys from right frame, similar to a SQL right outer join; preserve key order
- outer: use union of keys from both frames, similar to a SQL full outer join; sort keys lexicographically

- inner: use intersection of keys from both frames, similar to a SQL inner join; preserve the order of the left keys

on [label or list] Column or index level names to join on. These must be found in both DataFrames. If *on* is None and not merging on indexes then this defaults to the intersection of the columns in both DataFrames.

left_on [label or list, or array-like] Column or index level names to join on in the left DataFrame. Can also be an array or list of arrays of the length of the left DataFrame. These arrays are treated as if they are columns.

right_on [label or list, or array-like] Column or index level names to join on in the right DataFrame. Can also be an array or list of arrays of the length of the right DataFrame. These arrays are treated as if they are columns.

left_index [boolean, default False] Use the index from the left DataFrame as the join key(s). If it is a MultiIndex, the number of keys in the other DataFrame (either the index or a number of columns) must match the number of levels

right_index [boolean, default False] Use the index from the right DataFrame as the join key. Same caveats as left_index

sort [boolean, default False] Sort the join keys lexicographically in the result DataFrame. If False, the order of the join keys depends on the join type (how keyword)

suffixes [2-length sequence (tuple, list, . . .)] Suffix to apply to overlapping column names in the left and right side, respectively

copy [boolean, default True] If False, do not copy data unnecessarily

indicator [boolean or string, default False] If True, adds a column to output DataFrame called "_merge" with information on the source of each row. If string, column with information on source of each row will be added to output DataFrame, and column will be named value of string. Information column is Categorical-type and takes on a value of "left_only" for observations whose merge key only appears in 'left' DataFrame, "right_only" for observations whose merge key only appears in 'right' DataFrame, and "both" if the observation's merge key is found in both.

validate [string, default None] If specified, checks if merge is of specified type.

- "one_to_one" or "1:1": check if merge keys are unique in both left and right datasets.
- "one_to_many" or "1:m": check if merge keys are unique in left dataset.
- "many_to_one" or "m:1": check if merge keys are unique in right dataset.
- "many_to_many" or "m:m": allowed, but does not result in checks.

New in version 0.21.0.

Returns

merged [DataFrame] The output type will the be same as 'left', if it is a subclass of DataFrame.

See also:

`merge_ordered`, `merge_asof`, *`DataFrame.join`*

Notes

Support for specifying index levels as the *on*, *left_on*, and *right_on* parameters was added in version 0.23.0

Examples

```
>>> A              >>> B
    lkey value         rkey value
0   foo  1         0   foo  5
1   bar  2         1   bar  6
2   baz  3         2   qux  7
3   foo  4         3   bar  8
```

```
>>> A.merge(B, left_on='lkey', right_on='rkey', how='outer')
   lkey  value_x  rkey  value_y
0  foo   1        foo   5
1  foo   4        foo   5
2  bar   2        bar   6
3  bar   2        bar   8
4  baz   3        NaN   NaN
5  NaN   NaN      qux   7
```

min(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)

This method returns the minimum of the values in the object. If you want the *index* of the minimum, use `idxmin`. This is the equivalent of the `numpy.ndarray` method `argmin`.

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values when computing the result.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

min [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

mod(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Modulo of dataframe and other, element-wise (binary operator *mod*).

Equivalent to `dataframe % other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.rmod

Notes

Mismatched indices will be unioned together

Examples

None

mul(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Multiplication of dataframe and other, element-wise (binary operator *mul*).

Equivalent to `dataframe * other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.rmul

Notes

Mismatched indices will be unioned together

Examples

None

ndim
Return dimensionality

ne(*other*, *axis='columns'*, *level=None*)
Wrapper for flexible comparison methods ne

nlargest(*n=5*, *columns=None*, *split_every=None*)
Return the first *n* rows ordered by *columns* in descending order.

Return the first *n* rows with the largest values in *columns*, in descending order. The columns that are not specified are returned as well, but not used for ordering.

This method is equivalent to `df.sort_values(columns, ascending=False).head(n)`, but more performant.

Parameters

n [int] Number of rows to return.

columns [label or list of labels] Column label(s) to order by.

keep [{'first', 'last'}, default 'first'] Where there are duplicate values:

- *first* : prioritize the first occurrence(s)
- *last* : prioritize the last occurrence(s)

Returns

DataFrame The first *n* rows ordered by the given columns in descending order.

See also:

DataFrame.nsmallest Return the first *n* rows ordered by *columns* in ascending order.

DataFrame.sort_values Sort DataFrame by the values

DataFrame.head Return the first *n* rows without re-ordering.

Notes

This function cannot be used with all column types. For example, when specifying columns with *object* or *category* dtypes, `TypeError` is raised.

Examples

```
>>> df = pd.DataFrame({'a': [1, 10, 8, 10, -1],
...                    'b': list('abdce'),
...                    'c': [1.0, 2.0, np.nan, 3.0, 4.0]})
>>> df
    a  b    c
0   1  a  1.0
1  10  b  2.0
2   8  d  NaN
3  10  c  3.0
4  -1  e  4.0
```

In the following example, we will use `nlargest` to select the three rows having the largest values in column "a".

```
>>> df.nlargest(3, 'a')
    a  b    c
1  10  b  2.0
3  10  c  3.0
2   8  d  NaN
```

When using `keep='last'`, ties are resolved in reverse order:

```
>>> df.nlargest(3, 'a', keep='last')
    a  b    c
3  10  c  3.0
1  10  b  2.0
2   8  d  NaN
```

To order by the largest values in column "a" and then "c", we can specify multiple columns like in the next example.

```
>>> df.nlargest(3, ['a', 'c'])
    a  b    c
3  10  c  3.0
1  10  b  2.0
2   8  d  NaN
```

Attempting to use `nlargest` on non-numeric dtypes will raise a `TypeError`:

```
>>> df.nlargest(3, 'b')
Traceback (most recent call last):
TypeError: Column 'b' has dtype object, cannot use method 'nlargest'
```

notnull()

Detect existing (non-missing) values.

Return a boolean same-sized object indicating if the values are not NA. Non-missing values get mapped to True. Characters such as empty strings `''` or `numpy.inf` are not considered NA values (unless you set `pandas.options.mode.use_inf_as_na = True`). NA values, such as None or `numpy.NaN`, get mapped to False values.

Returns

DataFrame Mask of bool values for each element in DataFrame that indicates whether an element is not an NA value.

See also:

DataFrame.notnull alias of notna

DataFrame.isna boolean inverse of notna

DataFrame.dropna omit axes labels with missing values

notna top-level notna

Examples

Show which entries in a DataFrame are not NA.

```
>>> df = pd.DataFrame({'age': [5, 6, np.NaN],
...                    'born': [pd.NaT, pd.Timestamp('1939-05-27'),
...                             pd.Timestamp('1940-04-25')],
...                    'name': ['Alfred', 'Batman', ''],
...                    'toy': [None, 'Batmobile', 'Joker']})
>>> df
   age       born    name        toy
0  5.0        NaT  Alfred       None
1  6.0 1939-05-27  Batman  Batmobile
2  NaN 1940-04-25              Joker
```

```
>>> df.notna()
     age   born  name    toy
0   True  False  True  False
1   True   True  True   True
2  False   True  True   True
```

Show which entries in a Series are not NA.

```
>>> ser = pd.Series([5, 6, np.NaN])
>>> ser
0    5.0
1    6.0
2    NaN
dtype: float64
```

```
>>> ser.notna()
0     True
1     True
2    False
dtype: bool
```

npartitions
Return number of partitions

nsmallest(*n=5*, *columns=None*, *split_every=None*)
Get the rows of a DataFrame sorted by the *n* smallest values of *columns*.

Parameters

n [int] Number of items to retrieve

columns [list or str] Column name or names to order by

keep [{'first', 'last'}, default 'first'] Where there are duplicate values: - `first` : take the first occurrence. - `last` : take the last occurrence.

Returns

DataFrame

Notes

Dask doesn't support the following argument(s).

- keep

Examples

```
>>> df = pd.DataFrame({'a': [1, 10, 8, 11, -1],
...                    'b': list('abdce'),
...                    'c': [1.0, 2.0, np.nan, 3.0, 4.0]})
>>> df.nsmallest(3, 'a')
   a  b   c
4 -1  e   4
0  1  a   1
2  8  d NaN
```

nunique_approx(*split_every=None*)
Approximate number of unique rows.

This method uses the HyperLogLog algorithm for cardinality estimation to compute the approximate number of unique rows. The approximate error is 0.406%.

Parameters

split_every [int, optional] Group partitions into groups of this size while performing a tree-reduction. If set to False, no tree-reduction will be used. Default is 8.

Returns

a float representing the approximate number of elements

persist(***kwargs*)
Persist this dask collection into memory

This turns a lazy Dask collection into a Dask collection with the same metadata, but now with the results fully computed or actively computing in the background.

The action of function differs significantly depending on the active task scheduler. If the task scheduler supports asynchronous computing, such as is the case of the dask.distributed scheduler, then persist will return *immediately* and the return value's task graph will contain Dask Future objects. However if the task scheduler only supports blocking computation then the call to persist will *block* and the return value's task graph will contain concrete Python results.

This function is particularly useful when using distributed systems, because the results will be kept in distributed memory, rather than returned to the local process as with compute.

Parameters

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

optimize_graph [bool, optional] If True [default], the graph is optimized before computation. Otherwise the graph is run as is. This can be useful for debugging.

****kwargs** Extra keywords to forward to the scheduler function.

Returns

New dask collections backed by in-memory data

See also:

`dask.base.persist`

pipe(*func*, **args*, ***kwargs*)
Apply func(self, *args, **kwargs)

Parameters

func [function] function to apply to the NDFrame. `args`, and `kwargs` are passed into `func`. Alternatively a `(callable, data_keyword)` tuple where `data_keyword` is a string indicating the keyword of `callable` that expects the NDFrame.

args [iterable, optional] positional arguments passed into `func`.

kwargs [mapping, optional] a dictionary of keyword arguments passed into `func`.

Returns

object [the return type of `func`.]

See also:

`pandas.DataFrame.apply`, `pandas.DataFrame.applymap`, `pandas.Series.map`

Notes

Use `.pipe` when chaining together functions that expect Series, DataFrames or GroupBy objects. Instead of writing

```
>>> f(g(h(df), arg1=a), arg2=b, arg3=c)
```

You can write

```
>>> (df.pipe(h)
...     .pipe(g, arg1=a)
...     .pipe(f, arg2=b, arg3=c)
... )
```

If you have a function that takes the data as (say) the second argument, pass a tuple indicating which keyword expects the data. For example, suppose `f` takes its data as `arg2`:

```
>>> (df.pipe(h)
...     .pipe(g, arg1=a)
...     .pipe((f, 'arg2'), arg1=a, arg3=c)
...  )
```

pivot_table(*index=None*, *columns=None*, *values=None*, *aggfunc='mean'*)

Create a spreadsheet-style pivot table as a DataFrame. Target `columns` must have category dtype to infer result's `columns`. `index`, `columns`, `values` and `aggfunc` must be all scalar.

Parameters

values [scalar] column to aggregate

index [scalar] column to be index

columns [scalar] column to be columns

aggfunc [{'mean', 'sum', 'count'}, default 'mean']

Returns

table [DataFrame]

pow(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Exponential power of dataframe and other, element-wise (binary operator *pow*).

Equivalent to `dataframe ** other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.rpow

Notes

Mismatched indices will be unioned together

Examples

None

prod(*axis=None*, *skipna=True*, *split_every=False*, *dtype=None*, *out=None*)
Return the product of the values for the requested axis

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values when computing the result.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

min_count [int, default 0] The required number of valid values to perform the operation. If fewer than `min_count` non-NA values are present the result will be NA.

New in version 0.22.0: Added with the default being 0. This means the sum of an all-NA or empty Series is 0, and the product of an all-NA or empty Series is 1.

Returns

prod [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only
- min_count

Examples

By default, the product of an empty or all-NA Series is `1`

```
>>> pd.Series([]).prod()
1.0
```

This can be controlled with the `min_count` parameter

```
>>> pd.Series([]).prod(min_count=1)
nan
```

Thanks to the `skipna` parameter, `min_count` handles all-NA and empty series identically.

```
>>> pd.Series([np.nan]).prod()
1.0
```

```
>>> pd.Series([np.nan]).prod(min_count=1)
nan
```

quantile(*q=0.5*, *axis=0*)
Approximate row-wise and precise column-wise quantiles of DataFrame

Parameters

q [list/array of floats, default 0.5 (50%)] Iterable of numbers ranging from 0 to 1 for the desired quantiles

axis [{0, 1, 'index', 'columns'} (default 0)] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

query(*expr*, ***kwargs*)
Filter dataframe with complex expression

Blocked version of pd.DataFrame.query

This is like the sequential version except that this will also happen in many threads. This may conflict with `numexpr` which will use multiple threads itself. We recommend that you set numexpr to use a single thread

import numexpr numexpr.set_nthreads(1)

See also:

`pandas.DataFrame.query`

radd(*other*, *axis='columns'*, *level=None*, *fill_value=None*)
Addition of dataframe and other, element-wise (binary operator *radd*).

Equivalent to `other + dataframe`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.add

Notes

Mismatched indices will be unioned together

Examples

```
>>> a = pd.DataFrame([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'],
...                  columns=['one'])
>>> a
   one
a  1.0
b  1.0
c  1.0
d  NaN
>>> b = pd.DataFrame(dict(one=[1, np.nan, 1, np.nan],
...                       two=[np.nan, 2, np.nan, 2]),
...                  index=['a', 'b', 'd', 'e'])
>>> b
   one  two
a  1.0  NaN
b  NaN  2.0
d  1.0  NaN
e  NaN  2.0
>>> a.add(b, fill_value=0)
   one  two
a  2.0  NaN
b  1.0  2.0
c  1.0  NaN
d  1.0  NaN
e  NaN  2.0
```

random_split (*frac*, *random_state=None*)

Pseudorandomly split dataframe into different pieces row-wise

Parameters

frac [list] List of floats that should sum to one.

random_state: int or np.random.RandomState If int create a new RandomState with this as the seed

Otherwise draw from the passed RandomState

See also:

`dask.DataFrame.sample`

Examples

50/50 split

```
>>> a, b = df.random_split([0.5, 0.5])
```

80/10/10 split, consistent random_state

```
>>> a, b, c = df.random_split([0.8, 0.1, 0.1], random_state=123)
```

rdiv(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Floating division of dataframe and other, element-wise (binary operator *rtruediv*).

Equivalent to `other / dataframe`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.truediv

Notes

Mismatched indices will be unioned together

Examples

None

reduction(*chunk*, *aggregate=None*, *combine=None*, *meta='__no_default__'*, *token=None*, *split_every=None*, *chunk_kwargs=None*, *aggregate_kwargs=None*, *combine_kwargs=None*, ***kwargs*)

Generic row-wise reductions.

Parameters

chunk [callable] Function to operate on each partition. Should return a `pandas.DataFrame`, `pandas.Series`, or a scalar.

aggregate [callable, optional] Function to operate on the concatenated result of `chunk`. If not specified, defaults to `chunk`. Used to do the final aggregation in a tree reduction.

The input to `aggregate` depends on the output of `chunk`. If the output of `chunk` is a:

- scalar: Input is a Series, with one row per partition.
- Series: Input is a DataFrame, with one row per partition. Columns are the rows in the output series.
- DataFrame: Input is a DataFrame, with one row per partition. Columns are the columns in the output dataframes.

Should return a `pandas.DataFrame`, `pandas.Series`, or a scalar.

combine [callable, optional] Function to operate on intermediate concatenated results of `chunk` in a tree-reduction. If not provided, defaults to `aggregate`. The input/output requirements should match that of `aggregate` described above.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

token [str, optional] The name to use for the output keys.

split_every [int, optional] Group partitions into groups of this size while performing a tree-reduction. If set to False, no tree-reduction will be used, and all intermediates will be concatenated and passed to `aggregate`. Default is 8.

chunk_kwargs [dict, optional] Keyword arguments to pass on to `chunk` only.

aggregate_kwargs [dict, optional] Keyword arguments to pass on to `aggregate` only.

combine_kwargs [dict, optional] Keyword arguments to pass on to `combine` only.

kwargs : All remaining keywords will be passed to `chunk`, `combine`, and `aggregate`.

Examples

```
>>> import pandas as pd
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': range(50), 'y': range(50, 100)})
>>> ddf = dd.from_pandas(df, npartitions=4)
```

Count the number of rows in a DataFrame. To do this, count the number of rows in each partition, then sum the results:

```
>>> res = ddf.reduction(lambda x: x.count(),
...                     aggregate=lambda x: x.sum())
>>> res.compute()
x    50
y    50
dtype: int64
```

Count the number of rows in a Series with elements greater than or equal to a value (provided via a keyword).

```
>>> def count_greater(x, value=0):
...     return (x >= value).sum()
>>> res = ddf.x.reduction(count_greater, aggregate=lambda x: x.sum(),
...                       chunk_kwargs={'value': 25})
>>> res.compute()
25
```

Aggregate both the sum and count of a Series at the same time:

```
>>> def sum_and_count(x):
...     return pd.Series({'sum': x.sum(), 'count': x.count()})
>>> res = ddf.x.reduction(sum_and_count, aggregate=lambda x: x.sum())
>>> res.compute()
count      50
sum      1225
dtype: int64
```

Doing the same, but for a DataFrame. Here `chunk` returns a DataFrame, meaning the input to `aggregate` is a DataFrame with an index with non-unique entries for both 'x' and 'y'. We groupby the index, and sum each group to get the final result.

```
>>> def sum_and_count(x):
...     return pd.DataFrame({'sum': x.sum(), 'count': x.count()})
>>> res = ddf.reduction(sum_and_count,
...                     aggregate=lambda x: x.groupby(level=0).sum())
>>> res.compute()
   count   sum
x     50  1225
y     50  3725
```

rename(*index=None*, *columns=None*)

Alter axes labels.

Function / dict values must be unique (1-to-1). Labels not contained in a dict / Series will be left as-is. Extra labels listed don't throw an error.

See the user guide for more.

Parameters

mapper, index, columns [dict-like or function, optional] dict-like or functions transformations to apply to that axis' values. Use either `mapper` and `axis` to specify the axis to target with `mapper`, or `index` and `columns`.

axis [int or str, optional] Axis to target with `mapper`. Can be either the axis name ('index', 'columns') or number (0, 1). The default is 'index'.

copy [boolean, default True] Also copy underlying data

inplace [boolean, default False] Whether to return a new DataFrame. If True then value of copy is ignored.

level [int or level name, default None] In case of a MultiIndex, only rename labels in the specified level.

Returns

renamed [DataFrame]

See also:

`pandas.DataFrame.rename_axis`

Notes

Dask doesn't support the following argument(s).

- mapper
- axis
- copy
- inplace
- level
- index

Examples

`DataFrame.rename` supports two calling conventions

- `(index=index_mapper, columns=columns_mapper, ...)`
- `(mapper, axis={'index', 'columns'}, ...)`

We *highly* recommend using keyword arguments to clarify your intent.

```
>>> df = pd.DataFrame({"A": [1, 2, 3], "B": [4, 5, 6]})
>>> df.rename(index=str, columns={"A": "a", "B": "c"})
   a  c
0  1  4
1  2  5
2  3  6
```

```
>>> df.rename(index=str, columns={"A": "a", "C": "c"})
   a  B
0  1  4
1  2  5
2  3  6
```

Using axis-style parameters

```
>>> df.rename(str.lower, axis='columns')
   a  b
0  1  4
1  2  5
2  3  6
```

```
>>> df.rename({1: 2, 2: 4}, axis='index')
   A  B
0  1  4
2  2  5
4  3  6
```

repartition(*divisions=None*, *npartitions=None*, *freq=None*, *force=False*)
Repartition dataframe along new divisions

Parameters

divisions [list, optional] List of partitions to be used. If specified npartitions will be ignored.

npartitions [int, optional] Number of partitions of output. Only used if divisions isn't specified.

freq [str, pd.Timedelta] A period on which to partition timeseries data like `'7D'` or `'12h'` or `pd.Timedelta(hours=12)`. Assumes a datetime index.

force [bool, default False] Allows the expansion of the existing divisions. If False then the new divisions lower and upper bounds must be the same as the old divisions.

Examples

```
>>> df = df.repartition(npartitions=10)
>>> df = df.repartition(divisions=[0, 5, 10, 20])
>>> df = df.repartition(freq='7d')
```

resample(*rule*, *closed=None*, *label=None*)
Convenience method for frequency conversion and resampling of time series. Object must have a datetime-like index (DatetimeIndex, PeriodIndex, or TimedeltaIndex), or pass datetime-like values to the on or level keyword.

Parameters

rule [string] the offset string or object representing target conversion

axis [int, optional, default 0]

closed [{'right', 'left'}] Which side of bin interval is closed. The default is 'left' for all frequency offsets except for 'M', 'A', 'Q', 'BM', 'BA', 'BQ', and 'W' which all have a default of 'right'.

label [{'right', 'left'}] Which bin edge label to label bucket with. The default is 'left' for all frequency offsets except for 'M', 'A', 'Q', 'BM', 'BA', 'BQ', and 'W' which all have a default of 'right'.

convention [{'start', 'end', 's', 'e'}] For PeriodIndex only, controls whether to use the start or end of *rule*

kind: {'timestamp', 'period'}, optional Pass 'timestamp' to convert the resulting index to a `DateTimeIndex` or 'period' to convert it to a `PeriodIndex`. By default the input representation is retained.

loffset [timedelta] Adjust the resampled time labels

base [int, default 0] For frequencies that evenly subdivide 1 day, the "origin" of the aggregated intervals. For example, for '5min' frequency, base could range from 0 through 4. Defaults to 0

on [string, optional] For a DataFrame, column to use instead of index for resampling. Column must be datetime-like.

New in version 0.19.0.

level [string or int, optional] For a MultiIndex, level (name or number) to use for resampling. Level must be datetime-like.

New in version 0.19.0.

Returns

Resampler object

See also:

groupby Group by mapping, function, label, or list of labels.

Notes

See the user guide for more.

To learn more about the offset strings, please see this link.

Examples

Start by creating a series with 9 one minute timestamps.

```
>>> index = pd.date_range('1/1/2000', periods=9, freq='T')
>>> series = pd.Series(range(9), index=index)
>>> series
2000-01-01 00:00:00    0
2000-01-01 00:01:00    1
2000-01-01 00:02:00    2
2000-01-01 00:03:00    3
2000-01-01 00:04:00    4
2000-01-01 00:05:00    5
2000-01-01 00:06:00    6
2000-01-01 00:07:00    7
2000-01-01 00:08:00    8
Freq: T, dtype: int64
```

Downsample the series into 3 minute bins and sum the values of the timestamps falling into a bin.

```
>>> series.resample('3T').sum()
2000-01-01 00:00:00     3
2000-01-01 00:03:00    12
2000-01-01 00:06:00    21
Freq: 3T, dtype: int64
```

Downsample the series into 3 minute bins as above, but label each bin using the right edge instead of the left. Please note that the value in the bucket used as the label is not included in the bucket, which it labels. For example, in the original series the bucket `2000-01-01 00:03:00` contains the value 3, but the summed value in the resampled bucket with the label `2000-01-01 00:03:00` does not include 3 (if it did, the summed value would be 6, not 3). To include this value close the right side of the bin interval as illustrated in the example below this one.

```
>>> series.resample('3T', label='right').sum()
2000-01-01 00:03:00     3
2000-01-01 00:06:00    12
2000-01-01 00:09:00    21
Freq: 3T, dtype: int64
```

Downsample the series into 3 minute bins as above, but close the right side of the bin interval.

```
>>> series.resample('3T', label='right', closed='right').sum()
2000-01-01 00:00:00     0
2000-01-01 00:03:00     6
2000-01-01 00:06:00    15
2000-01-01 00:09:00    15
Freq: 3T, dtype: int64
```

Upsample the series into 30 second bins.

```
>>> series.resample('30S').asfreq()[0:5] #select first 5 rows
2000-01-01 00:00:00   0.0
2000-01-01 00:00:30   NaN
2000-01-01 00:01:00   1.0
2000-01-01 00:01:30   NaN
2000-01-01 00:02:00   2.0
Freq: 30S, dtype: float64
```

Upsample the series into 30 second bins and fill the `NaN` values using the `pad` method.

```
>>> series.resample('30S').pad()[0:5]
2000-01-01 00:00:00    0
2000-01-01 00:00:30    0
2000-01-01 00:01:00    1
2000-01-01 00:01:30    1
2000-01-01 00:02:00    2
Freq: 30S, dtype: int64
```

Upsample the series into 30 second bins and fill the `NaN` values using the `bfill` method.

```
>>> series.resample('30S').bfill()[0:5]
2000-01-01 00:00:00    0
2000-01-01 00:00:30    1
2000-01-01 00:01:00    1
2000-01-01 00:01:30    2
2000-01-01 00:02:00    2
Freq: 30S, dtype: int64
```

Pass a custom function via `apply`

```
>>> def custom_resampler(array_like):
...     return np.sum(array_like)+5
```

```
>>> series.resample('3T').apply(custom_resampler)
2000-01-01 00:00:00     8
2000-01-01 00:03:00    17
2000-01-01 00:06:00    26
Freq: 3T, dtype: int64
```

For a Series with a PeriodIndex, the keyword *convention* can be used to control whether to use the start or end of *rule*.

```
>>> s = pd.Series([1, 2], index=pd.period_range('2012-01-01',
                                                freq='A',
                                                periods=2))
>>> s
2012    1
2013    2
Freq: A-DEC, dtype: int64
```

Resample by month using 'start' *convention*. Values are assigned to the first month of the period.

```
>>> s.resample('M', convention='start').asfreq().head()
2012-01    1.0
2012-02    NaN
2012-03    NaN
2012-04    NaN
2012-05    NaN
Freq: M, dtype: float64
```

Resample by month using 'end' *convention*. Values are assigned to the last month of the period.

```
>>> s.resample('M', convention='end').asfreq()
2012-12    1.0
2013-01    NaN
2013-02    NaN
2013-03    NaN
2013-04    NaN
2013-05    NaN
2013-06    NaN
2013-07    NaN
2013-08    NaN
2013-09    NaN
2013-10    NaN
2013-11    NaN
2013-12    2.0
Freq: M, dtype: float64
```

For DataFrame objects, the keyword `on` can be used to specify the column instead of the index for resampling.

```
>>> df = pd.DataFrame(data=9*[range(4)], columns=['a', 'b', 'c', 'd'])
>>> df['time'] = pd.date_range('1/1/2000', periods=9, freq='T')
>>> df.resample('3T', on='time').sum()
                     a  b  c  d
time
2000-01-01 00:00:00  0  3  6  9
2000-01-01 00:03:00  0  3  6  9
2000-01-01 00:06:00  0  3  6  9
```

For a DataFrame with MultiIndex, the keyword `level` can be used to specify on level the resampling needs to take place.

```
>>> time = pd.date_range('1/1/2000', periods=5, freq='T')
>>> df2 = pd.DataFrame(data=10*[range(4)],
                       columns=['a', 'b', 'c', 'd'],
                       index=pd.MultiIndex.from_product([time, [1, 2]])
                       )
>>> df2.resample('3T', level=0).sum()
```

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```
                     a  b   c   d
2000-01-01 00:00:00  0  6  12  18
2000-01-01 00:03:00  0  4   8  12
```

reset_index(*drop=False*)

Reset the index to the default index.

Note that unlike in `pandas`, the reset `dask.dataframe` index will not be monotonically increasing from 0. Instead, it will restart at 0 for each partition (e.g. `index1 = [0, ..., 10], index2 = [0, ...]`). This is due to the inability to statically know the full length of the index.

For DataFrame with multi-level index, returns a new DataFrame with labeling information in the columns under the index names, defaulting to 'level_0', 'level_1', etc. if any are None. For a standard index, the index name will be used (if set), otherwise a default 'index' or 'level_0' (if 'index' is already taken) will be used.

Parameters

drop [boolean, default False] Do not try to insert index into dataframe columns.

rfloordiv(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Integer division of dataframe and other, element-wise (binary operator *rfloordiv*).

Equivalent to `other // dataframe`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.floordiv

Notes

Mismatched indices will be unioned together

Examples

None

rmod(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Modulo of dataframe and other, element-wise (binary operator *rmod*).

Equivalent to `other % dataframe`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.mod

Notes

Mismatched indices will be unioned together

Examples

None

rmul(*other*, *axis='columns'*, *level=None*, *fill_value=None*)
Multiplication of dataframe and other, element-wise (binary operator *rmul*).

Equivalent to `other * dataframe`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.mul

Notes

Mismatched indices will be unioned together

Examples

None

rolling(*window*, *min_periods=None*, *freq=None*, *center=False*, *win_type=None*, *axis=0*)
Provides rolling transformations.

Parameters

window [int, str, offset] Size of the moving window. This is the number of observations used for calculating the statistic. The window size must not be so large as to span more than one adjacent partition. If using an offset or offset alias like '5D', the data must have a `DatetimeIndex`

Changed in version 0.15.0: Now accepts offsets and string offset aliases

min_periods [int, default None] Minimum number of observations in window required to have a value (otherwise result is NA).

center [boolean, default False] Set the labels at the center of the window.

win_type [string, default None] Provide a window type. The recognized window types are identical to pandas.

axis [int, default 0]

Returns

a Rolling object on which to call a method to compute a statistic

Notes

The *freq* argument is not supported.

round(*decimals=0*)
Round a DataFrame to a variable number of decimal places.

Parameters

decimals [int, dict, Series] Number of decimal places to round each column to. If an int is given, round each column to the same number of places. Otherwise dict and Series round to variable numbers of places. Column names should be in the keys if *decimals* is a dict-like, or in the index if *decimals* is a Series. Any columns not included in *decimals* will be left as is. Elements of *decimals* which are not columns of the input will be ignored.

Returns

DataFrame object

See also:

`numpy.around`, *`Series.round`*

Examples

```
>>> df = pd.DataFrame(np.random.random([3, 3]),
...     columns=['A', 'B', 'C'], index=['first', 'second', 'third'])
>>> df
               A         B         C
first   0.028208  0.992815  0.173891
second  0.038683  0.645646  0.577595
third   0.877076  0.149370  0.491027
>>> df.round(2)
           A     B     C
first   0.03  0.99  0.17
second  0.04  0.65  0.58
third   0.88  0.15  0.49
>>> df.round({'A': 1, 'C': 2})
          A         B     C
first   0.0  0.992815  0.17
second  0.0  0.645646  0.58
third   0.9  0.149370  0.49
>>> decimals = pd.Series([1, 0, 2], index=['A', 'B', 'C'])
>>> df.round(decimals)
          A  B     C
first   0.0  1  0.17
second  0.0  1  0.58
third   0.9  0  0.49
```

rpow(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Exponential power of dataframe and other, element-wise (binary operator *rpow*).

Equivalent to `other ** dataframe`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.pow

Notes

Mismatched indices will be unioned together

Examples

None

rsub(*other*, *axis='columns'*, *level=None*, *fill_value=None*)
Subtraction of dataframe and other, element-wise (binary operator *rsub*).

Equivalent to `other - dataframe`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.sub

Notes

Mismatched indices will be unioned together

Examples

```
>>> a = pd.DataFrame([2, 1, 1, np.nan], index=['a', 'b', 'c', 'd'],
...                  columns=['one'])
>>> a
   one
a  2.0
b  1.0
c  1.0
d  NaN
>>> b = pd.DataFrame(dict(one=[1, np.nan, 1, np.nan],
...                       two=[3, 2, np.nan, 2]),
...                  index=['a', 'b', 'd', 'e'])
>>> b
   one  two
a  1.0  3.0
b  NaN  2.0
d  1.0  NaN
e  NaN  2.0
>>> a.sub(b, fill_value=0)
   one  two
a  1.0  -3.0
```

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```
b  1.0  -2.0
c  1.0  NaN
d  -1.0  NaN
e  NaN  -2.0
```

rtruediv(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Floating division of dataframe and other, element-wise (binary operator *rtruediv*).

Equivalent to `other / dataframe`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.truediv

Notes

Mismatched indices will be unioned together

Examples

None

sample(*n=None*, *frac=None*, *replace=False*, *random_state=None*)

Random sample of items

Parameters

n [int, optional] Number of items to return is not supported by dask. Use frac instead.

frac [float, optional] Fraction of axis items to return.

replace [boolean, optional] Sample with or without replacement. Default = False.

random_state [int or `np.random.RandomState`] If int we create a new RandomState with this as the seed Otherwise we draw from the passed RandomState

See also:

DataFrame.random_split, `pandas.DataFrame.sample`

select_dtypes(*include=None*, *exclude=None*)

Return a subset of the DataFrame's columns based on the column dtypes.

Parameters

include, exclude [scalar or list-like] A selection of dtypes or strings to be included/excluded. At least one of these parameters must be supplied.

Returns

subset [DataFrame] The subset of the frame including the dtypes in `include` and excluding the dtypes in `exclude`.

Raises

ValueError

- If both of `include` and `exclude` are empty
- If `include` and `exclude` have overlapping elements
- If any kind of string dtype is passed in.

Notes

- To select all *numeric* types, use `np.number` or `'number'`
- To select strings you must use the `object` dtype, but note that this will return *all* object dtype columns
- See the numpy dtype hierarchy
- To select datetimes, use `np.datetime64`, `'datetime'` or `'datetime64'`
- To select timedeltas, use `np.timedelta64`, `'timedelta'` or `'timedelta64'`
- To select Pandas categorical dtypes, use `'category'`
- To select Pandas datetimetz dtypes, use `'datetimetz'` (new in 0.20.0) or `'datetime64[ns, tz]'`

Examples

```
>>> df = pd.DataFrame({'a': [1, 2] * 3,
...                    'b': [True, False] * 3,
...                    'c': [1.0, 2.0] * 3})
>>> df
        a      b  c
0       1   True  1.0
1       2  False  2.0
2       1   True  1.0
3       2  False  2.0
4       1   True  1.0
5       2  False  2.0
```

```
>>> df.select_dtypes(include='bool')
   b
0  True
1  False
2  True
3  False
4  True
5  False
```

```
>>> df.select_dtypes(include=['float64'])
   c
0  1.0
1  2.0
2  1.0
3  2.0
4  1.0
5  2.0
```

```
>>> df.select_dtypes(exclude=['int'])
       b    c
0   True  1.0
1  False  2.0
2   True  1.0
3  False  2.0
4   True  1.0
5  False  2.0
```

sem(*axis=None*, *skipna=None*, *ddof=1*, *split_every=False*)
Return unbiased standard error of the mean over requested axis.

Normalized by N-1 by default. This can be changed using the ddof argument

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

ddof [int, default 1] Delta Degrees of Freedom. The divisor used in calculations is N - ddof, where N represents the number of elements.

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

sem [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

set_index(*other*, *drop=True*, *sorted=False*, *npartitions=None*, *divisions=None*, ***kwargs*)
Set the DataFrame index (row labels) using an existing column

This realigns the dataset to be sorted by a new column. This can have a significant impact on performance, because joins, groupbys, lookups, etc. are all much faster on that column. However, this performance increase comes with a cost, sorting a parallel dataset requires expensive shuffles. Often we `set_index` once directly after data ingest and filtering and then perform many cheap computations off of the sorted dataset.

This function operates exactly like `pandas.set_index` except with different performance costs (it is much more expensive). Under normal operation this function does an initial pass over the index column to compute approximate qunatiles to serve as future divisions. It then passes over the data a second time, splitting up each input partition into several pieces and sharing those pieces to all of the output partitions now in sorted order.

In some cases we can alleviate those costs, for example if your dataset is sorted already then we can avoid making many small pieces or if you know good values to split the new index column then we can avoid the initial pass over the data. For example if your new index is a datetime index and your data is already sorted by day then this entire operation can be done for free. You can control these options with the following parameters.

Parameters

df: Dask DataFrame

index: string or Dask Series

npartitions: int, None, or 'auto' The ideal number of output partitions. If None use the same as the input. If 'auto' then decide by memory use.

shuffle: string, optional Either `'disk'` for single-node operation or `'tasks'` for distributed operation. Will be inferred by your current scheduler.

sorted: bool, optional If the index column is already sorted in increasing order. Defaults to False

divisions: list, optional Known values on which to separate index values of the partitions. See https://docs.dask.org/en/latest/dataframe-design.html#partitions Defaults to computing this with a single pass over the data. Note that if `sorted=True`, specified divisions are assumed to match the existing partitions in the data. If this is untrue, you should leave divisions empty and call `repartition` after `set_index`.

compute: bool Whether or not to trigger an immediate computation. Defaults to False.

Examples

```
>>> df2 = df.set_index('x')
>>> df2 = df.set_index(d.x)
>>> df2 = df.set_index(d.timestamp, sorted=True)
```

A common case is when we have a datetime column that we know to be sorted and is cleanly divided by day. We can set this index for free by specifying both that the column is pre-sorted and the particular divisions along which is is separated

```
>>> import pandas as pd
>>> divisions = pd.date_range('2000', '2010', freq='1D')
>>> df2 = df.set_index('timestamp', sorted=True, divisions=divisions)
```

shape

Return a tuple representing the dimensionality of the DataFrame.

The number of rows is a Delayed result. The number of columns is a concrete integer.

Examples

```
>>> df.size
(Delayed('int-07f06075-5ecc-4d77-817e-63c69a9188a8'), 2)
```

shift(*periods=1*, *freq=None*, *axis=0*)
Shift index by desired number of periods with an optional time freq

Parameters

periods [int] Number of periods to move, can be positive or negative

freq [DateOffset, timedelta, or time rule string, optional] Increment to use from the tseries module or time rule (e.g. 'EOM'). See Notes.

axis [{0 or 'index', 1 or 'columns'}]

Returns

shifted [DataFrame]

Notes

If freq is specified then the index values are shifted but the data is not realigned. That is, use freq if you would like to extend the index when shifting and preserve the original data.

size
Size of the Series or DataFrame as a Delayed object.

Examples

```
>>> series.size
dd.Scalar<size-ag..., dtype=int64>
```

squeeze(*axis=None*)
Squeeze length 1 dimensions.

Parameters

axis [None, integer or string axis name, optional] The axis to squeeze if 1-sized.

New in version 0.20.0.

Returns

scalar if 1-sized, else original object

std(*axis=None*, *skipna=True*, *ddof=1*, *split_every=False*, *dtype=None*, *out=None*)
Return sample standard deviation over requested axis.

Normalized by N-1 by default. This can be changed using the ddof argument

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

ddof [int, default 1] Delta Degrees of Freedom. The divisor used in calculations is N - ddof, where N represents the number of elements.

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

std [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

sub(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Subtraction of dataframe and other, element-wise (binary operator *sub*).

Equivalent to `dataframe - other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.rsub

Notes

Mismatched indices will be unioned together

Examples

```
>>> a = pd.DataFrame([2, 1, 1, np.nan], index=['a', 'b', 'c', 'd'],
...                  columns=['one'])
>>> a
   one
a  2.0
b  1.0
c  1.0
d  NaN
>>> b = pd.DataFrame(dict(one=[1, np.nan, 1, np.nan],
...                       two=[3, 2, np.nan, 2]),
...                  index=['a', 'b', 'd', 'e'])
>>> b
   one  two
a  1.0  3.0
b  NaN  2.0
d  1.0  NaN
e  NaN  2.0
>>> a.sub(b, fill_value=0)
   one  two
a  1.0 -3.0
b  1.0 -2.0
c  1.0  NaN
d -1.0  NaN
e  NaN -2.0
```

sum(*axis=None*, *skipna=True*, *split_every=False*, *dtype=None*, *out=None*)

Return the sum of the values for the requested axis

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values when computing the result.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

min_count [int, default 0] The required number of valid values to perform the operation. If fewer than `min_count` non-NA values are present the result will be NA.

New in version 0.22.0: Added with the default being 0. This means the sum of an all-NA or empty Series is 0, and the product of an all-NA or empty Series is 1.

Returns

sum [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only
- min_count

Examples

By default, the sum of an empty or all-NA Series is `0`.

```
>>> pd.Series([]).sum()  # min_count=0 is the default
0.0
```

This can be controlled with the `min_count` parameter. For example, if you'd like the sum of an empty series to be NaN, pass `min_count=1`.

```
>>> pd.Series([]).sum(min_count=1)
nan
```

Thanks to the `skipna` parameter, `min_count` handles all-NA and empty series identically.

```
>>> pd.Series([np.nan]).sum()
0.0
```

```
>>> pd.Series([np.nan]).sum(min_count=1)
nan
```

tail (*n=5*, *compute=True*)
Last n rows of the dataset

Caveat, the only checks the last n rows of the last partition.

to_bag (*index=False*)
Create Dask Bag from a Dask DataFrame

Parameters

index [bool, optional] If True, the elements are tuples of `(index, value)`, otherwise they're just the `value`. Default is False.

Examples

```
>>> bag = df.to_bag()
```

to_csv (*filename*, ***kwargs*)
Store Dask DataFrame to CSV files

One filename per partition will be created. You can specify the filenames in a variety of ways.

Use a globstring:

```
>>> df.to_csv('/path/to/data/export-*.csv')
```

The * will be replaced by the increasing sequence 0, 1, 2, ...

```
/path/to/data/export-0.csv
/path/to/data/export-1.csv
```

Use a globstring and a `name_function=` keyword argument. The name_function function should expect an integer and produce a string. Strings produced by name_function must preserve the order of their respective partition indices.

```
>>> from datetime import date, timedelta
>>> def name(i):
...     return str(date(2015, 1, 1) + i * timedelta(days=1))
```

```
>>> name(0)
'2015-01-01'
>>> name(15)
'2015-01-16'
```

```
>>> df.to_csv('/path/to/data/export-*.csv', name_function=name)
```

```
/path/to/data/export-2015-01-01.csv
/path/to/data/export-2015-01-02.csv
...
```

You can also provide an explicit list of paths:

```
>>> paths = ['/path/to/data/alice.csv', '/path/to/data/bob.csv', ...]
>>> df.to_csv(paths)
```

Parameters

filename [string] Path glob indicating the naming scheme for the output files

name_function [callable, default None] Function accepting an integer (partition index) and producing a string to replace the asterisk in the given filename globstring. Should preserve the lexicographic order of partitions

compression [string or None] String like 'gzip' or 'xz'. Must support efficient random access. Filenames with extensions corresponding to known compression algorithms (gz, bz2) will be compressed accordingly automatically

sep [character, default ','] Field delimiter for the output file

na_rep [string, default ''] Missing data representation

float_format [string, default None] Format string for floating point numbers

columns [sequence, optional] Columns to write

header [boolean or list of string, default True] Write out column names. If a list of string is given it is assumed to be aliases for the column names

index [boolean, default True] Write row names (index)

index_label [string or sequence, or False, default None] Column label for index column(s) if desired. If None is given, and *header* and *index* are True, then the index names are used. A sequence should be given if the DataFrame uses MultiIndex. If False do not print fields for index names. Use index_label=False for easier importing in R

nanRep [None] deprecated, use na_rep

mode [str] Python write mode, default 'w'

encoding [string, optional] A string representing the encoding to use in the output file, defaults to 'ascii' on Python 2 and 'utf-8' on Python 3.

compression [string, optional] a string representing the compression to use in the output file, allowed values are 'gzip', 'bz2', 'xz', only used when the first argument is a filename

line_terminator [string, default '\n'] The newline character or character sequence to use in the output file

quoting [optional constant from csv module] defaults to csv.QUOTE_MINIMAL

quotechar [string (length 1), default '"'] character used to quote fields

doublequote [boolean, default True] Control quoting of *quotechar* inside a field

escapechar [string (length 1), default None] character used to escape *sep* and *quotechar* when appropriate

chunksize [int or None] rows to write at a time

tupleize_cols [boolean, default False] write multi_index columns as a list of tuples (if True) or new (expanded format) if False)

date_format [string, default None] Format string for datetime objects

decimal: string, default '.' Character recognized as decimal separator. E.g. use ',' for European data

storage_options: dict Parameters passed on to the backend filesystem class.

Returns

The names of the file written if they were computed right away

If not, the delayed tasks associated to the writing of the files

to_dask_array(*lengths=None*)

Convert a dask DataFrame to a dask array.

Parameters

lengths [bool or Sequence of ints, optional] How to determine the chunks sizes for the output array. By default, the output array will have unknown chunk lengths along the first axis, which can cause some later operations to fail.

- True : immediately compute the length of each partition
- Sequence : a sequence of integers to use for the chunk sizes on the first axis. These values are *not* validated for correctness, beyond ensuring that the number of items matches the number of partitions.

to_delayed(*optimize_graph=True*)

Convert into a list of `dask.delayed` objects, one per partition.

Parameters

optimize_graph [bool, optional] If True [default], the graph is optimized before converting into `dask.delayed` objects.

See also:

dask.dataframe.from_delayed

Examples

```
>>> partitions = df.to_delayed()
```

to_hdf(*path_or_buf*, *key*, *mode='a'*, *append=False*, ***kwargs*)
Store Dask Dataframe to Hierarchical Data Format (HDF) files

This is a parallel version of the Pandas function of the same name. Please see the Pandas docstring for more detailed information about shared keyword arguments.

This function differs from the Pandas version by saving the many partitions of a Dask DataFrame in parallel, either to many files, or to many datasets within the same file. You may specify this parallelism with an asterix `*` within the filename or datapath, and an optional `name_function`. The asterix will be replaced with an increasing sequence of integers starting from `0` or with the result of calling `name_function` on each of those integers.

This function only supports the Pandas `'table'` format, not the more specialized `'fixed'` format.

Parameters

path [string] Path to a target filename. May contain a `*` to denote many filenames

key [string] Datapath within the files. May contain a `*` to denote many locations

name_function [function] A function to convert the `*` in the above options to a string. Should take in a number from 0 to the number of partitions and return a string. (see examples below)

compute [bool] Whether or not to execute immediately. If False then this returns a `dask.Delayed` value.

lock [Lock, optional] Lock to use to prevent concurrency issues. By default a `threading.Lock`, `multiprocessing.Lock` or `SerializableLock` will be used depending on your scheduler if a lock is required. See dask.utils.get_scheduler_lock for more information about lock selection.

****other:** See pandas.to_hdf for more information

Returns

filenames [list] Returned if `compute` is True. List of file names that each partition is saved to.

delayed [dask.Delayed] Returned if `compute` is False. Delayed object to execute `to_hdf` when computed.

See also:

read_hdf, *to_parquet*

Examples

Save Data to a single file

```
>>> df.to_hdf('output.hdf', '/data')
```

Save data to multiple datapaths within the same file:

```
>>> df.to_hdf('output.hdf', '/data-*')
```

Save data to multiple files:

```
>>> df.to_hdf('output-*.hdf', '/data')
```

Save data to multiple files, using the multiprocessing scheduler:

```
>>> df.to_hdf('output-*.hdf', '/data', scheduler='processes')
```

Specify custom naming scheme. This writes files as '2000-01-01.hdf', '2000-01-02.hdf', '2000-01-03.hdf', etc..

```
>>> from datetime import date, timedelta
>>> base = date(year=2000, month=1, day=1)
>>> def name_function(i):
...     ''' Convert integer 0 to n to a string '''
...     return base + timedelta(days=i)
```

```
>>> df.to_hdf('*.hdf', '/data', name_function=name_function)
```

to_html (*max_rows=5*)

Render a DataFrame as an HTML table.

to_html-specific options:

bold_rows [boolean, default True] Make the row labels bold in the output

classes [str or list or tuple, default None] CSS class(es) to apply to the resulting html table

escape [boolean, default True] Convert the characters <, >, and & to HTML-safe sequences.

max_rows [int, optional] Maximum number of rows to show before truncating. If None, show all.

max_cols [int, optional] Maximum number of columns to show before truncating. If None, show all.

decimal [string, default '.'] Character recognized as decimal separator, e.g. ',' in Europe

New in version 0.18.0.

border [int] A `border=border` attribute is included in the opening <*table*> tag. Default `pd.options.html.border`.

New in version 0.19.0.

table_id [str, optional] A css id is included in the opening <*table*> tag if specified.

New in version 0.23.0.

Parameters

buf [StringIO-like, optional] buffer to write to

columns [sequence, optional] the subset of columns to write; default None writes all columns

col_space [int, optional] the minimum width of each column

header [bool, optional] whether to print column labels, default True

index [bool, optional] whether to print index (row) labels, default True

na_rep [string, optional] string representation of NAN to use, default 'NaN'

formatters [list or dict of one-parameter functions, optional] formatter functions to apply to columns' elements by position or name, default None. The result of each function must be a unicode string. List must be of length equal to the number of columns.

float_format [one-parameter function, optional] formatter function to apply to columns' elements if they are floats, default None. The result of this function must be a unicode string.

sparsify [bool, optional] Set to False for a DataFrame with a hierarchical index to print every multiindex key at each row, default True

index_names [bool, optional] Prints the names of the indexes, default True

line_width [int, optional] Width to wrap a line in characters, default no wrap

table_id [str, optional] id for the <table> element create by to_html

New in version 0.23.0.

justify [str, default None] How to justify the column labels. If None uses the option from the print configuration (controlled by set_option), 'right' out of the box. Valid values are

- left
- right
- center
- justify
- justify-all
- start
- end
- inherit
- match-parent
- initial
- unset

Returns

formatted [string (or unicode, depending on data and options)] Dask doesn't support the following argument(s).

- buf
- columns
- col_space
- header
- index
- na_rep
- formatters
- float_format
- sparsify
- index_names
- justify
- bold_rows

- classes
- escape
- max_cols
- show_dimensions
- notebook
- decimal
- border
- table_id

to_json (*filename*, **args*, ***kwargs*)
See dd.to_json docstring for more information

to_parquet (*path*, **args*, ***kwargs*)
Store Dask.dataframe to Parquet files

Parameters

df [dask.dataframe.DataFrame]

path [string] Destination directory for data. Prepend with protocol like `s3://` or `hdfs://` for remote data.

engine [{'auto', 'fastparquet', 'pyarrow'}, default 'auto'] Parquet library to use. If only one library is installed, it will use that one; if both, it will use 'fastparquet'.

compression [string or dict, optional] Either a string like `"snappy"` or a dictionary mapping column names to compressors like `{"name": "gzip", "values": "snappy"}`. The default is `"default"`, which uses the default compression for whichever engine is selected.

write_index [boolean, optional] Whether or not to write the index. Defaults to True *if* divisions are known.

append [bool, optional] If False (default), construct data-set from scratch. If True, add new row-group(s) to an existing data-set. In the latter case, the data-set must exist, and the schema must match the input data.

ignore_divisions [bool, optional] If False (default) raises error when previous divisions overlap with the new appended divisions. Ignored if append=False.

partition_on [list, optional] Construct directory-based partitioning by splitting on these fields' values. Each dask partition will result in one or more datafiles, there will be no global groupby.

storage_options [dict, optional] Key/value pairs to be passed on to the file-system backend, if any.

compute [bool, optional] If True (default) then the result is computed immediately. If False then a `dask.delayed` object is returned for future computation.

****kwargs** Extra options to be passed on to the specific backend.

See also:

read_parquet Read parquet data to dask.dataframe

Notes

Each partition will be written to a separate file.

Examples

```
>>> df = dd.read_csv(...)
>>> to_parquet('/path/to/output/', df, compression='snappy')
```

to_records(*index=False*)
Create Dask Array from a Dask Dataframe

Warning: This creates a dask.array without precise shape information. Operations that depend on shape information, like slicing or reshaping, will not work.

See also:

`dask.dataframe._Frame.values`, *dask.dataframe.from_dask_array*

Examples

```
>>> df.to_records()
dask.array<shape=(nan,), dtype=(numpy.record, [('ind', '<f8'), ('x', 'O'), (
↪'y', '<i8')]), chunksize=(nan,)>
```

to_string(*max_rows=5*)
Render a DataFrame to a console-friendly tabular output.

Parameters

buf [StringIO-like, optional] buffer to write to

columns [sequence, optional] the subset of columns to write; default None writes all columns

col_space [int, optional] the minimum width of each column

header [bool, optional] Write out the column names. If a list of strings is given, it is assumed to be aliases for the column names

index [bool, optional] whether to print index (row) labels, default True

na_rep [string, optional] string representation of NAN to use, default 'NaN'

formatters [list or dict of one-parameter functions, optional] formatter functions to apply to columns' elements by position or name, default None. The result of each function must be a unicode string. List must be of length equal to the number of columns.

float_format [one-parameter function, optional] formatter function to apply to columns' elements if they are floats, default None. The result of this function must be a unicode string.

sparsify [bool, optional] Set to False for a DataFrame with a hierarchical index to print every multiindex key at each row, default True

index_names [bool, optional] Prints the names of the indexes, default True

line_width [int, optional] Width to wrap a line in characters, default no wrap

table_id [str, optional] id for the <table> element create by to_html

New in version 0.23.0.

justify [str, default None] How to justify the column labels. If None uses the option from the print configuration (controlled by set_option), 'right' out of the box. Valid values are

- left
- right
- center
- justify
- justify-all
- start
- end
- inherit
- match-parent
- initial
- unset

Returns

formatted [string (or unicode, depending on data and options)] Dask doesn't support the following argument(s).

- buf
- columns
- col_space
- header
- index
- na_rep
- formatters
- float_format
- sparsify
- index_names
- justify
- line_width
- max_cols
- show_dimensions

to_timestamp (*freq=None*, *how='start'*, *axis=0*)

Cast to DatetimeIndex of timestamps, at *beginning* of period

Parameters

freq [string, default frequency of PeriodIndex] Desired frequency

how [{'s', 'e', 'start', 'end'}] Convention for converting period to timestamp; start of period vs. end

axis [{0 or 'index', 1 or 'columns'}, default 0] The axis to convert (the index by default)

copy [boolean, default True] If false then underlying input data is not copied

Returns

df [DataFrame with DatetimeIndex]

Notes

Dask doesn't support the following argument(s).

- copy

truediv(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Floating division of dataframe and other, element-wise (binary operator *truediv*).

Equivalent to `dataframe / other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series, DataFrame, or constant]

axis [{0, 1, 'index', 'columns'}] For Series input, axis to match Series index on

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

fill_value [None or float value, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing

Returns

result [DataFrame]

See also:

DataFrame.rtruediv

Notes

Mismatched indices will be unioned together

Examples

None

values

Return a dask.array of the values of this dataframe

Warning: This creates a dask.array without precise shape information. Operations that depend on shape information, like slicing or reshaping, will not work.

var(*axis=None*, *skipna=True*, *ddof=1*, *split_every=False*, *dtype=None*, *out=None*)
Return unbiased variance over requested axis.

Normalized by N-1 by default. This can be changed using the ddof argument

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

ddof [int, default 1] Delta Degrees of Freedom. The divisor used in calculations is N - ddof, where N represents the number of elements.

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

var [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

visualize(*filename='mydask'*, *format=None*, *optimize_graph=False*, ***kwargs*)
Render the computation of this object's task graph using graphviz.

Requires `graphviz` to be installed.

Parameters

filename [str or None, optional] The name (without an extension) of the file to write to disk. If *filename* is None, no file will be written, and we communicate with dot using only pipes.

format [{'png', 'pdf', 'dot', 'svg', 'jpeg', 'jpg'}, optional] Format in which to write output file. Default is 'png'.

optimize_graph [bool, optional] If True, the graph is optimized before rendering. Otherwise, the graph is displayed as is. Default is False.

color: {None, 'order'}, optional Options to color nodes. Provide `cmap=` keyword for additional colormap

****kwargs** Additional keyword arguments to forward to `to_graphviz`.

Returns

result [IPython.diplay.Image, IPython.display.SVG, or None] See dask.dot.dot_graph for more information.

See also:

`dask.base.visualize`, `dask.dot.dot_graph`

Notes

For more information on optimization see here:

https://docs.dask.org/en/latest/optimize.html

Examples

```
>>> x.visualize(filename='dask.pdf')
>>> x.visualize(filename='dask.pdf', color='order')
```

where(*cond*, *other=nan*)

Return an object of same shape as self and whose corresponding entries are from self where *cond* is True and otherwise are from *other*.

Parameters

cond [boolean NDFrame, array-like, or callable] Where *cond* is True, keep the original value. Where False, replace with corresponding value from *other*. If *cond* is callable, it is computed on the NDFrame and should return boolean NDFrame or array. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as cond.

other [scalar, NDFrame, or callable] Entries where *cond* is False are replaced with corresponding value from *other*. If other is callable, it is computed on the NDFrame and should return scalar or NDFrame. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as other.

inplace [boolean, default False] Whether to perform the operation in place on the data

axis [alignment axis if needed, default None]

level [alignment level if needed, default None]

errors [str, {'raise', 'ignore'}, default 'raise']

- `raise` : allow exceptions to be raised
- `ignore` : suppress exceptions. On error return original object

Note that currently this parameter won't affect the results and will always coerce to a suitable dtype.

try_cast [boolean, default False] try to cast the result back to the input type (if possible),

raise_on_error [boolean, default True] Whether to raise on invalid data types (e.g. trying to where on strings)

Deprecated since version 0.21.0.

Returns

wh [same type as caller]

See also:

DataFrame.mask()

Notes

The where method is an application of the if-then idiom. For each element in the calling DataFrame, if `cond` is `True` the element is used; otherwise the corresponding element from the DataFrame `other` is used.

The signature for *`DataFrame.where()`* differs from `numpy.where()`. Roughly `df1.where(m, df2)` is equivalent to `np.where(m, df1, df2)`.

For further details and examples see the `where` documentation in indexing.

Examples

```
>>> s = pd.Series(range(5))
>>> s.where(s > 0)
0    NaN
1    1.0
2    2.0
3    3.0
4    4.0
```

```
>>> s.mask(s > 0)
0    0.0
1    NaN
2    NaN
3    NaN
4    NaN
```

```
>>> s.where(s > 1, 10)
0    10.0
1    10.0
2    2.0
3    3.0
4    4.0
```

```
>>> df = pd.DataFrame(np.arange(10).reshape(-1, 2), columns=['A', 'B'])
>>> m = df % 3 == 0
>>> df.where(m, -df)
   A  B
0  0 -1
1 -2  3
2 -4 -5
3  6 -7
4 -8  9
>>> df.where(m, -df) == np.where(m, df, -df)
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
>>> df.where(m, -df) == df.mask(~m, -df)
      A     B
0  True  True
1  True  True
```

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```
2  True  True
3  True  True
4  True  True
```

Series Methods

class dask.dataframe.**Series**(*dsk*, *name*, *meta*, *divisions*)

Parallel Pandas Series

Do not use this class directly. Instead use functions like `dd.read_csv`, `dd.read_parquet`, or `dd.from_pandas`.

Parameters

dsk: dict The dask graph to compute this Series

_name: str The key prefix that specifies which keys in the dask comprise this particular Series

meta: pandas.Series An empty `pandas.Series` with names, dtypes, and index matching the expected output.

divisions: tuple of index values Values along which we partition our blocks on the index

See also:

dask.dataframe.DataFrame

abs()

Return a Series/DataFrame with absolute numeric value of each element.

This function only applies to elements that are all numeric.

Returns

abs Series/DataFrame containing the absolute value of each element.

See also:

numpy.absolute calculate the absolute value element-wise.

Notes

For `complex` inputs, `1.2 + 1j`, the absolute value is $\sqrt{a^2 + b^2}$.

Examples

Absolute numeric values in a Series.

```
>>> s = pd.Series([-1.10, 2, -3.33, 4])
>>> s.abs()
0    1.10
1    2.00
2    3.33
3    4.00
dtype: float64
```

Absolute numeric values in a Series with complex numbers.

```
>>> s = pd.Series([1.2 + 1j])
>>> s.abs()
0    1.56205
dtype: float64
```

Absolute numeric values in a Series with a Timedelta element.

```
>>> s = pd.Series([pd.Timedelta('1 days')])
>>> s.abs()
0   1 days
dtype: timedelta64[ns]
```

Select rows with data closest to certain value using argsort (from StackOverflow).

```
>>> df = pd.DataFrame({
...     'a': [4, 5, 6, 7],
...     'b': [10, 20, 30, 40],
...     'c': [100, 50, -30, -50]
... })
>>> df
     a    b    c
0    4   10  100
1    5   20   50
2    6   30  -30
3    7   40  -50
>>> df.loc[(df.c - 43).abs().argsort()]
     a    b    c
1    5   20   50
0    4   10  100
2    6   30  -30
3    7   40  -50
```

add(*other*, *level=None*, *fill_value=None*, *axis=0*)

Addition of series and other, element-wise (binary operator *add*).

Equivalent to `series + other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.radd

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

align(*other*, *join='outer'*, *axis=None*, *fill_value=None*)

Align two objects on their axes with the specified join method for each axis Index

Parameters

other [DataFrame or Series]

join [{'outer', 'inner', 'left', 'right'}, default 'outer']

axis [allowed axis of the other object, default None] Align on index (0), columns (1), or both (None)

level [int or level name, default None] Broadcast across a level, matching Index values on the passed MultiIndex level

copy [boolean, default True] Always returns new objects. If copy=False and no reindexing is required then original objects are returned.

fill_value [scalar, default np.NaN] Value to use for missing values. Defaults to NaN, but can be any "compatible" value

method [str, default None]

limit [int, default None]

fill_axis [{0 or 'index'}, default 0] Filling axis, method and limit

broadcast_axis [{0 or 'index'}, default None] Broadcast values along this axis, if aligning two objects of different dimensions

Returns

(left, right) [(Series, type of other)] Aligned objects

Notes

Dask doesn't support the following argument(s).

- level
- copy
- method
- limit
- fill_axis
- broadcast_axis

all(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)
Return whether all elements are True, potentially over an axis.

Returns True if all elements within a series or along a Dataframe axis are non-zero, not-empty or not-False.

Parameters

axis [{0 or 'index', 1 or 'columns', None}, default 0] Indicate which axis or axes should be reduced.

- 0 / 'index' : reduce the index, return a Series whose index is the original column labels.
- 1 / 'columns' : reduce the columns, return a Series whose index is the original index.
- None : reduce all axes, return a scalar.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

bool_only [boolean, default None] Include only boolean columns. If None, will attempt to use everything, then use only boolean data. Not implemented for Series.

****kwargs** [any, default None] Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

all [Series or DataFrame (if level specified)]

See also:

pandas.Series.all Return True if all elements are True

pandas.DataFrame.any Return True if one (or more) elements are True

Notes

Dask doesn't support the following argument(s).

- bool_only
- level

Examples

Series

```
>>> pd.Series([True, True]).all()
True
>>> pd.Series([True, False]).all()
False
```

DataFrames

Create a dataframe from a dictionary.

```
>>> df = pd.DataFrame({'col1': [True, True], 'col2': [True, False]})
>>> df
   col1   col2
0  True   True
1  True  False
```

Default behaviour checks if column-wise values all return True.

```
>>> df.all()
col1     True
col2    False
dtype: bool
```

Specify `axis='columns'` to check if row-wise values all return True.

```
>>> df.all(axis='columns')
0     True
1    False
dtype: bool
```

Or `axis=None` for whether every value is True.

```
>>> df.all(axis=None)
False
```

any(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)
Return whether any element is True over requested axis.

Unlike *DataFrame.all()*, this performs an *or* operation. If any of the values along the specified axis is True, this will return True.

Parameters

axis [{0 or 'index', 1 or 'columns', None}, default 0] Indicate which axis or axes should be reduced.

- 0 / 'index' : reduce the index, return a Series whose index is the original column labels.
- 1 / 'columns' : reduce the columns, return a Series whose index is the original index.
- None : reduce all axes, return a scalar.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

bool_only [boolean, default None] Include only boolean columns. If None, will attempt to use everything, then use only boolean data. Not implemented for Series.

****kwargs** [any, default None] Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

any [Series or DataFrame (if level specified)]

See also:

`pandas.DataFrame.all` Return whether all elements are True.

Notes

Dask doesn't support the following argument(s).

- bool_only
- level

Examples

Series

For Series input, the output is a scalar indicating whether any element is True.

```
>>> pd.Series([True, False]).any()
True
```

DataFrame

Whether each column contains at least one True element (the default).

```
>>> df = pd.DataFrame({"A": [1, 2], "B": [0, 2], "C": [0, 0]})
>>> df
   A  B  C
0  1  0  0
1  2  2  0
```

```
>>> df.any()
A     True
B     True
C    False
dtype: bool
```

Aggregating over the columns.

```
>>> df = pd.DataFrame({"A": [True, False], "B": [1, 2]})
>>> df
       A  B
0   True  1
1  False  2
```

```
>>> df.any(axis='columns')
0    True
1    True
dtype: bool
```

```
>>> df = pd.DataFrame({"A": [True, False], "B": [1, 0]})
>>> df
       A  B
0   True  1
1  False  0
```

```
>>> df.any(axis='columns')
0    True
1    False
dtype: bool
```

Aggregating over the entire DataFrame with `axis=None`.

```
>>> df.any(axis=None)
True
```

any for an empty DataFrame is an empty Series.

```
>>> pd.DataFrame([]).any()
Series([], dtype: bool)
```

append(*other*)

Concatenate two or more Series.

Parameters

to_append [Series or list/tuple of Series]

ignore_index [boolean, default False] If True, do not use the index labels.

New in version 0.19.0.

verify_integrity [boolean, default False] If True, raise Exception on creating index with duplicates

Returns

appended [Series]

See also:

`pandas.concat` General function to concatenate DataFrame, Series or Panel objects

Notes

Iteratively appending to a Series can be more computationally intensive than a single concatenate. A better solution is to append values to a list and then concatenate the list with the original Series all at once.

Examples

```
>>> s1 = pd.Series([1, 2, 3])
>>> s2 = pd.Series([4, 5, 6])
>>> s3 = pd.Series([4, 5, 6], index=[3,4,5])
>>> s1.append(s2)
0    1
1    2
2    3
0    4
1    5
2    6
dtype: int64
```

```
>>> s1.append(s3)
0    1
1    2
2    3
3    4
4    5
5    6
dtype: int64
```

With *ignore_index* set to True:

```
>>> s1.append(s2, ignore_index=True)
0    1
1    2
2    3
3    4
4    5
5    6
dtype: int64
```

With *verify_integrity* set to True:

```
>>> s1.append(s2, verify_integrity=True)
Traceback (most recent call last):
...
ValueError: Indexes have overlapping values: [0, 1, 2]
```

apply (*func*, *convert_dtype=True*, *meta='__no_default__'*, *args=()*, ***kwds*)
Parallel version of pandas.Series.apply

Parameters

func [function] Function to apply

convert_dtype [boolean, default True] Try to find better dtype for elementwise function results. If False, leave as dtype=object.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing

`meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

args [tuple] Positional arguments to pass to function in addition to the value.

Additional keyword arguments will be passed as keywords to the function.

Returns

applied [Series or DataFrame if func returns a Series.]

See also:

`dask.Series.map_partitions`

Examples

```
>>> import dask.dataframe as dd
>>> s = pd.Series(range(5), name='x')
>>> ds = dd.from_pandas(s, npartitions=2)
```

Apply a function elementwise across the Series, passing in extra arguments in `args` and `kwargs`:

```
>>> def myadd(x, a, b=1):
...     return x + a + b
>>> res = ds.apply(myadd, args=(2,), b=1.5)
```

By default, dask tries to infer the output metadata by running your provided function on some fake data. This works well in many cases, but can sometimes be expensive, or even fail. To avoid this, you can manually specify the output metadata with the `meta` keyword. This can be specified in many forms, for more information see `dask.dataframe.utils.make_meta`.

Here we specify the output is a Series with name `'x'`, and dtype `float64`:

```
>>> res = ds.apply(myadd, args=(2,), b=1.5, meta=('x', 'f8'))
```

In the case where the metadata doesn't change, you can also pass in the object itself directly:

```
>>> res = ds.apply(lambda x: x + 1, meta=ds)
```

astype(*dtype*)

Cast a pandas object to a specified dtype `dtype`.

Parameters

dtype [data type, or dict of column name -> data type] Use a numpy.dtype or Python type to cast entire pandas object to the same type. Alternatively, use {col: dtype, ...}, where col is a column label and dtype is a numpy.dtype or Python type to cast one or more of the DataFrame's columns to column-specific types.

copy [bool, default True.] Return a copy when `copy=True` (be very careful setting `copy=False` as changes to values then may propagate to other pandas objects).

errors [{'raise', 'ignore'}, default 'raise'.] Control raising of exceptions on invalid data for provided dtype.

- `raise` : allow exceptions to be raised
- `ignore` : suppress exceptions. On error return original object

New in version 0.20.0.

raise_on_error [raise on invalid input] Deprecated since version 0.20.0: Use `errors` instead

kwargs [keyword arguments to pass on to the constructor]

Returns

casted [type of caller]

See also:

pandas.to_datetime Convert argument to datetime.

pandas.to_timedelta Convert argument to timedelta.

pandas.to_numeric Convert argument to a numeric type.

numpy.ndarray.astype Cast a numpy array to a specified type.

Notes

Dask doesn't support the following argument(s).

- copy
- errors

Examples

```
>>> ser = pd.Series([1, 2], dtype='int32')
>>> ser
0    1
1    2
dtype: int32
>>> ser.astype('int64')
0    1
1    2
dtype: int64
```

Convert to categorical type:

```
>>> ser.astype('category')
0    1
1    2
dtype: category
Categories (2, int64): [1, 2]
```

Convert to ordered categorical type with custom ordering:

```
>>> ser.astype('category', ordered=True, categories=[2, 1])
0    1
1    2
dtype: category
Categories (2, int64): [2 < 1]
```

Note that using `copy=False` and changing data on a new pandas object may propagate changes:

```
>>> s1 = pd.Series([1,2])
>>> s2 = s1.astype('int64', copy=False)
>>> s2[0] = 10
>>> s1  # note that s1[0] has changed too
0    10
1     2
dtype: int64
```

autocorr (*lag=1*, *split_every=False*)
Lag-N autocorrelation

Parameters

lag [int, default 1] Number of lags to apply before performing autocorrelation.

Returns

autocorr [float]

between (*left*, *right*, *inclusive=True*)
Return boolean Series equivalent to left <= series <= right.

This function returns a boolean vector containing *True* wherever the corresponding Series element is between the boundary values *left* and *right*. NA values are treated as *False*.

Parameters

left [scalar] Left boundary.

right [scalar] Right boundary.

inclusive [bool, default True] Include boundaries.

Returns

Series Each element will be a boolean.

See also:

pandas.Series.gt Greater than of series and other

pandas.Series.lt Less than of series and other

Notes

This function is equivalent to `(left <= ser) & (ser <= right)`

Examples

```
>>> s = pd.Series([2, 0, 4, 8, np.nan])
```

Boundary values are included by default:

```
>>> s.between(1, 4)
0     True
1    False
2     True
3    False
```

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```
4    False
dtype: bool
```

With *inclusive* set to `False` boundary values are excluded:

```
>>> s.between(1, 4, inclusive=False)
0     True
1    False
2    False
3    False
4    False
dtype: bool
```

left and *right* can be any scalar value:

```
>>> s = pd.Series(['Alice', 'Bob', 'Carol', 'Eve'])
>>> s.between('Anna', 'Daniel')
0    False
1     True
2     True
3    False
dtype: bool
```

bfill (*axis=None*, *limit=None*)
Synonym for *DataFrame.fillna(method='bfill')*

Notes

Dask doesn't support the following argument(s).

- inplace
- downcast

clear_divisions ()
Forget division information

clip (*lower=None*, *upper=None*, *out=None*)
Trim values at input threshold(s).

Assigns values outside boundary to boundary values. Thresholds can be singular values or array like, and in the latter case the clipping is performed element-wise in the specified axis.

Parameters

lower [float or array_like, default None] Minimum threshold value. All values below this threshold will be set to it.

upper [float or array_like, default None] Maximum threshold value. All values above this threshold will be set to it.

axis [int or string axis name, optional] Align object with lower and upper along the given axis.

inplace [boolean, default False] Whether to perform the operation in place on the data.

New in version 0.21.0.

***args, **kwargs** Additional keywords have no effect but might be accepted for compatibility with numpy.

Returns

Series or DataFrame Same type as calling object with the values outside the clip boundaries replaced

See also:

clip_lower Clip values below specified threshold(s).

clip_upper Clip values above specified threshold(s).

Notes

Dask doesn't support the following argument(s).

- axis
- inplace

Examples

```
>>> data = {'col_0': [9, -3, 0, -1, 5], 'col_1': [-2, -7, 6, 8, -5]}
>>> df = pd.DataFrame(data)
>>> df
   col_0  col_1
0      9     -2
1     -3     -7
2      0      6
3     -1      8
4      5     -5
```

Clips per column using lower and upper thresholds:

```
>>> df.clip(-4, 6)
   col_0  col_1
0      6     -2
1     -3     -4
2      0      6
3     -1      6
4      5     -4
```

Clips using specific lower and upper thresholds per column element:

```
>>> t = pd.Series([2, -4, -1, 6, 3])
>>> t
0    2
1   -4
2   -1
3    6
4    3
dtype: int64
```

```
>>> df.clip(t, t + 4, axis=0)
   col_0  col_1
0      6      2
1     -3     -4
2      0      3
3      6      8
4      5      3
```

clip_lower(*threshold*)

Return copy of the input with values below a threshold truncated.

Parameters

threshold [numeric or array-like] Minimum value allowed. All values below threshold will be set to this value.

- float : every value is compared to *threshold*.
- array-like : The shape of *threshold* should match the object it's compared to. When *self* is a Series, *threshold* should be the length. When *self* is a DataFrame, *threshold* should 2-D and the same shape as *self* for `axis=None`, or 1-D and the same length as the axis being compared.

axis [{0 or 'index', 1 or 'columns'}, default 0] Align *self* with *threshold* along the given axis.

inplace [boolean, default False] Whether to perform the operation in place on the data.

New in version 0.21.0.

Returns

clipped [same type as input]

See also:

Series.clip Return copy of input with values below and above thresholds truncated.

Series.clip_upper Return copy of input with values above threshold truncated.

Notes

Dask doesn't support the following argument(s).

- axis
- inplace

Examples

Series single threshold clipping:

```
>>> s = pd.Series([5, 6, 7, 8, 9])
>>> s.clip_lower(8)
0    8
1    8
2    8
3    8
```

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```
4    9
dtype: int64
```

Series clipping element-wise using an array of thresholds. *threshold* should be the same length as the Series.

```
>>> elemwise_thresholds = [4, 8, 7, 2, 5]
>>> s.clip_lower(elemwise_thresholds)
0    5
1    8
2    7
3    8
4    9
dtype: int64
```

DataFrames can be compared to a scalar.

```
>>> df = pd.DataFrame({"A": [1, 3, 5], "B": [2, 4, 6]})
>>> df
   A  B
0  1  2
1  3  4
2  5  6
```

```
>>> df.clip_lower(3)
   A  B
0  3  3
1  3  4
2  5  6
```

Or to an array of values. By default, *threshold* should be the same shape as the DataFrame.

```
>>> df.clip_lower(np.array([[3, 4], [2, 2], [6, 2]]))
   A  B
0  3  4
1  3  4
2  6  6
```

Control how *threshold* is broadcast with *axis*. In this case *threshold* should be the same length as the axis specified by *axis*.

```
>>> df.clip_lower(np.array([3, 3, 5]), axis='index')
   A  B
0  3  3
1  3  4
2  5  6
```

```
>>> df.clip_lower(np.array([4, 5]), axis='columns')
   A  B
0  4  5
1  4  5
2  5  6
```

clip_upper(*threshold*)

Return copy of input with values above given value(s) truncated.

Parameters

threshold [float or array_like]

axis [int or string axis name, optional] Align object with threshold along the given axis.

inplace [boolean, default False] Whether to perform the operation in place on the data

New in version 0.21.0.

Returns

clipped [same type as input]

See also:

clip

Notes

Dask doesn't support the following argument(s).

- axis
- inplace

combine(*other*, *func*, *fill_value=None*)

Perform elementwise binary operation on two Series using given function with optional fill value when an index is missing from one Series or the other

Parameters

other [Series or scalar value]

func [function] Function that takes two scalars as inputs and return a scalar

fill_value [scalar value]

Returns

result [Series]

See also:

Series.combine_first Combine Series values, choosing the calling Series's values first

Examples

```
>>> s1 = Series([1, 2])
>>> s2 = Series([0, 3])
>>> s1.combine(s2, lambda x1, x2: x1 if x1 < x2 else x2)
0    0
1    2
dtype: int64
```

combine_first(*other*)

Combine Series values, choosing the calling Series's values first. Result index will be the union of the two indexes

Parameters

other [Series]

Returns

combined [Series]

See also:

Series.combine Perform elementwise operation on two Series using a given function

Examples

```
>>> s1 = pd.Series([1, np.nan])
>>> s2 = pd.Series([3, 4])
>>> s1.combine_first(s2)
0    1.0
1    4.0
dtype: float64
```

compute(***kwargs*)

Compute this dask collection

This turns a lazy Dask collection into its in-memory equivalent. For example a Dask.array turns into a `numpy.array()` and a Dask.dataframe turns into a Pandas dataframe. The entire dataset must fit into memory before calling this operation.

Parameters

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

optimize_graph [bool, optional] If True [default], the graph is optimized before computation. Otherwise the graph is run as is. This can be useful for debugging.

kwargs Extra keywords to forward to the scheduler function.

See also:

`dask.base.compute`

copy()

Make a copy of the dataframe

This is strictly a shallow copy of the underlying computational graph. It does not affect the underlying data

corr(*other*, *method='pearson'*, *min_periods=None*, *split_every=False*)

Compute correlation with *other* Series, excluding missing values

Parameters

other [Series]

method [{'pearson', 'kendall', 'spearman'}]

- pearson : standard correlation coefficient
- kendall : Kendall Tau correlation coefficient
- spearman : Spearman rank correlation

min_periods [int, optional] Minimum number of observations needed to have a valid result

Returns

correlation [float]

count (*split_every=False*)
Return number of non-NA/null observations in the Series

Parameters

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a smaller Series

Returns

nobs [int or Series (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level

cov (*other*, *min_periods=None*, *split_every=False*)
Compute covariance with Series, excluding missing values

Parameters

other [Series]

min_periods [int, optional] Minimum number of observations needed to have a valid result

Returns

covariance [float]

Normalized by N-1 (unbiased estimator).

cummax (*axis=None*, *skipna=True*, *out=None*)
Return cumulative maximum over a DataFrame or Series axis.

Returns a DataFrame or Series of the same size containing the cumulative maximum.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cummax [Series or DataFrame]

See also:

pandas.core.window.Expanding.max Similar functionality but ignores `NaN` values.

DataFrame.max Return the maximum over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])
>>> s
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cummax()
0    2.0
1    NaN
2    5.0
3    5.0
4    5.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cummax(skipna=False)
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the maximum in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cummax()
     A    B
0  2.0  1.0
1  3.0  NaN
2  3.0  1.0
```

To iterate over columns and find the maximum in each row, use `axis=1`

```
>>> df.cummax(axis=1)
     A    B
0  2.0  2.0
1  3.0  NaN
2  1.0  1.0
```

cummin (*axis=None*, *skipna=True*, *out=None*)

Return cumulative minimum over a DataFrame or Series axis.

Returns a DataFrame or Series of the same size containing the cumulative minimum.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cummin [Series or DataFrame]

See also:

pandas.core.window.Expanding.min Similar functionality but ignores `NaN` values.

DataFrame.min Return the minimum over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])
>>> s
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cummin()
0    2.0
1    NaN
2    2.0
```

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```
3   -1.0
4   -1.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cummin(skipna=False)
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the minimum in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cummin()
     A    B
0  2.0  1.0
1  2.0  NaN
2  1.0  0.0
```

To iterate over columns and find the minimum in each row, use `axis=1`

```
>>> df.cummin(axis=1)
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

cumprod(*axis=None*, *skipna=True*, *dtype=None*, *out=None*)

Return cumulative product over a DataFrame or Series axis.

Returns a DataFrame or Series of the same size containing the cumulative product.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cumprod [Series or DataFrame]

See also:

pandas.core.window.Expanding.prod Similar functionality but ignores `NaN` values.

DataFrame.prod Return the product over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])
>>> s
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cumprod()
0     2.0
1     NaN
2    10.0
3   -10.0
4    -0.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cumprod(skipna=False)
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df
     A    B
```

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```
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the product in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cumprod()
     A    B
0  2.0  1.0
1  6.0  NaN
2  6.0  0.0
```

To iterate over columns and find the product in each row, use `axis=1`

```
>>> df.cumprod(axis=1)
     A    B
0  2.0  2.0
1  3.0  NaN
2  1.0  0.0
```

cumsum(*axis=None*, *skipna=True*, *dtype=None*, *out=None*)

Return cumulative sum over a DataFrame or Series axis.

Returns a DataFrame or Series of the same size containing the cumulative sum.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cumsum [Series or DataFrame]

See also:

pandas.core.window.Expanding.sum Similar functionality but ignores `NaN` values.

DataFrame.sum Return the sum over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])
>>> s
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cumsum()
0    2.0
1    NaN
2    7.0
3    6.0
4    6.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cumsum(skipna=False)
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the sum in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cumsum()
     A    B
0  2.0  1.0
1  5.0  NaN
2  6.0  1.0
```

To iterate over columns and find the sum in each row, use `axis=1`

```
>>> df.cumsum(axis=1)
     A    B
0  2.0  3.0
1  3.0  NaN
2  1.0  1.0
```

describe(*split_every=False*)

Generates descriptive statistics that summarize the central tendency, dispersion and shape of a dataset's distribution, excluding `NaN` values.

Analyzes both numeric and object series, as well as `DataFrame` column sets of mixed data types. The output will vary depending on what is provided. Refer to the notes below for more detail.

Parameters

percentiles [list-like of numbers, optional] The percentiles to include in the output. All should fall between 0 and 1. The default is `[.25, .5, .75]`, which returns the 25th, 50th, and 75th percentiles.

include ['all', list-like of dtypes or None (default), optional] A white list of data types to include in the result. Ignored for `Series`. Here are the options:

- 'all' : All columns of the input will be included in the output.
- A list-like of dtypes : Limits the results to the provided data types. To limit the result to numeric types submit `numpy.number`. To limit it instead to object columns submit the `numpy.object` data type. Strings can also be used in the style of `select_dtypes` (e.g. `df.describe(include=['O'])`). To select pandas categorical columns, use `'category'`
- None (default) : The result will include all numeric columns.

exclude [list-like of dtypes or None (default), optional,] A black list of data types to omit from the result. Ignored for `Series`. Here are the options:

- A list-like of dtypes : Excludes the provided data types from the result. To exclude numeric types submit `numpy.number`. To exclude object columns submit the data type `numpy.object`. Strings can also be used in the style of `select_dtypes` (e.g. `df.describe(include=['O'])`). To exclude pandas categorical columns, use `'category'`
- None (default) : The result will exclude nothing.

Returns

summary: Series/DataFrame of summary statistics

See also:

DataFrame.count, *DataFrame.max*, *DataFrame.min*, *DataFrame.mean*, *DataFrame.std*, *DataFrame.select_dtypes*

Notes

For numeric data, the result's index will include `count`, `mean`, `std`, `min`, `max` as well as lower, `50` and upper percentiles. By default the lower percentile is `25` and the upper percentile is `75`. The `50` percentile is the same as the median.

For object data (e.g. strings or timestamps), the result's index will include `count`, `unique`, `top`, and `freq`. The `top` is the most common value. The `freq` is the most common value's frequency. Timestamps also include the `first` and `last` items.

If multiple object values have the highest count, then the `count` and `top` results will be arbitrarily chosen from among those with the highest count.

For mixed data types provided via a `DataFrame`, the default is to return only an analysis of numeric columns. If the dataframe consists only of object and categorical data without any numeric columns,

the default is to return an analysis of both the object and categorical columns. If `include='all'` is provided as an option, the result will include a union of attributes of each type.

The *include* and *exclude* parameters can be used to limit which columns in a `DataFrame` are analyzed for the output. The parameters are ignored when analyzing a `Series`.

Examples

Describing a numeric `Series`.

```
>>> s = pd.Series([1, 2, 3])
>>> s.describe()
count    3.0
mean     2.0
std      1.0
min      1.0
25%      1.5
50%      2.0
75%      2.5
max      3.0
```

Describing a categorical `Series`.

```
>>> s = pd.Series(['a', 'a', 'b', 'c'])
>>> s.describe()
count     4
unique    3
top       a
freq      2
dtype: object
```

Describing a timestamp `Series`.

```
>>> s = pd.Series([
...   np.datetime64("2000-01-01"),
...   np.datetime64("2010-01-01"),
...   np.datetime64("2010-01-01")
... ])
>>> s.describe()
count                       3
unique                      2
top       2010-01-01 00:00:00
freq                        2
first     2000-01-01 00:00:00
last      2010-01-01 00:00:00
dtype: object
```

Describing a `DataFrame`. By default only numeric fields are returned.

```
>>> df = pd.DataFrame({ 'object': ['a', 'b', 'c'],
...                     'numeric': [1, 2, 3],
...                     'categorical': pd.Categorical(['d','e','f'])
...                   })
>>> df.describe()
       numeric
count      3.0
mean       2.0
```

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```
std        1.0
min        1.0
25%        1.5
50%        2.0
75%        2.5
max        3.0
```

Describing all columns of a `DataFrame` regardless of data type.

```
>>> df.describe(include='all')
        categorical  numeric object
count             3      3.0      3
unique            3      NaN      3
top               f      NaN      c
freq              1      NaN      1
mean            NaN      2.0    NaN
std             NaN      1.0    NaN
min             NaN      1.0    NaN
25%             NaN      1.5    NaN
50%             NaN      2.0    NaN
75%             NaN      2.5    NaN
max             NaN      3.0    NaN
```

Describing a column from a `DataFrame` by accessing it as an attribute.

```
>>> df.numeric.describe()
count    3.0
mean     2.0
std      1.0
min      1.0
25%      1.5
50%      2.0
75%      2.5
max      3.0
Name: numeric, dtype: float64
```

Including only numeric columns in a `DataFrame` description.

```
>>> df.describe(include=[np.number])
       numeric
count      3.0
mean       2.0
std        1.0
min        1.0
25%        1.5
50%        2.0
75%        2.5
max        3.0
```

Including only string columns in a `DataFrame` description.

```
>>> df.describe(include=[np.object])
       object
count       3
unique      3
top         c
freq        1
```

Including only categorical columns from a `DataFrame` description.

```
>>> df.describe(include=['category'])
       categorical
count             3
unique            3
top               f
freq              1
```

Excluding numeric columns from a `DataFrame` description.

```
>>> df.describe(exclude=[np.number])
       categorical object
count             3      3
unique            3      3
top               f      c
freq              1      1
```

Excluding object columns from a `DataFrame` description.

```
>>> df.describe(exclude=[np.object])
        categorical  numeric
count             3      3.0
unique            3      NaN
top               f      NaN
freq              1      NaN
mean            NaN      2.0
std             NaN      1.0
min             NaN      1.0
25%             NaN      1.5
50%             NaN      2.0
75%             NaN      2.5
max             NaN      3.0
```

diff (*periods=1*, *axis=0*)

First discrete difference of element.

Calculates the difference of a DataFrame element compared with another element in the DataFrame (default is the element in the same column of the previous row).

Parameters

periods [int, default 1] Periods to shift for calculating difference, accepts negative values.

axis [{0 or 'index', 1 or 'columns'}, default 0] Take difference over rows (0) or columns (1).

New in version 0.16.1..

Returns

diffed [DataFrame]

See also:

Series.diff First discrete difference for a Series.

DataFrame.pct_change Percent change over given number of periods.

DataFrame.shift Shift index by desired number of periods with an optional time freq.

Examples

Difference with previous row

```
>>> df = pd.DataFrame({'a': [1, 2, 3, 4, 5, 6],
...                    'b': [1, 1, 2, 3, 5, 8],
...                    'c': [1, 4, 9, 16, 25, 36]})
>>> df
   a  b   c
0  1  1   1
1  2  1   4
2  3  2   9
3  4  3  16
4  5  5  25
5  6  8  36
```

```
>>> df.diff()
     a    b     c
0  NaN  NaN   NaN
1  1.0  0.0   3.0
2  1.0  1.0   5.0
3  1.0  1.0   7.0
4  1.0  2.0   9.0
5  1.0  3.0  11.0
```

Difference with previous column

```
>>> df.diff(axis=1)
    a    b     c
0 NaN  0.0   0.0
1 NaN -1.0   3.0
2 NaN -1.0   7.0
3 NaN -1.0  13.0
4 NaN  0.0  20.0
5 NaN  2.0  28.0
```

Difference with 3rd previous row

```
>>> df.diff(periods=3)
     a    b     c
0  NaN  NaN   NaN
1  NaN  NaN   NaN
2  NaN  NaN   NaN
3  3.0  2.0  15.0
4  3.0  4.0  21.0
5  3.0  6.0  27.0
```

Difference with following row

```
>>> df.diff(periods=-1)
     a    b     c
0 -1.0  0.0  -3.0
1 -1.0 -1.0  -5.0
2 -1.0 -1.0  -7.0
3 -1.0 -2.0  -9.0
4 -1.0 -3.0 -11.0
5  NaN  NaN   NaN
```

div(*other*, *level=None*, *fill_value=None*, *axis=0*)
Floating division of series and other, element-wise (binary operator *truediv*).

Equivalent to `series / other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.rtruediv

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

drop_duplicates(*split_every=None*, *split_out=1*, ***kwargs*)
Return DataFrame with duplicate rows removed, optionally only considering certain columns

Parameters

subset [column label or sequence of labels, optional] Only consider certain columns for identifying duplicates, by default use all of the columns

keep [{'first', 'last', False}, default 'first']

- `first` : Drop duplicates except for the first occurrence.

- `last` : Drop duplicates except for the last occurrence.
- False : Drop all duplicates.

inplace [boolean, default False] Whether to drop duplicates in place or to return a copy

Returns

deduplicated [DataFrame]

Notes

Dask doesn't support the following argument(s).

- subset
- keep
- inplace

dropna()

Return a new Series with missing values removed.

See the User Guide for more on which values are considered missing, and how to work with missing data.

Parameters

axis [{0 or 'index'}, default 0] There is only one axis to drop values from.

inplace [bool, default False] If True, do operation inplace and return None.

****kwargs** Not in use.

Returns

Series Series with NA entries dropped from it.

See also:

Series.isna Indicate missing values.

Series.notna Indicate existing (non-missing) values.

Series.fillna Replace missing values.

DataFrame.dropna Drop rows or columns which contain NA values.

Index.dropna Drop missing indices.

Notes

Dask doesn't support the following argument(s).

- axis
- inplace

Examples

```
>>> ser = pd.Series([1., 2., np.nan])
>>> ser
0    1.0
1    2.0
2    NaN
dtype: float64
```

Drop NA values from a Series.

```
>>> ser.dropna()
0    1.0
1    2.0
dtype: float64
```

Keep the Series with valid entries in the same variable.

```
>>> ser.dropna(inplace=True)
>>> ser
0    1.0
1    2.0
dtype: float64
```

Empty strings are not considered NA values. `None` is considered an NA value.

```
>>> ser = pd.Series([np.NaN, 2, pd.NaT, '', None, 'I stay'])
>>> ser
0       NaN
1         2
2       NaT
3
4      None
5    I stay
dtype: object
>>> ser.dropna()
1         2
3
5    I stay
dtype: object
```

dt

Namespace of datetime methods

dtype

Return data type

eq(*other*, *level=None*, *axis=0*)

Equal to of series and other, element-wise (binary operator *eq*).

Equivalent to `series == other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

`Series.None`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

ffill (*axis=None*, *limit=None*)
Synonym for *DataFrame.fillna(method='ffill')*

Notes

Dask doesn't support the following argument(s).

- inplace
- downcast

fillna (*value=None*, *method=None*, *limit=None*, *axis=None*)
Fill NA/NaN values using the specified method

Parameters

value [scalar, dict, Series, or DataFrame] Value to use to fill holes (e.g. 0), alternately a dict/Series/DataFrame of values specifying which value to use for each index (for a Series) or column (for a DataFrame). (values not in the dict/Series/DataFrame will not be filled). This value cannot be a list.

method [{'backfill', 'bfill', 'pad', 'ffill', None}, default None] Method to use for filling holes in reindexed Series pad / ffill: propagate last valid observation forward to next valid backfill / bfill: use NEXT valid observation to fill gap

axis [{0 or 'index', 1 or 'columns'}]

inplace [boolean, default False] If True, fill in place. Note: this will modify any other views on this object, (e.g. a no-copy slice for a column in a DataFrame).

limit [int, default None] If method is specified, this is the maximum number of consecutive NaN values to forward/backward fill. In other words, if there is a gap with more than this number of consecutive NaNs, it will only be partially filled. If method is not specified, this is the maximum number of entries along the entire axis where NaNs will be filled. Must be greater than 0 if not None.

downcast [dict, default is None] a dict of item->dtype of what to downcast if possible, or the string 'infer' which will try to downcast to an appropriate equal type (e.g. float64 to int64 if possible)

Returns

filled [DataFrame]

See also:

`interpolate` Fill NaN values using interpolation.

`reindex`, `asfreq`

Notes

Dask doesn't support the following argument(s).

- inplace
- downcast

Examples

```
>>> df = pd.DataFrame([[np.nan, 2, np.nan, 0],
...                    [3, 4, np.nan, 1],
...                    [np.nan, np.nan, np.nan, 5],
...                    [np.nan, 3, np.nan, 4]],
...                    columns=list('ABCD'))
>>> df
     A    B   C  D
0  NaN  2.0 NaN  0
1  3.0  4.0 NaN  1
2  NaN  NaN NaN  5
3  NaN  3.0 NaN  4
```

Replace all NaN elements with 0s.

```
>>> df.fillna(0)
    A   B   C   D
0   0.0 2.0 0.0 0
1   3.0 4.0 0.0 1
2   0.0 0.0 0.0 5
3   0.0 3.0 0.0 4
```

We can also propagate non-null values forward or backward.

```
>>> df.fillna(method='ffill')
    A   B   C   D
0   NaN 2.0 NaN 0
1   3.0 4.0 NaN 1
2   3.0 4.0 NaN 5
3   3.0 3.0 NaN 4
```

Replace all NaN elements in column 'A', 'B', 'C', and 'D', with 0, 1, 2, and 3 respectively.

```
>>> values = {'A': 0, 'B': 1, 'C': 2, 'D': 3}
>>> df.fillna(value=values)
    A   B   C   D
0   0.0 2.0 2.0 0
1   3.0 4.0 2.0 1
2   0.0 1.0 2.0 5
3   0.0 3.0 2.0 4
```

Only replace the first NaN element.

```
>>> df.fillna(value=values, limit=1)
    A   B   C   D
0   0.0 2.0 2.0 0
1   3.0 4.0 NaN 1
2   NaN 1.0 NaN 5
3   NaN 3.0 NaN 4
```

first(*offset*)

Convenience method for subsetting initial periods of time series data based on a date offset.

Parameters

offset [string, DateOffset, dateutil.relativedelta]

Returns

subset [type of caller]

Raises

TypeError If the index is not a `DatetimeIndex`

See also:

last Select final periods of time series based on a date offset

at_time Select values at a particular time of the day

between_time Select values between particular times of the day

Examples

```
>>> i = pd.date_range('2018-04-09', periods=4, freq='2D')
>>> ts = pd.DataFrame({'A': [1,2,3,4]}, index=i)
>>> ts
            A
2018-04-09  1
2018-04-11  2
2018-04-13  3
2018-04-15  4
```

Get the rows for the first 3 days:

```
>>> ts.first('3D')
            A
2018-04-09  1
2018-04-11  2
```

Notice the data for 3 first calender days were returned, not the first 3 days observed in the dataset, and therefore data for 2018-04-13 was not returned.

floordiv(*other*, *level=None*, *fill_value=None*, *axis=0*)

Integer division of series and other, element-wise (binary operator *floordiv*).

Equivalent to `series // other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.rfloordiv

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

ge(*other*, *level=None*, *axis=0*)
Greater than or equal to of series and other, element-wise (binary operator *ge*).

Equivalent to `series >= other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

`Series.None`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

get_partition(*n*)
Get a dask DataFrame/Series representing the *nth* partition.

groupby(*by=None*, ***kwargs*)
Group series using mapper (dict or key function, apply given function to group, return result as series) or by a series of columns.

Parameters

by [mapping, function, label, or list of labels] Used to determine the groups for the groupby. If `by` is a function, it's called on each value of the object's index. If a dict or Series is passed, the Series or dict VALUES will be used to determine the groups (the Series' values are first aligned; see `.align()` method). If an ndarray is passed, the values are used as-is determine the groups. A label or list of labels may be passed to group by the columns in `self`. Notice that a tuple is interpreted a (single) key.

axis [int, default 0]

level [int, level name, or sequence of such, default None] If the axis is a MultiIndex (hierarchical), group by a particular level or levels

as_index [boolean, default True] For aggregated output, return object with group labels as the index. Only relevant for DataFrame input. as_index=False is effectively "SQL-style" grouped output

sort [boolean, default True] Sort group keys. Get better performance by turning this off. Note this does not influence the order of observations within each group. groupby preserves the order of rows within each group.

group_keys [boolean, default True] When calling apply, add group keys to index to identify pieces

squeeze [boolean, default False] reduce the dimensionality of the return type if possible, otherwise return a consistent type

observed [boolean, default False] This only applies if any of the groupers are Categoricals If True: only show observed values for categorical groupers. If False: show all values for categorical groupers.

New in version 0.23.0.

Returns

GroupBy object

See also:

resample Convenience method for frequency conversion and resampling of time series.

Notes

See the user guide for more.

Examples

DataFrame results

```
>>> data.groupby(func, axis=0).mean()
>>> data.groupby(['col1', 'col2'])['col3'].mean()
```

DataFrame with hierarchical index

```
>>> data.groupby(['col1', 'col2']).mean()
```

gt(*other*, *level=None*, *axis=0*)
Greater than of series and other, element-wise (binary operator *gt*).

Equivalent to `series > other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

`Series.None`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

head(*n=5*, *npartitions=1*, *compute=True*)
First n rows of the dataset

Parameters

n [int, optional] The number of rows to return. Default is 5.

npartitions [int, optional] Elements are only taken from the first `npartitions`, with a default of 1. If there are fewer than `n` rows in the first `npartitions` a warning will be raised and any found rows returned. Pass -1 to use all partitions.

compute [bool, optional] Whether to compute the result, default is True.

idxmax(*axis=None*, *skipna=True*, *split_every=False*)

Return index of first occurrence of maximum over requested axis. NA/null values are excluded.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

Returns

idxmax [Series]

Raises

ValueError

- If the row/column is empty

See also:

Series.idxmax

Notes

This method is the DataFrame version of `ndarray.argmax`.

idxmin(*axis=None*, *skipna=True*, *split_every=False*)

Return index of first occurrence of minimum over requested axis. NA/null values are excluded.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

Returns

idxmin [Series]

Raises

ValueError

- If the row/column is empty

See also:

Series.idxmin

Notes

This method is the DataFrame version of `ndarray.argmin`.

index

Return dask Index instance

isin(*values*)

Check whether *values* are contained in Series.

Return a boolean Series showing whether each element in the Series matches an element in the passed sequence of *values* exactly.

Parameters

values [set or list-like] The sequence of values to test. Passing in a single string will raise a `TypeError`. Instead, turn a single string into a list of one element.

New in version 0.18.1: Support for values as a set.

Returns

isin [Series (bool dtype)]

Raises

TypeError

- If *values* is a string

See also:

pandas.DataFrame.isin equivalent method on DataFrame

Examples

```
>>> s = pd.Series(['lama', 'cow', 'lama', 'beetle', 'lama',
...                'hippo'], name='animal')
>>> s.isin(['cow', 'lama'])
0     True
1     True
2     True
3    False
4     True
5    False
Name: animal, dtype: bool
```

Passing a single string as `s.isin('lama')` will raise an error. Use a list of one element instead:

```
>>> s.isin(['lama'])
0     True
1    False
2     True
3    False
4     True
5    False
Name: animal, dtype: bool
```

isna()

Detect missing values.

Return a boolean same-sized object indicating if the values are NA. NA values, such as None or `numpy.NaN`, gets mapped to True values. Everything else gets mapped to False values. Characters such as empty strings `''` or `numpy.inf` are not considered NA values (unless you set `pandas.options.mode.use_inf_as_na = True`).

Returns

DataFrame Mask of bool values for each element in DataFrame that indicates whether an element is not an NA value.

See also:

DataFrame.isnull alias of isna

DataFrame.notna boolean inverse of isna

DataFrame.dropna omit axes labels with missing values

isna top-level isna

Examples

Show which entries in a DataFrame are NA.

```
>>> df = pd.DataFrame({'age': [5, 6, np.NaN],
...                    'born': [pd.NaT, pd.Timestamp('1939-05-27'),
...                             pd.Timestamp('1940-04-25')],
...                    'name': ['Alfred', 'Batman', ''],
...                    'toy': [None, 'Batmobile', 'Joker']})
>>> df
   age       born    name        toy
0  5.0        NaT  Alfred       None
1  6.0 1939-05-27  Batman  Batmobile
2  NaN 1940-04-25              Joker
```

```
>>> df.isna()
     age   born   name    toy
0  False   True  False   True
1  False  False  False  False
2   True  False  False  False
```

Show which entries in a Series are NA.

```
>>> ser = pd.Series([5, 6, np.NaN])
>>> ser
0    5.0
1    6.0
2    NaN
dtype: float64
```

```
>>> ser.isna()
0    False
1    False
2     True
dtype: bool
```

isnull()

Detect missing values.

Return a boolean same-sized object indicating if the values are NA. NA values, such as None or `numpy.NaN`, gets mapped to True values. Everything else gets mapped to False values. Characters such as empty strings `''` or `numpy.inf` are not considered NA values (unless you set `pandas.options.mode.use_inf_as_na = True`).

Returns

DataFrame Mask of bool values for each element in DataFrame that indicates whether an element is not an NA value.

See also:

DataFrame.isnull alias of isna

DataFrame.notna boolean inverse of isna

DataFrame.dropna omit axes labels with missing values

isna top-level isna

Examples

Show which entries in a DataFrame are NA.

```
>>> df = pd.DataFrame({'age': [5, 6, np.NaN],
...                    'born': [pd.NaT, pd.Timestamp('1939-05-27'),
...                             pd.Timestamp('1940-04-25')],
...                    'name': ['Alfred', 'Batman', ''],
...                    'toy': [None, 'Batmobile', 'Joker']})
>>> df
   age       born    name        toy
0  5.0        NaT  Alfred       None
1  6.0 1939-05-27  Batman  Batmobile
2  NaN 1940-04-25              Joker
```

```
>>> df.isna()
     age   born   name    toy
0  False   True  False   True
1  False  False  False  False
2   True  False  False  False
```

Show which entries in a Series are NA.

```
>>> ser = pd.Series([5, 6, np.NaN])
>>> ser
0    5.0
1    6.0
2    NaN
dtype: float64
```

```
>>> ser.isna()
0    False
1    False
2     True
dtype: bool
```

iteritems()
Lazily iterate over (index, value) tuples

known_divisions
Whether divisions are already known

last(*offset*)
Convenience method for subsetting final periods of time series data based on a date offset.

Parameters

offset [string, DateOffset, dateutil.relativedelta]

Returns

subset [type of caller]

Raises

TypeError If the index is not a `DatetimeIndex`

See also:

first Select initial periods of time series based on a date offset

at_time Select values at a particular time of the day

between_time Select values between particular times of the day

Examples

```
>>> i = pd.date_range('2018-04-09', periods=4, freq='2D')
>>> ts = pd.DataFrame({'A': [1,2,3,4]}, index=i)
>>> ts
            A
2018-04-09  1
2018-04-11  2
2018-04-13  3
2018-04-15  4
```

Get the rows for the last 3 days:

```
>>> ts.last('3D')
            A
2018-04-13  3
2018-04-15  4
```

Notice the data for 3 last calender days were returned, not the last 3 observed days in the dataset, and therefore data for 2018-04-11 was not returned.

le(*other*, *level=None*, *axis=0*)

Less than or equal to of series and other, element-wise (binary operator *le*).

Equivalent to `series <= other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

`Series.None`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

`loc`

Purely label-location based indexer for selection by label.

```
>>> df.loc["b"]
>>> df.loc["b":"d"]
```

`lt` (*other*, *level=None*, *axis=0*)

Less than of series and other, element-wise (binary operator *lt*).

Equivalent to `series < other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

`Series.None`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

map(*arg*, *na_action=None*, *meta='__no_default__'*)

Map values of Series using input correspondence (a dict, Series, or function).

Parameters

arg [function, dict, or Series] Mapping correspondence.

na_action [{None, 'ignore'}] If 'ignore', propagate NA values, without passing them to the mapping correspondence.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Returns

y [Series] Same index as caller.

See also:

Series.apply For applying more complex functions on a Series.

DataFrame.apply Apply a function row-/column-wise.

DataFrame.applymap Apply a function elementwise on a whole DataFrame.

Notes

When *arg* is a dictionary, values in Series that are not in the dictionary (as keys) are converted to `NaN`. However, if the dictionary is a `dict` subclass that defines `__missing__` (i.e. provides a method for default values), then this default is used rather than `NaN`:

```
>>> from collections import Counter
>>> counter = Counter()
>>> counter['bar'] += 1
>>> y.map(counter)
1    0
2    1
3    0
dtype: int64
```

Examples

Map inputs to outputs (both of type *Series*):

```
>>> x = pd.Series([1,2,3], index=['one', 'two', 'three'])
>>> x
one      1
two      2
three    3
dtype: int64
```

```
>>> y = pd.Series(['foo', 'bar', 'baz'], index=[1,2,3])
>>> y
1    foo
2    bar
3    baz
```

```
>>> x.map(y)
one   foo
two   bar
three baz
```

If *arg* is a dictionary, return a new Series with values converted according to the dictionary's mapping:

```
>>> z = {1: 'A', 2: 'B', 3: 'C'}
```

```
>>> x.map(z)
one   A
two   B
three C
```

Use na_action to control whether NA values are affected by the mapping function.

```
>>> s = pd.Series([1, 2, 3, np.nan])
```

```
>>> s2 = s.map('this is a string {}'.format, na_action=None)
0    this is a string 1.0
1    this is a string 2.0
2    this is a string 3.0
```

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```
3    this is a string nan
dtype: object
```

```
>>> s3 = s.map('this is a string {}'.format, na_action='ignore')
0    this is a string 1.0
1    this is a string 2.0
2    this is a string 3.0
3                    NaN
dtype: object
```

map_overlap (*func*, *before*, *after*, **args*, ***kwargs*)

Apply a function to each partition, sharing rows with adjacent partitions.

This can be useful for implementing windowing functions such as `df.rolling(...).mean()` or `df.diff()`.

Parameters

func [function] Function applied to each partition.

before [int] The number of rows to prepend to partition `i` from the end of partition `i - 1`.

after [int] The number of rows to append to partition `i` from the beginning of partition `i + 1`.

args, kwargs : Arguments and keywords to pass to the function. The partition will be the first argument, and these will be passed *after*.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Notes

Given positive integers `before` and `after`, and a function `func`, `map_overlap` does the following:

1. Prepend `before` rows to each partition `i` from the end of partition `i - 1`. The first partition has no rows prepended.
2. Append `after` rows to each partition `i` from the beginning of partition `i + 1`. The last partition has no rows appended.
3. Apply `func` to each partition, passing in any extra `args` and `kwargs` if provided.
4. Trim `before` rows from the beginning of all but the first partition.
5. Trim `after` rows from the end of all but the last partition.

Note that the index and divisions are assumed to remain unchanged.

Examples

Given a DataFrame, Series, or Index, such as:

```
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': [1, 2, 4, 7, 11],
...                    'y': [1., 2., 3., 4., 5.]})
>>> ddf = dd.from_pandas(df, npartitions=2)
```

A rolling sum with a trailing moving window of size 2 can be computed by overlapping 2 rows before each partition, and then mapping calls to `df.rolling(2).sum()`:

```
>>> ddf.compute()
    x    y
0   1  1.0
1   2  2.0
2   4  3.0
3   7  4.0
4  11  5.0
>>> ddf.map_overlap(lambda df: df.rolling(2).sum(), 2, 0).compute()
      x    y
0   NaN  NaN
1   3.0  3.0
2   6.0  5.0
3  11.0  7.0
4  18.0  9.0
```

The pandas `diff` method computes a discrete difference shifted by a number of periods (can be positive or negative). This can be implemented by mapping calls to `df.diff` to each partition after prepending/appending that many rows, depending on sign:

```
>>> def diff(df, periods=1):
...     before, after = (periods, 0) if periods > 0 else (0, -periods)
...     return df.map_overlap(lambda df, periods=1: df.diff(periods),
...                           periods, 0, periods=periods)
>>> diff(ddf, 1).compute()
     x    y
0  NaN  NaN
1  1.0  1.0
2  2.0  1.0
3  3.0  1.0
4  4.0  1.0
```

If you have a `DatetimeIndex`, you can use a `pd.Timedelta` for time- based windows.

```
>>> ts = pd.Series(range(10), index=pd.date_range('2017', periods=10))
>>> dts = dd.from_pandas(ts, npartitions=2)
>>> dts.map_overlap(lambda df: df.rolling('2D').sum(),
...                 pd.Timedelta('2D'), 0).compute()
2017-01-01     0.0
2017-01-02     1.0
2017-01-03     3.0
2017-01-04     5.0
2017-01-05     7.0
2017-01-06     9.0
2017-01-07    11.0
2017-01-08    13.0
```

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```
2017-01-09    15.0
2017-01-10    17.0
dtype: float64
```

map_partitions (*func*, **args*, ***kwargs*)

Apply Python function on each DataFrame partition.

Note that the index and divisions are assumed to remain unchanged.

Parameters

func [function] Function applied to each partition.

args, kwargs : Arguments and keywords to pass to the function. The partition will be the first argument, and these will be passed *after*. Arguments and keywords may contain `Scalar`, `Delayed` or regular python objects.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Examples

Given a DataFrame, Series, or Index, such as:

```
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': [1, 2, 3, 4, 5],
...                    'y': [1., 2., 3., 4., 5.]})
>>> ddf = dd.from_pandas(df, npartitions=2)
```

One can use `map_partitions` to apply a function on each partition. Extra arguments and keywords can optionally be provided, and will be passed to the function after the partition.

Here we apply a function with arguments and keywords to a DataFrame, resulting in a Series:

```
>>> def myadd(df, a, b=1):
...     return df.x + df.y + a + b
>>> res = ddf.map_partitions(myadd, 1, b=2)
>>> res.dtype
dtype('float64')
```

By default, dask tries to infer the output metadata by running your provided function on some fake data. This works well in many cases, but can sometimes be expensive, or even fail. To avoid this, you can manually specify the output metadata with the `meta` keyword. This can be specified in many forms, for more information see `dask.dataframe.utils.make_meta`.

Here we specify the output is a Series with no name, and dtype `float64`:

```
>>> res = ddf.map_partitions(myadd, 1, b=2, meta=(None, 'f8'))
```

Here we map a function that takes in a DataFrame, and returns a DataFrame with a new column:

```
>>> res = ddf.map_partitions(lambda df: df.assign(z=df.x * df.y))
>>> res.dtypes
x      int64
y    float64
z    float64
dtype: object
```

As before, the output metadata can also be specified manually. This time we pass in a `dict`, as the output is a DataFrame:

```
>>> res = ddf.map_partitions(lambda df: df.assign(z=df.x * df.y),
...                          meta={'x': 'i8', 'y': 'f8', 'z': 'f8'})
```

In the case where the metadata doesn't change, you can also pass in the object itself directly:

```
>>> res = ddf.map_partitions(lambda df: df.head(), meta=df)
```

Also note that the index and divisions are assumed to remain unchanged. If the function you're mapping changes the index/divisions, you'll need to clear them afterwards:

```
>>> ddf.map_partitions(func).clear_divisions()
```

mask(*cond*, *other=nan*)

Return an object of same shape as self and whose corresponding entries are from self where *cond* is False and otherwise are from *other*.

Parameters

cond [boolean NDFrame, array-like, or callable] Where *cond* is False, keep the original value. Where True, replace with corresponding value from *other*. If *cond* is callable, it is computed on the NDFrame and should return boolean NDFrame or array. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as cond.

other [scalar, NDFrame, or callable] Entries where *cond* is True are replaced with corresponding value from *other*. If other is callable, it is computed on the NDFrame and should return scalar or NDFrame. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as other.

inplace [boolean, default False] Whether to perform the operation in place on the data

axis [alignment axis if needed, default None]

level [alignment level if needed, default None]

errors [str, {'raise', 'ignore'}, default 'raise']

- `raise` : allow exceptions to be raised
- `ignore` : suppress exceptions. On error return original object

Note that currently this parameter won't affect the results and will always coerce to a suitable dtype.

try_cast [boolean, default False] try to cast the result back to the input type (if possible),

raise_on_error [boolean, default True] Whether to raise on invalid data types (e.g. trying to where on strings)

Deprecated since version 0.21.0.

Returns

wh [same type as caller]

See also:

DataFrame.where()

Notes

The mask method is an application of the if-then idiom. For each element in the calling DataFrame, if `cond` is `False` the element is used; otherwise the corresponding element from the DataFrame `other` is used.

The signature for *DataFrame.where()* differs from `numpy.where()`. Roughly `df1.where(m, df2)` is equivalent to `np.where(m, df1, df2)`.

For further details and examples see the `mask` documentation in indexing.

Examples

```
>>> s = pd.Series(range(5))
>>> s.where(s > 0)
0    NaN
1    1.0
2    2.0
3    3.0
4    4.0
```

```
>>> s.mask(s > 0)
0    0.0
1    NaN
2    NaN
3    NaN
4    NaN
```

```
>>> s.where(s > 1, 10)
0    10.0
1    10.0
2    2.0
3    3.0
4    4.0
```

```
>>> df = pd.DataFrame(np.arange(10).reshape(-1, 2), columns=['A', 'B'])
>>> m = df % 3 == 0
>>> df.where(m, -df)
   A  B
0  0 -1
1 -2  3
2 -4 -5
3  6 -7
4 -8  9
>>> df.where(m, -df) == np.where(m, df, -df)
```

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```
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
>>> df.where(m, -df) == df.mask(~m, -df)
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
```

max(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)

This method returns the maximum of the values in the object. If you want the *index* of the maximum, use `idxmax`. This is the equivalent of the `numpy.ndarray` method `argmax`.

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values when computing the result.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

max [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

mean(*axis=None*, *skipna=True*, *split_every=False*, *dtype=None*, *out=None*)

Return the mean of the values for the requested axis

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values when computing the result.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

mean [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

memory_usage(*index=True*, *deep=False*)

Return the memory usage of the Series.

The memory usage can optionally include the contribution of the index and of elements of *object* dtype.

Parameters

index [bool, default True] Specifies whether to include the memory usage of the Series index.

deep [bool, default False] If True, introspect the data deeply by interrogating *object* dtypes for system-level memory consumption, and include it in the returned value.

Returns

int Bytes of memory consumed.

See also:

numpy.ndarray.nbytes Total bytes consumed by the elements of the array.

DataFrame.memory_usage Bytes consumed by a DataFrame.

Examples

```
>>> s = pd.Series(range(3))
>>> s.memory_usage()
104
```

Not including the index gives the size of the rest of the data, which is necessarily smaller:

```
>>> s.memory_usage(index=False)
24
```

The memory footprint of *object* values is ignored by default:

```
>>> s = pd.Series(["a", "b"])
>>> s.values
array(['a', 'b'], dtype=object)
>>> s.memory_usage()
96
>>> s.memory_usage(deep=True)
212
```

min(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)

This method returns the minimum of the values in the object. If you want the *index* of the minimum, use `idxmin`. This is the equivalent of the `numpy.ndarray` method `argmin`.

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values when computing the result.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

min [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

mod(*other*, *level=None*, *fill_value=None*, *axis=0*)

Modulo of series and other, element-wise (binary operator *mod*).

Equivalent to `series % other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.rmod

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
```

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```
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

mul (*other*, *level=None*, *fill_value=None*, *axis=0*)

Multiplication of series and other, element-wise (binary operator *mul*).

Equivalent to `series * other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.rmul

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
```

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```
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

nbytes
Number of bytes

ndim
Return dimensionality

ne (*other*, *level=None*, *axis=0*)
Not equal to of series and other, element-wise (binary operator *ne*).

Equivalent to `series != other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

`Series.None`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
```

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```
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

nlargest(*n=5*, *split_every=None*)

Return the largest *n* elements.

Parameters

n [int] Return this many descending sorted values

keep [{'first', 'last'}, default 'first'] Where there are duplicate values: - `first` : take the first occurrence. - `last` : take the last occurrence.

Returns

top_n [Series] The n largest values in the Series, in sorted order

See also:

Series.nsmallest

Notes

Faster than `.sort_values(ascending=False).head(n)` for small *n* relative to the size of the `Series` object.

Examples

```
>>> import pandas as pd
>>> import numpy as np
>>> s = pd.Series(np.random.randn(10**6))
>>> s.nlargest(10)  # only sorts up to the N requested
219921    4.644710
82124     4.608745
421689    4.564644
425277    4.447014
718691    4.414137
43154     4.403520
283187    4.313922
595519    4.273635
503969    4.250236
121637    4.240952
dtype: float64
```

notnull()

Detect existing (non-missing) values.

Return a boolean same-sized object indicating if the values are not NA. Non-missing values get mapped to True. Characters such as empty strings `''` or `numpy.inf` are not considered NA values (unless you set `pandas.options.mode.use_inf_as_na = True`). NA values, such as None or `numpy.NaN`, get mapped to False values.

Returns

DataFrame Mask of bool values for each element in DataFrame that indicates whether an element is not an NA value.

See also:

DataFrame.notnull alias of notna

DataFrame.isna boolean inverse of notna

DataFrame.dropna omit axes labels with missing values

notna top-level notna

Examples

Show which entries in a DataFrame are not NA.

```
>>> df = pd.DataFrame({'age': [5, 6, np.NaN],
...                    'born': [pd.NaT, pd.Timestamp('1939-05-27'),
...                             pd.Timestamp('1940-04-25')],
...                    'name': ['Alfred', 'Batman', ''],
...                    'toy': [None, 'Batmobile', 'Joker']})
>>> df
   age       born    name        toy
0  5.0        NaT  Alfred       None
1  6.0 1939-05-27  Batman  Batmobile
2  NaN 1940-04-25              Joker
```

```
>>> df.notna()
     age   born  name    toy
0   True  False  True  False
1   True   True  True   True
2  False   True  True   True
```

Show which entries in a Series are not NA.

```
>>> ser = pd.Series([5, 6, np.NaN])
>>> ser
0    5.0
1    6.0
2    NaN
dtype: float64
```

```
>>> ser.notna()
0     True
1     True
2    False
dtype: bool
```

npartitions
Return number of partitions

nsmallest(*n=5*, *split_every=None*)
Return the smallest *n* elements.

Parameters

n [int] Return this many ascending sorted values

keep [{'first', 'last'}, default 'first'] Where there are duplicate values: - `first` : take the first occurrence. - `last` : take the last occurrence.

Returns

bottom_n [Series] The n smallest values in the Series, in sorted order

See also:

Series.nlargest

Notes

Faster than `.sort_values().head(n)` for small *n* relative to the size of the `Series` object.

Examples

```
>>> import pandas as pd
>>> import numpy as np
>>> s = pd.Series(np.random.randn(10**6))
>>> s.nsmallest(10)  # only sorts up to the N requested
288532   -4.954580
732345   -4.835960
64803    -4.812550
446457   -4.609998
501225   -4.483945
669476   -4.472935
973615   -4.401699
621279   -4.355126
773916   -4.347355
359919   -4.331927
dtype: float64
```

nunique(*split_every=None*)

Return number of unique elements in the object.

Excludes NA values by default.

Parameters

dropna [boolean, default True] Don't include NaN in the count.

Returns

nunique [int]

Notes

Dask doesn't support the following argument(s).

- dropna

nunique_approx(*split_every=None*)

Approximate number of unique rows.

This method uses the HyperLogLog algorithm for cardinality estimation to compute the approximate number of unique rows. The approximate error is 0.406%.

Parameters

split_every [int, optional] Group partitions into groups of this size while performing a tree-reduction. If set to False, no tree-reduction will be used. Default is 8.

Returns

a float representing the approximate number of elements

persist(***kwargs*)

Persist this dask collection into memory

This turns a lazy Dask collection into a Dask collection with the same metadata, but now with the results fully computed or actively computing in the background.

The action of function differs significantly depending on the active task scheduler. If the task scheduler supports asynchronous computing, such as is the case of the dask.distributed scheduler, then persist will return *immediately* and the return value's task graph will contain Dask Future objects. However if the task scheduler only supports blocking computation then the call to persist will *block* and the return value's task graph will contain concrete Python results.

This function is particularly useful when using distributed systems, because the results will be kept in distributed memory, rather than returned to the local process as with compute.

Parameters

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

optimize_graph [bool, optional] If True [default], the graph is optimized before computation. Otherwise the graph is run as is. This can be useful for debugging.

****kwargs** Extra keywords to forward to the scheduler function.

Returns

New dask collections backed by in-memory data

See also:

`dask.base.persist`

pipe(*func*, **args*, ***kwargs*)

Apply func(self, *args, **kwargs)

Parameters

func [function] function to apply to the NDFrame. `args`, and `kwargs` are passed into `func`. Alternatively a `(callable, data_keyword)` tuple where `data_keyword` is a string indicating the keyword of `callable` that expects the NDFrame.

args [iterable, optional] positional arguments passed into `func`.

kwargs [mapping, optional] a dictionary of keyword arguments passed into `func`.

Returns

object [the return type of `func`.]

See also:

`pandas.DataFrame.apply`, `pandas.DataFrame.applymap`, `pandas.Series.map`

Notes

Use `.pipe` when chaining together functions that expect Series, DataFrames or GroupBy objects. Instead of writing

```
>>> f(g(h(df), arg1=a), arg2=b, arg3=c)
```

You can write

```
>>> (df.pipe(h)
...     .pipe(g, arg1=a)
...     .pipe(f, arg2=b, arg3=c)
... )
```

If you have a function that takes the data as (say) the second argument, pass a tuple indicating which keyword expects the data. For example, suppose `f` takes its data as `arg2`:

```
>>> (df.pipe(h)
...     .pipe(g, arg1=a)
...     .pipe((f, 'arg2'), arg1=a, arg3=c)
...  )
```

pow(*other*, *level=None*, *fill_value=None*, *axis=0*)

Exponential power of series and other, element-wise (binary operator *pow*).

Equivalent to `series ** other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.rpow

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
```

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```
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

prod(*axis=None*, *skipna=True*, *split_every=False*, *dtype=None*, *out=None*)
Return the product of the values for the requested axis

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values when computing the result.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

min_count [int, default 0] The required number of valid values to perform the operation. If fewer than `min_count` non-NA values are present the result will be NA.

New in version 0.22.0: Added with the default being 0. This means the sum of an all-NA or empty Series is 0, and the product of an all-NA or empty Series is 1.

Returns

prod [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only
- min_count

Examples

By default, the product of an empty or all-NA Series is `1`

```
>>> pd.Series([]).prod()
1.0
```

This can be controlled with the `min_count` parameter

```
>>> pd.Series([]).prod(min_count=1)
nan
```

Thanks to the `skipna` parameter, `min_count` handles all-NA and empty series identically.

```
>>> pd.Series([np.nan]).prod()
1.0
```

```
>>> pd.Series([np.nan]).prod(min_count=1)
nan
```

quantile(*q=0.5*)

Approximate quantiles of Series

q [list/array of floats, default 0.5 (50%)] Iterable of numbers ranging from 0 to 1 for the desired quantiles

radd(*other*, *level=None*, *fill_value=None*, *axis=0*)

Addition of series and other, element-wise (binary operator *radd*).

Equivalent to `other + series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.add

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
```

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```
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

random_split (*frac*, *random_state=None*)

Pseudorandomly split dataframe into different pieces row-wise

Parameters

frac [list] List of floats that should sum to one.

random_state: int or np.random.RandomState If int create a new RandomState with this as the seed

Otherwise draw from the passed RandomState

See also:

`dask.DataFrame.sample`

Examples

50/50 split

```
>>> a, b = df.random_split([0.5, 0.5])
```

80/10/10 split, consistent random_state

```
>>> a, b, c = df.random_split([0.8, 0.1, 0.1], random_state=123)
```

rdiv (*other*, *level=None*, *fill_value=None*, *axis=0*)

Floating division of series and other, element-wise (binary operator *rtruediv*).

Equivalent to `other / series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.truediv

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

reduction(*chunk*, *aggregate=None*, *combine=None*, *meta='__no_default__'*, *token=None*, *split_every=None*, *chunk_kwargs=None*, *aggregate_kwargs=None*, *combine_kwargs=None*, ***kwargs*)

Generic row-wise reductions.

Parameters

chunk [callable] Function to operate on each partition. Should return a `pandas.DataFrame`, `pandas.Series`, or a scalar.

aggregate [callable, optional] Function to operate on the concatenated result of `chunk`. If not specified, defaults to `chunk`. Used to do the final aggregation in a tree reduction.

The input to `aggregate` depends on the output of `chunk`. If the output of `chunk` is a:

- scalar: Input is a Series, with one row per partition.
- Series: Input is a DataFrame, with one row per partition. Columns are the rows in the output series.
- DataFrame: Input is a DataFrame, with one row per partition. Columns are the columns in the output dataframes.

Should return a `pandas.DataFrame`, `pandas.Series`, or a scalar.

combine [callable, optional] Function to operate on intermediate concatenated results of `chunk` in a tree-reduction. If not provided, defaults to `aggregate`. The input/output requirements should match that of `aggregate` described above.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided.

Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

token [str, optional] The name to use for the output keys.

split_every [int, optional] Group partitions into groups of this size while performing a tree-reduction. If set to False, no tree-reduction will be used, and all intermediates will be concatenated and passed to `aggregate`. Default is 8.

chunk_kwargs [dict, optional] Keyword arguments to pass on to `chunk` only.

aggregate_kwargs [dict, optional] Keyword arguments to pass on to `aggregate` only.

combine_kwargs [dict, optional] Keyword arguments to pass on to `combine` only.

kwargs : All remaining keywords will be passed to `chunk`, `combine`, and `aggregate`.

Examples

```
>>> import pandas as pd
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': range(50), 'y': range(50, 100)})
>>> ddf = dd.from_pandas(df, npartitions=4)
```

Count the number of rows in a DataFrame. To do this, count the number of rows in each partition, then sum the results:

```
>>> res = ddf.reduction(lambda x: x.count(),
...                     aggregate=lambda x: x.sum())
>>> res.compute()
x    50
y    50
dtype: int64
```

Count the number of rows in a Series with elements greater than or equal to a value (provided via a keyword).

```
>>> def count_greater(x, value=0):
...     return (x >= value).sum()
>>> res = ddf.x.reduction(count_greater, aggregate=lambda x: x.sum(),
...                       chunk_kwargs={'value': 25})
>>> res.compute()
25
```

Aggregate both the sum and count of a Series at the same time:

```
>>> def sum_and_count(x):
...     return pd.Series({'sum': x.sum(), 'count': x.count()})
>>> res = ddf.x.reduction(sum_and_count, aggregate=lambda x: x.sum())
>>> res.compute()
count      50
sum      1225
dtype: int64
```

Doing the same, but for a DataFrame. Here `chunk` returns a DataFrame, meaning the input to `aggregate` is a DataFrame with an index with non-unique entries for both 'x' and 'y'. We groupby the index, and sum each group to get the final result.

```
>>> def sum_and_count(x):
...     return pd.DataFrame({'sum': x.sum(), 'count': x.count()})
>>> res = ddf.reduction(sum_and_count,
...                     aggregate=lambda x: x.groupby(level=0).sum())
>>> res.compute()
   count   sum
x     50  1225
y     50  3725
```

rename(*index=None*, *inplace=False*, *sorted_index=False*)

Alter Series index labels or name

Function / dict values must be unique (1-to-1). Labels not contained in a dict / Series will be left as-is. Extra labels listed don't throw an error.

Alternatively, change `Series.name` with a scalar value.

Parameters

index [scalar, hashable sequence, dict-like or callable, optional] If dict-like or callable, the transformation is applied to the index. Scalar or hashable sequence-like will alter the `Series.name` attribute.

inplace [boolean, default False] Whether to return a new Series or modify this one inplace.

sorted_index [bool, default False] If true, the output `Series` will have known divisions inferred from the input series and the transformation. Ignored for non-callable/dict-like `index` or when the input series has unknown divisions. Note that this may only be set to `True` if you know that the transformed index is monotonicly increasing. Dask will check that transformed divisions are monotonic, but cannot check all the values between divisions, so incorrectly setting this can result in bugs.

Returns

renamed [Series]

See also:

`pandas.Series.rename`

repartition(*divisions=None*, *npartitions=None*, *freq=None*, *force=False*)

Repartition dataframe along new divisions

Parameters

divisions [list, optional] List of partitions to be used. If specified npartitions will be ignored.

npartitions [int, optional] Number of partitions of output. Only used if divisions isn't specified.

freq [str, pd.Timedelta] A period on which to partition timeseries data like `'7D'` or `'12h'` or `pd.Timedelta(hours=12)`. Assumes a datetime index.

force [bool, default False] Allows the expansion of the existing divisions. If False then the new divisions lower and upper bounds must be the same as the old divisions.

Examples

```
>>> df = df.repartition(npartitions=10)
>>> df = df.repartition(divisions=[0, 5, 10, 20])
>>> df = df.repartition(freq='7d')
```

resample(*rule*, *closed=None*, *label=None*)

Convenience method for frequency conversion and resampling of time series. Object must have a datetime-like index (DatetimeIndex, PeriodIndex, or TimedeltaIndex), or pass datetime-like values to the on or level keyword.

Parameters

rule [string] the offset string or object representing target conversion

axis [int, optional, default 0]

closed [{'right', 'left'}] Which side of bin interval is closed. The default is 'left' for all frequency offsets except for 'M', 'A', 'Q', 'BM', 'BA', 'BQ', and 'W' which all have a default of 'right'.

label [{'right', 'left'}] Which bin edge label to label bucket with. The default is 'left' for all frequency offsets except for 'M', 'A', 'Q', 'BM', 'BA', 'BQ', and 'W' which all have a default of 'right'.

convention [{'start', 'end', 's', 'e'}] For PeriodIndex only, controls whether to use the start or end of *rule*

kind: {'timestamp', 'period'}, optional Pass 'timestamp' to convert the resulting index to a `DateTimeIndex` or 'period' to convert it to a `PeriodIndex`. By default the input representation is retained.

loffset [timedelta] Adjust the resampled time labels

base [int, default 0] For frequencies that evenly subdivide 1 day, the "origin" of the aggregated intervals. For example, for '5min' frequency, base could range from 0 through 4. Defaults to 0

on [string, optional] For a DataFrame, column to use instead of index for resampling. Column must be datetime-like.

New in version 0.19.0.

level [string or int, optional] For a MultiIndex, level (name or number) to use for resampling. Level must be datetime-like.

New in version 0.19.0.

Returns

Resampler object

See also:

groupby Group by mapping, function, label, or list of labels.

Notes

See the user guide for more.

To learn more about the offset strings, please see this link.

Examples

Start by creating a series with 9 one minute timestamps.

```
>>> index = pd.date_range('1/1/2000', periods=9, freq='T')
>>> series = pd.Series(range(9), index=index)
>>> series
2000-01-01 00:00:00    0
2000-01-01 00:01:00    1
2000-01-01 00:02:00    2
2000-01-01 00:03:00    3
2000-01-01 00:04:00    4
2000-01-01 00:05:00    5
2000-01-01 00:06:00    6
2000-01-01 00:07:00    7
2000-01-01 00:08:00    8
Freq: T, dtype: int64
```

Downsample the series into 3 minute bins and sum the values of the timestamps falling into a bin.

```
>>> series.resample('3T').sum()
2000-01-01 00:00:00     3
2000-01-01 00:03:00    12
2000-01-01 00:06:00    21
Freq: 3T, dtype: int64
```

Downsample the series into 3 minute bins as above, but label each bin using the right edge instead of the left. Please note that the value in the bucket used as the label is not included in the bucket, which it labels. For example, in the original series the bucket `2000-01-01 00:03:00` contains the value 3, but the summed value in the resampled bucket with the label `2000-01-01 00:03:00` does not include 3 (if it did, the summed value would be 6, not 3). To include this value close the right side of the bin interval as illustrated in the example below this one.

```
>>> series.resample('3T', label='right').sum()
2000-01-01 00:03:00     3
2000-01-01 00:06:00    12
2000-01-01 00:09:00    21
Freq: 3T, dtype: int64
```

Downsample the series into 3 minute bins as above, but close the right side of the bin interval.

```
>>> series.resample('3T', label='right', closed='right').sum()
2000-01-01 00:00:00     0
2000-01-01 00:03:00     6
2000-01-01 00:06:00    15
2000-01-01 00:09:00    15
Freq: 3T, dtype: int64
```

Upsample the series into 30 second bins.

```
>>> series.resample('30S').asfreq()[0:5] #select first 5 rows
2000-01-01 00:00:00   0.0
2000-01-01 00:00:30   NaN
2000-01-01 00:01:00   1.0
2000-01-01 00:01:30   NaN
2000-01-01 00:02:00   2.0
Freq: 30S, dtype: float64
```

Upsample the series into 30 second bins and fill the `NaN` values using the `pad` method.

```
>>> series.resample('30S').pad()[0:5]
2000-01-01 00:00:00    0
2000-01-01 00:00:30    0
2000-01-01 00:01:00    1
2000-01-01 00:01:30    1
2000-01-01 00:02:00    2
Freq: 30S, dtype: int64
```

Upsample the series into 30 second bins and fill the `NaN` values using the `bfill` method.

```
>>> series.resample('30S').bfill()[0:5]
2000-01-01 00:00:00    0
2000-01-01 00:00:30    1
2000-01-01 00:01:00    1
2000-01-01 00:01:30    2
2000-01-01 00:02:00    2
Freq: 30S, dtype: int64
```

Pass a custom function via `apply`

```
>>> def custom_resampler(array_like):
...     return np.sum(array_like)+5
```

```
>>> series.resample('3T').apply(custom_resampler)
2000-01-01 00:00:00     8
2000-01-01 00:03:00    17
2000-01-01 00:06:00    26
Freq: 3T, dtype: int64
```

For a Series with a PeriodIndex, the keyword *convention* can be used to control whether to use the start or end of *rule*.

```
>>> s = pd.Series([1, 2], index=pd.period_range('2012-01-01',
                                                freq='A',
                                                periods=2))
>>> s
2012    1
2013    2
Freq: A-DEC, dtype: int64
```

Resample by month using 'start' *convention*. Values are assigned to the first month of the period.

```
>>> s.resample('M', convention='start').asfreq().head()
2012-01    1.0
2012-02    NaN
2012-03    NaN
2012-04    NaN
2012-05    NaN
Freq: M, dtype: float64
```

Resample by month using 'end' *convention*. Values are assigned to the last month of the period.

```
>>> s.resample('M', convention='end').asfreq()
2012-12    1.0
2013-01    NaN
```

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```
2013-02    NaN
2013-03    NaN
2013-04    NaN
2013-05    NaN
2013-06    NaN
2013-07    NaN
2013-08    NaN
2013-09    NaN
2013-10    NaN
2013-11    NaN
2013-12    2.0
Freq: M, dtype: float64
```

For DataFrame objects, the keyword `on` can be used to specify the column instead of the index for resampling.

```
>>> df = pd.DataFrame(data=9*[range(4)], columns=['a', 'b', 'c', 'd'])
>>> df['time'] = pd.date_range('1/1/2000', periods=9, freq='T')
>>> df.resample('3T', on='time').sum()
                     a  b  c  d
time
2000-01-01 00:00:00  0  3  6  9
2000-01-01 00:03:00  0  3  6  9
2000-01-01 00:06:00  0  3  6  9
```

For a DataFrame with MultiIndex, the keyword `level` can be used to specify on level the resampling needs to take place.

```
>>> time = pd.date_range('1/1/2000', periods=5, freq='T')
>>> df2 = pd.DataFrame(data=10*[range(4)],
                       columns=['a', 'b', 'c', 'd'],
                       index=pd.MultiIndex.from_product([time, [1, 2]])
                       )
>>> df2.resample('3T', level=0).sum()
                     a  b   c   d
2000-01-01 00:00:00  0  6  12  18
2000-01-01 00:03:00  0  4   8  12
```

reset_index(*drop=False*)

Reset the index to the default index.

Note that unlike in `pandas`, the reset `dask.dataframe` index will not be monotonically increasing from 0. Instead, it will restart at 0 for each partition (e.g. `index1 = [0, ..., 10], index2 = [0, ...]`). This is due to the inability to statically know the full length of the index.

For DataFrame with multi-level index, returns a new DataFrame with labeling information in the columns under the index names, defaulting to 'level_0', 'level_1', etc. if any are None. For a standard index, the index name will be used (if set), otherwise a default 'index' or 'level_0' (if 'index' is already taken) will be used.

Parameters

drop [boolean, default False] Do not try to insert index into dataframe columns.

rfloordiv(*other*, *level=None*, *fill_value=None*, *axis=0*)

Integer division of series and other, element-wise (binary operator *rfloordiv*).

Equivalent to `other // series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.floordiv

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

rmod(*other*, *level=None*, *fill_value=None*, *axis=0*)

Modulo of series and other, element-wise (binary operator *rmod*).

Equivalent to `other % series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.mod

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

rmul(*other*, *level=None*, *fill_value=None*, *axis=0*)

Multiplication of series and other, element-wise (binary operator *rmul*).

Equivalent to `other * series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.mul

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

rolling(*window*, *min_periods=None*, *freq=None*, *center=False*, *win_type=None*, *axis=0*)
Provides rolling transformations.

Parameters

window [int, str, offset] Size of the moving window. This is the number of observations used for calculating the statistic. The window size must not be so large as to span more than one adjacent partition. If using an offset or offset alias like '5D', the data must have a `DatetimeIndex`

Changed in version 0.15.0: Now accepts offsets and string offset aliases

min_periods [int, default None] Minimum number of observations in window required to have a value (otherwise result is NA).

center [boolean, default False] Set the labels at the center of the window.

win_type [string, default None] Provide a window type. The recognized window types are identical to pandas.

axis [int, default 0]

Returns

a Rolling object on which to call a method to compute a statistic

Notes

The *freq* argument is not supported.

round(*decimals=0*)
Round each value in a Series to the given number of decimals.

Parameters

decimals [int] Number of decimal places to round to (default: 0). If decimals is negative, it specifies the number of positions to the left of the decimal point.

Returns

Series object

See also:

`numpy.around`, *`DataFrame.round`*

rpow (*other*, *level=None*, *fill_value=None*, *axis=0*)
Exponential power of series and other, element-wise (binary operator *rpow*).

Equivalent to `other ** series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

`Series.pow`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

rsub(*other*, *level=None*, *fill_value=None*, *axis=0*)
Subtraction of series and other, element-wise (binary operator *rsub*).

Equivalent to `other - series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.sub

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

rtruediv(*other*, *level=None*, *fill_value=None*, *axis=0*)
Floating division of series and other, element-wise (binary operator *rtruediv*).

Equivalent to `other / series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.truediv

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

sample(*n=None*, *frac=None*, *replace=False*, *random_state=None*)
Random sample of items

Parameters

n [int, optional] Number of items to return is not supported by dask. Use frac instead.

frac [float, optional] Fraction of axis items to return.

replace [boolean, optional] Sample with or without replacement. Default = False.

random_state [int or `np.random.RandomState`] If int we create a new RandomState with this as the seed Otherwise we draw from the passed RandomState

See also:

DataFrame.random_split, `pandas.DataFrame.sample`

sem(*axis=None*, *skipna=None*, *ddof=1*, *split_every=False*)
Return unbiased standard error of the mean over requested axis.

Normalized by N-1 by default. This can be changed using the ddof argument

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

ddof [int, default 1] Delta Degrees of Freedom. The divisor used in calculations is N - ddof, where N represents the number of elements.

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

sem [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

shape

Return a tuple representing the dimensionality of a Series.

The single element of the tuple is a Delayed result.

Examples

```
>>> series.shape
# (dd.Scalar<size-ag..., dtype=int64>,)
```

shift (*periods=1*, *freq=None*, *axis=0*)

Shift index by desired number of periods with an optional time freq

Parameters

periods [int] Number of periods to move, can be positive or negative

freq [DateOffset, timedelta, or time rule string, optional] Increment to use from the tseries module or time rule (e.g. 'EOM'). See Notes.

axis [{0 or 'index', 1 or 'columns'}]

Returns

shifted [DataFrame]

Notes

If freq is specified then the index values are shifted but the data is not realigned. That is, use freq if you would like to extend the index when shifting and preserve the original data.

size
Size of the Series or DataFrame as a Delayed object.

Examples

```
>>> series.size
dd.Scalar<size-ag..., dtype=int64>
```

squeeze()
Squeeze length 1 dimensions.

Parameters

axis [None, integer or string axis name, optional] The axis to squeeze if 1-sized.

New in version 0.20.0.

Returns

scalar if 1-sized, else original object

Notes

Dask doesn't support the following argument(s).

- axis

std(*axis=None*, *skipna=True*, *ddof=1*, *split_every=False*, *dtype=None*, *out=None*)
Return sample standard deviation over requested axis.

Normalized by N-1 by default. This can be changed using the ddof argument

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

ddof [int, default 1] Delta Degrees of Freedom. The divisor used in calculations is N - ddof, where N represents the number of elements.

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

std [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

str

Namespace for string methods

sub(*other*, *level=None*, *fill_value=None*, *axis=0*)

Subtraction of series and other, element-wise (binary operator *sub*).

Equivalent to `series - other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.rsub

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

sum(*axis=None*, *skipna=True*, *split_every=False*, *dtype=None*, *out=None*)
Return the sum of the values for the requested axis

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values when computing the result.

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

min_count [int, default 0] The required number of valid values to perform the operation. If fewer than `min_count` non-NA values are present the result will be NA.

New in version 0.22.0: Added with the default being 0. This means the sum of an all-NA or empty Series is 0, and the product of an all-NA or empty Series is 1.

Returns

sum [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only
- min_count

Examples

By default, the sum of an empty or all-NA Series is `0`.

```
>>> pd.Series([]).sum()  # min_count=0 is the default
0.0
```

This can be controlled with the `min_count` parameter. For example, if you'd like the sum of an empty series to be NaN, pass `min_count=1`.

```
>>> pd.Series([]).sum(min_count=1)
nan
```

Thanks to the `skipna` parameter, `min_count` handles all-NA and empty series identically.

```
>>> pd.Series([np.nan]).sum()
0.0
```

```
>>> pd.Series([np.nan]).sum(min_count=1)
nan
```

tail (*n=5*, *compute=True*)
Last n rows of the dataset

Caveat, the only checks the last n rows of the last partition.

to_bag (*index=False*)
Craeate a Dask Bag from a Series

to_csv (*filename*, ***kwargs*)
Store Dask DataFrame to CSV files

One filename per partition will be created. You can specify the filenames in a variety of ways.

Use a globstring:

```
>>> df.to_csv('/path/to/data/export-*.csv')
```

The * will be replaced by the increasing sequence 0, 1, 2, ...

```
/path/to/data/export-0.csv
/path/to/data/export-1.csv
```

Use a globstring and a `name_function=` keyword argument. The name_function function should expect an integer and produce a string. Strings produced by name_function must preserve the order of their respective partition indices.

```
>>> from datetime import date, timedelta
>>> def name(i):
...     return str(date(2015, 1, 1) + i * timedelta(days=1))
```

```
>>> name(0)
'2015-01-01'
>>> name(15)
'2015-01-16'
```

```
>>> df.to_csv('/path/to/data/export-*.csv', name_function=name)
```

```
/path/to/data/export-2015-01-01.csv
/path/to/data/export-2015-01-02.csv
...
```

You can also provide an explicit list of paths:

```
>>> paths = ['/path/to/data/alice.csv', '/path/to/data/bob.csv', ...]
>>> df.to_csv(paths)
```

Parameters

filename [string] Path glob indicating the naming scheme for the output files

name_function [callable, default None] Function accepting an integer (partition index) and producing a string to replace the asterisk in the given filename globstring. Should preserve the lexicographic order of partitions

compression [string or None] String like 'gzip' or 'xz'. Must support efficient random access. Filenames with extensions corresponding to known compression algorithms (gz, bz2) will be compressed accordingly automatically

sep [character, default ','] Field delimiter for the output file

na_rep [string, default ‘’] Missing data representation

float_format [string, default None] Format string for floating point numbers

columns [sequence, optional] Columns to write

header [boolean or list of string, default True] Write out column names. If a list of string is given it is assumed to be aliases for the column names

index [boolean, default True] Write row names (index)

index_label [string or sequence, or False, default None] Column label for index column(s) if desired. If None is given, and *header* and *index* are True, then the index names are used. A sequence should be given if the DataFrame uses MultiIndex. If False do not print fields for index names. Use index_label=False for easier importing in R

nanRep [None] deprecated, use na_rep

mode [str] Python write mode, default ‘w’

encoding [string, optional] A string representing the encoding to use in the output file, defaults to ‘ascii’ on Python 2 and ‘utf-8’ on Python 3.

compression [string, optional] a string representing the compression to use in the output file, allowed values are ‘gzip’, ‘bz2’, ‘xz’, only used when the first argument is a filename

line_terminator [string, default ‘\n’] The newline character or character sequence to use in the output file

quoting [optional constant from csv module] defaults to csv.QUOTE_MINIMAL

quotechar [string (length 1), default ‘”’] character used to quote fields

doublequote [boolean, default True] Control quoting of *quotechar* inside a field

escapechar [string (length 1), default None] character used to escape *sep* and *quotechar* when appropriate

chunksize [int or None] rows to write at a time

tupleize_cols [boolean, default False] write multi_index columns as a list of tuples (if True) or new (expanded format) if False)

date_format [string, default None] Format string for datetime objects

decimal: string, default ‘.’ Character recognized as decimal separator. E.g. use ‘,’ for European data

storage_options: dict Parameters passed on to the backend filesystem class.

Returns

The names of the file written if they were computed right away

If not, the delayed tasks associated to the writing of the files

to_dask_array(*lengths=None*)

Convert a dask DataFrame to a dask array.

Parameters

lengths [bool or Sequence of ints, optional] How to determine the chunks sizes for the output array. By default, the output array will have unknown chunk lengths along the first axis, which can cause some later operations to fail.

- True : immediately compute the length of each partition
- Sequence : a sequence of integers to use for the chunk sizes on the first axis. These values are *not* validated for correctness, beyond ensuring that the number of items matches the number of partitions.

to_delayed(*optimize_graph=True*)
Convert into a list of `dask.delayed` objects, one per partition.

Parameters

optimize_graph [bool, optional] If True [default], the graph is optimized before converting into `dask.delayed` objects.

See also:

dask.dataframe.from_delayed

Examples

```
>>> partitions = df.to_delayed()
```

to_frame(*name=None*)
Convert Series to DataFrame

Parameters

name [object, default None] The passed name should substitute for the series name (if it has one).

Returns

data_frame [DataFrame]

to_hdf(*path_or_buf*, *key*, *mode='a'*, *append=False*, ***kwargs*)
Store Dask Dataframe to Hierarchical Data Format (HDF) files

This is a parallel version of the Pandas function of the same name. Please see the Pandas docstring for more detailed information about shared keyword arguments.

This function differs from the Pandas version by saving the many partitions of a Dask DataFrame in parallel, either to many files, or to many datasets within the same file. You may specify this parallelism with an asterix `*` within the filename or datapath, and an optional `name_function`. The asterix will be replaced with an increasing sequence of integers starting from `0` or with the result of calling `name_function` on each of those integers.

This function only supports the Pandas `'table'` format, not the more specialized `'fixed'` format.

Parameters

path [string] Path to a target filename. May contain a `*` to denote many filenames

key [string] Datapath within the files. May contain a `*` to denote many locations

name_function [function] A function to convert the `*` in the above options to a string. Should take in a number from 0 to the number of partitions and return a string. (see examples below)

compute [bool] Whether or not to execute immediately. If False then this returns a `dask.Delayed` value.

lock [Lock, optional] Lock to use to prevent concurrency issues. By default a `threading.Lock`, `multiprocessing.Lock` or `SerializableLock` will be used depending on your scheduler if a lock is required. See dask.utils.get_scheduler_lock for more information about lock selection.

****other:** See pandas.to_hdf for more information

Returns

filenames [list] Returned if `compute` is True. List of file names that each partition is saved to.

delayed [dask.Delayed] Returned if `compute` is False. Delayed object to execute `to_hdf` when computed.

See also:

read_hdf, *to_parquet*

Examples

Save Data to a single file

```
>>> df.to_hdf('output.hdf', '/data')
```

Save data to multiple datapaths within the same file:

```
>>> df.to_hdf('output.hdf', '/data-*')
```

Save data to multiple files:

```
>>> df.to_hdf('output-*.hdf', '/data')
```

Save data to multiple files, using the multiprocessing scheduler:

```
>>> df.to_hdf('output-*.hdf', '/data', scheduler='processes')
```

Specify custom naming scheme. This writes files as '2000-01-01.hdf', '2000-01-02.hdf', '2000-01-03.hdf', etc..

```
>>> from datetime import date, timedelta
>>> base = date(year=2000, month=1, day=1)
>>> def name_function(i):
...     ''' Convert integer 0 to n to a string '''
...     return base + timedelta(days=i)
```

```
>>> df.to_hdf('*.hdf', '/data', name_function=name_function)
```

to_json (*filename*, **args*, ***kwargs*)
See dd.to_json docstring for more information

to_parquet (*path*, **args*, ***kwargs*)
Store Dask.dataframe to Parquet files

Parameters

df [dask.dataframe.DataFrame]

path [string] Destination directory for data. Prepend with protocol like `s3://` or `hdfs://` for remote data.

engine [{'auto', 'fastparquet', 'pyarrow'}, default 'auto'] Parquet library to use. If only one library is installed, it will use that one; if both, it will use 'fastparquet'.

compression [string or dict, optional] Either a string like `"snappy"` or a dictionary mapping column names to compressors like `{"name": "gzip", "values": "snappy"}`. The default is `"default"`, which uses the default compression for whichever engine is selected.

write_index [boolean, optional] Whether or not to write the index. Defaults to True *if* divisions are known.

append [bool, optional] If False (default), construct data-set from scratch. If True, add new row-group(s) to an existing data-set. In the latter case, the data-set must exist, and the schema must match the input data.

ignore_divisions [bool, optional] If False (default) raises error when previous divisions overlap with the new appended divisions. Ignored if append=False.

partition_on [list, optional] Construct directory-based partitioning by splitting on these fields' values. Each dask partition will result in one or more datafiles, there will be no global groupby.

storage_options [dict, optional] Key/value pairs to be passed on to the file-system backend, if any.

compute [bool, optional] If True (default) then the result is computed immediately. If False then a `dask.delayed` object is returned for future computation.

****kwargs** Extra options to be passed on to the specific backend.

See also:

read_parquet Read parquet data to dask.dataframe

Notes

Each partition will be written to a separate file.

Examples

```
>>> df = dd.read_csv(...)
>>> to_parquet('/path/to/output/', df, compression='snappy')
```

to_string(*max_rows=5*)

Render a string representation of the Series

Parameters

buf [StringIO-like, optional] buffer to write to

na_rep [string, optional] string representation of NAN to use, default 'NaN'

float_format [one-parameter function, optional] formatter function to apply to columns' elements if they are floats default None

header: boolean, default True Add the Series header (index name)

index [bool, optional] Add index (row) labels, default True

length [boolean, default False] Add the Series length

dtype [boolean, default False] Add the Series dtype

name [boolean, default False] Add the Series name if not None

max_rows [int, optional] Maximum number of rows to show before truncating. If None, show all.

Returns

formatted [string (if not buffer passed)]

Notes

Dask doesn't support the following argument(s).

- buf
- na_rep
- float_format
- header
- index
- length
- dtype
- name

to_timestamp (*freq=None*, *how='start'*, *axis=0*)

Cast to DatetimeIndex of timestamps, at *beginning* of period

Parameters

freq [string, default frequency of PeriodIndex] Desired frequency

how [{'s', 'e', 'start', 'end'}] Convention for converting period to timestamp; start of period vs. end

axis [{0 or 'index', 1 or 'columns'}, default 0] The axis to convert (the index by default)

copy [boolean, default True] If false then underlying input data is not copied

Returns

df [DataFrame with DatetimeIndex]

Notes

Dask doesn't support the following argument(s).

- copy

truediv (*other*, *level=None*, *fill_value=None*, *axis=0*)

Floating division of series and other, element-wise (binary operator *truediv*).

Equivalent to `series / other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.rtruediv

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])
>>> a
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])
>>> b
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

unique (*split_every=None*, *split_out=1*)

Return Series of unique values in the object. Includes NA values.

Returns

uniques [Series]

value_counts (*split_every=None*, *split_out=1*)

Returns object containing counts of unique values.

The resulting object will be in descending order so that the first element is the most frequently-occurring element. Excludes NA values by default.

Parameters

normalize [boolean, default False] If True then the object returned will contain the relative frequencies of the unique values.

sort [boolean, default True] Sort by values

ascending [boolean, default False] Sort in ascending order

bins [integer, optional] Rather than count values, group them into half-open bins, a convenience for pd.cut, only works with numeric data

dropna [boolean, default True] Don't include counts of NaN.

Returns

counts [Series]

Notes

Dask doesn't support the following argument(s).

- normalize
- sort
- ascending
- bins
- dropna

values

Return a dask.array of the values of this dataframe

Warning: This creates a dask.array without precise shape information. Operations that depend on shape information, like slicing or reshaping, will not work.

var(*axis=None*, *skipna=True*, *ddof=1*, *split_every=False*, *dtype=None*, *out=None*)

Return unbiased variance over requested axis.

Normalized by N-1 by default. This can be changed using the ddof argument

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA

level [int or level name, default None] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

ddof [int, default 1] Delta Degrees of Freedom. The divisor used in calculations is N - ddof, where N represents the number of elements.

numeric_only [boolean, default None] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

var [Series or DataFrame (if level specified)]

Notes

Dask doesn't support the following argument(s).

- level
- numeric_only

visualize(*filename='mydask'*, *format=None*, *optimize_graph=False*, ***kwargs*)
Render the computation of this object's task graph using graphviz.

Requires `graphviz` to be installed.

Parameters

filename [str or None, optional] The name (without an extension) of the file to write to disk. If *filename* is None, no file will be written, and we communicate with dot using only pipes.

format [{'png', 'pdf', 'dot', 'svg', 'jpeg', 'jpg'}, optional] Format in which to write output file. Default is 'png'.

optimize_graph [bool, optional] If True, the graph is optimized before rendering. Otherwise, the graph is displayed as is. Default is False.

color: {None, 'order'}, optional Options to color nodes. Provide `cmap=` keyword for additional colormap

****kwargs** Additional keyword arguments to forward to `to_graphviz`.

Returns

result [IPython.diplay.Image, IPython.display.SVG, or None] See dask.dot.dot_graph for more information.

See also:

`dask.base.visualize`, `dask.dot.dot_graph`

Notes

For more information on optimization see here:

https://docs.dask.org/en/latest/optimize.html

Examples

```
>>> x.visualize(filename='dask.pdf')
>>> x.visualize(filename='dask.pdf', color='order')
```

where(*cond*, *other=nan*)
Return an object of same shape as self and whose corresponding entries are from self where *cond* is True and otherwise are from *other*.

Parameters

cond [boolean NDFrame, array-like, or callable] Where *cond* is True, keep the original value. Where False, replace with corresponding value from *other*. If *cond* is callable, it is computed on the NDFrame and should return boolean NDFrame or array. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as cond.

other [scalar, NDFrame, or callable] Entries where *cond* is False are replaced with corresponding value from *other*. If other is callable, it is computed on the NDFrame and should return scalar or NDFrame. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as other.

inplace [boolean, default False] Whether to perform the operation in place on the data

axis [alignment axis if needed, default None]

level [alignment level if needed, default None]

errors [str, {'raise', 'ignore'}, default 'raise']

- `raise` : allow exceptions to be raised
- `ignore` : suppress exceptions. On error return original object

Note that currently this parameter won't affect the results and will always coerce to a suitable dtype.

try_cast [boolean, default False] try to cast the result back to the input type (if possible),

raise_on_error [boolean, default True] Whether to raise on invalid data types (e.g. trying to where on strings)

Deprecated since version 0.21.0.

Returns

wh [same type as caller]

See also:

DataFrame.mask()

Notes

The where method is an application of the if-then idiom. For each element in the calling DataFrame, if `cond` is `True` the element is used; otherwise the corresponding element from the DataFrame `other` is used.

The signature for *DataFrame.where()* differs from `numpy.where()`. Roughly `df1.where(m, df2)` is equivalent to `np.where(m, df1, df2)`.

For further details and examples see the `where` documentation in indexing.

Examples

```
>>> s = pd.Series(range(5))
>>> s.where(s > 0)
0    NaN
1    1.0
2    2.0
3    3.0
4    4.0
```

```
>>> s.mask(s > 0)
0    0.0
1    NaN
2    NaN
3    NaN
4    NaN
```

```
>>> s.where(s > 1, 10)
0    10.0
1    10.0
2    2.0
3    3.0
4    4.0
```

```
>>> df = pd.DataFrame(np.arange(10).reshape(-1, 2), columns=['A', 'B'])
>>> m = df % 3 == 0
>>> df.where(m, -df)
   A  B
0  0 -1
1 -2  3
2 -4 -5
3  6 -7
4 -8  9
>>> df.where(m, -df) == np.where(m, df, -df)
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
>>> df.where(m, -df) == df.mask(~m, -df)
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
```

DataFrameGroupBy

class dask.dataframe.groupby.**DataFrameGroupBy**(*df*, *by=None*, *slice=None*)

agg(*arg*, *split_every=None*, *split_out=1*)

Aggregate using one or more operations over the specified axis.

Parameters

func [function, string, dictionary, or list of string/functions] Function to use for aggregating the data. If a function, must either work when passed a DataFrame or when passed to DataFrame.apply. For a DataFrame, can pass a dict, if the keys are DataFrame column names.

Accepted combinations are:

- string function name.
- function.
- list of functions.
- dict of column names -> functions (or list of functions).

***args** Positional arguments to pass to *func*.

****kwargs** Keyword arguments to pass to *func*.

Returns

aggregated [DataFrame]

See also:

`pandas.DataFrame.groupby.apply`, `pandas.DataFrame.groupby.transform`, `pandas.DataFrame.aggregate`

Notes

agg is an alias for *aggregate*. Use the alias.

A passed user-defined-function will be passed a Series for evaluation.

Examples

```
>>> df = pd.DataFrame({'A': [1, 1, 2, 2],
...                    'B': [1, 2, 3, 4],
...                    'C': np.random.randn(4)})
```

```
>>> df
   A  B         C
0  1  1  0.362838
1  1  2  0.227877
2  2  3  1.267767
3  2  4 -0.562860
```

The aggregation is for each column.

```
>>> df.groupby('A').agg('min')
   B         C
A
1  1  0.227877
2  3 -0.562860
```

Multiple aggregations

```
>>> df.groupby('A').agg(['min', 'max'])
    B             C
  min max       min       max
A
1   1   2  0.227877  0.362838
2   3   4 -0.562860  1.267767
```

Select a column for aggregation

```
>>> df.groupby('A').B.agg(['min', 'max'])
   min  max
A
1    1    2
2    3    4
```

Different aggregations per column

```
>>> df.groupby('A').agg({'B': ['min', 'max'], 'C': 'sum'})
    B             C
  min max       sum
A
1   1   2  0.590716
2   3   4  0.704907
```

aggregate(*arg*, *split_every=None*, *split_out=1*)

Aggregate using one or more operations over the specified axis.

Parameters

func [function, string, dictionary, or list of string/functions] Function to use for aggregating the data. If a function, must either work when passed a DataFrame or when passed to DataFrame.apply. For a DataFrame, can pass a dict, if the keys are DataFrame column names.

Accepted combinations are:

- string function name.
- function.
- list of functions.
- dict of column names -> functions (or list of functions).

***args** Positional arguments to pass to *func*.

****kwargs** Keyword arguments to pass to *func*.

Returns

aggregated [DataFrame]

See also:

`pandas.DataFrame.groupby.apply`, `pandas.DataFrame.groupby.transform`, `pandas.DataFrame.aggregate`

Notes

agg is an alias for *aggregate*. Use the alias.

A passed user-defined-function will be passed a Series for evaluation.

Examples

```
>>> df = pd.DataFrame({'A': [1, 1, 2, 2],
...                    'B': [1, 2, 3, 4],
...                    'C': np.random.randn(4)})
```

```
>>> df
   A  B         C
0  1  1  0.362838
1  1  2  0.227877
2  2  3  1.267767
3  2  4 -0.562860
```

The aggregation is for each column.

```
>>> df.groupby('A').agg('min')
   B         C
A
1  1  0.227877
2  3 -0.562860
```

Multiple aggregations

```
>>> df.groupby('A').agg(['min', 'max'])
    B             C
  min max       min       max
A
1   1   2  0.227877  0.362838
2   3   4 -0.562860  1.267767
```

Select a column for aggregation

```
>>> df.groupby('A').B.agg(['min', 'max'])
   min  max
A
1    1    2
2    3    4
```

Different aggregations per column

```
>>> df.groupby('A').agg({'B': ['min', 'max'], 'C': 'sum'})
    B             C
  min max       sum
A
1   1   2  0.590716
2   3   4  0.704907
```

apply (*func*, **args*, ***kwargs*)

Parallel version of pandas GroupBy.apply

This mimics the pandas version except for the following:

1. The user should provide output metadata.
2. If the grouper does not align with the index then this causes a full shuffle. The order of rows within each group may not be preserved.

Parameters

func: function Function to apply

args, kwargs [Scalar, Delayed or object] Arguments and keywords to pass to the function.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Returns

applied [Series or DataFrame depending on columns keyword]

count(*split_every=None*, *split_out=1*)

Compute count of group, excluding missing values

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

cumcount(*axis=None*)

Number each item in each group from 0 to the length of that group - 1.

Essentially this is equivalent to

```
>>> self.apply(lambda x: Series(np.arange(len(x)), x.index))
```

Parameters

ascending [bool, default True] If False, number in reverse, from length of group - 1 to 0.

See also:

ngroup Number the groups themselves.

Notes

Dask doesn't support the following argument(s).

- ascending

Examples

```
>>> df = pd.DataFrame([['a'], ['a'], ['a'], ['b'], ['b'], ['a']],
...                   columns=['A'])
>>> df
   A
0  a
1  a
2  a
3  b
4  b
5  a
>>> df.groupby('A').cumcount()
0    0
1    1
2    2
3    0
4    1
5    3
dtype: int64
>>> df.groupby('A').cumcount(ascending=False)
0    3
1    2
2    1
```

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```
3    1
4    0
5    0
dtype: int64
```

cumprod(*axis=0*)
Cumulative product for each group

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

cumsum(*axis=0*)
Cumulative sum for each group

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

first(*split_every=None*, *split_out=1*)
Compute first of group values

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

get_group(*key*)
Constructs NDFrame from group with provided name

Parameters

name [object] the name of the group to get as a DataFrame

obj [NDFrame, default None] the NDFrame to take the DataFrame out of. If it is None, the object groupby was called on will be used

Returns

group [type of obj]

Notes

Dask doesn't support the following argument(s).

- name
- obj

last(*split_every=None*, *split_out=1*)
Compute last of group values

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

max(*split_every=None*, *split_out=1*)
Compute max of group values

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

mean(*split_every=None*, *split_out=1*)
Compute mean of groups, excluding missing values

For multiple groupings, the result index will be a MultiIndex

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

min(*split_every=None*, *split_out=1*)
Compute min of group values

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

size(*split_every=None*, *split_out=1*)
Compute group sizes

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

std(*ddof=1*, *split_every=None*, *split_out=1*)
Compute standard deviation of groups, excluding missing values

For multiple groupings, the result index will be a MultiIndex

Parameters

ddof [integer, default 1] degrees of freedom

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

sum(*split_every=None*, *split_out=1*)
Compute sum of group values

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

var(*ddof=1*, *split_every=None*, *split_out=1*)
Compute variance of groups, excluding missing values

For multiple groupings, the result index will be a MultiIndex

Parameters

ddof [integer, default 1] degrees of freedom

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

SeriesGroupBy

class dask.dataframe.groupby.**SeriesGroupBy**(*df*, *by=None*, *slice=None*)

agg(*arg*, *split_every=None*, *split_out=1*)
Aggregate using one or more operations over the specified axis.

Parameters

func [function, string, dictionary, or list of string/functions] Function to use for aggregating the data. If a function, must either work when passed a Series or when passed to Series.apply. For a DataFrame, can pass a dict, if the keys are DataFrame column names.

Accepted combinations are:

- string function name.
- function.
- list of functions.
- dict of column names -> functions (or list of functions).

***args** Positional arguments to pass to *func*.

****kwargs** Keyword arguments to pass to *func*.

Returns

aggregated [Series]

See also:

`pandas.Series.groupby.apply`, `pandas.Series.groupby.transform`, `pandas.Series.aggregate`

Notes

agg is an alias for *aggregate*. Use the alias.

A passed user-defined-function will be passed a Series for evaluation.

Examples

```
>>> s = Series([1, 2, 3, 4])
```

```
>>> s
0    1
1    2
2    3
3    4
dtype: int64
```

```
>>> s.groupby([1, 1, 2, 2]).min()
1    1
2    3
dtype: int64
```

```
>>> s.groupby([1, 1, 2, 2]).agg('min')
1    1
2    3
dtype: int64
```

```
>>> s.groupby([1, 1, 2, 2]).agg(['min', 'max'])
   min  max
1    1    2
2    3    4
```

aggregate(*arg*, *split_every=None*, *split_out=1*)

Aggregate using one or more operations over the specified axis.

Parameters

func [function, string, dictionary, or list of string/functions] Function to use for aggregating the data. If a function, must either work when passed a Series or when passed to Series.apply. For a DataFrame, can pass a dict, if the keys are DataFrame column names.

Accepted combinations are:

- string function name.
- function.
- list of functions.
- dict of column names -> functions (or list of functions).

***args** Positional arguments to pass to *func*.

****kwargs** Keyword arguments to pass to *func*.

Returns

aggregated [Series]

See also:

`pandas.Series.groupby.apply`, `pandas.Series.groupby.transform`, `pandas.Series.aggregate`

Notes

agg is an alias for *aggregate*. Use the alias.

A passed user-defined-function will be passed a Series for evaluation.

Examples

```
>>> s = Series([1, 2, 3, 4])
```

```
>>> s
0    1
1    2
2    3
3    4
dtype: int64
```

```
>>> s.groupby([1, 1, 2, 2]).min()
1    1
2    3
dtype: int64
```

```
>>> s.groupby([1, 1, 2, 2]).agg('min')
1    1
2    3
dtype: int64
```

```
>>> s.groupby([1, 1, 2, 2]).agg(['min', 'max'])
   min  max
1    1    2
2    3    4
```

apply (*func*, **args*, ***kwargs*)

Parallel version of pandas GroupBy.apply

This mimics the pandas version except for the following:

1. The user should provide output metadata.
2. If the grouper does not align with the index then this causes a full shuffle. The order of rows within each group may not be preserved.

Parameters

func: function Function to apply

args, kwargs [Scalar, Delayed or object] Arguments and keywords to pass to the function.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Returns

applied [Series or DataFrame depending on columns keyword]

count (*split_every=None*, *split_out=1*)

Compute count of group, excluding missing values

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

cumcount (*axis=None*)

Number each item in each group from 0 to the length of that group - 1.

Essentially this is equivalent to

```
>>> self.apply(lambda x: Series(np.arange(len(x)), x.index))
```

Parameters

ascending [bool, default True] If False, number in reverse, from length of group - 1 to 0.

See also:

ngroup Number the groups themselves.

Notes

Dask doesn't support the following argument(s).

- ascending

Examples

```
>>> df = pd.DataFrame([['a'], ['a'], ['a'], ['b'], ['b'], ['a']],
...                   columns=['A'])
>>> df
   A
0  a
1  a
2  a
3  b
4  b
5  a
>>> df.groupby('A').cumcount()
0    0
1    1
2    2
3    0
4    1
5    3
dtype: int64
>>> df.groupby('A').cumcount(ascending=False)
0    3
1    2
2    1
3    1
4    0
5    0
dtype: int64
```

cumprod (*axis=0*)
Cumulative product for each group

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

cumsum (*axis=0*)
Cumulative sum for each group

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

first(*split_every=None*, *split_out=1*)
Compute first of group values

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

get_group(*key*)
Constructs NDFrame from group with provided name

Parameters

name [object] the name of the group to get as a DataFrame

obj [NDFrame, default None] the NDFrame to take the DataFrame out of. If it is None, the object groupby was called on will be used

Returns

group [type of obj]

Notes

Dask doesn't support the following argument(s).

- name
- obj

last(*split_every=None*, *split_out=1*)
Compute last of group values

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

max(*split_every=None*, *split_out=1*)
Compute max of group values

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

mean(*split_every=None*, *split_out=1*)
Compute mean of groups, excluding missing values

For multiple groupings, the result index will be a MultiIndex

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

min(*split_every=None*, *split_out=1*)
Compute min of group values

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

size(*split_every=None*, *split_out=1*)
Compute group sizes

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

std(*ddof=1*, *split_every=None*, *split_out=1*)
Compute standard deviation of groups, excluding missing values

For multiple groupings, the result index will be a MultiIndex

Parameters

ddof [integer, default 1] degrees of freedom

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

sum(*split_every=None*, *split_out=1*)
Compute sum of group values

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

var(*ddof=1*, *split_every=None*, *split_out=1*)
Compute variance of groups, excluding missing values

For multiple groupings, the result index will be a MultiIndex

Parameters

ddof [integer, default 1] degrees of freedom

See also:

pandas.Series.groupby, pandas.DataFrame.groupby, pandas.Panel.groupby

Storage and Conversion

dask.dataframe.**read_csv**(*urlpath*, *blocksize=64000000*, *collection=True*, *lineterminator=None*, *compression=None*, *sample=256000*, *enforce=False*, *assume_missing=False*, *storage_options=None*, *include_path_column=False*, ***kwargs*)
Read CSV files into a Dask.DataFrame

This parallelizes the pandas.read_csv() function in the following ways:

- It supports loading many files at once using globstrings:

```
>>> df = dd.read_csv('myfiles.*.csv')
```

- In some cases it can break up large files:

```
>>> df = dd.read_csv('largefile.csv', blocksize=25e6)  # 25MB chunks
```

- It can read CSV files from external resources (e.g. S3, HDFS) by providing a URL:

```
>>> df = dd.read_csv('s3://bucket/myfiles.*.csv')
>>> df = dd.read_csv('hdfs:///myfiles.*.csv')
>>> df = dd.read_csv('hdfs://namenode.example.com/myfiles.*.csv')
```

Internally dd.read_csv uses pandas.read_csv() and supports many of the same keyword arguments with the same performance guarantees. See the docstring for pandas.read_csv() for more information on available keyword arguments.

Parameters

urlpath [string or list] Absolute or relative filepath(s). Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol.

blocksize [int or None, optional] Number of bytes by which to cut up larger files. Default value is computed based on available physical memory and the number of cores. If `None`, use a single block for each file.

collection [boolean, optional] Return a dask.dataframe if True or list of dask.delayed objects if False

sample [int, optional] Number of bytes to use when determining dtypes

assume_missing [bool, optional] If True, all integer columns that aren't specified in `dtype` are assumed to contain missing values, and are converted to floats. Default is False.

storage_options [dict, optional] Extra options that make sense for a particular storage connection, e.g. host, port, username, password, etc.

include_path_column [bool or str, optional] Whether or not to include the path to each particular file. If True a new column is added to the dataframe called `path`. If str, sets new column name. Default is False.

****kwargs** Extra keyword arguments to forward to `pandas.read_csv()`.

Notes

Dask dataframe tries to infer the `dtype` of each column by reading a sample from the start of the file (or of the first file if it's a glob). Usually this works fine, but if the `dtype` is different later in the file (or in other files) this can cause issues. For example, if all the rows in the sample had integer dtypes, but later on there was a `NaN`, then this would error at compute time. To fix this, you have a few options:

- Provide explicit dtypes for the offending columns using the `dtype` keyword. This is the recommended solution.
- Use the `assume_missing` keyword to assume that all columns inferred as integers contain missing values, and convert them to floats.
- Increase the size of the sample using the `sample` keyword.

It should also be noted that this function may fail if a CSV file includes quoted strings that contain the line terminator. To get around this you can specify `blocksize=None` to not split files into multiple partitions, at the cost of reduced parallelism.

`dask.dataframe.`**`read_table`**(*urlpath*, *blocksize=64000000*, *collection=True*, *lineterminator=None*, *compression=None*, *sample=256000*, *enforce=False*, *assume_missing=False*, *storage_options=None*, *include_path_column=False*, ***kwargs*)

Read delimited files into a Dask.DataFrame

This parallelizes the `pandas.read_table()` function in the following ways:

- It supports loading many files at once using globstrings:

```
>>> df = dd.read_table('myfiles.*.csv')
```

- In some cases it can break up large files:

```
>>> df = dd.read_table('largefile.csv', blocksize=25e6)  # 25MB chunks
```

- It can read CSV files from external resources (e.g. S3, HDFS) by providing a URL:

```
>>> df = dd.read_table('s3://bucket/myfiles.*.csv')
>>> df = dd.read_table('hdfs:///myfiles.*.csv')
>>> df = dd.read_table('hdfs://namenode.example.com/myfiles.*.csv')
```

Internally `dd.read_table` uses `pandas.read_table()` and supports many of the same keyword arguments with the same performance guarantees. See the docstring for `pandas.read_table()` for more information on available keyword arguments.

Parameters

urlpath [string or list] Absolute or relative filepath(s). Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol.

blocksize [int or None, optional] Number of bytes by which to cut up larger files. Default value is computed based on available physical memory and the number of cores. If `None`, use a single block for each file.

collection [boolean, optional] Return a dask.dataframe if True or list of dask.delayed objects if False

sample [int, optional] Number of bytes to use when determining dtypes

assume_missing [bool, optional] If True, all integer columns that aren't specified in `dtype` are assumed to contain missing values, and are converted to floats. Default is False.

storage_options [dict, optional] Extra options that make sense for a particular storage connection, e.g. host, port, username, password, etc.

include_path_column [bool or str, optional] Whether or not to include the path to each particular file. If True a new column is added to the dataframe called `path`. If str, sets new column name. Default is False.

****kwargs** Extra keyword arguments to forward to `pandas.read_table()`.

Notes

Dask dataframe tries to infer the `dtype` of each column by reading a sample from the start of the file (or of the first file if it's a glob). Usually this works fine, but if the `dtype` is different later in the file (or in other files) this can cause issues. For example, if all the rows in the sample had integer dtypes, but later on there was a `NaN`, then this would error at compute time. To fix this, you have a few options:

- Provide explicit dtypes for the offending columns using the `dtype` keyword. This is the recommended solution.
- Use the `assume_missing` keyword to assume that all columns inferred as integers contain missing values, and convert them to floats.
- Increase the size of the sample using the `sample` keyword.

It should also be noted that this function may fail if a delimited file includes quoted strings that contain the line terminator. To get around this you can specify `blocksize=None` to not split files into multiple partitions, at the cost of reduced parallelism.

`dask.dataframe.`**`read_parquet`**(*path*, *columns=None*, *filters=None*, *categories=None*, *index=None*, *storage_options=None*, *engine='auto'*, *infer_divisions=None*)

Read ParquetFile into a Dask DataFrame

This reads a directory of Parquet data into a Dask.dataframe, one file per partition. It selects the index among the sorted columns if any exist.

Parameters

path [string, list or fastparquet.ParquetFile] Source directory for data, or path(s) to individual parquet files. Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol. Alternatively, also accepts a previously opened fastparquet.ParquetFile()

columns [string, list or None (default)] Field name(s) to read in as columns in the output. By default all non-index fields will be read (as determined by the pandas parquet metadata, if present). Provide a single field name instead of a list to read in the data as a Series.

filters [list] List of filters to apply, like `[('x', '>', 0), ...]`. This implements row-group (partition) -level filtering only, i.e., to prevent the loading of some chunks of the data, and only if relevant statistics have been included in the metadata.

index [string, list, False or None (default)] Field name(s) to use as the output frame index. By default will be inferred from the pandas parquet file metadata (if present). Use False to read all fields as columns.

categories [list, dict or None] For any fields listed here, if the parquet encoding is Dictionary, the column will be created with dtype category. Use only if it is guaranteed that the column is encoded as dictionary in all row-groups. If a list, assumes up to 2**16-1 labels; if a dict, specify the number of labels expected; if None, will load categories automatically for data written by dask/fastparquet, not otherwise.

storage_options [dict] Key/value pairs to be passed on to the file-system backend, if any.

engine [{'auto', 'fastparquet', 'pyarrow'}, default 'auto'] Parquet reader library to use. If only one library is installed, it will use that one; if both, it will use 'fastparquet'

infer_divisions [bool or None (default).] By default, divisions are inferred if the read *engine* supports doing so efficiently and the *index* of the underlying dataset is sorted across the individual parquet files. Set to `True` to force divisions to be inferred in all cases. Note that this may require reading metadata from each file in the dataset, which may be expensive. Set to `False` to never infer divisions.

See also:

to_parquet

Examples

```
>>> df = dd.read_parquet('s3://bucket/my-parquet-data')
```

dask.dataframe.**read_orc**(*path*, *columns=None*, *storage_options=None*)

Read dataframe from ORC file(s)

Parameters

path: str or list(str) Location of file(s), which can be a full URL with protocol specifier, and may include glob character if a single string.

columns: None or list(str) Columns to load. If None, loads all.

storage_options: None or dict Further parameters to pass to the bytes backend.

Returns

Dask.DataFrame (even if there is only one column)

Examples

```
>>> df = dd.read_orc('https://github.com/apache/orc/raw/'
...                  'master/examples/demo-11-zlib.orc')
```

dask.dataframe.**read_hdf**(*pattern*, *key*, *start=0*, *stop=None*, *columns=None*, *chunksize=1000000*, *sorted_index=False*, *lock=True*, *mode='a'*)

Read HDF files into a Dask DataFrame

Read hdf files into a dask dataframe. This function is like `pandas.read_hdf`, except it can read from a single large file, or from multiple files, or from multiple keys from the same file.

Parameters

pattern [string, list] File pattern (string), buffer to read from, or list of file paths. Can contain wildcards.

key [group identifier in the store. Can contain wildcards]

start [optional, integer (defaults to 0), row number to start at]

stop [optional, integer (defaults to None, the last row), row number to] stop at

columns [list of columns, optional] A list of columns that if not None, will limit the return columns (default is None)

chunksize [positive integer, optional] Maximal number of rows per partition (default is 1000000).

sorted_index [boolean, optional] Option to specify whether or not the input hdf files have a sorted index (default is False).

lock [boolean, optional] Option to use a lock to prevent concurrency issues (default is True).

mode [{'a', 'r', 'r+'}, default 'a'. Mode to use when opening file(s).]

'r' Read-only; no data can be modified.

'a' Append; an existing file is opened for reading and writing, and if the file does not exist it is created.

'r+' It is similar to 'a', but the file must already exist.

Returns

dask.DataFrame

Examples

Load single file

```
>>> dd.read_hdf('myfile.1.hdf5', '/x')
```

Load multiple files

```
>>> dd.read_hdf('myfile.*.hdf5', '/x')
```

```
>>> dd.read_hdf(['myfile.1.hdf5', 'myfile.2.hdf5'], '/x')
```

Load multiple datasets

```
>>> dd.read_hdf('myfile.1.hdf5', '/*')
```

dask.dataframe.**read_json**(*url_path*, *orient='records'*, *lines=None*, *storage_options=None*, *blocksize=None*, *sample=1048576*, *encoding='utf-8'*, *errors='strict'*, *compression='infer'*, ***kwargs*)

Create a dataframe from a set of JSON files

This utilises `pandas.read_json()`, and most parameters are passed through - see its docstring.

Differences: orient is 'records' by default, with lines=True; this is appropriate for line-delimited "JSON-lines" data, the kind of JSON output that is most common in big-data scenarios, and which can be chunked when reading (see `read_json()`). All other options require blocksize=None, i.e., one partition per input file.

Parameters

url_path: str, list of str Location to read from. If a string, can include a glob character to find a set of file names. Supports protocol specifications such as `"s3://"`.

encoding, errors: The text encoding to implement, e.g., "utf-8" and how to respond to errors in the conversion (see `str.encode()`).

orient, lines, kwargs passed to pandas; if not specified, lines=True when orient='records', False otherwise.

storage_options: dict Passed to backend file-system implementation

blocksize: None or int If None, files are not blocked, and you get one partition per input file. If int, which can only be used for line-delimited JSON files, each partition will be approximately this size in bytes, to the nearest newline character.

sample: int Number of bytes to pre-load, to provide an empty dataframe structure to any blocks wihout data. Only relevant is using blocksize.

encoding, errors: Text conversion, `see bytes.decode()`

compression [string or None] String like 'gzip' or 'xz'.

Returns

dask.DataFrame

Examples

Load single file

```
>>> dd.read_json('myfile.1.json')
```

Load multiple files

```
>>> dd.read_json('myfile.*.json')
```

```
>>> dd.read_json(['myfile.1.json', 'myfile.2.json'])
```

Load large line-delimited JSON files using partitions of approx 256MB size

>> dd.read_json('data/file*.csv', blocksize=2**28)

dask.dataframe.**read_sql_table**(*table*, *uri*, *index_col*, *divisions=None*, *npartitions=None*, *limits=None*, *columns=None*, *bytes_per_chunk=268435456*, *head_rows=5*, *schema=None*, *meta=None*, ***kwargs*)

Create dataframe from an SQL table.

If neither divisions or npartitions is given, the memory footprint of the first few rows will be determined, and partitions of size ~256MB will be used.

Parameters

table [string or sqlalchemy expression] Select columns from here.

uri [string] Full sqlalchemy URI for the database connection

index_col [string] Column which becomes the index, and defines the partitioning. Should be a indexed column in the SQL server, and any orderable type. If the type is number or time, then partition boundaries can be inferred from npartitions or bytes_per_chunk; otherwide must supply explicit `divisions=`. `index_col` could be a function to return a value, e.g., `sql.func.abs(sql.column('value')).label('abs(value)')`. Labeling columns created by functions or arithmetic operations is required.

divisions: sequence Values of the index column to split the table by. If given, this will override npartitions and bytes_per_chunk. The divisions are the value boundaries of the index column used to define the partitions. For example, `divisions=list('acegikmoqsuwz')` could be used to partition a string column lexographically into 12 partitions, with the implicit assumption that each partition contains similar numbers of records.

npartitions [int] Number of partitions, if divisions is not given. Will split the values of the index column linearly between limits, if given, or the column max/min. The index column must be numeric or time for this to work

limits: 2-tuple or None Manually give upper and lower range of values for use with npartitions; if None, first fetches max/min from the DB. Upper limit, if given, is inclusive.

columns [list of strings or None] Which columns to select; if None, gets all; can include sqlalchemy functions, e.g., `sql.func.abs(sql.column('value')).label('abs(value)')`. Labeling columns created by functions or arithmetic operations is recommended.

bytes_per_chunk: int If both divisions and npartitions is None, this is the target size of each partition, in bytes

head_rows: int How many rows to load for inferring the data-types, unless passing meta

meta: empty DataFrame or None If provided, do not attempt to infer dtypes, but use these, coercing all chunks on load

schema: str or None If using a table name, pass this to sqlalchemy to select which DB schema to use within the URI connection

kwargs [dict] Additional parameters to pass to *pd.read_sql()*

Returns

dask.dataframe

Examples

```
>>> df = dd.read_sql('accounts', 'sqlite:///path/to/bank.db',
...                  npartitions=10, index_col='id')
```

`dask.dataframe.`**`from_array`**(*x*, *chunksize=50000*, *columns=None*)

Read any slicable array into a Dask Dataframe

Uses getitem syntax to pull slices out of the array. The array need not be a NumPy array but must support slicing syntax

x[50000:100000]

and have 2 dimensions:

x.ndim == 2

or have a record dtype:

x.dtype == [('name', 'O'), ('balance', 'i8')]

`dask.dataframe.`**`from_pandas`**(*data*, *npartitions=None*, *chunksize=None*, *sort=True*, *name=None*)
Construct a Dask DataFrame from a Pandas DataFrame

This splits an in-memory Pandas dataframe into several parts and constructs a dask.dataframe from those parts on which Dask.dataframe can operate in parallel.

Note that, despite parallelism, Dask.dataframe may not always be faster than Pandas. We recommend that you stay with Pandas for as long as possible before switching to Dask.dataframe.

Parameters

df [pandas.DataFrame or pandas.Series] The DataFrame/Series with which to construct a Dask DataFrame/Series

npartitions [int, optional] The number of partitions of the index to create. Note that depending on the size and index of the dataframe, the output may have fewer partitions than requested.

chunksize [int, optional] The number of rows per index partition to use.

sort: bool Sort input first to obtain cleanly divided partitions or don't sort and don't get cleanly divided partitions

name: string, optional An optional keyname for the dataframe. Defaults to hashing the input

Returns

dask.DataFrame or dask.Series A dask DataFrame/Series partitioned along the index

Raises

TypeError If something other than a `pandas.DataFrame` or `pandas.Series` is passed in.

See also:

`from_array` Construct a dask.DataFrame from an array that has record dtype

`read_csv` Construct a dask.DataFrame from a CSV file

Examples

```
>>> df = pd.DataFrame(dict(a=list('aabbcc'), b=list(range(6))),
...                   index=pd.date_range(start='20100101', periods=6))
>>> ddf = from_pandas(df, npartitions=3)
>>> ddf.divisions
(Timestamp('2010-01-01 00:00:00', freq='D'),
 Timestamp('2010-01-03 00:00:00', freq='D'),
 Timestamp('2010-01-05 00:00:00', freq='D'),
```

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```
 Timestamp('2010-01-06 00:00:00', freq='D'))
>>> ddf = from_pandas(df.a, npartitions=3)  # Works with Series too!
>>> ddf.divisions
(Timestamp('2010-01-01 00:00:00', freq='D'),
 Timestamp('2010-01-03 00:00:00', freq='D'),
 Timestamp('2010-01-05 00:00:00', freq='D'),
 Timestamp('2010-01-06 00:00:00', freq='D'))
```

dask.dataframe.**from_bcolz**(*x*, *chunksize=None*, *categorize=True*, *index=None*, *lock=<unlocked _thread.lock object>*, ***kwargs*)

Read BColz CTable into a Dask Dataframe

BColz is a fast on-disk compressed column store with careful attention given to compression. https://bcolz.readthedocs.io/en/latest/

Parameters

x [bcolz.ctable]

chunksize [int, optional] The size(rows) of blocks to pull out from ctable.

categorize [bool, defaults to True] Automatically categorize all string dtypes

index [string, optional] Column to make the index

lock: bool or Lock Lock to use when reading or False for no lock (not-thread-safe)

See also:

from_array more generic function not optimized for bcolz

dask.dataframe.**from_dask_array**(*x*, *columns=None*, *index=None*)

Create a Dask DataFrame from a Dask Array.

Converts a 2d array into a DataFrame and a 1d array into a Series.

Parameters

x [da.Array]

columns [list or string] list of column names if DataFrame, single string if Series

index [dask.dataframe.Index, optional] An optional *dask* Index to use for the output Series or DataFrame.

The default output index depends on whether *x* has any unknown chunks. If there are any unknown chunks, the output has `None` for all the divisions (one per chunk). If all the chunks are known, a default index with known divsions is created.

Specifying *index* can be useful if you're conforming a Dask Array to an existing dask Series or DataFrame, and you would like the indices to match.

See also:

dask.bag.to_dataframe from dask.bag

dask.dataframe._Frame.values Reverse conversion

dask.dataframe._Frame.to_records Reverse conversion

Examples

```
>>> import dask.array as da
>>> import dask.dataframe as dd
>>> x = da.ones((4, 2), chunks=(2, 2))
>>> df = dd.io.from_dask_array(x, columns=['a', 'b'])
>>> df.compute()
     a    b
0  1.0  1.0
1  1.0  1.0
2  1.0  1.0
3  1.0  1.0
```

dask.dataframe.**from_delayed**(*dfs*, *meta=None*, *divisions=None*, *prefix='from-delayed'*)

Create Dask DataFrame from many Dask Delayed objects

Parameters

dfs [list of Delayed] An iterable of `dask.delayed.Delayed` objects, such as come from `dask.delayed` These comprise the individual partitions of the resulting dataframe.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

divisions [tuple, str, optional] Partition boundaries along the index. For tuple, see https://docs.dask.org/en/latest/dataframe-design.html#partitions For string 'sorted' will compute the delayed values to find index values. Assumes that the indexes are mutually sorted. If None, then won't use index information

prefix [str, optional] Prefix to prepend to the keys.

dask.dataframe.**to_records**(*df*)

Create Dask Array from a Dask Dataframe

Warning: This creates a dask.array without precise shape information. Operations that depend on shape information, like slicing or reshaping, will not work.

See also:

`dask.dataframe._Frame.values`, *dask.dataframe.from_dask_array*

Examples

```
>>> df.to_records()
dask.array<shape=(nan,), dtype=(numpy.record, [('ind', '<f8'), ('x', 'O'), ('y', '
↪<i8')]), chunksize=(nan,)>
```

dask.dataframe.**to_csv**(*df*, *filename*, *name_function=None*, *compression=None*, *compute=True*, *get=None*, *scheduler=None*, *storage_options=None*, ***kwargs*)

Store Dask DataFrame to CSV files

One filename per partition will be created. You can specify the filenames in a variety of ways.

Use a globstring:

```
>>> df.to_csv('/path/to/data/export-*.csv')
```

The * will be replaced by the increasing sequence 0, 1, 2, ...

```
/path/to/data/export-0.csv
/path/to/data/export-1.csv
```

Use a globstring and a `name_function=` keyword argument. The name_function function should expect an integer and produce a string. Strings produced by name_function must preserve the order of their respective partition indices.

```
>>> from datetime import date, timedelta
>>> def name(i):
...     return str(date(2015, 1, 1) + i * timedelta(days=1))
```

```
>>> name(0)
'2015-01-01'
>>> name(15)
'2015-01-16'
```

```
>>> df.to_csv('/path/to/data/export-*.csv', name_function=name)
```

```
/path/to/data/export-2015-01-01.csv
/path/to/data/export-2015-01-02.csv
...
```

You can also provide an explicit list of paths:

```
>>> paths = ['/path/to/data/alice.csv', '/path/to/data/bob.csv', ...]
>>> df.to_csv(paths)
```

Parameters

filename [string] Path glob indicating the naming scheme for the output files

name_function [callable, default None] Function accepting an integer (partition index) and producing a string to replace the asterisk in the given filename globstring. Should preserve the lexicographic order of partitions

compression [string or None] String like 'gzip' or 'xz'. Must support efficient random access. Filenames with extensions corresponding to known compression algorithms (gz, bz2) will be compressed accordingly automatically

sep [character, default ','] Field delimiter for the output file

na_rep [string, default ''] Missing data representation

float_format [string, default None] Format string for floating point numbers

columns [sequence, optional] Columns to write

header [boolean or list of string, default True] Write out column names. If a list of string is given it is assumed to be aliases for the column names

index [boolean, default True] Write row names (index)

index_label [string or sequence, or False, default None] Column label for index column(s) if desired. If None is given, and *header* and *index* are True, then the index names are used.

A sequence should be given if the DataFrame uses MultiIndex. If False do not print fields for index names. Use index_label=False for easier importing in R

nanRep [None] deprecated, use na_rep

mode [str] Python write mode, default 'w'

encoding [string, optional] A string representing the encoding to use in the output file, defaults to 'ascii' on Python 2 and 'utf-8' on Python 3.

compression [string, optional] a string representing the compression to use in the output file, allowed values are 'gzip', 'bz2', 'xz', only used when the first argument is a filename

line_terminator [string, default '\n'] The newline character or character sequence to use in the output file

quoting [optional constant from csv module] defaults to csv.QUOTE_MINIMAL

quotechar [string (length 1), default '"'] character used to quote fields

doublequote [boolean, default True] Control quoting of *quotechar* inside a field

escapechar [string (length 1), default None] character used to escape *sep* and *quotechar* when appropriate

chunksize [int or None] rows to write at a time

tupleize_cols [boolean, default False] write multi_index columns as a list of tuples (if True) or new (expanded format) if False)

date_format [string, default None] Format string for datetime objects

decimal: string, default '.' Character recognized as decimal separator. E.g. use ',' for European data

storage_options: dict Parameters passed on to the backend filesystem class.

Returns

The names of the file written if they were computed right away

If not, the delayed tasks associated to the writing of the files

`dask.dataframe.`**`to_bag`**(*df*, *index=False*)

Create Dask Bag from a Dask DataFrame

Parameters

index [bool, optional] If True, the elements are tuples of `(index, value)`, otherwise they're just the `value`. Default is False.

Examples

```
>>> bag = df.to_bag()
```

`dask.dataframe.`**`to_hdf`**(*df*, *path*, *key*, *mode='a'*, *append=False*, *get=None*, *scheduler=None*, *name_function=None*, *compute=True*, *lock=None*, *dask_kwargs={}*, ***kwargs*)

Store Dask Dataframe to Hierarchical Data Format (HDF) files

This is a parallel version of the Pandas function of the same name. Please see the Pandas docstring for more detailed information about shared keyword arguments.

This function differs from the Pandas version by saving the many partitions of a Dask DataFrame in parallel, either to many files, or to many datasets within the same file. You may specify this parallelism with an asterix `*` within the filename or datapath, and an optional `name_function`. The asterix will be replaced with an increasing sequence of integers starting from `0` or with the result of calling `name_function` on each of those integers.

This function only supports the Pandas `'table'` format, not the more specialized `'fixed'` format.

Parameters

path [string] Path to a target filename. May contain a `*` to denote many filenames

key [string] Datapath within the files. May contain a `*` to denote many locations

name_function [function] A function to convert the `*` in the above options to a string. Should take in a number from 0 to the number of partitions and return a string. (see examples below)

compute [bool] Whether or not to execute immediately. If False then this returns a `dask.Delayed` value.

lock [Lock, optional] Lock to use to prevent concurrency issues. By default a `threading.Lock`, `multiprocessing.Lock` or `SerializableLock` will be used depending on your scheduler if a lock is required. See dask.utils.get_scheduler_lock for more information about lock selection.

****other:** See pandas.to_hdf for more information

Returns

filenames [list] Returned if `compute` is True. List of file names that each partition is saved to.

delayed [dask.Delayed] Returned if `compute` is False. Delayed object to execute `to_hdf` when computed.

See also:

read_hdf, *to_parquet*

Examples

Save Data to a single file

```
>>> df.to_hdf('output.hdf', '/data')
```

Save data to multiple datapaths within the same file:

```
>>> df.to_hdf('output.hdf', '/data-*')
```

Save data to multiple files:

```
>>> df.to_hdf('output-*.hdf', '/data')
```

Save data to multiple files, using the multiprocessing scheduler:

```
>>> df.to_hdf('output-*.hdf', '/data', scheduler='processes')
```

Specify custom naming scheme. This writes files as ‘2000-01-01.hdf’, ‘2000-01-02.hdf’, ‘2000-01-03.hdf’, etc..

```
>>> from datetime import date, timedelta
>>> base = date(year=2000, month=1, day=1)
>>> def name_function(i):
...     ''' Convert integer 0 to n to a string '''
...     return base + timedelta(days=i)
```

```
>>> df.to_hdf('*.hdf', '/data', name_function=name_function)
```

dask.dataframe.**to_parquet**(*df*, *path*, *engine='auto'*, *compression='default'*, *write_index=None*, *append=False*, *ignore_divisions=False*, *partition_on=None*, *storage_options=None*, *compute=True*, ***kwargs*)

Store Dask.dataframe to Parquet files

Parameters

df [dask.dataframe.DataFrame]

path [string] Destination directory for data. Prepend with protocol like `s3://` or `hdfs://` for remote data.

engine [{'auto', 'fastparquet', 'pyarrow'}, default 'auto'] Parquet library to use. If only one library is installed, it will use that one; if both, it will use 'fastparquet'.

compression [string or dict, optional] Either a string like `"snappy"` or a dictionary mapping column names to compressors like `{"name": "gzip", "values": "snappy"}`. The default is `"default"`, which uses the default compression for whichever engine is selected.

write_index [boolean, optional] Whether or not to write the index. Defaults to True *if* divisions are known.

append [bool, optional] If False (default), construct data-set from scratch. If True, add new row-group(s) to an existing data-set. In the latter case, the data-set must exist, and the schema must match the input data.

ignore_divisions [bool, optional] If False (default) raises error when previous divisions overlap with the new appended divisions. Ignored if append=False.

partition_on [list, optional] Construct directory-based partitioning by splitting on these fields' values. Each dask partition will result in one or more datafiles, there will be no global groupby.

storage_options [dict, optional] Key/value pairs to be passed on to the file-system backend, if any.

compute [bool, optional] If True (default) then the result is computed immediately. If False then a `dask.delayed` object is returned for future computation.

****kwargs** Extra options to be passed on to the specific backend.

See also:

read_parquet Read parquet data to dask.dataframe

Notes

Each partition will be written to a separate file.

Examples

```
>>> df = dd.read_csv(...)
>>> to_parquet('/path/to/output/', df, compression='snappy')
```

dask.dataframe.**to_json**(*df*, *url_path*, *orient='records'*, *lines=None*, *storage_options=None*, *compute=True*, *encoding='utf-8'*, *errors='strict'*, *compression=None*, ***kwargs*)

Write dataframe into JSON text files

This utilises `pandas.DataFrame.to_json()`, and most parameters are passed through - see its docstring.

Differences: orient is 'records' by default, with lines=True; this produces the kind of JSON output that is most common in big-data applications, and which can be chunked when reading (see `read_json()`).

Parameters

df: dask.DataFrame Data to save

url_path: str, list of str Location to write to. If a string, and there are more than one partitions in df, should include a glob character to expand into a set of file names, or provide a `name_function=` parameter. Supports protocol specifications such as `"s3://"`.

encoding, errors: The text encoding to implement, e.g., "utf-8" and how to respond to errors in the conversion (see `str.encode()`).

orient, lines, kwargs passed to pandas; if not specified, lines=True when orient='records', False otherwise.

storage_options: dict Passed to backend file-system implementation

compute: bool If true, immediately executes. If False, returns a set of delayed objects, which can be computed at a later time.

encoding, errors: Text conversion, `see str.encode()`

compression [string or None] String like 'gzip' or 'xz'.

Rolling

dask.dataframe.rolling.**map_overlap**(*func*, *df*, *before*, *after*, **args*, ***kwargs*)

Apply a function to each partition, sharing rows with adjacent partitions.

Parameters

func [function] Function applied to each partition.

df [dd.DataFrame, dd.Series]

before [int or timedelta] The rows to prepend to partition `i` from the end of partition `i - 1`.

after [int or timedelta] The rows to append to partition `i` from the beginning of partition `i + 1`.

args, kwargs : Arguments and keywords to pass to the function. The partition will be the first argument, and these will be passed *after*.

See also:

`dd.DataFrame.map_overlap`

Other functions

dask.dataframe.**compute**(**args*, ***kwargs*)
Compute several dask collections at once.

Parameters

args [object] Any number of objects. If it is a dask object, it's computed and the result is returned. By default, python builtin collections are also traversed to look for dask objects (for more information see the `traverse` keyword). Non-dask arguments are passed through unchanged.

traverse [bool, optional] By default dask traverses builtin python collections looking for dask objects passed to `compute`. For large collections this can be expensive. If none of the arguments contain any dask objects, set `traverse=False` to avoid doing this traversal.

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

optimize_graph [bool, optional] If True [default], the optimizations for each collection are applied before computation. Otherwise the graph is run as is. This can be useful for debugging.

kwargs Extra keywords to forward to the scheduler function.

Examples

```
>>> import dask.array as da
>>> a = da.arange(10, chunks=2).sum()
>>> b = da.arange(10, chunks=2).mean()
>>> compute(a, b)
(45, 4.5)
```

By default, dask objects inside python collections will also be computed:

```
>>> compute({'a': a, 'b': b, 'c': 1})
({'a': 45, 'b': 4.5, 'c': 1},)
```

dask.dataframe.**map_partitions**(*func*, **args*, ***kwargs*)
Apply Python function on each DataFrame partition.

Parameters

func [function] Function applied to each partition.

args, kwargs : Arguments and keywords to pass to the function. At least one of the args should be a Dask.dataframe. Arguments and keywords may contain `Scalar`, `Delayed` or regular python objects.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

dask.dataframe.multi.**concat**(*dfs*, *axis=0*, *join='outer'*, *interleave_partitions=False*)

Concatenate DataFrames along rows.

- When axis=0 (default), concatenate DataFrames row-wise:
  - If all divisions are known and ordered, concatenate DataFrames keeping divisions. When divisions are not ordered, specifying interleave_partition=True allows concatenate divisions each by each.
  - If any of division is unknown, concatenate DataFrames resetting its division to unknown (None)
- When axis=1, concatenate DataFrames column-wise:
  - Allowed if all divisions are known.
  - If any of division is unknown, it raises ValueError.

Parameters

dfs [list] List of dask.DataFrames to be concatenated

axis [{0, 1, 'index', 'columns'}, default 0] The axis to concatenate along

join [{'inner', 'outer'}, default 'outer'] How to handle indexes on other axis

interleave_partitions [bool, default False] Whether to concatenate DataFrames ignoring its order. If True, every divisions are concatenated each by each.

Notes

This differs in from `pd.concat` in the when concatenating Categoricals with different categories. Pandas currently coerces those to objects before concatenating. Coercing to objects is very expensive for large arrays, so dask preserves the Categoricals by taking the union of the categories.

Examples

If all divisions are known and ordered, divisions are kept.

```
>>> a
dd.DataFrame<x, divisions=(1, 3, 5)>
>>> b
dd.DataFrame<y, divisions=(6, 8, 10)>
>>> dd.concat([a, b])
dd.DataFrame<concat-..., divisions=(1, 3, 6, 8, 10)>
```

Unable to concatenate if divisions are not ordered.

```
>>> a
dd.DataFrame<x, divisions=(1, 3, 5)>
>>> b
dd.DataFrame<y, divisions=(2, 3, 6)>
>>> dd.concat([a, b])
ValueError: All inputs have known divisions which cannot be concatenated
in order. Specify interleave_partitions=True to ignore order
```

Specify interleave_partitions=True to ignore the division order.

```
>>> dd.concat([a, b], interleave_partitions=True)
dd.DataFrame<concat-..., divisions=(1, 2, 3, 5, 6)>
```

If any of division is unknown, the result division will be unknown

```
>>> a
dd.DataFrame<x, divisions=(None, None)>
>>> b
dd.DataFrame<y, divisions=(1, 4, 10)>
>>> dd.concat([a, b])
dd.DataFrame<concat-..., divisions=(None, None, None, None)>
```

Different categoricals are unioned

>> dd.concat([# doctest: +SKIP ... dd.from_pandas(pd.Series(['a', 'b'], dtype='category'), 1), ... dd.from_pandas(pd.Series(['a', 'c'], dtype='category'), 1), ...], interleave_partitions=True).dtype CategoricalDtype(categories=['a', 'b', 'c'], ordered=False)

dask.dataframe.multi.**merge**(*left*, *right*, *how='inner'*, *on=None*, *left_on=None*, *right_on=None*, *left_index=False*, *right_index=False*, *sort=False*, *suffixes=('_x', '_y')*, *copy=True*, *indicator=False*, *validate=None*)

Merge DataFrame objects by performing a database-style join operation by columns or indexes.

If joining columns on columns, the DataFrame indexes *will be ignored*. Otherwise if joining indexes on indexes or indexes on a column or columns, the index will be passed on.

Parameters

left [DataFrame]

right [DataFrame]

how [{'left', 'right', 'outer', 'inner'}, default 'inner']

- left: use only keys from left frame, similar to a SQL left outer join; preserve key order
- right: use only keys from right frame, similar to a SQL right outer join; preserve key order
- outer: use union of keys from both frames, similar to a SQL full outer join; sort keys lexicographically
- inner: use intersection of keys from both frames, similar to a SQL inner join; preserve the order of the left keys

on [label or list] Column or index level names to join on. These must be found in both DataFrames. If *on* is None and not merging on indexes then this defaults to the intersection of the columns in both DataFrames.

left_on [label or list, or array-like] Column or index level names to join on in the left DataFrame. Can also be an array or list of arrays of the length of the left DataFrame. These arrays are treated as if they are columns.

right_on [label or list, or array-like] Column or index level names to join on in the right DataFrame. Can also be an array or list of arrays of the length of the right DataFrame. These arrays are treated as if they are columns.

left_index [boolean, default False] Use the index from the left DataFrame as the join key(s). If it is a MultiIndex, the number of keys in the other DataFrame (either the index or a number of columns) must match the number of levels

right_index [boolean, default False] Use the index from the right DataFrame as the join key. Same caveats as left_index

sort [boolean, default False] Sort the join keys lexicographically in the result DataFrame. If False, the order of the join keys depends on the join type (how keyword)

suffixes [2-length sequence (tuple, list, . . .)] Suffix to apply to overlapping column names in the left and right side, respectively

copy [boolean, default True] If False, do not copy data unnecessarily

indicator [boolean or string, default False] If True, adds a column to output DataFrame called "_merge" with information on the source of each row. If string, column with information on source of each row will be added to output DataFrame, and column will be named value of string. Information column is Categorical-type and takes on a value of "left_only" for observations whose merge key only appears in 'left' DataFrame, "right_only" for observations whose merge key only appears in 'right' DataFrame, and "both" if the observation's merge key is found in both.

validate [string, default None] If specified, checks if merge is of specified type.

- "one_to_one" or "1:1": check if merge keys are unique in both left and right datasets.
- "one_to_many" or "1:m": check if merge keys are unique in left dataset.
- "many_to_one" or "m:1": check if merge keys are unique in right dataset.
- "many_to_many" or "m:m": allowed, but does not result in checks.

New in version 0.21.0.

Returns

merged [DataFrame] The output type will the be same as 'left', if it is a subclass of DataFrame.

See also:

`merge_ordered`, `merge_asof`, `DataFrame.join`

Notes

Support for specifying index levels as the *on*, *left_on*, and *right_on* parameters was added in version 0.23.0

Examples

```
>>> A              >>> B
    lkey value         rkey value
0   foo  1         0   foo  5
1   bar  2         1   bar  6
2   baz  3         2   qux  7
3   foo  4         3   bar  8
```

```
>>> A.merge(B, left_on='lkey', right_on='rkey', how='outer')
   lkey  value_x  rkey  value_y
0  foo   1        foo   5
1  foo   4        foo   5
2  bar   2        bar   6
3  bar   2        bar   8
4  baz   3        NaN   NaN
5  NaN   NaN      qux   7
```

4.9.2 Create and Store Dask DataFrames

Dask can create dataframes from various data storage formats like CSV, HDF, Apache Parquet, and others. For most formats this data can live on various storage systems including local disk, network file systems (NFS), the Hadoop File System (HDFS), and Amazon's S3 (excepting HDF, which is only available on POSIX like file systems).

See the Overview section for an in depth discussion of `dask.dataframe` scope, use, limitations.

API

The following functions provide access to convert between Dask Dataframes, file formats, and other Dask or Python collections.

File Formats:

read_csv(urlpath[, blocksize, collection, ...])	Read CSV files into a Dask.DataFrame
read_parquet(path[, columns, filters, ...])	Read ParquetFile into a Dask DataFrame
read_hdf(pattern, key[, start, stop, ...])	Read HDF files into a Dask DataFrame
read_orc(path[, columns, storage_options])	Read dataframe from ORC file(s)
read_json(url_path[, orient, lines, ...])	Create a dataframe from a set of JSON files
read_sql_table(table, uri, index_col[, ...])	Create dataframe from an SQL table.
from_bcolz(x[, chunksize, categorize, ...])	Read BColz CTable into a Dask Dataframe
from_array(x[, chunksize, columns])	Read any slicable array into a Dask Dataframe
to_csv(df, filename[, name_function, ...])	Store Dask DataFrame to CSV files
to_parquet(df, path[, engine, compression, ...])	Store Dask.dataframe to Parquet files
to_hdf(df, path, key[, mode, append, get, ...])	Store Dask Dataframe to Hierarchical Data Format (HDF) files

Dask Collections:

from_delayed(dfs[, meta, divisions, prefix])	Create Dask DataFrame from many Dask Delayed objects
from_dask_array(x[, columns, index])	Create a Dask DataFrame from a Dask Array.
dask.bag.core.Bag.to_dataframe([meta, columns])	Create Dask Dataframe from a Dask Bag.
DataFrame.to_delayed([optimize_graph])	Convert into a list of `dask.delayed` objects, one per partition.
to_records(df)	Create Dask Array from a Dask Dataframe
to_bag(df[, index])	Create Dask Bag from a Dask DataFrame

Pandas:

from_pandas(data[, npartitions, chunksize, ...])	Construct a Dask DataFrame from a Pandas DataFrame

Locations

For text, CSV, and Apache Parquet formats data can come from local disk, from the Hadoop File System, from S3FS, or others, by prepending the filenames with a protocol.

```
>>> df = dd.read_csv('my-data-*.csv')
>>> df = dd.read_csv('hdfs:///path/to/my-data-*.csv')
```

(continues on next page)

(continued from previous page)

```
>>> df = dd.read_csv('s3://bucket-name/my-data-*.csv')
```

For remote systems like HDFS or S3 credentials may be an issue. Usually these are handled by configuration files on disk (such as a `.boto` file for S3) but in some cases you may want to pass storage-specific options through to the storage backend. You can do this with the `storage_options=` keyword.

```
>>> df = dd.read_csv('s3://bucket-name/my-data-*.csv',
...                  storage_options={'anon': True})
```

Dask Delayed

For more complex situations not covered by the functions above you may want to use *dask.delayed* , which lets you construct Dask.dataframes out of arbitrary Python function calls that load dataframes. This can allow you to handle new formats easily, or bake in particular logic around loading data if, for example, your data is stored with some special

See *documentation on using dask.delayed with collections* or an example notebook showing how to create a Dask DataFrame from a nested directory structure of Feather files (as a stand in for any custom file format).

Dask.delayed is particularly useful when simple `map` operations aren't sufficient to capture the complexity of your data layout.

From Raw Dask Graphs

This section is mainly for developers wishing to extend dask.dataframe. It discusses internal API not normally needed by users. Everything below can be done just as effectively with *dask.delayed* described just above. You should never need to create a dataframe object by hand.

To construct a DataFrame manually from a dask graph you need the following information:

1. dask: a dask graph with keys like `{(name, 0): ..., (name, 1): ...}` as well as any other tasks on which those tasks depend. The tasks corresponding to `(name, i)` should produce `pandas.DataFrame` objects that correspond to the columns and divisions information discussed below.
2. name: The special name used above
3. columns: A list of column names
4. divisions: A list of index values that separate the different partitions. Alternatively, if you don't know the divisions (this is common) you can provide a list of `[None, None, None, ...]` with as many partitions as you have plus one. For more information see the Partitions section in the *dataframe documentation*.

As an example, we build a DataFrame manually that reads several CSV files that have a datetime index separated by day. Note, you should never do this. The `dd.read_csv` function does this for you.

```
dsk = {('mydf', 0): (pd.read_csv, 'data/2000-01-01.csv'),
       ('mydf', 1): (pd.read_csv, 'data/2000-01-02.csv'),
       ('mydf', 2): (pd.read_csv, 'data/2000-01-03.csv')}
name = 'mydf'
columns = ['price', 'name', 'id']
divisions = [Timestamp('2000-01-01 00:00:00'),
             Timestamp('2000-01-02 00:00:00'),
             Timestamp('2000-01-03 00:00:00'),
             Timestamp('2000-01-03 23:59:59')]

df = dd.DataFrame(dsk, name, columns, divisions)
```

4.9.3 Dask DataFrame Performance Tips

Use Pandas

For data that fits into RAM, Pandas can often be faster and easier to use than Dask.dataframe. While "Big Data" tools can be exciting, they are almost always worse than normal data tools while those remain appropriate.

Pandas Performance Tips Apply to Dask.dataframe

Normal Pandas performance tips, like avoiding apply, using vectorized operations, using categoricals, etc. all apply equally to Dask.dataframe. See Modern Pandas by Tom Augspurger is a good read here.

Use the Index

Dask.dataframe can be optionally sorted along a single index column. Some operations against this column can be very fast. For example if your dataset is sorted by time you can quickly select data for a particular day, perform time series joins, etc. You can check if your data is sorted by looking at the `df.known_divisions` attribute. You can set an index column using the `.set_index(columnname)` method. This operation is expensive though, so use it sparingly (see below).

```
df = df.set_index('timestamp')  # set the index to make some operations fast

df.loc['2001-01-05':'2001-01-12']  # this is very fast if you have an index
df.merge(df2, left_index=True, right_index=True)  # this is also very fast
```

Avoid Shuffles

Setting an index is an important (see above) but expensive operation. You should do it infrequently and you should persist afterwards (see below).

Some operations like `set_index` and `merge/join` are harder to do in a parallel or distributed setting than they are in-memory on a single machine. In particular *shuffling operations* that rearrange data become much more communication intensive. For example if your data is arranged by customer ID but now you want to arrange it by time all of your partitions will have to talk to each other to exchange shards of data. This can be an intense process, particularly on a cluster.

So definitely set the index, but try do so infrequently. After you set the index then you may want to `persist` your data if you are on a cluster.

```
df = df.set_index('column-name')  # do this infrequently
```

Additionally, set_index has a few options that can accelerate it in some situations. For example if you know that your dataset is sorted or you already know the values by which it is divided you can provide these to accelerate the set_index operation. See the set_index docstring for more information.

```
df2 = df.set_index(d.timestamp, sorted=True)
```

Persist Intelligently

This section is only relevant to users on distributed systems.

Often dataframe workloads look like the following:

1. Load data from files
2. Filter data to a particular subset
3. Shuffle data to set an intelligent index
4. Several complex queries on top of this indexed data

It is often ideal to load, filter, and shuffle data once and keep this result in memory. Afterwards each of the several complex queries can be based off of this in-memory data rather than have to repeat the full load-filter-shuffle process each time. To do this, use the client.persist method.

```
df = dd.read_csv('s3://bucket/path/to/*.csv')
df = df[df.balance < 0]
df = client.persist(df)

df = df.set_index('timestamp')
df = client.persist(df)

>>> df.customer_id.nunique().compute()
18452844

>>> df.groupby(df.city).size().compute()
...
```

Persist is important because Dask.dataframe is *lazy by default*. Persist is a way of telling the cluster that it should start computing on the computations that you have defined so far and that it should try to keep those results in memory. You will get back a new dataframe that is semantically equivalent to your old dataframe, but now points to running data. Your old dataframe still points to lazy computations

```
# Don't do this
client.persist(df)  # Persist doesn't change the input in-place

# Do this instead
df = client.persist(df)  # Replace your old lazy dataframe
```

Repartition to Reduce Overhead

Your Dask.dataframe is split up into many Pandas dataframes. We sometimes call these "partitions". Often the number of partitions is decided for you; for example it might be the number of CSV files from which you are reading. However over time as you reduce or increase the size of your pandas dataframes by filtering or joining it may be wise to reconsider how many partitions you need. There is a cost to having too many or having too few.

Partitions should fit comfortably in memory (smaller than a gigabyte) but also not be too numerous. Every operation on every partition takes the central scheduler a few hundred microseconds to process. If you have a few thousand tasks this is barely noticeable, but it is nice to reduce the number if possible.

A common situation is that you load lots of data into reasonably sized partitions (dask's defaults make decent choices) but then you filter down your dataset to only a small fraction of the original. At this point it is wise to regroup your many small partitions into a few larger ones. You can do this with the `repartition` method:

```
df = dd.read_csv('s3://bucket/path/to/*.csv')
df = df[df.name == 'Alice']  # only 1/100th of the data
df = df.repartition(npartitions=df.npartitions // 100)

df = client.persist(df)  # if on a distributed system
```

This helps to reduce overhead and increase the effectiveness of vectorized Pandas operations. You should aim for partitions that have around 100MB of data each.

Additionally, reducing partitions is very helpful just before shuffling, which creates `n log(n)` tasks relative to the number of partitions. Dataframes with less than 100 partitions are much easier to shuffle than dataframes with tens of thousands.

Joins

Joining two dataframes can be either very expensive or very cheap depending on the situation. It is cheap in the following cases:

1. Joining a Dask.dataframe with a Pandas dataframe
2. Joining a Dask.dataframe with a Dask.dataframe of a single partition.
3. Joining Dask.dataframes along their indexes

It is expensive in the following case:

1. Joining Dask.dataframes along columns that are not their index

The expensive case requires a shuffle. This is fine, and Dask.dataframe will complete the job well, but it will be more expensive than a typical linear-time operation.

```
dd.merge(a, pandas_df)  # fast
dd.merge(a, b, left_index=True, right_index=True)  # fast
dd.merge(a, b, left_index=True, right_on='id')  # half-fast, half-slow
dd.merge(a, b, left_on='id', right_on='id')  # slow
```

Store Data in Apache Parquet Format

HDF5 is a popular choice for Pandas users with high performance needs. We encourage Dask.dataframe users to store and load data dataframe-create> using Parquet instead. Apache Parquet is a columnar binary format that is easy to split into multiple files (easier for parallel loading) and is generally much simpler to deal with than HDF5 (from the library's perspective). It is also a common format used by other big data systems like Apache Spark and Apache Impala and so is useful to interchange with other systems.

```
df.to_parquet('path/to/my-results/')
df = dd.read_parquet('path/to/my-results/')
```

Dask supports reading with multiple implementations of the Apache Parquet format for Python.

```
df1 = dd.read_parquet('path/to/my-results/', engine='fastparquet')
df2 = dd.read_parquet('path/to/my-results/', engine='pyarrow')
```

These libraries be installed using

```
conda install fastparquet pyarrow -c conda-forge
```

Fastparquet is a Python-based implementation that uses the Numba Python-to-LLVM compiler. PyArrow is part of the Apache Arrow project and uses the C++ implementation of Apache Parquet.

4.9.4 Internal Design

Dask dataframes coordinate many Pandas DataFrames/Series arranged along an index. We define a `dask.dataframe` object with the following components:

- A dask graph with a special set of keys designating partitions, such as `('x', 0), ('x', 1), ...`.
- A name to identify which keys in the dask graph refer to this dataframe, such as `'x'`.
- An empty pandas object containing appropriate metadata (e.g. column names, dtypes, etc...).
- A sequence of partition boundaries along the index, called `divisions`.

Metadata

Many dataframe operations rely on knowing the name and dtype of columns. To keep track of this information, all `dask.dataframe` objects have a `_meta` attribute which contains an empty pandas object with the same dtypes and names. For example:

```
>>> df = pd.DataFrame({'a': [1, 2, 3], 'b': ['x', 'y', 'z']})
>>> ddf = dd.from_pandas(df, npartitions=2)
>>> ddf._meta
Empty DataFrame
Columns: [a, b]
Index: []
>>> ddf._meta.dtypes
a     int64
b    object
dtype: object
```

Internally `dask.dataframe` does its best to propagate this information through all operations, so most of the time a user shouldn't have to worry about this. Usually this is done by evaluating the operation on a small sample of fake data, which can be found on the `_meta_nonempty` attribute:

```
>>> ddf._meta_nonempty
   a    b
0  1  foo
1  1  foo
```

Sometimes this operation may fail in user defined functions (e.g. when using `DataFrame.apply`), or may be prohibitively expensive. For these cases, many functions support an optional `meta` keyword, which allows specifying the metadata directly, avoiding the inference step. For convenience, this supports several options:

1. A pandas object with appropriate dtypes and names. If not empty, an empty slice will be taken:

```
>>> ddf.map_partitions(foo, meta=pd.DataFrame({'a': [1], 'b': [2]}))
```

2. A description of the appropriate names and dtypes. This can take several forms:
   - A `dict` of `{name: dtype}` or an iterable of `(name, dtype)` specifies a dataframe
   - A tuple of `(name, dtype)` specifies a series
   - A dtype object or string (e.g. `'f8'`) specifies a scalar

This keyword is available on all functions/methods that take user provided callables (e.g. `DataFrame.map_partitions`, `DataFrame.apply`, etc...), as well as many creation functions (e.g. `dd.from_delayed`).

Categoricals

Dask dataframe divides categorical data into two types:

- Known categoricals have the `categories` known statically (on the `_meta` attribute). Each partition **must** have the same categories as found on the `_meta` attribute.

- Unknown categoricals don't know the categories statically, and may have different categories in each partition. Internally, unknown categoricals are indicated by the presence of `dd.utils.UNKNOWN_CATEGORIES` in the categories on the `_meta` attribute. Since most dataframe operations propagate the categories, the known/unknown status should propagate through operations (similar to how `NaN` propagates).

For metadata specified as a description (option 2 above), unknown categoricals are created.

Certain operations are only available for known categoricals. For example, `df.col.cat.categories` would only work if `df.col` has known categories, since the categorical mapping is only known statically on the metadata of known categoricals.

The known/unknown status for a categorical column can be found using the `known` property on the categorical accessor:

```
>>> ddf.col.cat.known
False
```

Additionally, an unknown categorical can be converted to known using `.cat.as_known()`. If you have multiple categorical columns in a dataframe, you may instead want to use `df.categorize(columns=...)`, which will convert all specified columns to known categoricals. Since getting the categories requires a full scan of the data, using `df.categorize()` is more efficient than calling `.cat.as_known()` for each column (which would result in multiple scans).

```
>>> col_known = ddf.col.cat.as_known()  # use for single column
>>> col_known.cat.known
True
>>> ddf_known = ddf.categorize()        # use for multiple columns
>>> ddf_known.col.cat.known
True
```

To convert a known categorical to an unknown categorical, there is also the `.cat.as_unknown()` method. This requires no computation, as it's just a change in the metadata.

Non-categorical columns can be converted to categoricals in a few different ways:

```
# astype operates lazily, and results in unknown categoricals
ddf = ddf.astype({'mycol': 'category', ...})
# or
ddf['mycol'] = ddf.mycol.astype('category')

# categorize requires computation, and results in known categoricals
ddf = ddf.categorize(columns=['mycol', ...])
```

Additionally, with pandas 0.19.2 and up `dd.read_csv` and `dd.read_table` can read data directly into unknown categorical columns by specifying a column dtype as `'category'`:

```
>>> ddf = dd.read_csv(..., dtype={col_name: 'category'})
```

With pandas 0.21.0 and up, `dd.read_csv` and `dd.read_table` can read data directly into *known* categoricals by specifying instances of `pd.api.types.CategoricalDtype`:

```
>>> dtype = {'col': pd.api.types.CategoricalDtype(['a', 'b', 'c'])}
>>> ddf = dd.read_csv(..., dtype=dtype)
```

Partitions

Internally a dask dataframe is split into many partitions, and each partition is one pandas dataframe. These dataframes are split vertically along the index. When our index is sorted and we know the values of the divisions of our partitions,

then we can be clever and efficient with expensive algorithms (e.g. groupby's, joins, etc...).

For example, if we have a time-series index then our partitions might be divided by month. All of January will live in one partition while all of February will live in the next. In these cases operations like `loc`, `groupby`, and `join/merge` along the index can be *much* more efficient than would otherwise be possible in parallel. You can view the number of partitions and divisions of your dataframe with the following fields:

```
>>> df.npartitions
4
>>> df.divisions
['2015-01-01', '2015-02-01', '2015-03-01', '2015-04-01', '2015-04-31']
```

Divisions includes the minimum value of every partition's index and the maximum value of the last partition's index. In the example above if the user searches for a specific datetime range then we know which partitions we need to inspect and which we can drop:

```
>>> df.loc['2015-01-20': '2015-02-10']  # Must inspect first two partitions
```

Often we do not have such information about our partitions. When reading CSV files for example we do not know, without extra user input, how the data is divided. In this case `.divisions` will be all `None`:

```
>>> df.divisions
[None, None, None, None, None]
```

In these cases any operation that requires a cleanly partitioned dataframe with known divisions will have to perform a sort. This can generally achieved by calling `df.set_index(...)`.

4.9.5 Shuffling for GroupBy and Join

Operations like `groupby`, `join`, and `set_index` have special performance considerations that are different from normal Pandas due to the parallel, larger-than-memory, and distributed nature of dask.dataframe.

Easy Case

To start off, common groupby operations like `df.groupby(columns).reduction()` for known reductions like `mean, sum, std, var, count, nunique` are all quite fast and efficient, even if partitions are not cleanly divided with known divisions. This is the common case.

Additionally, if divisions are known then applying an arbitrary function to groups is efficient when the grouping columns include the index.

Joins are also quite fast when joining a Dask dataframe to a Pandas dataframe or when joining two Dask dataframes along their index. No special considerations need to be made when operating in these common cases.

So if you're doing common groupby and join operations then you can stop reading this. Everything will scale nicely. Fortunately this is true most of the time.

```
>>> df.groupby(columns).known_reduction()              # Fast and common case
>>> df.groupby(columns_with_index).apply(user_fn)      # Fast and common case
>>> dask_df.join(pandas_df, on=column)                 # Fast and common case
>>> lhs.join(rhs)                                      # Fast and common case
>>> lhs.merge(rhs, on=columns_with_index)              # Fast and common case
```

Difficult Cases

In some cases, such as when applying an arbitrary function to groups (when not grouping on index with known divisions), when joining along non-index columns, or when explicitly setting an unsorted column to be the index, we may need to trigger a full dataset shuffle

```
>>> df.groupby(columns_no_index).apply(user_fn)    # Requires shuffle
>>> lhs.join(rhs, on=columns_no_index)             # Requires shuffle
>>> df.set_index(column)                           # Requires shuffle
```

A shuffle is necessary when we need to re-sort our data along a new index. For example if we have banking records that are organized by time and we now want to organize them by user ID then we'll need to move a lot of data around. In Pandas all of this data fit in memory, so this operation was easy. Now that we don't assume that all data fits in memory we must be a bit more careful.

Re-sorting the data can be avoided by restricting yourself to the easy cases mentioned above.

Shuffle Methods

There are currently two strategies to shuffle data depending on whether you are on a single machine or on a distributed cluster.

Shuffle on Disk

When operating on larger-than-memory data on a single machine we shuffle by dumping intermediate results to disk. This is done using the partd project for on-disk shuffles.

Shuffle over the Network

When operating on a distributed cluster the Dask workers may not have access to a shared hard drive. In this case we shuffle data by breaking input partitions into many pieces based on where they will end up and moving these pieces throughout the network. This prolific expansion of intermediate partitions can stress the task scheduler. To manage for many-partitioned datasets we sometimes shuffle in stages, causing undue copies but reducing the `n**2` effect of shuffling to something closer to `n log(n)` with `log(n)` copies.

Selecting methods

Dask will use on-disk shuffling by default but will switch to task-based distributed shuffling if the default scheduler is set to use a `dask.distributed.Client` such as would be the case if the user sets the Client as default:

```
client = Client('scheduler:8786', set_as_default=True)
```

Alternatively, if you prefer to avoid defaults, you can configure the global shuffling method by using the `dask.config.set(shuffle=...)` command. This can be done globally,

```
dask.config.set(shuffle='tasks')

df.groupby(...).apply(...)
```

or as a context manager

```
with dask.config.set(shuffle='tasks'):
    df.groupby(...).apply(...)
```

In addition, `set_index` also accepts a `shuffle` keyword argument that can be used to select either on-disk or task-based shuffling

```
df.set_index(column, shuffle='disk')
df.set_index(column, shuffle='tasks')
```

4.9.6 Aggregate

Dask support Pandas' `aggregate` syntax to run multiple reductions on the same groups. Common reductions, such as `max`, `sum`, `mean` are directly supported:

```
>>> df.groupby(columns).aggregate(['sum', 'mean', 'max', 'min'])
```

Dask also supports user defined reductions. To ensure proper performance, the reduction has to be formulated in terms of three independent steps. The `chunk` step is applied to each partition independently and reduces the data within a partition. The `aggregate` combines the within partition results. The optional `finalize` step combines the results returned from the `aggregate` step and should return a single final column. For Dask to recognize the reduction, it has to be passed as an instance of `dask.dataframe.Aggregation`.

For example, `sum` could be implemented as

```
custom_sum = dd.Aggregation('custom_sum', lambda s: s.sum(), lambda s0: s0.sum())
df.groupby('g').agg(custom_sum)
```

The name argument should be different from existing reductions to avoid data corruption. The arguments to each function are pre-grouped series objects, similar to `df.groupby('g')['value']`.

Many reductions can only be implemented with multiple temporaries. To implement these reductions, the steps should return tuples and expect multiple arguments. A mean function can be implemented as

```
custom_mean = dd.Aggregation(
    'custom_mean',
    lambda s: (s.count(), s.sum()),
    lambda count, sum: (count.sum(), sum.sum()),
    lambda count, sum: sum / count,
)
df.groupby('g').agg(custom_mean)
```

4.9.7 Indexing into Dask DataFrames

Dask DataFrame supports some of pandas' indexing behavior.

DataFrame.iloc	Purely integer-location based indexing for selection by position.
DataFrame.loc	Purely label-location based indexer for selection by label.

Label-based Indexing

Just like pandas, Dask DataFrame supports label-based indexing with the `.loc` accessor for selecting rows or columns, and `__getitem__` (square brackets) for selecting just columns.

Note: To select rows, the DataFrame's divisions must be known (see *Internal Design* and *Dask DataFrame Performance Tips*) for more.

```
>>> import dask.dataframe as dd
>>> import pandas as pd
>>> df = pd.DataFrame({"A": [1, 2, 3], "B": [3, 4, 5]},
...                   index=['a', 'b', 'c'])
>>> ddf = dd.from_pandas(df, npartitions=2)
>>> ddf
Dask DataFrame Structure:
                    A      B
npartitions=1
a               int64  int64
c                 ...    ...
Dask Name: from_pandas, 1 tasks
```

Selecting columns:

```
>>> ddf[['B', 'A']]
Dask DataFrame Structure:
                    B      A
npartitions=1
a               int64  int64
c                 ...    ...
Dask Name: getitem, 2 tasks
```

Selecting a single column reduces to a Dask Series:

```
>>> ddf['A']
Dask Series Structure:
npartitions=1
a    int64
c      ...
Name: A, dtype: int64
Dask Name: getitem, 2 tasks
```

Slicing rows and (optionally) columns with `.loc`:

```
>>> ddf.loc[['b', 'c'], ['A']]
Dask DataFrame Structure:
                    A
npartitions=1
b               int64
c                 ...
Dask Name: loc, 2 tasks
```

Dask DataFrame supports pandas' partial-string indexing:

```
>>> ts = dd.demo.make_timeseries()
>>> ts
Dask DataFrame Structure:
```

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```
                   id    name        x        y
npartitions=11
2000-01-31      int64  object  float64  float64
2000-02-29        ...     ...      ...      ...
...               ...     ...      ...      ...
2000-11-30        ...     ...      ...      ...
2000-12-31        ...     ...      ...      ...
Dask Name: make-timeseries, 11 tasks

>>> ts.loc['2000-02-12']
Dask DataFrame Structure:
                                   id    name        x        y
npartitions=1
2000-02-12 00:00:00.000000000  int64  object  float64  float64
2000-02-12 23:59:59.999999999    ...     ...      ...      ...
Dask Name: loc, 12 tasks
```

Positional Indexing

Dask DataFrame does not track the length of partitions, making positional indexing with `.iloc` inefficient for selecting rows. *`DataFrame.iloc()`* only supports indexers where the row indexer is `slice(None)` (which `:` is a shorthand for.)

```
>>> ddf.iloc[:, [1, 0]]
Dask DataFrame Structure:
                   B      A
npartitions=1
a              int64  int64
c                ...    ...
Dask Name: iloc, 2 tasks
```

Trying to select specific rows with `iloc` will raise an exception:

```
>>> ddf.iloc[[0, 2], [1]]
Traceback (most recent call last)
  File "<stdin>", line 1, in <module>
ValueError: 'DataFrame.iloc' does not support slicing rows. The indexer must be a 2-
↪tuple whose first item is 'slice(None)'.
```

4.9.8 Subclass DataFrames

There are a few projects that subclass or replicate the functionality of Pandas objects:

- GeoPandas: for Geospatial analytics
- PyGDF: for data analysis on GPUs
- ...

These projects may also want to produce parallel variants of themselves with Dask, and may want to reuse some of the code in Dask Dataframe. This document describes how to do this. It is intended for maintainers of these libraries, and not for general users.

Implement dask, name, meta, and divisions

You will need to implement `._meta`, `.dask`, `.divisions`, and `._name` as defined in the *dataframe design docs*.

Extend Dispatched Methods

If you are going to pass around Pandas-like objects that are not normal Pandas objects then we ask you to extend a few dispatched methods.

make_meta

This function returns an empty version of one of your non-Dask objects, given a non-empty non-Dask object.

```
from dask.dataframe import make_meta

@make_meta.register(MyDataFrame)
def make_meta_dataframe(df):
    return df.head(0)


@make_meta.register(MySeries)
def make_meta_series(s):
    return s.head(0)


@make_meta.register(MyIndex)
def make_meta_index(ind):
    return ind[:0]
```

Additionally you should create a similar function that returns a non-empty version of your non-Dask dataframe objects, filled with a few rows of representative or random data. This is used to guess types when they are not provided. It should expect an empty version of your object with columns, dtypes, index name, and it should return a non-empty version.

```
from dask.dataframe.utils import meta_nonempty

@meta_nonempty.register(MyDataFrame)
def meta_nonempty_dataframe(df):
    ...
    return MyDataFrame(..., columns=df.columns,
                       index=MyIndex(..., name=df.index.name)


@meta_nonempty.register(MySeries)
def meta_nonempty_series(s):
    ...


@meta_nonempty.register(MyIndex)
def meta_nonempty_index(ind):
    ...
```

get_parallel_type

Given a non-Dask dataframe object, return the Dask equivalent

```
from dask.dataframe.core import get_parallel_type

@get_parallel_type.register(MyDataFrame)
def get_parallel_type_dataframe(df):
    return MyDaskDataFrame


@get_parallel_type.register(MySeries)
def get_parallel_type_series(s):
    return MyDaskSeries


@get_parallel_type.register(MyIndex)
def get_parallel_type_index(ind):
    return MyDaskIndex
```

concat

Concatenate many of your non-Dask dataframe objects together. It should expect a list of your objects (homogeneously typed).

```
from dask.dataframe.methods import concat_dispatch

@concat_dispatch.register((MyDataFrame, MySeries, MyIndex))
def concat_pandas(dfs, axis=0, join='outer', uniform=False, filter_warning=True):
    ...
```

Extension Arrays

Rather than subclassing Pandas dataframes, you may be interested in extending Pandas with Extension Arrays.

API support for extension arrays isn't in Dask Dataframe yet (though this would be a good contribution), but many of the complications above will go away if your objects are genuinely Pandas dataframes, rather than a subclass.

A Dask DataFrame is a large parallel dataframe composed of many smaller Pandas dataframes, split along the index. These pandas dataframes may live on disk for larger-than-memory computing on a single machine, or on many different machines in a cluster. One Dask dataframe operation triggers many operations on the constituent Pandas dataframes.

4.9.9 Design

Dask dataframes coordinate many Pandas DataFrames/Series arranged along the index. Dask.dataframe is partitioned *row-wise*, grouping rows by index value for efficiency. These Pandas objects may live on disk or on other machines.

4.9.10 Dask.dataframe copies the Pandas API

Because the `dask.dataframe` application programming interface (API) is a subset of the Pandas API it should be familiar to Pandas users. There are some slight alterations due to the parallel nature of dask:

```
>>> import dask.dataframe as dd
>>> df = dd.read_csv('2014-*.csv')
>>> df.head()
   x  y
0  1  a
1  2  b
2  3  c
3  4  a
4  5  b
5  6  c

>>> df2 = df[df.y == 'a'].x + 1
```

As with all dask collections one triggers computation by calling the `.compute()` method:

```
>>> df2.compute()
0    2
3    5
Name: x, dtype: int64
```

4.9.11 Common Uses and Anti-Uses

Dask.dataframe is used in situations where Pandas is commonly needed, but when Pandas fails due to data size or computation speed.

- Manipulating large datasets, even when those datasets don't fit in memory
- Accelerating long computations by using many cores
- Distributed computing on large datasets with standard Pandas operations like groupby, join, and time series computations

Dask dataframe may not be the best choice in the following situations:

- If your dataset fits comfortably into RAM on your laptop then you may be better off just using Pandas . There may be simpler ways to improve performance than through parallelism.
- If your dataset doesn't fit neatly into the Pandas tabular model then you might find more use in *dask.bag* or *dask.array*
- If you need functions that are not implemented in Dask dataframe then you might want to look at *dask.delayed* which offers more flexibility.
- If you need a proper database with all that databases offer you might prefer something like Postgres

4.9.12 Scope

Dask.dataframe covers a well-used portion of the Pandas API. The following class of computations works well:

- **Trivially parallelizable operations (fast):**
  - Elementwise operations: `df.x + df.y`, `df * df`
  - Row-wise selections: `df[df.x > 0]`

  - Loc: `df.loc[4.0:10.5]`
  - Common aggregations: `df.x.max()`, `df.max()`
  - Is in: `df[df.x.isin([1, 2, 3])]`
  - Datetime/string accessors: `df.timestamp.month`
- **Cleverly parallelizable operations (fast):**
  - groupby-aggregate (with common aggregations): `df.groupby(df.x).y.max()`, `df.groupby('x').max()`
  - groupby-apply on index: `df.groupby(['idx', 'x']).apply(myfunc)`, where `idx` is the index level name
  - value_counts: `df.x.value_counts()`
  - Drop duplicates: `df.x.drop_duplicates()`
  - Join on index: `dd.merge(df1, df2, left_index=True, right_index=True)` or `dd.merge(df1, df2, on=['idx', 'x'])` where `idx` is the index name for both `df1` and `df2`
  - Join with Pandas DataFrames: `dd.merge(df1, df2, on='id')`
  - Elementwise operations with different partitions / divisions: `df1.x + df2.y`
  - Datetime resampling: `df.resample(...)`
  - Rolling averages: `df.rolling(...)`
  - Pearson Correlations: `df[['col1', 'col2']].corr()`
- **Operations requiring a shuffle (slow-ish, unless on index)**
  - Set index: `df.set_index(df.x)`
  - groupby-apply not on index (with anything): `df.groupby(df.x).apply(myfunc)`
  - Join not on the index: `dd.merge(df1, df2, on='name')`

However Dask dataframe does not implement the entire Pandas interface. Users expecting this will be disappointed. Notably, Dask dataframe has the following limitations:

1. Setting a new index from an unsorted column is expensive
2. Many operations, like groupby-apply and join on unsorted columns require setting the index, which as mentioned above, is expensive
3. The Pandas API is very large. Dask dataframe does not attempt to implement many Pandas features or any of the more exotic data structures like NDFrames
4. Operations that were slow on Pandas, like iterating through row-by-row, remain slow on Dask dataframe

See *DataFrame API documentation* for a more extensive list.

4.9.13 Execution

By default `dask.dataframe` uses the multi-threaded scheduler. This exposes some parallelism when Pandas or the underlying numpy operations release the global interpreter lock (GIL). Generally Pandas is more GIL bound than NumPy, so multi-core speed-ups are not as pronounced for `dask.dataframe` as they are for `dask.array`. This is changing, and the Pandas development team is actively working on releasing the GIL.

When dealing with text data you may see speedups by switching to the newer *distributed scheduler* either on a cluster or single machine.

4.10 Delayed

4.10.1 API

The `dask.delayed` interface consists of one function, `delayed`:

- `delayed` wraps functions

  Wraps functions. Can be used as a decorator, or around function calls directly (i.e. `delayed(foo)(a, b, c)`). Outputs from functions wrapped in `delayed` are proxy objects of type `Delayed` that contain a graph of all operations done to get to this result.

- `delayed` wraps objects

  Wraps objects. Used to create `Delayed` proxies directly.

`Delayed` objects can be thought of as representing a key in the dask. A `Delayed` supports *most* python operations, each of which creates another `Delayed` representing the result:

- Most operators (`*`, `-`, and so on)
- Item access and slicing (`a[0]`)
- Attribute access (`a.size`)
- Method calls (`a.index(0)`)

Operations that aren't supported include:

- Mutating operators (`a += 1`)
- Mutating magics such as `__setitem__`/`__setattr__` (`a[0] = 1`, `a.foo = 1`)
- Iteration. (`for i in a: ...`)
- Use as a predicate (`if a: ...`)

The last two points in particular mean that `Delayed` objects cannot be used for control flow, meaning that no `Delayed` can appear in a loop or if statement. In other words you can't iterate over a `Delayed` object, or use it as part of a condition in an if statement, but `Delayed` object can be used in a body of a loop or if statement (i.e. the example above is fine, but if `data` was a `Delayed` object it wouldn't be). Even with this limitation, many workflows can easily be parallelized.

delayed	Wraps a function or object to produce a `Delayed`.

`dask.delayed.`**`delayed`**`()`

Wraps a function or object to produce a `Delayed`.

`Delayed` objects act as proxies for the object they wrap, but all operations on them are done lazily by building up a dask graph internally.

Parameters

obj [object] The function or object to wrap

name [string or hashable, optional] The key to use in the underlying graph for the wrapped object. Defaults to hashing content. Note that this only affects the name of the object wrapped by this call to delayed, and *not* the output of delayed function calls - for that use `dask_key_name=` as described below.

pure [bool, optional] Indicates whether calling the resulting `Delayed` object is a pure operation. If True, arguments to the call are hashed to produce deterministic keys. If not

provided, the default is to check the global `delayed_pure` setting, and fallback to `False` if unset.

nout [int, optional] The number of outputs returned from calling the resulting `Delayed` object. If provided, the `Delayed` output of the call can be iterated into `nout` objects, allowing for unpacking of results. By default iteration over `Delayed` objects will error. Note, that `nout=1` expects `obj`, to return a tuple of length 1, and consequently for `nout=0`, `obj` should return an empty tuple.

traverse [bool, optional] By default dask traverses builtin python collections looking for dask objects passed to `delayed`. For large collections this can be expensive. If `obj` doesn't contain any dask objects, set `traverse=False` to avoid doing this traversal.

Examples

Apply to functions to delay execution:

```
>>> def inc(x):
...     return x + 1
```

```
>>> inc(10)
11
```

```
>>> x = delayed(inc, pure=True)(10)
>>> type(x) == Delayed
True
>>> x.compute()
11
```

Can be used as a decorator:

```
>>> @delayed(pure=True)
... def add(a, b):
...     return a + b
>>> add(1, 2).compute()
3
```

`delayed` also accepts an optional keyword `pure`. If False, then subsequent calls will always produce a different `Delayed`. This is useful for non-pure functions (such as `time` or `random`).

```
>>> from random import random
>>> out1 = delayed(random, pure=False)()
>>> out2 = delayed(random, pure=False)()
>>> out1.key == out2.key
False
```

If you know a function is pure (output only depends on the input, with no global state), then you can set `pure=True`. This will attempt to apply a consistent name to the output, but will fallback on the same behavior of `pure=False` if this fails.

```
>>> @delayed(pure=True)
... def add(a, b):
...     return a + b
>>> out1 = add(1, 2)
>>> out2 = add(1, 2)
```

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```
>>> out1.key == out2.key
True
```

Instead of setting `pure` as a property of the callable, you can also set it contextually using the `delayed_pure` setting. Note that this influences the *call* and not the *creation* of the callable:

```
>>> import dask
>>> @delayed
... def mul(a, b):
...     return a * b
>>> with dask.config.set(delayed_pure=True):
...     print(mul(1, 2).key == mul(1, 2).key)
True
>>> with dask.config.set(delayed_pure=False):
...     print(mul(1, 2).key == mul(1, 2).key)
False
```

The key name of the result of calling a delayed object is determined by hashing the arguments by default. To explicitly set the name, you can use the `dask_key_name` keyword when calling the function:

```
>>> add(1, 2)
Delayed('add-3dce7c56edd1ac2614add714086e950f')
>>> add(1, 2, dask_key_name='three')
Delayed('three')
```

Note that objects with the same key name are assumed to have the same result. If you set the names explicitly you should make sure your key names are different for different results.

```
>>> add(1, 2, dask_key_name='three')
>>> add(2, 1, dask_key_name='three')
>>> add(2, 2, dask_key_name='four')
```

`delayed` can also be applied to objects to make operations on them lazy:

```
>>> a = delayed([1, 2, 3])
>>> isinstance(a, Delayed)
True
>>> a.compute()
[1, 2, 3]
```

The key name of a delayed object is hashed by default if `pure=True` or is generated randomly if `pure=False` (default). To explicitly set the name, you can use the `name` keyword:

```
>>> a = delayed([1, 2, 3], name='mylist')
>>> a
Delayed('mylist')
```

Delayed results act as a proxy to the underlying object. Many operators are supported:

```
>>> (a + [1, 2]).compute()
[1, 2, 3, 1, 2]
>>> a[1].compute()
2
```

Method and attribute access also works:

```
>>> a.count(2).compute()
1
```

Note that if a method doesn't exist, no error will be thrown until runtime:

```
>>> res = a.not_a_real_method()
>>> res.compute()
AttributeError("'list' object has no attribute 'not_a_real_method'")
```

"Magic" methods (e.g. operators and attribute access) are assumed to be pure, meaning that subsequent calls must return the same results. This behavior is not overrideable through the `delayed` call, but can be modified using other ways as described below.

To invoke an impure attribute or operator, you'd need to use it in a delayed function with `pure=False`:

```
>>> class Incrementer(object):
...     def __init__(self):
...         self._n = 0
...     @property
...     def n(self):
...         self._n += 1
...         return self._n
...
>>> x = delayed(Incrementer())
>>> x.n.key == x.n.key
True
>>> get_n = delayed(lambda x: x.n, pure=False)
>>> get_n(x).key == get_n(x).key
False
```

In contrast, methods are assumed to be impure by default, meaning that subsequent calls may return different results. To assume purity, set *pure=True*. This allows sharing of any intermediate values.

```
>>> a.count(2, pure=True).key == a.count(2, pure=True).key
True
```

As with function calls, method calls also respect the global `delayed_pure` setting and support the `dask_key_name` keyword:

```
>>> a.count(2, dask_key_name="count_2")
Delayed('count_2')
>>> with dask.config.set(delayed_pure=True):
...     print(a.count(2).key == a.count(2).key)
True
```

4.10.2 Working with Collections

Often we want to do a bit of custom work with `dask.delayed` (for example for complex data ingest), then leverage the algorithms in `dask.array` or `dask.dataframe`, and then switch back to custom work. To this end, all collections support `from_delayed` functions and `to_delayed` methods.

As an example, consider the case where we store tabular data in a custom format not known by `dask.dataframe`. This format is naturally broken apart into pieces and we have a function that reads one piece into a Pandas DataFrame. We use `dask.delayed` to lazily read these files into Pandas DataFrames, use `dd.from_delayed` to wrap these pieces up into a single `dask.dataframe`, use the complex algorithms within `dask.dataframe` (groupby, join, etc..) and then switch back to delayed to save our results back to the custom format.

```
import dask.dataframe as dd
from dask.delayed import delayed

from my_custom_library import load, save

filenames = ...
dfs = [delayed(load)(fn) for fn in filenames]

df = dd.from_delayed(dfs)
df = ... # do work with dask.dataframe

dfs = df.to_delayed()
writes = [delayed(save)(df, fn) for df, fn in zip(dfs, filenames)]

dd.compute(*writes)
```

Data science is often complex, `dask.delayed` provides a release valve for users to manage this complexity on their own, and solve the last mile problem for custom formats and complex situations.

4.10.3 Best Practices

It is easy to get started with Dask delayed, but using it *well* does require some experience. This page contains suggestions for best practices, and includes solutions to common problems:

Call delayed on the function, not the result

Dask.delayed operates on functions, like `dask.delayed(f)(x, y)`, not on their results like `dask.delayed(f(x, y))`. When you do the latter Python first calculates `f(x, y)` before Dask has a chance to step in

Don't

```
dask.delayed(f(x, y))
```

Do

```
dask.delayed(f)(x, y)
```

Compute on lots of computation at once

To improve parallelism you want to include lots of computation in each compute call. Ideally you want to make many dask.delayed calls to define your computation and then only call `dask.compute` at the end. It's ok to call `dask.compute` in the middle of your computation as well, but everything will stop there as Dask computes those results before moving forward with your code.

Don't

```
for x in L:
    y = dask.delayed(f)(x)
    y.compute()  # calling compute after every delayed call stops parallelism
```

Do

```
results = []
for x in L:
    y = dask.delayed(f)(x)
    results.append(y)

results = dask.compute(*results)  # call compute after you have collected many␣
↪delayed calls
```

Don't mutate inputs

Your functions should not change the inputs directly

Don't

```
@dask.delayed
def f(x):
    x += 1
    return x
```

Do

```
@dask.delayed
def f(x):
    return x + 1
```

If you need to use a mutable operation then make a copy within your function first

```
@dask.delayed
def f(x):
    x = copy(x)
    x += 1
    return x
```

Avoid global state

Ideally your operations shouldn't rely on global state. Using global state *might* work if you only use threads, but when you move to multiprocessing or distributed computing then you will likely encounter confusing errors

Don't

```
L = []

@dask.delayed
def f(x):
    L.append(x)
```

Don't rely on side effects

Delayed functions only do something if they are computed. You will always need to pass the output to something that eventually calls compute.

Don't

```
dask.delayed(f)(1, 2, 3)  # this has no effect
```

Do

```
x = dask.delayed(f)(1, 2, 3)
...
dask.compute(x, ...)  # need to call compute for something to happen
```

Break up computations into many pieces

Every dask.delayed function call is a single operation from Dask's perspective. You achieve parallelism by having many dask.delayed calls, not by using only a single one. Dask will not look inside a function decorated with dask.delayed and parallelize that code internally. It needs your help to find good places to break up a computation.

Don't

```
def load(filename):
    ...

def process(data):
    ...

def save(data):
    ...

@dask.delayed
def f(filenames):
    results = []
    for filename in filenames:
        data = load(filename)
        data = process(data)
        result = save(data)

    return results

dask.compute(f(filenames))  # this is only a single task
```

Do

```
@dask.delayed
def load(filename):
    ...

@dask.delayed
def process(data):
    ...

@dask.delayed
def save(data):
    ...

def f(filenames):
    results = []
    for filename in filenames:
        data = load(filename)
        data = process(data)
```

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```
        result = save(data)

    return results

dask.compute(f(filenames))  # this has many tasks and so will parallelize
```

Avoid too many tasks

Every delayed task has an overhead of a few hundred microseconds. Usually this is ok, but it can become a problem if you apply dask.delayed too finely. In this case it's often best to break up your many tasks into batches, or use one of the dask collections to help you.

Don't

```
results = []
for x in range(1000000000):  # Too many dask.delayed calls
    y = dask.delayed(f)(x)
    results.append(y)
```

Do

```
# Use collections

import dask.bag as db
b = db.from_sequence(1000000000, npartitions=1000)
b = b.map(f)
```

```
# Or batch manually

def batch(seq):
    sub_results = []
    for x in seq:
        result = f(x)
        sub_results.append(result)
    return sub_results

batches = []
for i in range(0, 1000000000, 1000000):  # in steps of 1000000
    result_batch = dask.delayed(batch, range(i, i + 1000000))
    batches.append(result_batch)
```

Avoid calling delayed within delayed functions

Often if you are new to using Dask.delayed you place dask.delayed calls everywhere and hope for the best. While this may actually work it's usually slow and results in hard-to-understand solutions.

Usually you never call dask.delayed within dask.delayed functions.

Don't

```
@dask.delayed
def process_all(L):
    result = []
    for x in L:
```

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```
        y = dask.delayed(f)(x)
        result.append(y)
    return result
```

Do

Instead, because this function only does delayed work it is very fast and so there is no reason to delay it.

```
def process_all(L):
    result = []
    for x in L:
        y = dask.delayed(f)(x)
        result.append(y)
    return result
```

Don't call dask.delayed on other Dask collections

When you place a dask array or dask dataframe into a delayed call that function will receive the Numpy or Pandas equivalent. Beware that if your array is large then this might crash your workers.

Instead, it's more common to use methods like `da.map_blocks` or `df.map_partitions`, or to turn your arrays or dataframes into *many* delayed objects

Don't

```
import dask.dataframe as dd
df = dd.read_csv('/path/to/*.csv')

dask.delayed(train)(df)  # might as well have used Pandas instead
```

Do

```
import dask.dataframe as dd
df = dd.read_csv('/path/to/*.csv')

df.map_partitions(train)
# or
partitions = df.to_delayed()

delayed_values = [dask.delayed(train)(part) for part in partitions]
```

However, if you don't mind turning your dask array/dataframe into a single chunk then this is ok.

```
dask.delayed(train)(..., y=df.sum())
```

Avoid repeatedly putting large inputs into delayed calls

Every time you pass a concrete result (anything that isn't delayed) Dask will hash it by default to give it a name. This is fairly fast (around 500 MB/s) but can be slow if you do it over and over again. Instead, it is better to delay your data as well.

This is especially important when using a distributed cluster to avoid sending your data separately for each function call.

Don't

```
x = np.array(...)  # some large array

results = [dask.delayed(train)(x, i) for i in range(1000)]
```

Every call to `dask.delayed(train)(x, ...)` has to hash the numpy array `x`, which slows things down.

Do

```
x = np.array(...)  # some large array
x = dask.delayed(x)  # delay the data, hashing once

results = [dask.delayed(train)(x, i) for i in range(1000)]
```

Sometimes problems don't fit into one of the collections like `dask.array` or `dask.dataframe`. In these cases, users can parallelize custom algorithms using the simpler `dask.delayed` interface. This allows one to create graphs directly with a light annotation of normal python code.

```
>>> x = dask.delayed(inc)(1)
>>> y = dask.delayed(inc)(2)
>>> z = dask.delayed(add)(x, y)
>>> z.compute()
5
>>> z.vizualize()
```

4.10.4 Example

Sometimes we face problems that are parallelizable, but don't fit high-level abstractions Dask array or Dask dataframe. Consider the following example:

```
def inc(x):
    return x + 1

def double(x):
    return x + 2

def add(x, y):
    return x + y

data = [1, 2, 3, 4, 5]

output = []
for x in data:
    a = inc(x)
    b = double(x)
    c = add(a, b)
    output.append(c)

total = sum(output)
```

There is clearly parallelism in this problem (many of the `inc` and `double` and `add` functions can evaluate independently), but it's not clear how to convert this to a big array or big dataframe computation.

As written this code runs sequentially in a single thread. However we see that a lot of this could be executed in parallel.

The Dask `delayed` function decorates your functions so that they operate *lazily*. Rather than executing your function immediately it will defer execution, placing the function and its arguments into a task graph.

delayed	Wraps a function or object to produce a `Delayed`.

We slightly modify our code by wrapping functions in `delayed`. This delays the execution of the function and generates a dask graph instead.

```
import dask

output = []
for x in data:
    a = dask.delayed(inc)(x)
    b = dask.delayed(double)(x)
    c = dask.delayed(add)(a, b)
    output.append(c)

total = dask.delayed(sum)(output)
```

We used the `dask.delayed` function to wrap the function calls that we want to turn into tasks. None of the `inc`, `double`, `add` or `sum` calls have happened yet, instead the object `total` is a `Delayed` result that contains a task graph of the entire computation. Looking at the graph we see clear opportunities for parallel execution. The dask schedulers will exploit this parallelism, generally improving performance. (although not in this example, because these functions are already very small and fast.)

```
total.visualize()  # see image to the right
```

We can now compute this lazy result to execute the graph in parallel:

```
>>> total.compute()
45
```

4.10.5 Decorator

It is also common to see the delayed function used as a decorator. Here is a reproduction of our original problem as a parallel code.

```
import dask

@dask.delayed
def inc(x):
    return x + 1

@dask.delayed
def double(x):
    return x + 2

@dask.delayed
def add(x, y):
    return x + y

data = [1, 2, 3, 4, 5]
```

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```
output = []
for x in data:
    a = inc(x)
    b = double(x)
    c = add(a, b)
    output.append(c)

total = dask.delayed(sum)(output)
```

4.10.6 Real time

Sometimes you want to create and destroy work during execution, launch tasks from other tasks, etc.. For this, see the *Futures* interface.

4.10.7 Best Practices

For a list of common problems and recommendations see *Delayed Best Practices*

4.11 Futures

Dask supports a real-time task framework that extends Python's concurrent.futures interface. This interface is good for arbitrary task scheduling, like *dask.delayed*, but is immediate rather than lazy, which provides some more flexibility in situations where the computations may evolve over time.

These features depend on the second generation task scheduler found in dask.distributed (which, despite its name, runs very well on a single machine).

4.11.1 Start Dask Client

You must start a `Client` to use the futures interface. This tracks state among the various worker processes or threads.

```
from dask.distributed import Client

client = Client()  # start local workers as processes
# or
client = Client(processes=False)  # start local workers as threads
```

If you have Bokeh installed then this starts up a diagnostic dashboard at http://localhost:8787 .

4.11.2 Submit Tasks

Client.submit(func, *args, **kwargs)	Submit a function application to the scheduler
Client.map(func, *iterables, **kwargs)	Map a function on a sequence of arguments
Future.result([timeout])	Wait until computation completes, gather result to local process.

Then you can submit individual tasks using the `submit` method.

```
def inc(x):
    return x + 1

def add(x, y):
    return x + y

a = client.submit(inc, 10)  # calls inc(10) in background thread or process
b = client.submit(inc, 20)  # calls inc(20) in background thread or process
```

Submit returns a `Future`, which refers to a remote result. This result may not yet be completed:

```
>>> a
<Future: status: pending, key: inc-b8aaf26b99466a7a1980efa1ade6701d>
```

Eventually it will complete. The result stays in the remote thread/process/worker until you ask for it back explicitly.

```
>>> a
<Future: status: finished, type: int, key: inc-b8aaf26b99466a7a1980efa1ade6701d>

>>> a.result()  # blocks until task completes and data arrives
11
```

You can pass futures as inputs to submit. Dask automatically handles dependency tracking; once all input futures have completed they will be moved onto a single worker (if necessary), and then the computation that depends on them will be started. You do not need to wait for inputs to finish before submitting a new task; Dask will handle this automatically.

```
c = client.submit(add, a, b)  # calls add on the results of a and b
```

Similar to Python's `map` you can use `Client.map` to call the same function and many inputs:

```
futures = client.map(inc, range(1000))
```

However note that each task comes with about 1ms of overhead. If you want to map a function over a large number of inputs then you might consider *dask.bag* or *dask.dataframe* instead.

4.11.3 Move Data

Future.result([timeout])	Wait until computation completes, gather result to local process.
Client.gather(futures[, errors, maxsize, ...])	Gather futures from distributed memory
Client.scatter(data[, workers, broadcast, ...])	Scatter data into distributed memory

Given any future you can call the `.result` method to gather the result. This will block until the future is done computing and then transfer the result back to your local process if necessary.

```
>>> c.result()
32
```

You can gather many results concurrently using the `Client.gather` method. This can be more efficient than calling `.result()` on each future sequentially.

```
>>> # results = [future.result() for future in futures]
>>> results = client.gather(futures)  # this can be faster
```

If you have important local data that you want to include in your computation you can either include it as a normal input to a submit or map call:

```
>>> df = pd.read_csv('training-data.csv')
>>> future = client.submit(my_function, df)
```

Or you can `scatter` it explicitly. Scattering moves your data to a worker and returns a future pointing to that data:

```
>>> remote_df = client.scatter(df)
>>> remote_df
<Future: status: finished, type: DataFrame, key: bbd0ca93589c56ea14af49cba470006e>

>>> future = client.submit(my_function, remote_df)
```

Both of these accomplish the same result, but using scatter can sometimes be faster. This is especially true if you use processes or distributed workers (where data transfer is necessary) and you want to use `df` in many computations. Scattering the data beforehand avoids excessive data movement.

Calling scatter on a list scatters all elements individually. Dask will spread these elements evenly throughout workers in a round-robin fashion:

```
>>> client.scatter([1, 2, 3])
[<Future: status: finished, type: int, key: c0a8a20f903a4915b94db8de3ea63195>,
 <Future: status: finished, type: int, key: 58e78e1b34eb49a68c65b54815d1b158>,
 <Future: status: finished, type: int, key: d3395e15f605bc35ab1bac6341a285e2>]
```

4.11.4 References, Cancellation, and Exceptions

Future.cancel(**kwargs)	Cancel request to run this future
Future.exception([timeout])	Return the exception of a failed task
Future.traceback([timeout])	Return the traceback of a failed task
Client.cancel(futures[, asynchronous, force])	Cancel running futures

Dask will only compute and hold onto results for which there are active futures. In this way your local variables define what is active in Dask. When a future is garbage collected by your local Python session, Dask will feel free to delete that data or stop ongoing computations that were trying to produce it.

```
>>> del future  # deletes remote data once future is garbage collected
```

You can also explicitly cancel a task using the `Future.cancel` or `Client.cancel` methods.

```
>>> future.cancel()  # deletes data even if other futures point to it
```

If a future fails, then Dask will raise the remote exceptions and tracebacks if you try to get the result.

```
def div(x, y):
    return x / y

>>> a = client.submit(div, 1, 0)  # 1 / 0 raises a ZeroDivisionError
>>> a
<Future: status: error, key: div-3601743182196fb56339e584a2bf1039>

>>> a.result()
      1 def div(x, y):
```

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```
----> 2     return x / y

ZeroDivisionError: division by zero
```

All futures that depend on an erred future also err with the same exception:

```
>>> b = client.submit(inc, a)
>>> b
<Future: status: error, key: inc-15e2e4450a0227fa38ede4d6b1a952db>
```

You can collect the exception or traceback explicitly with the `Future.exception` or `Future.traceback` methods.

4.11.5 Waiting on Futures

as_completed([futures, loop, with_results, ...])	Return futures in the order in which they complete
wait(fs[, timeout, return_when])	Wait until all futures are complete

You can wait on a future or collection of futures using the `wait` function:

```
from dask.distributed import wait

>>> wait(futures)
```

This blocks until all futures are finished or have erred.

You can also iterate over the futures as they complete using the `as_completed` function:

```
from dask.distributed import as_completed

futures = client.map(score, x_values)

best = -1
for future in as_completed(futures):
   y = future.result()
   if y > best:
       best = y
```

For greater efficiency you can also ask `as_completed` to gather the results in the background.

```
for future, result in as_completed(futures, with_results=True):
    # y = future.result()  # don't need this
   ...
```

Or collect futures all futures in batches that had arrived since the last iteration

```
for batch in as_completed(futures, with_results=True).batches():
   for future, result in batch:
       ...
```

Additionally, for iterative algorithms you can add more futures into the `as_completed` iterator *during* iteration.

```
seq = as_completed(futures)
```

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```
for future in seq:
    y = future.result()
    if condition(y):
        new_future = client.submit(...)
        seq.add(new_future)  # add back into the loop
```

4.11.6 Fire and Forget

fire_and_forget(obj)	Run tasks at least once, even if we release the futures

Sometimes we don't care about gathering the result of a task, and only care about side effects that it might have, like writing a result to a file.

```
>>> a = client.submit(load, filename)
>>> b = client.submit(process, a)
>>> c = client.submit(write, c, out_filename)
```

As noted above, Dask will stop work that doesn't have any active futures. It thinks that because no one has a pointer to this data that no one cares. You can tell Dask to compute a task anyway, even if there are no active futures, using the `fire_and_forget` function:

```
from dask.distributed import fire_and_forget

>>> fire_and_forget(c)
```

This is particularly useful when a future may go out of scope, for example as part of a function:

```
def process(filename):
    out_filename = 'out-' + filename
    a = client.submit(load, filename)
    b = client.submit(process, a)
    c = client.submit(write, c, out_filename)
    fire_and_forget(c)
    return  # here we lose the reference to c, but that's now ok

for filename in filenames:
    process(filename)
```

4.11.7 Submit Tasks from Tasks

get_client([address, timeout, resolve_address])	Get a client while within a task.
rejoin()	Have this thread rejoin the ThreadPoolExecutor
secede()	Have this task secede from the worker's thread pool

This is an advanced feature and is rarely necessary in the common case.

Tasks can launch other tasks by getting their own client. This enables complex and highly dynamic workloads.

```
from dask.distributed import get_client
```

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```
def my_function(x):
    ...

    # Get locally created client
    client = get_client()

    # Do normal client operations, asking cluster for computation
    a = client.submit(...)
    b = client.submit(...)
    a, b = client.gather([a, b])

    return a + b
```

It also allows you to set up long running tasks that watch other resources like sockets or physical sensors:

```
def monitor(device):
   client = get_client()
   while True:
       data = device.read_data()
       future = client.submit(process, data)
       fire_and_forget(future)

for device in devices:
    fire_and_forget(client.submit(monitor))
```

However, each running task takes up a single thread, and so if you launch many tasks that launch other tasks then it is possible to deadlock the system if you are not careful. You can call the `secede` function from within a task to have it remove itself from the dedicated thread pool into an administrative thread that does not take up a slot within the Dask worker:

```
from dask.distributed import get_client, secede

def monitor(device):
   client = get_client()
   secede()  # remove this task from the thread pool
   while True:
       data = device.read_data()
       future = client.submit(process, data)
       fire_and_forget(future)
```

If you intend to do more work in the same thread after waiting on client work, you may want to explicitly block until the thread is able to *rejoin* the thread pool. This allows some control over the number of threads that are created and stops too many threads from being active at once, over-saturating your hardware.

```
def f(n):  # assume that this runs as a task
   client = get_client()

   secede()  # secede while we wait for results to come back
   futures = client.map(func, range(n))
   results = client.gather(futures)

   rejoin()  # block until a slot is open in the thread pool
   result = analyze(results)
   return result
```

Alternatively, you can just use the normal `dask.compute` function *within* a task. This will automatically call `secede` and `rejoin` appropriately.

```
def f(name, fn):
    df = dd.read_csv(fn)  # note that this is a dask collection
    result = df[df.name == name].count()

    # This calls secede
    # Then runs the computation on the cluster (including this worker)
    # Then blocks on rejoin, and finally delivers the answer
    result = result.compute()

    return result
```

4.11.8 Coordination Primitives

Queue([name, client, maxsize])	Distributed Queue
Variable([name, client, maxsize])	Distributed Global Variable
Lock([name, client])	Distributed Centralized Lock
Pub(name[, worker, client])	Publish data with Publish-Subscribe pattern
Sub(name[, worker, client])	Subscribe to a Publish/Subscribe topic

Sometimes situations arise where tasks, workers, or clients need to coordinate with each other in ways beyond normal task scheduling with futures. In these cases Dask provides additional primitives to help in complex situations.

Dask provides distributed versions of coordination primitives like locks, queues, global variables, and pub-sub systems that, where appropriate, match their in-memory counterparts. These can be used to control access to external resources, track progress of ongoing computations, or share data in side-channels between many workers, clients, and tasks sensibly.

These features are rarely necessary for common use of Dask. We recommend that beginning users stick with using the simpler futures found above (like `Client.submit` and `Client.gather`) rather than embracing needlessly complex techniques.

Queues

Queue([name, client, maxsize])	Distributed Queue

Dask queues follow the API for the standard Python Queue, but now move futures or small messages between clients. Queues serialize sensibly and reconnect themselves on remote clients if necessary.

```
from dask.distributed import Queue

def load_and_submit(filename):
    data = load(filename)
    client = get_client()
    future = client.submit(process, data)
    queue.put(future)

client = Client()

queue = Queue()

for filename in filenames:
    future = client.submit(load_and_submit, filename)
```

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```
    fire_and_forget(filename)

while True:
    future = queue.get()
    print(future.result())
```

Queues can also send small pieces of information, anything that is msgpack encodable (ints, strings, bools, lists, dicts, etc..). This can be useful to send back small scores or administrative messages:

```
def func(x):
    try:
        ...
    except Exception as e:
        error_queue.put(str(e))

error_queue = Queue()
```

Queues are mediated by the central scheduler, and so they are not ideal for sending large amounts of data (everything you send will be routed through a central point). They are well suited to move around small bits of metadata, or futures. These futures may point to much larger pieces of data safely.

```
>>> x = ... # my large numpy array

# Don't do this!
>>> q.put(x)

# Do this instead
>>> future = client.scatter(x)
>>> q.put(future)

# Or use futures for metadata
>>> q.put({'status': 'OK', 'stage=': 1234})
```

If you're looking to move large amounts of data between workers then you might also want to consider the Pub/Sub system described a few sections below.

Global Variables

Variable([name, client, maxsize])	Distributed Global Variable

Variables are like Queues in that they communicate futures and small data between clients. However variables hold only a single value. You can get or set that value at any time.

```
>>> var = Variable('stopping-criterion')
>>> var.set(False)

>>> var.get()
False
```

This is often used to signal stopping criteria or current parameters, etc. between clients.

If you want to share large pieces of information then scatter the data first

```
>>> parameters = np.array(...)
>>> future = client.scatter(parameters)
>>> var.set(future)
```

Locks

Lock([name, client])	Distributed Centralized Lock

You can also hold onto cluster-wide locks using the `Lock` object. Dask Locks have the same API as normal `threading.Lock` objects, except that they work across the cluster:

```
from dask.distributed import Lock
lock = Lock()

with lock:
    # access protected resource
```

You can manage several locks at the same time. Lock can either be given a consistent name, or you can pass the lock object around itself.

Using a consistent name is convenient when you want to lock some known named resource.

```
from dask.distributed import Lock

def load(fn):
    with Lock('the-production-database'):
        # read data from filename using some sensitive source
        return ...

futures = client.map(load, filenames)
```

Passing around a lock works as well, and is easier when you want to create short-term locks for a particular situation.

```
from dask.distributed import Lock
lock = Lock()

def load(fn, lock=None):
    with lock:
        # read data from filename using some sensitive source
        return ...

futures = client.map(load, filenames, lock=lock)
```

This can be useful if you want to control concurrent access to some external resource like a database or un-thread-safe library.

Publish-Subscribe

Pub(name[, worker, client])	Publish data with Publish-Subscribe pattern
Sub(name[, worker, client])	Subscribe to a Publish/Subscribe topic

Dask implements the Publish Subscribe pattern, providing an additional channel of communication between ongoing tasks.

class distributed.**Pub**(*name*, *worker=None*, *client=None*)

Publish data with Publish-Subscribe pattern

This allows clients and workers to directly communicate data between each other with a typical Publish-Subscribe pattern. This involves two components,

Pub objects, into which we put data:

```
>>> pub = Pub('my-topic')
>>> pub.put(123)
```

And Sub objects, from which we collect data:

```
>>> sub = Sub('my-topic')
>>> sub.get()
123
```

Many Pub and Sub objects can exist for the same topic. All data sent from any Pub will be sent to all Sub objects on that topic that are currently connected. Pub's and Sub's find each other using the scheduler, but they communicate directly with each other without coordination from the scheduler.

Pubs and Subs use the central scheduler to find each other, but not to mediate the communication. This means that there is very little additional latency or overhead, and they are appropriate for very frequent data transfers. For context, most data transfer first checks with the scheduler to find which workers should participate, and then does direct worker-to-worker transfers. This checking in with the scheduler provides some stability guarnatees, but also adds in a few extra network hops. PubSub doesn't do this, and so is faster, but also can easily drop messages if Pubs or Subs disappear without notice.

When using a Pub or Sub from a Client all communications will be routed through the scheduler. This can cause some performance degredation. Pubs an Subs only operate at top-speed when they are both on workers.

Parameters

name: object (msgpack serializable) The name of the group of Pubs and Subs on which to participate

See also:

Sub

Examples

```
>>> pub = Pub('my-topic')
>>> sub = Sub('my-topic')
>>> pub.put([1, 2, 3])
>>> sub.get()
[1, 2, 3]
```

You can also use sub within a for loop:

```
>>> for msg in sub:
...     print(msg)
```

or an async for loop

```
>>> async for msg in sub:
...     print(msg)
```

Similarly the `.get` method will return an awaitable if used by an async client or within the IOLoop thread of a worker

```
>>> await sub.get()
```

You can see the set of connected worker subscribers by looking at the `.subscribers` attribute:

```
>>> pub.subscribers
{'tcp://...': {},
 'tcp://...': {}}
```

put(*msg*)
Publish a message to all subscribers of this topic

4.11.9 Actors

Actors allow workers to manage rapidly changing state without coordinating with the central scheduler. This has the advantage of reducing latency (worker-to-worker roundtrip latency is around 1ms), reducing pressure on the centralized scheduler (workers can coordinate actors entirely among each other) and also enabling workflows that require stateful or in-place memory manipulation.

However, these benefits come at a cost. The scheduler is unaware of actors and so they don't benefit from diagnostics, load balancing, or resilience. Once an actor is running on a worker it is forever tied to that worker. If that worker becomes overburdened or dies then there is not opportunity to recover the workload.

Because Actors avoid the central scheduler they can be high-performing, but not resilient.

Example: Counter

An actor is a class containing both state and methods that is submitted to a worker.

```
class Counter:
    n = 0

    def __init__(self):
        self.n = 0

    def increment(self):
        self.n += 1
        return self.n

from dask.distributed import Client
client = Client()

future = client.submit(Counter, actor=True)
counter = future.result()

>>> counter
<Actor: Counter, key=Counter-afa1cdfb6b4761e616fa2cfab42398c8>
```

Method calls on this object produce `ActorFutures`, which are similar to normal Futures, but interact only with the worker holding the Actor:

```
>>> future = counter.increment()
>>> future
```

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```
<ActorFuture>

>>> future.result()
1
```

Attribute access is synchronous and blocking:

```
>>> counter.n
1
```

Example: Parameter Server

```
import numpy as np

from dask.distributed import Client
client = Client(processes=False)

class ParameterServer:
    def __init__(self):
        self.data = dict()

    def put(self, key, value):
        self.data[key] = value

    def get(self, key):
        return self.data[key]

ps_future = client.submit(ParameterServer, actor=True)
ps = ps_future.result()

ps.put('parameters', np.random.random(1000))

def train(batch, ps):
    params = ps.get('parameters')

for batch in batches:
```

Asynchronous Operation

All operations that require talking to the remote worker are awaitable

```
async def f():
    future = client.submit(Counter, actor=True)
    counter = await future  # gather actor object locally

    counter.increment()  # send off a request asynchronously
    await counter.increment()  # or wait until it was received

    n = await counter.n  # attribute access also must be awaited
```

Usually Dask computations are composed of tasks that build off of each other in a pure functional way. They're centrally manathat are managed by the central scheduler and

Because tasks are assumed to be pure (they don't change their inputs) and are known and coordinated by the central scheduler they are safe and

4.11.10 API

Client

Client([address, loop, timeout, ...])	Connect to and drive computation on a distributed Dask cluster
Client.cancel(futures[, asynchronous, force])	Cancel running futures
Client.compute(collections[, sync, ...])	Compute dask collections on cluster
Client.gather(futures[, errors, maxsize, ...])	Gather futures from distributed memory
Client.get(dsk, keys[, restrictions, ...])	Compute dask graph
Client.get_dataset(name, **kwargs)	Get named dataset from the scheduler
Client.get_executor(**kwargs)	Return a concurrent.futures Executor for submitting tasks on this Client
Client.has_what([workers])	Which keys are held by which workers
Client.list_datasets(**kwargs)	List named datasets available on the scheduler
Client.map(func, *iterables, **kwargs)	Map a function on a sequence of arguments
Client.ncores([workers])	The number of threads/cores available on each worker node
Client.persist(collections[, ...])	Persist dask collections on cluster
Client.publish_dataset(*args, **kwargs)	Publish named datasets to scheduler
Client.rebalance([futures, workers])	Rebalance data within network
Client.replicate(futures[, n, workers, ...])	Set replication of futures within network
Client.restart(**kwargs)	Restart the distributed network
Client.run(function, *args, **kwargs)	Run a function on all workers outside of task scheduling system
Client.run_on_scheduler(function, *args, ...)	Run a function on the scheduler process
Client.scatter(data[, workers, broadcast, ...])	Scatter data into distributed memory
Client.shutdown(*args, **kwargs)	Deprecated, see close instead
Client.scheduler_info(**kwargs)	Basic information about the workers in the cluster
Client.shutdown(*args, **kwargs)	Deprecated, see close instead
Client.start_ipython_workers([workers, ...])	Start IPython kernels on workers
Client.start_ipython_scheduler([magic_name, ...])	Start IPython kernel on the scheduler
Client.submit(func, *args, **kwargs)	Submit a function application to the scheduler
Client.unpublish_dataset(name, **kwargs)	Remove named datasets from scheduler
Client.upload_file(filename, **kwargs)	Upload local package to workers
Client.who_has([futures])	The workers storing each future's data

Future

Future(key[, client, inform, state])	A remotely running computation
Future.add_done_callback(fn)	Call callback on future when callback has finished
Future.cancel(**kwargs)	Cancel request to run this future
Future.cancelled()	Returns True if the future has been cancelled
Future.done()	Is the computation complete?
Future.exception([timeout])	Return the exception of a failed task

Continued on next page

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Future.result([timeout])	Wait until computation completes, gather result to local process.
Future.traceback([timeout])	Return the traceback of a failed task

Functions

as_completed([futures, loop, with_results, ...])	Return futures in the order in which they complete
fire_and_forget(obj)	Run tasks at least once, even if we release the futures
get_client([address, timeout, resolve_address])	Get a client while within a task.
secede()	Have this task secede from the worker's thread pool
rejoin()	Have this thread rejoin the ThreadPoolExecutor
wait(fs[, timeout, return_when])	Wait until all futures are complete

distributed.**as_completed**(*futures=None*, *loop=None*, *with_results=False*, *raise_errors=True*)

Return futures in the order in which they complete

This returns an iterator that yields the input future objects in the order in which they complete. Calling `next` on the iterator will block until the next future completes, irrespective of order.

Additionally, you can also add more futures to this object during computation with the `.add` method

Parameters

futures: Collection of futures A list of Future objects to be iterated over in the order in which they complete

with_results: bool (False) Whether to wait and include results of futures as well; in this case *as_completed* yields a tuple of (future, result)

raise_errors: bool (True) Whether we should raise when the result of a future raises an exception; only affects behavior when *with_results=True*.

Examples

```
>>> x, y, z = client.map(inc, [1, 2, 3])
>>> for future in as_completed([x, y, z]):
...     print(future.result())
3
2
4
```

Add more futures during computation

```
>>> x, y, z = client.map(inc, [1, 2, 3])
>>> ac = as_completed([x, y, z])
>>> for future in ac:
...     print(future.result())
...     if random.random() < 0.5:
...         ac.add(c.submit(double, future))
4
2
8
3
6
```

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```
12
24
```

Optionally wait until the result has been gathered as well

```
>>> ac = as_completed([x, y, z], with_results=True)
>>> for future, result in ac:
...     print(result)
2
4
3
```

distributed.**fire_and_forget**(*obj*)

Run tasks at least once, even if we release the futures

Under normal operation Dask will not run any tasks for which there is not an active future (this avoids unnecessary work in many situations). However sometimes you want to just fire off a task, not track its future, and expect it to finish eventually. You can use this function on a future or collection of futures to ask Dask to complete the task even if no active client is tracking it.

The results will not be kept in memory after the task completes (unless there is an active future) so this is only useful for tasks that depend on side effects.

Parameters

obj: Future, list, dict, dask collection The futures that you want to run at least once

Examples

```
>>> fire_and_forget(client.submit(func, *args))
```

distributed.**get_client**(*address=None*, *timeout=3*, *resolve_address=True*)

Get a client while within a task.

This client connects to the same scheduler to which the worker is connected

Parameters

address [str, optional] The address of the scheduler to connect to. Defaults to the scheduler the worker is connected to.

timeout [int, default 3] Timeout (in seconds) for getting the Client

resolve_address [bool, default True] Whether to resolve *address* to its canonical form.

Returns

Client

See also:

`get_worker`, `worker_client`, *secede*

Examples

```
>>> def f():
...     client = get_client()
...     futures = client.map(lambda x: x + 1, range(10))  # spawn many tasks
...     results = client.gather(futures)
...     return sum(results)
```

```
>>> future = client.submit(f)
>>> future.result()
55
```

distributed.**secede**()

Have this task secede from the worker's thread pool

This opens up a new scheduling slot and a new thread for a new task. This enables the client to schedule tasks on this node, which is especially useful while waiting for other jobs to finish (e.g., with `client.gather`).

See also:

get_client, get_worker

Examples

```
>>> def mytask(x):
...     # do some work
...     client = get_client()
...     futures = client.map(...)  # do some remote work
...     secede()  # while that work happens, remove ourself from the pool
...     return client.gather(futures)  # return gathered results
```

distributed.**rejoin**()

Have this thread rejoin the ThreadPoolExecutor

This will block until a new slot opens up in the executor. The next thread to finish a task will leave the pool to allow this one to join.

See also:

secede leave the thread pool

distributed.**wait**(*fs*, *timeout=None*, *return_when='ALL_COMPLETED'*)

Wait until all futures are complete

Parameters

fs: list of futures

timeout: number, optional Time in seconds after which to raise a `dask.distributed.TimeoutError`

———-

Named tuple of completed, not completed

class distributed.**Client**(*address=None, loop=None, timeout='__no_default__', set_as_default=True, scheduler_file=None, security=None, asynchronous=False, name=None, heartbeat_interval=None, serializers=None, deserializers=None, extensions=[<class 'distributed.pubsub.PubSubClientExtension'>], direct_to_workers=False, **kwargs*)

Connect to and drive computation on a distributed Dask cluster

The Client connects users to a dask.distributed compute cluster. It provides an asynchronous user interface around functions and futures. This class resembles executors in `concurrent.futures` but also allows `Future` objects within `submit/map` calls.

Parameters

address: string, or Cluster This can be the address of a `Scheduler` server like a string `'127.0.0.1:8786'` or a cluster object like `LocalCluster()`

timeout: int Timeout duration for initial connection to the scheduler

set_as_default: bool (True) Claim this scheduler as the global dask scheduler

scheduler_file: string (optional) Path to a file with scheduler information if available

security: (optional) Optional security information

asynchronous: bool (False by default) Set to True if using this client within async/await functions or within Tornado gen.coroutines. Otherwise this should remain False for normal use.

name: string (optional) Gives the client a name that will be included in logs generated on the scheduler for matters relating to this client

direct_to_workers: bool (optional) Can this client connect directly to workers or should it proxy through the scheduler?

heartbeat_interval: int Time in milliseconds between heartbeats to scheduler

See also:

`distributed.scheduler.Scheduler` Internal scheduler

Examples

Provide cluster's scheduler node address on initialization:

```
>>> client = Client('127.0.0.1:8786')
```

Use `submit` method to send individual computations to the cluster

```
>>> a = client.submit(add, 1, 2)
>>> b = client.submit(add, 10, 20)
```

Continue using submit or map on results to build up larger computations

```
>>> c = client.submit(add, a, b)
```

Gather results with the `gather` method.

```
>>> client.gather(c)
33
```

`asynchronous`

Are we running in the event loop?

This is true if the user signaled that we might be when creating the client as in the following:

```
client = Client(asynchronous=True)
```

However, we override this expectation if we can definitively tell that we are running from a thread that is not the event loop. This is common when calling get_client() from within a worker task. Even though the client was originally created in asynchronous mode we may find ourselves in contexts when it is better to operate synchronously.

call_stack (*futures=None*, *keys=None*)
The actively running call stack of all relevant keys

You can specify data of interest either by providing futures or collections in the `futures=` keyword or a list of explicit keys in the `keys=` keyword. If neither are provided then all call stacks will be returned.

Parameters

futures: list (optional) List of futures, defaults to all data

keys: list (optional) List of key names, defaults to all data

Examples

```
>>> df = dd.read_parquet(...).persist()
>>> client.call_stack(df)  # call on collections
```

```
>>> client.call_stack()  # Or call with no arguments for all activity
```

cancel (*futures*, *asynchronous=None*, *force=False*)
Cancel running futures

This stops future tasks from being scheduled if they have not yet run and deletes them if they have already run. After calling, this result and all dependent results will no longer be accessible

Parameters

futures: list of Futures

force: boolean (False) Cancel this future even if other clients desire it

close (*timeout='__no_default__'*)
Close this client

Clients will also close automatically when your Python session ends

If you started a client without arguments like `Client()` then this will also close the local cluster that was started at the same time.

See also:

Client.restart

compute (*collections*, *sync=False*, *optimize_graph=True*, *workers=None*, *allow_other_workers=False*, *resources=None*, *retries=0*, *priority=0*, *fifo_timeout='60s'*, *actors=None*, ***kwargs*)
Compute dask collections on cluster

Parameters

collections: iterable of dask objects or single dask object Collections like dask.array or dataframe or dask.value objects

sync: bool (optional) Returns Futures if False (default) or concrete values if True

optimize_graph: bool Whether or not to optimize the underlying graphs

workers: str, list, dict Which workers can run which parts of the computation If a string a list then the output collections will run on the listed workers, but other sub-computations can run anywhere If a dict then keys should be (tuples of) collections and values should be addresses or lists.

allow_other_workers: bool, list If True then all restrictions in workers= are considered loose If a list then only the keys for the listed collections are loose

retries: int (default to 0) Number of allowed automatic retries if computing a result fails

priority: Number Optional prioritization of task. Zero is default. Higher priorities take precedence

fifo_timeout: timedelta str (defaults to '60s') Allowed amount of time between calls to consider the same priority

****kwargs:** Options to pass to the graph optimize calls

Returns

List of Futures if input is a sequence, or a single future otherwise

See also:

Client.get Normal synchronous dask.get function

Examples

```
>>> from dask import delayed
>>> from operator import add
>>> x = delayed(add)(1, 2)
>>> y = delayed(add)(x, x)
>>> xx, yy = client.compute([x, y])
>>> xx
<Future: status: finished, key: add-8f6e709446674bad78ea8aeecfee188e>
>>> xx.result()
3
>>> yy.result()
6
```

Also support single arguments

```
>>> xx = client.compute(x)
```

classmethod current()
Return global client if one exists, otherwise raise ValueError

gather(*futures*, *errors='raise'*, *maxsize=0*, *direct=None*, *asynchronous=None*)
Gather futures from distributed memory

Accepts a future, nested container of futures, iterator, or queue. The return type will match the input type.

Parameters

futures: Collection of futures This can be a possibly nested collection of Future objects. Collections can be lists, sets, iterators, queues or dictionaries

errors: string Either 'raise' or 'skip' if we should raise if a future has erred or skip its inclusion in the output collection

maxsize: int If the input is a queue then this produces an output queue with a maximum size.

Returns

results: a collection of the same type as the input, but now with

gathered results rather than futures

See also:

Client.scatter Send data out to cluster

Examples

```
>>> from operator import add
>>> c = Client('127.0.0.1:8787')
>>> x = c.submit(add, 1, 2)
>>> c.gather(x)
3
>>> c.gather([x, [x], x])  # support lists and dicts
[3, [3], 3]
```

```
>>> seq = c.gather(iter([x, x]))  # support iterators
>>> next(seq)
3
```

get(*dsk*, *keys*, *restrictions=None*, *loose_restrictions=None*, *resources=None*, *sync=True*, *asynchronous=None*, *direct=None*, *retries=None*, *priority=0*, *fifo_timeout='60s'*, ***kwargs*)
Compute dask graph

Parameters

dsk: dict

keys: object, or nested lists of objects

restrictions: dict (optional) A mapping of {key: {set of worker hostnames}} that restricts where jobs can take place

retries: int (default to 0) Number of allowed automatic retries if computing a result fails

priority: Number Optional prioritization of task. Zero is default. Higher priorities take precedence

sync: bool (optional) Returns Futures if False or concrete values if True (default).

direct: bool Gather results directly from workers

See also:

Client.compute Compute asynchronous collections

Examples

```
>>> from operator import add
>>> c = Client('127.0.0.1:8787')
>>> c.get({'x': (add, 1, 2)}, 'x')
3
```

get_dataset(*name*, ***kwargs*)
Get named dataset from the scheduler

See also:

Client.publish_dataset, *Client.list_datasets*

get_executor(***kwargs*)
Return a concurrent.futures Executor for submitting tasks on this Client

Parameters

****kwargs:** Any submit()- or map()- compatible arguments, such as *workers* or *resources*.

Returns

An Executor object that's fully compatible with the concurrent.futures

API.

get_metadata(*keys*, *default='__no_default__'*)
Get arbitrary metadata from scheduler

See set_metadata for the full docstring with examples

Parameters

keys: key or list Key to access. If a list then gets within a nested collection

default: optional If the key does not exist then return this value instead. If not provided then this raises a KeyError if the key is not present

See also:

Client.set_metadata

classmethod get_restrictions(*collections*, *workers*, *allow_other_workers*)
Get restrictions from inputs to compute/persist

get_scheduler_logs(*n=None*)
Get logs from scheduler

Parameters

n: int Number of logs to retrive. Maxes out at 10000 by default, confiruable in config.yaml::log-length

Returns

Logs in reversed order (newest first)

get_task_stream(*start=None*, *stop=None*, *count=None*, *plot=False*, *filename='task-stream.html'*)
Get task stream data from scheduler

This collects the data present in the diagnostic "Task Stream" plot on the dashboard. It includes the start, stop, transfer, and deserialization time of every task for a particular duration.

Note that the task stream diagnostic does not run by default. You may wish to call this function once before you start work to ensure that things start recording, and then again after you have completed.

Parameters

start: Number or string When you want to start recording If a number it should be the result of calling time() If a string then it should be a time difference before now, like '60s' or '500 ms'

stop: Number or string When you want to stop recording

count: int The number of desired records, ignored if both start and stop are specified

plot: boolean, str If true then also return a Bokeh figure If plot == 'save' then save the figure to a file

filename: str (optional) The filename to save to if you set `plot='save'`

Returns

L: List[Dict]

See also:

get_task_stream a context manager version of this method

Examples

```
>>> client.get_task_stream()  # prime plugin if not already connected
>>> x.compute()  # do some work
>>> client.get_task_stream()
[{'task': ...,
  'type': ...,
  'thread': ...,
  ...}]
```

Pass the `plot=True` or `plot='save'` keywords to get back a Bokeh figure

```
>>> data, figure = client.get_task_stream(plot='save', filename='myfile.html
↪')
```

Alternatively consider the context manager

```
>>> from dask.distributed import get_task_stream
>>> with get_task_stream() as ts:
...     x.compute()
>>> ts.data
[...]
```

get_versions(*check=False*, *packages=[]*)

Return version info for the scheduler, all workers and myself

Parameters

check [boolean, default False] raise ValueError if all required & optional packages do not match

packages [List[str]] Extra package names to check

Examples

```
>>> c.get_versions()
```

```
>>> c.get_versions(packages=['sklearn', 'geopandas'])
```

get_worker_logs(*n=None*, *workers=None*)

Get logs from workers

Parameters

n: int Number of logs to retrive. Maxes out at 10000 by default, confiruable in config.yaml::log-length

workers: iterable List of worker addresses to retrive. Gets all workers by default.

Returns

Dictionary mapping worker address to logs.

Logs are returned in reversed order (newest first)

has_what(*workers=None*, ***kwargs*)
Which keys are held by which workers

This returns the keys of the data that are held in each worker's memory.

Parameters

workers: list (optional) A list of worker addresses, defaults to all

See also:

Client.who_has, *Client.ncores*, *Client.processing*

Examples

```
>>> x, y, z = c.map(inc, [1, 2, 3])
>>> wait([x, y, z])
>>> c.has_what()
{'192.168.1.141:46784': ['inc-1c8dd6be1c21646c71f76c16d09304ea',
                         'inc-fd65c238a7ea60f6a01bf4c8a5fcf44b',
                         'inc-1e297fc27658d7b67b3a758f16bcf47a']}
```

list_datasets(***kwargs*)
List named datasets available on the scheduler

See also:

Client.publish_dataset, *Client.get_dataset*

map(*func*, **iterables*, ***kwargs*)
Map a function on a sequence of arguments

Arguments can be normal objects or Futures

Parameters

func: callable

iterables: Iterables, Iterators, or Queues

key: str, list Prefix for task names if string. Explicit names if list.

pure: bool (defaults to True) Whether or not the function is pure. Set `pure=False` for impure functions like `np.random.random`.

workers: set, iterable of sets A set of worker hostnames on which computations may be performed. Leave empty to default to all workers (common case)

retries: int (default to 0) Number of allowed automatic retries if a task fails

priority: Number Optional prioritization of task. Zero is default. Higher priorities take precedence

fifo_timeout: str timedelta (default '100ms') Allowed amount of time between calls to consider the same priority

****kwargs: dict** Extra keywords to send to the function. Large values will be included explicitly in the task graph.

Returns

List, iterator, or Queue of futures, depending on the type of the

inputs.

See also:

Client.submit Submit a single function

Examples

```
>>> L = client.map(func, sequence)
```

nbytes(*keys=None*, *summary=True*, ***kwargs*)
The bytes taken up by each key on the cluster

This is as measured by `sys.getsizeof` which may not accurately reflect the true cost.

Parameters

keys: list (optional) A list of keys, defaults to all keys

summary: boolean, (optional) Summarize keys into key types

See also:

Client.who_has

Examples

```
>>> x, y, z = c.map(inc, [1, 2, 3])
>>> c.nbytes(summary=False)
{'inc-1c8dd6be1c21646c71f76c16d09304ea': 28,
 'inc-1e297fc27658d7b67b3a758f16bcf47a': 28,
 'inc-fd65c238a7ea60f6a01bf4c8a5fcf44b': 28}
```

```
>>> c.nbytes(summary=True)
{'inc': 84}
```

ncores(*workers=None*, ***kwargs*)
The number of threads/cores available on each worker node

Parameters

workers: list (optional) A list of workers that we care about specifically. Leave empty to receive information about all workers.

See also:

Client.who_has, *Client.has_what*

Examples

```
>>> c.ncores()
{'192.168.1.141:46784': 8,
 '192.167.1.142:47548': 8,
 '192.167.1.143:47329': 8,
 '192.167.1.144:37297': 8}
```

normalize_collection(*collection*)

Replace collection's tasks by already existing futures if they exist

This normalizes the tasks within a collections task graph against the known futures within the scheduler. It returns a copy of the collection with a task graph that includes the overlapping futures.

See also:

Client.persist trigger computation of collection's tasks

Examples

```
>>> len(x.__dask_graph__())  # x is a dask collection with 100 tasks
100
>>> set(client.futures).intersection(x.__dask_graph__())  # some overlap␣
↪exists
10
```

```
>>> x = client.normalize_collection(x)
>>> len(x.__dask_graph__())  # smaller computational graph
20
```

persist(*collections*, *optimize_graph=True*, *workers=None*, *allow_other_workers=None*, *resources=None*, *retries=None*, *priority=0*, *fifo_timeout='60s'*, *actors=None*, ***kwargs*)

Persist dask collections on cluster

Starts computation of the collection on the cluster in the background. Provides a new dask collection that is semantically identical to the previous one, but now based off of futures currently in execution.

Parameters

collections: sequence or single dask object Collections like dask.array or dataframe or dask.value objects

optimize_graph: bool Whether or not to optimize the underlying graphs

workers: str, list, dict Which workers can run which parts of the computation If a string a list then the output collections will run on the listed workers, but other sub-computations can run anywhere If a dict then keys should be (tuples of) collections and values should be addresses or lists.

allow_other_workers: bool, list If True then all restrictions in workers= are considered loose If a list then only the keys for the listed collections are loose

retries: int (default to 0) Number of allowed automatic retries if computing a result fails

priority: Number Optional prioritization of task. Zero is default. Higher priorities take precedence

fifo_timeout: timedelta str (defaults to '60s') Allowed amount of time between calls to consider the same priority

kwargs: Options to pass to the graph optimize calls

Returns

List of collections, or single collection, depending on type of input.

See also:

Client.compute

Examples

```
>>> xx = client.persist(x)
>>> xx, yy = client.persist([x, y])
```

processing(*workers=None*)

The tasks currently running on each worker

Parameters

workers: list (optional) A list of worker addresses, defaults to all

See also:

Client.who_has, *Client.has_what*, *Client.ncores*

Examples

```
>>> x, y, z = c.map(inc, [1, 2, 3])
>>> c.processing()
{'192.168.1.141:46784': ['inc-1c8dd6be1c21646c71f76c16d09304ea',
                         'inc-fd65c238a7ea60f6a01bf4c8a5fcf44b',
                         'inc-1e297fc27658d7b67b3a758f16bcf47a']}
```

profile(*key=None*, *start=None*, *stop=None*, *workers=None*, *merge_workers=True*)

Collect statistical profiling information about recent work

Parameters

key: str Key prefix to select, this is typically a function name like 'inc' Leave as None to collect all data

start: time

stop: time

workers: list List of workers to restrict profile information

Examples

```
>>> client.profile()  # call on collections
```

publish_dataset(**args*, ***kwargs*)

Publish named datasets to scheduler

This stores a named reference to a dask collection or list of futures on the scheduler. These references are available to other Clients which can download the collection or futures with `get_dataset`.

Datasets are not immediately computed. You may wish to call `Client.persist` prior to publishing a dataset.

Parameters

args [list of objects to publish as name]

name [optional name of the dataset to publish]

kwargs: dict named collections to publish on the scheduler

Returns

None

See also:

Client.list_datasets, *Client.get_dataset*, *Client.unpublish_dataset*, *Client.persist*

Examples

Publishing client:

```
>>> df = dd.read_csv('s3://...')
>>> df = c.persist(df)
>>> c.publish_dataset(my_dataset=df)
```

Alternative invocation >>> c.publish_dataset(df, name='my_dataset')

Receiving client:

```
>>> c.list_datasets()
['my_dataset']
>>> df2 = c.get_dataset('my_dataset')
```

rebalance (*futures=None*, *workers=None*, ***kwargs*)
Rebalance data within network

Move data between workers to roughly balance memory burden. This either affects a subset of the keys/workers or the entire network, depending on keyword arguments.

This operation is generally not well tested against normal operation of the scheduler. It it not recommended to use it while waiting on computations.

Parameters

futures: list, optional A list of futures to balance, defaults all data

workers: list, optional A list of workers on which to balance, defaults to all workers

register_worker_callbacks (*setup=None*)
Registers a setup callback function for all current and future workers.

This registers a new setup function for workers in this cluster. The function will run immediately on all currently connected workers. It will also be run upon connection by any workers that are added in the future. Multiple setup functions can be registered - these will be called in the order they were added.

If the function takes an input argument named `dask_worker` then that variable will be populated with the worker itself.

Parameters

setup [callable(dask_worker: Worker) -> None] Function to register and run on all workers

replicate (*futures*, *n=None*, *workers=None*, *branching_factor=2*, ***kwargs*)
Set replication of futures within network

Copy data onto many workers. This helps to broadcast frequently accessed data and it helps to improve resilience.

This performs a tree copy of the data throughout the network individually on each piece of data. This operation blocks until complete. It does not guarantee replication of data to future workers.

Parameters

futures: list of futures Futures we wish to replicate

n: int, optional Number of processes on the cluster on which to replicate the data. Defaults to all.

workers: list of worker addresses Workers on which we want to restrict the replication. Defaults to all.

branching_factor: int, optional The number of workers that can copy data in each generation

See also:

Client.rebalance

Examples

```
>>> x = c.submit(func, *args)
>>> c.replicate([x])  # send to all workers
>>> c.replicate([x], n=3)  # send to three workers
>>> c.replicate([x], workers=['alice', 'bob'])  # send to specific
>>> c.replicate([x], n=1, workers=['alice', 'bob'])  # send to one of␣
↪specific workers
>>> c.replicate([x], n=1)  # reduce replications
```

restart (***kwargs*)
Restart the distributed network

This kills all active work, deletes all data on the network, and restarts the worker processes.

retire_workers (*workers=None*, *close_workers=True*, ***kwargs*)
Retire certain workers on the scheduler

See dask.distributed.Scheduler.retire_workers for the full docstring.

See also:

dask.distributed.Scheduler.retire_workers

Examples

You can get information about active workers using the following: >>> workers = client.scheduler_info()['workers']

From that list you may want to select some workers to close >>> client.retire_workers(workers=['tcp://address:port', ...])

run (*function*, **args*, ***kwargs*)
Run a function on all workers outside of task scheduling system

This calls a function on all currently known workers immediately, blocks until those results come back, and returns the results asynchronously as a dictionary keyed by worker address. This method if generally used for side effects, such and collecting diagnostic information or installing libraries.

If your function takes an input argument named `dask_worker` then that variable will be populated with the worker itself.

Parameters

function: callable

***args: arguments for remote function**

****kwargs: keyword arguments for remote function**

workers: list Workers on which to run the function. Defaults to all known workers.

Examples

```
>>> c.run(os.getpid)
{'192.168.0.100:9000': 1234,
 '192.168.0.101:9000': 4321,
 '192.168.0.102:9000': 5555}
```

Restrict computation to particular workers with the `workers=` keyword argument.

```
>>> c.run(os.getpid, workers=['192.168.0.100:9000',
...                           '192.168.0.101:9000'])
{'192.168.0.100:9000': 1234,
 '192.168.0.101:9000': 4321}
```

```
>>> def get_status(dask_worker):
...     return dask_worker.status
```

```
>>> c.run(get_hostname)
{'192.168.0.100:9000': 'running',
 '192.168.0.101:9000': 'running}
```

run_coroutine (*function*, **args*, ***kwargs*)
Spawn a coroutine on all workers.

This spaws a coroutine on all currently known workers and then waits for the coroutine on each worker. The coroutines' results are returned as a dictionary keyed by worker address.

Parameters

function: a coroutine function

(typically a function wrapped in gen.coroutine or a Python 3.5+ async function)

***args: arguments for remote function**

****kwargs: keyword arguments for remote function**

wait: boolean (default True) Whether to wait for coroutines to end.

workers: list Workers on which to run the function. Defaults to all known workers.

run_on_scheduler(*function*, **args*, ***kwargs*)
Run a function on the scheduler process

This is typically used for live debugging. The function should take a keyword argument `dask_scheduler=`, which will be given the scheduler object itself.

See also:

Client.run Run a function on all workers

Client.start_ipython_scheduler Start an IPython session on scheduler

Examples

```
>>> def get_number_of_tasks(dask_scheduler=None):
...     return len(dask_scheduler.tasks)
```

```
>>> client.run_on_scheduler(get_number_of_tasks)
100
```

scatter(*data*, *workers=None*, *broadcast=False*, *direct=None*, *hash=True*, *maxsize=0*, *time-out='__no_default__'*, *asynchronous=None*)
Scatter data into distributed memory

This moves data from the local client process into the workers of the distributed scheduler. Note that it is often better to submit jobs to your workers to have them load the data rather than loading data locally and then scattering it out to them.

Parameters

data: list, iterator, dict, Queue, or object Data to scatter out to workers. Output type matches input type.

workers: list of tuples (optional) Optionally constrain locations of data. Specify workers as hostname/port pairs, e.g. `('127.0.0.1', 8787)`.

broadcast: bool (defaults to False) Whether to send each data element to all workers. By default we round-robin based on number of cores.

direct: bool (defaults to automatically check) Send data directly to workers, bypassing the central scheduler This avoids burdening the scheduler but assumes that the client is able to talk directly with the workers.

maxsize: int (optional) Maximum size of queue if using queues, 0 implies infinite

hash: bool (optional) Whether or not to hash data to determine key. If False then this uses a random key

Returns

List, dict, iterator, or queue of futures matching the type of input.

See also:

Client.gather Gather data back to local process

Examples

```
>>> c = Client('127.0.0.1:8787')
>>> c.scatter(1)
<Future: status: finished, key: c0a8a20f903a4915b94db8de3ea63195>
```

```
>>> c.scatter([1, 2, 3])
[<Future: status: finished, key: c0a8a20f903a4915b94db8de3ea63195>,
 <Future: status: finished, key: 58e78e1b34eb49a68c65b54815d1b158>,
 <Future: status: finished, key: d3395e15f605bc35ab1bac6341a285e2>]
```

```
>>> c.scatter({'x': 1, 'y': 2, 'z': 3})
{'x': <Future: status: finished, key: x>,
 'y': <Future: status: finished, key: y>,
 'z': <Future: status: finished, key: z>}
```

Constrain location of data to subset of workers

```
>>> c.scatter([1, 2, 3], workers=[('hostname', 8788)])
```

Handle streaming sequences of data with iterators or queues

```
>>> seq = c.scatter(iter([1, 2, 3]))
>>> next(seq)
<Future: status: finished, key: c0a8a20f903a4915b94db8de3ea63195>,
```

Broadcast data to all workers

```
>>> [future] = c.scatter([element], broadcast=True)
```

scheduler_info (***kwargs*)

Basic information about the workers in the cluster

Examples

```
>>> c.scheduler_info()
{'id': '2de2b6da-69ee-11e6-ab6a-e82aea155996',
 'services': {},
 'type': 'Scheduler',
 'workers': {'127.0.0.1:40575': {'active': 0,
                                 'last-seen': 1472038237.4845693,
                                 'name': '127.0.0.1:40575',
                                 'services': {},
                                 'stored': 0,
                                 'time-delay': 0.0061032772064208984}}}
```

set_metadata (*key*, *value*)

Set arbitrary metadata in the scheduler

This allows you to store small amounts of data on the central scheduler process for administrative purposes. Data should be msgpack serializable (ints, strings, lists, dicts)

If the key corresponds to a task then that key will be cleaned up when the task is forgotten by the scheduler.

If the key is a list then it will be assumed that you want to index into a nested dictionary structure using those keys. For example if you call the following:

```
>>> client.set_metadata(['a', 'b', 'c'], 123)
```

Then this is the same as setting

```
>>> scheduler.task_metadata['a']['b']['c'] = 123
```

The lower level dictionaries will be created on demand.

See also:

get_metadata

Examples

```
>>> client.set_metadata('x', 123)
>>> client.get_metadata('x')
123
```

```
>>> client.set_metadata(['x', 'y'], 123)
>>> client.get_metadata('x')
{'y': 123}
```

```
>>> client.set_metadata(['x', 'w', 'z'], 456)
>>> client.get_metadata('x')
{'y': 123, 'w': {'z': 456}}
```

```
>>> client.get_metadata(['x', 'w'])
{'z': 456}
```

shutdown (**args*, ***kwargs*)
Deprecated, see close instead

This was deprecated because "shutdown" was sometimes confusingly thought to refer to the cluster rather than the client

start (***kwargs*)
Start scheduler running in separate thread

start_ipython_scheduler (*magic_name='scheduler_if_ipython'*, *qtconsole=False*, *qtconsole_args=None*)
Start IPython kernel on the scheduler

Parameters

magic_name: str or None (optional) If defined, register IPython magic with this name for executing code on the scheduler. If not defined, register %scheduler magic if IPython is running.

qtconsole: bool (optional) If True, launch a Jupyter QtConsole connected to the worker(s).

qtconsole_args: list(str) (optional) Additional arguments to pass to the qtconsole on startup.

Returns

connection_info: dict connection_info dict containing info necessary to connect Jupyter clients to the scheduler.

See also:

Client.start_ipython_workers Start IPython on the workers

Examples

```
>>> c.start_ipython_scheduler()
>>> %scheduler scheduler.processing
{'127.0.0.1:3595': {'inc-1', 'inc-2'},
 '127.0.0.1:53589': {'inc-2', 'add-5'}}
```

```
>>> c.start_ipython_scheduler(qtconsole=True)
```

start_ipython_workers(*workers=None*, *magic_names=False*, *qtconsole=False*, *qtconsole_args=None*)

Start IPython kernels on workers

Parameters

workers: list (optional) A list of worker addresses, defaults to all

magic_names: str or list(str) (optional) If defined, register IPython magics with these names for executing code on the workers. If string has asterix then expand asterix into 0, 1, . . . , n for n workers

qtconsole: bool (optional) If True, launch a Jupyter QtConsole connected to the worker(s).

qtconsole_args: list(str) (optional) Additional arguments to pass to the qtconsole on startup.

Returns

iter_connection_info: list List of connection_info dicts containing info necessary to connect Jupyter clients to the workers.

See also:

Client.start_ipython_scheduler start ipython on the scheduler

Examples

```
>>> info = c.start_ipython_workers()
>>> %remote info['192.168.1.101:5752'] worker.data
{'x': 1, 'y': 100}
```

```
>>> c.start_ipython_workers('192.168.1.101:5752', magic_names='w')
>>> %w worker.data
{'x': 1, 'y': 100}
```

```
>>> c.start_ipython_workers('192.168.1.101:5752', qtconsole=True)
```

Add asterix * in magic names to add one magic per worker

```
>>> c.start_ipython_workers(magic_names='w_*')
>>> %w_0 worker.data
{'x': 1, 'y': 100}
>>> %w_1 worker.data
{'z': 5}
```

submit (*func*, **args*, ***kwargs*)
Submit a function application to the scheduler

Parameters

func: callable

***args:**

****kwargs:**

pure: bool (defaults to True) Whether or not the function is pure. Set `pure=False` for impure functions like `np.random.random`.

workers: set, iterable of sets A set of worker hostnames on which computations may be performed. Leave empty to default to all workers (common case)

key: str Unique identifier for the task. Defaults to function-name and hash

allow_other_workers: bool (defaults to False) Used with *workers*. Indicates whether or not the computations may be performed on workers that are not in the *workers* set(s).

retries: int (default to 0) Number of allowed automatic retries if the task fails

priority: Number Optional prioritization of task. Zero is default. Higher priorities take precedence

fifo_timeout: str timedelta (default '100ms') Allowed amount of time between calls to consider the same priority

Returns

Future

See also:

Client.map Submit on many arguments at once

Examples

```
>>> c = client.submit(add, a, b)
```

unpublish_dataset (*name*, ***kwargs*)
Remove named datasets from scheduler

See also:

Client.publish_dataset

Examples

```
>>> c.list_datasets()
['my_dataset']
>>> c.unpublish_datasets('my_dataset')
>>> c.list_datasets()
[]
```

upload_file(*filename*, ***kwargs*)
Upload local package to workers

This sends a local file up to all worker nodes. This file is placed into a temporary directory on Python's system path so any .py, .egg or .zip files will be importable.

Parameters

filename: string Filename of .py, .egg or .zip file to send to workers

Examples

```
>>> client.upload_file('mylibrary.egg')
>>> from mylibrary import myfunc
>>> L = c.map(myfunc, seq)
```

who_has(*futures=None*, ***kwargs*)
The workers storing each future's data

Parameters

futures: list (optional) A list of futures, defaults to all data

See also:

Client.has_what, *Client.ncores*

Examples

```
>>> x, y, z = c.map(inc, [1, 2, 3])
>>> wait([x, y, z])
>>> c.who_has()
{'inc-1c8dd6be1c21646c71f76c16d09304ea': ['192.168.1.141:46784'],
 'inc-1e297fc27658d7b67b3a758f16bcf47a': ['192.168.1.141:46784'],
 'inc-fd65c238a7ea60f6a01bf4c8a5fcf44b': ['192.168.1.141:46784']}
```

```
>>> c.who_has([x, y])
{'inc-1c8dd6be1c21646c71f76c16d09304ea': ['192.168.1.141:46784'],
 'inc-1e297fc27658d7b67b3a758f16bcf47a': ['192.168.1.141:46784']}
```

write_scheduler_file(*scheduler_file*)
Write the scheduler information to a json file.

This facilitates easy sharing of scheduler information using a file system. The scheduler file can be used to instantiate a second Client using the same scheduler.

Parameters

scheduler_file: str Path to a write the scheduler file.

Examples

```
>>> client = Client()
>>> client.write_scheduler_file('scheduler.json')
# connect to previous client's scheduler
>>> client2 = Client(scheduler_file='scheduler.json')
```

class distributed.**Future**(*key*, *client=None*, *inform=True*, *state=None*)

A remotely running computation

A Future is a local proxy to a result running on a remote worker. A user manages future objects in the local Python process to determine what happens in the larger cluster.

Parameters

key: str, or tuple Key of remote data to which this future refers

client: Client Client that should own this future. Defaults to _get_global_client()

inform: bool Do we inform the scheduler that we need an update on this future

See also:

Client Creates futures

Examples

Futures typically emerge from Client computations

```
>>> my_future = client.submit(add, 1, 2)
```

We can track the progress and results of a future

```
>>> my_future
<Future: status: finished, key: add-8f6e709446674bad78ea8aeecfee188e>
```

We can get the result or the exception and traceback from the future

```
>>> my_future.result()
```

add_done_callback(*fn*)

Call callback on future when callback has finished

The callback `fn` should take the future as its only argument. This will be called regardless of if the future completes successfully, errs, or is cancelled

The callback is executed in a separate thread.

cancel(***kwargs*)

Cancel request to run this future

See also:

Client.cancel

cancelled()

Returns True if the future has been cancelled

done()

Is the computation complete?

exception (*timeout=None*, ***kwargs*)
Return the exception of a failed task

If *timeout* seconds are elapsed before returning, a `dask.distributed.TimeoutError` is raised.

See also:

Future.traceback

result (*timeout=None*)
Wait until computation completes, gather result to local process.

If *timeout* seconds are elapsed before returning, a `dask.distributed.TimeoutError` is raised.

traceback (*timeout=None*, ***kwargs*)
Return the traceback of a failed task

This returns a traceback object. You can inspect this object using the `traceback` module. Alternatively if you call `future.result()` this traceback will accompany the raised exception.

If *timeout* seconds are elapsed before returning, a `dask.distributed.TimeoutError` is raised.

See also:

Future.exception

Examples

```
>>> import traceback
>>> tb = future.traceback()
>>> traceback.export_tb(tb)
[...]
```

class distributed.**Queue** (*name=None*, *client=None*, *maxsize=0*)
Distributed Queue

This allows multiple clients to share futures or small bits of data between each other with a multi-producer/multi-consumer queue. All metadata is sequentialized through the scheduler.

Elements of the Queue must be either Futures or msgpack-encodable data (ints, strings, lists, dicts). All data is sent through the scheduler so it is wise not to send large objects. To share large objects scatter the data and share the future instead.

Warning: This object is experimental and has known issues in Python 2

See also:

Variable shared variable between clients

Examples

```
>>> from dask.distributed import Client, Queue
>>> client = Client()
>>> queue = Queue('x')
>>> future = client.submit(f, x)
>>> queue.put(future)
```

get(*timeout=None*, *batch=False*, ***kwargs*)
Get data from the queue

Parameters

timeout: Number (optional) Time in seconds to wait before timing out

batch: boolean, int (optional) If True then return all elements currently waiting in the queue. If an integer than return that many elements from the queue If False (default) then return one item at a time

put(*value*, *timeout=None*, ***kwargs*)
Put data into the queue

qsize(***kwargs*)
Current number of elements in the queue

class distributed.**Variable**(*name=None*, *client=None*, *maxsize=0*)
Distributed Global Variable

This allows multiple clients to share futures and data between each other with a single mutable variable. All metadata is sequentialized through the scheduler. Race conditions can occur.

Values must be either Futures or msgpack-encodable data (ints, lists, strings, etc..) All data will be kept and sent through the scheduler, so it is wise not to send too much. If you want to share a large amount of data then `scatter` it and share the future instead.

Warning: This object is experimental and has known issues in Python 2

See also:

Queue shared multi-producer/multi-consumer queue between clients

Examples

```
>>> from dask.distributed import Client, Variable
>>> client = Client()
>>> x = Variable('x')
>>> x.set(123)  # docttest: +SKIP
>>> x.get()  # docttest: +SKIP
123
>>> future = client.submit(f, x)
>>> x.set(future)
```

delete()
Delete this variable

Caution, this affects all clients currently pointing to this variable.

get(*timeout=None*, ***kwargs*)
Get the value of this variable

set(*value*, ***kwargs*)
Set the value of this variable

Parameters

value: Future or object Must be either a Future or a msgpack-encodable value

class distributed.**Lock**(*name=None*, *client=None*)
Distributed Centralized Lock

Parameters

name: string Name of the lock to acquire. Choosing the same name allows two disconnected processes to coordinate a lock.

Examples

```
>>> lock = Lock('x')
>>> lock.acquire(timeout=1)
>>> # do things with protected resource
>>> lock.release()
```

acquire(*timeout=None*)
Acquire the lock

Parameters

timeout: number Seconds to wait on the lock in the scheduler. This does not include local coroutine time, network transfer time, etc..

Returns

True or False whether or not it sucessfully acquired the lock

Examples

```
>>> lock = Lock('x')
>>> lock.acquire(timeout=1)
```

release()
Release the lock if already acquired

class distributed.**Pub**(*name*, *worker=None*, *client=None*)
Publish data with Publish-Subscribe pattern

This allows clients and workers to directly communicate data between each other with a typical Publish-Subscribe pattern. This involves two components,

Pub objects, into which we put data:

```
>>> pub = Pub('my-topic')
>>> pub.put(123)
```

And Sub objects, from which we collect data:

```
>>> sub = Sub('my-topic')
>>> sub.get()
123
```

Many Pub and Sub objects can exist for the same topic. All data sent from any Pub will be sent to all Sub objects on that topic that are currently connected. Pub's and Sub's find each other using the scheduler, but they communicate directly with each other without coordination from the scheduler.

Pubs and Subs use the central scheduler to find each other, but not to mediate the communication. This means that there is very little additional latency or overhead, and they are appropriate for very frequent data transfers.

For context, most data transfer first checks with the scheduler to find which workers should participate, and then does direct worker-to-worker transfers. This checking in with the scheduler provides some stability guarnatees, but also adds in a few extra network hops. PubSub doesn't do this, and so is faster, but also can easily drop messages if Pubs or Subs disappear without notice.

When using a Pub or Sub from a Client all communications will be routed through the scheduler. This can cause some performance degredation. Pubs an Subs only operate at top-speed when they are both on workers.

Parameters

name: object (msgpack serializable) The name of the group of Pubs and Subs on which to participate

See also:

Sub

Examples

```
>>> pub = Pub('my-topic')
>>> sub = Sub('my-topic')
>>> pub.put([1, 2, 3])
>>> sub.get()
[1, 2, 3]
```

You can also use sub within a for loop:

```
>>> for msg in sub:
...     print(msg)
```

or an async for loop

```
>>> async for msg in sub:
...     print(msg)
```

Similarly the `.get` method will return an awaitable if used by an async client or within the IOLoop thread of a worker

```
>>> await sub.get()
```

You can see the set of connected worker subscribers by looking at the `.subscribers` attribute:

```
>>> pub.subscribers
{'tcp://...': {},
 'tcp://...': {}}
```

put(*msg*)
Publish a message to all subscribers of this topic

class distributed.**Sub**(*name*, *worker=None*, *client=None*)
Subscribe to a Publish/Subscribe topic

See also:

Pub for full docstring

get(*timeout=None*)
Get a single message

next(*timeout=None*)
Get a single message

4.12 API

Dask APIs generally follow from upstream APIs:

- The *Dask Array API* follows the Numpy API
- The *Dask Dataframe API* follows the Pandas API
- The Dask-ML API follows the Scikit-Learn API and other related machine learning libraries
- The *Dask Bag API* follows the map/filter/groupby/reduce API common in PySpark, PyToolz, and the Python standard library
- The *Dask Delayed API* wraps general Python code
- The *Real-time Futures API* follows the concurrent.futures API from the standard library.

Additionally, Dask has its own functions to start computations, persist data in memory, check progress, and so forth that complement the APIs above. These more general Dask functions are described below:

compute(*args, **kwargs)	Compute several dask collections at once.
is_dask_collection(x)	Returns `True` if `x` is a dask collection
optimize(*args, **kwargs)	Optimize several dask collections at once.
persist(*args, **kwargs)	Persist multiple Dask collections into memory
visualize(*args, **kwargs)	Visualize several dask graphs at once.

These functions work with any scheduler. More advanced operations are available when using the newer scheduler and starting a `dask.distributed.Client` (which, despite its name, runs nicely on a single machine). This API provides the ability to submit, cancel, and track work asynchronously, and includes many functions for complex inter-task workflows. These are not necessary for normal operation, but can be useful for real-time or advanced operation.

This more advanced API is available in the Dask distributed documentation

`dask.`**compute**(**args*, ***kwargs*)
Compute several dask collections at once.

Parameters

args [object] Any number of objects. If it is a dask object, it's computed and the result is returned. By default, python builtin collections are also traversed to look for dask objects (for more information see the `traverse` keyword). Non-dask arguments are passed through unchanged.

traverse [bool, optional] By default dask traverses builtin python collections looking for dask objects passed to `compute`. For large collections this can be expensive. If none of the arguments contain any dask objects, set `traverse=False` to avoid doing this traversal.

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

optimize_graph [bool, optional] If True [default], the optimizations for each collection are applied before computation. Otherwise the graph is run as is. This can be useful for debugging.

kwargs Extra keywords to forward to the scheduler function.

Examples

```
>>> import dask.array as da
>>> a = da.arange(10, chunks=2).sum()
>>> b = da.arange(10, chunks=2).mean()
>>> compute(a, b)
(45, 4.5)
```

By default, dask objects inside python collections will also be computed:

```
>>> compute({'a': a, 'b': b, 'c': 1})
({'a': 45, 'b': 4.5, 'c': 1},)
```

dask.**is_dask_collection**(*x*)

Returns `True` if `x` is a dask collection

dask.**optimize**(**args*, ***kwargs*)

Optimize several dask collections at once.

Returns equivalent dask collections that all share the same merged and optimized underlying graph. This can be useful if converting multiple collections to delayed objects, or to manually apply the optimizations at strategic points.

Note that in most cases you shouldn't need to call this method directly.

Parameters

***args** [objects] Any number of objects. If a dask object, its graph is optimized and merged with all those of all other dask objects before returning an equivalent dask collection. Non-dask arguments are passed through unchanged.

traverse [bool, optional] By default dask traverses builtin python collections looking for dask objects passed to `optimize`. For large collections this can be expensive. If none of the arguments contain any dask objects, set `traverse=False` to avoid doing this traversal.

optimizations [list of callables, optional] Additional optimization passes to perform.

****kwargs** Extra keyword arguments to forward to the optimization passes.

Examples

```
>>> import dask.array as da
>>> a = da.arange(10, chunks=2).sum()
>>> b = da.arange(10, chunks=2).mean()
>>> a2, b2 = optimize(a, b)
```

```
>>> a2.compute() == a.compute()
True
>>> b2.compute() == b.compute()
True
```

dask.**persist**(**args*, ***kwargs*)

Persist multiple Dask collections into memory

This turns lazy Dask collections into Dask collections with the same metadata, but now with their results fully computed or actively computing in the background.

For example a lazy dask.array built up from many lazy calls will now be a dask.array of the same shape, dtype, chunks, etc., but now with all of those previously lazy tasks either computed in memory as many small `numpy.array` (in the single-machine case) or asynchronously running in the background on a cluster (in the distributed case).

This function operates differently if a `dask.distributed.Client` exists and is connected to a distributed scheduler. In this case this function will return as soon as the task graph has been submitted to the cluster, but before the computations have completed. Computations will continue asynchronously in the background. When using this function with the single machine scheduler it blocks until the computations have finished.

When using Dask on a single machine you should ensure that the dataset fits entirely within memory.

Parameters

***args: Dask collections**

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

traverse [bool, optional] By default dask traverses builtin python collections looking for dask objects passed to `persist`. For large collections this can be expensive. If none of the arguments contain any dask objects, set `traverse=False` to avoid doing this traversal.

optimize_graph [bool, optional] If True [default], the graph is optimized before computation. Otherwise the graph is run as is. This can be useful for debugging.

****kwargs** Extra keywords to forward to the scheduler function.

Returns

New dask collections backed by in-memory data

Examples

```
>>> df = dd.read_csv('/path/to/*.csv')
>>> df = df[df.name == 'Alice']
>>> df['in-debt'] = df.balance < 0
>>> df = df.persist()  # triggers computation
```

```
>>> df.value().min()  # future computations are now fast
-10
>>> df.value().max()
100
```

```
>>> from dask import persist  # use persist function on multiple collections
>>> a, b = persist(a, b)
```

`dask.`**`visualize`**(**args*, ***kwargs*)

Visualize several dask graphs at once.

Requires `graphviz` to be installed. All options that are not the dask graph(s) should be passed as keyword arguments.

Parameters

dsk [dict(s) or collection(s)] The dask graph(s) to visualize.

filename [str or None, optional] The name (without an extension) of the file to write to disk. If *filename* is None, no file will be written, and we communicate with dot using only pipes.

format [{'png', 'pdf', 'dot', 'svg', 'jpeg', 'jpg'}, optional] Format in which to write output file. Default is 'png'.

optimize_graph [bool, optional] If True, the graph is optimized before rendering. Otherwise, the graph is displayed as is. Default is False.

color: {None, 'order'}, optional Options to color nodes. Provide `cmap=` keyword for additional colormap

****kwargs** Additional keyword arguments to forward to `to_graphviz`.

Returns

result [IPython.diplay.Image, IPython.display.SVG, or None] See dask.dot.dot_graph for more information.

See also:

`dask.dot.dot_graph`

Notes

For more information on optimization see here:

https://docs.dask.org/en/latest/optimize.html

Examples

```
>>> x.visualize(filename='dask.pdf')
>>> x.visualize(filename='dask.pdf', color='order')
```

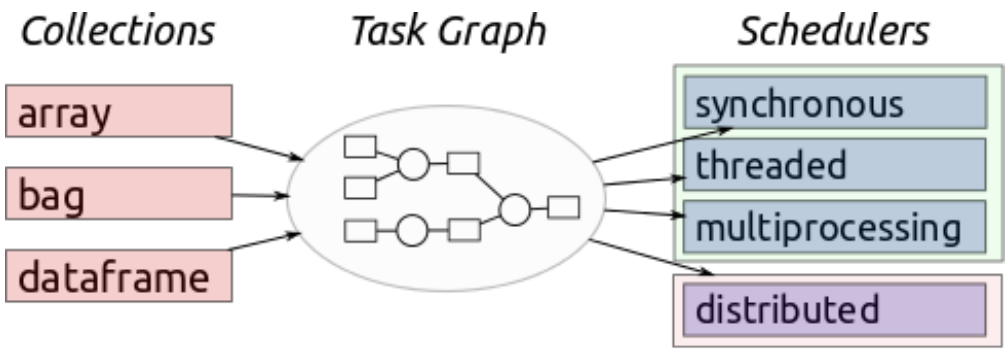
Scheduling

Schedulers execute task graphs. Dask currently has two main schedulers: one for local processing using threads or processes; and one for distributed memory clusters.

- *Scheduling*
- *Distributed Scheduling*

4.13 Scheduling

All of the large-scale Dask collections like *Dask Array*, *Dask dataframe*, and *Dask bag* and the fine-grained APIs like *delayed* and *futures* generate task graphs where each node in the graph is a normal Python function, and edges between nodes are normal Python objects that are created by one task as ouptuts and used as inputs in another task. After Dask generates these task graphs it needs to execute them on parallel hardware. This is the job of a *task scheduler*. Different task schedulers exist. Each will consume a task graph and compute the same result, but with different performance characteristics.



Dask has two families of task schedulers:

1. **Single machine scheduler**: This scheduler provides basic features on a local process or thread pool. This scheduler was made first and is the default. It is simple and cheap to use. It can only be used on a single machine and does not scale.
2. **Distributed scheduler**: This scheduler is more sophisticated, offers more features, but also requires a bit more effort to set up. It can run locally or distributed across a cluster.

For different computations you may find better performance with particular scheduler settings. This document helps you understand how to choose between and configure different schedulers, and provides guidelines on when one might be more appropriate.

4.13.1 Local Threads

```
import dask
dask.config.set(scheduler='threads')  # overwrite default with threaded scheduler
```

The threaded scheduler executes computations with a local `multiprocessing.pool.ThreadPool`. It is lightweight and requires no setup. It introduces very little task overhead, around 50us per task, and because everything occurs in the same process, it incurs no costs to transfer data between tasks. However due to Python's Global Interpreter Lock (GIL), this scheduler only provides parallelism when your computation is dominated by non-Python code, such as is the case when operating on numeric data in NumPy arrays, Pandas dataframes, or using any of the other C/C++/Cython based projects in the ecosystem.

The threaded scheduler is the default choice for *dask array*, *dask dataframe*, and *dask delayed*. However if your computation is dominated by processing pure Python objects like strings, dicts, or lists, then you may want to try one of the process-based schedulers below (we currently recommend the distributed scheduler on a local machine).

4.13.2 Local Processes

Note: the distributed scheduler described a couple sections below is often a better choice today. we encourage readers to continue reading after this section

```
import dask.multiprocessing
dask.config.set(scheduler='processes')  # overwrite default with multiprocessing␣
↪scheduler
```

The multiprocessing scheduler executes computations with a local `multiprocessing.Pool`. It is lightweight to use and requires no setup. Every task and all of its dependencies are shipped to a local process, executed, and then their result is shipped back to the main process. This means that it is able to bypass issues with the GIL and provide parallelism even on computations are are dominated by Pure Python code, such as those that process strings, dicts, and lists.

However moving data to remote processes and back can introduce performance penalties, particularly when the data being transferred between processes is large. The multiprocessing scheduler is an excellent choice when workflows are relatively linear, and so do not involve significant inter-task data transfer, and when inputs and outputs are both small, like filenames and counts.

This is common in basic data ingestion workloads, such as those are common in *dask bag*, where the multiprocessing scheduler is the default.

```
>>> import dask.bag as db
>>> db.read_text('*.json').map(json.loads).pluck('name').frequencies().compute()
{'alice': 100, 'bob': 200, 'charlie': 300}
```

For more complex workloads, where large intermediate results may be depended upon by multiple downstream tasks, we generally recommend the use of the distributed scheduler on a local machine. The distributed scheduler is more intelligent about moving around large intermediate results.

4.13.3 Single Thread

```
import dask
dask.config.set(scheduler='synchronous')  # overwrite default with single-threaded␣
↪scheduler
```

The single-threaded synchronous scheduler executes all computations in the local thread, with no parallelism at all. This is particularly valuable for debugging and profiling, which are more difficult when using threads or processes.

For example, when using IPython or Jupyter notebooks the `%debug`, `%pdb`, or `%prun` magics will not work well when using the parallel dask schedulers; they were not designed to be used in a parallel computing context. However if you run into an exception and want to step into the debugger you may wish to rerun your computation under the single-threaded scheduler, where these tools will function properly.

4.13.4 Dask Distributed (local)

```
from dask.distributed import Client
client = Client()
# or
client = Client(processes=False)
```

The dask.distributed scheduler can either be *setup on a cluster* or run locally on a personal machine. Despite having the name "distributed" it is often pragmatic on local machines for a few reasons:

1. It provides access to asynchronous API, notably *Futures*
2. It provides a diagnostic dashboard that can provide valuable insight on performance and progress
3. It handles data locality with more sophistication, and so can be more efficient than the multiprocessing scheduler on workloads that require multiple processes.

You can read more about using the dask.distributed scheduler on a single machine in *these docs*.

4.13.5 Dask Distributed (Cluster)

You can also run Dask on a distributed cluster. There are a variety of ways to set this up depending on your cluster. We recommend referring to the *setup documentation* for more information.

4.13.6 Configuration

You can configure the global default scheduler by using the `dask.config.set(scheduler...)` command. This can be done globally,

```
dask.config.set(scheduler='threads')

x.compute()
```

or as a context manager

```
with dask.config.set(scheduler='threads'):
    x.compute()
```

or within a single compute call

```
x.compute(scheduler='threads')
```

Additionally some of the scheduler support other keyword arguments. For example the Pool-based single-machine scheduler allow you to provide custom pools, or specify the desired number of workers.

```
from multiprocessing.pool import ThreadPool
with dask.config.set(pool=ThreadPool(4)):
    ...

with dask.config.set(num_workers=4):
    ...
```

4.14 Distributed Scheduling

Dask can run on a cluster of hundreds of machines and thousands of cores. Technical documentation for the distributed system is located on a separate website located here:

- https://distributed.dask.org/en/latest/

Diagnosing Performance

Parallel code can be tricky to debug and profile. Dask provides several tools to help make debugging and profiling graph execution easier.

- *Understanding Performance*
- *Visualize task graphs*
- *Diagnostics (local)*
- *Diagnostics (distributed)*
- *Debugging*

4.15 Understanding Performance

The first step to making computations run quickly is to understand the costs involved. In Python we often rely on tools like the CProfile module, the %%prun IPython magic the VMProf module or the snakeviz module to understand the costs associated with our code. However, few of these tools work well on multi-threaded or multi-process code, and

fewer still on computations distributed among many machines. We also have new costs like data transfer, serialization, task scheduling overhead, and more that we may not be accustomed to tracking.

Fortunately the Dask schedulers come with diagnostics to help you understand the performance characteristics of your computations. By using these diagnostics and a little thought we can often identify the slow parts of troublesome computations.

The *single-machine and distributed schedulers* come with *different* diagnostic tools. These tools are deeply integrated into each scheduler so a tool designed for one will not transfer over to the other.

These pages provide four options for profiling parallel code:

1. *Visualize task graphs*
2. *Single threaded scheduler and a normal Python profiler*
3. *Diagnostics for the single-machine scheduler*
4. *Dask.distributed dashboard*

4.16 Visualize task graphs

`visualize`(*args, **kwargs)	Visualize several dask graphs at once.

Before executing your computation you might consider visualizing the underlying task graph. By looking at the interconnectedness of tasks you can learn more about potential bottlenecks where parallelism may not be possile, or areas where many tasks depend on each other, which may cause a great deal of communication.

The `.visualize` method and `dask.visualize` function work exactly like the `.compute` method and `dask.compute` function, except that rather than computing the result, they produce an image of the task graph.

By default the task graph is rendered from top to bottom. In the case that you prefer to visualize it from left to right, pass `rankdir="LR"` as a keyword argument to `.visualize`.

```
import dask.array as da
x = da.ones((15, 15), chunks=(5, 5))

y = x + x.T

# y.compute()
y.visualize(filename='transpose.svg')
```

Note that the `visualize` function is powered by the GraphViz system library. This library has a few considerations:

1. You must install both the graphviz system library (with tools like apt-get, yum, or brew) *and* the graphviz Python library. If you use Conda then you need to install `python-graphviz`, which will bring along the `graphviz` system library as a dependency.
2. Graphviz takes a while on graphs larger than about 100 nodes. For large computations you might have to simplify your computation a bit for the visualize method to work well.

4.17 Diagnostics (local)

Profiling parallel code can be challening, but `dask.diagnostics` provides functionality to aid in profiling and inspecting execution with the *local task scheduler*.

This page describes the following few built-in options:

1. ProgressBar
2. Profiler
3. ResourceProfiler
4. CacheProfiler

This page then provides instructions on how to build your own custom diagnostic.

4.17.1 Progress Bar

ProgressBar([minimum, width, dt, out])	A progress bar for dask.

The `ProgressBar` class builds on the scheduler callbacks described above to display a progress bar in the terminal or notebook during computation. This can be a nice feedback during long running graph execution. It can be used as a context manager around calls to `get` or `compute` to profile the computation:

```
>>> from dask.diagnostics import ProgressBar
>>> a = da.random.normal(size=(10000, 10000), chunks=(1000, 1000))
>>> res = a.dot(a.T).mean(axis=0)

>>> with ProgressBar():
...     out = res.compute()
[########################################] | 100% Completed | 17.1 s
```

Or registered globally using the `register` method.

```
>>> pbar = ProgressBar()
>>> pbar.register()
>>> out = res.compute()
[########################################] | 100% Completed | 17.1 s
```

To unregister from the global callbacks, call the `unregister` method:

```
>>> pbar.unregister()
```

4.17.2 Profiler

Profiler()	A profiler for dask execution at the task level.

Dask provides a few tools for profiling execution. As with the `ProgressBar`, they each can be used as context managers, or registered globally.

The `Profiler` class is used to profile dask execution at the task level. During execution it records the following information for each task:

1. Key
2. Task
3. Start time in seconds since the epoch
4. Finish time in seconds since the epoch
5. Worker id

4.17.3 ResourceProfiler

ResourceProfiler([dt])	A profiler for resource use.

The `ResourceProfiler` class is used to profile dask execution at the resource level. During execution it records the following information for each timestep

1. Time in seconds since the epoch
2. Memory usage in MB
3. % CPU usage

The default timestep is 1 second, but can be set manually using the `dt` keyword.

```
>>> from dask.diagnostics import ResourceProfiler
>>> rprof = ResourceProfiler(dt=0.5)
```

4.17.4 CacheProfiler

CacheProfiler([metric, metric_name])	A profiler for dask execution at the scheduler cache level.

The `CacheProfiler` class is used to profile dask execution at the scheduler cache level. During execution it records the following information for each task:

1. Key
2. Task
3. Size metric
4. Cache entry time in seconds since the epoch
5. Cache exit time in seconds since the epoch

Where the size metric is the output of a function called on the result of each task. The default metric is to count each task (`metric` is 1 for all tasks). Other functions may be used as a metric instead through the `metric` keyword. For example, the `nbytes` function found in `cachey` can be used to measure the number of bytes in the scheduler cache:

```
>>> from dask.diagnostics import CacheProfiler
>>> from cachey import nbytes
>>> cprof = CacheProfiler(metric=nbytes)
```

4.17.5 Example

As an example to demonstrate using the diagnostics, we'll profile some linear algebra done with `dask.array`. We'll create a random array, take its QR decomposition, and then reconstruct the initial array by multiplying the Q and R components together. Note that since the profilers (and all diagnostics) are just context managers, multiple profilers can be used in a with block:

```
>>> import dask.array as da
>>> from dask.diagnostics import Profiler, ResourceProfiler, CacheProfiler
>>> a = da.random.random(size=(10000, 1000), chunks=(1000, 1000))
>>> q, r = da.linalg.qr(a)
>>> a2 = q.dot(r)

>>> with Profiler() as prof, ResourceProfiler(dt=0.25) as rprof,
...          CacheProfiler() as cprof:
...      out = a2.compute()
```

The results of each profiler are stored in their `results` attribute as a list of `namedtuple` objects:

```
>>> prof.results[0]
TaskData(key=('tsqr-8d16e396b237bf7a731333130d310cb9_QR_st1', 5, 0),
         task=(qr, (_apply_random, 'random_sample', 1060164455, (1000, 1000), (), {}
↪)),
         start_time=1454368444.493292,
         end_time=1454368444.902987,
         worker_id=4466937856)

>>> rprof.results[0]
ResourceData(time=1454368444.078748, mem=74.100736, cpu=0.0)

>>> cprof.results[0]
CacheData(key=('tsqr-8d16e396b237bf7a731333130d310cb9_QR_st1', 7, 0),
          task=(qr, (_apply_random, 'random_sample', 1310656009, (1000, 1000), (), {}
↪)),
          metric=1,
          cache_time=1454368444.49662,
          free_time=1454368446.769452)
```

These can be analyzed separately, or viewed in a bokeh plot using the provided `visualize` method on each profiler:

```
>>> prof.visualize()
```

To view multiple profilers at the same time, the `dask.diagnostics.visualize` function can be used. This takes a list of profilers, and creates a vertical stack of plots aligned along the x-axis:

```
>>> from dask.diagnostics import visualize
>>> visualize([prof, rprof, cprof])
```

Looking at the above figure, from top to bottom:

1. The results from the `Profiler` object. This shows the execution time for each task as a rectangle, organized along the y-axis by worker (in this case threads). Similar tasks are grouped by color, and by hovering over each task one can see the key and task that each block represents.
2. The results from the `ResourceProfiler` object. This shows two lines, one for total CPU percentage used by all the workers, and one for total memory usage.
3. The results from the `CacheProfiler` object. This shows a line for each task group, plotting the sum of the current `metric` in the cache against time. In this case it's the default metric (count), and the lines represent

the number of each object in the cache at time. Note that the grouping and coloring is the same as for the `Profiler` plot, and that the task represented by each line can be found by hovering over the line.

From these plots we can see that the initial tasks (calls to `numpy.random.random` and `numpy.linalg.qr` for each chunk) are run concurrently, but only use slightly more than 100% CPU. This is because the call to `numpy.linalg.qr` currently doesn't release the global interpreter lock, so those calls can't truly be done in parallel. Next, there's a reduction step where all the blocks are combined. This requires all the results from the first step to be held in memory, as shown by the increased number of results in the cache, and increase in memory usage. Immediately after this task ends, the number of elements in the cache decreases, showing that they were only needed for this step. Finally, there's an interleaved set of calls to `dot` and `sum`. Looking at the CPU plot shows that these run both concurrently and in parallel, as the CPU percentage spikes up to around 350%.

4.17.6 Custom Callbacks

Callback([start, start_state, pretask, ...])	Base class for using the callback mechanism

Schedulers based on `dask.local.get_async` (currently `dask.get`, `dask.threaded.get`, and `dask.multiprocessing.get`) accept five callbacks, allowing for inspection of scheduler execution.

The callbacks are:

1. `start(dsk)`

   Run at the beginning of execution, right before the state is initialized. Receives the dask graph.

2. `start_state(dsk, state)`

   Run at the beginning of execution, right after the state is initialized. Receives the dask graph and scheduler state.

3. `pretask(key, dsk, state)`

   Run every time a new task is started. Receives the key of the task to be run, the dask graph, and the scheduler state.

4. `posttask(key, result, dsk, state, id)`

   Run every time a task is finished. Receives the key of the task that just completed, the result, the dask graph, the scheduler state, and the id of the worker that ran the task.

5. `finish(dsk, state, errored)`

   Run at the end of execution, right before the result is returned. Receives the dask graph, the scheduler state, and a boolean indicating whether or not the exit was due to an error.

Custom diagnostics can be created either by instantiating the `Callback` class with the some of above methods as keywords or by subclassing the `Callback` class. Here we create a class that prints the name of every key as it's computed:

```
from dask.callbacks import Callback
class PrintKeys(Callback):
    def _pretask(self, key, dask, state):
        """Print the key of every task as it's started"""
        print("Computing: {0}!".format(repr(key)))
```

This can now be used as a context manager during computation:

```
>>> from operator import add, mul
>>> dsk = {'a': (add, 1, 2), 'b': (add, 3, 'a'), 'c': (mul, 'a', 'b')}
```

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```
>>> with PrintKeys():
...     get(dsk, 'c')
Computing 'a'!
Computing 'b'!
Computing 'c'!
```

Alternatively, functions may be passed in as keyword arguments to `Callback`:

```
>>> def printkeys(key, dask, state):
...     print("Computing: {0}!".format(repr(key)))

>>> with Callback(pretask=printkeys):
...     get(dsk, 'c')
Computing 'a'!
Computing 'b'!
Computing 'c'!
```

4.17.7 API

CacheProfiler([metric, metric_name])	A profiler for dask execution at the scheduler cache level.
Callback([start, start_state, pretask, ...])	Base class for using the callback mechanism
Profiler()	A profiler for dask execution at the task level.
ProgressBar([minimum, width, dt, out])	A progress bar for dask.
ResourceProfiler([dt])	A profiler for resource use.
visualize(profilers[, file_path, show, save])	Visualize the results of profiling in a bokeh plot.

dask.diagnostics.**ProgressBar**(*minimum=0*, *width=40*, *dt=0.1*, *out=None*)

A progress bar for dask.

Parameters

minimum [int, optional] Minimum time threshold in seconds before displaying a progress bar. Default is 0 (always display)

width [int, optional] Width of the bar

dt [float, optional] Update resolution in seconds, default is 0.1 seconds

Examples

Below we create a progress bar with a minimum threshold of 1 second before displaying. For cheap computations nothing is shown:

```
>>> with ProgressBar(minimum=1.0):
...     out = some_fast_computation.compute()
```

But for expensive computations a full progress bar is displayed:

```
>>> with ProgressBar(minimum=1.0):
...     out = some_slow_computation.compute()
[########################################] | 100% Completed | 10.4 s
```

The duration of the last computation is available as an attribute

```
>>> pbar = ProgressBar()
>>> with pbar:
...     out = some_computation.compute()
[########################################] | 100% Completed | 10.4 s
>>> pbar.last_duration
10.4
```

You can also register a progress bar so that it displays for all computations:

```
>>> pbar = ProgressBar()
>>> pbar.register()
>>> some_slow_computation.compute()
[########################################] | 100% Completed | 10.4 s
```

dask.diagnostics.**Profiler**()

A profiler for dask execution at the task level.

Records the following information for each task:

1. Key
2. Task
3. Start time in seconds since the epoch
4. Finish time in seconds since the epoch
5. Worker id

Examples

```
>>> from operator import add, mul
>>> from dask.threaded import get
>>> dsk = {'x': 1, 'y': (add, 'x', 10), 'z': (mul, 'y', 2)}
>>> with Profiler() as prof:
...     get(dsk, 'z')
22
```

```
>>> prof.results
[('y', (add, 'x', 10), 1435352238.48039, 1435352238.480655, 140285575100160),
 ('z', (mul, 'y', 2), 1435352238.480657, 1435352238.480803, 140285566707456)]
```

These results can be visualized in a bokeh plot using the `visualize` method. Note that this requires bokeh to be installed.

```
>>> prof.visualize()
```

You can activate the profiler globally

```
>>> prof.register()
```

If you use the profiler globally you will need to clear out old results manually.

```
>>> prof.clear()
```

dask.diagnostics.**ResourceProfiler**(*dt=1*)

A profiler for resource use.

Records the following each timestep

1. Time in seconds since the epoch
2. Memory usage in MB
3. % CPU usage

Examples

```
>>> from operator import add, mul
>>> from dask.threaded import get
>>> dsk = {'x': 1, 'y': (add, 'x', 10), 'z': (mul, 'y', 2)}
>>> with ResourceProfiler() as prof:
...     get(dsk, 'z')
22
```

These results can be visualized in a bokeh plot using the `visualize` method. Note that this requires bokeh to be installed.

```
>>> prof.visualize()
```

You can activate the profiler globally

```
>>> prof.register()
```

If you use the profiler globally you will need to clear out old results manually.

```
>>> prof.clear()
```

Note that when used as a context manager data will be collected throughout the duration of the enclosed block. In contrast, when registered globally data will only be collected while a dask scheduler is active.

dask.diagnostics.**CacheProfiler**(*metric=None*, *metric_name=None*)

A profiler for dask execution at the scheduler cache level.

Records the following information for each task:

1. Key
2. Task
3. Size metric
4. Cache entry time in seconds since the epoch
5. Cache exit time in seconds since the epoch

Examples

```
>>> from operator import add, mul
>>> from dask.threaded import get
>>> dsk = {'x': 1, 'y': (add, 'x', 10), 'z': (mul, 'y', 2)}
>>> with CacheProfiler() as prof:
```

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```
...     get(dsk, 'z')
22
```

```
>>> prof.results
[CacheData('y', (add, 'x', 10), 1, 1435352238.48039, 1435352238.480655),
 CacheData('z', (mul, 'y', 2), 1, 1435352238.480657, 1435352238.480803)]
```

The default is to count each task (`metric` is 1 for all tasks). Other functions may used as a metric instead through the `metric` keyword. For example, the `nbytes` function found in `cachey` can be used to measure the number of bytes in the cache.

```
>>> from cachey import nbytes
>>> with CacheProfiler(metric=nbytes) as prof:
...     get(dsk, 'z')
```

The profiling results can be visualized in a bokeh plot using the `visualize` method. Note that this requires bokeh to be installed.

```
>>> prof.visualize()
```

You can activate the profiler globally

```
>>> prof.register()
```

If you use the profiler globally you will need to clear out old results manually.

```
>>> prof.clear()
```

dask.diagnostics.**Callback**(*start=None*, *start_state=None*, *pretask=None*, *posttask=None*, *finish=None*)

Base class for using the callback mechanism

Create a callback with functions of the following signatures:

```
>>> def start(dsk):
...     pass
>>> def start_state(dsk, state):
...     pass
>>> def pretask(key, dsk, state):
...     pass
>>> def posttask(key, result, dsk, state, worker_id):
...     pass
>>> def finish(dsk, state, failed):
...     pass
```

You may then construct a callback object with any number of them

```
>>> cb = Callback(pretask=pretask, finish=finish)
```

And use it either as a context manager over a compute/get call

```
>>> with cb:
...     x.compute()
```

Or globally with the `register` method

```
>>> cb.register()
>>> cb.unregister()
```

Alternatively subclass the `Callback` class with your own methods.

```
>>> class PrintKeys(Callback):
...     def _pretask(self, key, dask, state):
...         print("Computing: {0}!".format(repr(key)))
```

```
>>> with PrintKeys():
...     x.compute()
```

dask.diagnostics.**visualize**(*profilers*, *file_path=None*, *show=True*, *save=True*, ***kwargs*)

Visualize the results of profiling in a bokeh plot.

If multiple profilers are passed in, the plots are stacked vertically.

Parameters

profilers [profiler or list] Profiler or list of profilers.

file_path [string, optional] Name of the plot output file.

show [boolean, optional] If True (default), the plot is opened in a browser.

save [boolean, optional] If True (default), the plot is saved to disk.

****kwargs** Other keyword arguments, passed to bokeh.figure. These will override all defaults set by visualize.

Returns

The completed bokeh plot object.

4.18 Diagnostics (distributed)

The *Dask distributed scheduler* provides feedback in two forms:

1. A progress bar suitable for interactive use in consoles or notebooks
2. An interactive dashboard, containing several plots and tables with live information

4.18.1 Progress bar

progress(*futures, **kwargs)	Track progress of futures

The dask.distributed progress bar differs from the `ProgressBar` used for *local diagnostics*. The `progress` function takes a Dask object that is executing in the background.

```
# Single machine progress bar
from dask.diagnostics import ProgressBar

with ProgressBar():
    x.compute()

# Distributed scheduler ProgressBar
```

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```
from dask.distributed import Client, progress

client = Client()  # use dask.distributed by default

x = x.persist()  # start computation in the background
progress(x)      # watch progress

x.compute()      # convert to final result when done if desired
```

4.18.2 Dashboard

`Client`([address, loop, timeout, ...])	Connect to and drive computation on a distributed Dask cluster

If Bokeh is installed then the dashboard will start up automatically whenever the scheduler is created. For local use this happens automatically when you create a client with no arguments

```
from dask.distributed import Client
client = Client()  # start distributed scheduler locally.  Launch dashboard
```

It is typically served at http://localhost:8787/status , but may be served elsewhere if this port is taken. The address of the dashboard will be displayed if you are in a Jupyter Notebook.

There are numerous pages with information about task runtimes, communication, statistical profiling, load balancing, memory use, and much more. For more information we recommend the following video guide:

4.18.3 External Documentation

More in-depth technical documentation about Dask's distributed scheduler is available at https://distributed.dask.org/en/latest

4.18.4 API

`dask.distributed.`**`progress`**(**futures*, ***kwargs*)

Track progress of futures

This operates differently in the notebook and the console

- Notebook: This returns immediately, leaving an IPython widget on screen
- Console: This blocks until the computation completes

Parameters

futures: Futures A list of futures or keys to track

notebook: bool (optional) Running in the notebook or not (defaults to guess)

multi: bool (optional) Track different functions independently (defaults to True)

complete: bool (optional) Track all keys (True) or only keys that have not yet run (False) (defaults to True)

Notes

In the notebook, the output of *progress* must be the last statement in the cell. Typically, this means calling *progress* at the end of a cell.

Examples

```
>>> progress(futures)
[########################################] | 100% Completed |  1.7s
```

4.19 Debugging

Debugging parallel programs is hard. Normal debugging tools like logging and using `pdb` to interact with tracebacks stop working normally when exceptions occur in far-away machines or different processes or threads.

Dask has a variety of mechanisms to make this process easier. Depending on your situation some of these approaches may be more appropriate than others.

These approaches are ordered from lightweight or easy solutions to more involved solutions.

4.19.1 Exceptions

When a task in your computation fails the standard way of understanding what went wrong is to look at the exception and traceback. Often people do this with the `pdb` module, IPython `%debug` or `%pdb` magics, or by just looking at the traceback and investigating where in their code the exception occurred.

Normally when a computation computes in a separate thread or a different machine these approaches break down. Dask provides a few mechanisms to recreate the normal Python debugging experience.

Inspect Exceptions and Tracebacks

By default, Dask already copies the exception and traceback wherever they occur and reraises that exception locally. If your task failed with a `ZeroDivisionError` remotely then you'll get a `ZeroDivisionError` in your interactive session. Similarly you'll see a full traceback of where this error occurred, which, just like in normal Python, can help you to identify the troublsome spot in your code.

However, you cannot use the `pdb` module or `%debug` IPython magics with these tracebacks to look at the value of variables during failure. You can only inspect things visually. Additionally, the top of the traceback may be filled with functions that are dask-specific and not relevant to your problem, you can safely ignore these.

Both the single-machine and distributed schedulers do this.

Use the Single-Threaded Scheduler

Dask ships with a simple single-threaded scheduler. This doesn't offer any parallel performance improvements, but does run your Dask computation faithfully in your local thread, allowing you to use normal tools like `pdb`, `%debug` IPython magics, the profiling tools like the `cProfile` module and snakeviz. This allows you to use all of your normal Python debugging tricks in Dask computations, as long as you don't need parallelism.

The single-threaded scheduler can be used, for example, by setting `scheduler='single-threaded'` in a compute call

```
>>> x.compute(scheduler='single-threaded')
```

For more ways to configure schedulers, see the *scheduler configuration documentation*.

This only works for single-machine schedulers. It does not work with dask.distributed unless you are comfortable using the Tornado API (look at the testing infrastructure docs, which accomplish this). Also, because this operates on a single machine it assumes that your computation can run on a single machine without exceeding memory limits. It may be wise to use this approach on smaller versions of your problem if possible.

Rerun Failed Task Locally

If a remote task fails, we can collect the function and all inputs, bring them to the local thread, and then rerun the function in hopes of triggering the same exception locally, where normal debugging tools can be used.

With the single machine schedulers, use the `rerun_exceptions_locally=True` keyword.

```
>>> x.compute(rerun_exceptions_locally=True)
```

On the distributed scheduler use the `recreate_error_locally` method on anything that contains `Futures` :

```
>>> x.compute()
ZeroDivisionError(...)

>>> %pdb
>>> future = client.compute(x)
>>> client.recreate_error_locally(future)
```

Remove Failed Futures Manually

Sometimes only parts of your computations fail, for example if some rows of a CSV dataset are faulty in some way. When running with the distributed scheduler you can remove chunks of your data that have produced bad results if you switch to dealing with Futures.

```
>>> import dask.dataframe as dd
>>> df = ...            # create dataframe
>>> df = df.persist()   # start computing on the cluster

>>> from distributed.client import futures_of
>>> futures = futures_of(df)   # get futures behind dataframe
>>> futures
[<Future: status: finished, type: pd.DataFrame, key: load-1>
 <Future: status: finished, type: pd.DataFrame, key: load-2>
 <Future: status: error, key: load-3>
 <Future: status: pending, key: load-4>
 <Future: status: error, key: load-5>]

>>> # wait until computation is done
>>> while any(f.status == 'pending' for f in futures):
...     sleep(0.1)

>>> # pick out only the successful futures and reconstruct the dataframe
>>> good_futures = [f for f in futures if f.status == 'finished']
>>> df = dd.from_delayed(good_futures, meta=df._meta)
```

This is a bit of a hack, but often practical when first exploring messy data. If you are using the concurrent.futures API (map, submit, gather) then this approach is more natural.

4.19.2 Inspect Scheduling State

Not all errors present themselves as Exceptions. For example in a distributed system workers may die unexpectedly or your computation may be unreasonably slow due to inter-worker communication or scheduler overhead or one of several other issues. Getting feedback about what's going on can help to identify both failures and general performance bottlenecks.

For the single-machine scheduler see *diagnostics* documentation. The rest of the section will assume that you are using the distributed scheduler where these issues arise more commonly.

Web Diagnostics

First, the distributed scheduler has a number of diagnostic web pages showing dozens of recorded metrics like CPU, memory, network, and disk use, a history of previous tasks, allocation of tasks to workers, worker memory pressure, work stealing, open file handle limits, etc.. *Many* problems can be correctly diagnosed by inspecting these pages. By default these are available at `http://scheduler:8787/` `http://scheduler:8788/` and `http://worker:8789/` where `scheduler` and `worker` should be replaced by the addresses of the scheduler and each of the workers. See web diagnostic docs for more information.

Logs

The scheduler and workers and client all emits logs using Python's standard logging module. By default these emit to standard error. When Dask is launched by a cluster job scheduler (SGE/SLURM/YARN/Mesos/Marathon/Kubernetes/whatever) that system will track these logs and will have an interface to help you access them. If you are launching Dask on your own they will probably dump to the screen unless you redirect stderr to a file .

You can control the logging verbosity in the `~/.dask/config.yaml` file. Defaults currently look like the following:

```
logging:
  distributed: info
  distributed.client: warning
  bokeh: error
```

So for example you could add a line like `distributed.worker: debug` to get *very* verbose output from the workers.

4.19.3 LocalCluster

If you are using the distributed scheduler from a single machine you may be setting up workers manually using the command line interface or you may be using LocalCluster which is what runs when you just call `Client()`

```
>>> from dask.distributed import Client, LocalCluster
>>> client = Client()  # This is actually the following two commands

>>> cluster = LocalCluster()
>>> client = Client(cluster.scheduler.address)
```

LocalCluster is useful because the scheduler and workers are in the same process with you, so you can easily inspect their state while they run (they are running in a separate thread).

```
>>> cluster.scheduler.processing
{'worker-one:59858': {'inc-123', 'add-443'},
 'worker-two:48248': {'inc-456'}}
```

You can also do this for the workers *if* you run them without nanny processes.

```
>>> cluster = LocalCluster(nanny=False)
>>> client = Client(cluster)
```

This can be very helpful if you want to use the dask.distributed API and still want to investigate what is going on directly within the workers. Information is not distilled for you like it is in the web diagnostics, but you have full low-level access.

4.19.4 Inspect state with IPython

Sometimes you want to inspect the state of your cluster, but you don't have the luxury of operating on a single machine. In these cases you can launch an IPython kernel on the scheduler and on every worker, which lets you inspect state on the scheduler and workers as computations are completing.

This does not give you the ability to run `%pdb` or `%debug` on remote machines, the tasks are still running in separate threads, and so are not easily accessible from an interactive IPython session.

For more details, see the Dask.distributed IPython docs.

Graph Internals

Internally, Dask encodes algorithms in a simple format involving Python dicts, tuples, and functions. This graph format can be used in isolation from the dask collections. Working directly with dask graphs is rare, unless you intend to develop new modules with Dask. Even then, *dask.delayed* is often a better choice. If you are a *core developer*, then you should start here.

- *Overview*
- *Specification*
- *Custom Graphs*
- *Optimization*
- *Custom Collections*

4.20 Overview

An explanation of dask task graphs.

4.20.1 Motivation

Normally, humans write programs and then compilers/interpreters interpret them (for example `python`, `javac`, `clang`). Sometimes humans disagree with how these compilers/interpreters choose to interpret and execute their programs. In these cases humans often bring the analysis, optimization, and execution of code into the code itself.

Commonly a desire for parallel execution causes this shift of responsibility from compiler to human developer. In these cases, we often represent the structure of our program explicitly as data within the program itself.

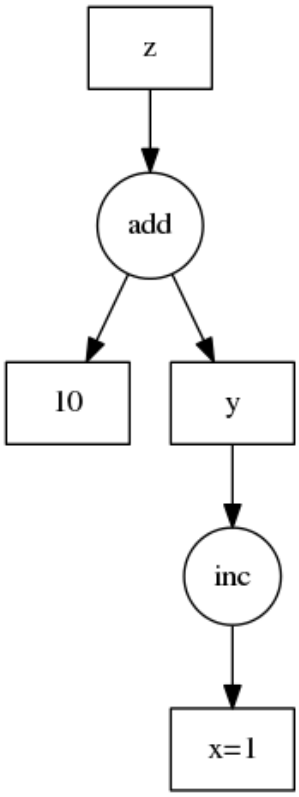
A common approach to parallel execution in user-space is *task scheduling*. In task scheduling we break our program into many medium-sized tasks or units of computation, often a function call on a non-trivial amount of data. We

represent these tasks as nodes in a graph with edges between nodes if one task depends on data produced by another. We call upon a *task scheduler* to execute this graph in a way that respects these data dependencies and leverages parallelism where possible, multiple independent tasks can be run simultaneously.

Many solutions exist. This is a common approach in parallel execution frameworks. Often task scheduling logic hides within other larger frameworks (Luigi, Storm, Spark, IPython Parallel, and so on) and so is often reinvented.

Dask is a specification that encodes task schedules with minimal incidental complexity using terms common to all Python projects, namely dicts, tuples, and callables. Ideally this minimum solution is easy to adopt and understand by a broad community.

4.20.2 Example



Consider the following simple program:

```
def inc(i):
    return i + 1

def add(a, b):
    return a + b

x = 1
y = inc(x)
z = add(y, 10)
```

We encode this as a dictionary in the following way:

```
d = {'x': 1,
     'y': (inc, 'x'),
     'z': (add, 'y', 10)}
```

While less pleasant than our original code, this representation can be analyzed and executed by other Python code, not just the CPython interpreter. We don't recommend that users write code in this way, but rather that it is an appropriate target for automated systems. Also, in non-toy examples, the execution times are likely much larger than for `inc` and `add`, warranting the extra complexity.

4.20.3 Schedulers

The `dask` library currently contains a few schedulers to execute these graphs. Each scheduler works differently, providing different performance guarantees and operating in different contexts. These implementations are not special and others can write different schedulers better suited to other applications or architectures easily. Systems that emit dask graphs (like `dask.array`, `dask.bag`, and so on) may leverage the appropriate scheduler for the application and hardware.

4.21 Specification

Dask is a specification to encode a graph – specifically, a directed acyclic graph of tasks with data dependencies – using ordinary Python data structures, namely dicts, tuples, functions, and arbitrary Python values.

4.21.1 Definitions

A **dask graph** is a dictionary mapping **keys** to **computations**:

```
{'x': 1,
 'y': 2,
 'z': (add, 'x', 'y'),
 'w': (sum, ['x', 'y', 'z']),
 'v': [(sum, ['w', 'z']), 2]}
```

A **key** is any hashable value that is not a **task**:

```
'x'
('x', 2, 3)
```

A **task** is a tuple with a callable first element. Tasks represent atomic units of work meant to be run by a single worker. Example:

```
(add, 'x', 'y')
```

We represent a task as a tuple such that the *first element is a callable function* (like `add`), and the succeeding elements are *arguments* for that function. An *argument* may be any valid **computation**.

A **computation** may be one of the following:

1. Any **key** present in the dask graph like `'x'`
2. Any other value like `1`, to be interpreted literally
3. A **task** like `(inc, 'x')` (see below)
4. A list of **computations**, like `[1, 'x', (inc, 'x')]`

So all of the following are valid **computations**:

```
np.array([...])
(add, 1, 2)
(add, 'x', 2)
(add, (inc, 'x'), 2)
(sum, [1, 2])
(sum, ['x', (inc, 'x')])
(np.dot, np.array([...]), np.array([...]))
[(sum, ['x', 'y']), 'z']
```

To encode keyword arguments, we recommend the use of `functools.partial` or `toolz.curry`.

4.21.2 What functions should expect

In cases like `(add, 'x', 'y')`, functions like `add` receive concrete values instead of keys. A dask scheduler replaces keys (like `'x'` and `'y'`) with their computed values (like `1`, and `2`) *before* calling the `add` function.

4.21.3 Entry Point - The `get` function

The `get` function serves as entry point to computation for all schedulers. This function gets the value associated to the given key. That key may refer to stored data, as is the case with `'x'`, or a task as is the case with `'z'`. In the latter case, `get` should perform all necessary computation to retrieve the computed value.

```
>>> from dask.threaded import get

>>> from operator import add

>>> dsk = {'x': 1,
...        'y': 2,
...        'z': (add, 'x', 'y'),
...        'w': (sum, ['x', 'y', 'z'])}
```

```
>>> get(dsk, 'x')
1

>>> get(dsk, 'z')
3

>>> get(dsk, 'w')
6
```

Additionally if given a `list`, get should simultaneously acquire values for multiple keys:

```
>>> get(dsk, ['x', 'y', 'z'])
[1, 2, 3]
```

Because we accept lists of keys as keys, we support nested lists.

```
>>> get(dsk, [['x', 'y'], ['z', 'w']])
[[1, 2], [3, 6]]
```

Internally `get` can be arbitrarily complex, calling out to distributed computing, using caches, and so on.

4.21.4 Why use tuples

With `(add, 'x', 'y')` we wish to encode "the result of calling `add` on the values corresponding to the keys `'x'` and `'y'`.

We intend the following meaning:

```
add('x', 'y')  # after x and y have been replaced
```

But this will err because Python executes the function immediately, before we know values for `'x'` and `'y'`.

We delay the execution by moving the opening parenthesis one term to the left, creating a tuple:

```
Before: add( 'x', 'y')
After: (add, 'x', 'y')
```

This lets us store the desired computation as data that we can analyze using other Python code, rather than cause immediate execution.

LISP users will identify this as an s-expression, or as a rudimentary form of quoting.

4.22 Custom Graphs

There may be times that you want to do parallel computing, but your application doesn't fit neatly into something like `dask.array` or `dask.bag`. In these cases, you can interact directly with the dask schedulers. These schedulers operate well as standalone modules.

This separation provides a release valve for complex situations and allows advanced projects additional opportunities for parallel execution, even if those projects have an internal representation for their computations. As dask schedulers improve or expand to distributed memory, code written to use dask schedulers will advance as well.

4.22.1 Example

As discussed in the *motivation* and *specification* sections, the schedulers take a task graph which is a dict of tuples of functions, and a list of desired keys from that graph.

Here is a mocked out example building a graph for a traditional clean and analyze pipeline:

```
def load(filename):
    ...

def clean(data):
    ...

def analyze(sequence_of_data):
    ...

def store(result):
    with open(..., 'w') as f:
        f.write(result)
```

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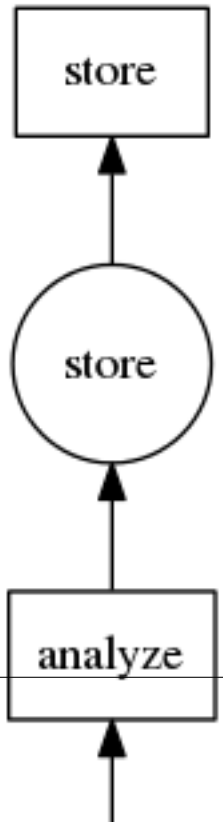

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```
dsk = {'load-
↪1': (load, 'myfile.a.data'),
       'load-
↪2': (load, 'myfile.b.data'),
       'load-
↪3': (load, 'myfile.c.data'),
      ␣
↪'clean-1': (clean, 'load-1'),
      ␣
↪'clean-2': (clean, 'load-2'),
      ␣
↪'clean-3': (clean, 'load-3'),
      ␣
↪'analyze': (analyze, ['clean-
↪%d' % i for i in [1, 2, 3]]),
     ␣
↪ 'store': (store, 'analyze')}

from dask.
↪multiprocessing import get
get(dsk, 'store
↪')  # executes in parallel
```

4.22.2 Related Projects

The following excellent projects also provide parallel execution:

- Joblib
- Multiprocessing
- IPython Parallel
- Concurrent.futures
- Luigi

Each library lets you dictate how your tasks relate to each other with various levels of sophistication. Each library executes those tasks with some internal logic.

Dask schedulers differ in the following ways:

1. You specify the entire graph as a Python dict rather than using a specialized API
2. You get a variety of schedulers ranging from single machine single core, to threaded, to multiprocessing, to distributed, and
3. The dask single-machine schedulers have logic to execute the graph

in a way that minimizes memory footprint.

But the other projects offer different advantages and different programming paradigms. One should inspect all such projects before selecting one.

4.23 Optimization

Performance can be significantly improved in different contexts by making small optimizations on the dask graph before calling the scheduler.

The `dask.optimization` module contains several functions to transform graphs in a variety of useful ways. In most cases, users won't need to interact with these functions directly, as specialized subsets of these transforms are done automatically in the dask collections (`dask.array`, `dask.bag`, and `dask.dataframe`). However, users working with custom graphs or computations may find that applying these methods results in substantial speedups.

In general, there are two goals when doing graph optimizations:

1. Simplify computation
2. Improve parallelism.

Simplifying computation can be done on a graph level by removing unnecessary tasks (`cull`), or on a task level by replacing expensive operations with cheaper ones (`RewriteRule`).

Parallelism can be improved by reducing inter-task communication, whether by fusing many tasks into one (`fuse`), or by inlining cheap operations (`inline`, `inline_functions`).

Below, we show an example walking through the use of some of these to optimize a task graph.

4.23.1 Example

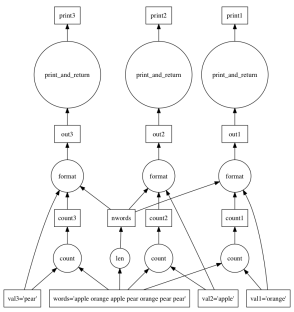
Suppose you had a custom dask graph for doing a word counting task:

```
>>> from __future__ import␣
↪print_function

>>> def print_and_
↪return(string):
...     print(string)
...     return string

>>> def format_str(count, val,␣
↪nwords):
...     return ('word list has
↪{0} occurrences of {1}, '
...             'out of {2}␣
↪words').format(count, val,␣
↪nwords)

>>> dsk = {'words': 'apple␣
↪orange apple pear orange␣
↪pear pear',
...        'nwords': (len,␣
↪(str.split, 'words')),
...        'val1': 'orange',
...        'val2': 'apple',
...        'val3': 'pear',
...        'count1': (str.
↪count, 'words', 'val1'),
...        'count2': (str.
↪count, 'words', 'val2'),
...        'count3': (str.
↪count, 'words', 'val3'),
...        'out1': (format_str,
↪ 'count1', 'val1', 'nwords'),
...        'out2': (format_str,
↪ 'count2', 'val2', 'nwords'),
...        'out3': (format_str,
↪ 'count3', 'val3', 'nwords'),
...        'print1': (print_
↪and_return, 'out1'),
...        'print2': (print_
↪and_return, 'out2'),
...        'print3': (print_
↪and_return, 'out3')}
```



Here we're counting the occurrence of the words `'orange'`, `'apple'`, and `'pear'` in the list of words, formatting an output string reporting the results, printing the output, then returning the output string.

To perform the computation, we pass the dask graph and the desired output keys to a scheduler `get` function:

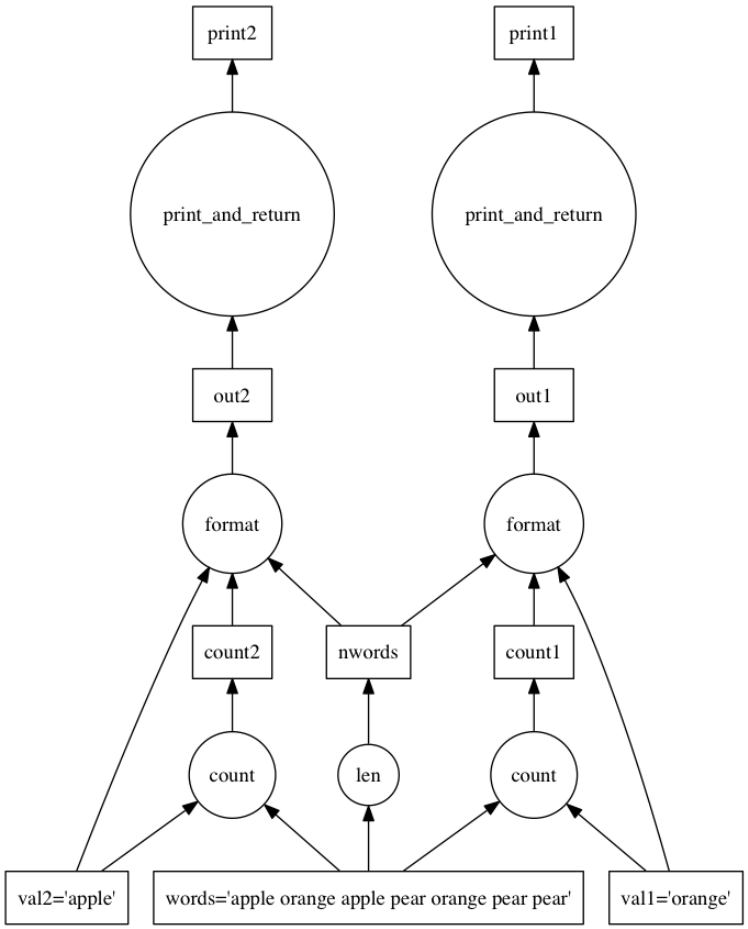
```
>>> from dask.threaded import get

>>> outputs = ['print1', 'print2']
>>> results = get(dsk, outputs)
word list has 2 occurrences of apple, out of 7 words
word list has 2 occurrences of orange, out of 7 words

>>> results
('word list has 2 occurrences of orange, out of 7 words',
 'word list has 2 occurrences of apple, out of 7 words')
```

As can be seen above, the scheduler computed only the requested outputs (`'print3'` was never computed). This is because the scheduler internally calls `cull`, which removes the unnecessary tasks from the graph. Even though this is done internally in the scheduler, it can be beneficial to call it at the start of a series of optimizations to reduce the amount of work done in later steps:

```
>>> from dask.optimization import cull
>>> dsk1, dependencies = cull(dsk, outputs)
```



Looking at the task graph above, there are multiple accesses to constants such as `'val1'` or `'val2'` in the dask graph. These can be inlined into the tasks to improve efficiency using the `inline` function. For example:

```
>>> from dask.optimization import inline
>>> dsk2 = inline(dsk1, dependencies=dependencies)
>>> results = get(dsk2, outputs)
```

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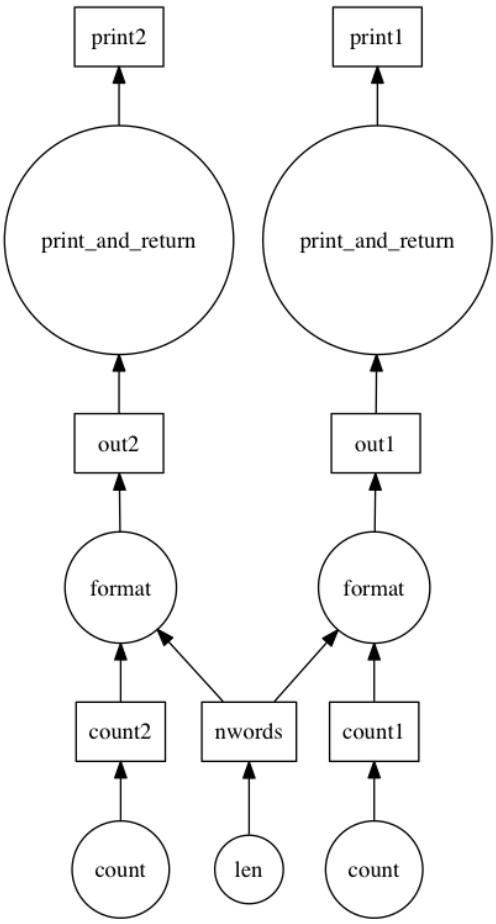
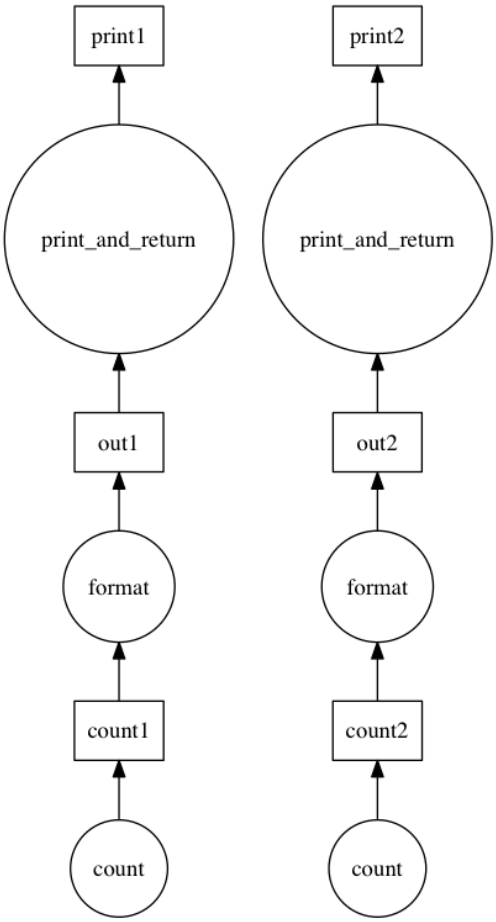
```
word list has 2 occurrences of apple, out of 7 words
word list has 2 occurrences of orange, out of 7 words
```



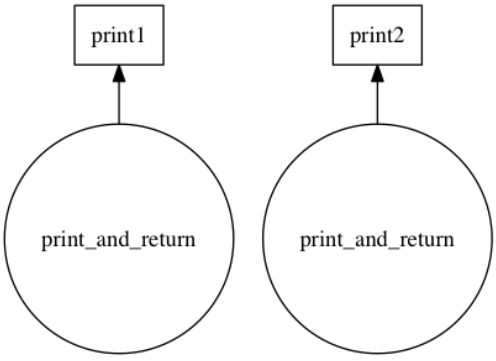
Now we have two sets of *almost* linear task chains. The only link between them is the word counting function. For cheap operations like this, the serialization cost may be larger than the actual computation, so it may be faster to do the computation more than once, rather than passing the results to all nodes. To perform this function inlining, the `inline_functions` function can be used:

```
>>> from dask.optimization import inline_functions
>>> dsk3 = inline_functions(dsk2, outputs, [len, str.split],
...                         dependencies=dependencies)
>>> results = get(dsk3, outputs)
word list has 2 occurrences of apple, out of 7 words
word list has 2 occurrences of orange, out of 7 words
```



Now we have a set of purely linear tasks. We'd like to have the scheduler run all of these on the same worker to reduce data serialization between workers. One option is just to merge these linear chains into one big task using the `fuse` function:

```
>>> from dask.optimization import fuse
>>> dsk4, dependencies = fuse(dsk3)
>>> results = get(dsk4, outputs)
word list has 2 occurrences of apple, out of 7 words
word list has 2 occurrences of orange, out of 7 words
```



Putting it all together:

```
>>> def optimize_and_get(dsk, keys):
...     dsk1, deps = cull(dsk, keys)
...     dsk2 = inline(dsk1, dependencies=deps)
...     dsk3 = inline_functions(dsk2, keys, [len, str.split],
...                             dependencies=deps)
...     dsk4, deps = fuse(dsk3)
...     return get(dsk4, keys)

>>> optimize_and_get(dsk, outputs)
word list has 2 occurrences of apple, out of 7 words
word list has 2 occurrences of orange, out of 7 words
```

In summary, the above operations accomplish the following:

1. Removed tasks unnecessary for the desired output using `cull`.
2. Inlined constants using `inline`.
3. Inlined cheap computations using `inline_functions`, improving parallelism.
4. Fused linear tasks together to ensure they run on the same worker using `fuse`.

As stated previously, these optimizations are already performed automatically in the dask collections. Users not working with custom graphs or computations should rarely need to directly interact with them.

These are just a few of the optimizations provided in `dask.optimization`. For more information, see the API below.

4.23.2 Rewrite Rules

For context based optimizations, `dask.rewrite` provides functionality for pattern matching and term rewriting. This is useful for replacing expensive computations with equivalent, cheaper computations. For example, `dask.array` uses the rewrite functionality to replace series of array slicing operations with a more efficient single slice.

The interface to the rewrite system consists of two classes:

1. `RewriteRule(lhs, rhs, vars)`

   Given a left-hand-side (`lhs`), a right-hand-side (`rhs`), and a set of variables (`vars`), a rewrite rule declaratively encodes the following operation:

   `lhs -> rhs if task matches lhs over variables`

2. `RuleSet(*rules)`

   A collection of rewrite rules. The design of `RuleSet` class allows for efficient "many-to-one" pattern matching, meaning that there is minimal overhead for rewriting with multiple rules in a rule set.

Example

Here we create two rewrite rules expressing the following mathematical transformations:

1. `a + a -> 2*a`
2. `a * a -> a**2`

where `'a'` is a variable:

```
>>> from dask.rewrite import RewriteRule, RuleSet
>>> from operator import add, mul, pow

>>> variables = ('a',)

>>> rule1 = RewriteRule((add, 'a', 'a'), (mul, 'a', 2), variables)

>>> rule2 = RewriteRule((mul, 'a', 'a'), (pow, 'a', 2), variables)

>>> rs = RuleSet(rule1, rule2)
```

The `RewriteRule` objects describe the desired transformations in a declarative way, and the `RuleSet` builds an efficient automata for applying that transformation. Rewriting can then be done using the `rewrite` method:

```
>>> rs.rewrite((add, 5, 5))
(mul, 5, 2)

>>> rs.rewrite((mul, 5, 5))
(pow, 5, 2)

>>> rs.rewrite((mul, (add, 3, 3), (add, 3, 3)))
(pow, (mul, 3, 2), 2)
```

The whole task is traversed by default. If you only want to apply a transform to the top-level of the task, you can pass in `strategy='top_level'` as shown:

```
# Transforms whole task
>>> rs.rewrite((sum, [(add, 3, 3), (mul, 3, 3)]))
(sum, [(mul, 3, 2), (pow, 3, 2)])

# Only applies to top level, no transform occurs
>>> rs.rewrite((sum, [(add, 3, 3), (mul, 3, 3)]), strategy='top_level')
(sum, [(add, 3, 3), (mul, 3, 3)])
```

The rewriting system provides a powerful abstraction for transforming computations at a task level. Again, for many users, directly interacting with these transformations will be unnecessary.

4.23.3 Keyword Arguments

Some optimizations take optional keyword arguments. To pass keywords from the compute call down to the right optimization, prepend the keyword with the name of the optimization. For example to send a `keys=` keyword argument to the `fuse` optimization from a compute call, use the `fuse_keys=` keyword:

```
def fuse(dsk, keys=None):
    ...

x.compute(fuse_keys=['x', 'y', 'z'])
```

4.23.4 Customizing Optimization

Dask defines a default optimization strategy for each collection type (Array, Bag, DataFrame, Delayed). However different applications may have different needs. To address this variability of needs, you can construct your own custom optimization function and use it instead of the default. An optimization function takes in a task graph and list of desired keys and returns a new task graph.

```
def my_optimize_function(dsk, keys):
    new_dsk = {...}
    return new_dsk
```

You can then register this optimization class against whichever collection type you prefer and it will be used instead of the default scheme.

```
with dask.config.set(array_optimize=my_optimize_function):
    x, y = dask.compute(x, y)
```

You can register separate optimization functions for different collections, or you can register `None` if you do not want particular types of collections to be optimized.

```
with dask.config.set(array_optimize=my_optimize_function,
                     dataframe_optimize=None,
                     delayed_optimize=my_other_optimize_function):
    ...
```

You need not specify all collections. Collections will default to their standard optimization scheme (which is usually a good choice).

4.23.5 API

Top level optimizations

cull(dsk, keys)	Return new dask with only the tasks required to calculate keys.
fuse(dsk[, keys, dependencies, ave_width, ...])	Fuse tasks that form reductions; more advanced than `fuse_linear`
inline(dsk[, keys, inline_constants, ...])	Return new dask with the given keys inlined with their values.
inline_functions(dsk, output[, ...])	Inline cheap functions into larger operations

Utility functions

functions_of(task)	Set of functions contained within nested task

Rewrite Rules

RewriteRule(lhs, rhs[, vars])	A rewrite rule.
RuleSet(*rules)	A set of rewrite rules.

Definitions

`dask.optimization.`**`cull`**(*dsk*, *keys*)

Return new dask with only the tasks required to calculate keys.

In other words, remove unnecessary tasks from dask. `keys` may be a single key or list of keys.

Returns

dsk: culled dask graph

dependencies: Dict mapping {key: [deps]}. Useful side effect to accelerate other optimizations, notably fuse.

Examples

```
>>> d = {'x': 1, 'y': (inc, 'x'), 'out': (add, 'x', 10)}
>>> dsk, dependencies = cull(d, 'out')
>>> dsk
{'x': 1, 'out': (add, 'x', 10)}
>>> dependencies
{'x': set(), 'out': set(['x'])}
```

dask.optimization.**fuse**(*dsk*, *keys=None*, *dependencies=None*, *ave_width=None*, *max_width=None*, *max_height=None*, *max_depth_new_edges=None*, *rename_keys=None*, *fuse_subgraphs=None*)

Fuse tasks that form reductions; more advanced than `fuse_linear`

This trades parallelism opportunities for faster scheduling by making tasks less granular. It can replace `fuse_linear` in optimization passes.

This optimization applies to all reductions–tasks that have at most one dependent–so it may be viewed as fusing "multiple input, single output" groups of tasks into a single task. There are many parameters to fine tune the behavior, which are described below. `ave_width` is the natural parameter with which to compare parallelism to granularity, so it should always be specified. Reasonable values for other parameters with be determined using `ave_width` if necessary.

Parameters

dsk: dict dask graph

keys: list or set, optional Keys that must remain in the returned dask graph

dependencies: dict, optional {key: [list-of-keys]}. Must be a list to provide count of each key This optional input often comes from `cull`

ave_width: float (default 2) Upper limit for `width = num_nodes / height`, a good measure of parallelizability

max_width: int Don't fuse if total width is greater than this

max_height: int Don't fuse more than this many levels

max_depth_new_edges: int Don't fuse if new dependencies are added after this many levels

rename_keys: bool or func, optional Whether to rename the fused keys with `default_fused_keys_renamer` or not. Renaming fused keys can keep the graph more understandable and comprehensive, but it comes at the cost of additional processing. If False, then the top-most key will be used. For advanced usage, a function to create the new name is also accepted.

fuse_subgraphs [bool, optional] Whether to fuse multiple tasks into `SubgraphCallable` objects.

Returns

dsk: output graph with keys fused

dependencies: dict mapping dependencies after fusion. Useful side effect to accelerate other downstream optimizations.

dask.optimization.**inline**(*dsk*, *keys=None*, *inline_constants=True*, *dependencies=None*)
Return new dask with the given keys inlined with their values.

Inlines all constants if `inline_constants` keyword is True. Note that the constant keys will remain in the graph, to remove them follow `inline` with `cull`.

Examples

```
>>> d = {'x': 1, 'y': (inc, 'x'), 'z': (add, 'x', 'y')}
>>> inline(d)
{'x': 1, 'y': (inc, 1), 'z': (add, 1, 'y')}
```

```
>>> inline(d, keys='y')
{'x': 1, 'y': (inc, 1), 'z': (add, 1, (inc, 1))}
```

```
>>> inline(d, keys='y', inline_constants=False)
{'x': 1, 'y': (inc, 1), 'z': (add, 'x', (inc, 'x'))}
```

dask.optimization.**inline_functions**(*dsk*, *output*, *fast_functions=None*, *inline_constants=False*, *dependencies=None*)
Inline cheap functions into larger operations

Examples

```
>>> dsk = {'out': (add, 'i', 'd'),
...        'i': (inc, 'x'),
...        'd': (double, 'y'),
...        'x': 1, 'y': 1}
>>> inline_functions(dsk, [], [inc])
{'out': (add, (inc, 'x'), 'd'),
 'd': (double, 'y'),
 'x': 1, 'y': 1}
```

Protect output keys. In the example below `i` is not inlined because it is marked as an output key.

```
>>> inline_functions(dsk, ['i', 'out'], [inc, double])
{'out': (add, 'i', (double, 'y')),
 'i': (inc, 'x'),
 'x': 1, 'y': 1}
```

dask.optimization.**functions_of**(*task*)
Set of functions contained within nested task

Examples

```
>>> task = (add, (mul, 1, 2), (inc, 3))
>>> functions_of(task)
set([add, mul, inc])
```

dask.rewrite.**RewriteRule**(*lhs*, *rhs*, *vars=()*)
A rewrite rule.

Expresses *lhs* -> *rhs*, for variables *vars*.

Parameters

lhs [task] The left-hand-side of the rewrite rule.

rhs [task or function] The right-hand-side of the rewrite rule. If it's a task, variables in *rhs* will be replaced by terms in the subject that match the variables in *lhs*. If it's a function, the function will be called with a dict of such matches.

vars: tuple, optional Tuple of variables found in the lhs. Variables can be represented as any hashable object; a good convention is to use strings. If there are no variables, this can be omitted.

Examples

Here's a *RewriteRule* to replace all nested calls to *list*, so that *(list, (list, 'x'))* is replaced with *(list, 'x')*, where *'x'* is a variable.

```
>>> lhs = (list, (list, 'x'))
>>> rhs = (list, 'x')
>>> variables = ('x',)
>>> rule = RewriteRule(lhs, rhs, variables)
```

Here's a more complicated rule that uses a callable right-hand-side. A callable *rhs* takes in a dictionary mapping variables to their matching values. This rule replaces all occurrences of *(list, 'x')* with *'x'* if *'x'* is a list itself.

```
>>> lhs = (list, 'x')
>>> def repl_list(sd):
...     x = sd['x']
...     if isinstance(x, list):
...         return x
...     else:
...         return (list, x)
>>> rule = RewriteRule(lhs, repl_list, variables)
```

dask.rewrite.**RuleSet**(**rules*)

A set of rewrite rules.

Forms a structure for fast rewriting over a set of rewrite rules. This allows for syntactic matching of terms to patterns for many patterns at the same time.

Examples

```
>>> def f(*args): pass
>>> def g(*args): pass
>>> def h(*args): pass
>>> from operator import add
```

```
>>> rs = RuleSet(                  # Make RuleSet with two Rules
...         RewriteRule((add, 'x', 0), 'x', ('x',)),
...         RewriteRule((f, (g, 'x'), 'y'),
...                     (h, 'x', 'y'),
...                     ('x', 'y')))
```

```
>>> rs.rewrite((add, 2, 0))        # Apply ruleset to single task
2
```

```
>>> rs.rewrite((f, (g, 'a', 3)))
(h, 'a', 3)
```

```
>>> dsk = {'a': (add, 2, 0),       # Apply ruleset to full dask graph
...        'b': (f, (g, 'a', 3))}
```

```
>>> from toolz import valmap
>>> valmap(rs.rewrite, dsk)
{'a': 2,
 'b': (h, 'a', 3)}
```

Attributes

rules [list] A list of *RewriteRule's included in the 'RuleSet*.

4.24 Custom Collections

For many problems the built-in dask collections (`dask.array`, `dask.dataframe`, `dask.bag`, and `dask.delayed`) are sufficient. For cases where they aren't it's possible to create your own dask collections. Here we describe the required methods to fullfill the dask collection interface.

Warning: The custom collection API is experimental and subject to change without going through a deprecation cycle.

Note: This is considered an advanced feature. For most cases the built-in collections are probably sufficient.

Before reading this you should read and underestand:

- *overview*
- *graph specification*
- *custom graphs*

Contents

- *Description of the dask collection interface*
- *How this interface is used to implement the core dask methods*
- *How to add the core methods to your class*
- *Example Dask Collection*
- *How to check if something is a dask collection*
- *How to make tokenize work with your collection*

4.24.1 The Dask Collection Interface

To create your own dask collection, you need to fullfill the following interface. Note that there is no required base class.

It's recommended to also read *Internals of the Core Dask Methods* to see how this interface is used inside dask.

__dask_graph__(*self*)
The dask graph.

dsk [MutableMapping, None] The dask graph. If `None`, this instance will not be interpreted as a dask collection, and none of the remaining interface methods will be called.

__dask_keys__(*self*)
The output keys for the dask graph.

keys [list] A possibly nested list of keys that represent the outputs of the graph. After computation, the results will be returned in the same layout, with the keys replaced with their corresponding outputs.

static __dask_optimize__(*dsk*, *keys*, ***kwargs*)
Given a graph and keys, return a new optimized graph.

This method can be either a `staticmethod` or a `classmethod`, but not an instancemethod.

Note that graphs and keys are merged before calling `__dask_optimize__`; as such the graph and keys passed to this method may represent more than one collection sharing the same optimize method.

If not implemented, defaults to returning the graph unchanged.

dsk [MutableMapping] The merged graphs from all collections sharing the same `__dask_optimize__` method.

keys [list] A list of the outputs from `__dask_keys__` from all collections sharing the same `__dask_optimize__` method.

****kwargs** Extra keyword arguments forwarded from the call to `compute` or `persist`. Can be used or ignored as needed.

optimized_dsk [MutableMapping] The optimized dask graph.

static __dask_scheduler__(*dsk*, *keys*, ***kwargs*)
The default scheduler `get` to use for this object.

Usually attached to the class as a staticmethod, e.g.

```
>>> import dask.threaded
>>> class MyCollection(object):
...     # Use the threaded scheduler by default
...     __dask_scheduler__ = staticmethod(dask.threaded.get)
```

__dask_postcompute__(*self*)
Return the finalizer and (optional) extra arguments to convert the computed results into their in-memory representation.

Used to implement `dask.compute`.

finalize [callable] A function with the signature `finalize(results, *extra_args)`. Called with the computed results in the same structure as the corresponding keys from `__dask_keys__`, as well as any extra arguments as specified in `extra_args`. Should perform any necessary finalization before returning the corresponding in-memory collection from `compute`. For example, the `finalize` function for `dask.array.Array` concatenates all the individual array chunks into one large numpy array, which is then the result of `compute`.

extra_args [tuple] Any extra arguments to pass to `finalize` after `results`. If no extra arguments should be an empty tuple.

__dask_postpersist__(*self*)
Return the rebuilder and (optional) extra arguments to rebuild an equivalent dask collection from a persisted graph.

Used to implement `dask.persist`.

rebuild [callable] A function with the signature `rebuild(dsk, *extra_args)`. Called with a persisted graph containing only the keys and results from `__dask_keys__`, as well as any extra arguments as specified in `extra_args`. Should return an equivalent dask collection with the same keys as `self`, but with the results already computed. For example, the `rebuild` function for `dask.array.Array` is just the `__init__` method called with the new graph but the same metadata.

extra_args [tuple] Any extra arguments to pass to `rebuild` after `dsk`. If no extra arguments should be an empty tuple.

Note: It's also recommended to define `__dask_tokenize__`, see *Implementing Deterministic Hashing*.

4.24.2 Internals of the Core Dask Methods

Dask has a few *core* functions (and corresponding methods) that implement common operations:

- `compute`: convert one or more dask collections into their in-memory counterparts
- `persist`: convert one or more dask collections into equivalent dask collections with their results already computed and cached in memory.
- `optimize`: convert one or more dask collections into equivalent dask collections sharing one large optimized graph.
- `visualize`: given one or more dask collections, draw out the graph that would be passed to the scheduler during a call to `compute` or `persist`

Here we briefly describe the internals of these functions to illustrate how they relate to the above interface.

Compute

The operation of `compute` can be broken into three stages:

1. **Graph Merging & Optimization**

   First the individual collections are converted to a single large graph and nested list of keys. How this happens depends on the value of the `optimize_graph` keyword, which each function takes:

   - If `optimize_graph` is `True` (default) then the collections are first grouped by their `__dask_optimize__` methods. All collections with the same `__dask_optimize__` method have their graphs merged and keys concatenated, and then a single call to each respective `__dask_optimize__` is made with the merged graphs and keys. The resulting graphs are then merged.
   - If `optimize_graph` is `False` then all the graphs are merged and all the keys concatenated.

   After this stage there is a single large graph and nested list of keys which represents all the collections.

2. **Computation**

   After the graphs are merged and any optimizations performed, the resulting large graph and nested list of keys are passed on to the scheduler. The scheduler to use is chosen as follows:

   - If a `get` function is specified directly as a keyword, use that.
   - Otherwise, if a global scheduler is set, use that.
   - Otherwise fall back to the default scheduler for the given collections. Note that if all collections don't share the same `__dask_scheduler__` then an error will be raised.

Once the appropriate scheduler `get` function is determined, it's called with the merged graph, keys, and extra keyword arguments. After this stage `results` is a nested list of values. The structure of this list mirrors that of `keys`, with each key substituted with its corresponding result.

3. **Postcompute**

   After the results are generated the output values of `compute` need to be built. This is what the `__dask_postcompute__` method is for. `__dask_postcompute__` returns two things:

   - A `finalize` function, which takes in the results for the corresponding keys
   - A tuple of extra arguments to pass to `finalize` after the results

   To build the outputs, the list of collections and results is iterated over, and the finalizer for each collection is called on its respective results.

In pseudocode this process looks like:

```
def compute(*collections, **kwargs):
    # 1. Graph Merging & Optimization
    # -------------------------------
    if kwargs.pop('optimize_graph', True):
        # If optimization is turned on, group the collections by
        # optimization method, and apply each method only once to the merged
        # sub-graphs.
        optimization_groups = groupby_optimization_methods(collections)
        graphs = []
        for optimize_method, cols in optimization_groups:
            # Merge the graphs and keys for the subset of collections that
            # share this optimization method
            sub_graph = merge_graphs([x.__dask_graph__() for x in cols])
            sub_keys = [x.__dask_keys__() for x in cols]
            # kwargs are forwarded to ``__dask_optimize__`` from compute
            optimized_graph = optimize_method(sub_graph, sub_keys, **kwargs)
            graphs.append(optimized_graph)
        graph = merge_graphs(graphs)
    else:
        graph = merge_graphs([x.__dask_graph__() for x in collections])
    # Keys are always the same
    keys = [x.__dask_keys__() for x in collections]

    # 2. Computation
    # --------------
    # Determine appropriate get function based on collections, global
    # settings, and keyword arguments
    get = determine_get_function(collections, **kwargs)
    # Pass the merged graph, keys, and kwargs to ``get``
    results = get(graph, keys, **kwargs)

    # 3. Postcompute
    # --------------
    output = []
    # Iterate over the results and collections
    for res, collection in zip(results, collections):
        finalize, extra_args = collection.__dask_postcompute__()
        out = finalize(res, **extra_args)
        output.append(out)

    # `dask.compute` always returns tuples
    return tuple(output)
```

Persist

Persist is very similar to `compute`, except for how the return values are created. It too has three stages:

1. **Graph Merging & Optimization**

   Same as in `compute`.

2. **Computation**

   Same as in `compute`, except in the case of the distributed scheduler, where the values in `results` are futures instead of values.

3. **Postpersist**

   Similar to `__dask_postcompute__`, `__dask_postpersist__` is used to rebuild values in a call to `persist`. `__dask_postpersist__` returns two things:

   - A `rebuild` function, which takes in a persisted graph. The keys of this graph are the same as `__dask_keys__` for the corresponding collection, and the values are computed results (for the single machine scheduler) or futures (for the distributed scheduler).
   - A tuple of extra arguments to pass to `rebuild` after the graph

   To build the outputs of `persist`, the list of collections and results is iterated over, and the rebuilder for each collection is called on the graph for its respective results.

In pseudocode this looks like:

```
def persist(*collections, **kwargs):
    # 1. Graph Merging & Optimization
    # -------------------------------
    # **Same as in compute**
    graph = ...
    keys = ...

    # 2. Computation
    # --------------
    # **Same as in compute**
    results = ...

    # 3. Postpersist
    # --------------
    output = []
    # Iterate over the results and collections
    for res, collection in zip(results, collections):
        # res has the same structure as keys
        keys = collection.__dask_keys__()
        # Get the computed graph for this collection.
        # Here flatten converts a nested list into a single list
        subgraph = {k: r for (k, r) in zip(flatten(keys), flatten(res))}

        # Rebuild the output dask collection with the computed graph
        rebuild, extra_args = collection.__dask_postpersist__()
        out = rebuild(subgraph, *extra_args)

        output.append(out)

    # dask.persist always returns tuples
    return tuple(output)
```

Optimize

The operation of `optimize` can be broken into two stages:

1. **Graph Merging & Optimization**

   Same as in `compute`.

2. **Rebuilding**

   Similar to `persist`, the `rebuild` function and arguments from `__dask_postpersist__` are used to reconstruct equivalent collections from the optimized graph.

In pseudocode this looks like:

```
def optimize(*collections, **kwargs):
    # 1. Graph Merging & Optimization
    # -------------------------------
    # **Same as in compute**
    graph = ...

    # 2. Rebuilding
    # -------------
    # Rebuild each dask collection using the same large optimized graph
    output = []
    for collection in collections:
        rebuild, extra_args = collection.__dask_postpersist__()
        out = rebuild(graph, *extra_args)
        output.append(out)

    # dask.optimize always returns tuples
    return tuple(output)
```

Visualize

Visualize is the simplest of the 4 core functions. It only has two stages:

1. **Graph Merging & Optimization**

   Same as in `compute`

2. **Graph Drawing**

   The resulting merged graph is drawn using `graphviz` and output to the specified file.

In pseudocode this looks like:

```
def visualize(*collections, **kwargs):
    # 1. Graph Merging & Optimization
    # -------------------------------
    # **Same as in compute**
    graph = ...

    # 2. Graph Drawing
    # ----------------
    # Draw the graph with graphviz's `dot` tool and return the result.
    return dot_graph(graph, **kwargs)
```

4.24.3 Adding the Core Dask Methods to Your Class

Defining the above interface will allow your object to used by the core dask functions (`dask.compute`, `dask.persist`, `dask.visualize`, etc...). To add corresponding method versions of these subclass from `dask.base.DaskMethodsMixin`, which adds implementations of `compute`, `persist`, and `visualize` based on the interface above.

4.24.4 Example Dask Collection

Here we create a dask collection representing a tuple. Every element in the tuple is represented as a task in the graph. Note that this is for illustration purposes only - the same user experience could be done using normal tuples with elements of `dask.delayed`.

```
# Saved as dask_tuple.py
from dask.base import DaskMethodsMixin
from dask.optimization import cull

# We subclass from DaskMethodsMixin to add common dask methods to our
# class. This is nice but not necessary for creating a dask collection.
class Tuple(DaskMethodsMixin):
    def __init__(self, dsk, keys):
        # The init method takes in a dask graph and a set of keys to use
        # as outputs.
        self._dsk = dsk
        self._keys = keys

    def __dask_graph__(self):
        return self._dsk

    def __dask_keys__(self):
        return self._keys

    @staticmethod
    def __dask_optimize__(dsk, keys, **kwargs):
        # We cull unnecessary tasks here. Note that this isn't necessary,
        # dask will do this automatically, this just shows one optimization
        # you could do.
        dsk2, _ = cull(dsk, keys)
        return dsk2

    # Use the threaded scheduler by default.
    __dask_scheduler__ = staticmethod(dask.threaded.get)

    def __dask_postcompute__(self):
        # We want to return the results as a tuple, so our finalize
        # function is `tuple`. There are no extra arguments, so we also
        # return an empty tuple.
        return tuple, ()

    def __dask_postpersist__(self):
        # Since our __init__ takes a graph as its first argument, our
        # rebuild function can just be the class itself. For extra
        # arguments we also return a tuple containing just the keys.
        return Tuple, (self._keys,)

    def __dask_tokenize__(self):
```

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```
        # For tokenize to work we want to return a value that fully
        # represents this object. In this case it's the list of keys
        # to be computed.
        return tuple(self._keys)
```

Demonstrating this class:

```
>>> from dask_tuple import Tuple
>>> from operator import add, mul

# Define a dask graph
>>> dsk = {'a': 1,
...        'b': 2,
...        'c': (add, 'a', 'b'),
...        'd': (mul, 'b', 2),
...        'e': (add, 'b', 'c')}

# The output keys for this graph
>>> keys = ['b', 'c', 'd', 'e']

>>> x = Tuple(dsk, keys)

# Compute turns Tuple into a tuple
>>> x.compute()
(2, 3, 4, 5)

# Persist turns Tuple into a Tuple, with each task already computed
>>> x2 = x.persist()
>>> isinstance(x2, Tuple)
True
>>> x2.__dask_graph__()
{'b': 2,
 'c': 3,
 'd': 4,
 'e': 5}
>>> x2.compute()
(2, 3, 4, 5)
```

4.24.5 Checking if an object is a dask collection

To check if an object is a dask collection, use `dask.base.is_dask_collection`:

```
>>> from dask.base import is_dask_collection
>>> from dask import delayed

>>> x = delayed(sum)([1, 2, 3])
>>> is_dask_collection(x)
True
>>> is_dask_collection(1)
False
```

4.24.6 Implementing Deterministic Hashing

Dask implements its own deterministic hash function to generate keys based on the value of arguments. This function is available as `dask.base.tokenize`. Many common types already have implementations of `tokenize`, which can be found in `dask/base.py`.

When creating your own custom classes you may need to register a `tokenize` implementation. There are two ways to do this:

Note: Both dask collections and normal python objects can have implementations of `tokenize` using either of the methods described below.

---

1. The `__dask_tokenize__` method

   Where possible, it's recommended to define the `__dask_tokenize__` method. This method takes no arguments and should return a value fully representative of the object.

2. Register a function with `dask.base.normalize_token`

   If defining a method on the class isn't possible, you can register a tokenize function with the `normalize_token` dispatch. The function should have the same signature as described above.

In both cases the implementation should be the same, only the location of the definition is different.

Example

```
>>> from dask.base import tokenize, normalize_token

# Define a tokenize implementation using a method.
>>> class Foo(object):
...     def __init__(self, a, b):
...         self.a = a
...         self.b = b
...
...     def __dask_tokenize__(self):
...         # This tuple fully represents self
...         return (Foo, self.a, self.b)

>>> x = Foo(1, 2)
>>> tokenize(x)
'5988362b6e07087db2bc8e7c1c8cc560'
>>> tokenize(x) == tokenize(x)  # token is deterministic
True

# Register an implementation with normalize_token
>>> class Bar(object):
...     def __init__(self, x, y):
...         self.x = x
...         self.y = y

>>> @normalize_token.register(Bar)
... def tokenize_bar(x):
...     return (Bar, x.x, x.x)

>>> y = Bar(1, 2)
>>> tokenize(y)
```

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```
'5a7e9c3645aa44cf13d021c14452152e'
>>> tokenize(y) == tokenize(y)
True
>>> tokenize(y) == tokenize(x)  # tokens for different objects aren't equal
False
```

For more examples please see `dask/base.py` or any of the built-in dask collections.

Help & reference

- *Development Guidelines*
- *Changelog*
- *Configuration*
- *Presentations On Dask*
- *Dask Cheat Sheet*
- *Comparison to Spark*
- *Opportunistic Caching*
- *Internal Data Ingestion*
- *Remote Data*
- *Citations*
- *Funding*
- *Images and Logos*

4.25 Development Guidelines

Dask is a community maintained project. We welcome contributions in the form of bug reports, documentation, code, design proposals, and more. This page provides resources on how best to contribute.

4.25.1 Where to ask for help

Dask conversation happens in the following places:

1. StackOverflow #dask tag: for usage questions
2. Github Issue Tracker: for discussions around new features or established bugs
3. Gitter chat: for real-time discussion

For usage questions and bug reports we strongly prefer the use of StackOverflow and Github issues over gitter chat. Github and StackOverflow are more easily searchable by future users and so is more efficient for everyone's time. Gitter chat is generally reserved for community discussion.

4.25.2 Separate Code Repositories

Dask maintains code and documentation in a few git repositories hosted on the Github `dask` organization, http://github.com/dask. This includes the primary repository and several other repositories for different components. A non-exhaustive list follows:

- http://github.com/dask/dask: The main code repository holding parallel algorithms, the single-machine scheduler, and most documentation.
- http://github.com/dask/distributed: The distributed memory scheduler
- http://github.com/dask/dask-ml: Machine learning algorithms
- http://github.com/dask/s3fs: S3 Filesystem interface
- http://github.com/dask/gcsfs: GCS Filesystem interface
- http://github.com/dask/hdfs3: Hadoop Filesystem interface
- ...

Git and Github can be challenging at first. Fortunately good materials exist on the internet. Rather than repeat these materials here we refer you to Pandas' documentation and links on this subject at http://pandas.pydata.org/pandas-docs/stable/contributing.html

4.25.3 Issues

The community discusses and tracks known bugs and potential features in the Github Issue Tracker. If you have a new idea or have identified a bug then you should raise it there to start public discussion.

If you are looking for an introductory issue to get started with development then check out the introductory label, which contains issues that are good for starting developers. Generally familiarity with Python, NumPy, Pandas, and some parallel computing are assumed.

4.25.4 Development Environment

Download code

Clone the main dask git repository (or whatever repository you're working on.):

```
git clone git@github.com:dask/dask.git
```

Install

You may want to install larger dependencies like NumPy and Pandas using a binary package manager, like conda. You can skip this step if you already have these libraries, don't care to use them, or have sufficient build environment on your computer to compile them when installing with `pip`:

```
conda install -y numpy pandas scipy bokeh
```

Install dask and dependencies:

```
cd dask
pip install -e .[complete]
```

For development dask uses the following additional dependencies:

```
pip install pytest moto mock
```

Run Tests

Dask uses py.test for testing. You can run tests from the main dask directory as follows:

```
py.test dask --verbose
```

4.25.5 Contributing to Code

Dask maintains development standards that are similar to most PyData projects. These standards include language support, testing, documentation, and style.

Python Versions

Dask supports Python versions 2.7, 3.4, 3.5, and 3.6 in a single codebase. Name changes are handled by the `dask/compatibility.py` file.

Test

Dask employs extensive unit tests to ensure correctness of code both for today and for the future. Test coverage is expected for all code contributions.

Tests are written in a py.test style with bare functions.

```
def test_fibonacci():
    assert fib(0) == 0
    assert fib(1) == 0
    assert fib(10) == 55
    assert fib(8) == fib(7) + fib(6)

    for x in [-3, 'cat', 1.5]:
        with pytest.raises(ValueError):
            fib(x)
```

These tests should compromise well between covering all branches and fail cases and running quickly (slow test suites get run less often.)

You can run tests locally by running `py.test` in the local dask directory:

```
py.test dask --verbose
```

You can also test certain modules or individual tests for faster response:

```
py.test dask/dataframe --verbose

py.test dask/dataframe/tests/test_dataframe_core.py::test_set_index
```

Tests run automatically on the Travis.ci and Appveyor continuous testing frameworks on every push to every pull request on GitHub.

Tests are organized within the various modules' subdirectories:

```
dask/array/tests/test_*.py
dask/bag/tests/test_*.py
dask/dataframe/tests/test_*.py
dask/diagnostics/tests/test_*.py
```

For the Dask collections like dask.array and dask.dataframe behavior is typically tested directly against the Numpy or Pandas libraries using the `assert_eq` functions:

```
import numpy as np
import dask.array as da
from dask.array.utils import assert_eq

def test_aggregations():
    nx = np.random.random(100)
    dx = da.from_array(x, chunks=(10,))

    assert_eq(nx.sum(), dx.sum())
    assert_eq(nx.min(), dx.min())
    assert_eq(nx.max(), dx.max())
    ...
```

This technique helps to ensure compatibility with upstream libraries, and tends to be simpler than testing correctness directly. Additionally, by passing Dask collections directly to the `assert_eq` function rather than call compute manually the testing suite is able to run a number of checks on the lazy collections themselves.

Docstrings

User facing functions should roughly follow the numpydoc standard, including sections for `Parameters`, `Examples` and general explanatory prose.

By default examples will be doc-tested. Reproducible examples in documentation is valuable both for testing and, more importantly, for communication of common usage to the user. Documentation trumps testing in this case and clear examples should take precedence over using the docstring as testing space. To skip a test in the examples add the comment `# doctest: +SKIP` directly after the line.

```
def fib(i):
    """ A single line with a brief explanation

    A more thorough description of the function, consisting of multiple
    lines or paragraphs.

    Parameters
    ----------
    i: int
         A short description of the argument if not immediately clear

    Examples
    --------
    >>> fib(4)
    3
    >>> fib(5)
    5
    >>> fib(6)
    8
    >>> fib(-1)  # Robust to bad inputs
    ValueError(...)
    """
```

Docstrings are currently tested under Python 3.6 on travis.ci. You can test docstrings with pytest as follows:

```
py.test dask --doctest-modules
```

Docstring testing requires graphviz to be installed. This can be done via:

```
conda install -y graphviz
```

Style

Dask verifies style uniformity with the `flake8` tool.:

```
pip install flake8
flake8 dask
```

Changelog

Every significative code contribution should be listed in the *Changelog* under the corresponding version. When submitting a Pull Request in Github please add to that file explaining what was added/modified.

4.25.6 Contributing to Documentation

Dask uses Sphinx for documentation, hosted on http://readthedocs.org . Documentation is maintained in the RestructuredText markup language (`.rst` files) in `dask/docs/source`. The documentation consists both of prose and API documentation.

To build the documentation locally, first install requirements:

```
cd docs/
pip install -r requirements-docs.txt
```

Then build documentation with `make`:

```
make html
```

The resulting HTML files end up in the `build/html` directory.

You can now make edits to rst files and run `make html` again to update the affected pages.

4.26 Changelog

4.26.1 0.19.3 / 2018-10-05

Array

- Make da.RandomState extensible to other modules (GH#4041) Matthew Rocklin
- Support unknown dims in ravel no-op case (GH#4055) Jim Crist
- Add basic infrastructure for cupy (GH#4019) Matthew Rocklin
- Avoid asarray and lock arguments for from_array(getitem‘) (GH#4044) Matthew Rocklin
- Move local imports in *corrcoef* to global imports (GH#4030) John A Kirkham
- Move local *indices* import to global import (GH#4029) John A Kirkham
- Fix-up Dask Array’s fromfunction w.r.t. dtype and kwargs (GH#4028) John A Kirkham

- Don't use dummy expansion for trim_internal in overlapped (GH#3964) Mark Harfouche
- Add unravel_index (GH#3958) John A Kirkham

Bag

- Sort result in Bag.frequencies (GH#4033) Matthew Rocklin
- Add support for npartitions=1 edge case in groupby (GH#4050) James Bourbeau
- Add new random dataset for people (GH#4018) Matthew Rocklin
- Improve performance of bag.read_text on small files (GH#4013) Eric Wolak
- Add bag.read_avro (GH#4000) (GH#4007) Martin Durant

Dataframe

- Added an `index` parameter to *`dask.dataframe.from_dask_array()`* for creating a dask DataFrame from a dask Array with a given index. (GH#3991) Tom Augspurger
- Improve sub-classability of dask dataframe (GH#4015) Matthew Rocklin
- Fix failing hdfs test [test-hdfs] (GH#4046) Jim Crist
- fuse_subgraphs works without normal fuse (GH#4042) Jim Crist
- Make path for reading many parquet files without prescan (GH#3978) Martin Durant
- Index in dd.from_dask_array (GH#3991) Tom Augspurger
- Making skiprows accept lists (GH#3975) Julia Signell
- Fail early in fastparquet read for nonexistent column (GH#3989) Martin Durant

Core

- Add support for npartitions=1 edge case in groupby (GH#4050) James Bourbeau
- Automatically wrap large arguments with dask.delayed in map_blocks/partitions (GH#4002) Matthew Rocklin
- Fuse linear chains of subgraphs (GH#3979) Jim Crist
- Make multiprocessing context configurable (GH#3763) Itamar Turner-Trauring

Documentation

- Extensive copy-editing (GH#4049), (GH#4034), (GH#4031), (GH#4020), (GH#4021), (GH#4022), (GH#4023), (GH#4016), (GH#4017), (GH#4010), (GH#3997), (GH#3996), Miguel Farrajota
- Update shuffle method selection docs [skip ci] (GH#4048) James Bourbeau
- Remove docs/source/examples, point to examples.dask.org (GH#4014) Matthew Rocklin
- Replace readthedocs links with dask.org (GH#4008) Matthew Rocklin
- Updates DataFrame.to_hdf docstring for returned values [skip ci] (GH#3992) James Bourbeau

4.26.2 0.19.2 / 2018-09-17

Array

- `apply_gufunc` implements automatic infer of functions output dtypes (GH#3936) Markus Gonser
- Fix array histogram range error when array has nans (GH#3980) James Bourbeau
- Issue 3937 follow up, int type checks. (GH#3956) Yu Feng
- from_array: add @martindurant's explaining of how hashing is done for an array. (GH#3965) Mark Harfouche
- Support gradient with coordinate (GH#3949) Keisuke Fujii

Core

- Fix use of has_keyword with partial in Python 2.7 (GH#3966) Mark Harfouche
- Set pyarrow as default for HDFS (GH#3957) Matthew Rocklin

Documentation

- Use dask_sphinx_theme (GH#3963) Matthew Rocklin
- Use JupyterLab in Binder links from main page Matthew Rocklin
- DOC: fixed sphinx syntax (GH#3960) Tom Augspurger

4.26.3 0.19.1 / 2018-09-06

Array

- Don't enforce dtype if result has no dtype (GH#3928) Matthew Rocklin
- Fix NumPy issubtype deprecation warning (GH#3939) Bruce Merry
- Fix arg reduction tokens to be unique with different arguments (GH#3955) Tobias de Jong
- Coerce numpy integers to ints in slicing code (GH#3944) Yu Feng
- Linalg.norm ndim along axis partial fix (GH#3933) Tobias de Jong

Dataframe

- Deterministic DataFrame.set_index (GH#3867) George Sakkis
- Fix divisions in read_parquet when dealing with filters #3831 #3930 (GH#3923) (GH#3931) @andrethrill
- Fixing returning type in categorical.as_known (GH#3888) Sriharsha Hatwar
- Fix DataFrame.assign for callables (GH#3919) Tom Augspurger
- Include partitions with no width in repartition (GH#3941) Matthew Rocklin
- Don't constrict stage/k dtype in dataframe shuffle (GH#3942) Matthew Rocklin

Documentation

- DOC: Add hint on how to render task graphs horizontally (GH#3922) Uwe Korn
- Add try-now button to main landing page (GH#3924) Matthew Rocklin

4.26.4 0.19.0 / 2018-08-29

Array

- Support coordinate in gradient (GH#3949) Keisuke Fujii
- Fix argtopk split_every bug (GH#3810) Guido Imperiale
- Ensure result computing dask.array.isnull() always gives a numpy array (GH#3825) Stephan Hoyer
- Support concatenate for scipy.sparse in dask array (GH#3836) Matthew Rocklin
- Fix argtopk on 32-bit systems. (GH#3823) Elliott Sales de Andrade
- Normalize keys in rechunk (GH#3820) Matthew Rocklin
- Allow shape of dask.array to be a numpy array (GH#3844) Mark Harfouche
- Fix numpy deprecation warning on tuple indexing (GH#3851) Tobias de Jong
- Rename ghost module to overlap (GH#3830) Robert Sare
- Re-add the ghost import to da __init__ (GH#3861) Jim Crist
- Ensure copy preserves masked arrays (GH#3852) Tobias de Jong

DataFrame

- Added `dtype` and `sparse` keywords to `dask.dataframe.get_dummies()` (GH#3792) Tom Augspurger
- Added `dask.dataframe.to_dask_array()` for converting a Dask Series or DataFrame to a Dask Array, possibly with known chunk sizes (GH#3884) *Tom Augspurger*
- Changed the behavior for *`dask.array.asarray()`* for dask dataframe and series inputs. Previously, the series was eagerly converted to an in-memory NumPy array before creating a dask array with known chunks sizes. This caused unexpectedly high memory usage. Now, no intermediate NumPy array is created, and a Dask array with unknown chunk sizes is returned (GH#3884) *Tom Augspurger*
- DataFrame.iloc (GH#3805) Tom Augspurger
- When reading multiple paths, expand globs. (GH#3828) Irina Truong
- Added index column name after resample (GH#3833) Eric Bonfadini
- Add (lazy) shape property to dataframe and series (GH#3212) Henrique Ribeiro
- Fix failing hdfs test [test-hdfs] (GH#3858) Jim Crist
- Fixes for pyarrow 0.10.0 release (GH#3860) Jim Crist
- Rename to_csv keys for diagnostics (GH#3890) Matthew Rocklin
- Match pandas warnings for concat sort (GH#3897) Tom Augspurger
- Include filename in read_csv (GH#3908) Julia Signell

Core

- Better error message on import when missing common dependencies (GH#3771) Danilo Horta
- Drop Python 3.4 support (GH#3840) Jim Crist
- Remove expired deprecation warnings (GH#3841) Jim Crist
- Add DASK_ROOT_CONFIG environment variable (GH#3849) Joe Hamman
- Don't cull in local scheduler, do cull in delayed (GH#3856) Jim Crist
- Increase conda download retries (GH#3857) Jim Crist
- Add python_requires and Trove classifiers (GH#3855) @hugovk
- Fix collections.abc deprecation warnings in Python 3.7.0 (GH#3876) Jan Margeta
- Allow dot jpeg to xfail in visualize tests (GH#3896) Matthew Rocklin
- Add Python 3.7 to travis.yml (GH#3894) Matthew Rocklin
- Add expand_environment_variables to dask.config (GH#3893) Joe Hamman

Docs

- Fix typo in import statement of diagnostics (GH#3826) John Mrziglod
- Add link to YARN docs (GH#3838) Jim Crist
- fix of minor typos in landing page index.html (GH#3746) Christoph Moehl
- Update delayed-custom.rst (GH#3850) Anderson Banihirwe
- DOC: clarify delayed docstring (GH#3709) Scott Sievert
- Add new presentations (GH#3880) @javad94
- Add dask array normalize_chunks to documentation (GH#3878) Daniel Rothenberg
- Docs: Fix link to snakeviz (GH#3900) Hans Moritz Günther
- Add missing ‘ to docstring (GH#3915) @rtobar

4.26.5 0.18.2 / 2018-07-23

Array

- Reimplemented `argtopk` to make it release the GIL (GH#3610) Guido Imperiale
- Don't overlap on non-overlapped dimensions in `map_overlap` (GH#3653) Matthew Rocklin
- Fix `linalg.tsqr` for dimensions of uncertain length (GH#3662) Jeremy Chen
- Break apart uneven array-of-int slicing to separate chunks (GH#3648) Matthew Rocklin
- Align auto chunks to provided chunks, rather than shape (GH#3679) Matthew Rocklin
- Adds endpoint and retstep support for linspace (GH#3675) James Bourbeau
- Implement `.blocks` accessor (GH#3689) Matthew Rocklin
- Add `block_info` keyword to `map_blocks` functions (GH#3686) Matthew Rocklin
- Slice by dask array of ints (GH#3407) Guido Imperiale

- Support `dtype` in `arange` (GH#3722) Guido Imperiale
- Fix `argtopk` with uneven chunks (GH#3720) Guido Imperiale
- Raise error when `replace=False` in `da.choice` (GH#3765) James Bourbeau
- Update chunks in `Array.__setitem__` (GH#3767) Itamar Turner-Trauring
- Add a `chunksize` convenience property (GH#3777) Jacob Tomlinson
- Fix and simplify array slicing behavior when `step < 0` (GH#3702) Ziyao Wei
- Ensure `to_zarr` with `return_stored True` returns a Dask Array (GH#3786) John A Kirkham

Bag

- Add `last_endline` optional parameter in `to_textfiles` (GH#3745) George Sakkis

Dataframe

- Add aggregate function for rolling objects (GH#3772) Gerome Pistre
- Properly tokenize cumulative groupby aggregations (GH#3799) Cloves Almeida

Delayed

- Add the `@` operator to the delayed objects (GH#3691) Mark Harfouche
- Add delayed best practices to documentation (GH#3737) Matthew Rocklin
- Fix `@delayed` decorator for methods and add tests (GH#3757) Ziyao Wei

Core

- Fix extra progressbar (GH#3669) Mike Neish
- Allow tasks back onto ordering stack if they have one dependency (GH#3652) Matthew Rocklin
- Prefer end-tasks with low numbers of dependencies when ordering (GH#3588) Tom Augspurger
- Add `assert_eq` to top-level modules (GH#3726) Matthew Rocklin
- Test that dask collections can hold `scipy.sparse` arrays (GH#3738) Matthew Rocklin
- Fix setup of lz4 decompression functions (GH#3782) Elliott Sales de Andrade
- Add datasets module (GH#3780) Matthew Rocklin

4.26.6 0.18.1 / 2018-06-22

Array

- `from_array` now supports scalar types and nested lists/tuples in input, just like all numpy functions do; it also produces a simpler graph when the input is a plain ndarray (GH#3568) Guido Imperiale
- Fix slicing of big arrays due to cumsum dtype bug (GH#3620) Marco Rossi
- Add Dask Array implementation of pad (GH#3578) John A Kirkham

- Fix array random API examples (GH#3625) James Bourbeau
- Add average function to dask array (GH#3640) James Bourbeau
- Tokenize ghost_internal with axes (GH#3643) Matthew Rocklin
- Add outer for Dask Arrays (GH#3658) John A Kirkham

DataFrame

- Add Index.to_series method (GH#3613) Henrique Ribeiro
- Fix missing partition columns in pyarrow-parquet (GH#3636) Martin Durant

Core

- Minor tweaks to CI (GH#3629) Guido Imperiale
- Add back dask.utils.effective_get (GH#3642) Matthew Rocklin
- DASK_CONFIG dictates config write location (GH#3621) Jim Crist
- Replace 'collections' key in unpack_collections with unique key (GH#3632) Yu Feng
- Avoid deepcopy in dask.config.set (GH#3649) Matthew Rocklin

4.26.7 0.18.0 / 2018-06-14

Array

- Add to/read_zarr for Zarr-format datasets and arrays (GH#3460) Martin Durant
- Experimental addition of generalized ufunc support, `apply_gufunc`, `gufunc`, and `as_gufunc` (GH#3109) (GH#3526) (GH#3539) Markus Gonser
- Avoid unnecessary rechunking tasks (GH#3529) Matthew Rocklin
- Compute dtypes at runtime for fft (GH#3511) Matthew Rocklin
- Generate UUIDs for all da.store operations (GH#3540) Martin Durant
- Correct internal dimension of Dask's SVD (GH#3517) John A Kirkham
- BUG: do not raise IndexError for identity slice in array.vindex (GH#3559) Scott Sievert
- Adds *isneginf* and *isposinf* (GH#3581) John A Kirkham
- Drop Dask Array's *learn* module (GH#3580) John A Kirkham
- added sfqr (short-and-fat) as a counterpart to tsqr... (GH#3575) Jeremy Chen
- Allow 0-width chunks in dask.array.rechunk (GH#3591) Marc Pfister
- Document Dask Array's *nan_to_num* in public API (GH#3599) John A Kirkham
- Show block example (GH#3601) John A Kirkham
- Replace token= keyword with name= in map_blocks (GH#3597) Matthew Rocklin
- Disable locking in to_zarr (needed for using to_zarr in a distributed context) (GH#3607) John A Kirkham
- Support Zarr Arrays in *to_zarr/from_zarr* (GH#3561) John A Kirkham

- Added recursion to array/linalg/tsqr to better manage the single core bottleneck (GH#3586) Jeremy Chan (GH#3396) Guido Imperiale

Dataframe

- Add to/read_json (GH#3494) Martin Durant
- Adds `index` to unsupported arguments for `DataFrame.rename` method (GH#3522) James Bourbeau
- Adds support to subset Dask DataFrame columns using `numpy.ndarray`, `pandas.Series`, and `pandas.Index` objects (GH#3536) James Bourbeau
- Raise error if meta columns do not match dataframe (GH#3485) Christopher Ren
- Add index to unsupprted argument for DataFrame.rename (GH#3522) James Bourbeau
- Adds support for subsetting DataFrames with pandas Index/Series and numpy ndarrays (GH#3536) James Bourbeau
- Dataframe sample method docstring fix (GH#3566) James Bourbeau
- fixes dd.read_json to infer file compression (GH#3594) Matt Lee
- Adds n to sample method (GH#3606) James Bourbeau
- Add fastparquet ParquetFile object support (GH#3573) @andrethrill

Bag

- Rename method= keyword to shuffle= in bag.groupby (GH#3470) Matthew Rocklin

Core

- Replace get= keyword with scheduler= keyword (GH#3448) Matthew Rocklin
- Add centralized dask.config module to handle configuration for all Dask subprojects (GH#3432) (GH#3513) (GH#3520) Matthew Rocklin
- Add *dask-ssh* CLI Options and Description. (GH#3476) @beomi
- Read whole files fix regardless of header for HTTP (GH#3496) Martin Durant
- Adds synchronous scheduler syntax to debugging docs (GH#3509) James Bourbeau
- Replace dask.set_options with dask.config.set (GH#3502) Matthew Rocklin
- Update sphinx readthedocs-theme (GH#3516) Matthew Rocklin
- Introduce "auto" value for normalize_chunks (GH#3507) Matthew Rocklin
- Fix check in configuration with env=None (GH#3562) Simon Perkins
- Update sizeof definitions (GH#3582) Matthew Rocklin
- Remove –verbose flag from travis-ci (GH#3477) Matthew Rocklin
- Remove "da.random" from random array keys (GH#3604) Matthew Rocklin

4.26.8 0.17.5 / 2018-05-16

Array

- Fix `rechunk` with chunksize of -1 in a dict (GH#3469) Stephan Hoyer
- `einsum` now accepts the `split_every` parameter (GH#3471) Guido Imperiale
- Improved slicing performance (GH#3479) Yu Feng

DataFrame

- Compatibility with pandas 0.23.0 (GH#3499) Tom Augspurger

4.26.9 0.17.4 / 2018-05-03

Dataframe

- Add support for indexing Dask DataFrames with string subclasses (GH#3461) James Bourbeau
- Allow using both sorted_index and chunksize in read_hdf (GH#3463) Pierre Bartet
- Pass filesystem to arrow piece reader (GH#3466) Martin Durant
- Switches to using dask.compat string_types (GH#3462) James Bourbeau

4.26.10 0.17.3 / 2018-05-02

Array

- Add `einsum` for Dask Arrays (GH#3412) Simon Perkins
- Add `piecewise` for Dask Arrays (GH#3350) John A Kirkham
- Fix handling of `nan` in `broadcast_shapes` (GH#3356) John A Kirkham
- Add `isin` for dask arrays (GH#3363). Stephan Hoyer
- Overhauled `topk` for Dask Arrays: faster algorithm, particularly for large k's; added support for multiple axes, recursive aggregation, and an option to pick the bottom k elements instead. (GH#3395) Guido Imperiale
- The `topk` API has changed from topk(k, array) to the more conventional topk(array, k). The legacy API still works but is now deprecated. (GH#2965) Guido Imperiale
- New function `argtopk` for Dask Arrays (GH#3396) Guido Imperiale
- Fix handling partial depth and boundary in `map_overlap` (GH#3445) John A Kirkham
- Add `gradient` for Dask Arrays (GH#3434) John A Kirkham

DataFrame

- Allow *t* as shorthand for *table* in *to_hdf* for pandas compatibility (GH#3330) Jörg Dietrich
- Added top level *isna* method for Dask DataFrames (GH#3294) Christopher Ren
- Fix selection on partition column on `read_parquet` for `engine="pyarrow"` (GH#3207) Uwe Korn

- Added DataFrame.squeeze method (GH#3366) Christopher Ren
- Added *infer_divisions* option to `read_parquet` to specify whether read engines should compute divisions (GH#3387) Jon Mease
- Added support for inferring division for `engine="pyarrow"` (GH#3387) Jon Mease
- Provide more informative error message for meta= errors (GH#3343) Matthew Rocklin
- add orc reader (GH#3284) Martin Durant
- Default compression for parquet now always Snappy, in line with pandas (GH#3373) Martin Durant
- Fixed bug in Dask DataFrame and Series comparisons with NumPy scalars (GH#3436) James Bourbeau
- Remove outdated requirement from repartition docstring (GH#3440) Jörg Dietrich
- Fixed bug in aggregation when only a Series is selected (GH#3446) Jörg Dietrich
- Add default values to make_timeseries (GH#3421) Matthew Rocklin

Core

- Support traversing collections in persist, visualize, and optimize (GH#3410) Jim Crist
- Add schedule= keyword to compute and persist. This replaces common use of the get= keyword (GH#3448) Matthew Rocklin

4.26.11 0.17.2 / 2018-03-21

Array

- Add `broadcast_arrays` for Dask Arrays (GH#3217) John A Kirkham
- Add `bitwise_*` ufuncs (GH#3219) John A Kirkham
- Add optional `axis` argument to `squeeze` (GH#3261) John A Kirkham
- Validate inputs to atop (GH#3307) Matthew Rocklin
- Avoid calls to astype in concatenate if all parts have the same dtype (GH#3301) Martin Durant

DataFrame

- Fixed bug in shuffle due to aggressive truncation (GH#3201) Matthew Rocklin
- Support specifying categorical columns on `read_parquet` with `categories=[...]` for `engine="pyarrow"` (GH#3177) Uwe Korn
- Add `dd.tseries.Resampler.agg` (GH#3202) Richard Postelnik
- Support operations that mix dataframes and arrays (GH#3230) Matthew Rocklin
- Support extra Scalar and Delayed args in `dd.groupby._Groupby.apply` (GH#3256) Gabriele Lanaro

Bag

- Support joining against single-partitioned bags and delayed objects (GH#3254) Matthew Rocklin

Core

- Fixed bug when using unexpected but hashable types for keys (GH#3238) Daniel Collins
- Fix bug in task ordering so that we break ties consistently with the key name (GH#3271) Matthew Rocklin
- Avoid sorting tasks in order when the number of tasks is very large (GH#3298) Matthew Rocklin

4.26.12 0.17.1 / 2018-02-22

Array

- Corrected dimension chunking in indices (GH#3166, GH#3167) Simon Perkins
- Inline `store_chunk` calls for `store`'s `return_stored` option (GH#3153) John A Kirkham
- Compatibility with struct dtypes for NumPy 1.14.1 release (GH#3187) Matthew Rocklin

DataFrame

- Bugfix to allow column assignment of pandas datetimes(GH#3164) Max Epstein

Core

- New file-system for HTTP(S), allowing direct loading from specific URLs (GH#3160) Martin Durant
- Fix bug when tokenizing partials with no keywords (GH#3191) Matthew Rocklin
- Use more recent LZ4 API (GH#3157) Thrasibule
- Introduce output stream parameter for progress bar (GH#3185) Dieter Weber

4.26.13 0.17.0 / 2018-02-09

Array

- Added a support object-type arrays for nansum, nanmin, and nanmax (GH#3133) Keisuke Fujii
- Update error handling when len is called with empty chunks (GH#3058) Xander Johnson
- Fixes a metadata bug with `store`'s `return_stored` option (GH#3064) John A Kirkham
- Fix a bug in `optimization.fuse_slice` to properly handle when first input is `None` (GH#3076) James Bourbeau
- Support arrays with unknown chunk sizes in percentile (GH#3107) Matthew Rocklin
- Tokenize scipy.sparse arrays and np.matrix (GH#3060) Roman Yurchak

DataFrame

- Support month timedeltas in repartition(freq=...) (GH#3110) Matthew Rocklin
- Avoid mutation in dataframe groupby tests (GH#3118) Matthew Rocklin
- `read_csv`, `read_table`, and `read_parquet` accept iterables of paths (GH#3124) Jim Crist

- Deprecates the `dd.to_delayed` *function* in favor of the existing method (GH#3126) Jim Crist
- Return dask.arrays from df.map_partitions calls when the UDF returns a numpy array (GH#3147) Matthew Rocklin
- Change handling of `columns` and `index` in `dd.read_parquet` to be more consistent, especially in handling of multi-indices (GH#3149) Jim Crist
- fastparquet append=True allowed to create new dataset (GH#3097) Martin Durant
- dtype rationalization for sql queries (GH#3100) Martin Durant

Bag

- Document `bag.map_paritions` function may recieve either a list or generator. (GH#3150) Nir

Core

- Change default task ordering to prefer nodes with few dependents and then many downstream dependencies (GH#3056) Matthew Rocklin
- Add color= option to visualize to color by task order (GH#3057) (GH#3122) Matthew Rocklin
- Deprecate `dask.bytes.open_text_files` (GH#3077) Jim Crist
- Remove short-circuit hdfs reads handling due to maintenance costs. May be re-added in a more robust manner later (GH#3079) Jim Crist
- Add `dask.base.optimize` for optimizing multiple collections without computing. (GH#3071) Jim Crist
- Rename `dask.optimize` module to `dask.optimization` (GH#3071) Jim Crist
- Change task ordering to do a full traversal (GH#3066) Matthew Rocklin
- Adds an `optimize_graph` keyword to all `to_delayed` methods to allow controlling whether optimizations occur on conversion. (GH#3126) Jim Crist
- Support using `pyarrow` for hdfs integration (GH#3123) Jim Crist
- Move HDFS integration and tests into dask repo (GH#3083) Jim Crist
- Remove write_bytes (GH#3116) Jim Crist

4.26.14 0.16.1 / 2018-01-09

Array

- Fix handling of scalar percentile values in `percentile` (GH#3021) James Bourbeau
- Prevent `bool()` coercion from calling compute (GH#2958) Albert DeFusco
- Add `matmul` (GH#2904) John A Kirkham
- Support N-D arrays with `matmul` (GH#2909) John A Kirkham
- Add `vdot` (GH#2910) John A Kirkham
- Explicit `chunks` argument for `broadcast_to` (GH#2943) Stephan Hoyer
- Add `meshgrid` (GH#2938) John A Kirkham and (GH#3001) Markus Gonser
- Preserve singleton chunks in `fftshift`/`ifftshift` (GH#2733) John A Kirkham

- Fix handling of negative indexes in `vindex` and raise errors for out of bounds indexes (GH#2967) Stephan Hoyer
- Add `flip`, `flipud`, `fliplr` (GH#2954) John A Kirkham
- Add `float_power` ufunc (GH#2962) (GH#2969) John A Kirkham
- Compatability for changes to structured arrays in the upcoming NumPy 1.14 release (GH#2964) Tom Augspurger
- Add `block` (GH#2650) John A Kirkham
- Add `frompyfunc` (GH#3030) Jim Crist
- Add the `return_stored` option to `store` for chaining stored results (GH#2980) John A Kirkham

DataFrame

- Fixed naming bug in cumulative aggregations (GH#3037) Martijn Arts
- Fixed `dd.read_csv` when `names` is given but `header` is not set to `None` (GH#2976) Martijn Arts
- Fixed `dd.read_csv` so that passing instances of `CategoricalDtype` in `dtype` will result in known categoricals (GH#2997) Tom Augspurger
- Prevent `bool()` coercion from calling compute (GH#2958) Albert DeFusco
- `DataFrame.read_sql()` (GH#2928) to an empty database tables returns an empty dask dataframe Apostolos Vlachopoulos
- Compatability for reading Parquet files written by PyArrow 0.8.0 (GH#2973) Tom Augspurger
- Correctly handle the column name (*df.columns.name*) when reading in `dd.read_parquet` (GH#2973) Tom Augspurger
- Fixed `dd.concat` losing the index dtype when the data contained a categorical (GH#2932) Tom Augspurger
- Add `dd.Series.rename` (GH#3027) Jim Crist
- `DataFrame.merge()` now supports merging on a combination of columns and the index (GH#2960) Jon Mease
- Removed the deprecated `dd.rolling*` methods, in preperation for their removal in the next pandas release (GH#2995) Tom Augspurger
- Fix metadata inference bug in which single-partition series were mistakenly special cased (GH#3035) Jim Crist
- Add support for `Series.str.cat` (GH#3028) Jim Crist

Core

- Improve 32-bit compatibility (GH#2937) Matthew Rocklin
- Change task prioritization to avoid upwards branching (GH#3017) Matthew Rocklin

4.26.15 0.16.0 / 2017-11-17

This is a major release. It includes breaking changes, new protocols, and a large number of bug fixes.

Array

- Add `atleast_1d`, `atleast_2d`, and `atleast_3d` (GH#2760) (GH#2765) John A Kirkham
- Add `allclose` (GH#2771) by John A Kirkham
- Remove `random.different_seeds` from Dask Array API docs (GH#2772) John A Kirkham
- Deprecate `vnorm` in favor of `dask.array.linalg.norm` (GH#2773) John A Kirkham
- Reimplement `unique` to be lazy (GH#2775) John A Kirkham
- Support broadcasting of Dask Arrays with 0-length dimensions (GH#2784) John A Kirkham
- Add `asarray` and `asanyarray` to Dask Array API docs (GH#2787) James Bourbeau
- Support `unique`'s `return_*` arguments (GH#2779) John A Kirkham
- Simplify `_unique_internal` (GH#2850) (GH#2855) John A Kirkham
- Avoid removing some getter calls in array optimizations (GH#2826) Jim Crist

DataFrame

- Support `pyarrow` in `dd.to_parquet` (GH#2868) Jim Crist
- Fixed `DataFrame.quantile` and `Series.quantile` returning `nan` when missing values are present (GH#2791) Tom Augspurger
- Fixed `DataFrame.quantile` losing the result `.name` when `q` is a scalar (GH#2791) Tom Augspurger
- Fixed `dd.concat` return a `dask.Dataframe` when concatenating a single series along the columns, matching pandas' behavior (GH#2800) James Munroe
- Fixed default inplace parameter for `DataFrame.eval` to match the pandas defualt for pandas >= 0.21.0 (GH#2838) Tom Augspurger
- Fix exception when calling `DataFrame.set_index` on text column where one of the partitions was empty (GH#2831) Jesse Vogt
- Do not raise exception when calling `DataFrame.set_index` on empty dataframe (GH#2827) Jesse Vogt
- Fixed bug in `Dataframe.fillna` when filling with a `Series` value (GH#2810) Tom Augspurger
- Deprecate old argument ordering in `dd.to_parquet` to better match convention of putting the dataframe first (GH#2867) Jim Crist
- df.astype(categorical_dtype -> known categoricals (GH#2835) Jim Crist
- Test against Pandas release candidate (GH#2814) Tom Augspurger
- Add more tests for read_parquet(engine='pyarrow') (GH#2822) Uwe Korn
- Remove unnecessary map_partitions in aggregate (GH#2712) Christopher Prohm
- Fix bug calling sample on empty partitions (GH#2818) @xwang777
- Error nicely when parsing dates in read_csv (GH#2863) Jim Crist
- Cleanup handling of passing filesystem objects to PyArrow readers (GH#2527) @fjetter
- Support repartitioning even if there are no divisions (GH#2873) @Ced4
- Support reading/writing to hdfs using `pyarrow` in `dd.to_parquet` (GH#2894, GH#2881) Jim Crist

Core

- Allow tuples as sharedict keys (GH#2763) Matthew Rocklin
- Calling compute within a dask.distributed task defaults to distributed scheduler (GH#2762) Matthew Rocklin
- Auto-import gcsfs when gcs:// protocol is used (GH#2776) Matthew Rocklin
- Fully remove dask.async module, use dask.local instead (GH#2828) Thomas Caswell
- Compatability with bokeh 0.12.10 (GH#2844) Tom Augspurger
- Reduce test memory usage (GH#2782) Jim Crist
- Add Dask collection interface (GH#2748) Jim Crist
- Update Dask collection interface during XArray integration (GH#2847) Matthew Rocklin
- Close resource profiler process on __exit__ (GH#2871) Jim Crist
- Fix S3 tests (GH#2875) Jim Crist
- Fix port for bokeh dashboard in docs (GH#2889) Ian Hopkinson
- Wrap Dask filesystems for PyArrow compatibility (GH#2881) Jim Crist

4.26.16 0.15.4 / 2017-10-06

Array

- `da.random.choice` now works with array arguments (GH#2781)
- Support indexing in arrays with np.int (fixes regression) (GH#2719)
- Handle zero dimension with rechunking (GH#2747)
- Support -1 as an alias for "size of the dimension" in `chunks` (GH#2749)
- Call mkdir in array.to_npy_stack (GH#2709)

DataFrame

- Added the *.str* accessor to Categoricals with string categories (GH#2743)
- Support int96 (spark) datetimes in parquet writer (GH#2711)
- Pass on file scheme to fastparquet (GH#2714)
- Support Pandas 0.21 (GH#2737)

Bag

- Add tree reduction support for foldby (GH#2710)

Core

- Drop s3fs from `pip install dask[complete]` (GH#2750)

4.26.17 0.15.3 / 2017-09-24

Array

- Add masked arrays (GH#2301)
- Add `*_like array creation functions` (GH#2640)
- Indexing with unsigned integer array (GH#2647)
- Improved slicing with boolean arrays of different dimensions (GH#2658)
- Support literals in `top` and `atop` (GH#2661)
- Optional axis argument in cumulative functions (GH#2664)
- Improve tests on scalars with `assert_eq` (GH#2681)
- Fix norm keepdims (GH#2683)
- Add `ptp` (GH#2691)
- Add apply_along_axis (GH#2690) and apply_over_axes (GH#2702)

DataFrame

- Added `Series.str[index]` (GH#2634)
- Allow the groupby by param to handle columns and index levels (GH#2636)
- **`DataFrame.to_csv` and `Bag.to_textfiles` now return the filenames to** which they have written (GH#2655)
- Fix combination of `partition_on` and `append` in `to_parquet` (GH#2645)
- Fix for parquet file schemes (GH#2667)
- Repartition works with mixed categoricals (GH#2676)

Core

- `python setup.py test` now runs tests (GH#2641)
- Added new cheatsheet (GH#2649)
- Remove resize tool in Bokeh plots (GH#2688)

4.26.18 0.15.2 / 2017-08-25

Array

- Remove spurious keys from map_overlap graph (GH#2520)
- where works with non-bool condition and scalar values (GH#2543) (GH#2549)
- Improve compress (GH#2541) (GH#2545) (GH#2555)
- Add argwhere, _nonzero, and where(cond) (GH#2539)
- Generalize vindex in dask.array to handle multi-dimensional indices (GH#2573)
- Add choose method (GH#2584)

- Split code into reorganized files (GH#2595)
- Add linalg.norm (GH#2597)
- Add diff, ediff1d (GH#2607), (GH#2609)
- Improve dtype inference and reflection (GH#2571)

Bag

- Remove deprecated Bag behaviors (GH#2525)

DataFrame

- Support callables in assign (GH#2513)
- better error messages for read_csv (GH#2522)
- Add dd.to_timedelta (GH#2523)
- Verify metadata in from_delayed (GH#2534) (GH#2591)
- Add DataFrame.isin (GH#2558)
- Read_hdf supports iterables of files (GH#2547)

Core

- Remove bare `except:` blocks everywhere (GH#2590)

4.26.19 0.15.1 / 2017-07-08

- Add storage_options to to_textfiles and to_csv (GH#2466)
- Rechunk and simplify rfftfreq (GH#2473), (GH#2475)
- Better support ndarray subclasses (GH#2486)
- Import star in dask.distributed (GH#2503)
- Threadsafe cache handling with tokenization (GH#2511)

4.26.20 0.15.0 / 2017-06-09

Array

- Add dask.array.stats submodule (GH#2269)
- Support `ufunc.outer` (GH#2345)
- Optimize fancy indexing by reducing graph overhead (GH#2333) (GH#2394)
- Faster array tokenization using alternative hashes (GH#2377)
- Added the matmul `@` operator (GH#2349)
- Improved coverage of the `numpy.fft` module (GH#2320) (GH#2322) (GH#2327) (GH#2323)
- Support NumPy's `__array_ufunc__` protocol (GH#2438)

Bag

- Fix bug where reductions on bags with no partitions would fail (GH#2324)
- Add broadcasting and variadic `db.map` top-level function. Also remove auto-expansion of tuples as map arguments (GH#2339)
- Rename `Bag.concat` to `Bag.flatten` (GH#2402)

DataFrame

- Parquet improvements (GH#2277) (GH#2422)

Core

- Move dask.async module to dask.local (GH#2318)
- Support callbacks with nested scheduler calls (GH#2397)
- Support pathlib.Path objects as uris (GH#2310)

4.26.21 0.14.3 / 2017-05-05

DataFrame

- Pandas 0.20.0 support

4.26.22 0.14.2 / 2017-05-03

Array

- Add da.indices (GH#2268), da.tile (GH#2153), da.roll (GH#2135)
- Simultaneously support drop_axis and new_axis in da.map_blocks (GH#2264)
- Rechunk and concatenate work with unknown chunksizes (GH#2235) and (GH#2251)
- Support non-numpy container arrays, notably sparse arrays (GH#2234)
- Tensordot contracts over multiple axes (GH#2186)
- Allow delayed targets in da.store (GH#2181)
- Support interactions against lists and tuples (GH#2148)
- Constructor plugins for debugging (GH#2142)
- Multi-dimensional FFTs (single chunk) (GH#2116)

Bag

- to_dataframe enforces consistent types (GH#2199)

DataFrame

- Set_index always fully sorts the index (GH#2290)
- Support compatibility with pandas 0.20.0 (GH#2249), (GH#2248), and (GH#2246)
- Support Arrow Parquet reader (GH#2223)
- Time-based rolling windows (GH#2198)
- Repartition can now create more partitions, not just less (GH#2168)

Core

- Always use absolute paths when on POSIX file system (GH#2263)
- Support user provided graph optimizations (GH#2219)
- Refactor path handling (GH#2207)
- Improve fusion performance (GH#2129), (GH#2131), and (GH#2112)

4.26.23 0.14.1 / 2017-03-22

Array

- Micro-optimize optimizations (GH#2058)
- Change slicing optimizations to avoid fusing raw numpy arrays (GH#2075) (GH#2080)
- Dask.array operations now work on numpy arrays (GH#2079)
- Reshape now works in a much broader set of cases (GH#2089)
- Support deepcopy python protocol (GH#2090)
- Allow user-provided FFT implementations in `da.fft` (GH#2093)

DataFrame

- Fix to_parquet with empty partitions (GH#2020)
- Optional `npartitions='auto'` mode in `set_index` (GH#2025)
- Optimize shuffle performance (GH#2032)
- Support efficient repartitioning along time windows like `repartition(freq='12h')` (GH#2059)
- Improve speed of categorize (GH#2010)
- Support single-row dataframe arithmetic (GH#2085)
- Automatically avoid shuffle when setting index with a sorted column (GH#2091)
- Improve handling of integer-na handling in read_csv (GH#2098)

Delayed

- Repeated attribute access on delayed objects uses the same key (GH#2084)

Core

- Improve naming of nodes in dot visuals to avoid generic `apply` (GH#2070)
- Ensure that worker processes have different random seeds (GH#2094)

4.26.24 0.14.0 / 2017-02-24

Array

- Fix corner cases with zero shape and misaligned values in `arange` (GH#1902), (GH#1904), (GH#1935), (GH#1955), (GH#1956)
- Improve concatenation efficiency (GH#1923)
- Avoid hashing in `from_array` if name is provided (GH#1972)

Bag

- Repartition can now increase number of partitions (GH#1934)
- Fix bugs in some reductions with empty partitions (GH#1939), (GH#1950), (GH#1953)

DataFrame

- Support non-uniform categoricals (GH#1877), (GH#1930)
- Groupby cumulative reductions (GH#1909)
- DataFrame.loc indexing now supports lists (GH#1913)
- Improve multi-level groupbys (GH#1914)
- Improved HTML and string repr for DataFrames (GH#1637)
- Parquet append (GH#1940)
- Add `dd.demo.daily_stock` function for teaching (GH#1992)

Delayed

- Add `traverse=` keyword to delayed to optionally avoid traversing nested data structures (GH#1899)
- Support Futures in from_delayed functions (GH#1961)
- Improve serialization of decorated delayed functions (GH#1969)

Core

- Improve windows path parsing in corner cases (GH#1910)
- Rename tasks when fusing (GH#1919)
- Add top level `persist` function (GH#1927)
- Propagate `errors=` keyword in byte handling (GH#1954)
- Dask.compute traverses Python collections (GH#1975)

- Structural sharing between graphs in dask.array and dask.delayed (GH#1985)

4.26.25 0.13.0 / 2017-01-02

Array

- Mandatory dtypes on dask.array. All operations maintain dtype information and UDF functions like map_blocks now require a dtype= keyword if it can not be inferred. (GH#1755)
- Support arrays without known shapes, such as arises when slicing arrays with arrays or converting dataframes to arrays (GH#1838)
- Support mutation by setting one array with another (GH#1840)
- Tree reductions for covariance and correlations. (GH#1758)
- Add SerializableLock for better use with distributed scheduling (GH#1766)
- Improved atop support (GH#1800)
- Rechunk optimization (GH#1737), (GH#1827)

Bag

- Avoid wrong results when recomputing the same groupby twice (GH#1867)

DataFrame

- Add `map_overlap` for custom rolling operations (GH#1769)
- Add `shift` (GH#1773)
- Add Parquet support (GH#1782) (GH#1792) (GH#1810), (GH#1843), (GH#1859), (GH#1863)
- Add missing methods combine, abs, autocorr, sem, nsmallest, first, last, prod, (GH#1787)
- Approximate nunique (GH#1807), (GH#1824)
- Reductions with multiple output partitions (for operations like drop_duplicates) (GH#1808), (GH#1823) (GH#1828)
- Add delitem and copy to DataFrames, increasing mutation support (GH#1858)

Delayed

- Changed behaviour for `delayed(nout=0)` and `delayed(nout=1)`: `delayed(nout=1)` does not default to `out=None` anymore, and `delayed(nout=0)` is also enabled. I.e. functions with return tuples of length 1 or 0 can be handled correctly. This is especially handy, if functions with a variable amount of outputs are wrapped by `delayed`. E.g. a trivial example: `delayed(lambda *args: args, nout=len(vals))(*vals)`

Core

- Refactor core byte ingest (GH#1768), (GH#1774)
- Improve import time (GH#1833)

4.26.26 0.12.0 / 2016-11-03

DataFrame

- Return a series when functions given to `dataframe.map_partitions` return scalars (GH#1515)
- Fix type size inference for series (GH#1513)
- `dataframe.DataFrame.categorize` no longer includes missing values in the `categories`. This is for compatibility with a pandas change (GH#1565)
- Fix head parser error in `dataframe.read_csv` when some lines have quotes (GH#1495)
- Add `dataframe.reduction` and `series.reduction` methods to apply generic row-wise reduction to dataframes and series (GH#1483)
- Add `dataframe.select_dtypes`, which mirrors the pandas method (GH#1556)
- `dataframe.read_hdf` now supports reading `Series` (GH#1564)
- Support Pandas 0.19.0 (GH#1540)
- Implement `select_dtypes` (GH#1556)
- String accessor works with indexes (GH#1561)
- Add pipe method to dask.dataframe (GH#1567)
- Add `indicator` keyword to merge (GH#1575)
- Support Series in `read_hdf` (GH#1575)
- Support Categories with missing values (GH#1578)
- Support inplace operators like `df.x += 1` (GH#1585)
- Str accessor passes through args and kwargs (GH#1621)
- Improved groupby support for single-machine multiprocessing scheduler (GH#1625)
- Tree reductions (GH#1663)
- Pivot tables (GH#1665)
- Add clip (GH#1667), align (GH#1668), combine_first (GH#1725), and any/all (GH#1724)
- Improved handling of divisions on dask-pandas merges (GH#1666)
- Add `groupby.aggregate` method (GH#1678)
- Add `dd.read_table` function (GH#1682)
- Improve support for multi-level columns (GH#1697) (GH#1712)
- Support 2d indexing in `loc` (GH#1726)
- Extend `resample` to include DataFrames (GH#1741)
- Support dask.array ufuncs on dask.dataframe objects (GH#1669)

Array

- Add information about how `dask.array` `chunks` argument work (GH#1504)
- Fix field access with non-scalar fields in `dask.array` (GH#1484)
- Add concatenate= keyword to atop to concatenate chunks of contracted dimensions

- Optimized slicing performance (GH#1539) (GH#1731)
- Extend `atop` with a `concatenate=` (GH#1609) `new_axes=` (GH#1612) and `adjust_chunks=` (GH#1716) keywords
- Add clip (GH#1610) swapaxes (GH#1611) round (GH#1708) repeat
- Automatically align chunks in `atop`-backed operations (GH#1644)
- Cull dask.arrays on slicing (GH#1709)

Bag

- Fix issue with callables in `bag.from_sequence` being interpreted as tasks (GH#1491)
- Avoid non-lazy memory use in reductions (GH#1747)

Administration

- Added changelog (GH#1526)
- Create new threadpool when operating from thread (GH#1487)
- Unify example documentation pages into one (GH#1520)
- Add versioneer for git-commit based versions (GH#1569)
- Pass through node_attr and edge_attr keywords in dot visualization (GH#1614)
- Add continuous testing for Windows with Appveyor (GH#1648)
- Remove use of multiprocessing.Manager (GH#1653)
- Add global optimizations keyword to compute (GH#1675)
- Micro-optimize get_dependencies (GH#1722)

4.26.27 0.11.0 / 2016-08-24

Major Points

DataFrames now enforce knowing full metadata (columns, dtypes) everywhere. Previously we would operate in an ambiguous state when functions lost dtype information (such as `apply`). Now all dataframes always know their dtypes and raise errors asking for information if they are unable to infer (which they usually can). Some internal attributes like `_pd` and `_pd_nonempty` have been moved.

The internals of the distributed scheduler have been refactored to transition tasks between explicit states. This improves resilience, reasoning about scheduling, plugin operation, and logging. It also makes the scheduler code easier to understand for newcomers.

Breaking Changes

- The `distributed.s3` and `distributed.hdfs` namespaces are gone. Use protocols in normal methods like `read_text('s3://...'` instead.
- `Dask.array.reshape` now errs in some cases where previously it would have create a very large number of tasks

4.26.28 0.10.2 / 2016-07-27

- More Dataframe shuffles now work in distributed settings, ranging from setting-index to hash joins, to sorted joins and groupbys.
- Dask passes the full test suite when run when under in Python's optimized-OO mode.
- On-disk shuffles were found to produce wrong results in some highly-concurrent situations, especially on Windows. This has been resolved by a fix to the partd library.
- Fixed a growth of open file descriptors that occurred under large data communications
- Support ports in the `--bokeh-whitelist` option ot dask-scheduler to better routing of web interface messages behind non-trivial network settings
- Some improvements to resilience to worker failure (though other known failures persist)
- You can now start an IPython kernel on any worker for improved debugging and analysis
- Improvements to `dask.dataframe.read_hdf`, especially when reading from multiple files and docs

4.26.29 0.10.0 / 2016-06-13

Major Changes

- This version drops support for Python 2.6
- Conda packages are built and served from conda-forge
- The `dask.distributed` executables have been renamed from dfoo to dask-foo. For example dscheduler is renamed to dask-scheduler
- Both Bag and DataFrame include a preliminary distributed shuffle.

Bag

- Add task-based shuffle for distributed groupbys
- Add accumulate for cumulative reductions

DataFrame

- Add a task-based shuffle suitable for distributed joins, groupby-applys, and set_index operations. The single-machine shuffle remains untouched (and much more efficient.)
- Add support for new Pandas rolling API with improved communication performance on distributed systems.
- Add `groupby.std/var`
- Pass through S3/HDFS storage options in `read_csv`
- Improve categorical partitioning
- Add eval, info, isnull, notnull for dataframes

Distributed

- Rename executables like dscheduler to dask-scheduler
- Improve scheduler performance in the many-fast-tasks case (important for shuffling)
- Improve work stealing to be aware of expected function run-times and data sizes. The drastically increases the breadth of algorithms that can be efficiently run on the distributed scheduler without significant user expertise.
- Support maximum buffer sizes in streaming queues
- Improve Windows support when using the Bokeh diagnostic web interface
- Support compression of very-large-bytestrings in protocol
- Support clean cancellation of submitted futures in Joblib interface

Other

- All dask-related projects (dask, distributed, s3fs, hdfs, partd) are now building conda packages on conda-forge.
- Change credential handling in s3fs to only pass around delegated credentials if explicitly given secret/key. The default now is to rely on managed environments. This can be changed back by explicitly providing a keyword argument. Anonymous mode must be explicitly declared if desired.

4.26.30 0.9.0 / 2016-05-11

API Changes

- `dask.do` and `dask.value` have been renamed to `dask.delayed`
- `dask.bag.from_filenames` has been renamed to `dask.bag.read_text`
- All S3/HDFS data ingest functions like `db.from_s3` or `distributed.s3.read_csv` have been moved into the plain `read_text`, `read_csv functions`, which now support protocols, like `dd.read_csv('s3://bucket/keys*.csv')`

Array

- Add support for `scipy.LinearOperator`
- Improve optional locking to on-disk data structures
- Change rechunk to expose the intermediate chunks

Bag

- Rename `from_filenames` to `read_text`
- Remove `from_s3` in favor of `read_text('s3://...')`

DataFrame

- Fixed numerical stability issue for correlation and covariance
- Allow no-hash `from_pandas` for speedy round-trips to and from-pandas objects
- Generally reengineered `read_csv` to be more in line with Pandas behavior
- Support fast `set_index` operations for sorted columns

Delayed

- Rename `do/value` to `delayed`
- Rename `to/from_imperative` to `to/from_delayed`

Distributed

- Move s3 and hdfs functionality into the dask repository
- Adaptively oversubscribe workers for very fast tasks
- Improve PyPy support
- Improve work stealing for unbalanced workers
- Scatter data efficiently with tree-scatters

Other

- Add lzma/xz compression support
- Raise a warning when trying to split unsplittable compression types, like gzip or bz2
- Improve hashing for single-machine shuffle operations
- Add new callback method for start state
- General performance tuning

4.26.31 0.8.1 / 2016-03-11

Array

- Bugfix for range slicing that could periodically lead to incorrect results.
- Improved support and resiliency of `arg` reductions (`argmin`, `argmax`, etc.)

Bag

- Add `zip` function

DataFrame

- Add `corr` and `cov` functions
- Add `melt` function
- Bugfixes for io to bcolz and hdf5

4.26.32 0.8.0 / 2016-02-20

Array

- Changed default array reduction split from 32 to 4
- Linear algebra, `tril`, `triu`, `LU`, `inv`, `cholesky`, `solve`, `solve_triangular`, `eye`, `lstsq`, `diag`, `corrcoef`.

Bag

- Add tree reductions
- Add range function
- drop `from_hdfs` function (better functionality now exists in hdfs3 and distributed projects)

DataFrame

- Refactor `dask.dataframe` to include a full empty pandas dataframe as metadata. Drop the `.columns` attribute on Series
- Add Series categorical accessor, series.nunique, drop the `.columns` attribute for series.
- `read_csv` fixes (multi-column parse_dates, integer column names, etc.)
- Internal changes to improve graph serialization

Other

- Documentation updates
- Add from_imperative and to_imperative functions for all collections
- Aesthetic changes to profiler plots
- Moved the dask project to a new dask organization

4.26.33 0.7.6 / 2016-01-05

Array

- Improve thread safety
- Tree reductions
- Add `view`, `compress`, `hstack`, `dstack`, `vstack` methods
- `map_blocks` can now remove and add dimensions

DataFrame

- Improve thread safety
- Extend sampling to include replacement options

Imperative

- Removed optimization passes that fused results.

Core

- Removed `dask.distributed`
- Improved performance of blocked file reading
- Serialization improvements
- Test Python 3.5

4.26.34 0.7.4 / 2015-10-23

This was mostly a bugfix release. Some notable changes:

- Fix minor bugs associated with the release of numpy 1.10 and pandas 0.17
- Fixed a bug with random number generation that would cause repeated blocks due to the birthday paradox
- Use locks in `dask.dataframe.read_hdf` by default to avoid concurrency issues
- Change `dask.get` to point to `dask.async.get_sync` by default
- Allow visualization functions to accept general graphviz graph options like rankdir='LR'
- Add reshape and ravel to `dask.array`
- Support the creation of `dask.arrays` from `dask.imperative` objects

Deprecation

This release also includes a deprecation warning for `dask.distributed`, which will be removed in the next version.

Future development in distributed computing for dask is happening here: https://distributed.dask.org . General feedback on that project is most welcome from this community.

4.26.35 0.7.3 / 2015-09-25

Diagnostics

- A utility for profiling memory and cpu usage has been added to the `dask.diagnostics` module.

DataFrame

This release improves coverage of the pandas API. Among other things it includes `nunique`, `nlargest`, `quantile`. Fixes encoding issues with reading non-ascii csv files. Performance improvements and bug fixes with resample. More flexible read_hdf with globbing. And many more. Various bug fixes in `dask.imperative` and `dask.bag`.

4.26.36 0.7.0 / 2015-08-15

DataFrame

This release includes significant bugfixes and alignment with the Pandas API. This has resulted both from use and from recent involvement by Pandas core developers.

- New operations: query, rolling operations, drop
- Improved operations: quantiles, arithmetic on full dataframes, dropna, constructor logic, merge/join, elemwise operations, groupby aggregations

Bag

- Fixed a bug in fold where with a null default argument

Array

- New operations: da.fft module, da.image.imread

Infrastructure

- The array and dataframe collections create graphs with deterministic keys. These tend to be longer (hash strings) but should be consistent between computations. This will be useful for caching in the future.
- All collections (Array, Bag, DataFrame) inherit from common subclass

4.26.37 0.6.1 / 2015-07-23

Distributed

- Improved (though not yet sufficient) resiliency for `dask.distributed` when workers die

DataFrame

- Improved writing to various formats, including to_hdf, to_castra, and to_csv
- Improved creation of dask DataFrames from dask Arrays and Bags
- Improved support for categoricals and various other methods

Array

- Various bug fixes
- Histogram function

Scheduling

- Added tie-breaking ordering of tasks within parallel workloads to better handle and clear intermediate results

Other

- Added the dask.do function for explicit construction of graphs with normal python code
- Traded pydot for graphviz library for graph printing to support Python3
- There is also a gitter chat room and a stackoverflow tag

4.27 Configuration

Taking full advantage of Dask sometimes requires user configuration. This might be to control logging verbosity, specify cluster configuration, provide credentials for security, or any of several other options that arise in production.

Configuration is specified in one of the following ways:

1. YAML files in `~/.config/dask/` or `/etc/dask/`
2. Environment variables like `DASK_DISTRIBUTED__SCHEDULER__WORK_STEALING=True`
3. Default settings within sub-libraries

This combination makes it easy to specify configuration in a variety of settings ranging from personal workstations, to IT-mandated configuration, to docker images.

4.27.1 Access Configuration

dask.config.get(key[, default, config])	Get elements from global config

Configuration is usually read by using the `dask.config` module, either with the `config` dictionary or the `get` function:

```
>>> import dask
>>> import dask.distributed  # populate config with distributed defaults
>>> dask.config.config
{
  'logging': {
    'distributed': 'info',
    'bokeh': 'critical',
    'tornado': 'critical',
  }
  'admin': {
    'log-format': '%(name)s - %(levelname)s - %(message)s'
  }
```

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```
}

>>> dask.config.get('logging')
{'distributed': 'info',
 'bokeh': 'critical',
 'tornado': 'critical'}

>>> dask.config.get('logging.bokeh')  # use `.` for nested access
'critical'
```

You may wish to inspect the `dask.config.config` dictionary to get a sense for what configuration is being used by your current system.

4.27.2 Specify Configuration

YAML files

You can specify configuration values in YAML files like the following:

```
logging:
  distributed: info
  bokeh: critical
  tornado: critical

scheduler:
  work-stealing: True
  allowed-failures: 5

 admin:
   log-format: '%(name)s - %(levelname)s - %(message)s'
```

These files can live in any of the following locations:

1. The `~/.config/dask` directory in the user's home directory
2. The `{sys.prefix}/etc/dask` directory local to Python
3. The root directory (specified by the `DASK_ROOT_CONFIG` environment variable or `/etc/dask/` by default)

Dask searches for *all* YAML files within each of these directories and merges them together, preferring configuration files closer to the user over system configuration files (preference follows the order in the list above). Additionally users can specify a path with the `DASK_CONFIG` environment variable, that takes precedence at the top of the list above.

The contents of these YAML files are merged together, allowing different dask subprojects like `dask-kubernetes` or `dask-ml` to manage configuration files separately, but have them merge into the same global configuration.

Note: for historical reasons we also look in the ''~/.dask'' directory for config files. This is deprecated and will soon be removed.

Environment Variables

You can also specify configuration values with environment variables like the following:

```
export DASK_DISTRIBUTED__SCHEDULER__WORK_STEALING=True
export DASK_DISTRIBUTED__SCHEDULER__ALLOWED_FAILURES=5
```

resulting in configuration values like the following:

```
{'distributed':
  {'scheduler':
    {'work-stealing': True,
     'allowed-failures': 5}
  }
}
```

Dask searches for all environment variables that start with `DASK_`, then transforms keys by converting to lower case, changing double-underscores to nested structures, and changing single underscores to hyphens.

Dask tries to parse all values with ast.literal_eval, letting users pass numeric and boolean values (such as `True` in the example above) as well as lists, dictionaries, and so on with normal Python syntax.

Environment variables take precedence over configuration values found in YAML files.

Defaults

Additionally, individual subprojects may add their own default values when they are imported. These are always added with lower priority than the YAML files or environment variables mentioned above

```
>>> import dask.config
>>> dask.config.config  # no configuration by default
{}

>>> import dask.distributed
>>> dask.config.config  # New values have been added
{'scheduler': ...,
 'worker': ...,
 'tls': ...}
```

Directly within Python

dask.config.set([arg, config, lock])	Temporarily set configuration values within a context manager

Configuration is stored within a normal Python dictionary in `dask.config.config` and can be modified using normal Python operations.

Additionally, you can temporarily set a configuration value using the `dask.config.set` function. This function accepts a dictionary as an input and interprets `"."` as nested access

```
>>> dask.config.set({'scheduler.work-stealing': True})
```

This function can also be used as a context manager for consistent cleanup.

```
with dask.config.set({'scheduler.work-stealing': True}):
    ...
```

4.27.3 Updating Configuration

Manipulating configuration dictionaries

dask.config.merge(*dicts)	Update a sequence of nested dictionaries
dask.config.update(old, new[, priority])	Update a nested dictionary with values from another
dask.config.expand_environment_variables([config])	Expand environment variables in a nested config dictionary

As described above, configuration can come from many places, including several YAML files, environment variables, and project defaults. Each of these provides a configuration that is possibly nested like the following:

```
x = {'a': 0, 'c': {'d': 4}}
y = {'a': 1, 'b': 2, 'c': {'e': 5}}
```

Dask will merge these configurations respecting nested data structures, and respecting order.

```
>>> dask.config.merge(x, y)
{'a': 1, 'b': 2, 'c': {'d': 4, 'e': 5}}
```

You can also use the `update` function to update the existing configuration in place with a new configuration. This can be done with priority being given to either config. This is often used to update the global configuration in `dask.config.config`

```
dask.config.update(dask.config, new, priority='new')  # Give priority to new values
dask.config.update(dask.config, new, priority='old')  # Give priority to old values
```

Sometimes it is useful to expand environment variables stored within a configuration. This can be done with the `expand_environment_variables` function:

```
dask.config.config = dask.config.expand_environment_variables(dask.config.config)
```

Refreshing Configuration

dask.config.collect([paths, env])	Collect configuration from paths and environment variables
dask.config.refresh([config, defaults])	Update configuration by re-reading yaml files and env variables

If you change your environment variables or YAML files Dask will not immediately see the changes. Instead, you can call `refresh` to go through the configuration collection process and update the default configuration.

```
>>> dask.config.config
{}

>>> # make some changes to yaml files

>>> dask.config.refresh()
>>> dask.config.config
{...}
```

This function uses `dask.config.collect`, which returns the configuration without modifying the global config-

uration. You might use this to determine the configuration of particular paths not yet on the config path.

```
>>> dask.config.collect(paths=[...])
{...}
```

4.27.4 Downstream Libraries

dask.config.ensure_file(source[, ...])	Copy file to default location if it does not already exist
dask.config.update(old, new[, priority])	Update a nested dictionary with values from another
dask.config.update_defaults(new[, config, ...])	Add a new set of defaults to the configuration

Downstream Dask libraries often follow a standard convention to use the central Dask configuration. This section provides recommendations for integration, using a fictional project, `dask-foo`, as an example.

Downstream projects typically follow the following convention:

1. Maintain default configuration in a YAML file within their source directory:

   ```
   setup.py
   dask_foo/__init__.py
   dask_foo/config.py
   dask_foo/core.py
   dask_foo/foo.yaml   # <---
   ```

2. Place configuration in that file within a namespace for the project

   ```
   # dask_foo/foo.yaml

   foo:
     color: red
     admin:
       a: 1
       b: 2
   ```

3. Within a config.py file (or anywhere) load that default config file and update it into the global configuration

   ```
   # dask_foo/config.py
   import os
   import yaml

   import dask.config

   fn = os.path.join(os.path.dirname(__file__), 'foo.yaml')

   with open(fn) as f:
       defaults = yaml.load(f)

   dask.config.update_defaults(defaults)
   ```

4. Within that same config.py file, copy the `'foo.yaml'` file to the user's configuration directory if it doesn't already exist.

   We also comment the file to make it easier for us to change defaults in the future.

```
# ... continued from above

dask.config.ensure_file(source=fn, comment=True)
```

The user can investigate `~/.config/dask/*.yaml` to see all of the commented out configuration files to which they have access.

5. Ensure that this file is run on import by including it in `__init__.py`

```
# dask_foo/__init__.py

from . import config
```

6. Within `dask_foo` code, use the `dask.config.get` function to access configuration values

```
# dask_foo/core.py

def process(fn, color=dask.config.get('foo.color')):
    ...
```

7. You may also want to ensure that your yaml configuration files are included in your package. This can be accomplished by including the following line in your MANIFEST.in:

```
recursive-include <PACKAGE_NAME> *.yaml
```

and the following in your setup.py `setup` call

```
from setuptools import setup

setup(...,
      include_package_data=True,
      ...)
```

This process keeps configuration in a central place, but also keeps it safe within namespaces. It places config files in an easy to access location ,‘‘~/.config/dask/*.yaml‘‘ by default so that users can easily discover what they can change, but maintains the actual defaults within the source code, so that they more closely track changes in the library.

However, downstream libraries may choose alternative solutions, such as isolating their configuration within their library, rather than using the global dask.config system. All functions in the `dask.config` module also work with parameters, and do not need to mutate global state.

4.27.5 API

`dask.config.get`(*key*, *default='__no_default__'*, *config={'array': {'rechunk-threshold': 4, 'chunk-size': '128MiB'}}*)

Get elements from global config

Use ‘.’ for nested access

See also:

dask.config.set

Examples

```
>>> from dask import config
>>> config.get('foo')
{'x': 1, 'y': 2}
```

```
>>> config.get('foo.x')
1
```

```
>>> config.get('foo.x.y', default=123)
123
```

dask.config.**set**(*arg=None*, *config={'array': {'rechunk-threshold': 4, 'chunk-size': '128MiB'}}*, *lock=<unlocked _thread.lock object>*, ***kwargs*)

Temporarily set configuration values within a context manager

See also:

dask.config.get

Examples

```
>>> import dask
>>> with dask.config.set({'foo': 123}):
...     pass
```

dask.config.**merge**(**dicts*)

Update a sequence of nested dictionaries

This prefers the values in the latter dictionaries to those in the former

See also:

dask.config.update

Examples

```
>>> a = {'x': 1, 'y': {'a': 2}}
>>> b = {'y': {'b': 3}}
>>> merge(a, b)
{'x': 1, 'y': {'a': 2, 'b': 3}}
```

dask.config.**update**(*old*, *new*, *priority='new'*)

Update a nested dictionary with values from another

This is like dict.update except that it smoothly merges nested values

This operates in-place and modifies old

Parameters

priority: string {'old', 'new'} If new (default) then the new dictionary has preference. Otherwise the old dictionary does.

See also:

dask.config.merge

Examples

```
>>> a = {'x': 1, 'y': {'a': 2}}
>>> b = {'x': 2, 'y': {'b': 3}}
>>> update(a, b)
{'x': 2, 'y': {'a': 2, 'b': 3}}
```

```
>>> a = {'x': 1, 'y': {'a': 2}}
>>> b = {'x': 2, 'y': {'b': 3}}
>>> update(a, b, priority='old')
{'x': 1, 'y': {'a': 2, 'b': 3}}
```

dask.config.**collect**(*paths=['/etc/dask', '/home/docs/checkouts/readthedocs.org/user_builds/dask/envs/latest/etc/dask', '/home/docs/.config/dask', '/home/docs/.dask'], env=None*)

Collect configuration from paths and environment variables

Parameters

paths [List[str]] A list of paths to search for yaml config files

env [dict] The system environment variables

Returns

config: dict

See also:

dask.config.refresh collect configuration and update into primary config

dask.config.**refresh**(*config={'array': {'rechunk-threshold': 4, 'chunk-size': '128MiB'}}, defaults=[{'array': {'rechunk-threshold': 4, 'chunk-size': '128MiB'}}], **kwargs*)

Update configuration by re-reading yaml files and env variables

This mutates the global dask.config.config, or the config parameter if passed in.

This goes through the following stages:

1. Clearing out all old configuration
2. Updating from the stored defaults from downstream libraries (see update_defaults)
3. Updating from yaml files and environment variables

Note that some functionality only checks configuration once at startup and may not change behavior, even if configuration changes. It is recommended to restart your python process if convenient to ensure that new configuration changes take place.

See also:

dask.config.collect for parameters

dask.config.update_defaults

dask.config.**ensure_file**(*source*, *destination=None*, *comment=True*)

Copy file to default location if it does not already exist

This tries to move a default configuration file to a default location if if does not already exist. It also comments out that file by default.

This is to be used by downstream modules (like dask.distributed) that may have default configuration files that they wish to include in the default configuration path.

Parameters

source [string, filename] Source configuration file, typically within a source directory.

destination [string, directory] Destination directory. Configurable by `DASK_CONFIG` environment variable, falling back to ~/.config/dask.

comment [bool, True by default] Whether or not to comment out the config file when copying.

`dask.config.`**`expand_environment_variables`**`(`*`config`*`)`

Expand environment variables in a nested config dictionary

This function will recursively search through any nested dictionaries and/or lists.

Parameters

config [dict, iterable, or str] Input object to search for environment variables

Returns

config [same type as input]

Examples

```
>>> expand_environment_variables({'x': [1, 2, '$USER']})
{'x': [1, 2, 'my-username']}
```

4.28 Presentations On Dask

- SciPy 2018, July 2018
  - Scalable Machine Learning with Dask (30 minutes)
- AMS & ESIP, January 2018
  - Pangeo quick demo: Dask, XArray, Zarr on the cloud with JupyterHub (3 minutes)
  - Pangeo talk: An open-source big data science platform with Dask, XArray, Zarr on the cloud with JupyterHub (43 minutes)
- PYCON.DE 2017, November 2017
  - Dask: Parallelism in Python (1 hour, 2 minutes)
- PYCON 2017, May 2017
  - Dask: A Pythonic Distributed Data Science Framework (46 minutes)
- PLOTCON 2016, December 2016
  - Visualizing Distributed Computations with Dask and Bokeh (33 minutes)
- PyData DC, October 2016
  - Using Dask for Parallel Computing in Python (44 minutes)
- SciPy 2016, July 2016
  - Dask Parallel and Distributed Computing (28 minutes)

- PyData NYC, December 2015
  - Dask Parallelizing NumPy and Pandas through Task Scheduling (33 minutes)
- PyData Seattle, August 2015
  - Dask: out of core arrays with task scheduling (1 hour, 50 minutes)
- SciPy 2015, July 2015
  - Dask Out of core NumPy:Pandas through Task Scheduling (16 minutes)

4.29 Dask Cheat Sheet

The 300KB pdf `dask cheat sheet` is a single page summary about using dask. It is commonly distributed at conferences and trade shows.

4.30 Comparison to Spark

Apache Spark is a popular distributed computing tool for tabular datasets that is growing to become a dominant name in Big Data analysis today. Dask has several elements that appear to intersect this space and we are often asked, "How does Dask compare with Spark?"

Answering such comparison questions in an unbiased and informed way is hard, particularly when the differences can be somewhat technical. This document tries to do this; we welcome any corrections.

4.30.1 Summary

Generally Dask is smaller and lighter weight than Spark. This means that it has fewer features and instead is intended to be used in conjunction with other libraries, particularly those in the numeric Python ecosystem. It couples with other libraries like Pandas or Scikit-Learn to achieve high-level functionality.

- **Language**
  - Spark is written in Scala with some support for Python and R. It interoperates well with other JVM code.
  - Dask is written in Python and only really supports Python. It interoperates well with C/C++/Fortran/LLVM or other natively compiled code linked through Python.
- **Ecosystem**
  - Spark is an all-in-one project that has inspired its own ecosystem. It integrates well with many other Apache projects.
  - Dask is a component of the larger Python ecosystem. It couples with and enhances other libraries like NumPy, Pandas, and Scikit-Learn.
- **Age and Trust**
  - Spark is older (since 2010) and has become a dominant and well-trusted tool in the Big Data enterprise world.
  - Dask is younger (since 2014) and is an extension of the well trusted NumPy/Pandas/Scikit-learn/Jupyter stack.
- **Scope**

  - Spark is more focused on traditional business intelligence operations like SQL and lightweight machine learning.
  - Dask is applied more generally both to business intelligence applications, as well as a number of scientific and custom situations

- **Internal Design**
  - Spark's internal model is higher level, providing good high level optimizations on uniformly applied computations, but lacking flexibility for more complex algorithms or ad-hoc systems. It is fundamentally an extension of the Map-Shuffle-Reduce paradigm.
  - Dask's internal model is lower level, and so lacks high level optimizations, but is able to implement more sophisticated algorithms and build more complex bespoke systems. It is fundamentally based on generic task scheduling.

- **Scale**
  - Spark scales from a single node to thousand-node clusters
  - Dask scales from a single node to thousand-node clusters

- **APIs**
  - **Dataframes**
    - Spark dataframe has its own API and memory model. It also implements a large subset of the SQL language. Spark includes a high-level query optimizer for complex queries.
    - Dask.dataframe reuses the Pandas API and memory model. It implements neither SQL nor a query optimizer. It is able to do random access, efficient time series operations, and other Pandas-style indexed operations.
  - **Machine Learning**
    - Spark MLLib is a cohesive project with support for common operations that are easy to implement with Spark's Map-Shuffle-Reduce style system. People considering MLLib might also want to consider *other* JVM-based machine learning libraries like H2O, which may have better performance.
    - Dask relies on and interoperates with existing libraries like Scikit-Learn and XGBoost. These can be more familiar or higher performance, but generally results in a less-cohesive whole. See the dask-ml project for integrations.
  - **Arrays**
    - Spark does not include support for multi-dimensional arrays natively (this would be challenging given their computation model) although some support for two-dimensional matrices may be found in MLLib. People may also want to look at the Thunder project, which combines Apache Spark with NumPy arrays.
    - Dask fully supports the NumPy model for *scalable multi-dimensional arrays*.
  - **Streaming**
    - Spark's support for streaming data is first-class and integrates well into their other APIs. It follows a mini-batch approach. This provides decent performance on large uniform streaming operations
    - Dask provides a *real-time futures interface* that is lower-level than Spark streaming. This enables more creative and complex use-cases, but requires more work than Spark streaming.
  - **Graphs / complex networks**
    - Spark provides GraphX, a library for graph processing

    * Dask provides no such library

  - **Custom parallelism**

    * Spark generally expects users to compose computations out of their high-level primitives (map, reduce, groupby, join, ...). It is also possible to extend Spark through subclassing RDDs, although this is rarely done.
    * Dask allows you to specify arbitrary task graphs for more complex and custom systems that are not part of the standard set of collections.

4.30.2 Reasons you might choose Spark

- You prefer Scala or the SQL language
- You have mostly JVM infrastructure and legacy systems
- You want an established and trusted solution for business
- You are mostly doing business analytics with some lightweight machine learning
- You want an all-in-one solution

4.30.3 Reasons you might choose Dask

- You prefer Python or native code, or have large legacy code bases that you do not want to entirely rewrite
- Your use case is complex or does not cleanly fit the Spark computing model
- You want a lighter-weight transition from local computing to cluster computing
- You want to interoperate with other technologies and don't mind installing multiple packages

4.30.4 Developer-Facing Differences

Graph Granularity

Both Spark and Dask represent computations with directed acyclic graphs. These graphs however represent computations at very different granularities.

One operation on a Spark RDD might add a node like `Map` and `Filter` to the graph. These are high-level operations that convey meaning and will eventually be turned into many little tasks to execute on individual workers. This many-little-tasks state is only available internally to the Spark scheduler.

Dask graphs skip this high-level representation and go directly to the many-little-tasks stage. As such one `map` operation on a dask collection will immediately generate and add possibly thousands of tiny tasks to the dask graph.

This difference in the scale of the underlying graph has implications on the kinds of analysis and optimizations one can do and also on the generality that one exposes to users. Dask is unable to perform some optimizations that Spark can because Dask schedulers do not have a top-down picture of the computation they were asked to perform. However, dask is able to easily represent far more complex algorithms and expose the creation of these algorithms to normal users.

4.30.5 Conclusion

Spark is mature and all-inclusive. If you want a single project that does everything and you're already on Big Data hardware then Spark is a safe bet, especially if your use cases are typical ETL + SQL and you're already using Scala.

Dask is lighter weight and is easier to integrate into existing code and hardware. If your problems vary beyond typical ETL + SQL and you want to add flexible parallelism to existing solutions then dask may be a good fit, especially if you are already using Python and associated libraries like NumPy and Pandas.

If you are looking to manage a terabyte or less of tabular CSV or JSON data then you should forget both Spark and Dask and use Postgres or MongoDB.

4.31 Opportunistic Caching

EXPERIMENTAL FEATURE added to Version 0.6.2 and above - see *disclaimer*.

Dask usually removes intermediate values as quickly as possible in order to make space for more data to flow through your computation. However, in some cases, we may want to hold onto intermediate values, because they might be useful for future computations in an interactive session.

We need to balance the following concerns:

1. Intermediate results might be useful in future unknown computations
2. Intermediate results also fill up memory, reducing space for the rest of our current computation.

Negotiating between these two concerns helps us to leverage the memory that we have available to speed up future, unanticipated computations. Which intermediate results should we keep?

This document explains an experimental, opportunistic caching mechanism that automatically picks out and stores useful tasks.

4.31.1 Motivating Example

Consider computing the maximum value of a column in a CSV file:

```
>>> import dask.dataframe as dd
>>> df = dd.read_csv('myfile.csv')
>>> df.columns
['first-name', 'last-name', 'amount', 'id', 'timestamp']

>>> df.amount.max().compute()
1000
```

Even though our full dataset may be too large to fit in memory, the single `df.amount` column may be small enough to hold in memory just in case it might be useful in the future. This is often the case during data exploration, because we investigate the same subset of our data repeatedly before moving on.

For example, we may now want to find the minimum of the amount column:

```
>>> df.amount.min().compute()
-1000
```

Under normal operations, this would need to read through the entire CSV file over again. This is somewhat wasteful, and stymies interactive data exploration.

4.31.2 Two Simple Solutions

If we know ahead of time that we want both the maximum and minimum, we can compute them simultaneously. Dask will share intermediates intelligently, reading through the dataset only once:

```
>>> dd.compute(df.amount.max(), df.amount.min())
(1000, -1000)
```

If we know that this column fits in memory then we can also explicitly compute the column and then continue forward with straight Pandas:

```
>>> amount = df.amount.compute()
>>> amount.max()
1000
>>> amount.min()
-1000
```

If either of these solutions work for you, great. Otherwise, continue on for a third approach.

4.31.3 Automatic Opportunistic Caching

Another approach is to watch *all* intermediate computations, and *guess* which ones might be valuable to keep for the future. Dask has an *opportunistic caching mechanism* that stores intermediate tasks that show the following characteristics:

1. Expensive to compute
2. Cheap to store
3. Frequently used

We can activate a fixed sized cache as a callback.

```
>>> from dask.cache import Cache
>>> cache = Cache(2e9)  # Leverage two gigabytes of memory
>>> cache.register()    # Turn cache on globally
```

Now the cache will watch every small part of the computation and judge the value of that part based on the three characteristics listed above (expensive to compute, cheap to store, and frequently used).

Dask will hold on to 2GB of the best intermediate results it can find, evicting older results as better results come in. If the `df.amount` column fits in 2GB then probably all of it will be stored while we keep working on it.

If we start work on something else, then the `df.amount` column will likely be evicted to make space for other more timely results:

```
>>> df.amount.max().compute()  # slow the first time
1000
>>> df.amount.min().compute()  # fast because df.amount is in the cache
-1000
>>> df.id.nunique().compute()  # starts to push out df.amount from cache
```

4.31.4 Cache tasks, not expressions

This caching happens at the low-level scheduling layer, not the high-level dask.dataframe or dask.array layer. We don't explicitly cache the column `df.amount`. Instead, we cache the hundreds of small pieces of that column that form the dask graph. It could be that we end up caching only a fraction of the column.

This means that the opportunistic caching mechanism described above works for *all* dask computations, as long as those computations employ a consistent naming scheme (as all of dask.dataframe, dask.array, and dask.delayed do.)

You can see which tasks are held by the cache by inspecting the following attributes of the cache object:

```
>>> cache.cache.data
<stored values>
>>> cache.cache.heap.heap
<scores of items in cache>
>>> cache.cache.nbytes
<number of bytes per item in cache>
```

The cache object is powered by cachey, a tiny library for opportunistic caching.

4.31.5 Disclaimer

This feature is still experimental, and can cause your computation to fill up RAM.

Restricting your cache to a fixed size like 2GB requires dask to accurately count the size of each of our objects in memory. This can be tricky, particularly for Pythonic objects like lists and tuples, and for DataFrames that contain object dtypes.

It is entirely possible that the caching mechanism will *undercount* the size of objects, causing it to use up more memory than anticipated which can lead to blowing up RAM and crashing your session.

4.32 Internal Data Ingestion

Dask contains internal tools for extensible data ingestion in the `dask.bytes` package. *These functions are developer-focused rather than for direct consumption by users. These functions power user facing functions like ‘‘dd.read_csv‘‘ and ‘‘db.read_text‘‘ which are probably more useful for most users.*

read_bytes(urlpath[, delimiter, not_zero, ...])	Given a path or paths, return delayed objects that read from those paths.
open_files(urlpath[, mode, compression, ...])	Given a path or paths, return a list of `OpenFile` objects.

These functions are extensible in their output formats (bytes, file objects), their input locations (file system, S3, HDFS), line delimiters, and compression formats.

These functions provide data as `dask.delayed` objects. These objects either point to blocks of bytes (`read_bytes`) or open file objects (`open_files`). They can handle different compression formats by prepending protocols like `s3://` or `hdfs://`. They handle compression formats listed in the `dask.bytes.compression` module.

These functions are not used for all data sources. Some data sources like HDF5 are quite particular and receive custom treatment.

4.32.1 Delimiters

The `read_bytes` function takes a path (or globstring of paths) and produces a sample of the first file and a list of delayed objects for each of the other files. If passed a delimiter such as `delimiter=b'\n'` it will ensure that the blocks of bytes start directly after a delimiter and end directly before a delimiter. This allows other functions, like `pd.read_csv`, to operate on these delayed values with expected behavior.

These delimiters are useful both for typical line-based formats (log files, CSV, JSON) as well as other delimited formats like Avro, which may separate logical chunks by a complex sentinel string.

4.32.2 Locations

These functions dispatch to other functions that handle different storage backends, like S3 and HDFS. These storage backends register themselves with protocols and so are called whenever the path is prepended with a string like the following:

```
s3://bucket/keys-*.csv
```

The various back-ends accept optional extra keywords, detailing authentication and other parameters, see *remote data services*

4.32.3 Compression

These functions support widely available compression technologies like `gzip`, `bz2`, `xz`, `snappy`, and `lz4`. More compressions can be easily added by inserting functions into dictionaries available in the `dask.bytes.compression` module. This can be done at runtime and need not be added directly to the codebase.

However, not all compression technologies are available for all functions. In particular, compression technologies like `gzip` do not support efficient random access and so are useful for streaming `open_files` but not useful for `read_bytes` which splits files at various points.

4.32.4 Functions

`dask.bytes.`**`read_bytes`**(*urlpath*, *delimiter=None*, *not_zero=False*, *blocksize=134217728*, *sample=True*, *compression=None*, *include_path=False*, ***kwargs*)

Given a path or paths, return delayed objects that read from those paths.

The path may be a filename like `'2015-01-01.csv'` or a globstring like `'2015-*-*.csv'`.

The path may be preceded by a protocol, like `s3://` or `hdfs://` if those libraries are installed.

This cleanly breaks data by a delimiter if given, so that block boundaries start directly after a delimiter and end on the delimiter.

Parameters

urlpath [string or list] Absolute or relative filepath(s). Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol.

delimiter [bytes] An optional delimiter, like `b'\n'` on which to split blocks of bytes.

not_zero [bool] Force seek of start-of-file delimiter, discarding header.

blocksize [int (=128MB)] Chunk size in bytes

compression [string or None] String like 'gzip' or 'xz'. Must support efficient random access.

sample [bool or int] Whether or not to return a header sample. If an integer is given it is used as sample size, otherwise the default sample size is 10kB.

include_path [bool] Whether or not to include the path with the bytes representing a particular file. Default is False.

****kwargs** [dict] Extra options that make sense to a particular storage connection, e.g. host, port, username, password, etc.

Returns

sample [bytes] The sample header

blocks [list of lists of `dask.Delayed`] Each list corresponds to a file, and each delayed object computes to a block of bytes from that file.

paths [list of strings, only included if include_path is True] List of same length as blocks, where each item is the path to the file represented in the corresponding block.

Examples

```
>>> sample, blocks = read_bytes('2015-*-*.csv', delimiter=b'\n')
>>> sample, blocks = read_bytes('s3://bucket/2015-*-*.csv', delimiter=b'\n')
>>> sample, paths, blocks = read_bytes('2015-*-*.csv', include_path=True)
```

`dask.bytes.`**`open_files`**(*urlpath*, *mode='rb'*, *compression=None*, *encoding='utf8'*, *errors=None*, *name_function=None*, *num=1*, ***kwargs*)

Given a path or paths, return a list of `OpenFile` objects.

Parameters

urlpath [string or list] Absolute or relative filepath(s). Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol.

mode ['rb', 'wt', etc.]

compression [string] Compression to use. See `dask.bytes.compression.files` for options.

encoding [str] For text mode only

errors [None or str] Passed to TextIOWrapper in text mode

name_function [function or None] if opening a set of files for writing, those files do not yet exist, so we need to generate their names by formatting the urlpath for each sequence number

num [int [1]] if writing mode, number of files we expect to create (passed to name+function)

****kwargs** [dict] Extra options that make sense to a particular storage connection, e.g. host, port, username, password, etc.

Returns

List of ''OpenFile'' objects.

Examples

```
>>> files = open_files('2015-*-*.csv')
>>> files = open_files('s3://bucket/2015-*-*.csv.gz', compression='gzip')
```

4.33 Remote Data

Dask can read data from a variety data stores including local file systems, network file systems, cloud object stores, and Hadoop. Typically this is done by prepending a protocol like `"s3://"` to paths used in common data access functions like `dd.read_csv`

```
import dask.dataframe as dd
df = dd.read_csv('s3://bucket/path/to/data-*.csv')
df = dd.read_parquet('gcs://bucket/path/to/data-*.parq')

import dask.bag as db
b = db.read_text('hdfs://path/to/*.json').map(json.loads)
```

The following remote services are well supported and tested against the main codebase:

- **Local or Network File System**: `file://` - the local file system, default in the absence of any protocol
- **Hadoop File System**: `hdfs://` - Hadoop Distributed File System, for resilient, replicated files within a cluster. Can use either hdfs3 or pyarrow.
- **Amazon S3**: `s3://` - Amazon S3 remote binary store, often used with Amazon EC2, using the library s3fs
- **Google Cloud Storage**: `gcs://` or `gs:` - Google Cloud Storage, typically used with Google Compute resource, using gcsfs (in development)
- **HTTP(s)**: `http://` or `https://` for reading data directly from HTTP web servers

When specifying a storage location, a URL should be provided using the general form `protocol://path/to/data`. If no protocol is provided, the local file-system is assumed (same as `file://`).

Lower-level details on how Dask handles remote data is described in Section *Internal Data Ingestion*.

4.33.1 Optional Parameters

Two methods exist for passing parameters to the backend file-system driver: extending the URL to include username, password, server, port, etc.; and providing `storage_options`, a dictionary of parameters to pass on. Examples:

```
df = dd.read_csv('hdfs://user@server:port/path/*.csv')

df = dd.read_parquet('s3://bucket/path',
                     storage_options={'anon': True, 'use_ssl': False})
```

Further details on how to provide configuration for each backend is listed next.

Each back-end has additional installation requirements and may not be available at runtime. The dictionary `dask.bytes.core._filesystems` contains the currently available file-systems. Some require appropriate imports before use.

The following list gives the protocol shorthands and the back-ends to which they refer.

4.33.2 Local File System

Local files are always accessible, and all parameters passed as part of the URL (beyond the path itself) or with the `storage_options` dictionary will be ignored.

This is the default back-end, and the one used if no protocol is passed at all.

We assume here that each worker has access to the same file-system - either the workers are co-located on the same machine, or a network file system is mounted and referenced at the same path location for every worker node.

Locations specified relative to the current working directory will, in general, be respected (as they would be with the built-in python `open`), but this may fail in the case that the client and worker processes do not necessarily have the same working directory.

4.33.3 Hadoop File System

The Hadoop File System (HDFS) is a widely deployed, distributed, data-local file system written in Java. This file system backs many clusters running Hadoop and Spark.

HDFS support can be provided by either hdfs3 or pyarrow, defaulting to the first library installed in that order. To explicitly set which library to use, set `hdfs_driver` using `dask.config.set`:

```
# Use first available option in [hdfs3, pyarrow]
 dd.read_csv('hdfs:///path/to/*.csv')

# Use hdfs3 for HDFS I/O
with dask.config.set(hdfs_driver='hdfs3'):
    dd.read_csv('hdfs:///path/to/*.csv')

# Use pyarrow for HDFS I/O
with dask.config.set(hdfs_driver='pyarrow'):
    dd.read_csv('hdfs:///path/to/*.csv')

# Set pyarrow as the global hdfs driver
dask.config.set(hdfs_driver='pyarrow')
```

By default, both libraries attempt to read the default server and port from local Hadoop configuration files on each node, so it may be that no configuration is required. However, the server, port and user can be passed as part of the url: `hdfs://user:pass@server:port/path/to/data`.

Extra Configuration for HDFS3

The following additional options may be passed to the `hdfs3` driver via `storage_options`:

- `host`, `port`, `user`: basic authentication
- `ticket_cache`, `token`: kerberos authentication
- `pars`: dictionary of further parameters (e.g., for high availability)

The `hdfs3` driver can also be affected by a few environment variables. For information on these see the hdfs3 documentation.

Extra Configuration for PyArrow

The following additional options may be passed to the `pyarrow` driver via `storage_options`:

- `host`, `port`, `user`: basic authentication
- `kerb_ticket`: path to kerberos ticket cache

PyArrow's `libhdfs` driver can also be affected by a few environment variables. For information on these see the pyarrow documentation.

4.33.4 Amazon S3

Amazon S3 (Simple Storage Service) is a web service offered by Amazon Web Services.

The S3 back-end will be available to dask is s3fs is importable when dask is imported.

Authentication for S3 is provided by the underlying library boto3. As described in the auth docs this could be achieved by placing credentials files in one of several locations on each node: `~/.aws/credentials`, `~/.aws/config`, `/etc/boto.cfg` and `~/.boto`. Alternatively, for nodes located within Amazon EC2, IAM roles can be set up for each node, and then no further configuration is required. The final authentication option, is for user credentials can be passed directly in the URL (`s3://keyID:keySecret/bucket/key/name`) or using `storage_options`. In this case, however, the key/secret will be passed to all workers in-the-clear, so this method is only recommended on well-secured networks.

The following parameters may be passed to s3fs using `storage_options`:

- anon: whether access should be anonymous (default False)
- key, secret: for user authentication
- token: if authentication has been done with some other S3 client
- use_ssl: whether connections are encrypted and secure (default True)
- client_kwargs: dict passed to the boto3 client, with keys such as *region_name*, *endpoint_url*
- requester_pays: set True if the authenticated user will assume transfer costs, which is required by some providers of bulk data
- default_block_size, default_fill_cache: these are not of particular interest to dask users, as they concern the behaviour of the buffer between successive reads
- kwargs: other parameters are passed to the boto3 Session object, such as *profile_name*, to pick one of the authentication sections from the configuration files referred to above (see here)

4.33.5 Google Cloud Storage

(gcsfs is in early development, expect the details here to change)

Google Cloud Storage is a RESTful online file storage web service for storing and accessing data on Google's infrastructure.

The GCS backend will be available only after importing gcsfs. The protocol identifiers `gcs` and `gs` are identical in their effect.

Authentication for GCS is based on OAuth2, and designed for user verification. Interactive authentication is available when `token==None` using the local browser, or by using gcloud to produce a JSON token file and passing that. In either case, gcsfs stores a cache of tokens in a local file, so subsequent authentication will not be necessary.

Possible additional storage options:

- access : 'read_only', 'read_write', 'full_control', access privilege level (note that the token cache uses a separate token for each level)
- token: either an actual dictionary of a google token, or location of a JSON file created by gcloud.

4.33.6 HTTP(s)

Direct file-like access to arbitrary URLs is available over HTTP and HTTPS. However, there is no such thing as `glob` functionality over HTTP, so only explicit lists of files can be used.

Server implementations differ in the information they provide - they may or may not specify the size of a file via a HEAD request or at the start of a download - and some servers may not respect bytes range requests. The HTTPFileSystem therefore offers best-effort behaviour: the download is streamed, but if more data is seen than the configured block-size, an error will be raised. To be able to access such data, you must read the whole file in one shot (and it must fit in memory).

Note that, currently, `http://` and `https://` are treated as separate protocols, and cannot be mixed.

4.33.7 Developer API

The prototype for any file-system back-end can be found in `bytes.local.LocalFileSystem`. Any new implementation should provide the same API, and make itself available as a protocol to dask. For example, the following would register the protocol "myproto", described by the implementation class `MyProtoFileSystem`. URLs of the form `myproto://` would thereafter be dispatched to the methods of this class.

```
dask.bytes.core._filesystems['myproto'] = MyProtoFileSystem
```

For a more complicated example, users may wish to also see `dask.bytes.s3.DaskS3FileSystem`.

class dask.bytes.local.**LocalFileSystem**(***storage_options*)

API spec for the methods a filesystem

A filesystem must provide these methods, if it is to be registered as a backend for dask.

Implementation for local disc

glob(*path*)

For a template path, return matching files

mkdirs(*path*)

Make any intermediate directories to make path writable

open(*path*, *mode='rb'*, ***kwargs*)

Make a file-like object

Parameters

mode: string normally "rb", "wb" or "ab" or other.

kwargs: key-value Any other parameters, such as buffer size. May be better to set these on the filesystem instance, to apply to all files created by it. Not used for local.

size(*path*)

Size in bytes of the file at path

ukey(*path*)

Unique identifier, so we can tell if a file changed

4.34 Citations

Dask is developed by many people from many institutions. Some of these developers are academics who depend on academic citations to justify their efforts. Unfortunately, no single citation can do all of these developers (and the developers to come) sufficient justice. Instead, we choose to use a single blanket citation for all developers past and present.

To cite Dask in publications, please use the following:

```
Dask Development Team (2016). Dask: Library for dynamic task scheduling
URL https://dask.org
```

A BibTeX entry for LaTeX users follows:

```
@Manual{,
  title = {Dask: Library for dynamic task scheduling},
  author = {{Dask Development Team}},
  year = {2016},
  url = {https://dask.org},
}
```

The full author list is available using git, or by looking at the AUTHORS file.

4.34.1 Papers about parts of Dask

Rocklin, Matthew. "Dask: Parallel Computation with Blocked algorithms and Task Scheduling." (2015). PDF.

```
@InProceedings{ matthew_rocklin-proc-scipy-2015,
  author    = { Matthew Rocklin },
  title     = { Dask: Parallel Computation with Blocked algorithms and Task␣
↪Scheduling },
  booktitle = { Proceedings of the 14th Python in Science Conference },
  pages     = { 130 - 136 },
  year      = { 2015 },
  editor    = { Kathryn Huff and James Bergstra }
}
```

4.35 Funding

Dask receives generous funding and support from the following sources:

1. The time and effort of numerous open source contributors
2. The DARPA XData program
3. The Moore Foundation's Data Driven Discovery program
4. Anaconda Inc
5. A variety of private companies who sponsor the development of particular open source features

We encourage monetary donations to NumFOCUS to support open source scientific computing software.

4.36 Images and Logos

Dask is supported by Anaconda Inc and develops under the BSD 3-clause license.

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