LSU INFORMATION TECHNOLOGY SERVICES

Parallelizing Massively Independent Tasks

GNU Parallel & Job Arrays

Siva Prasad Kasetti

HPC User Services

LSU & LONI HPC

sys-help@loni.org

Louisiana State University

Baton Rouge

08 April 2025

http://www.hpc.lsu.edu/training/archive/tutorials.php

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  - **SLURM Job Arrays**

Outline

- **Introduction**
  - What is GNU Parallel and SLURM Job arrays?
  - When and Why to use GNU Parallel and SLURM Job arrays (Previous Slide)
- **Basic Usage**
  - GNU Parallel Syntax and Options
  - Running jobs with GNU Parallel:
    - Serial Tasks & Multi-Threaded Tasks - Run each LAMMPS task
  - Running jobs with Job arrays
    - Submit and manage large sets of similar jobs using array indexing (--array)
- **Proper usage**
  - Memory consideration (GNU Parallel)
  - Task granularity (GNU Parallel)
  - Best practices with Job arrays

What is GNU Parallel and Job Arrays?

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Parallelizing Massive Individual Tasks

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What is GNU Parallel and Job Arrays?

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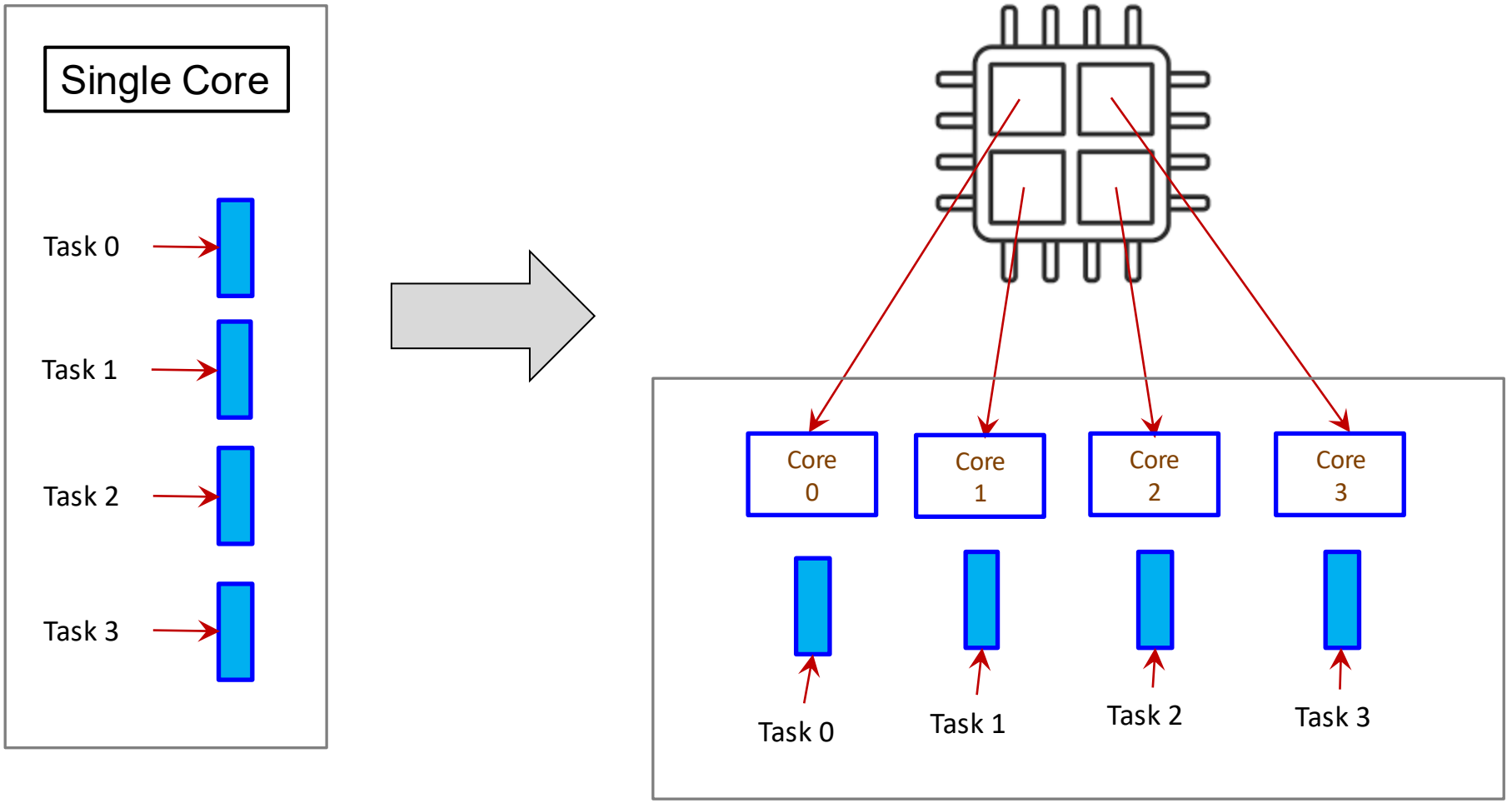
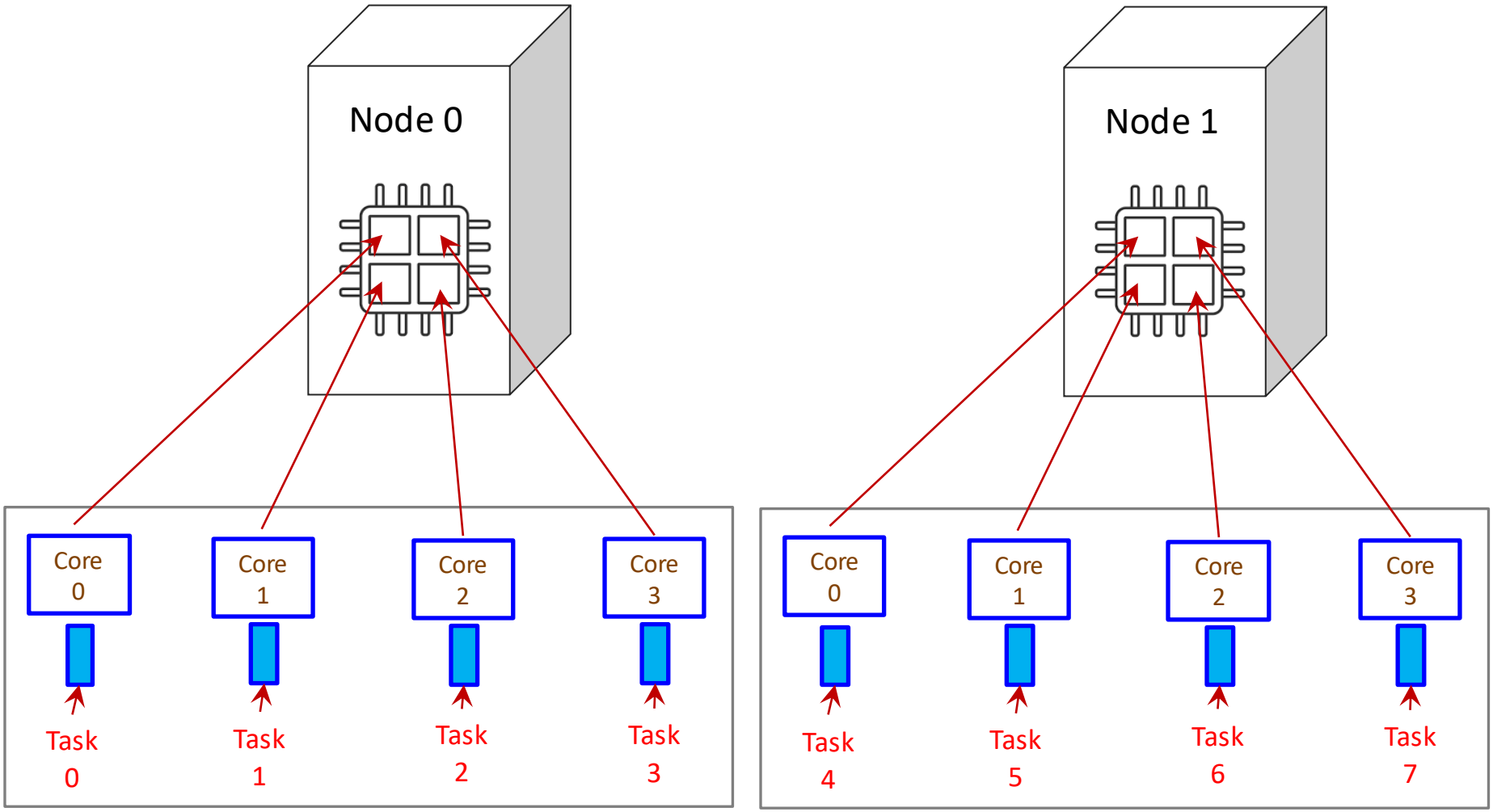
- **Individual (Independent)**
  - Each task operates independently of the others. This means there's no dependency between tasks, allowing them to be executed in parallel without waiting for one another.
- **Tasks**
  - These are the units of work or commands you want to execute. Each task could be a program, script, or function that processes a specific set of inputs.

What do we want to accomplish?

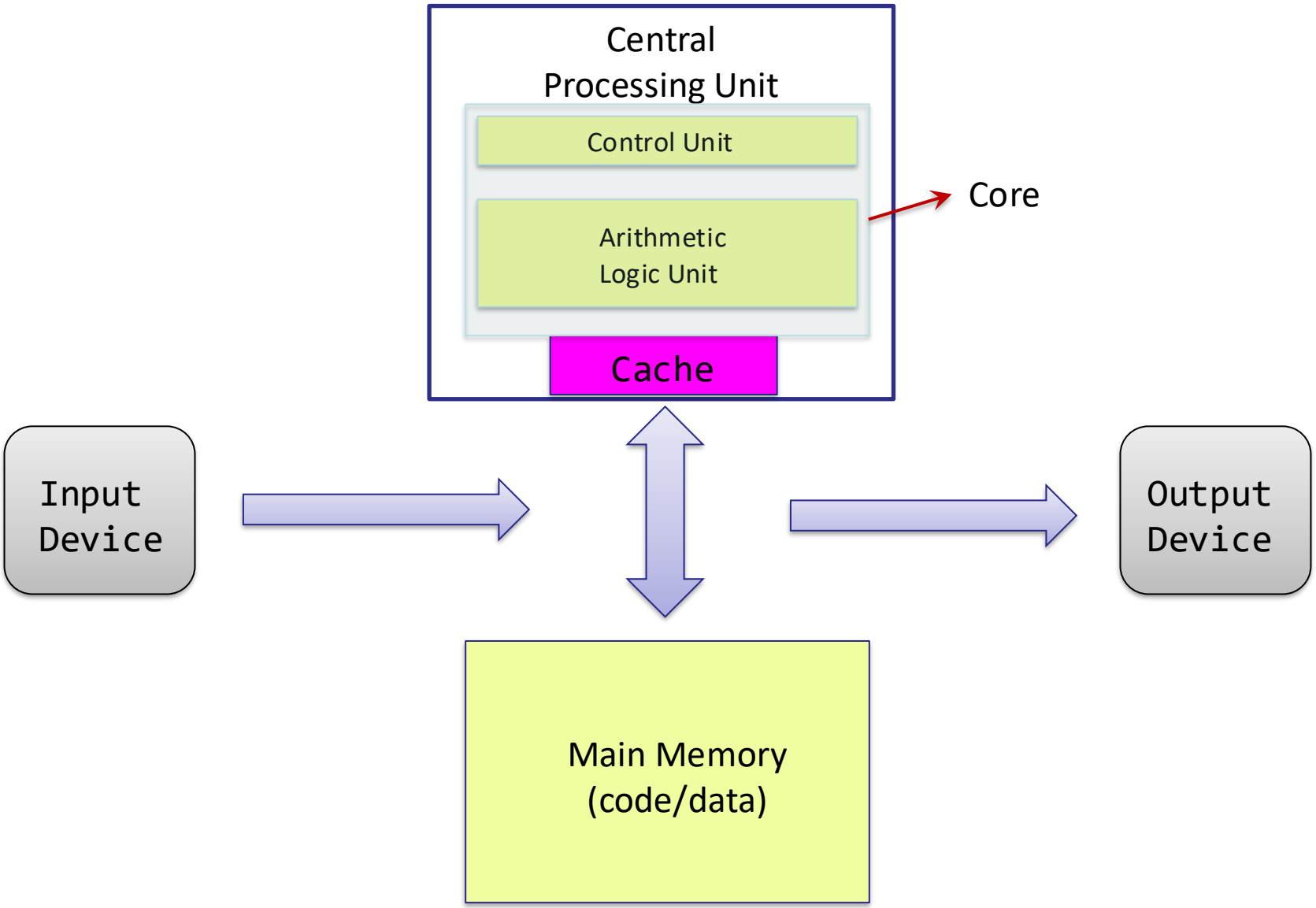
- **Parallize lots of small independent tasks on a multi-core platform (compute nodes)**



Background and Distribute



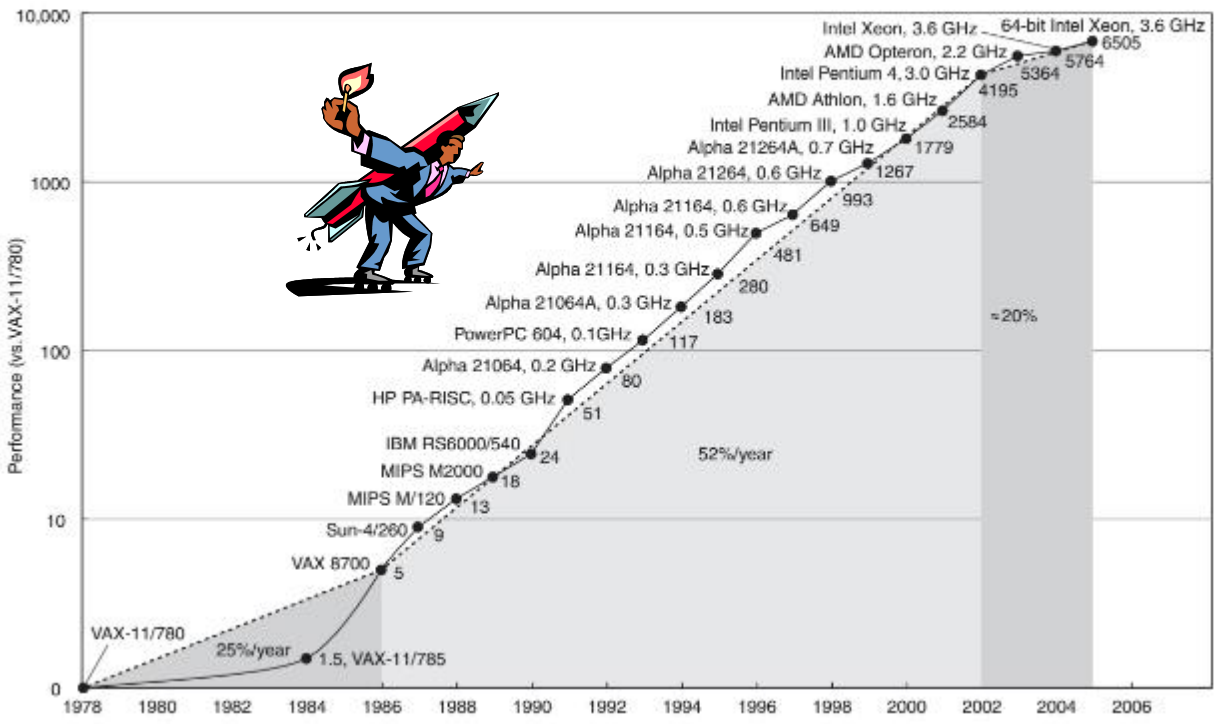
The von Neumann Architecture



Changing Times

- **From 1986 - 2002, microprocessors were speeding like a rocket, increasing in performance an average of 50% per year.**
- **Since then, it's dropped to about 20% increase per year.**

History of Processor Performance



Moore's Law states that transistor counts on chips double roughly every two years.

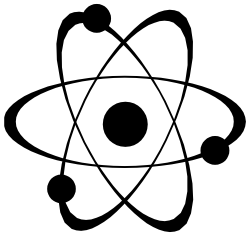
Limitation:

2 GHz Consumer
4 GHz Server

Source:
http://www.cs.columbia.edu/~sedwards/classes/2012/3827-spring/

A Little Physics Problem

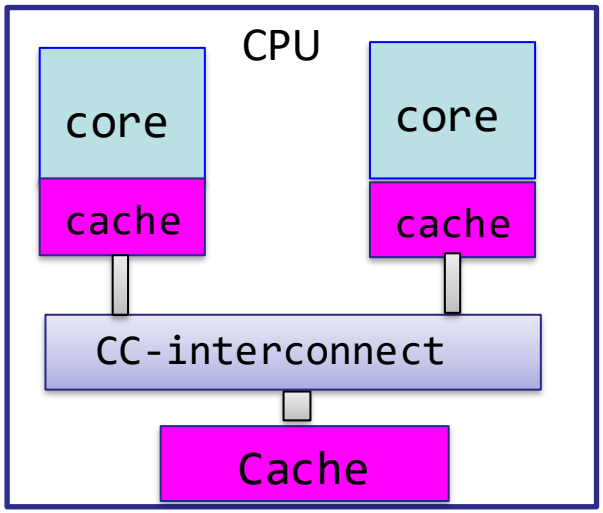
- **Smaller transistors = faster processors.**
- **Faster processors = increased power consumption.**
- **Increased power consumption = increased heat.**
- **Increased heat = unreliable processors.**

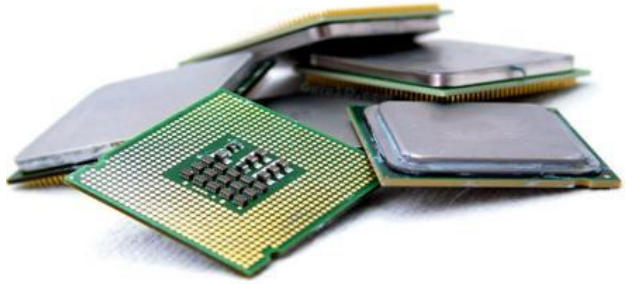


- **Solution:**
  - Move away from single-core systems to multicore processors.
  - "core" = central processing unit (CPU)
  - Introducing parallelism
    - *What if your problem is also not CPU dominant?*

The von Neumann Architecture

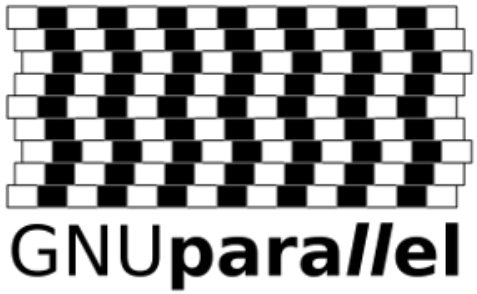
Around year 2005





GNU Parallel

- **GNU parallel is a shell tool for executing "embarrassingly parallel" tasks using one or more computers (*compute nodes*).**
- **Terminology:**
  - **Task**: Each ***small, independent*** piece of computation work to be finished, e.g., a single genome computation, a single MD simulation
  - **Job**: The list of tasks to be completed on a set of nodes (cores)
- **A task can be a *single command or a small script* that must be run for each of the lines in the input.**
- **The typical input is a *list of files*, a list of hosts, a list of users, a list of URLs, or a list of tables.**
- **See more at: https://www.gnu.org/software/parallel/**



Introduction to GNU Parallel

GNU Parallel Syntax

Adding GNU Parallel to Environment

- **On SuperMike3:**

```
[fchen14@mike139 ~]$ module av parallel
---- /usr/local/packages/Modules/default/modulefiles/linux-rhel8-icelake ----
parallel-netcdf/1.12.2/intel-2021.5.0
parallel/20210922/intel-2021.5.0
parallel-netcdf/1.12.2/intel-2021.5.0-intel-mpi-2021.5.1

# load the module to environment
[fchen14@mike139 ~]$ module load parallel/20210922/intel-2021.5.0

[fchen14@mike139 ~]$ which parallel
/usr/local/packages/parallel/20210922/hrsviur/bin/parallel

[fchen14@mike139 ~]$ parallel –version # check GNU parallel version
GNU parallel 20210922
Copyright (C) 2007-2021 Ole Tange, http://ole.tange.dk and Free Software
Foundation, Inc.
...
```

GNU Parallel Syntax

- **Reading commands to be run in parallel from an input file:**

```
parallel [OPTIONS] < CMDFILE
```

- **Reading command arguments on the command line:**

```
parallel [OPTIONS] COMMAND [ARGUMENTS] ::: ARGLIST
```

- **Reading command arguments from an input file:**

```
parallel [OPTIONS] COMMAND [ARGUMENTS] :::: ARGFILE
```

ARGLIST from command line

- **parallel [OPTIONS] COMMAND [ARGUMENTS] ::: ARGLIST**
- **Examples:**

```
[fchen14@mike139 ~]$ parallel echo ::: A B C
A
B
C
[fchen14@mike139 ~]$ parallel echo ::: `seq 1 3`
1
2
3
[fchen14@mike139 ~]$ parallel echo ::: {A..Z}
A
B
...
Z
[fchen14@mike139 test]$ ls -1 | parallel echo
2013-06-18.tgz
backups.sh
bigmem_test.pbs
...
```

ARGLIST from file

- **parallel [OPTIONS] COMMAND [ARGUMENTS] :::: ARGFILE**

```
[fchen14@mike139 GNU_PARALLEL]$ pwd
/project/fchen14/GNU_PARALLEL
[fchen14@mike139 GNU_PARALLEL]$ cat input.lst | head
01.lj
02.lj
03.lj
...
[fchen14@mike139 GNU_PARALLEL]$ head input.lst -n 5 | parallel echo
01.lj
02.lj
03.lj
04.lj
05.lj
[fchen14@mike139 GNU_PARALLEL]$ parallel echo :::: input.lst
01.lj
02.lj
...
```

Replacement Strings

- '{}' returns a full line read from the input source .

```
[fchen14@mike139 GNU_PARALLEL]$ parallel echo {} ::: data/in.lj
data/in.lj
```

- '{/}' removes everything up to and including the last forward slash:

```
[fchen14@mike139 GNU_PARALLEL]$ parallel echo {/} ::: data/in.lj
in.lj
```

- '{//}' returns the directory name of input line.

```
[fchen14@mike139 GNU_PARALLEL]$ parallel echo {//} ::: data/in.lj
data
```

- '{.}' removes any filename extension:

```
[fchen14@mike139 GNU_PARALLEL]$ parallel echo {.} ::: data/in.lj
data/in
```

- '{/.}' returns the basename of the input line without extension. It is a combination of {/} and {.}:

```
[fchen14@mike139 GNU_PARALLEL]$ parallel echo {/.} ::: data/in.lj
in
```

- See "man parallel" for more detailed explanation.

Replacement String Example

- **Print the full path of the input file, and then print the desired output file name, e.g.:**
  - Input file: `data/lj.in`
  - Output file name: `output/lj.out`

```
# Process data/lj.in and send result to output/lj.out
$ parallel echo {} output/{/.}.out ::: data/lj.in
data/lj.in output/lj.out
```

Parallelize Job Script

- **GNU parallel is often called as this:**

```
cat input_file | parallel command
parallel command ::: foo bar
```

- **If command is a script, parallel can be combined into a single file so this will run the script in parallel:**

```
parallel [OPTIONS] script [ARGUMENTS] ::: ARGLIST
```

  - or

```
parallel [OPTIONS] script [ARGUMENTS] :::: ARGFILE
```

- **See next slide for example…**

Parallize Script Example

- **This is the script we want to parallize "cmd_ex.sh":**

```
#!/bin/bash
# print the input, on which host, which working directory
echo "This script uses input: $1 on $HOSTNAME:$PWD"
```

- **Parallize the script using ARGLIST from command line:**

```
[fchen14@mike139 GNU_PARALLEL]$ parallel --wd $PWD ./cmd_ex.sh ::: A B C
This script uses input: A on mike139:/project/fchen14/GNU_PARALLEL
This script uses input: B on mike139:/project/fchen14/GNU_PARALLEL
This script uses input: C on mike139:/project/fchen14/GNU_PARALLEL
```

- **Parallize the script using ARGFILE:**

```
[fchen14@mike139 GNU_PARALLEL]$ cat argfile
A
B
C
[fchen14@mike139 GNU_PARALLEL]$ parallel --wd $PWD ./cmd_ex.sh :::: argfile
This script uses input: A on mike139:/project/fchen14/GNU_PARALLEL
This script uses input: B on mike139:/project/fchen14/GNU_PARALLEL
This script uses input: C on mike139:/project/fchen14/GNU_PARALLEL
```

- **Can parallize Python/Perl scripts, see "man parallel" for details**

Common OPTIONS --jobs (-j)

- **--jobs N (-j N)**
  - Number of jobslots on each machine (node). Run up to N jobs in parallel. 0 means as many as possible. Default is 100% which will run one job per CPU core on each machine.
  - On HPC/LONI clusters, **N** is number of jobslots per node.
  - Make sure you use GNU Parallel version **>=20161022** to avoid a "Max jobs to run" bug

```
[fchen14@mike139 test]$ parallel --version
GNU parallel 20210922
...
```

- **-j +N**
  - Add N to the number of CPU cores. Run this many jobs in parallel.
- **-j -N**
  - Subtract N from the number of CPU cores. Run this many jobs in parallel. If the evaluated number is less than 1 then 1 will be used.

Common OPTIONS --slf (Slurm)

- **--slf filename (--sshloginfile filename)**
  - To get the sshloginfile on Slurm job session, use the below command:

```
scontrol show hostname $SLURM_NODELIST > nodefile
```

  - A typical example on HPC/LONI clusters while running batch jobs:

```
--slf nodefile
```

  - Look at $SLURM_NODELIST and nodefile

```
# start an interactive job requesting 2 nodes (64x2=128 cores)
[kasetti@mike4 ~]$ srun -N2 -n128 -p workq --cpu-bind none --pty bash
srun: Job is in held state, pending scheduler release
srun: job 39474 queued and waiting for resources
Interactive job 39474 waiting:
srun: job 39474 has been allocated resources # we got mike157 and mike158
[kasetti@mike157 ~]$ echo $SLURM_NODELIST
mike[157-158]
[kasetti@mike157 ~]$ scontrol show hostname $SLURM_NODELIST > nodefile
[kasetti@mike157 ~]$ cat nodefile
mike157
mike158
```

Common OPTIONS --sshdelay

- **If many tasks are started on the same compute node, sshd can be overloaded. On SuperMike3/QB3, some of the tasks might fail to start, e.g., starting all 64/48 tasks at the same time.**
- **GNU parallel can insert a delay between each task run on the same server:**

```
[fchen14@mike139 GNU_PARALLEL]$ parallel --sshdelay 0.1 echo ::: A B C
A
B
C
```

Common OPTIONS --wd

- **`--wd mydir (--workdir mydir)`**
  - Designate the working directory of your commands.
  - A typical value can be:
    - `$PBS_O_WORDIR (PBS)`
    - `$SLURM_SUMBIT_DIR (Slurm)`

Common OPTIONS --env

- **`--env ENV_VAR`**
  - --env to tell GNU parallel to transfer an environment variable to the remote system.
  - A typical usage:

```
export OMP_NUM_THREADS=5
parallel --env OMP_NUM_THREADS cmd ::: ARGLIST
```

Common OPTIONS --progress

- **--progress**
  - Show progress of computations. (**Not recommended for batch jobs**)
  - List the computers involved in the task with number of CPU cores detected and the max number of jobs to run.
  - After that show progress for each node: number of running jobs, number of completed jobs, and percentage of all jobs done by this computer.
  - Example:

```
[fchen14@mike139 ~]$ parallel --progress echo ::: A B C

Computers / CPU cores / Max jobs to run
1:local / 64 / 3

Computer:jobs running/jobs completed/%of started jobs/Average seconds to complete
local:3/0/100%/0.0s A
local:2/1/100%/1.0s B
local:1/2/100%/0.5s C
local:0/3/100%/0.3s
```

- See also **--bar**

Common OPTIONS --joblog

- **--joblog logfile**
  - Creates a record for each completed subjob (task) to be written to LOGFILE, with info on how long they took, their exit status, etc.
  - Can be used to identify failed jobs, e.g.:

```
[fchen14@mike139 misc]$ parallel --joblog logfile exit ::: 1 2 0 0
[fchen14@mike139 misc]$ cat logfile
Seq     Host    Starttime       JobRuntime      Send    Receive Exitval Signal  Command
1       :       1477514132.358      0.019       0       0       1       0       exit 1
2       :       1477514132.375      0.003       0       0       2       0       exit 2
3       :       1477514132.376      0.002       0       0       0       0       exit 0
4       :       1477514132.377      0.003       0       0       0       0       exit 0
```

Common OPTIONS `--timeout`

- **`--timeout secs`**
  - Time out for command. If the command runs for longer than secs (seconds) it will get killed.
  - If secs is followed by a % then the timeout will dynamically be computed as a percentage of the median average runtime. Only values > 100% will make sense.

  - Useful if you know the command has failed if it runs longer than a threshold.

- **Download the material for this training at:**
  - wget http://www.hpc.lsu.edu/training/weekly-materials/Downloads/gnu_parallel_tut-main-fall2025.tar.gz

Introduction to GNU Parallel

Serial Jobs Example

LAMMPS Introduction

- **LAMMPS is a classical molecular dynamics code with a focus on materials modeling. https://www.lammps.org/**
- **You don't need any background in molecular dynamics/LAMMPS to understand today's example.**
- **Typical LAMMPS Syntax**
  - Serial run

```
lmp_serial -in in.script
```

  - Multi-Threaded run

```
env OMP_NUM_THREADS=4 lmp_omp -sf omp -in in.script # use OMP_NUM_THREADS
lmp_omp -sf omp -pk omp 5 -in in.script # use -pk omp to specify threads
```

  - MPI run

```
srun --overlap -n 4 lmp_mpi -in in.script # Slurm version, --overlap only needed for interactive job
mpirun -n 4 lmp_mpi -in in.script # PBS version
```

  - Custom command:

```
lmp_serial -var nsteps 200 –in in.script # we defined a custom variable in the input file to let nsteps control total steps to run,
The above command will run our input for 200 steps
```

LAMMPS Input File Used Today

```
# 3d Lennard-Jones melt
variable  x index 1
variable  y index 1
variable  z index 1
variable  xx equal 80*$x
variable  yy equal 80*$y
variable  zz equal 80*$z
units                  lj
atom_style             atomic
lattice                fcc 0.8442
region                 box block 0 ${xx} 0 ${yy} 0 ${zz}
create_box             1 box
create_atoms           1 box
mass                   1 1.0
velocity  all create 1.44 87287 loop geom
pair_style             lj/cut 2.5
pair_coeff             1 1 1.0 1.0 2.5
neighbor  0.3 bin
neigh_modify           delay 0 every 20 check no
fix                    1 all nve
# ${nsteps} is the parameter passing from LAMMPS command line "-var nsteps 200"
run                    ${nsteps}
```

Distribute Serial Jobs LAMMPS (Slurm)

```
#!/bin/bash
#SBATCH -N 2                          # request two nodes
#SBATCH -n 128                        # specify 128 process
#SBATCH -t 2:00:00
#SBATCH -p checkpt
#SBATCH -A hpc_hpcadmin8
#SBATCH -o gp-serial.out

TASKS_PER_NODE=16
SECONDS=0
scontrol show hostname $SLURM_NODELIST > nodefile
parallel --joblog lmp.serial.log \
         -j $TASKS_PER_NODE \
         --slf nodefile \
         --workdir $SLURM_SUBMIT_DIR \
         --sshdelay 0.1 \
         `which lmp_serial` -in {} -var nsteps 200 :::: input.lst
echo "took $SECONDS sec"
```

```
[fchen14@mike2 GNU_PARALLEL]$ head input.lst
data/01.lj.in
data/02.lj.in
data/03.lj.in
data/04.lj.in
data/05.lj.in
...
```

In case the task command is too long (complex)

- **Use a script for each task to be distributed, example here (`call_lmp.sh`)**
- **GNU Parallel will distribute each task script**

```
TASKS_PER_NODE=16

scontrol show hostname $SLURM_NODELIST > nodefile
parallel --joblog lmp.serial.log \
         -j $TASKS_PER_NODE \
         --slf nodefile \
         --workdir $SLURM_SUBMIT_DIR \
         --sshdelay 0.1 \
         ./call_lmp.sh {} 200 :::: input.lst
```

```
# content of call_lmp.sh
#!/bin/bash
echo "\$1=$1,\$2=$2"
lmp_serial -in $1 -var nsteps $2
```

$2 is the input parameter 200

$1 is the input from input.lst, e.g. data/01.lj.in

Introduction to GNU Parallel

Multi-Threaded Example

Distribute Multi-Threaded Jobs

- **Distribute Multi-Threaded jobs is very similar to the pure serial job example, the only difference is** TASKS_PER_NODE**:**
  - TASKS_PER_NODE=CPU_CORES_PER_NODE / NUM_THREADS_PER_TASK
- **If each job uses 4 threads, each node on SuperMike3 has 64 cores, then**
  - TASKS_PER_NODE=64/4=16
- **Slurm script (#SBATCH comments omitted):**

```
TASKS_PER_NODE=16
export OMP_NUM_THREADS=4
SECONDS=0
scontrol show hostname $SLURM_NODELIST > nodefile
parallel -j $TASKS_PER_NODE \
         --slf nodefile \
         --workdir $WDIR \
         --sshdelay 0.1 \
         --env OMP_NUM_THREADS \
         `which lmp_omp` -sf omp -in {} -var nsteps 200 :::: input.lst
echo "took $SECONDS sec"
```

Put 64/4=16 tasks per node

Pass the environmental variable OMP_NUM_THREADS to each task

OpenMP switch in lammps

Multi-Threaded LAMMPS (Slurm)

```
#!/bin/bash
#SBATCH -N 2                          # request two nodes
#SBATCH -n 128                        # specify 128 process
#SBATCH -t 2:00:00
#SBATCH -p checkpt
#SBATCH -A hpc_hpcadmin8
#SBATCH -o gp-omp.out

TASKS_PER_NODE=16
export OMP_NUM_THREADS=4
SECONDS=0
scontrol show hostname $SLURM_NODELIST > nodefile

parallel --joblog lmp.omp.log \
         -j $TASKS_PER_NODE \
         --slf nodefile \
         --workdir $SLURM_SUBMIT_DIR \
         --sshdelay 0.1 \
         --env OMP_NUM_THREADS \
         `which lmp_omp` -sf omp -in {} -var nsteps 200 :::: input.lst
echo "took $SECONDS sec"
```

This script is on SuperMike3, 64 cores per node, so TASKS_PER_NODE=64/4=16

Use 4 OMP threads per task

OpenMP switch in lammps

Introduction to GNU Parallel

Multi-Process (MPI) Example

Distribute MPI Jobs - LAMMPS

- **This section describes how to distribute small MPI jobs.**
- **Example problem - LAMMPS MPI**
  - Using the same input file, but with multiple MPI process for each task.
  - For simplicity, each MPI process will use only one thread

Distributing MPI Jobs (Slurm)

```
#!/bin/bash
#SBATCH -N 2          # request two nodes
#SBATCH -n 128        # specify 128 process
#SBATCH -t 2:00:00
#SBATCH -p checkpt
#SBATCH -A hpc_hpcadmin8
#SBATCH -o gp-mpi.out

TASKS_PER_NODE=16
PROC_PER_TASK=4
SECONDS=0
scontrol show hostname $SLURM_NODELIST > nodefile

parallel --joblog lmp.mpi.log \
         -j $TASKS_PER_NODE \
         --slf nodefile \
         --workdir $SLURM_SUBMIT_DIR \
         --sshdelay 0.1 \
         srun --overlap -n $PROC_PER_TASK `which lmp` -in {} -var nsteps 200 :::: input.lst
echo "took $SECONDS sec"
```

```
[fchen14@mike4 GNU_PARALLEL]$ head input.lst
data/01.lj.in
data/02.lj.in
data/03.lj.in
data/04.lj.in
data/05.lj.in
...
```

This script is on SuperMike3, 64 cores per node, so TASKS_PER_NODE=64/4=16

Use 4 MPI processes per task

Running Jobs With SLURM Job Arrays

Running Jobs with SLURM Job Arrays

- **Definition:** A SLURM Job Array allows you to submit and manage a large number of similar, independent jobs efficiently using a single batch script and one submission command.
- **Purpose:** Designed for large-scale workloads (e.g., parameter sweeps, simulations, bioinformatics pipelines) where each task runs independently but under the same resource settings.
- **Job Type:** Job arrays are supported only for batch jobs (not interactive jobs).
- **Efficiency:** SLURM launches and schedules many jobs within seconds, minimizing submission overhead.
- **Configuration & Resource Specification:**
  - All array tasks share the same batch script and requested resources (CPUs, memory, time), ensuring consistency across jobs.
  - Each task receives its own independent allocation within those resources — allowing SLURM to schedule and manage them efficiently.

Running Jobs with SLURM Job Arrays

- Every task is automatically assigned a unique index, available as $SLURM_ARRAY_TASK_ID, which is commonly used to pick input/output files dynamically.
- For serial or multi-threaded workloads, SLURM handles CPU and memory distribution automatically.
- For MPI or multi-node workloads, explicitly specify --nodes, --ntasks, or --cpus-per-task as needed.

- **Advantages**
  - Simplifies and automates submission of large parameter sweeps or ensemble simulations.
  - Reduces scheduler load — one submission command for thousands of jobs.
  - Easy monitoring and management using squeue, scontrol.
  - Fault-tolerant: Failed tasks can be re-run individually using their array index.

Running Jobs with SLURM Job Arrays

- **Syntax**
  - #SBATCH --array=<index_list> or #SBATCH -a=<index_list>
  - where "index_list"
    a. **Range:** a range of index values - #SBATCH --array=**n-m**, where ***n*** is the starting index, ***m*** is the ending index
    b. **Step size:** an optional step size - #SBATCH --array=**n-m:step_length**
    c. **Specific Values**: specific array index values - #SBATCH --array=1,3,5,7
    d. **Concurrency Limit:** You can limit how many tasks run at the same time using the "%" modifier, for example, --array=0-15%4 runs only 4 tasks concurrently.

Job Arrays Environment Variables

- Job arrays will have additional environment variables set.
  - **SLURM_ARRAY_JOB_ID** - the first job ID of the array.
  - **SLURM_ARRAY_TASK_ID -** the job array index value.
  - **SLURM_ARRAY_TASK_COUNT -** the number of tasks in the job array.
  - **SLURM_ARRAY_TASK_MAX -** the highest job array index value.
  - **SLURM_ARRAY_TASK_MIN -** the lowest job array index value.
- File Names:
  - **%A** will be replaced by the value of SLURM_ARRAY_JOB_ID
  - **%a** will be replaced by the value of SLURM_ARRAY_TASK_ID.
  - Example: slurm_%A_%a.out, slurm_%A_%a.err

Running Jobs with SLURM Job Arrays

```
#!/bin/bash
#SBATCH --job-name=demo_jobarray
#SBATCH --array=1-32 #or -a 1-32
#SBATCH -o output_%A_%a.out
#SBATCH -e error_%A_%a.err
#SBATCH --time=00:02:00
#SBATCH --cpus-per-task=1

module load parallel/20210922/intel-2021.5.0
module load lammps/23Jun2022/intel-2021.5.0-intel-mpi-2021.5.1

# Read the nth line from the input list file (matching array index)
INPUT_FILE=$(sed -n "${SLURM_ARRAY_TASK_ID}p" input.lst)

echo "Running job array task $SLURM_ARRAY_TASK_ID on $(hostname)"
echo "Input file: $INPUT_FILE"

# Run LAMMPS serial mode
`which lmp_serial` -in "$INPUT_FILE" -var nsteps 100
```

Running Jobs with SLURM Job Arrays

```
#!/bin/bash
#SBATCH --job-name=demo_jobarray
#SBATCH --array=1-32 #or -a 1-32
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#SBATCH -e error_%A_%a.err
#SBATCH --time=00:02:00
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```

Defines Job array with –array or -a with <index_list>

Running Jobs with SLURM Job Arrays

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#!/bin/bash
#SBATCH --job-name=demo_jobarray
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INPUT_FILE=$(sed -n "${SLURM_ARRAY_TASK_ID}p" input.lst)

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# Run LAMMPS serial mode
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```

Defines output files with
$SLURM_ARRAY_JOB_ID
$SLURM_ARRAY_TASK_ID

Running Jobs with SLURM Job Arrays

```
#!/bin/bash
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INPUT_FILE=$(sed -n "${SLURM_ARRAY_TASK_ID}p" input.lst)

echo "Running job array task $SLURM_ARRAY_TASK_ID on $(hostname)"
echo "Input file: $INPUT_FILE"

# Run LAMMPS serial mode
`which lmp_serial` -in "$INPUT_FILE" -var nsteps 100
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$SLURM_ARRAY_TASK_ID

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#SBATCH --job-name=demo_jobarray
#SBATCH --array=1-32 #or -a 1-32
#SBATCH -o output_%A_%a.out
#SBATCH -e error_%A_%a.err
#SBATCH --time=00:02:00
#SBATCH --cpus-per-task=1

module load parallel/20210922/intel-2021.5.0
module load lammps/23Jun2022/intel-2021.5.0-intel-mpi-2021.5.1

# Read the nth line from the input list file (matching array index)
INPUT_FILE=$(sed -n "${SLURM_ARRAY_TASK_ID}p" input.lst)

echo "Running job array task $SLURM_AR
echo "Input file: $INPUT_FILE"

# Run LAMMPS serial mode
`which lmp_serial` -in "$INPUT_FILE" -var nsteps 100
```

Input files indexed with $SLURM_ARRAY_TASK_ID

GNU Parallel
vs
SLURM Job Arrays

GNU Parallel vs. Job Arrays

GNU Parallel

Job arrays

GNU Parallel vs. Job Arrays

GNU Parallel	Execution Scope	Job arrays
Runs commands locally within an existing allocation		Each array element is submitted to the scheduler as a separate job

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GNU Parallel vs. Job Arrays

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Appears as one job to the scheduler	Visibility	Every task has its own job ID and status

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GNU Parallel vs. Job Arrays

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Basic progress output from GNU Parallel	Monitoring tools	Full integration with cluster tools like squeue, qstat

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Basic progress output from GNU Parallel	Monitoring tools	Full integration with cluster tools like squeue, qstat
File conversions, preprocessing, small parameter sweeps	Typical use cases	Genome analyses, simulations, large-scale sweeps

Introduction to GNU Parallel

Proper Usage of GNU Parallel

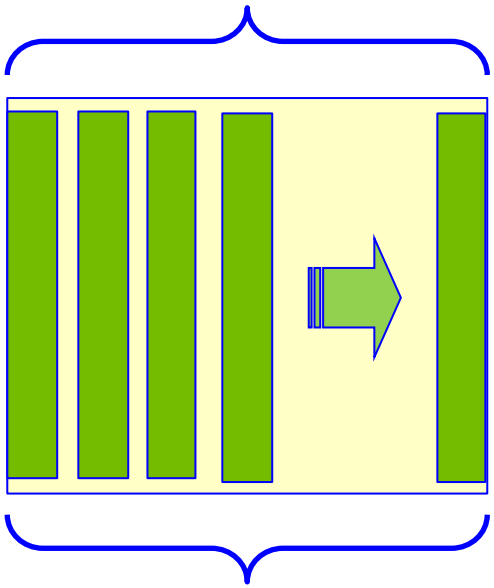
Common Rules

- Don't use more than one node when you are debugging/testing your code
- Know the performance of single task
- Start with only a few tasks in your **`input.lst`**
- **After you are comfortable with one node job, start with two node job first before jumping to more than three nodes**
- **Typically use no more than 5 nodes.**

Memory Consideration

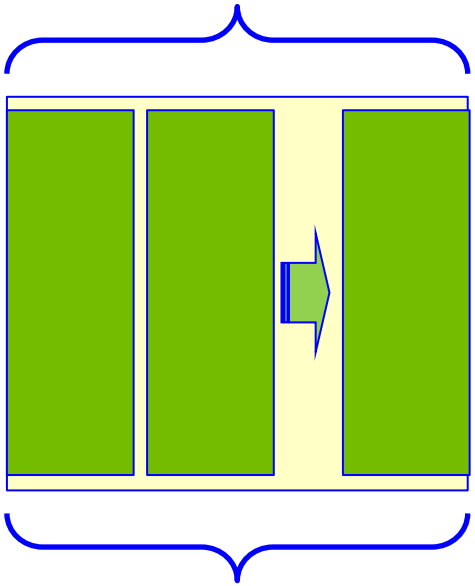
- Relationship between node memory and cores
  - Rule of Thumb: cannot exceed the available memory on a node

Available node memory 256 GB



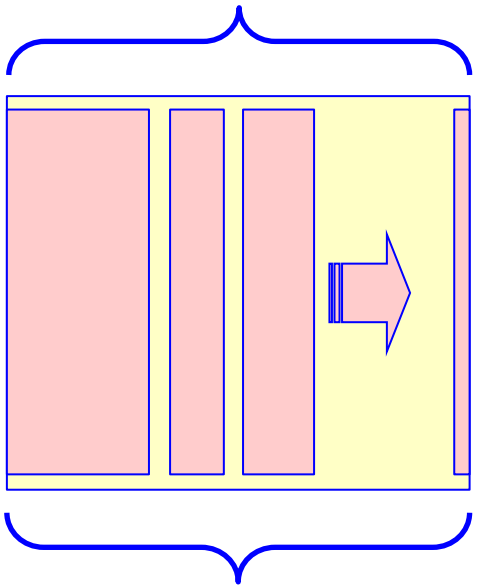
4 GB mem per task,
How many tasks per node?

Available node memory 256 GB



8 GB mem per task,
How many tasks per node?

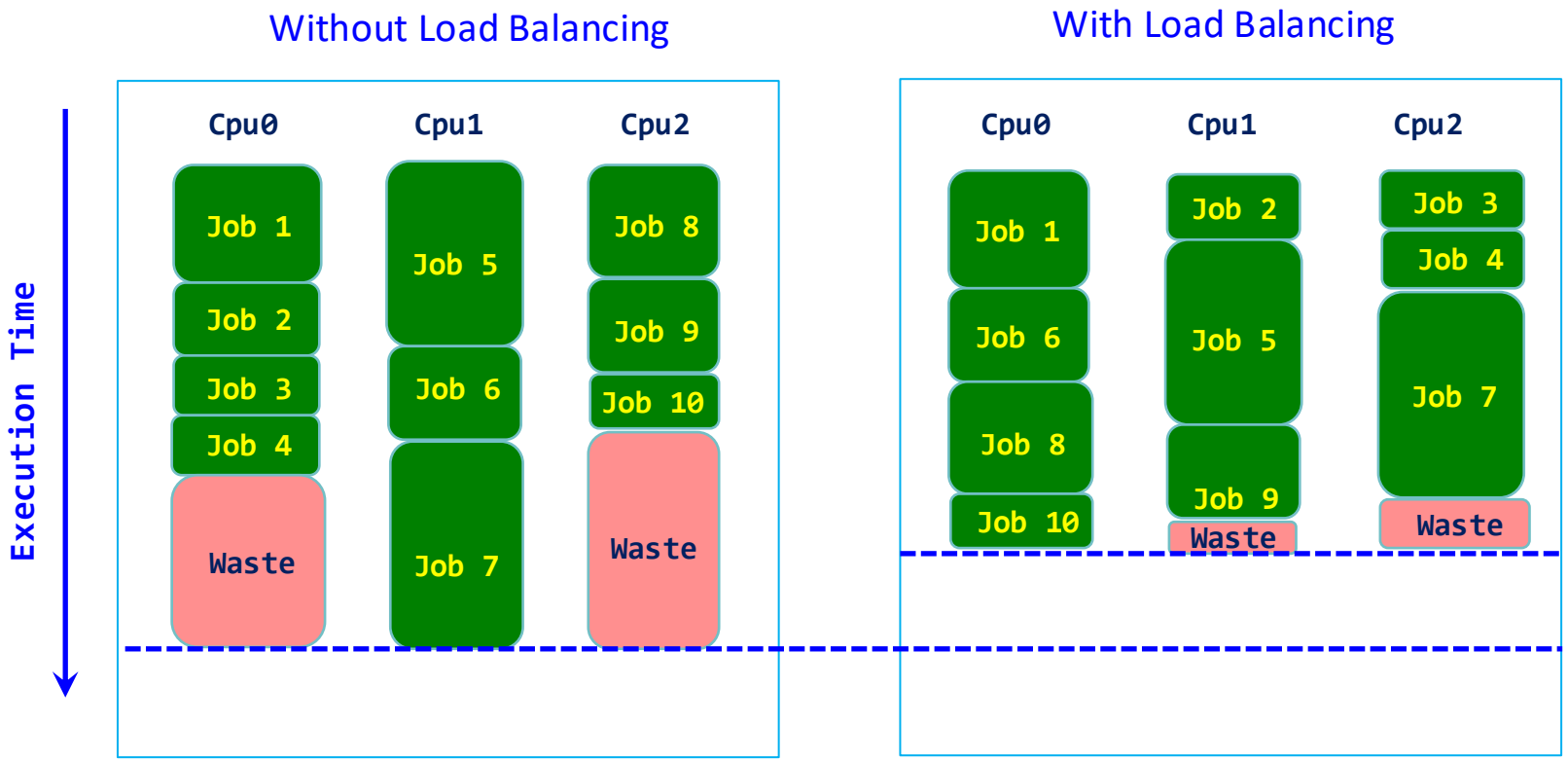
Available node memory 256 GB



Avoid this situation, hard to calculate/predict memory usage

Load Balancing in GNU Parallel

- **GNU Parallel spawns the next job when one finishes - keeping the CPUs active and thus saving time.**

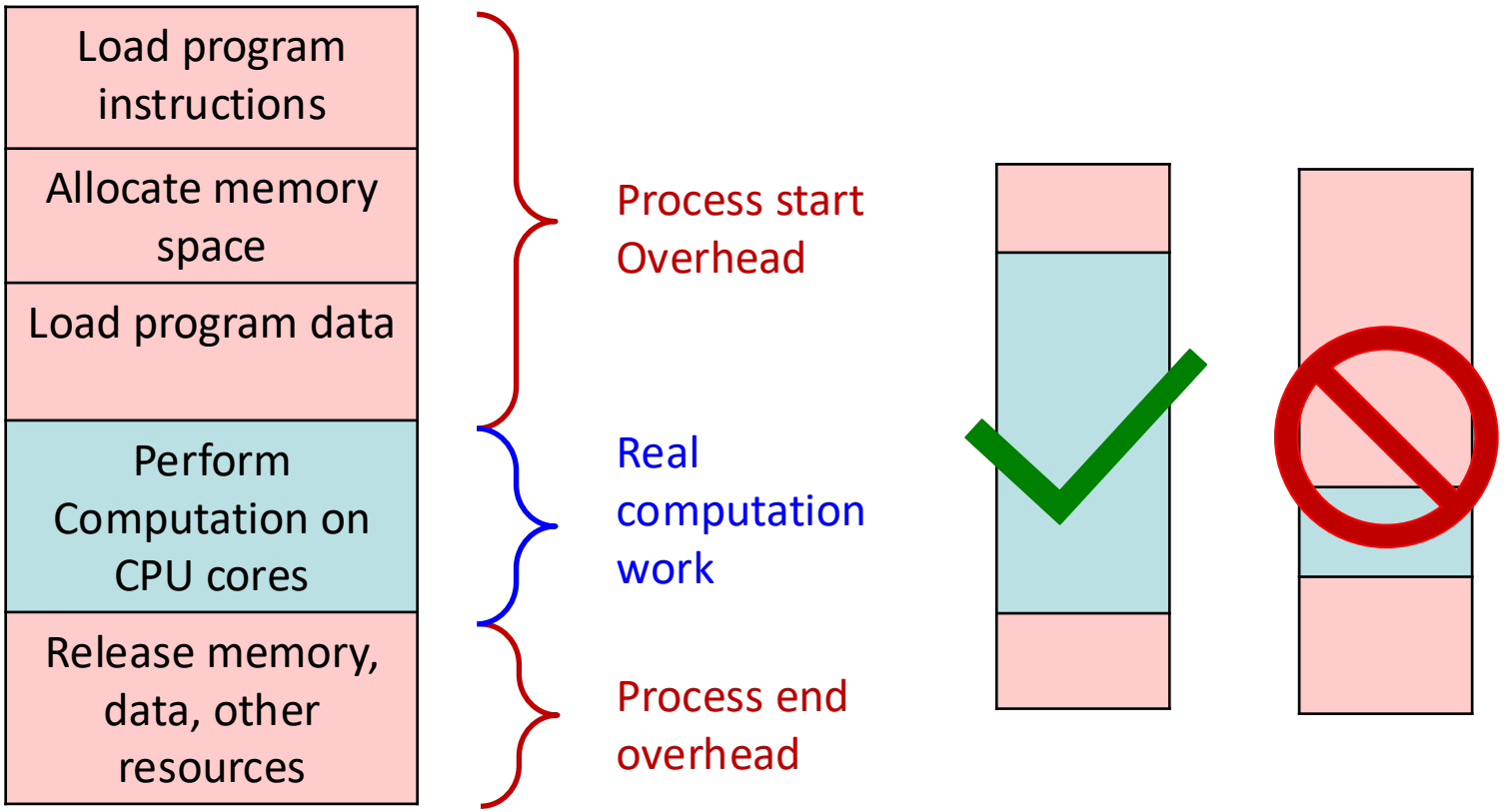


Task Granularity

- **In parallel computing, granularity (or grain size) of a task is a measure of the amount of work (or computation) which is performed by that task.**
- **Impact of granularity on performance**
  - Using fine grains or small tasks results in more parallelism and hence increases the speedup. However, synchronization overhead, scheduling strategies etc. can negatively impact the performance of fine-grained tasks.
  - Simply increasing parallelism alone cannot give the best performance.
  - In order to reduce the communication overhead, granularity can be increased. Coarse grained tasks have less communication overhead but they often cause load imbalance. Hence optimal performance is achieved between the two extremes of fine-grained and coarse-grained parallelism.

Ref: https://en.wikipedia.org/wiki/Granularity_(parallel_computing)

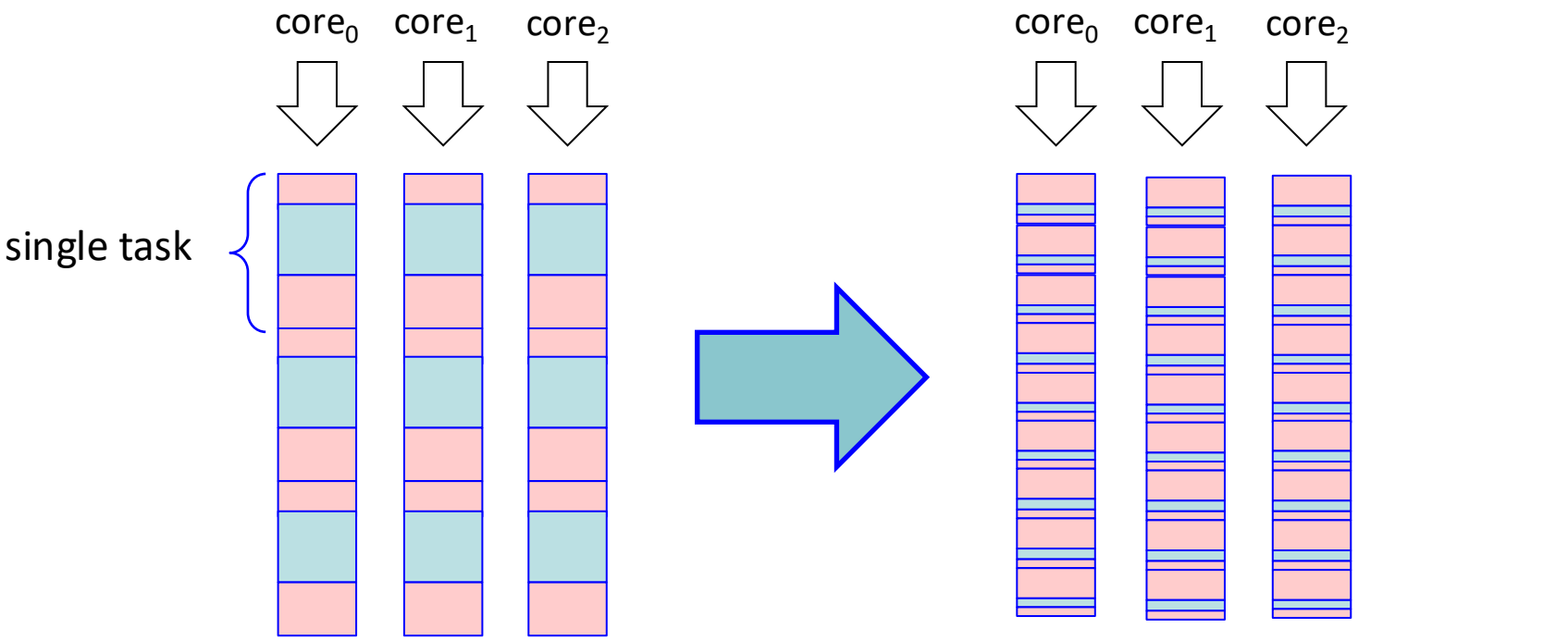
Components of a Task (Process)



Typical Misuse - Tiny grain size case

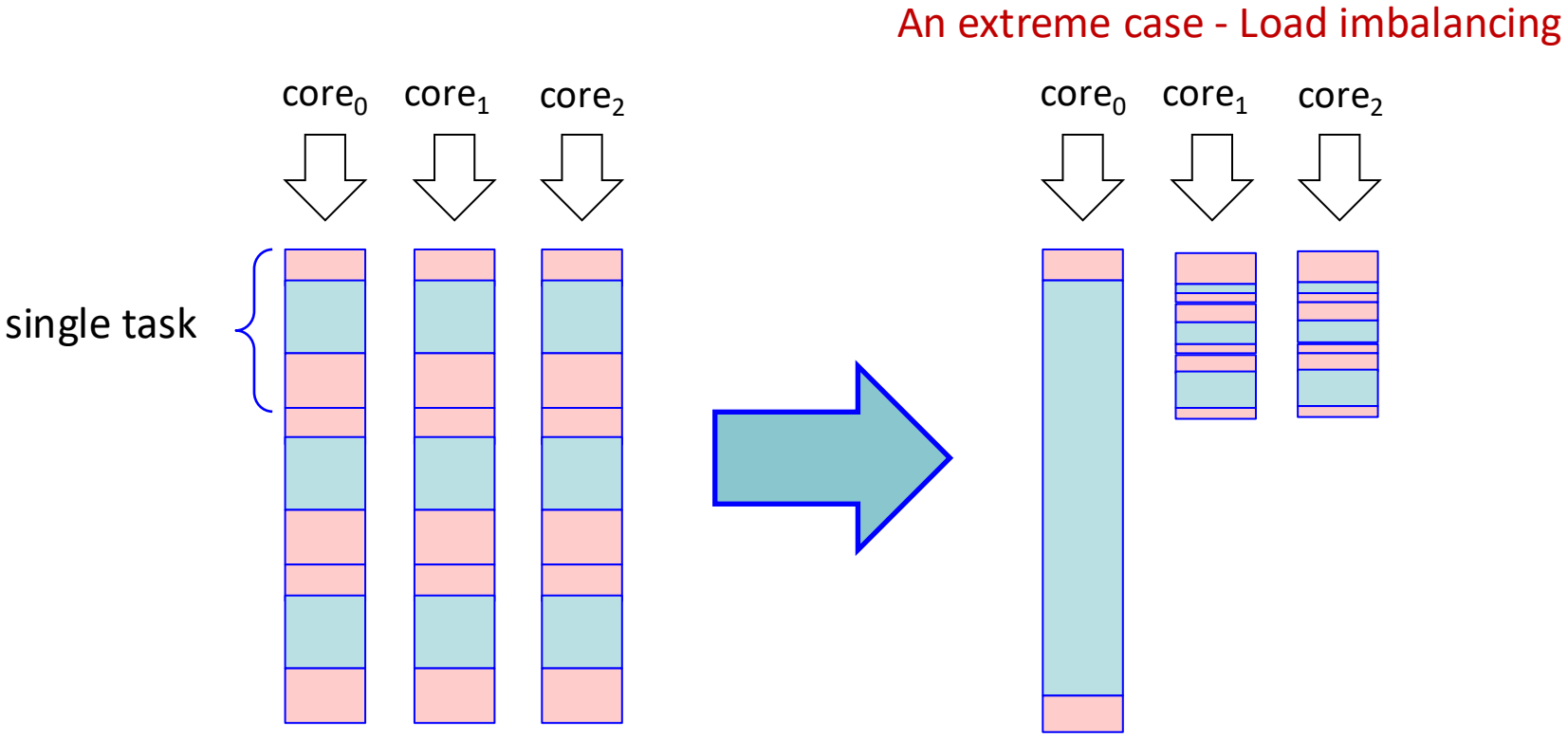
- **Tiny grain size**
  - E.g., each task takes little time (e.g., less than a second)
  - Most time will be spent on overhead

An extreme case - Cores are just idling



Typical Misuse - Large grain size case

- **Large grain size**
  - Some tasks are much longer than the rest
  - Load balancing can never be achieved



Proper Usage of Job Arrays

- **Best Practices:**
  - Use for many similar, independent tasks (e.g., simulations, parameter sweeps).
  - Use $SLURM_ARRAY_TASK_ID to assign unique inputs/outputs per task.
  - Limit concurrency with % (e.g., --array=1-1000%50) to control system load.
  - Avoid tiny jobs — combine short tasks to reduce overhead.
  - Organize output files with %A and %a in names.
  - Re-run failed tasks by specifying their indices (e.g., --array=5,9,13).

Summary

- **In today's training, we have covered**
  - Why need GNU Parallel or SLURM Job arrays?
  - Basic syntax of GNU Parallel and examples
  - How to run jobs with Job arrays?
  - How to use these tools wisely.

- **For more information about GNU Parallel and SLURM Job Arrays, refer to:**
  - https://www.gnu.org/software/parallel/parallel_tutorial.html
  - https://slurm.schedmd.com/job_array.html

Appendix

Introduction to GNU Parallel

Multi-Process (MPI) Example

Distribute MPI Jobs - LAMMPS

- **This section describes how to distribute small MPI jobs.**
- **Example problem - LAMMPS MPI**
  - Using the same input file, but with multiple MPI process for each task.
  - For simplicity, each MPI process will use only one thread

Distributing MPI Jobs (Slurm)

```
#!/bin/bash
#SBATCH -N 2          # request two nodes
#SBATCH -n 128        # specify 128 process
#SBATCH -t 2:00:00
#SBATCH -p checkpt
#SBATCH -A hpc_hpcadmin8
#SBATCH -o gp-mpi.out

TASKS_PER_NODE=16
PROC_PER_TASK=4
SECONDS=0
scontrol show hostname $SLURM_NODELIST > nodefile

parallel --joblog lmp.mpi.log \
         -j $TASKS_PER_NODE \
         --slf nodefile \
         --workdir $SLURM_SUBMIT_DIR \
         --sshdelay 0.1 \
         srun --overlap -n $PROC_PER_TASK `which lmp` -in {} -var nsteps 200 :::: input.lst
echo "took $SECONDS sec"
```

```
[fchen14@mike4 GNU_PARALLEL]$ head input.lst
data/01.lj.in
data/02.lj.in
data/03.lj.in
data/04.lj.in
data/05.lj.in
...
```

This script is on SuperMike3, 64 cores per node, so TASKS_PER_NODE=64/4=16

Use 4 MPI processes per task

Distributing MPI Jobs (PBS)

```
#!/bin/bash
#PBS -l nodes=2:ppn=20
#PBS -l walltime=1:00:00
#PBS -q checkpt
#PBS -A hpc_hpcadmin8
#PBS -j oe
#PBS -o gp-omp-pbs.out

module purge
module load parallel
module load lammps
TASKS_PER_NODE=4
SECONDS=0
cd $PBS_O_WORKDIR
parallel --joblog lmp.mpi.pbs.log \
         -j $TASKS_PER_NODE \
         --slf $PBS_NODEFILE \
         --workdir $PBS_O_WORKDIR \
         --sshdelay 0.1 \
         mpirun -np 5 `which lmp` -in {} -var nsteps 200 :::: input.lst
echo "took $SECONDS sec"
```

```
[fchen14@mike4 GNU_PARALLEL]$ head input.lst
data/01.lj.in
data/02.lj.in
data/03.lj.in
data/04.lj.in
data/05.lj.in
...
```

This script is on SuperMIC, 20 cores per node, so TASKS_PER_NODE=20/5=4

Use 5 MPI processes per task