Jobs – from one to many

Promise: You will learn techniques to scale up work + some other useful things.

Prerequisites: UNIX shell, editor, basic knowledge of jobs & Slurm

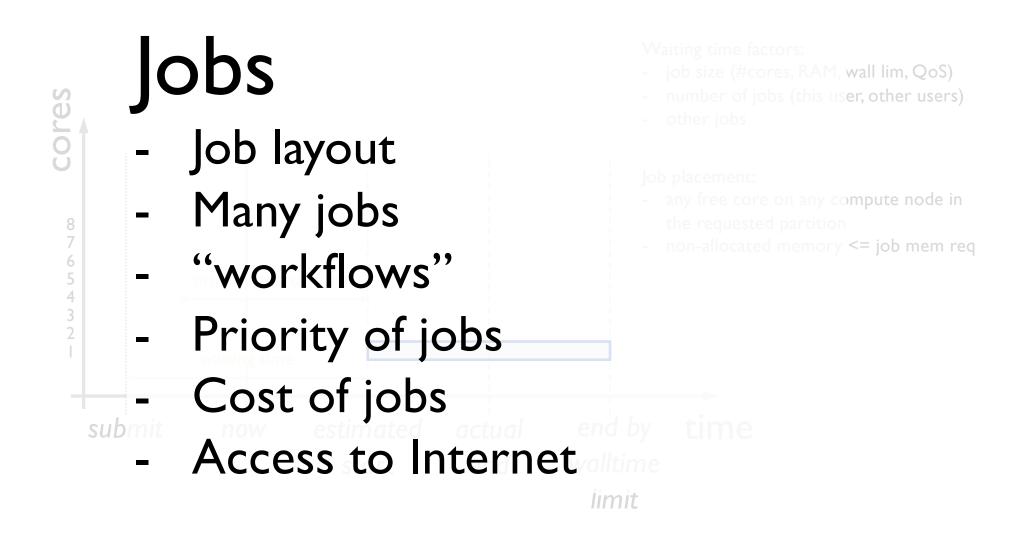
Me

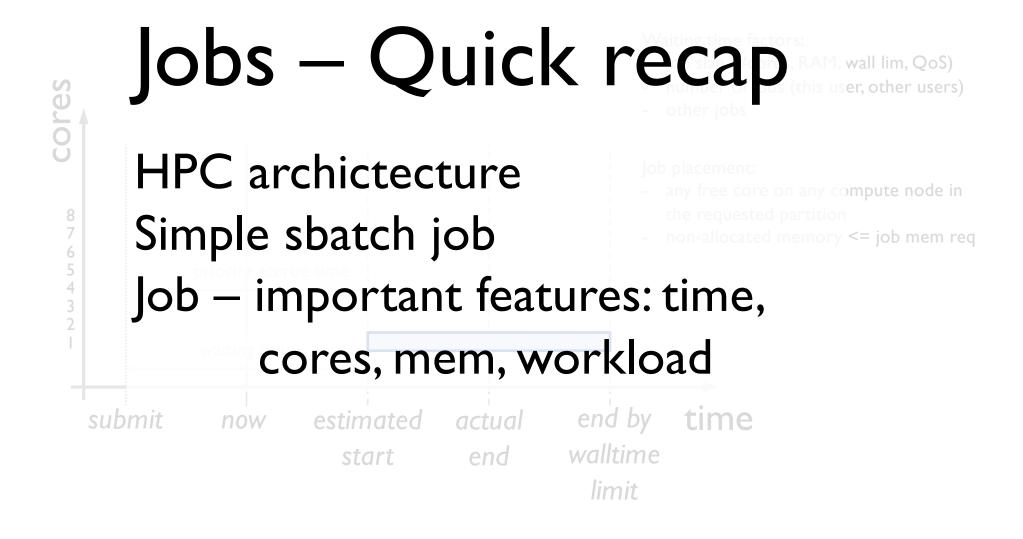
- Waiting time factors:
- job size (#cores, RAM, wall lim, QoS)
- number of jobs (this user, other users)
- other jobs
- 10 years research in computer science
- 10 years HPC sysadmin
- Projects: {N,E}ESSI & LUMI User Support

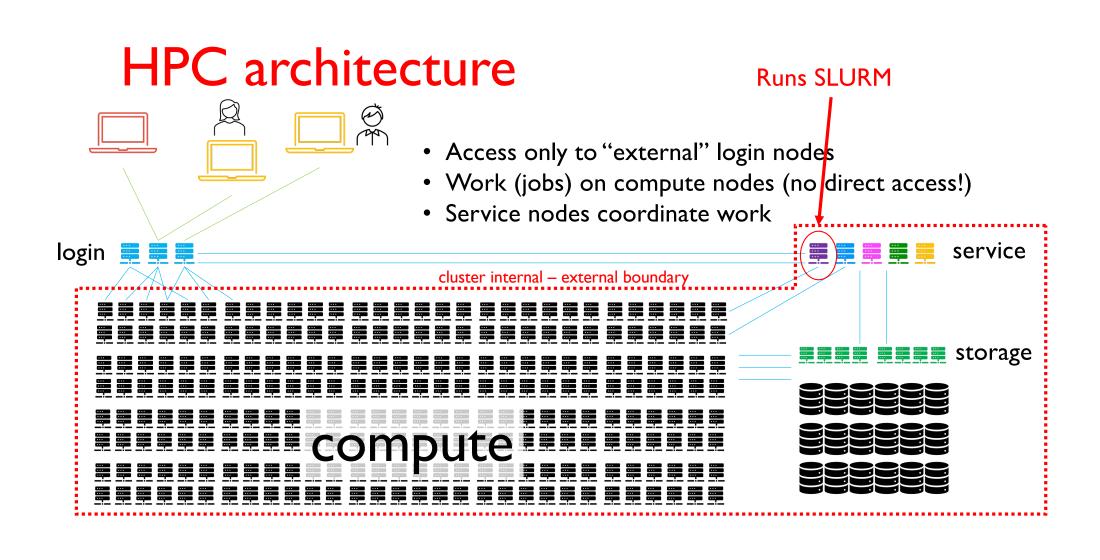


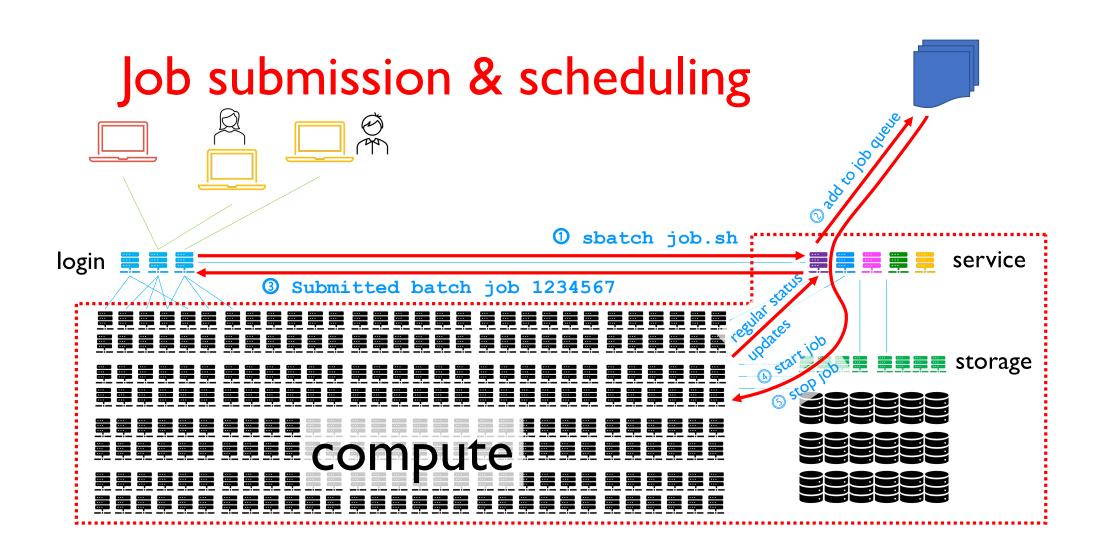
actual











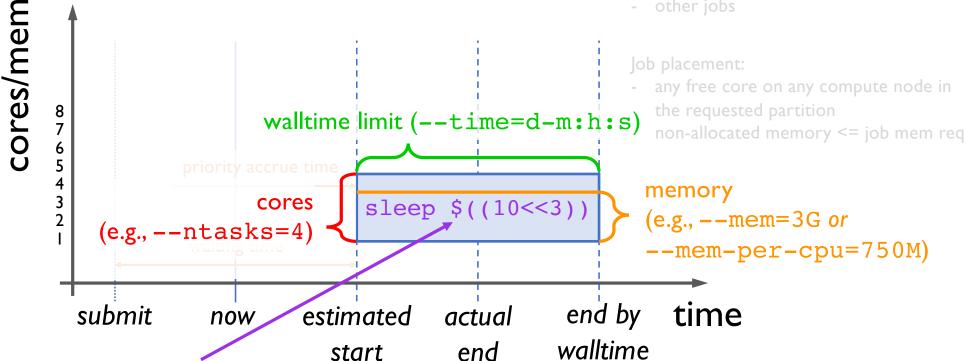
Jobs – important features

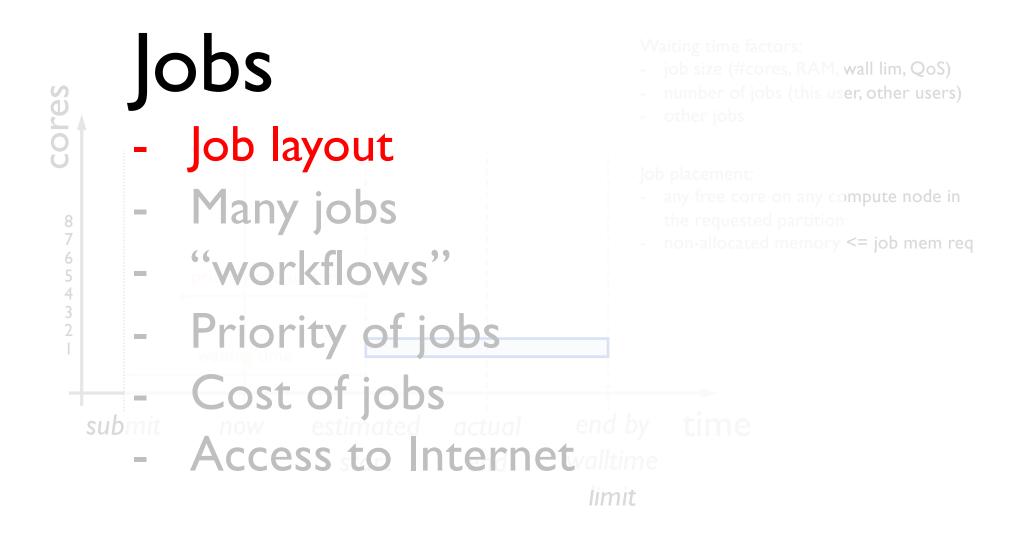
workload

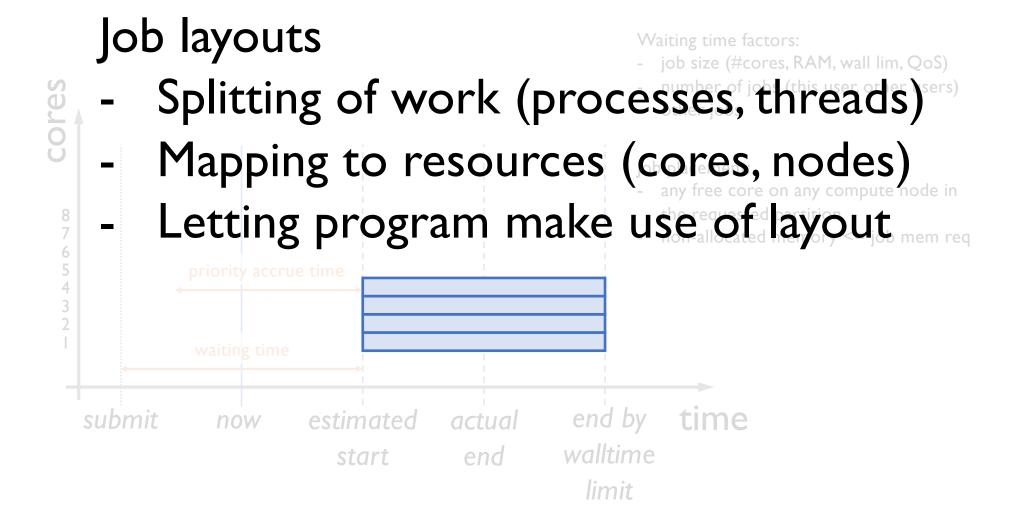
Waiting time factors:

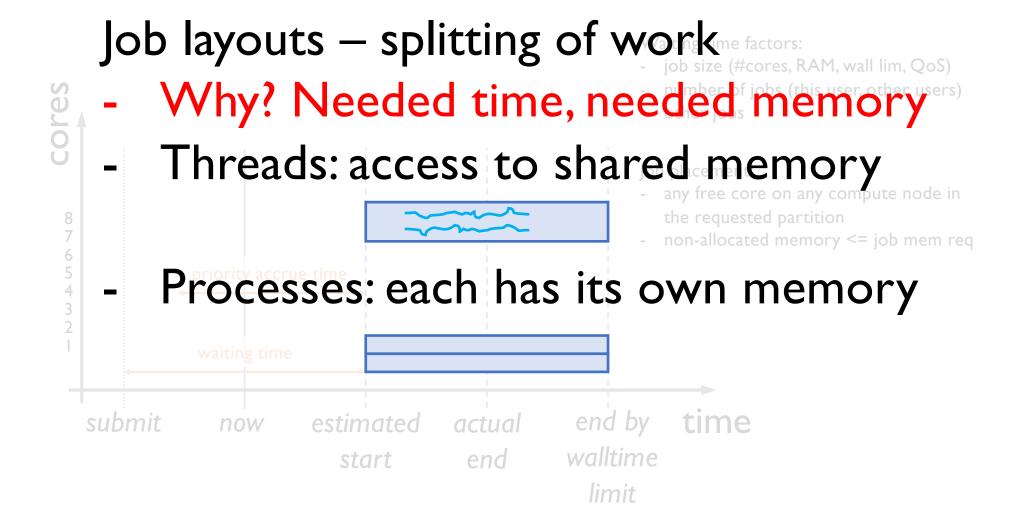
- job size (#cores, RAM, wall lim, QoS)
- number of jobs (this user, other users)

limit

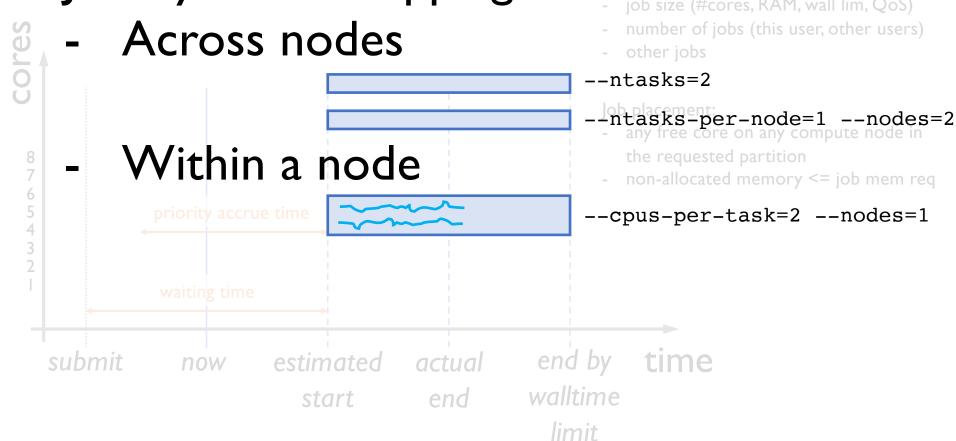


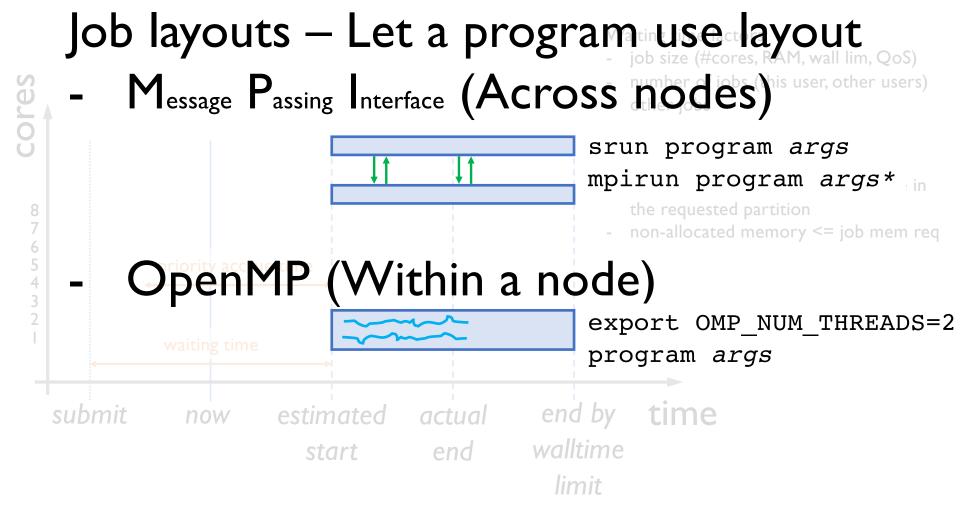






Job layouts — Mapping to resources job size (#cores, RAM, wall lim, QoS)





(*) We recommend to use srun. See documentation at https://documentation.sigma2.no/jobs/guides/running_mpi_jobs.html?highlight=mpirun

Job uses 4 threads in 1 process (task)

```
#SBATCH --ntasks=1
#SBATCH --cpus-per-tasks=4
```

program args

000

000

000

000

- Job uses 4 processes (tasks) anywhere

```
#SBATCH --ntasks=4

srun program args

significant now estimated actual end by time
```

000

000

000

- 2 nodes, 4 processes (tasks)

```
#SBATCH --nodes=2
#SBATCH --ntasks=4
```

srun program args

000

000

000

- 2 nodes, 2 processes (tasks) on each

```
#SBATCH --nodes=2
#SBATCH --ntasks-per-node=2
```

srun program args

000

000

000

- 4 processes (tasks), 2 on each node

```
#SBATCH --ntasks-4 #SBATCH --ntasks-per-node=2
```

srun program args

Job layouts – What to use & when?

- Computing effort
- (Parallelism) and size. How long does it run? test sma"
- Problem size

 How much mer case cast small, read doc

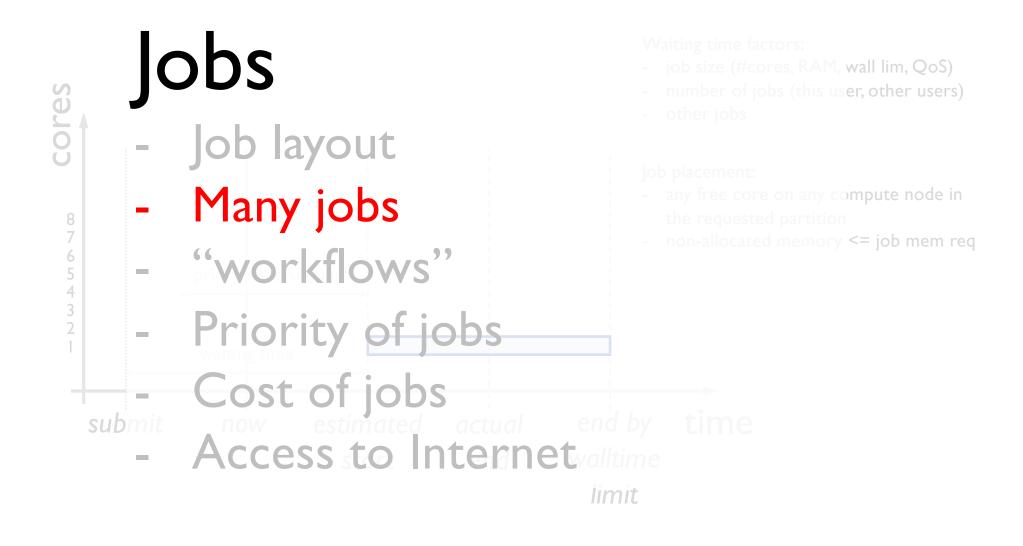
 Program then increase cast small, read doc

 Program then increase cast small, read doc

 and small, then increase cast small, read doc

 and small, then increase cast small, read doc

 If possible (time, mem) run sequential.
 - Either OpenMP or MPI. Lastly, both.



Many jobs

- Why? 1000 images, 1000 DNA seqs, ...
- Array jobs Slurm feature
- Parameter Sweep Jobs "manually"

Many jobs – Array jobs

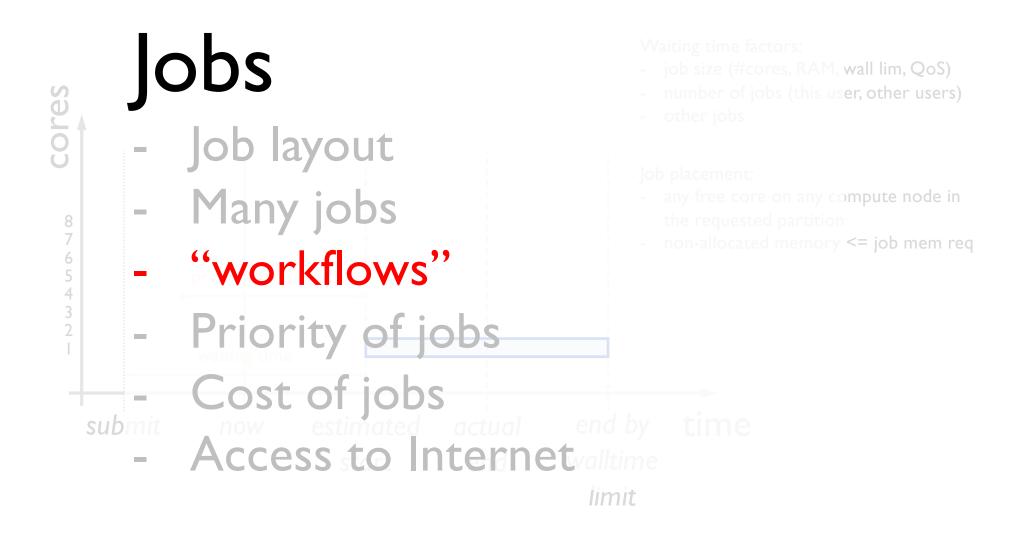
```
#SBATCH --array=1-10
...
program ${SLURM ARRAY TASK ID} args
```

- only one jobscript & sbatch call necessary
- squeue will show array workers as n_1, n_2,...
- max array size: scontrol show config | grep -i array
- program can make use of index(ed data)
- When? workload easily splitable and enumerable

Parameter Sweep Jobs

```
FEATURES="A1 A2 B3 D8 CC"
for f in ${FEATURES}
do
   program $f args
done
```

- iterate sequentially over inputs/features
- can be part of any (job)script
- nested loops (combinations of features possible)
- When? workload not easily enumerable

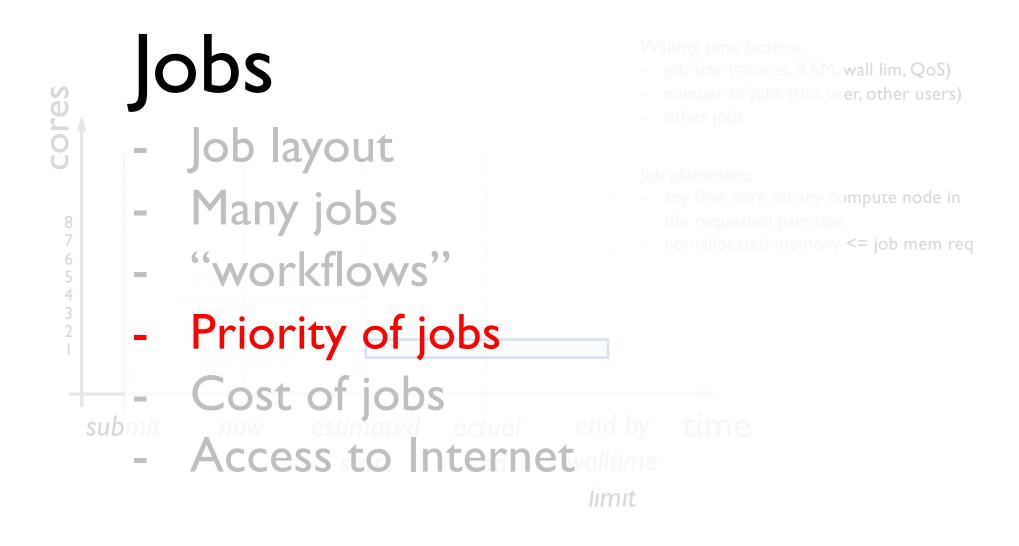


Dependent jobs ("workflows") me factors: - job size (#cores, RAM, wall lim, QoS) job B can only run after job A jobs (this user, other users) sbatch jobA.sh any free core on any compute node in Submitted batch job 1234 the requested partition \$ sbatch --dependency=afterok:1234 jobB.sh Submitted batch job 1240 В squeue -u \$USER actual JOBID PARTITION NAME USER ST TIME NODES NODELIST (REASON) normal OpenFOAM thomarob PDC110 0:00 (Dependency) 2211325

https://documentation.sigma2.no/jobs/guides/job_dependencies.html

normal OpenFOAM thomarob R

2211324



Priority of jobs

- means to distinguish jobs: age, QoS,
- optimization sched.: only top-prio jobs considered
- users cannot set a specific priority for a job
- List priorities of current jobs

```
$ sprio -S -y | head

JOBID PARTITION PRIORITY SITE AGE QOS

1629131 normal 29840 0 10080 19760

1629137 normal 29840 0 10080 19760
```

Priority of jobs - Example

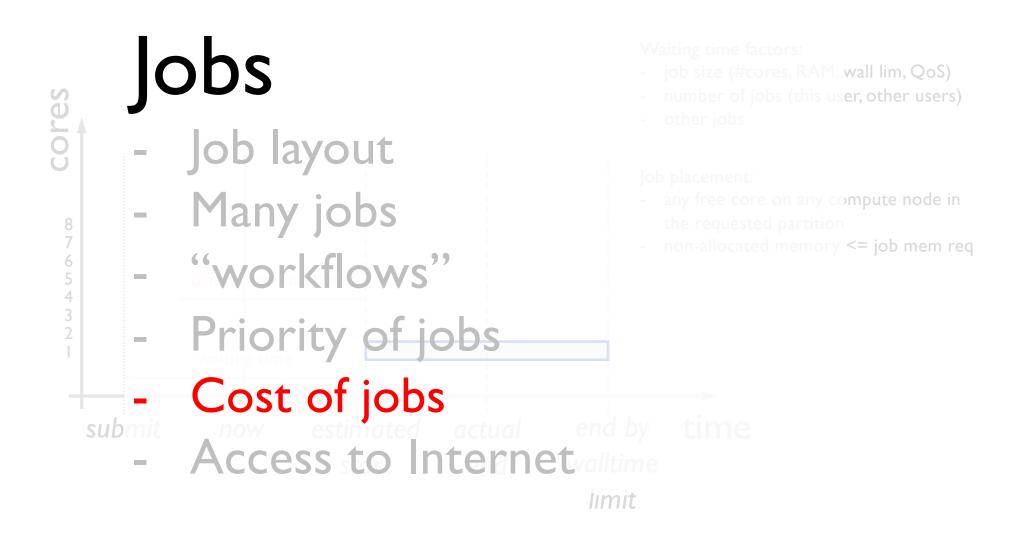
```
$ sbatch big.sh; date; sprio -u $USER
$ sleep 120; date; sprio -u $USER
• every minute job ages by one
```

- every influte job ages by on
- max age 10080 (7 days)
- devel qos start priority is 120 higher
- only 10 jobs per user age

```
$ for i in $(seq 1 11); do sbatch —
job-name=big-$i big.sh; done
$ date; sprio —u $USER
$ close 120: date: sprio —u $USER
```

Priority of jobs - Example

```
$ for i in $(seq 1 11)
do
sbatch --job-name=big-$i big.sh
done
$ date; sprio -u $USER
$ sleep 120; date; sprio -u $USER
```



Job accounting

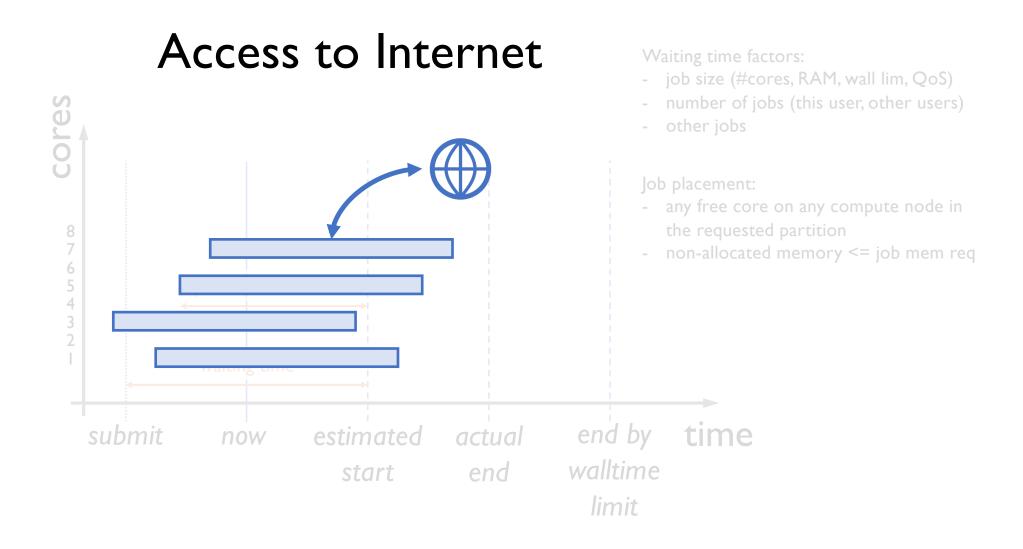
- Every project (nnABCDk) has a quota (BU hours)
- BU = billing unit
- Job submission only successful when enough quota left
 - → error label: AssocGrpBillingMinutes
- Jobs accounted for time actually used (not for time limit)
- Number of billing units = f(cores, RAM, GPUs)
- Cost = requested #BU x actually used time
- Resources allocated to a job cannot be used by other jobs.

Job accounting – calculate cost

- #BU is maximum for BU for cores, memory and GPUs
- every core costs one BU (everywhere)
- every GPU costs six BU (Saga only)
- Memory costs proportionally to node "size"
- Higher costs on Saga's bigmem nodes
- Request all mem incurs cost as if all CPU/GPU were used.
 - 377 GB on GPU nodes cost 24 BU
 - 186 GB on normal Saga nodes costs 40 BU
- 377/3021 GB on bigmem Saga nodes costs 40/320 BU

Job accounting – Examples

- Saga: 40G, 4 cores, normal \rightarrow max(8.6,4) = 8.6
 - If your job can use more cores, you get 4 for free!
- Saga: 40G, 4 cores, bigmem \rightarrow max(4.2,4) = 4.2
 - Well balanced.
- Saga: 40G, 4 cores, I GPU \rightarrow max(2.5,4,6) = 6
 - You could consider using more memory & cores.
- Fram: I node, normal → 32 (node has 32 cores)
- Betzy: 4 nodes, normal → 512 (node has 128 cores)



Access to Internet

- From jobs running on compute nodes
- GitHub (git clone)
- pages which contain data (wget, curl)
- Configured on Saga & Fram

```
$ srun --ntasks=1 --mem-per-cpu=4G --time=0:30:0 --
account=nn9989k --pty bash -i
...
git clone https://github.com/EESSI/docs.git
wget https://eessi-hpc.org
curl -I https://www.sigma2.no
```