

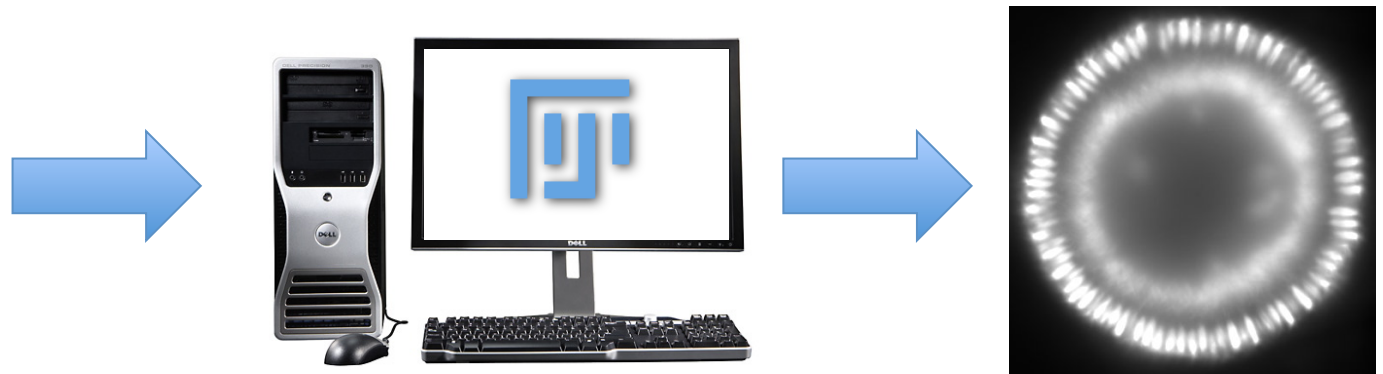
Processing SPIM data on a cluster

Lightsheet microscopy

EMBO Practical course 2014

Christopher Schmied & Pavel Tomancak

SPIMage processing

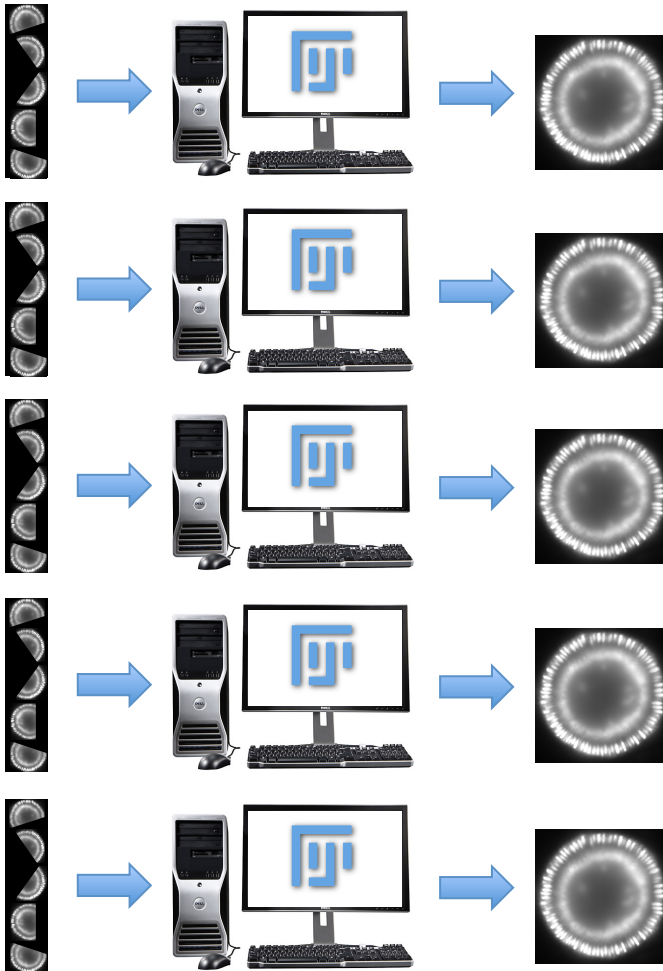


Lets assume 1 time point takes 5 min to process

But you have 200 time points

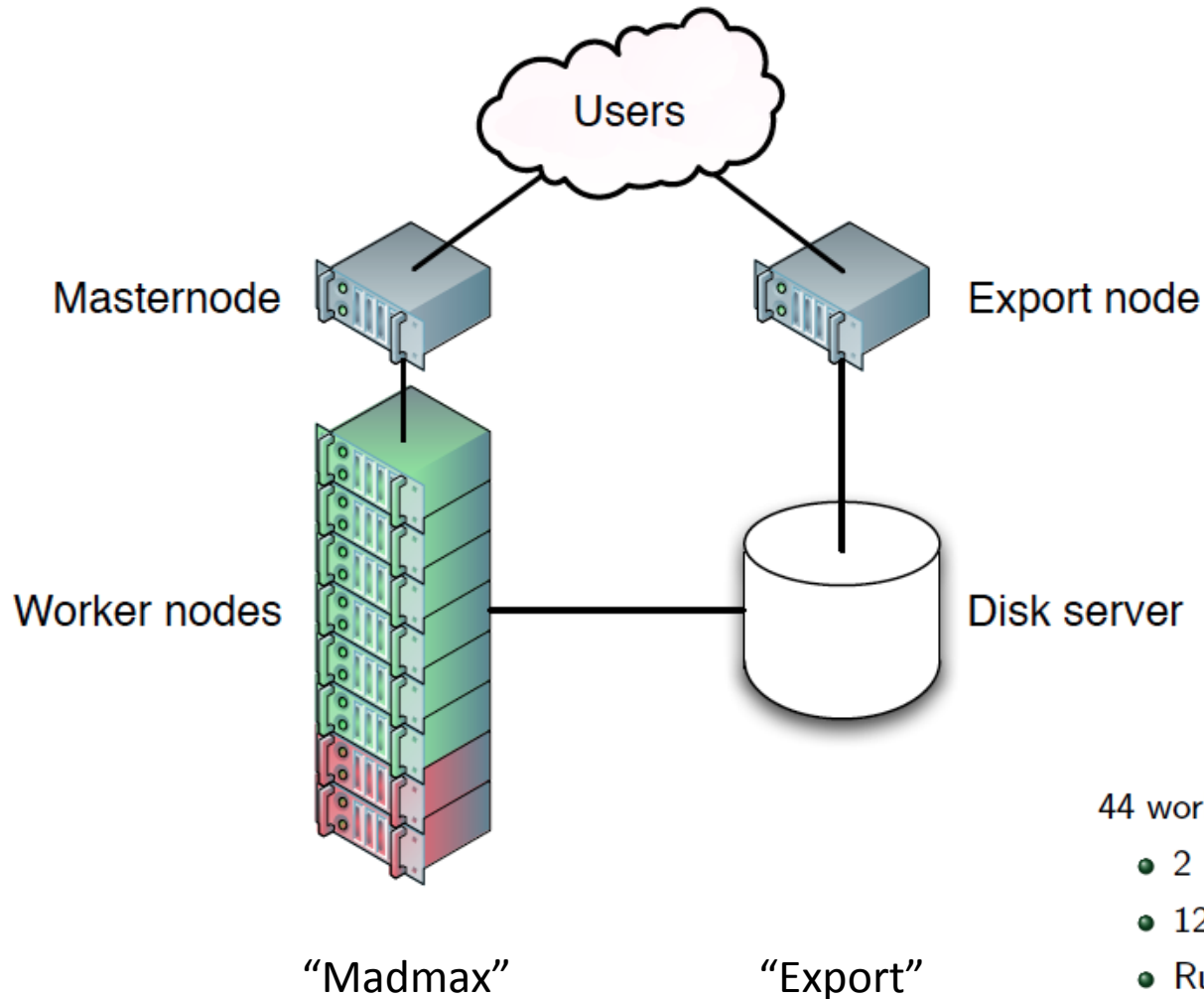
It will take more than 16h to process the dataset on 1 computer

SPIMage processing on a cluster



Instead of 1 computer use many!

High performance cluster (HPC)



44 worker nodes:

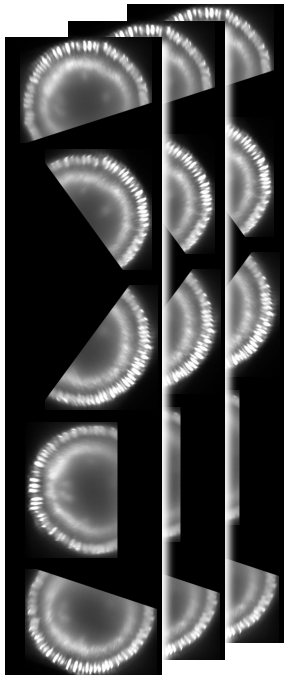
- 2 hexa-core CPU (i.e. 12 cores)
- 128 GB of RAM
- Running under CentOS 6.3

4 of them have 1 GPU each

Scripts

Master file

Directories
Angles
Time points
Reference time point
Processing parameters
...



Tp 1, Tp 2, Tp 3 ...

create-registration-jobs

Splits processing in
individual jobs



register-1.job



register-2.job



register-3.job



register-4.job



register-5.job



...

submit-jobs

To queuing
system

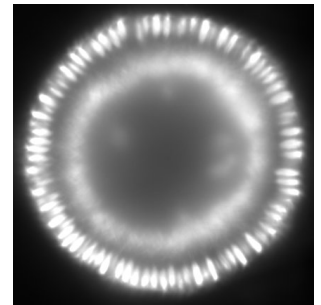
registration.bsh

Carries out
processing

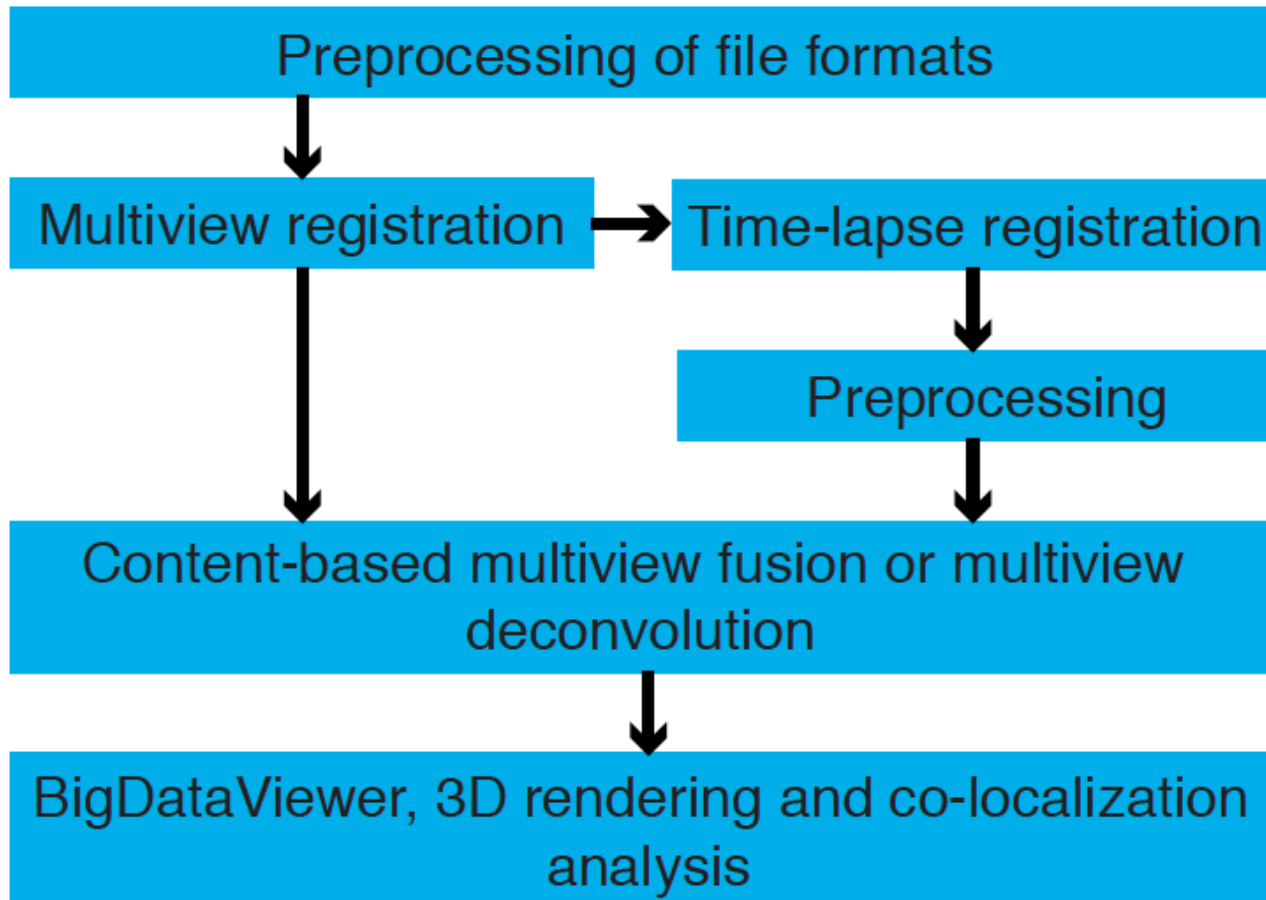


Output:

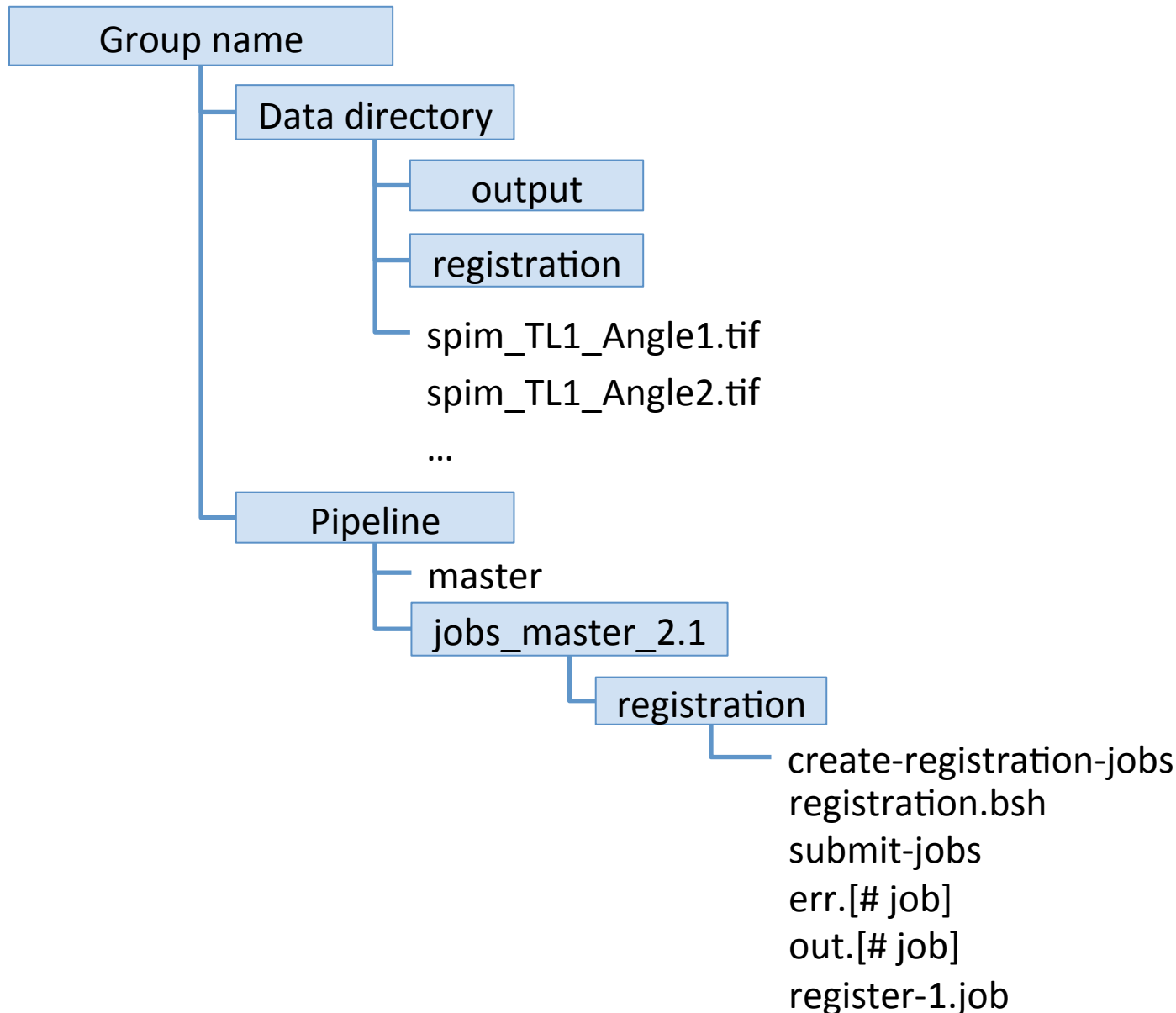
err.[# of job]
out.[# job]



Pipeline



Directory structure



Command line

```
$ ssh {username}@madmax; ssh {username}@export
$ pwd
$ cd /projects/embo2014/username
$ cd ..
$ ls
$ nano {script}
$ cat {text file}
$ ./{executable_script}
$ ./submit-jobs .
$ bjobs
$ bqueues
```