



# Parallelisation via srun and GNU parallel



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### GNU parallel allows to

- run any (executable) program(s) in parallel with no communication between program instances
- Allows to run many parallelisations on a fixed number of nodes: one finishes the next starts
- Does not have to be loaded via **module load**

Why GNU parallel?

- Not much overhead for learning standard usage (+ a bit more)
- Nice features, e.g. rerun only failed jobs

What does GNU parallel not do (well)?

- Parallelisation with (meaningful) communication between instances
- Efficient multi-node use
- Collection of output

O. Tange (2018): GNU Parallel 2018, March 2018, <u>https://doi.org/10.5281/zenodo.1146014.</u> https://www.gnu.org/software/parallel/







Running in parallel with **srun** - 1st example



- Our focus is on working on the <u>bwUniCluster</u> which e.g. uses SLURM as a workload manager and has GNU parallel installed. All examples are run on bwUniCluster's command line. If run elsewhere, you need to adjust some commands.
- Let's start an interactive session for 30 min w. 2 cores \$ salloc -t 30 -p dev\_single -n 2
- We will often run the executable bash script scr1 with 2 arguments

GNU nano 2.9.8

scr1

```
#!/bin/sh
date '+%X' #Gives the system time
sleep $((3*$1)) #Sleeps for 3x arg #1 seconds
echo "this is job $2" #Prints the text string w. arg #2 inserted
echo "I slept 3 x $1 seconds" #different text, different insert
```





Generate the executable scr1



1. Copy & paste into a (text) file scr1

#!/bin/sh
date '+%X'
sleep \$((3\*\$1))
echo "this is job \$2"
echo "I slept 3 x \$1 seconds"

2. Make it executable via \$ chmod u+x scr1







**\$ parallel** [options] *executable* **:::** *arg1 arg2 arg3 ...* 

Runs the executable in parallel: 1x with arg1, 1x with arg2, .... (options are ... optional and are set via -optionname)

We start an interactive session and try this out

\$ date '+%X' && parallel echo ::: 10 10 && date '+%X' \$ date '+%X' && parallel sleep ::: 10 10 && date '+%X'

Commands after && get executed directly after the one(s) in front - given everything in front ran successful)







Instead of manually providing arguments, you can use a file (one line=one argument for parallel)

\$ parallel -a argfile executable

#different order than on last slide, since #provided via option -a

For many runs in parallel (# runs > 2\*ntasks):

\$ parallel -j how\_many\_in\_parallel -a argfile executable

- -j specifies how many jobs (at most) are run in parallel at a given time
- if j is not specified, it runs as many jobs at the same time as there are cores







Combining multiple arguments with

\$ parallel executable {1} {2} ::: arguments1 ::: arguments2

runs the executable with **all combinations** of *arguments1* and *arguments2* 

\$ parallel --link executable {1} {2} ::: args1 ::: args2

runs the executable with combining arg #1 from *args1* with arg #1 from *args2*, arg #2 with arg #2, ..... If arguments differ in length, shorter one gets recycled

Examples:

\$ parallel --link ./scr1 {1} {2} ::: 5 2 5 2 ::: 1 2 3 4 \$ parallel -j 2 --link ./scr1 {1} {2} ::: 5 2 ::: 1 2 3 4 What do the commands do?







Helpful bash commands to use w. GNU parallel:

Let x,y,z be numbers

- seq x y z: series from x to z in steps of y
- Can be used as input arguments for GNU parallel by \$(seq x y z)
- pipe operator | allows to generate arguments from other commands
- Brace expansion to mix words with numbers (see example below)
- Many more

Examples:

```
$ parallel --link ./scr1 ::: 1 2 ::: $(seq 1 10 1)
$ parallel --link ./scr1 ::: 12 ::: job{1..10}
$ ls | parallel echo "FILE IS " {}
```

#works also without {}

What do these commands do?

Using pipes etc. may lead to some trial&error (syntax needs to be met)...





## GNU parallel

- some more job control options



<b>Option (short)</b>	Meaning
-a f1 -a f2	Run with all combinations from two input files f1 and f2
	Addlink to run 1st argument w. 1st argument,
joblog f1 resume-failed (resume)	1st run: run wjoblog to add journal log f1 (filename) 2nd run: run w. both options to rerun only the failed jobs from f1 (Alternatively for 2nd run: rerun jobs not run yet)
{#}	Instead of an argument provided after ::: or via -a, inputs the job number among all parallelised instances
citation	Citation info, please cite it if you use it for publications

Many more: Either \$ man parallel or

https://www.gnu.org/software/parallel/parallel.html#options

Nice tutorial: <u>https://www.gnu.org/software/parallel/parallel\_tutorial.html</u>

(you don't need remote running via -S or -ssh, since we run via SBATCH-scripts directly on the cluster)







srun allows to

- run any (executable) program(s) in parallel with no communication between program instances
- Allows to run MPI-using programs that allow communication between program instances ٠
- Does not have to be loaded via module load ٠

### Why **srun**?

- You can control how the program instances are distributed across cores/nodes
- Allows mpi use, i.e. It is the built-in SLURM machinery to run mpi programs ٠
- SLURM allows a lot of reporting ٠

Where does **srun** need help?

- It starts all jobs in parallel workarounds needed if you want to run more than the requested number of tasks
- Collection of output (when running independent instances) ٠

SLURM: https://slurm.schedmd.com/overview.html

srun man page: https://slurm.schedmd.com/srun.html







- While srun can also request resources alongside the program call, we use it here only within a SBATCH script (or analogously within resources allocated via salloc)
- General syntax: \$ **srun** *srun-options executable executable-args/opts*
- Simplest way to run it:
   \$ srun -n no\_tasks executable [args\_ex1]

Runs an executable file (via *.lexecutable\_1*, via program path) n times in parallel (<u>optionally</u> with arguments args\_ex1)

- Use this e.g. when collecting all output from simulations in the same file in parallel
- Or for a multi-threaded program that runs on multiple cores

Example: \$ srun -n 2 ./scr1 5 1







Run multiple instances of srun with one command, separated by colons :
 \$ srun srun-opt1 exec1 exec1-args : srun-opt2 exec2 exec2-args : ...

 e.g.
 \$ srun -n 4 exec1 : -n 3 exec2 : -n 2 exec 3

runs exec1 4 times, exec2 3 times and exec3 2 times (all in parallel). However, each instance runs on a <u>separate node</u> (produces an error if not enough nodes allocated).

 Better way to run it, <u>works on a single node</u>: \$ srun -n *no\_jobs* --multiprog *input\_file*

The input file is a text file, where each line shows, separated by a blank space,

- Which task to run with these arguments (indicated by number 0,1,...,n-1)
- Program to be run
- Program parameters





srun - the next example



Run scr1 w. two different sets of arguments

```
$ srun -n 1 ./scr1 5 1 : -n 1 ./scr1 2 2
```

What does the command do? Does it run on our resources? Why not?

• Exercise: Do the exact same via --multiprog.

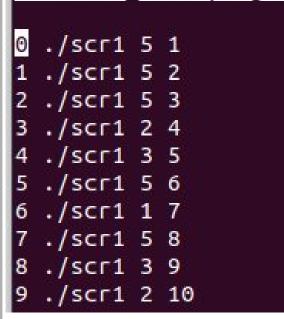
See the next slide for an example file for --multiprog







#### conf\_multiprog.txt



- If multiple tasks have the same arguments, you can separate them via comma an/or specify a range *from-to* Example: 0,3-5 ./fun1 7 runs ./fun1 w. argument 7 as tasks 0,3,4,5
- Setting \* as task number runs all tasks not specified in lines above it with the arguments in that line







Option (short)	Meaning
exclusive	Only allocate memory matching to the number of cores used for srun
-N <i>min-max</i>	Spread job over at least min nodes, at most max nodes
spread-job	Spreads jobs across nodes in a balanced manner
-r offset	Start distributing process instances on node <i>offset</i> of the current allocation (default value 0)
-c tasks-per	Each invoked process instance gets tasks-per cores allocated
-v [-v]	shows details of how srun distributes the jobs. Adding it multiple times increases the show information.
gpus-per-task= <i>number</i>	Take number of GPUs per invoked process

All entries in italics are integer-valued

Full (long) list: <u>https://slurm.schedmd.com/srun.html</u> worth looking at, e.g --distribution to have precise control over how tasks are distributed





A word on output files from running many tasks via GNU parallel



- GNU parallel allows to run many tasks, which possibly all write an output into a file
- Writing many files (e.g. tens of thousands, millions) within a workspace is not ideal for the memory system underlying the workspaces (and really bad on \$HOME)
- Solution (within SBATCH or salloc): Write the ouput files to the temporary directory
  - Each salloc or sbatch job has its own temporal directory while it exists
  - Its path is stored in the variable **\$TMP** (within the job allocation)
  - Write output there, and then move it back at the end of the SBATCH script/interactive session

\$ echo \$TMP \$ cd \$TMP \$ echo "THIS IS THE TMP: " \$TMP > temp1.txt \$ cp temp1.txt \$HOME/temp1.txt





Combining srun and GNU parallel to (comfortably) run on multiple nodes



 Run many jobs in parallel by GNU parallel, but wrap the executable into a srun to use srun's job control

Example (needs two cores to run, so you'd need a new resource call):

**\$** parallel -j 8 --link srun --exclusive -N 1 -n 1 -r {1} ./scr1 {2} {#} ::: 0 1 ::: 6 1 1 1 1 1 6 7 1 2 1 2 5 6 7 8 1 2 3 1 2 4 7

Runs 24 instances of exec1 with different parameters, at most 8 at one time, each one on one core/one node. Each second instance runs on node 2, all others on node 1. All instances get only default memory per node allocated

IMPORTANT!! You need to set --exclusive, otherwise the first instance gets all resources allocated

