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Deutsches Elektronen-Synchrotron

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Scientific perspective

- 1. Open Laptop
- 2. ...
- 3. ...
- 4. ...
- n. Do Science

Scientific perspective

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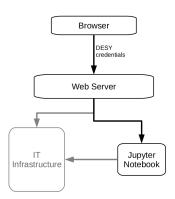
We do not care & it should be easy!

- Slurm scheduler for batch processing [1]
- Slurm submission nodes:
 - max-fsc | max-fsg
 - max-display
 - max-jhub

```
# simple job which prints hostname
[@max-wqs ~]$ cat hostname.sh
#!/bin/bash
#SBATCH --partition=maxwell
#SBATCH --time=00:10:00
                                                  # Maxi
#SBATCH --nodes=1
                                                  # Numb
##### note: from Slurm news file 17.11.0rcl:
##### Change --workdir in sbatch to be --chdir as in all
#####SBATCH --workdir /home/mmuster/slurm/output
                                                  # dire
#SBATCH --chdir /home/mmuster/slurm/output
#SBATCH --iob-name hostname
#SBATCH --output hostname-%N-%j.out
                                                  # File
                                                  # File
#SBATCH --error
                   hostname-%N-%i.err
#SBATCH --mail-type END
                                                  # Type
#SBATCH --mail-user max.muster@desv.de
                                                  # Emai
/bin/hostname
# submit to batch queue for one node with one task
# requesting 10 mins of wall time
[@max-wgs ~1$ sbatch hostname.sh
Submitted batch job 2163
[@max-wgs ~1$ ls
hostname.sh slurm-2163.out
[@max-wgs ~]$ cat slurm-2163.out
max-wn004.desv.de
```

- IPython Console
- Jupyter Notebooks
- JupyterLab

• JupyterHub @DESY [2]



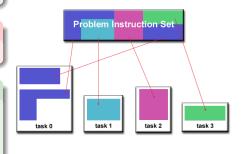
- Anaconda: venvs
 - requirements.txt

You shall not

import mpi4py

Use external framework

- Dask for parallel computing.
 - Dynamic task scheduling
 - "Big Data" collections for distributed environments or larger-than-memory



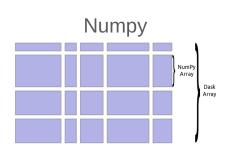
computing. IIn I. gov

Demo

Demo #1

- DESY's JupyterHub
- dask.delayed as way to parallelize existing code
- fetch via: git clone https://github.com/chrispassow/dask_demo.git

dask.array & dask.dataframe





 $\mathsf{https:}//\mathsf{dask.org}/$

- for distributed environments or larger-than-memory
- most of Numpy & Pandas methods are implemented

Demo

Demo #2

- using a single node on Maxwell via sbatch
- compare *numpy.array* and *dask.array*

Demo

Demo #3

• using multipile nodes on Maxwell interactivly via dask_jobqueue

Terminate Idle Slurm Jobs

Danger Zone

"With great power there must also come – great responsibility!" [3]

Below is an (automatically generated) list of partitions and the limits applying

Partition	# of nodes	Nodes/Job	Max Number of Jobs	Default Time	Maximum Time	Allowed groups
ps	35	1	5	1:00:00	14-00:00:00	max-ps2-users
psx	16	1	5	1:00:00	7-00:00:00	max-psx2-users

Emergancy Commands [4]

scancel -u your_uid

Summary and Outlook

Current situation

- manual work is lengthy and prone to error
- Conda envs already simplify
- Slurm batch procession

The other side of the fence

- Frameworks to speed up analytics or scale to large data
- Dask as a state-of-the-art solution
- Jupyter notebooks for interactive data exploration
- JupyterHub as easy to use gateway

Great responsibility

Be careful about the resources you allocate.

References

- [1] https://confluence.desy.de/display/IS/Running+Jobs+on+Maxwell
- [2] https://confluence.desy.de/display/IS/JupyterHub+on+Maxwell
- [3] Uncle Ben, Amazing Fantasy #15, Marvel Comics
- [4] https://www.rc.fas.harvard.edu/resources/documentation/convenient-slurm-commands/