Managing task-parallel computations with jobber

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https://thomas.orgis.org/jobber

teaser

- university compute cluster with very diverse user base
- many inexperienced users with serial or at most node-local parallel computations
- enabling them to fill cluster node allocations sensibly
- prerequisite: learning to phrase the set of tasks as shell script lines as universally applicable skill
- no need for details on the batch system, re-use personal setup on different sites

teaser example

- medical parameter study with statistics over generated data sets of certain size (one crucial parameter) and combinations of analysis methods
- researcher knows R and the science at hand, but not much else regarding computer use
- a bit of help to pass parameters into the existing R script from shell wrapper

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(Researcher was rather happy about that and did not hesitate to try the larger data set sizes after all.)

teaser batch script

```
#!/bin/bash
#SBATCH --job-name=someRstuff
#SBATCH --partition=std
#SBATCH --nodes=1
#SBATCH --tasks-per-node=1
#SBATCH --time=06:00:00
#SBATCH --export=NONE
. /sw/batch/init.sh
module switch env env/2020Q3-gcc-openmpi
module load R/4.0.2
module load jobber/r1254
# Simplest case. Could run multiple jobs of differing runtime
# sequentially or in parallel here (with or without srun).
jobber task.list 1
if jobber task.list more; then
 sbatch $0
fi
```

teaser job chain control

- stop execution of job chain: jobber task.list stop
- enable executon again: jobber task.list start
- make things more parallel: for n in \$(seq 1 \$N); do sbatch batch.sh; done
- check progress: jobber task.list done failed todo

but first ...

Why was this inevitable?

once upon a time, a physics student

Data analysis for student lab experiments via office spreadsheet software?

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- Data analysis for student lab experiments via office spreadsheet software?
- Write Perl scripts for common computations on measurements in text files (Text::NumericData on CPAN) and for automated plotting using scriptable tools.

taking the routine out of routine

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- ► Locate the scripting mechanism in that software, but in the end ...
- ... write more of the text data scripts and configurations for analysis pipes with a GUI for the colleagues to do the routine analyses on a batch of measurements.

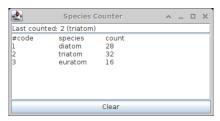
counting with your fingers

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- Working alongside biologists who look at dead things through microscopes, counting different types of dead things, manually writing down counts in spreadsheets software?
- Write a trivial Java GUI that counts key presses for a massive productivity boost

counting with your fingers



(a useful Java program, 2009 vintage)

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(Bonus: Does not crash all the time!)

Organize things differently for fun and profit!

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▶ **simple big problem:** high-resolution simulation run that can be split into consecutive pieces on the time axis

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- simple big problem: high-resolution simulation run that can be split into consecutive pieces on the time axis
- parallelize with OpenMP and/or MPI, just one chain of jobs or a single big one if HPC site permits it (we rather don't;-)

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solving my numerous problems

- lots of little problems amounting to a big one: a parameter study with varying resolutions and dynamics, a pile of model runs with varying runtimes
- lots of trial and error with job parameters, re-running failed computations

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- ► Keeping track in spreadsheets? No!
- ▶ Domain-specific, fat, hungy & fragile GUI? No!
- ► Got something that nicely works as a simple shell tool? Well ...

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- xargs: similar, good for ad-hoc parallelism

jobber features

- organize a list of tasks, posed as lines of shell script
- syncronize access while picking tasks
- record and manage state of each task, to know what to re-run
- pack multiple small/short tasks to better fill job time slots and allocated compute resources
- work on the same tasks in batch system or just a random personal computer, possibly going back and forth
- easy job chains via generic batch script

generic batch script

```
#!/bin/bash
#SBATCH -- job-name=manytasks
# we got 16-core nodes, not shared
#SBATCH --nodes=1
#SBATCH --time=12:00:00
# cluster-specific init stuff
# maybe load some modules
# Pack many single-processor-jobs into our time slot,
# until time runs out.
jobber --parallel=16 --time=$((11*3600)) task.list all
# Continue work in next batch job.
if jobber task.list more; then
  sbatch $0
fi
                            (pretty generic)
```

one way (for HPC people)

- master-worker program using OpenMP on a node
- some number of OMP threads
- #pragma omp critical section around a function that determines the next piece of work to do, if any
- actual work with custom code, or maybe using system()

another way (for HPC people)

- proper master-worker program using MPI
- central process distributing tasks
- ► MPI_Recv() and MPI_Send() on both sides
- worker processes getting bits of work from master
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Who writes real programs these days?

jobber implementation

- no central server process for management (serverless;-)
- safe operations on a single database file with POSIX rename semantics, also on network file systems
- flush and sync, see Stewart Smith: "Eat My Data How everybody gets file I/O wrong" (https://www.slideshare.net/nan1nan1/eat-my-data, https://www.youtube.com/watch?v=LMe7hf2G1po)
- behaves like a database with server backend, but still just plain files for data and control
- ▶ limitation: transaction rate low, but no issue for sensible tasks needing more than a few seconds each

one thing left to do

```
#!/bin.sh
LANG=C; set -ex
test -e jobber ||
wget https://thomas.orgis.org/jobber/jobber
test -e jobber.sig ||
wget https://thomas.orgis.org/jobber/jobber.sig
#gpg --search-key thomas@orgis.org
gpg --verify jobber.sig
chmod +x jobber
mkdir -p man1
./jobber -h=-100 | pod2man > man1/jobber.1
./jobber -h=-100 | pod2text > jobber.txt
```