Performantly Scaling Machine Learning Algorithms

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What is scaling?

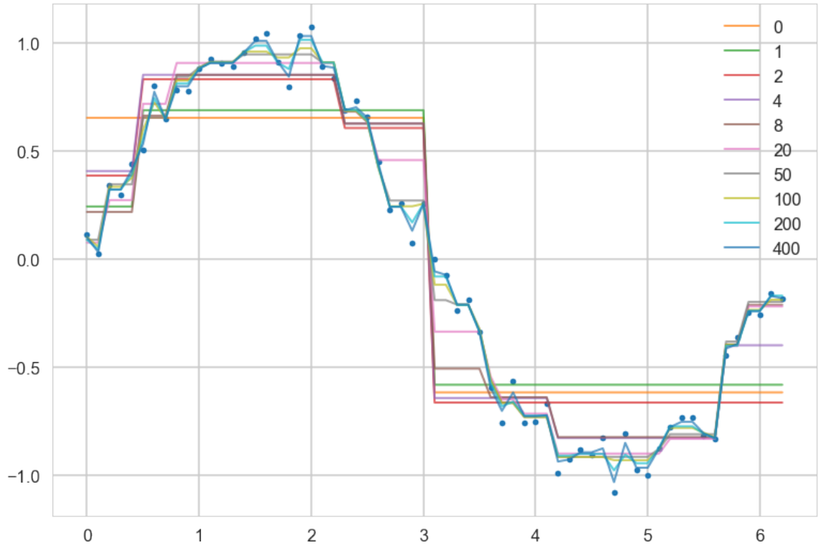
- Running experiments reproducibly, and keeping track
- Running in parallel, for speed and resilience
- Dealing with large data sets
- Grid or other Hyper-parameter optimization
- optimizing Gradient Descent

Hyper-parameter optimization

Eg, **Gradient boosting**: The basic idea is to fit the residuals of tree based regression models again and again. Peter Prettenhofer, who wrote sklearns GBRT implementation writes in his pydata14 talk:

I usually follow this recipe to tune the hyperparameters:

- Pick `n_estimators` as large as (computationally) possible (e.g. 3000)
- Tune `max_depth/min_samples_leaf`, `learning_rate`, and `max_features` via grid search
- A lower `learning_rate` requires a higher number of `n_estimators`. Thus increase `n_estimators` even more and tune `learning_rate` again holding the other params fixed.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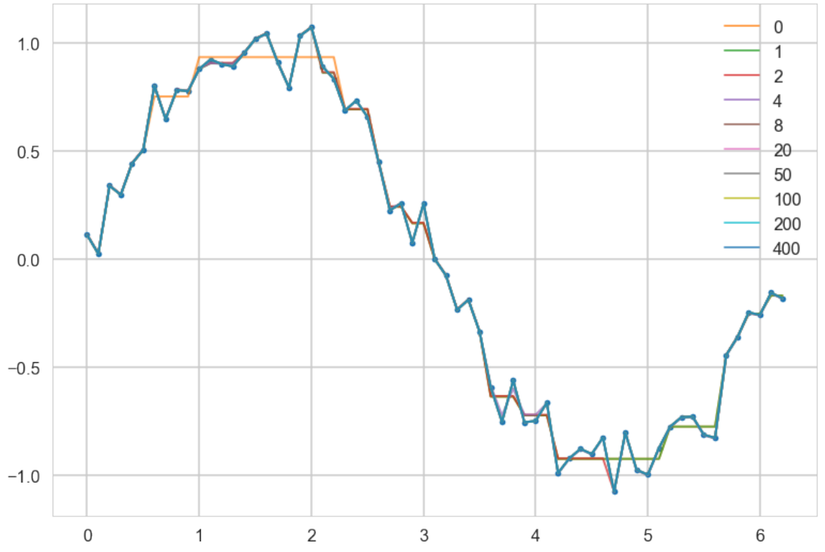
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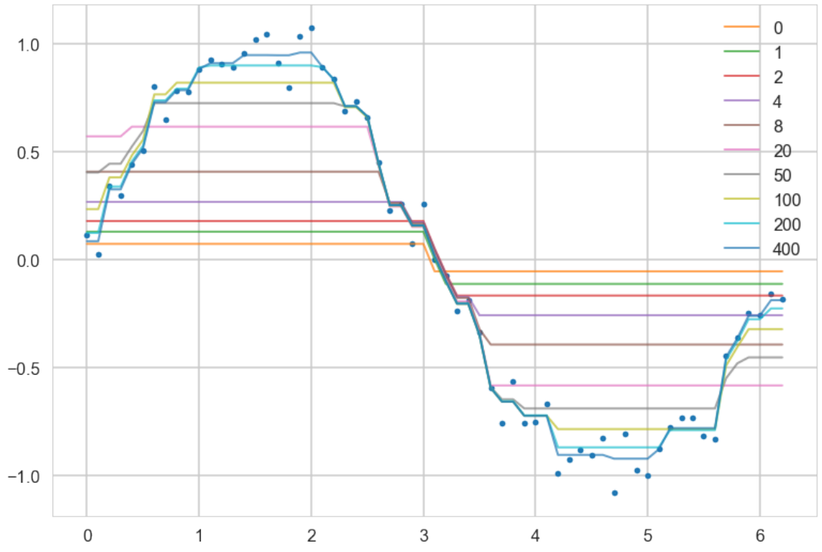
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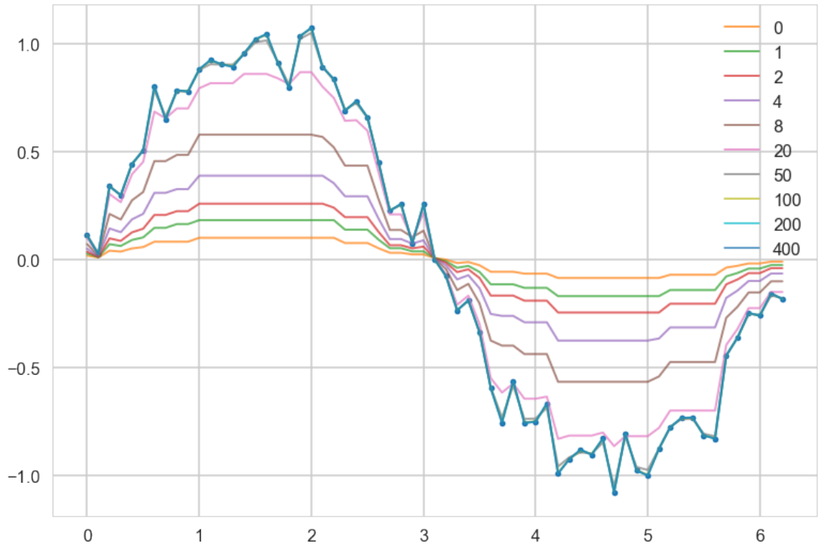
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Why is this bad? Or, why pipelines?

```
from sklearn.model_selection import GridSearchCV

vectorizer = TfidfVectorizer()
vectorizer.fit(text_train)

X_train = vectorizer.transform(text_train)
X_test = vectorizer.transform(text_test)

clf = LogisticRegression()
grid = GridSearchCV(clf, param_grid={'C': [.1, 1, 10, 100]}, cv=5)
grid.fit(X_train, y_train)
```

The purpose of the pipeline is to assemble several steps that can be cross-validated together while setting different parameters.

Grid search on pipelines

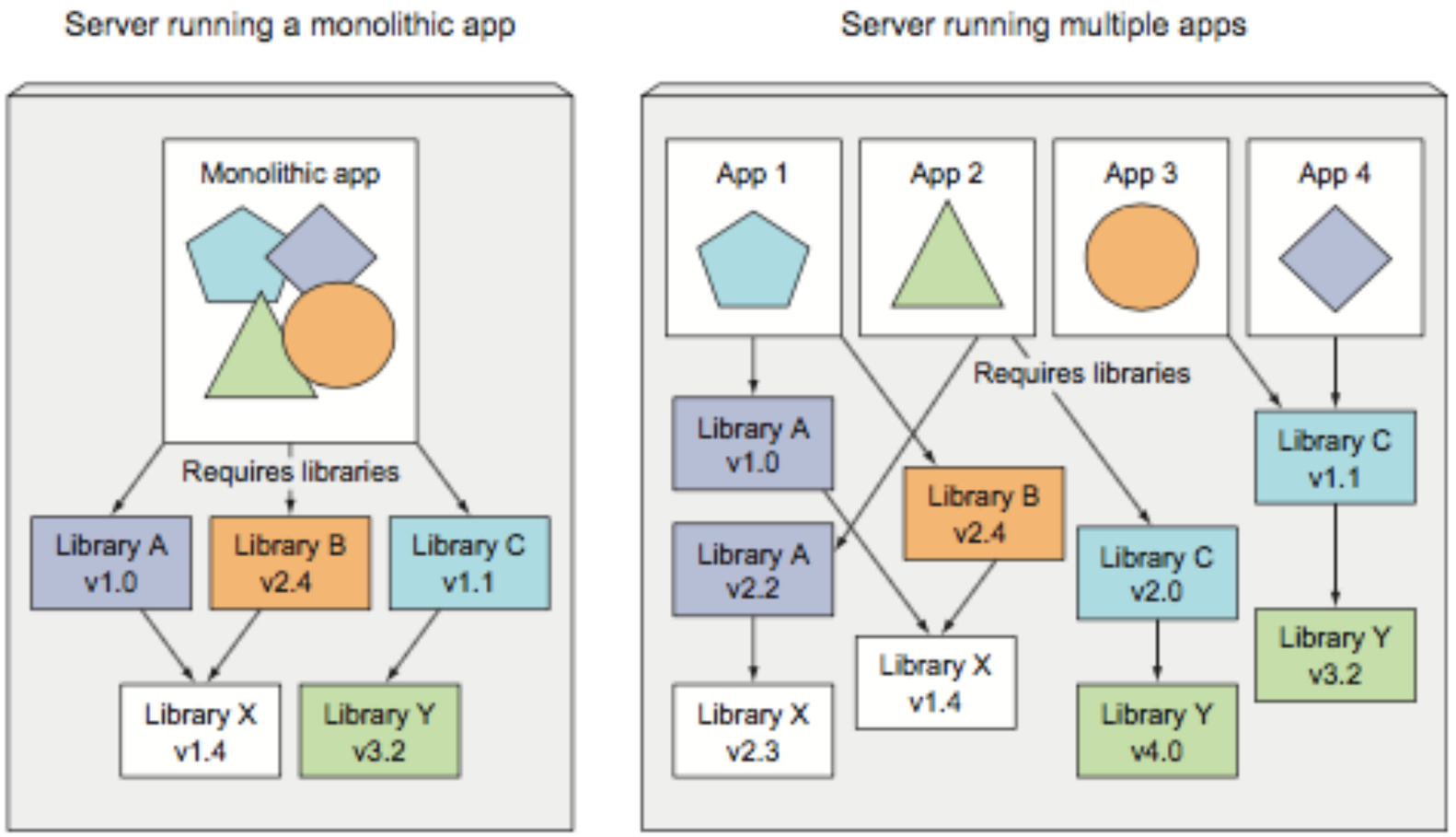
```
from sklearn.feature_extraction.text import CountVectorizer, TfidfTransformer
from sklearn.linear_model import SGDClassifier
from sklearn.pipeline import Pipeline
from sklearn.model_selection import GridSearchCV
from sklearn.datasets import fetch_20newsgroups

categories = [
    'alt.atheism',
    'talk.religion.misc',
]
data = fetch_20newsgroups(subset='train', categories=categories)
pipeline = Pipeline([('vect', CountVectorizer()),
                     ('tfidf', TfidfTransformer()),
                     ('clf', SGDClassifier())])
grid = {'vect__ngram_range': [(1, 1)],
        'tfidf__norm': ['l1', 'l2'],
        'clf__alpha': [1e-3, 1e-4, 1e-5]}

if __name__=='__main__':
    grid_search = GridSearchCV(pipeline, grid, cv=5, n_jobs=-1)
    grid_search.fit(data.data, data.target)
    print("Best score: %0.3f" % grid_search.best_score_)
    print("Best parameters set:", grid_search.best_estimator_.get_params())
```

ok, so you want to do this

PERFORMANTLY, AND REPRODUCIBLY

- same random seed
- same programming environment on multiple machines (ideally same version of OS/python-conda stack/BLAS libraries, etc)
- then run the same code with a different parameter combination on each machine
- deal with the possible loss of some machines in this computation (they die, you got an amazon spot instance..)
- combine all the data output from these runs to make hyperparameter choices

Programming environment: The multiple libraries problem



The python part: Conda environments

- create a conda environment for each new project
- put an `environment.yml` in each project folder
- at least have one for each new class, or class of projects
- environment for class of projects may grow organically, but capture its requirements from time-to-time.

see here

```yaml
# file name: environment.yml

# Give your project an informative name
name: project-name

# Specify the conda channels that you wish to grab packages from, in order of priority.
channels:
- defaults
- conda-forge

# Specify the packages that you would like to install inside your environment.
#Version numbers are allowed, and conda will automatically use its dependency
#solver to ensure that all packages work with one another.
dependencies:
- python=3.7
- conda
- scipy
- numpy
- pandas
- scikit-learn

# There are some packages which are not conda-installable. You can put the pip dependencies here instead.
- pip:
    - tqdm  # for example only, tqdm is actually available by conda.
```

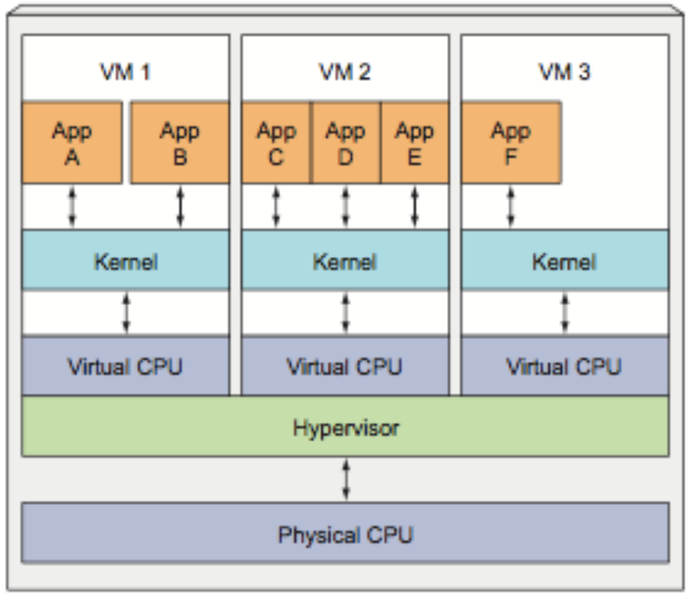
(from http://ericmjl.com/blog/2018/12/25/conda-hacks-for-data-science-efficiency/)

- `conda create --name environment-name [python=3.6]`
- `source[conda] activate environment-name` or project-name in the 1 environment per project paradigm
- `conda env create` in project folder
- `conda install <packagename>`
- or add the package to spec file, type `conda env update environment.yml` in appropriate folder
- `conda env export > environment.yml`

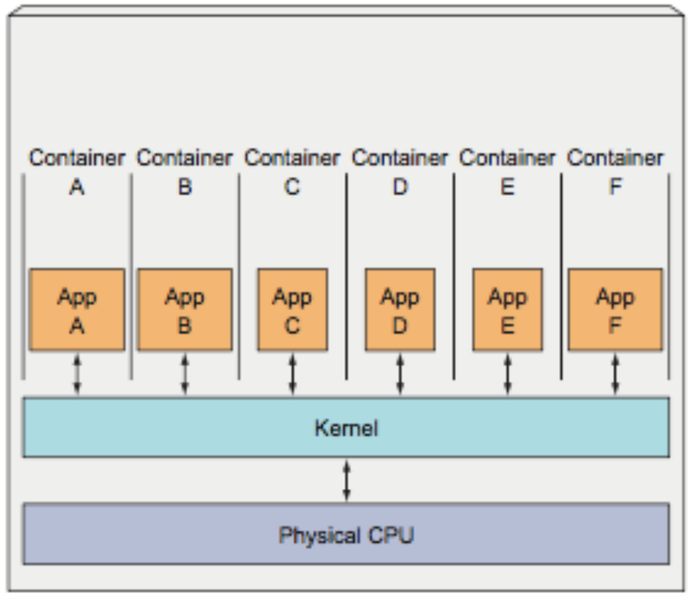
Rest of it: Docker

- More than python libs
- C-library, BLAS, linux kernel, etc
- we could use virtual machines (VMs) like vmware/virtualbox/lvm
- but these are heavy duty, OS level "hypervisor"s
- more general, but resource hungry

Apps running in multiple VMs



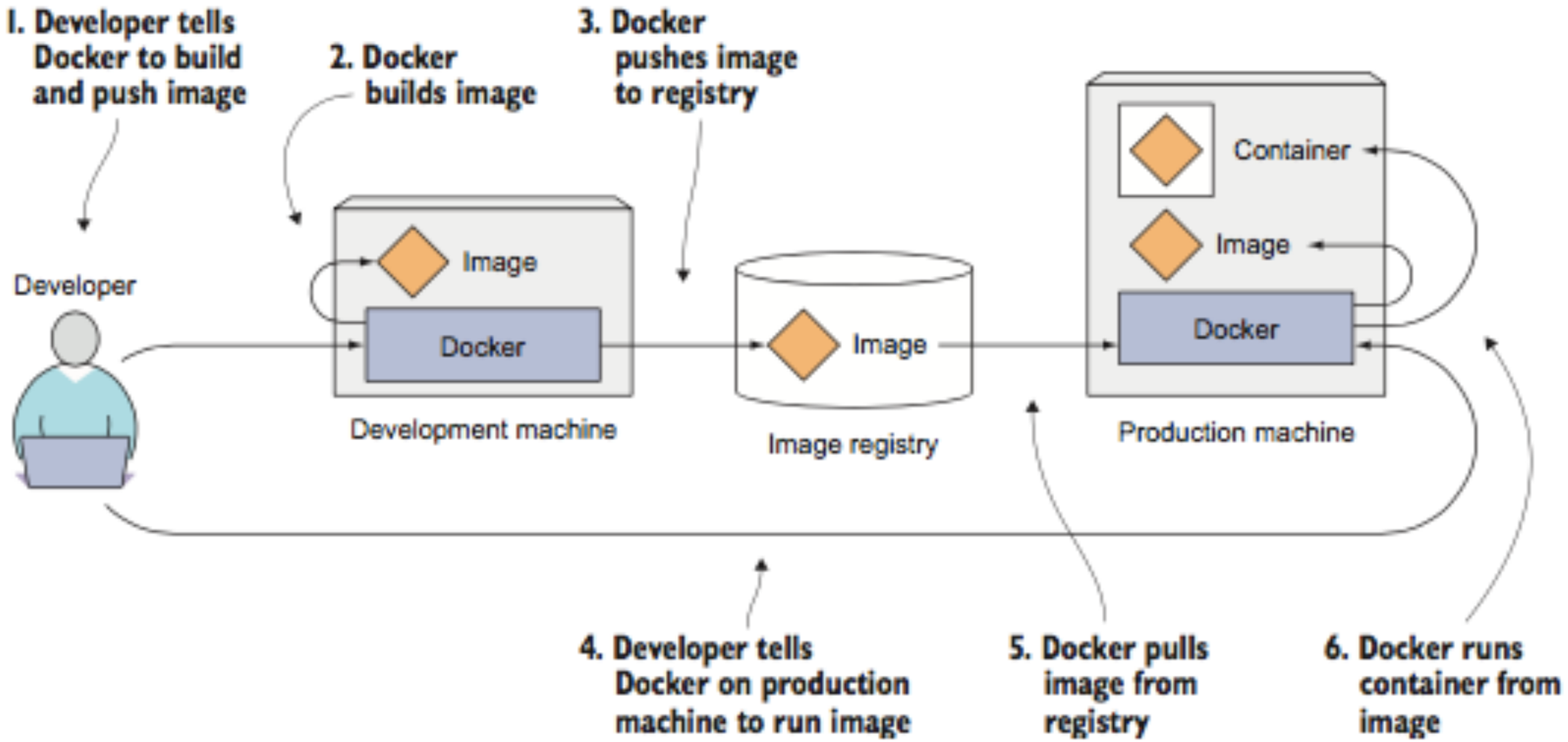
Apps running in isolated containers



Containers vs Virtual Machines

- containers provide process isolation, process throttling
- but work at library and kernel level, and can access hardware more easily
- hardware access important for gpu access
- containers can run on VMS, this is how docker runs on mac, and on many cloud providers. They can also run on a host linux OS on bare metal

Docker Architecture



Docker images

- docker is linux only, but other OS's now have support
- allow for environment setting across languages and runtimes
- can be chained together to create outcomes
- base image is a linux (full) image, others are just layers on top
- side benefit: integration testing and testing for CI

An Example

base notebook -> minimal notebook -> scipy notebook -> tensorflow notebook

```
# Copyright (c) Jupyter Development Team.
# Distributed under the terms of the Modified BSD License.
ARG BASE_CONTAINER=jupyter/scipy-notebook
FROM $BASE_CONTAINER

LABEL maintainer="Jupyter Project <jupyter@googlegroups.com>"

# Install Tensorflow
RUN conda install --quiet --yes \
    'tensorflow=1.12*' \
    'keras=2.2*' && \
    conda clean -tipsy && \
    fix-permissions $CONDA_DIR && \
    fix-permissions /home/$NB_USER
```

```
ARG BASE_CONTAINER=jupyter/minimal-notebook
FROM $BASE_CONTAINER
...
# ffmpeg for matplotlib anim
RUN apt-get update && \
    apt-get install -y --no-install-recommends ffmpeg && \
    rm -rf /var/lib/apt/lists/*
RUN conda install --quiet --yes \
    'conda-forge::blas=*=openblas' \
    'ipywidgets=7.4*' \
    'pandas=0.23*' \
    'numexpr=2.6*' \
    'matplotlib=2.2*' \
    'scipy=1.1*' \
    'seaborn=0.9*' \
    'scikit-learn=0.20*' \
    'scikit-image=0.14*' \
    'sympy=1.1*' \
    'cython=0.28*' \
    'patsy=0.5*' \
    'statsmodels=0.9*' \
    'cloudpickle=0.5*' \
    'dill=0.2*' \
    'numba=0.38*' \
    'bokeh=0.13*' \
    'sqlalchemy=1.2*' \
    'hdf5=1.10*' \
    'h5py=2.7*' \
    'vincent=0.4.*' \
    'beautifulsoup4=4.6.*' \
    'protobuf=3.*' \
    'xlrd'  && \
    conda remove --quiet --yes --force qt pyqt && \
    ...

# Install facets which does not have a pip or conda package at the moment
RUN cd /tmp && \
    git clone https://github.com/PAIR-code/facets.git && \
    cd facets && \
    jupyter nbextension install facets-dist/ --sys-prefix && \
    cd && ...
```

```
ARG
BASE_CONTAINER=ubuntu:bionic-20180526@sha256:c8c275751219dadad8fa56b3ac41ca6c
b22219ff117ca98fe82b42f24e1ba64e
FROM $BASE_CONTAINER
ARG NB_USER="jovyan"
...
USER root
RUN apt-get update && apt-get -yq dist-upgrade \
 && apt-get install -yq --no-install-recommends \
    wget \
    ...
RUN echo "en_US.UTF-8 UTF-8" > /etc/locale.gen && \
    locale-gen
ENV CONDA_DIR=/opt/conda \
    NB_USER=$NB_USER \
    ...
ADD fix-permissions /usr/local/bin/fix-permissions
RUN groupadd wheel -g 11 && \
    useradd -m -s /bin/bash -N -u $NB_UID $NB_USER && \
    ...
USER $NB_UID
...
ENV MINICONDA_VERSION 4.5.11
RUN cd /tmp && \
    wget --quiet https://repo.continuum.io/miniconda/Miniconda3-$
    {MINICONDA_VERSION}-Linux-x86_64.sh && \
    echo "e1045ee415162f944b6aebfe560b8fee *Miniconda3-${MINICONDA_VERSION}
    -Linux-x86_64.sh" | md5sum -c - && \
    /bin/bash Miniconda3-${MINICONDA_VERSION}-Linux-x86_64.sh -f -b -p
    $CONDA_DIR && \
    ...
RUN conda install --quiet --yes 'tini=0.18.0' && \
    ...
RUN conda install --quiet --yes \
'notebook=5.7.2' \
'jupyterhub=0.9.4' \
'jupyterlab=0.35.4' && ...
USER root
EXPOSE 8888
ENTRYPOINT ["tini", "-g", "--"]
CMD ["start-notebook.sh"]
COPY start.sh /usr/local/bin/
...
USER $NB_UID
```

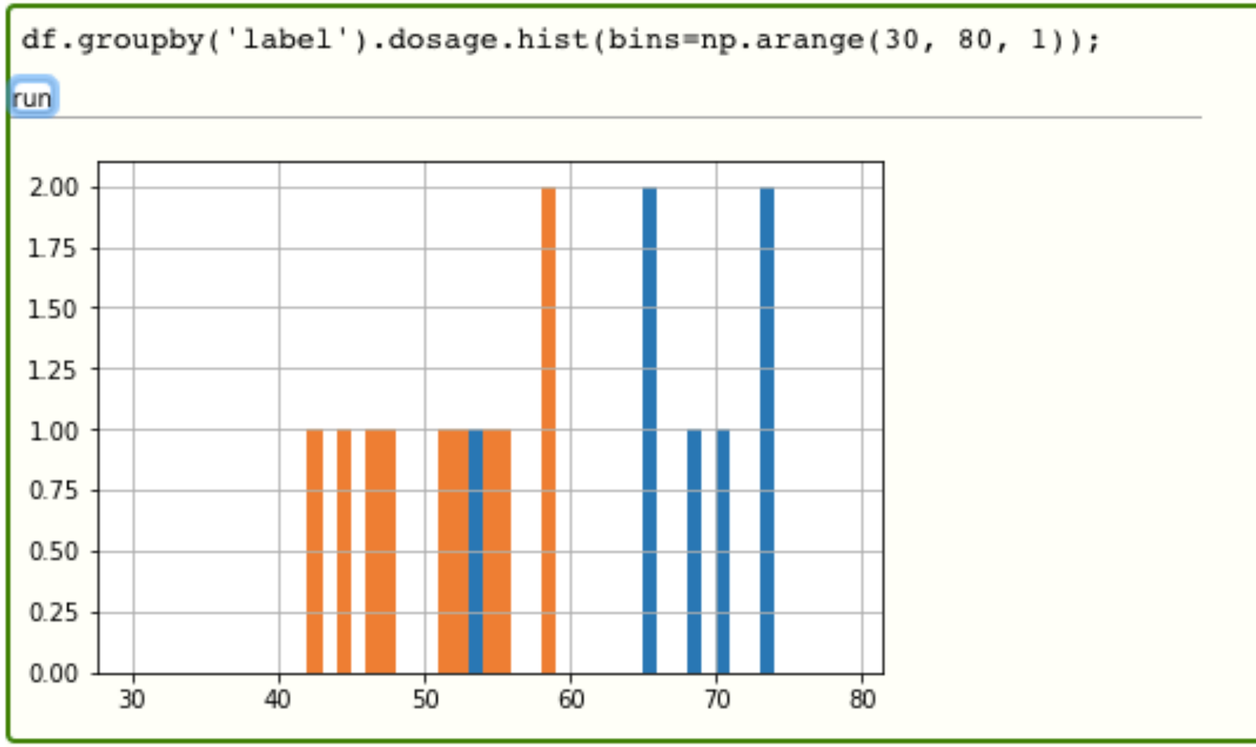
```
ARG BASE_CONTAINER=jupyter/base-notebook
FROM $BASE_CONTAINER

LABEL maintainer="Jupyter Project <jupyter@googlegroups.com>"

USER root

# Install all OS dependencies for fully functional notebook server
RUN apt-get update && apt-get install -yq --no-install-recommends \
    build-essential \
    emacs \
    git \
    inkscape \
    jed \
    libsm6 \
    libxext-dev \
    libxrender1 \
    lmodern \
    netcat \
    pandoc \
    python-dev \
    texlive-fonts-extra \
    texlive-fonts-recommended \
    texlive-generic-recommended \
    texlive-latex-base \
    texlive-latex-extra \
    texlive-xetex \
    unzip \
    nano \
    && rm -rf /var/lib/apt/lists/*

# Switch back to jovyan to avoid accidental container runs as root
USER $NB_UID
```

repo2docker and binder

- building docker images is not dead simple
- the Jupyter folks created repo2docker for this.
- provide a github repo, and repo2docker makes a docker image and uploads it to the docker image repository for you
- binder builds on this to provide a service where you provide a github repo, and it gives you a working jupyterhub where you can "publish" your project/demo/etc
- built repo's can be used with multiple software such as jupyterhub/dask/kubernetes, etc

usage example: AM207 and thebe-lab/juniper

- see https://github.com/am207/shadowbinder , a repository with an environment file only
- this repo is used to build a jupyterlab with some requirements where you can work.
- see here for example
- uses thebelab
- juniper used in the Spacy Course



Ok, so you now got repeatable environments. We next need to be

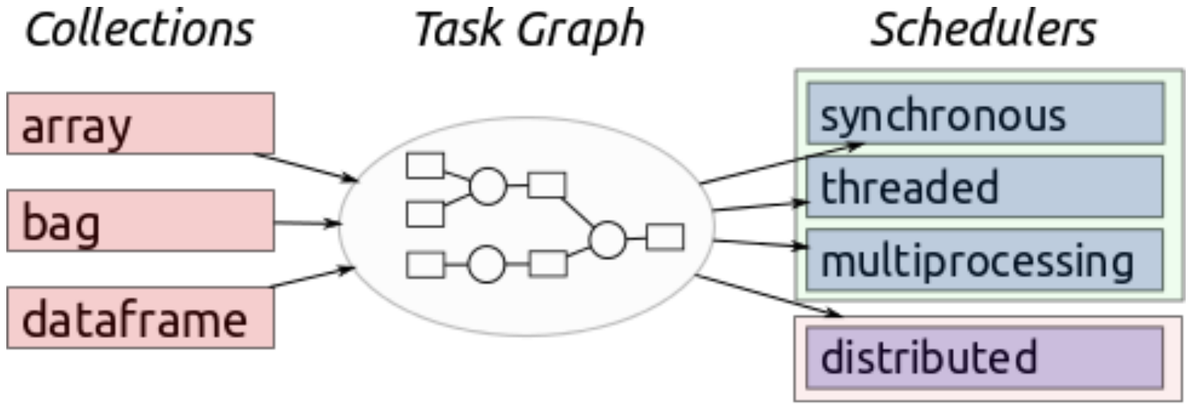
Running in parallel

and somehow manage all these machines...

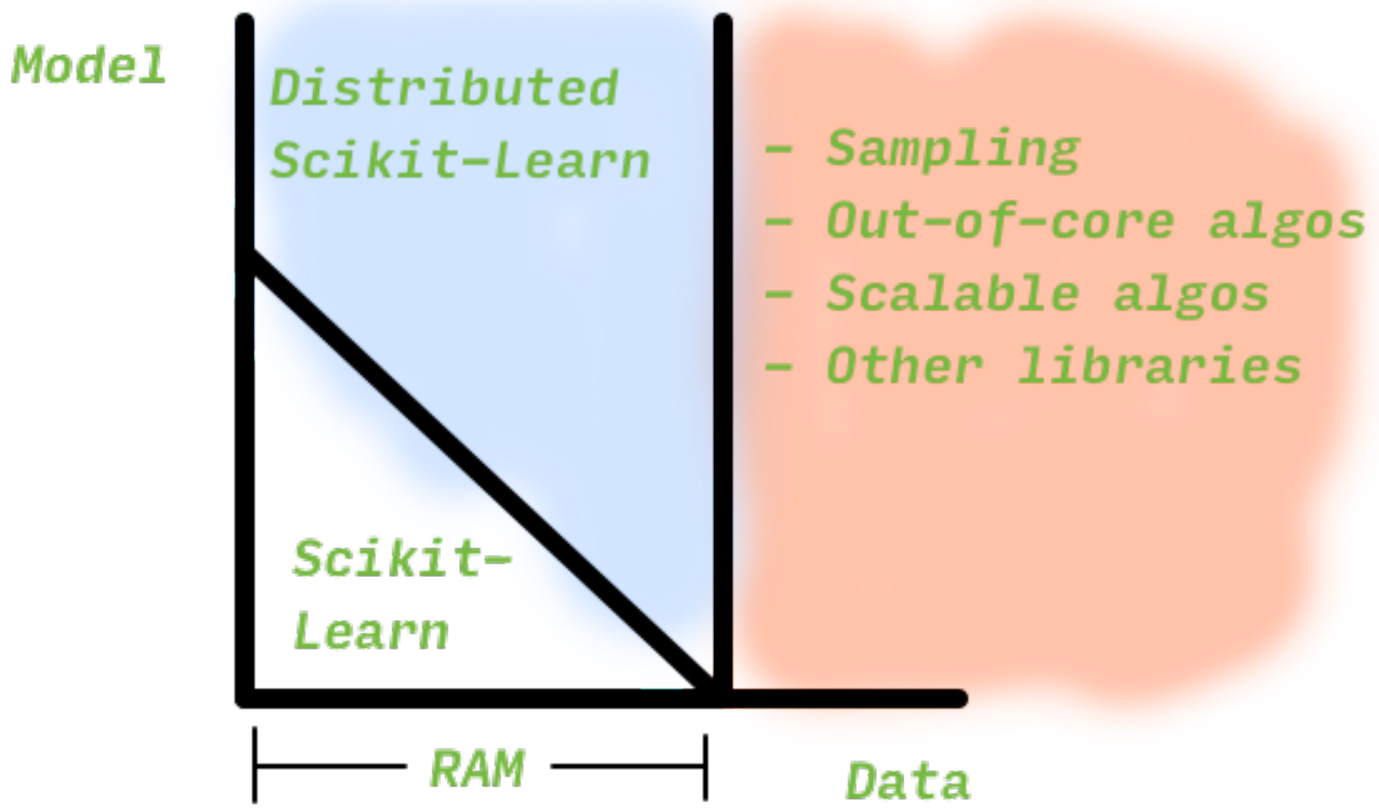
deal with downtime...

enable fast iteration...

Running in parallel: Dask



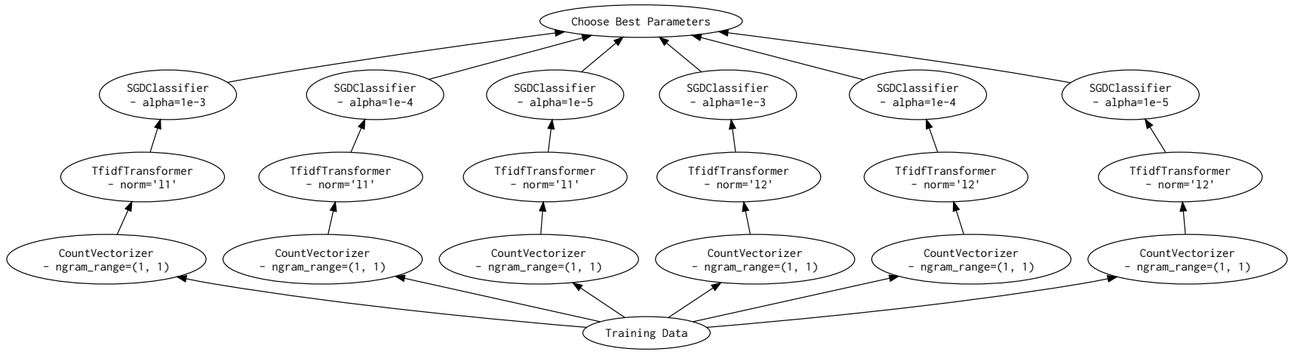
- library for parallel computing in Python.
- 2 parts. Dynamic task scheduling optimized for computation like `Airflow`. “Big Data” collections like parallel (numpy) arrays, (pandas) dataframes, and lists
- scales up (1000 core cluster) and down (laptop)
- designed with interactive computing in mind, with web based diagnostics



(from https://github.com/TomAugspurger/dask-tutorial-pycon-2018)

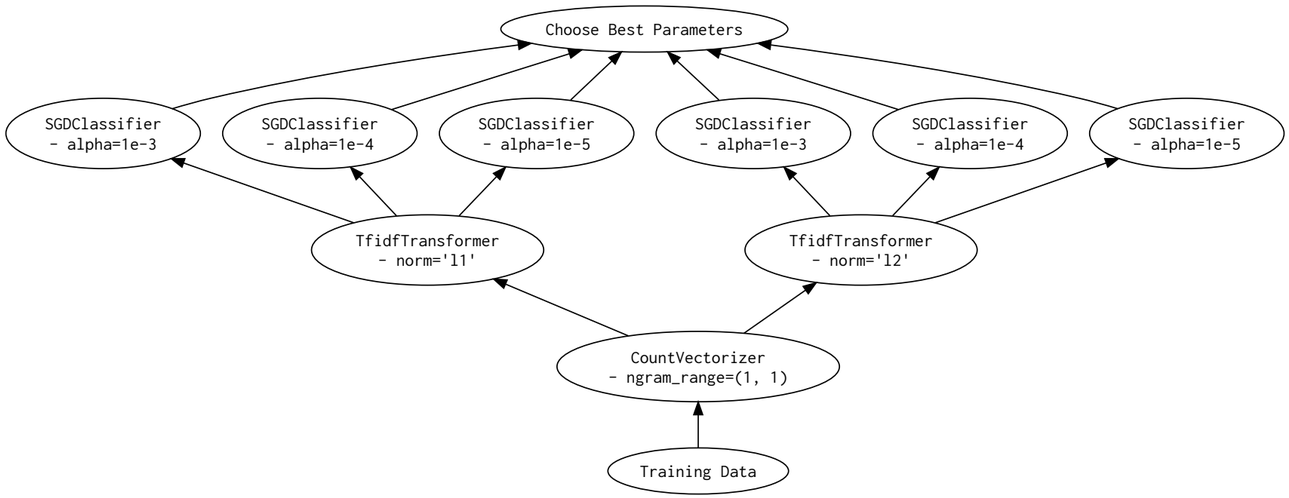
sklearn pipelines: the bad

```
scores = []
for ngram_range in parameters['vect__ngram_range']:
        for norm in parameters['tfidf__norm']:
                for alpha in parameters['clf__alpha']:
                        vect = CountVectorizer(ngram_range=ngram_range)
                        X2 = vect.fit_transform(X, y)
                        tfidf = TfidfTransformer(norm=norm)
                        X3 = tfidf.fit_transform(X2, y)
                        clf = SGDClassifier(alpha=alpha)
                        clf.fit(X3, y)
                        scores.append(clf.score(X3, y))
best = choose_best_parameters(scores, parameters)
```



dask pipelines: the good

```
scores = []
for ngram_range in parameters['vect__ngram_range']:
        vect = CountVectorizer(ngram_range=ngram_range)
        X2 = vect.fit_transform(X, y)
        for norm in parameters['tfidf__norm']:
                tfidf = TfidfTransformer(norm=norm)
                X3 = tfidf.fit_transform(X2, y)
                for alpha in parameters['clf__alpha']:
                        clf = SGDClassifier(alpha=alpha)
                        clf.fit(X3, y)
                        scores.append(clf.score(X3, y))
best = choose_best_parameters(scores, parameters)
```



Hyperparameter optimization using dask (locally)

```
from keras.models import Sequential
from keras.layers import Dense
from keras.wrappers.scikit_learn import KerasClassifier
from sklearn.datasets import load_breast_cancer
from sklearn.model_selection import train_test_split
from dask_ml.model_selection import GridSearchCV
from sklearn.externals import joblib

def simple_nn(hidden_neurons):
  model = Sequential()
  model.add(Dense(hidden_neurons, activation='relu', input_dim=30))
  model.add(Dense(1, activation='sigmoid'))
  model.compile(loss='binary_crossentropy', optimizer='rmsprop', metrics=['accuracy'])
  return model

param_grid = {'hidden_neurons': [100, 200, 300]}
if __name__=='__main__':
    cv = GridSearchCV(KerasClassifier(build_fn=simple_nn, epochs=30), param_grid)
    X, y = load_breast_cancer(return_X_y=True)
    X_train, X_test, y_train, y_test = train_test_split(X, y)
    with joblib.parallel_backend("dask", scatter=[X_train, y_train]):
        cv.fit(X_train, y_train)
    print(f'Best Accuracy for {cv.best_score_:.4} using {cv.best_params_}')
```

Large Data Sets

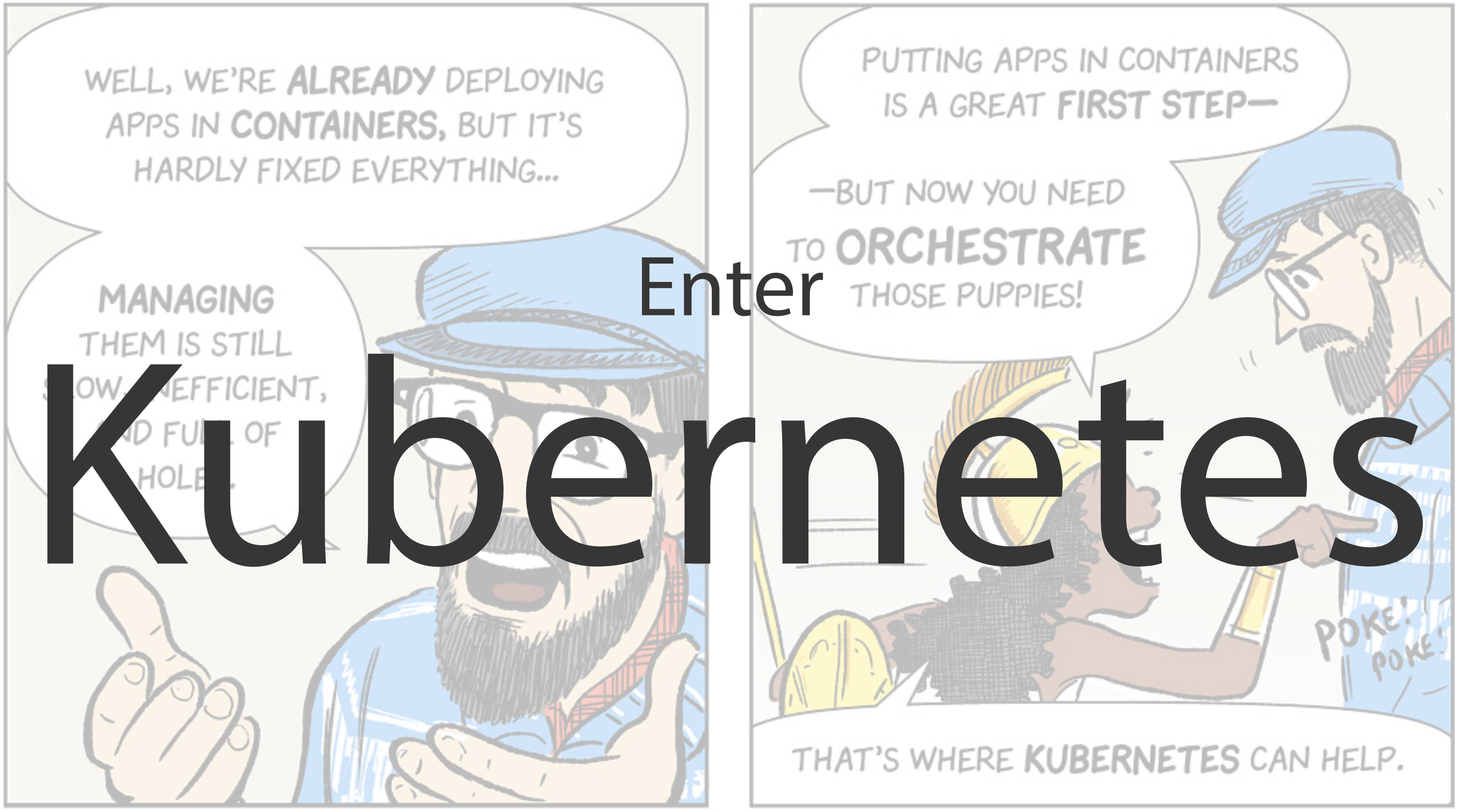
- important for pre-processing,
- also important for prediction on large data (test) sets
- dask provides scalable algoritms which can be run over clusters and are drop-in replacements for the `sklearn` equivalents
- Dask separates computation description (task graphs) from execution (schedulers).
- Write code once, and run it locally or scale it out across a cluster.

```
# Setup a local cluster.
import dask.array as da
import dask.delayed
from sklearn.datasets import make_blobs
import numpy as np
from dask_ml.cluster import KMeans


n_centers = 12
n_features = 20
X_small, y_small = make_blobs(n_samples=1000, centers=n_centers, n_features=n_features, random_state=
0)
centers = np.zeros((n_centers, n_features))
for i in range(n_centers):
    centers[i] = X_small[y_small == i].mean(0)
print(centers)

n_samples_per_block = 20000 # 0
n_blocks = 500
delayeds = [dask.delayed(make_blobs)(n_samples=n_samples_per_block,
                                     centers=centers,
                                     n_features=n_features,
                                     random_state=i)[0] for i in range(n_blocks)]
arrays = [da.from_delayed(obj, shape=(n_samples_per_block, n_features), dtype=X_small.dtype) for obj
in delayeds]
X = da.concatenate(arrays)
print(X.nbytes / 1e9)
X = X.persist() #actually run the stuff

clf = KMeans(init_max_iter=3, oversampling_factor=10)
clf.fit(X)
print(clf.labels_[:10].compute()) #actually run the stuff
```

- the previous code runs locally. ideally we want to run on a cloud-provisioned cluster
- and we'd like this cluster to be self-repairing
- and then we'd like our code to respond to failures.
- and expand onto more machines if we need them

We need a:

cluster manager!



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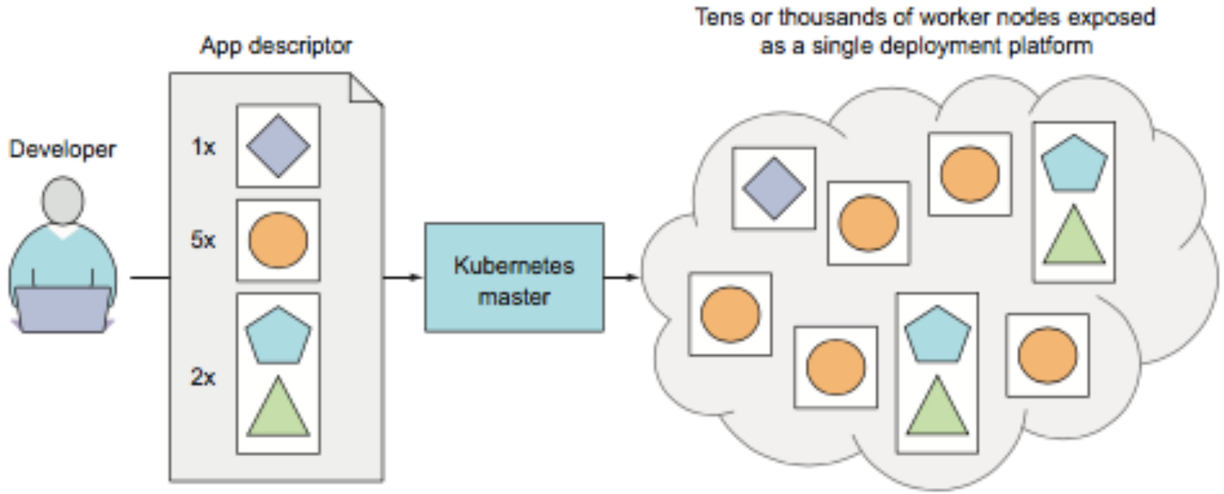
Kubernetes

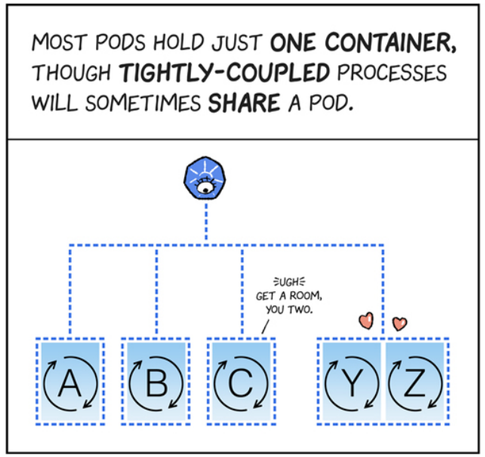


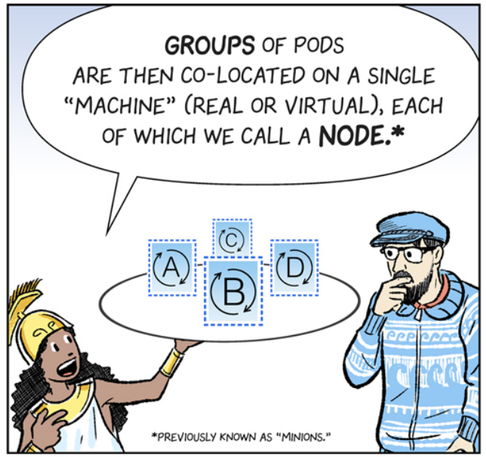
- OS for the cluster
- provides service discovery, scaling, load-balancing, self-healing, leader election
- think of applications as stateless, and movable from one machine to another to enable better resource utilization
- thus does not cover mutable databases which must remain outside the cluster
- there is a controlling master node, and worker nodes

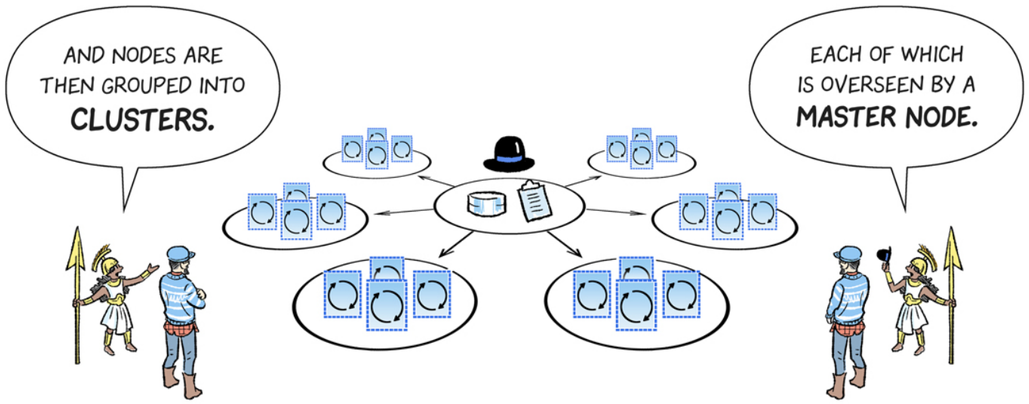
Open AI deep learning setup

- "operate several Kubernetes clusters (some in the cloud and some on physical hardware), the largest of which we've pushed to over 2,500 nodes. This cluster runs in Azure on a combination of D15v2 and NC24 VMs." (https://openai.com/blog/scaling-kubernetes-to-2500-nodes/)
- each job must be a Docker container. They provide tooling to transparently ship code from a researcher's laptop into a standard image.
- they use autoscaling

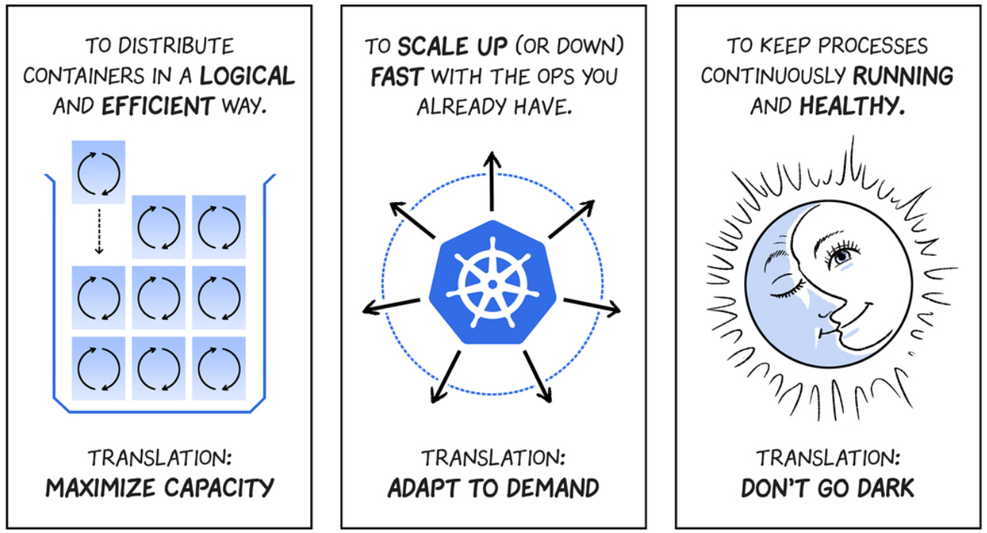
Basic Structure

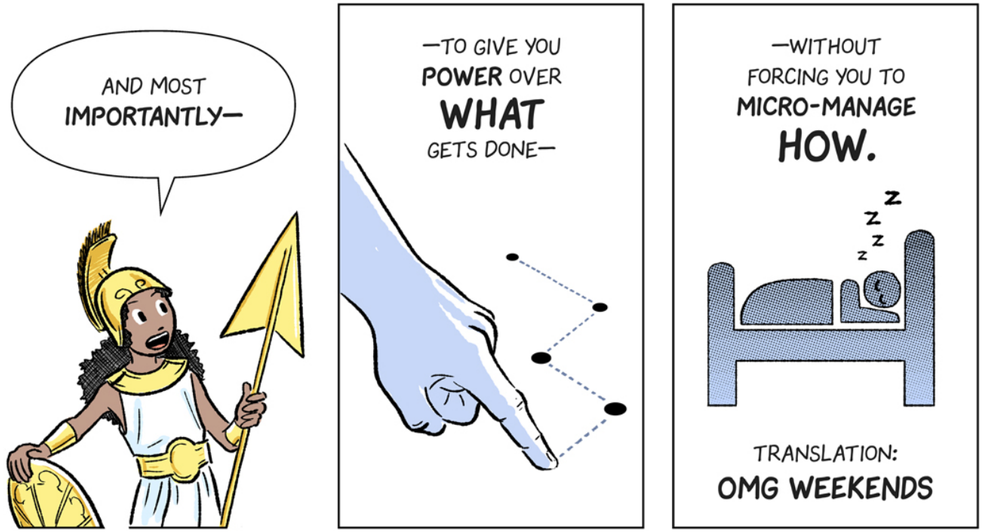




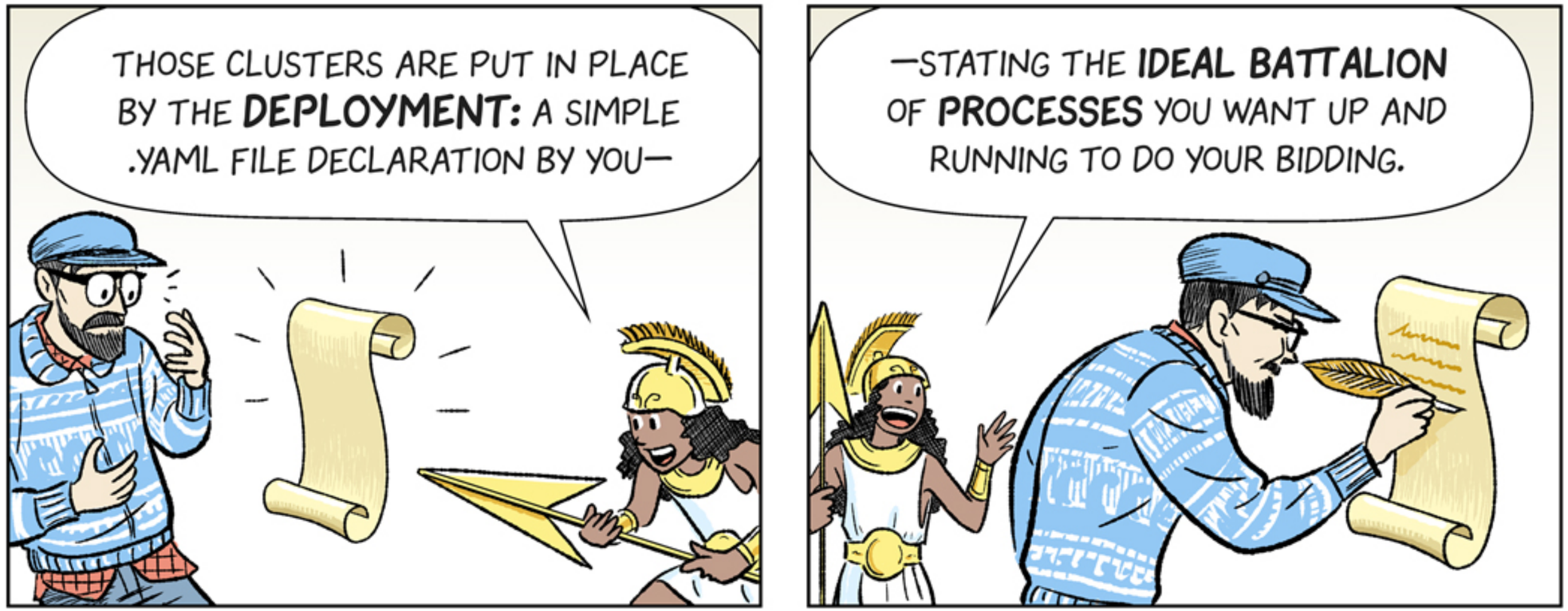


Kubernetes Goals





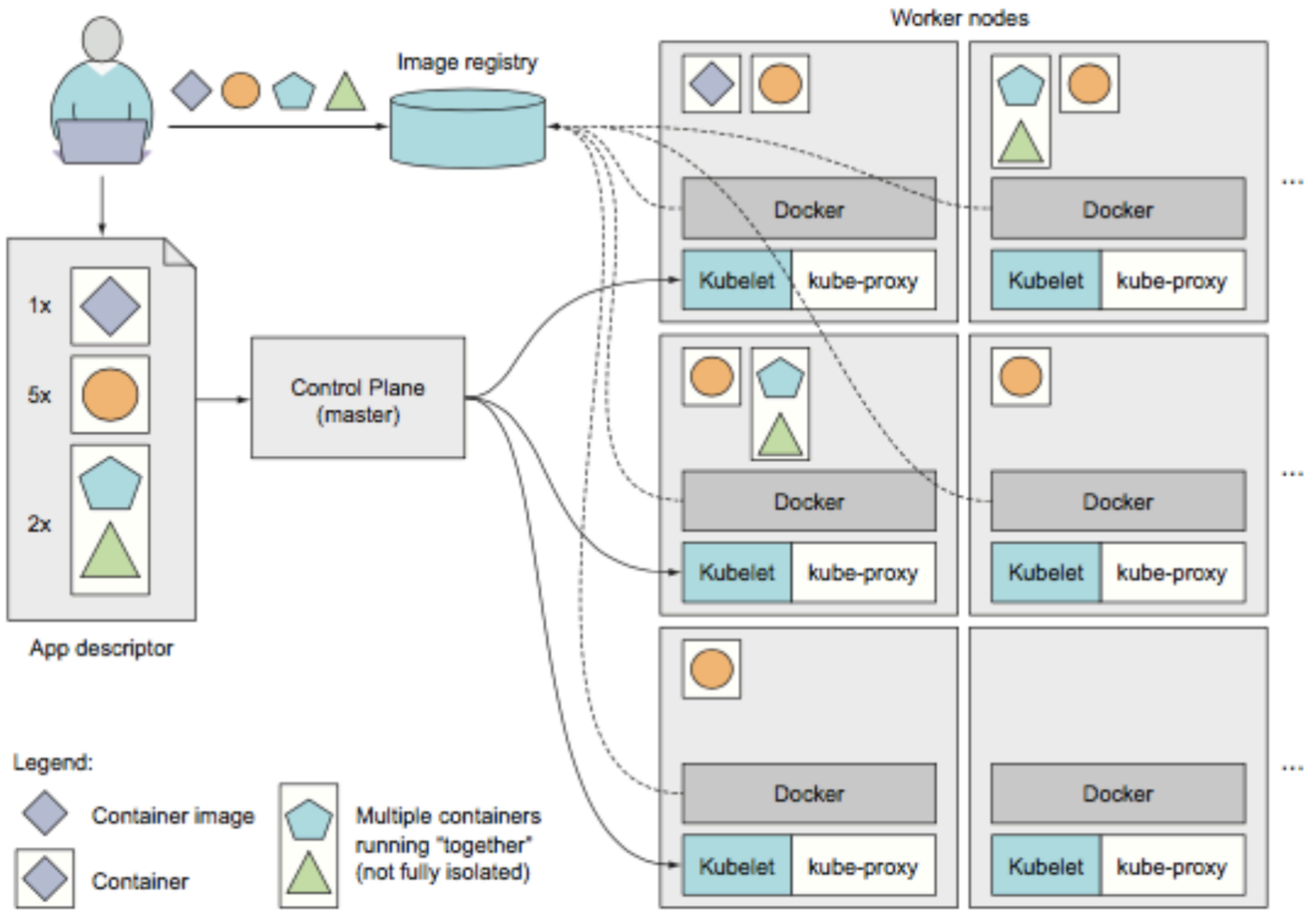
Deployment using `deployment.yaml`



Create a kubernetes cluster

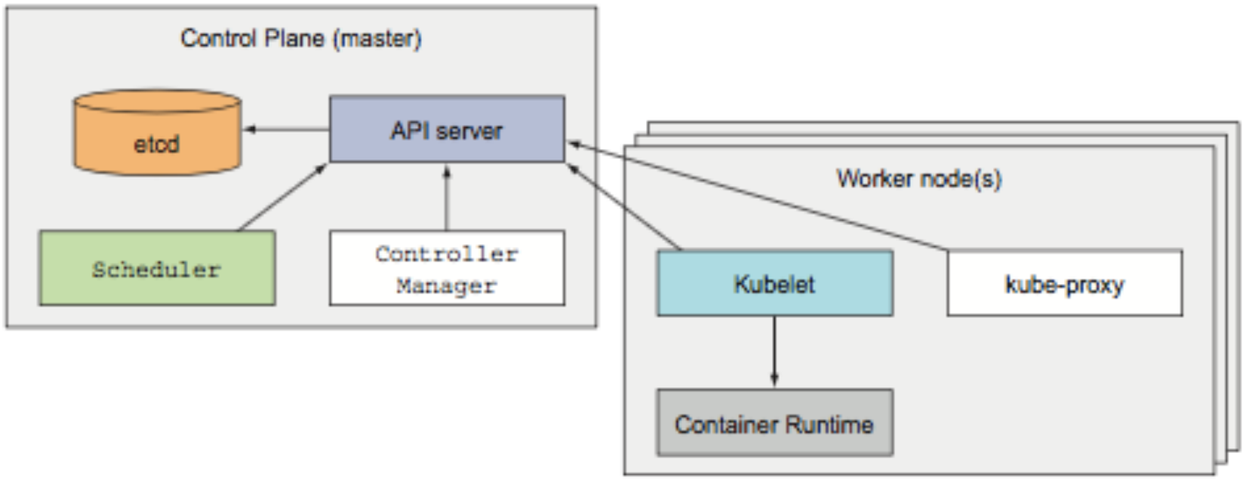
LETS DO IT TOGETHER

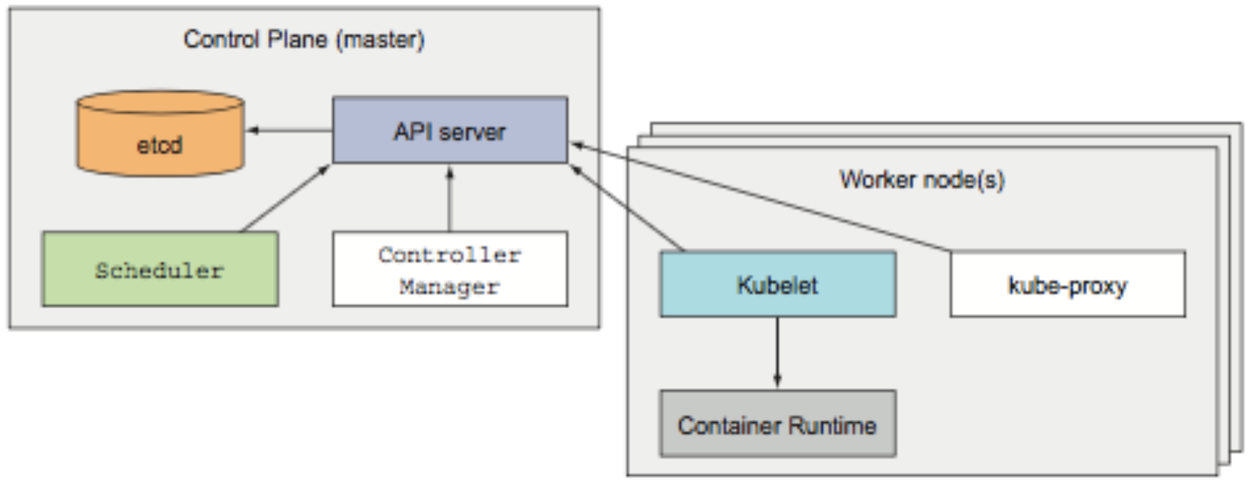
Kubernetes Architecture



master node:

- API server, communicated with my control-plane components and you (using `kubectl`)
- Scheduler, assigns a worker node to each application
- Controller Manager, performs cluster-level functions, such as replicating components, keeping track of worker nodes, handling node failures
- etcd, a reliable distributed data store that persistently stores the cluster configuration.



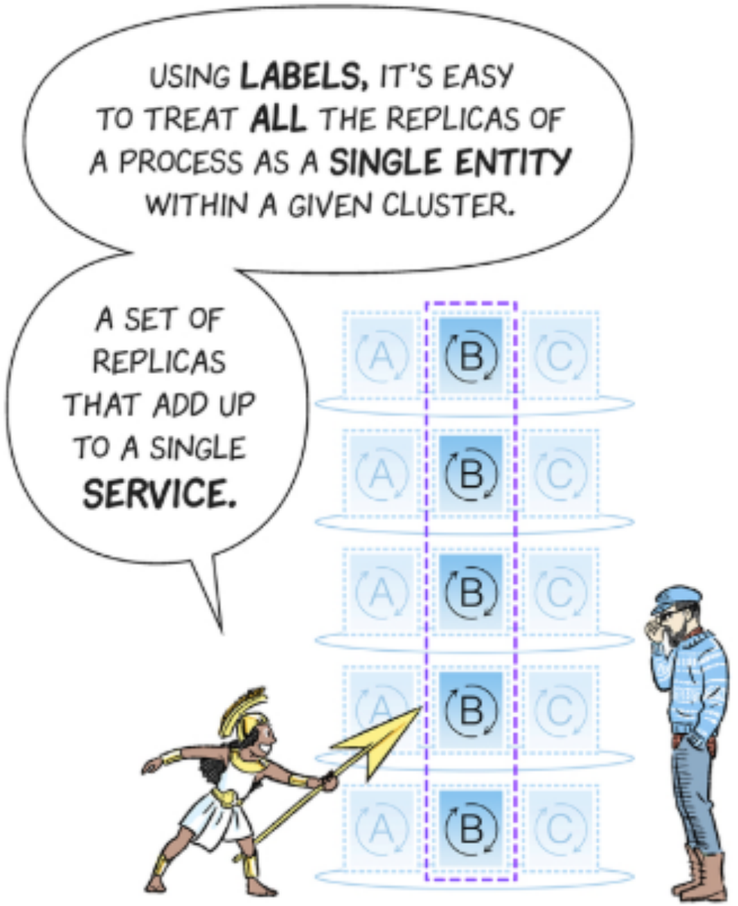


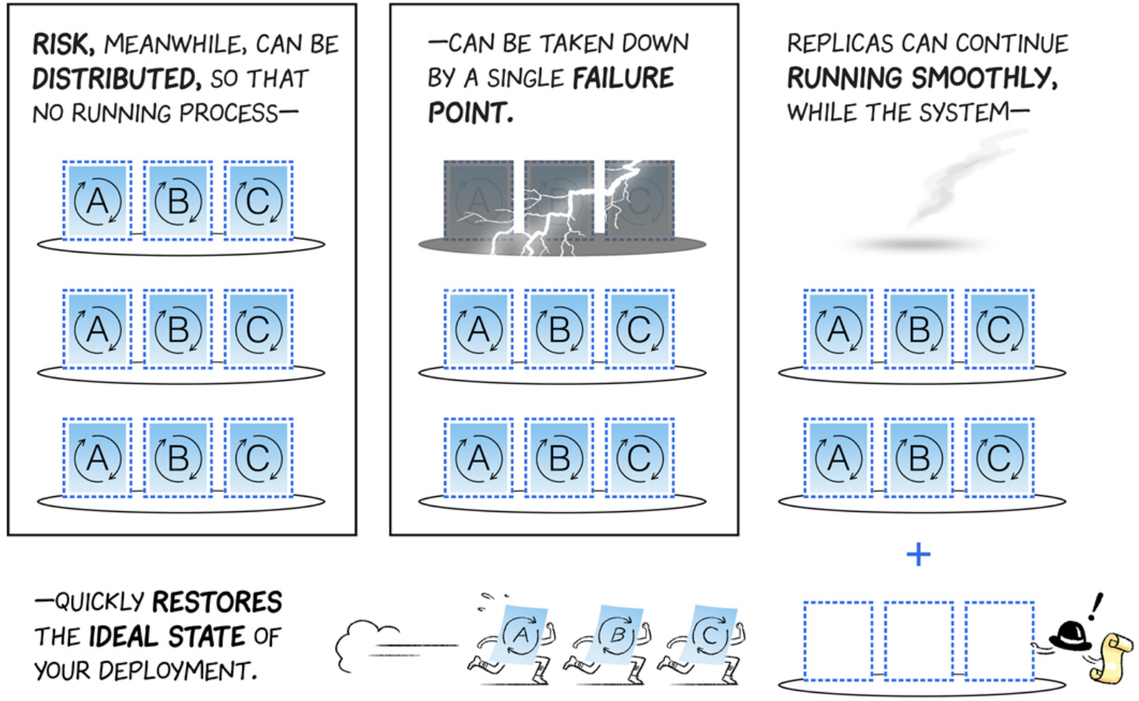
worker node:

- Docker, to run your containers
- you package your apps components into 1 or more docker images, and push them to a registry
- Kubelet, which talks to the API server and manages containers on its node
- kube-proxy, which load-balances network traffic between application components

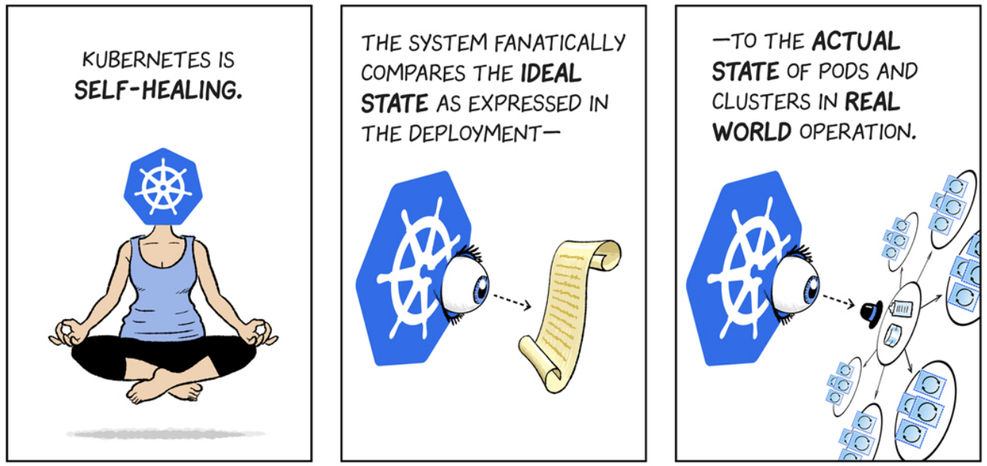
- To run an application in Kubernetes, you post a description of your app to the Kubernetes API server.
- people have created canned "descriptions" for multi-component software, which you can reuse. These use a "package manager" called `helm`, and its what is used to install dask and jupyterhub on a cluster
- description includes info on component images, their relationship, which ones need co-location, and how many replicas
- internal or external network services are also described. A lookup service is provided, and a given service is exposed at a particular ip address. kube-proxy makes sure connec- tions to the service are load balanced
- master continuously makes sure that the deployed state of the application matches description

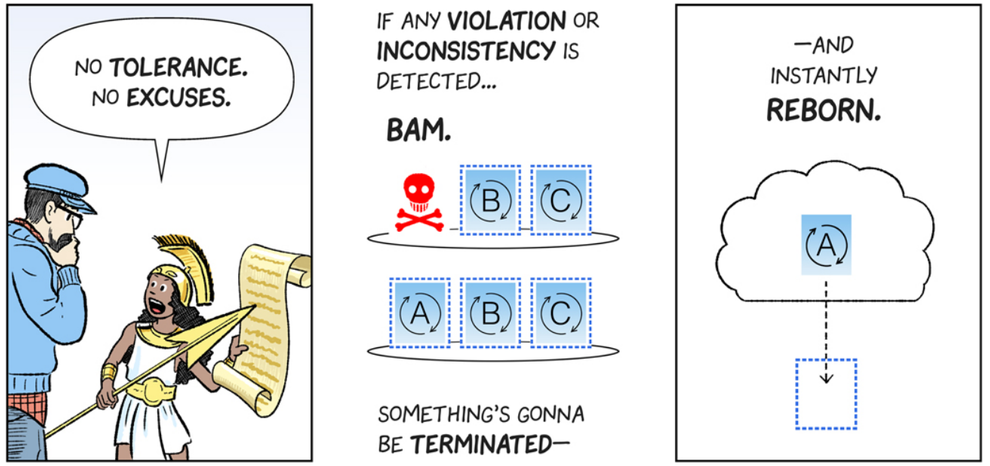
From nodes to horizontal labels





Self Healing Deployments





Used for deaths, consistency, and updating.

Now, lets parallelize DASK

- for data that fits into memory, we simply copy the memory to each node and run the algorithm there
- if you have created a re-sizable cluster of parallel machines, dask can even dynamically send parameter combinations to more and more machines

Dask can run on Kubernetes

Hyperparameter optimization using dask ON CLOUD

```
from keras.models import Sequential
from keras.layers import Dense
from keras.wrappers.scikit_learn import KerasClassifier
from sklearn.datasets import load_breast_cancer
from sklearn.model_selection import train_test_split
from dask_ml.model_selection import GridSearchCV
from dask.distributed import Client
from sklearn.externals import joblib

def simple_nn(hidden_neurons):
  model = Sequential()
  model.add(Dense(hidden_neurons, activation='relu', input_dim=30))
  model.add(Dense(1, activation='sigmoid'))
  model.compile(loss='binary_crossentropy', optimizer='rmsprop', metrics=['accuracy'])
  return model

param_grid = {'hidden_neurons': [100, 200, 300]}
if __name__=='__main__':
  client = Client()
  print(client.cluster)
    cv = GridSearchCV(KerasClassifier(build_fn=simple_nn, epochs=30), param_grid)
    X, y = load_breast_cancer(return_X_y=True)
    X_train, X_test, y_train, y_test = train_test_split(X, y)
    with joblib.parallel_backend("dask", scatter=[X_train, y_train]):
        cv.fit(X_train, y_train)
    print(f'Best Accuracy for {cv.best_score_:.4} using {cv.best_params_}')
```

```python
# run using local distributed scheduler
import dask.array as da
import dask.delayed
from sklearn.datasets import make_blobs
import numpy as np
from dask_ml.cluster import KMeans

n_centers = 12
n_features = 20
X_small, y_small = make_blobs(n_samples=1000, centers=n_centers, n_features=n_features, random_state=0)
centers = np.zeros((n_centers, n_features))
for i in range(n_centers):
    centers[i] = X_small[y_small == i].mean(0)
print(centers)

from dask.distributed import Client

# Setup a local cluster.
# By default this sets up 1 worker per core
if __name__=='__main__':
    client = Client()
    print(client.cluster)
    n_samples_per_block = 20000 # 0
    n_blocks = 500
    delayeds = [dask.delayed(make_blobs)(n_samples=n_samples_per_block,
                                         centers=centers,
                                         n_features=n_features,
                                         random_state=i)[0] for i in range(n_blocks)]
    arrays = [da.from_delayed(obj, shape=(n_samples_per_block, n_features), dtype=X_small.dtype) for obj in delayeds]
    X = da.concatenate(arrays)
    print(X.nbytes / 1e9)
    X = X.persist() #actually run the stuff

    clf = KMeans(init_max_iter=3, oversampling_factor=10)
    clf.fit(X)
    print(clf.labels_[:10].compute()) #actually run the stuff
```

Dask cloud deployment

Kubernetes is recommended

This can be done on your local machine using Minikube or on any of the 3 major cloud providers, Azure, GCP, or AWS. We will use GCP.

1. We will set up a Kubernetes cluster
2. Next you will set up Helm, which is a package maner for Kubernetes which works simply by filling templated yaml files with variables also stored in another yaml file `values.yaml`.
3. Finally you will install dask. First `helm repo update` and then `helm install stable/dask`.

See https://docs.dask.org/en/latest/setup/kubernetes-helm.html for all the details.

Dask Setup

LETS DO IT TOGETHER

Intro to Kubeflow

The basic idea in Kubeflow is:

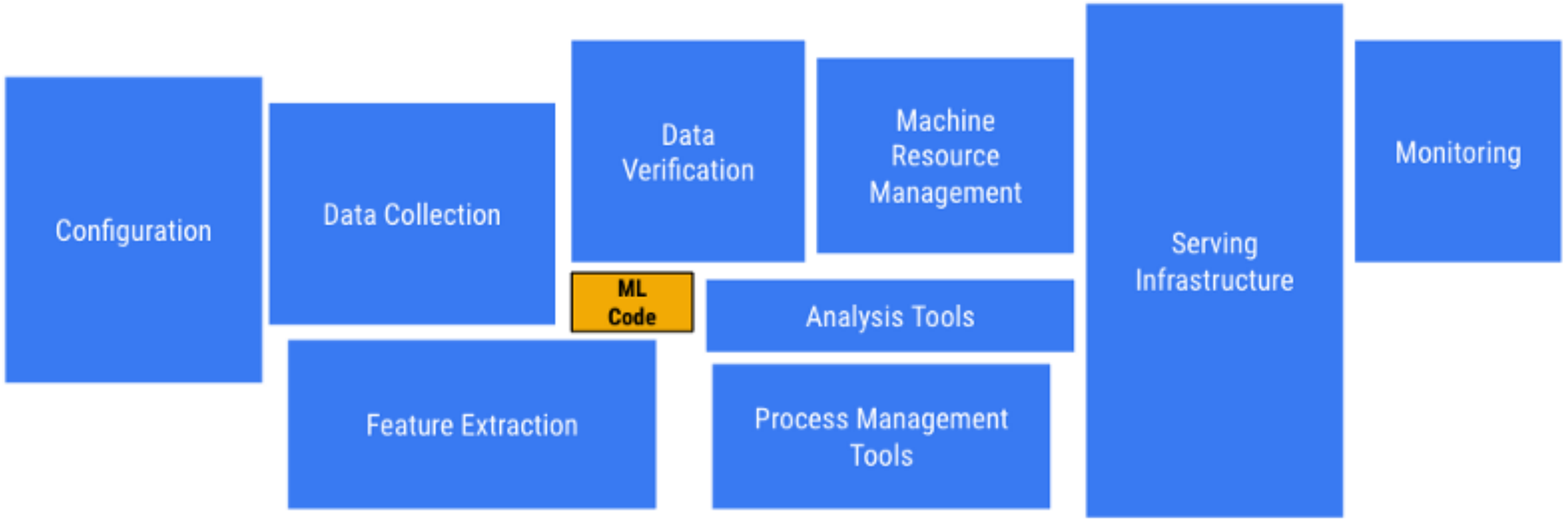
Everything runs in a docker container under Kubernetes.

This allows for autoscaling, revovery from downtime, and reproducibility.

Thus each hyperparameter tuning run happens on a pod in a docker container. Each part of a pipeline runs in a pod in a docker container. Each part of a distributed deep learning run happens in docker containers running in multiple pods.

Components are Notebooks, Hyperparameter Optimization (Katib), Pipelines, Model Serving (using Seldon and tf-serving).

Support for Tensorflow, pytorch, Mxnet, etc



(image from Hidden Technical Debt in ML systems)

Kubeflow provides nice visualization for pipelines, hyperparameter runs, tensorflow runs, and more.

Kubeflow Setup

LETS DO IT TOGETHER

KSonnet

- a ksonnet application? Think of an application as a well-structured directory of Kubernetes manifests, which typically tie together in some way.
- yet another way of combining the yaml kubernetes needs. Start with`ks init guestbook --context ks-dev`
- Generation from prototype: e.g.

```
ks generate deployed-service guestbook-ui \
--image gcr.io/heptio-images/ks-guestbook-demo:0.1 \
--type ClusterIP
```

- Apply multiple generated components sequentially, do `ks apply default` multiple times

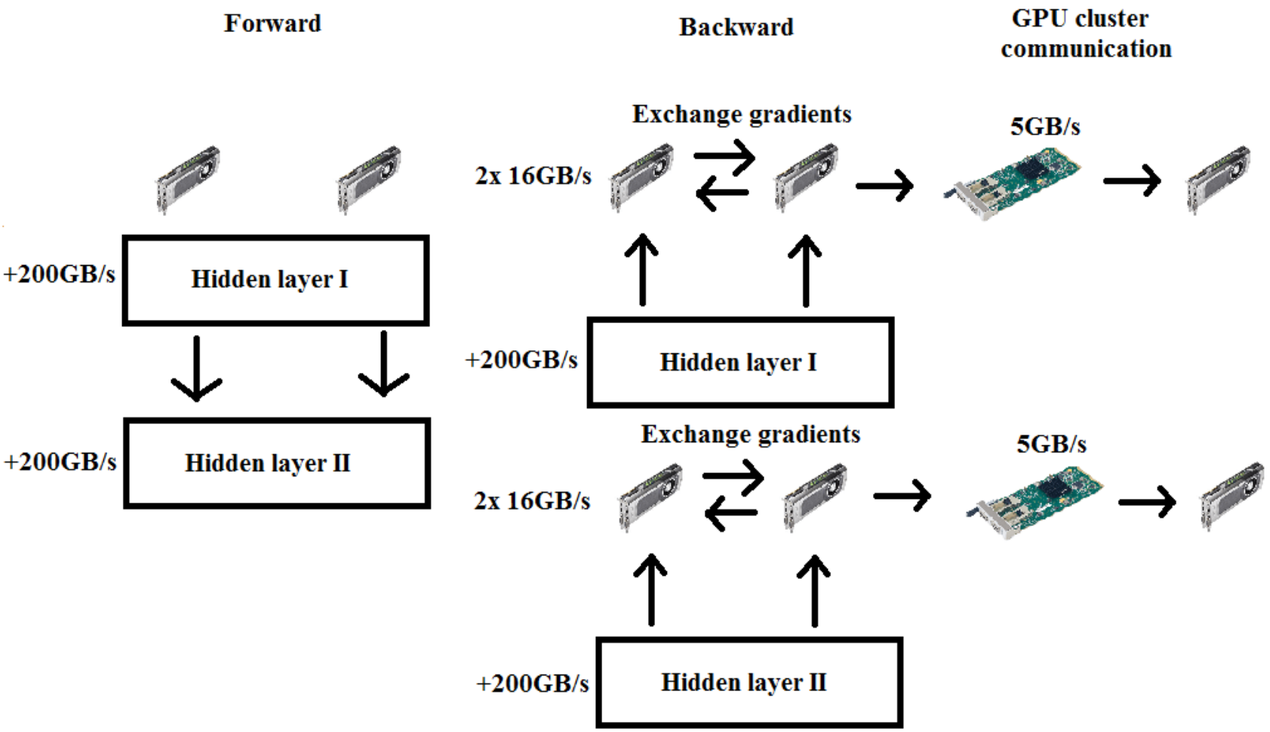
Deep Learning on the cloud

- tensorflow can be put on the cloud using `tf.distributed` of `kubeflow`
- parallelism can be trivially used at prediction time--you just need to distribute your weights
- as in our keras example you might have grid optimization
- but it would seem SGD is sequential

Data parallel vs compute parallel

- **Data Parallel**: split a batch over multiple gpus on one machine or multiple gpus
- use horovod or kubeflow
- **Program Parallel**: like hyperparameter optimization
- Train entire model asynchronously using parameter servers. use `tf.distributed` or kubeflow.

Data Parallel



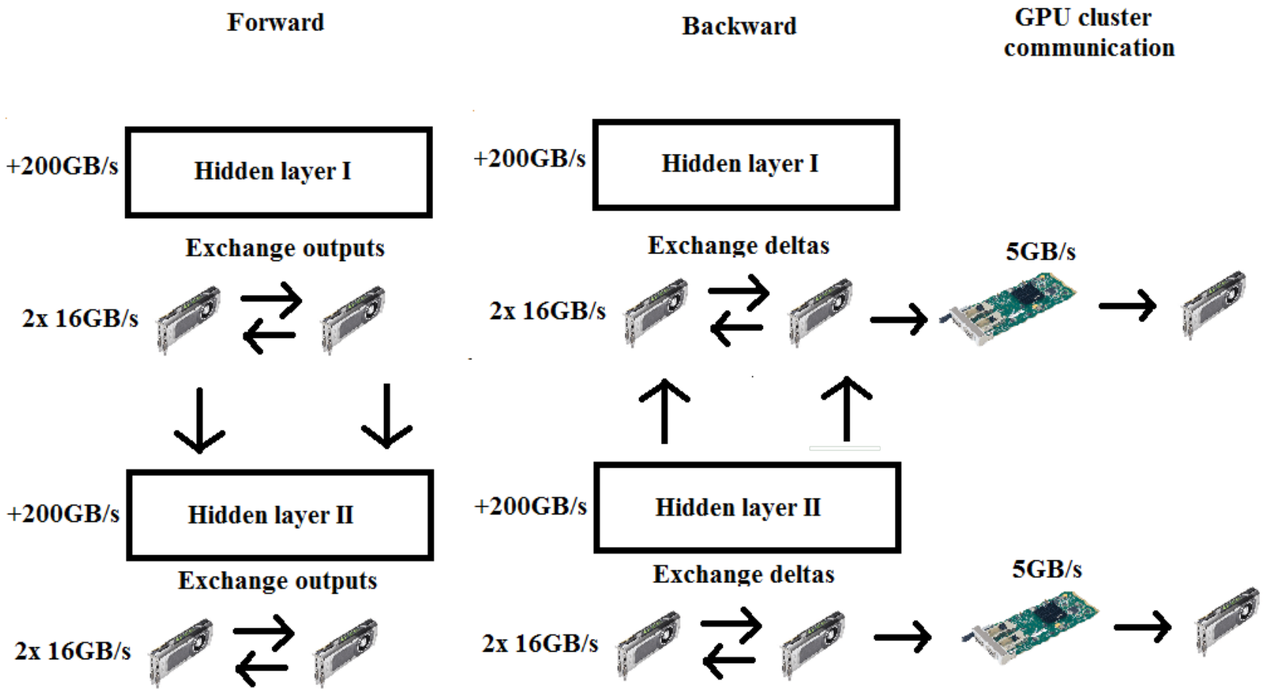
- use the same model for every thread, but feed it with different parts of the data
- 4 GPUs, you split a mini-batch with 128 examples into 32 examples for each GPU
- obtain gradients for each split batch, then average them
- problem: in backward pass you have to pass the whole gradient to ALL other GPUs. Thus use max-pool or other where params are less..conv layers
- better for smaller models like CNN

Model small batch sizes vs large batch sizes

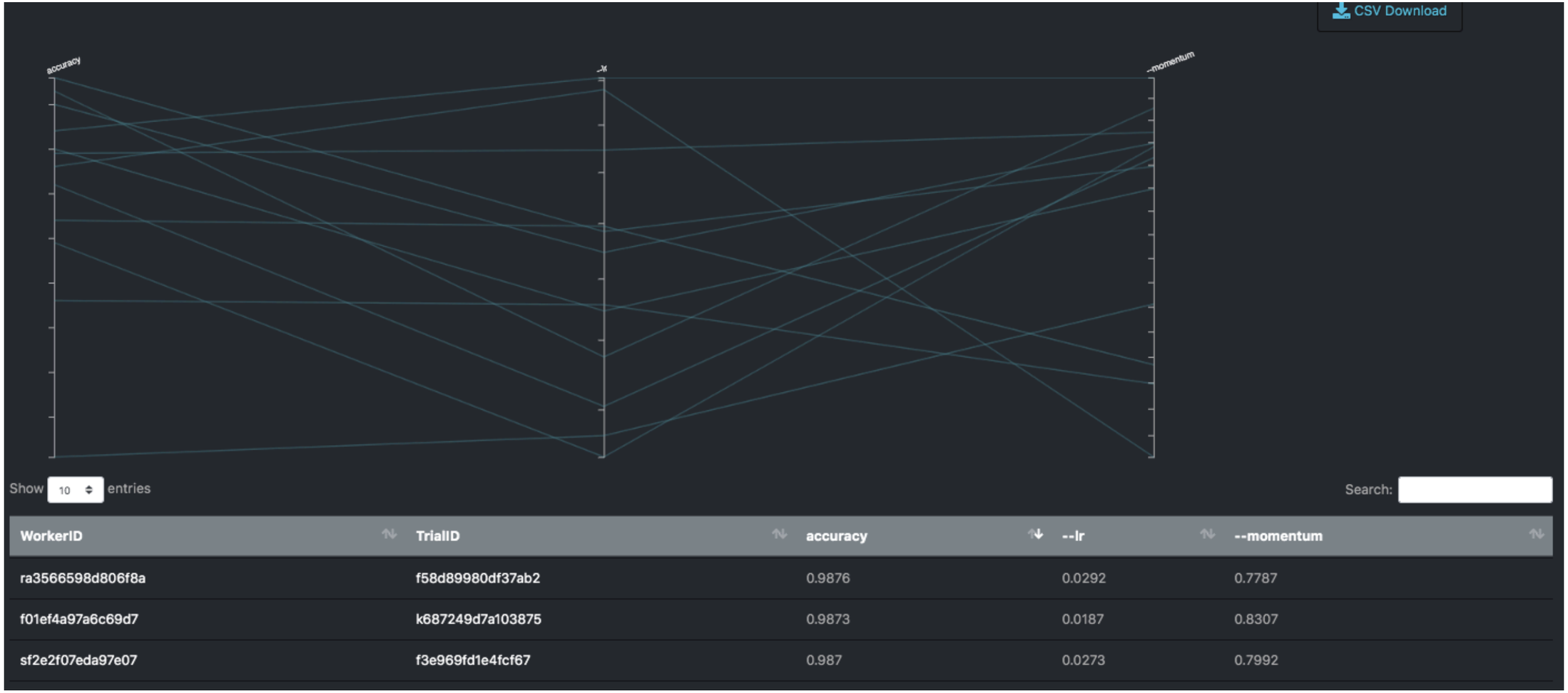
- smaller batch size captures obvious, common errors
- larger batch size also captures subtler, smaller errors.
- in the beginning a model had major errors so you dont want to fine tune too much, so smaller size better
- but not too small as you will even miss these larger errors
- hardware limits us in practice. When you split on gpu dont go below 64 as cuBLAS needs this for efficiency

Model Parallel

- supports large models. thus better for fully connected layers, transformers, etc
- might be really important in future for unsupervised learning
- synchronization needed after each dot product with the weight matrix for both forward and backward pass.
- but less data is transferred because of chunking in any weight matrix direction
- See Alex Krizhevsky, uses data parallelism in the convolutional layers and model parallelism in the dense layers.



Hyperparameter optimization is a (simple) model parallel



WorkerID	TrialID	accuracy	--lr	--momentum
ra3566598d806f8a	f58d89980df37ab2	0.9876	0.0292	0.7787
f01ef4a97a6c69d7	k687249d7a103875	0.9873	0.0187	0.8307
sf2e2f07eda97e07	f3e969fd1e4fcf67	0.987	0.0273	0.7992

Kubeflow Katib

LETS DO IT TOGETHER

What just happened? (is hapenning)

- we launched a pytorch job on our kubernetes cluster
- it is distributed with 1 master and 2 workers
- a different set of pods is created for each run
- k8s takes care of scheduling the runs

We'll do a more detailed example next, with distributing, but with serving, for tensorflow.

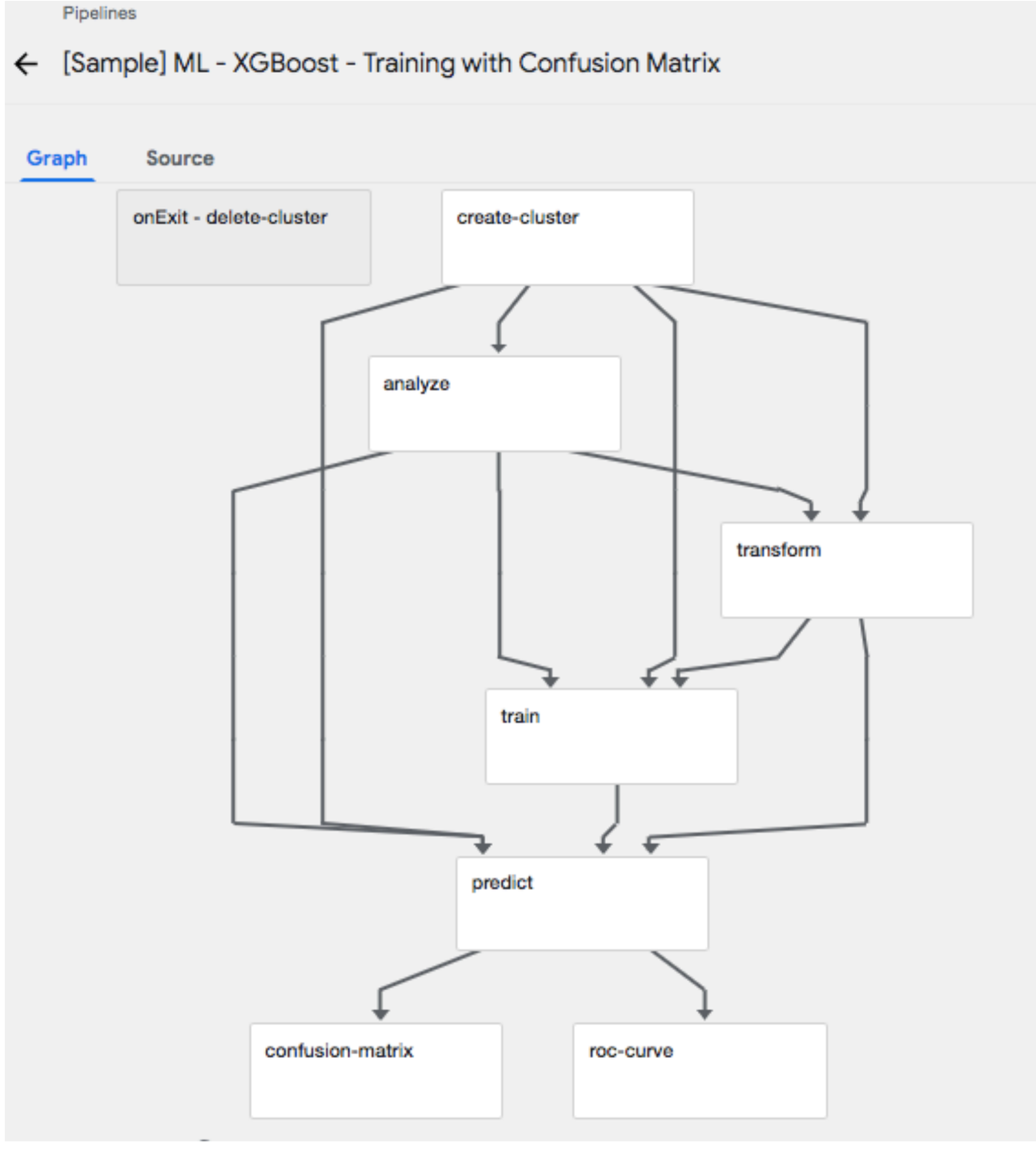
Running a deep learning model in Kubeflow

LETS DO IT TOGETHER

Kubeflow supports pipelines!

- as usual, each stage is a docker container, though there are lighter weight options defined in a python SDK.
- run the basic parellel join pipeline here

```
def gcs_download_op(url):
    return dsl.ContainerOp(
        name='GCS - Download', image='google/cloud-sdk:216.0.0',
        command=['sh', '-c'],
        arguments=['gsutil cat $0 | tee $1', url, '/tmp/results.txt'],
        file_outputs={
            'data': '/tmp/results.txt',
        }
    )
def echo2_op(text1, text2):
    return dsl.ContainerOp(
        name='echo', image='library/bash:4.4.23',
        command=['sh', '-c'],
        arguments=['echo "Text 1: $0"; echo "Text 2: $1"', text1, text2]
    )
@dsl.pipeline(
  name='Parallel pipeline',
  description='Download two messages in parallel and prints the concatenated result.'
)
def download_and_join(
    url1='gs://ml-pipeline-playground/shakespeare1.txt',
    url2='gs://ml-pipeline-playground/shakespeare2.txt'
):
    """A three-step pipeline with first two running in parallel."""
    download1_task = gcs_download_op(url1)
    download2_task = gcs_download_op(url2)
    echo_task = echo2_op(download1_task.output, download2_task.output)
```



FIN

- making things work performantly in the cloud is not easy
- but has huge time saving benefits
- this has been barely an introduction
- bit its been conceptual, so should help you implement
- there is another workshop on kubeflow at ODSC
- binge watch: https://fullstackdeeplearning.com/march2019#
- Reading: Kubernetes in Action, Cloud Native Devops with Kubernetes, Dask docs, Kubeflow docs.