



Clusters formation

Introduction

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<https://espri.ipsl.fr/about-espri/acknowledgement/>



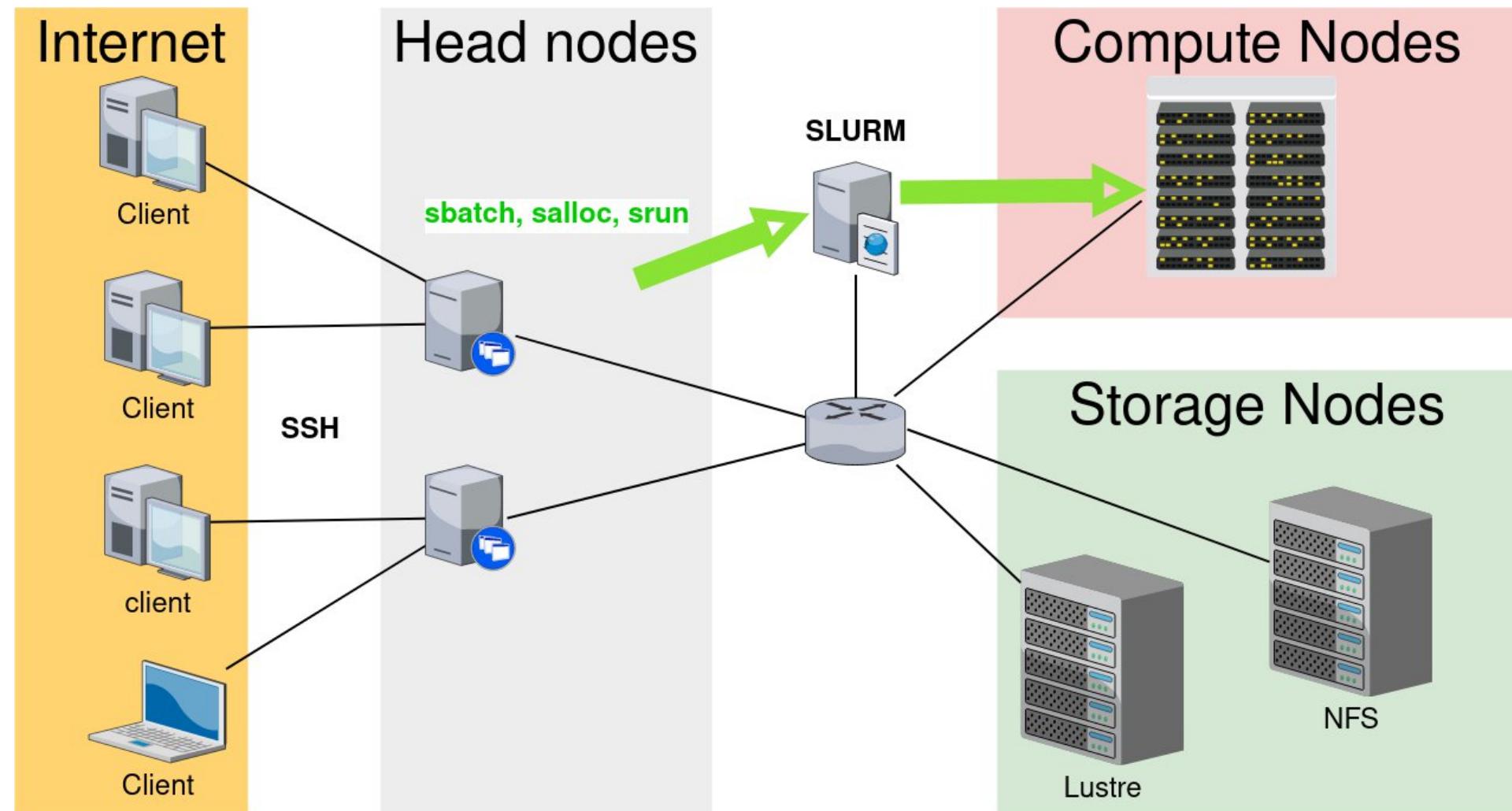
- **IPSL Clusters** [https://documentations.ipsl.fr/spirit/getting_started/cluster.html]
- Node hardware and architecture [socket, core, memory (NUMA), GPU]
 - https://documentations.ipsl.fr/spirit/spirit_clusters/computing_nodes.html
- SLURM (Job Management) [<https://documentations.ipsl.fr/spirit/common/slurm.html>]
- Software and modules [https://documentations.ipsl.fr/spirit/common/module_command.html]
- Storage spaces and I/O https://documentations.ipsl.fr/spirit/spirit_clusters/user_spaces.html
- Container with apptainer [singularity successor]
- IPSL support [meso-support]
 - https://documentations.ipsl.fr/spirit/getting_started/support.html

IPSL clusters



Head Nodes:

- IPSL-SU, Spirit:
 - spirit1.ipsl.fr
 - spirit2.ipsl.fr
- IPSL-X, SpiritX:
 - spiritx1.ipsl.fr
 - spiritx2.ipsl.fr
- IPSL-G, HAL:
 - hal.ipsl.fr





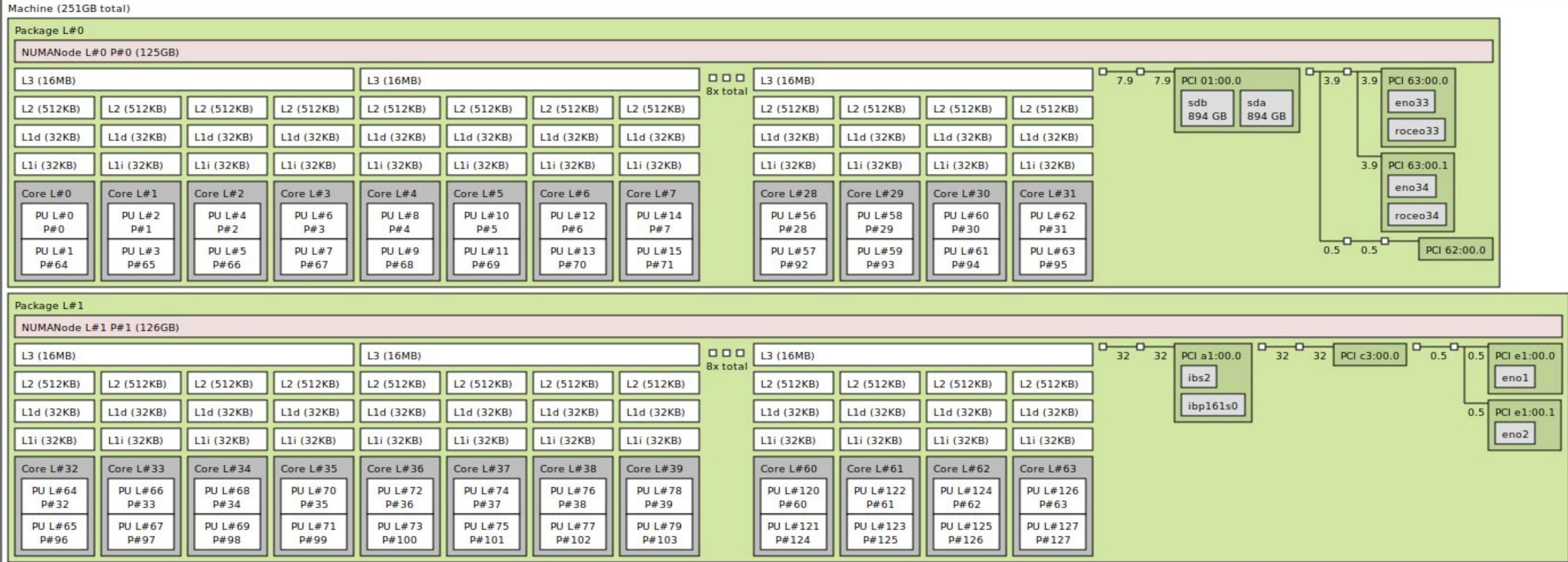
A cluster is like a hotel complex

Cluster	Hotel Complex
User	Client
Head Node	Entrance building
Slurm Resource Manager (controller)	Reception + reservation system
Node	Room building (2 floors)
Socket	Floor
Memory	Room surface
Core	Bed(2 places)
GPU	Balcony
Zen4 Partition node	Standard room building
Zen16 Partition node	Premium room building (suite)



- IPSL clusters [https://documentations.ipsl.fr/spirit/getting_started/cluster.html]
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Node architecture: zen4 partition (Spirit/SpiritX)



IPSL-X, SpiritX / IPSL-SU, Spirit

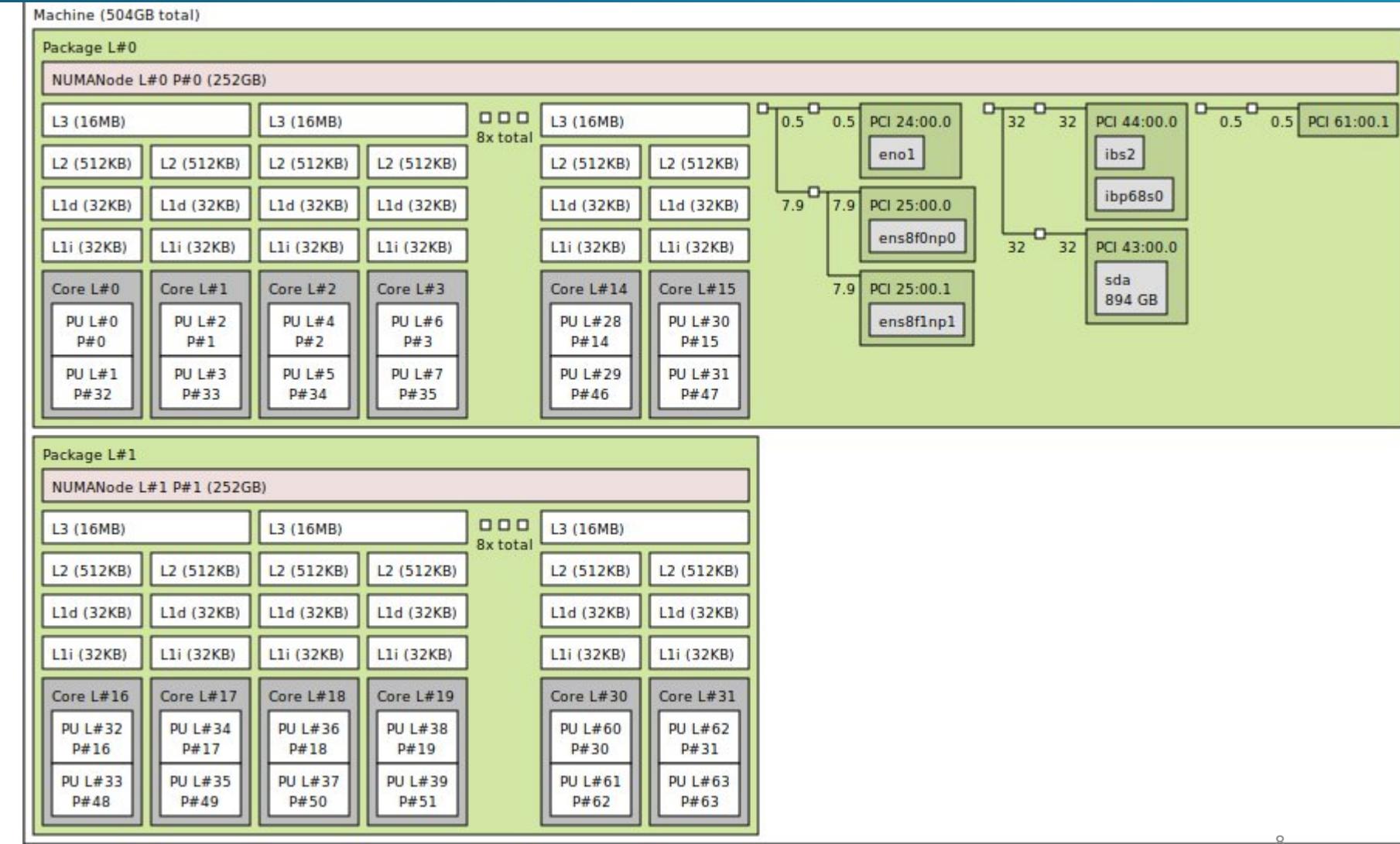
AMD ZEN2 (10K€) processor: 2 sockets, 32 Cores per socket, 4 Go memory per core 3840Mo/core for job .
NUMA: Non Uniform Memory Access

Accessing memory from one socket to another is really slower



Node architecture: zen16 partition (Spirit/SpiritX)

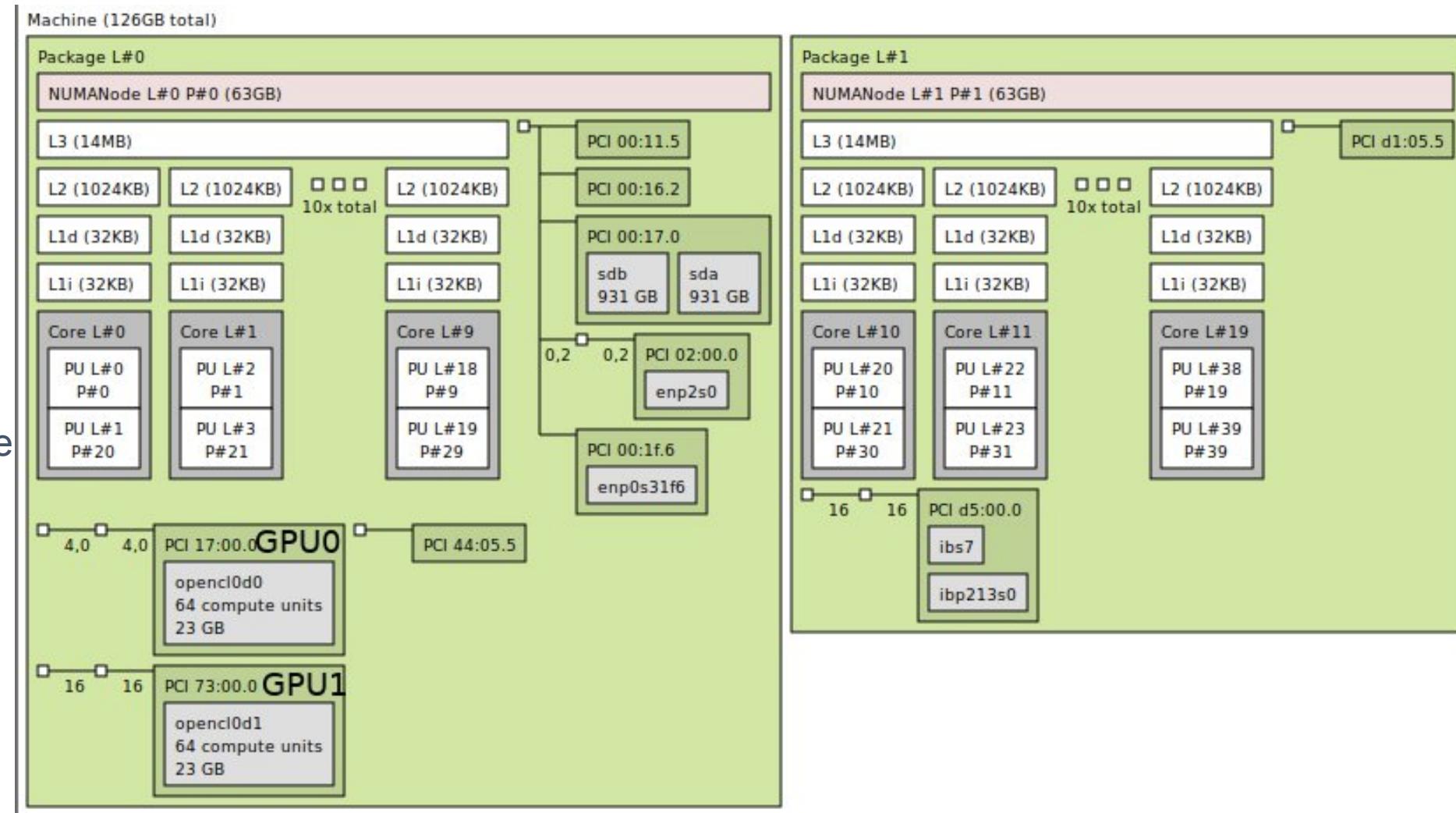
- IPSL-X, SpiritX
- IPSL-SU, Spirit
- AMD ZEN2 processor(7K€)
- 2 sockets
- 16 cores per socket
- Memory/core: 16 Go
- Memory/core for job: 15872Mo





Node architecture: GPU (HAL)

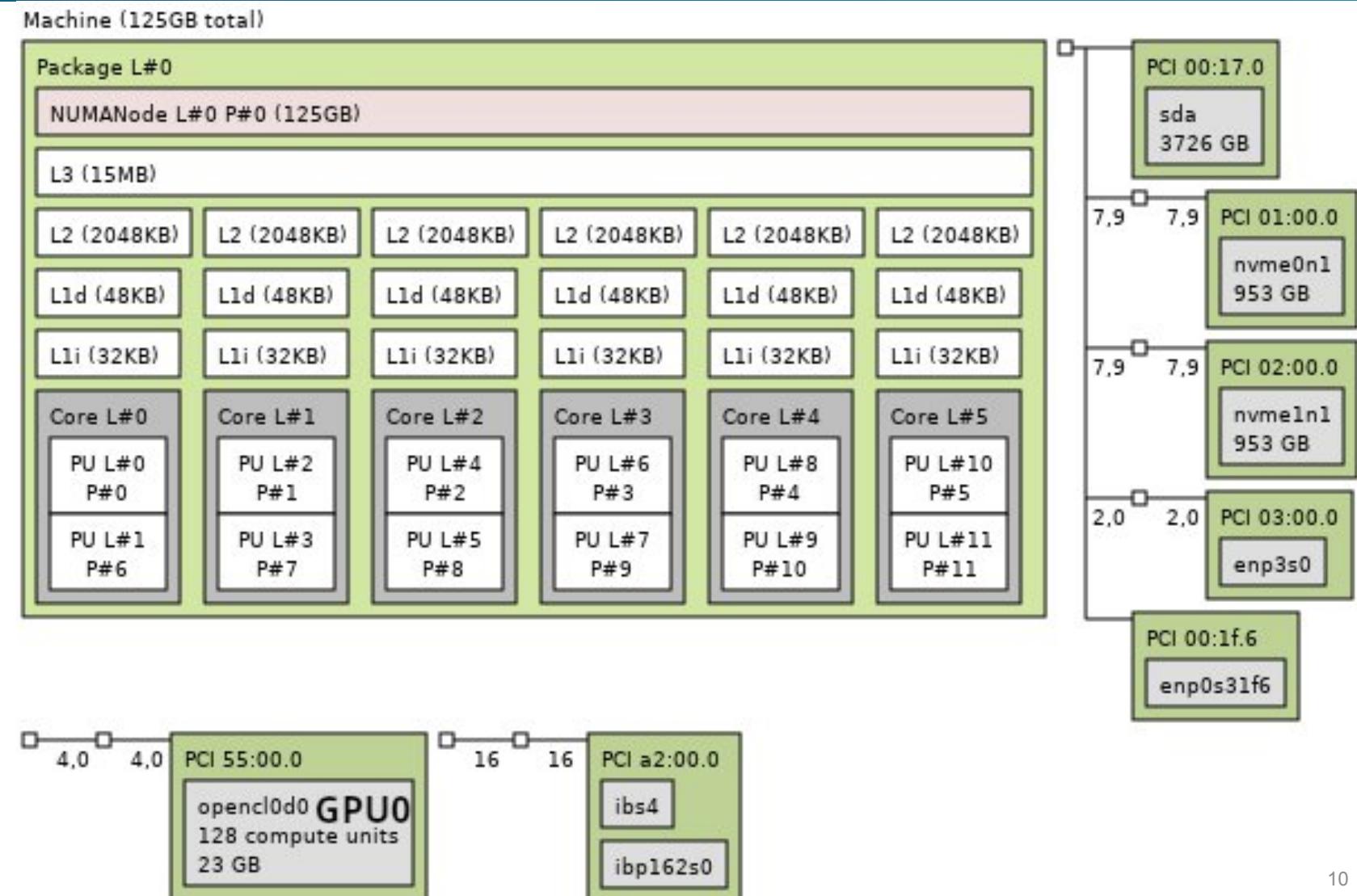
- IPSL-G, HAL
- INTEL processor
- 1 or 2 sockets
- 6 to 10 cores per socket
- Memory per core : variable
- GPUs: 1 per socket





Node architecture: GPU (HAL)

- IPSL-G, HAL
- INTEL processor
- 1 socket
- 6 core
- Memory per core : variable
- GPUs: 1





- IPSL clusters
- Node architecture
- **SLURM (Job Management)** (<https://documentations.ipsl.fr/spirit/common/slurm.html>)
 - **Introduction**
 - Computing task types (serial, parallel, distributed, hybrid)
 - Job types and job submission (interactive/batch)
 - Job array
 - Pipeline of jobs (dependency, chaining and recursive)
 - Job practice
 - Jobs control commands
 - Jobs monitoring, statistics and best practices



SLURM: Simple Linux Utility for Resource Management

Slurm is an orchestrator that manages jobs on a cluster

- Resources are:
 - **nodes**,
 - **CPU cores**,
 - **memory**,
 - **time**,
 - **GPUs**,
 - etc.
- **Resources requested are exclusive to a job**:
 - Nodes can host different jobs, but
 - Memory and CPU cores are never shared between the jobs.
- **Only request the necessary resources**: check resource utilization!

SLURM: resources and partitions



spirit - spiritx : see “**check-cluster**” command

Partitions limit	mem/cpu	time	NB node max
zen4 (default)	3 840 Mo/cpu max:64cpu	default 1h Max: 168h	1
zen16	15 872 Mo/cpu max:32cpu	default 1h Max: 72h	1

Interactive job : max time 10h and only one per user

Users limit	CPU max	MEM max	NB Jobs max	MaxSubmitJobs
Internal Users	96	256G	64	1000
External Users	48	128G	32	500

HAL: see “**check-cluster**” command

Partitions limit	GPU	time	NB Jobs max	MaxSubmitJobs
interactive (default)	max: 2	default: 1h Max: 10h	2	500
batch	max: 2	default: 1h Max: 72h	2	500



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Slurm computing task types



- **Sequential**: 1 node, 1 process, 1 computation at the same time on 1 CPU core
- **Parallel** (memory shared): only on 1 node, 1 process, several computations at the same time on different CPU cores
 - OpenMP
 - POSIX Threads
 - Some functions of certain Python computation libraries (not all functions of Numpy!)
- **Distributed**: same or different nodes, several processes that communicate with each other, 1 computation at the same time per process on 1 CPU core
 - MPI
 - Multiple Slurm jobs or Slurm job arrays
 - Python Dask
- **Hybrid**: distributed and parallel
 - MPI + OpenMP / POSIX threads
 - Python Dask with some functions of certain Python computation libraries



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Two types of SLURM job:

- Interactive (max 10 hours on all clusters and only one per user on Spirit[X], 2h for HAL).
 - Enable foreground computing and exploratory development (like JupyterLab).
 - Enable IO adjustments (ex: computation parameters, plots, etc.)
 - Debug scripts.
 - Disconnection ends the job!
- Batch
 - Enable background computing without any user interaction.
 - Jobs run even while the users are not connected.
 - Enable running several jobs (user limit) at the same time and queue several others (<= 1000).
 - Job parameters are given by shell script (ex: Bash).

Job submission: interactive job



Interactive jobs are submitted using the command `srun` with `--pty` option and the argument `bash`.

Syntax: `srun --pty [option1] [options2] [...optionsn] bash`

Example of the submission of an interactive job with default resources (1 node, 1 task, 1 CPU core, 1 hour, default partition `zen4`, default associated partition memory 4 Go) on Spirit:

```
user@spirit1:~$ srun --pty bash
user@spirit64-04:~$ slqueue --me # Display user's submitted jobs.
      JOBID PARTITION      NAME     USER   ST       TIME   NODES NODELIST(REASON)
        643373      zen4      bash    user     R       0:57       1 spirit64-04
user@spirit64-04:~$ # Do some cool stuff!
```



Job submission interactive job: srun options

- General options

```
--x11           # Enable x11 forwarding(Graphic).  
--partition=<string> # Set the partition. zen4 (default) or zen16 on Spirit[X] clusters ;  
interactive or batch on HAL.  
--time=<dd-HH:mm:ss> # The maximum elapsed time. Must fit the partition limit!
```

- Resources options (ignored on HAL except --gpus)

- Absolute options

```
--ntasks=<integer>   # The total number of tasks/processes.  
--mem=<integer><g|m> # The total amount of memory. Also influences the number of CPU cores!  
--gpus=[ampere:|turing:|ada:]<1|2> # The total number of GPU and their architecture, only on HAL.
```

- Relative options

```
--ntasks-per-node=<integer>   # The number of tasks/processes executed per node (distributed jobs)  
--cpus-per-task=<integer>     # The number of CPU cores per task/process (parallel jobs)  
--mem-per-cpu=<integer><g|m> # The amount of memory requested per CPU core.
```

Job submission interactive job: examples 1/2



1. Request an interactive job on Spirit[X] zen4 with the shell Bash, enabling X11 forwarding, leveraging 6 GB memory and 2 CPU cores, during up to 2 hours:

```
user@spirit1:~$ srun --pty --x11 --mem 6G --time 2:00:00 bash
```

2. Request an interactive job on Spirit[X] zen16 with the shell Bash, enabling X11 forwarding, leveraging 6 GB memory and 1 CPU cores, during up to 2 hours:

```
user@spirit1:~$ srun --pty --x11 --partition zen16 --mem 6G --time 2:00:00 bash
```

3. Request an interactive job on Spirit[X] zen4 with the shell Bash, leveraging 16 GB memory and 4 CPU cores, during 1 hour:

```
user@spirit1:~$ srun --pty --cpus-per-task=4 bash
```

4. Request an interactive job on HAL interactive with the shell Bash, leveraging 1 GPU and eventually competing for the memory and CPU cores of the node with the other jobs, during up to 2 hours:

```
user@hal:~$ srun --pty --gpus=1 --time 2:00:00 bash
```

Job submission interactive job: examples 2/2



5. Request an interactive job on HAL interactive with the shell Bash, leveraging 2 turing GPU and all the memory and CPU cores of the node, during up to 2 hours:

```
user@hal:~$ srun --pty --gpus=turing:2 --time 2:00:00 bash
```

Batch job: slurm script



Slurm script

```
#!/bin/bash  
#SBATCH ...  
#SBATCH ...  
#SBATCH ...
```

```
python my_script.py
```

Computation script / binary

```
print("Hello World")
```

Interpreted by SLURM and
Bash **on head node**

Interpreted by Python
on computing node

Batch job: submission



Batch jobs are submitted using the command `sbatch`.

Syntax:

```
sbatch [option1] [option2] <slurm_script_path> [slurm_script_arg1] [slurm_script_arg2]
```

Example of the submission of a batch job with default resources (1 node, 1 task, 1 CPU core, 1 hour, default partition, default associated partition memory) on Spirit:

```
job id -----  
user@spirit1:~$ sbatch script.slurm  
Submitted batch job 645486  
user@spirit1:~$ ls  
script.slurm slurm-645486.out
```

```
#!/bin/bash  
echo 'hello world'  
=====TASK PROLOG=====  
Job 645486 submitted on cluster spirit from spirit1.ipsl.fr  
Job 645486 submitted by user xxxx with account yyyy  
Job 645486 is running with 1 nodes and 1 cores on spirit64-0  
Job 645486 memory requirements are 3840 MB per node  
Job 645486 starting at 2023/12/18 14:42:25  
=====  
hello world
```

Batch job: sbatch options



The `sbatch` options are the same as the options of `srun`. The slurm script may contain job specs (sbatch instructions ; next slide). The `sbatch` line options may supersede the sbatch instructions.

▪ More general options

```
--mail-user=<email address>          # Specify an email address.  
--mail-type=<ALL|BEGIN|END|FAIL|...> # Send an email according to the argument.  
--job-name=<string>      # The name of the job.  
--chdir=<dir_path>        # Change directory before executing the script.  
--output=<file_path>       # Log the standard output.  
--error=<file_path>        # Log the error output. Can be the same file as the standard output.
```

▪ More resources options (ignored on HAL)

▪ Absolute options

```
--nodes=<integer>    # The total number of nodes (distributed jobs).  
--ntasks=<integer>   # The total number of tasks/processes (distributed jobs).
```

▪ Relative options

```
--ntasks-per-node=<integer> # The number of tasks/processes executed per node (distributed jobs).
```

Batch job: sbatch script instructions



Sbatch script instructions are made up with the previous options prefixed with a hash tag (a second hash tag disables the instruction). **Sbatch instructions must be located at the beginning of the slurm scripts.**

```
#!/bin/bash # This instruction is not part of the sbatch instructions, but it is mandatory!
#SBATCH --partition=<string> # Set the partition. zen4 or zen16 on Spirit[X] and batch on HAL.
#SBATCH --time=<dd-HH:mm:ss> # The maximum elapsed time. Must fit the partition limit!
etc.
```

Shell environment variables automatically set by Slurm:

- SLURM_JOB_ID
- SLURM_JOB_START_TIME
- And many more!

Sbatch instruction environment variables automatically set by Slurm:

- %j # job identifier (ex: 645486)
- %u # user name
- %x # job name
- And more.

Batch job: submission examples 1/4



1. Submit a batch job, requesting 1 node, 1 task, 2 CPU cores and 8 Go memory ([zen4](#)) during 2 hours:

```
user@spirit1:~$ sbatch script.slurm ----->
```

Command line options add some flexibility!

```
#!/bin/bash  
#SBATCH --time=2:00:00  
#SBATCH --cpus-per-task=2  
# do some cool stuff!
```

2. The same, but 30 Go memory and during up to 3 hours:

```
user@spirit1:~$ sbatch --time=3:00:00 --mem=30g --partition zen16 script.slurm
```

3. Slurm script for a parallel OpenMP batch job:

```
#!/bin/bash  
  
#SBATCH --cpus-per-task=2  
  
module purge  
  
module load gcc/9.4.0 openblas/0.3.17-openmp  
  
export OMP_NUM_THREADS=$SLURM_CPUS_PER_TASK  
  
cd /path/to/my/environment  
  
./my_binary
```

Batch job: submission examples 2/4



4. Slurm script for a POSIX threads parallel batch job, example for Python:

```
#!/bin/bash

#SBATCH --cpus-per-task=2

module purge

module load pangeo-meso/2023.04.15

export PYTHONUNBUFFERED=1 # Enable real-time standard and error outputs for Python.

python my_script.py
```

5. Slurm script for a MPI distributed batch job:

```
#!/bin/bash

#SBATCH --ntasks=2

module purge

module load gcc/11.2.0 openmpi/4.0.7

mpirun my_binary
```

Batch job: submission examples 3/4



6. Slurm script for a hybrid OpenMP/MPI batch job:

```
#!/bin/bash

#SBATCH --ntasks=2
#SBATCH --cpus-per-task=2

module purge

module load intel openmpi/4.0.7 intel-mkl/2020.4.304-openmp
export OMP_NUM_THREADS=$SLURM_CPUS_PER_TASK
mpirun my_binary
```

Batch job: submission examples 4/4



7. Slurm script for a Deep Learning training batch job on HAL:

```
#!/bin/bash  
  
#SBATCH --gpus=1  
  
module purge  
module load pytorch/2.1.2  
export PYTHONUNBUFFERED=1  
python pytorch_training_script.py
```

A complete example is available [here](#).

Batch job: passing parameters



- Submission

```
sbatch script.slurm param1 param2
```

- Slurm script

```
#!/bin/bash

#SBATCH --output=job_%j.log # Create a log file in the current directory.
#SBATCH --error=job_%j.log # Append error statements in the same file.

module purge
module load your_module
# The optional command line arguments of the job script are passed to your binary
# ($@).
my_binary $@ # Or python my_script.py $@
returned_code=$? # the returned code of the previous instruction.
echo "> script completed with exit code ${returned_code}"
exit ${returned_code}
```



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Job array offers a convenient mechanism to submit a collection of similar jobs at one time. Submitted jobs differ from their "task" id (not job id!) It is up to the user job script to exploit the task id.

Submitted jobs share the same resource specifications (but don't share the same resources!)

Advantages:

- Massive job submissions made easier (useful for optimization). Keep control of max number of running jobs.
- Unique id generator that bootstraps your parameters controller (will see).
- Only one [master] job id: convenient for cancellation, monitoring, etc.
- Maximum task id is 3000 on our Slurm configuration

Range syntax:

```
sbatch --array=<first_task_id>-<last_task_id>[%max_nb_running_jobs] <slurm_script_path> [args1] [args2]
```

Task ids are integers!

#SBATCH --array also available!

List syntax:

```
sbatch --array=<first_task_id>[,<second_task_id>] [%max_nb_running_jobs] <slurm_script_path> [args1] [args2]
```



More useful shell environment variables set:

- `SLURM_ARRAY_JOB_ID` # master job id
- `SLURM_ARRAY_TASK_ID` # task id (from the range or list)
- `SLURM_ARRAY_TASK_COUNT` # number of jobs
- `SLURM_ARRAY_TASK_MAX` # last job id < 3000 (which can be different from number of jobs!)
- `SLURM_ARRAY_TASK_MIN` # first job id

More useful sbatch instruction environment variables set:

- `%A` # master job id
- `%a` # task id

Job array example



▪ Slurm script

```
#!/bin/bash

#SBATCH --array=1,3,5%20
#SBATCH --output=job_%A_%a.log
#SBATCH --error=job_%A_%a.log

echo "I'am job ${SLURM_ARRAY_TASK_ID}/${SLURM_ARRAY_TASK_MAX}, \
part of the job array ${SLURM_ARRAY_JOB_ID} that counts ${SLURM_ARRAY_TASK_COUNT} jobs"
```

▪ Submission

```
user@spirit1:~$ sbatch script.slurm
Submitted batch job 647464
user@spirit1:~$ ls
job_647464_1.log  job_647464_3.log<-----
job_647464_5.log  script.slurm
```

```
=====
===== TASK PROLOG =====
Job 647466 submitted on cluster spirit from spirit1.ipsl.fr
Job 647466 submitted by user with account ipsl
Job 647466 is running with 1 nodes and 1 cores on spirit64-07
Job 647466 memory requirements are 4000 MB per node
Job 647466 starting at 2023/12/19 17:06:02
=====
I'am job 3/5, part of the job array 647464 that counts 334jobs
```

Job array mapping parameters 1/2



1. Passing task id as a parameter:

```
my_binary ${SLURM_ARRAY_TASK_ID} # or python my_script.py ${SLURM_ARRAY_TASK_ID}
```

Then exploit task id in code:

```
int main(int argc, char* argv[]) # for C  
import sys ; sys.argv[1] # for Python
```

2. Parameters from a specific parameters file:

```
my_binary < parameters_${SLURM_ARRAY_TASK_ID}.in
```

3. Parameters from a specific line in a parameters file:

```
my_binary $(sed -n "${SLURM_ARRAY_TASK_ID}p" parameters.in)
```

Job array mapping parameters 2/2



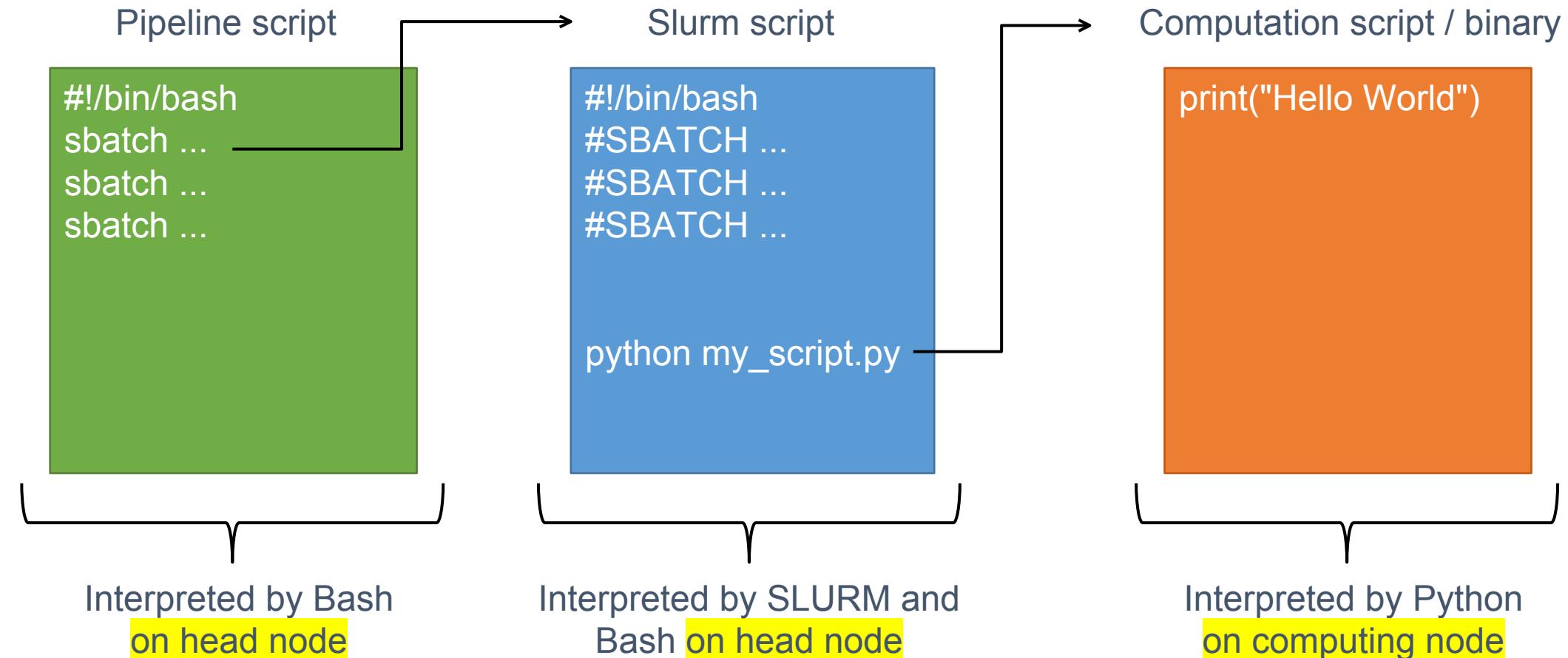
4. Fetch environment variables, example for a Python script:

```
import os  
  
slurm_task_id = int(os.environ['SLURM_ARRAY_TASK_ID'])  
  
# map slurm_task_id to a set of parameters (ex: Pandas's DataFrame index) and do cool  
stuff.
```



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Pipelines of jobs





Sbatch option `--dependency` enables various pipelines of jobs (graphs).

- Syntax

```
sbatch --dependency <dependency_type:job_id[:job_id] [,dependency_type:job_id[:job_id]]>  
sbatch --dependency <dependency_type:job_id[:job_id] [?dependency_type:job_id[:job_id]]>
```

All dependencies must be satisfied if the , separator is used (logical AND).

Any dependency may be satisfied if the ? separator is used (logical OR).

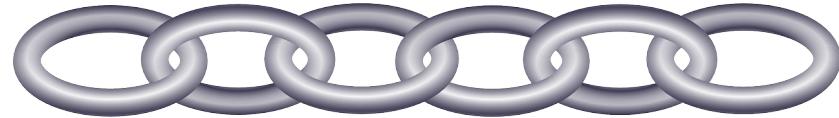
- Dependency types:

- afterok Job starts only if the dependencies have run successfully (ex: chain of jobs and barrier).
- afternotok Job starts only if the dependencies have failed (ex: cleaning/error handler jobs).
- afterany Job starts only if one of the dependencies have run successfully (ex: exploratory jobs).
- And more.



Pipeline of jobs examples 1/2

- Chain of jobs



pipeline.sh script:

```
#!/bin/bash

first_link_id=$(sbatch --parsable link_1.slurm)
second_link_id=$(sbatch --parsable --dependency=afterok:${first_link_id} link_2.slurm)
sbatch --dependency=afterok:${second_link_id} last_link.slurm
```

Script execution:

```
user@spirit1:~$ ./pipeline.sh # Don't forget to chmod +x pipeline.sh!
```

```
Submitted batch job 650560
```

```
user@spirit1:~$ squeue --me
```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST (REASON)
650560	zen4	last_lin	user	PD	0:00	1	(Dependency)
650559	zen4	link_2.s	user	PD	0:00	1	(Dependency)
650558	zen4	link_1.s	user	R	0:01	1	spirit64-02

Pipeline of jobs examples 2/2



- Job barrier

pipeline.sh script:

```
#!/bin/bash

job_id_0=$(sbatch --parsable job_1.slurm)
job_id_1=$(sbatch --parsable job_2.slurm)

sbatch --dependency=afterok:${job_id_0}:${job_id_1} barrier.slurm
```



Script execution:

```
user@spirit1:~$ ./pipeline.sh # Don't forget to chmod +x pipeline.sh!
```

```
user@spirit1:~$ squeue --me
```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST (REASON)
650603	zen4	barrier.	user	PD	0:00	1	(Dependency)
650601	zen4	job_1.sl	user	R	0:03	1	spirit64-03
650602	zen4	job_2.sl	user	R	0:03	1	spirit64-01



Recursive job: resubmit the same job inside a job with sbatch

This could cause problem if new job start before a complete end of the precedent, you must know that there is a system epilog at the end of your job causing delay

- To achieve this, the best way is :
 - sbatch must be the last command of your job
 - Run the next job only if the current is finished ok

The next command ensure the current job is really terminated before starting the next one, SLURM_JOB_ID variable contain the current jobid

```
sbatch --dependency=afterok:${SLURM_JOB_ID} script.slurm
```



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- Create a Job Array slurm script accepting two arguments *year month* and running a task for each day of month
- Create the same job using only one multitask job without job array



- Create a Job Array slurm script accepting two arguments *year month* and running a task *My_Prog* for each day of month

```
#!/bin/bash

#SBATCH --array 1-31
# fist ARG is $1 in shell
# second arg is $2 ....

if [ $# -ne 2 ];then # $# is number of argument
    echo $0 YYYY MM    # $0 is the name of the script
    exit 1
fi

YEAR="$1"
MONTH="$2"
DAY=${SLURM_TASK_ID} # problem DAY is 1 but i need 01
DAY=$(printf "%02d" ${SLURM_TASK_ID})
FILE=/bdd/dataset/truc/${YEAR}/${MONTH}/${DAY}/xx${YEAR}${MONTH}${DAY}.dat

if [ -r $FILE ]; then
    time My_prog $FILE
fi
```



- Create one Multitask Job slurm script accepting two arguments year month and running a task My_Prog for each day of month

```
#!/bin/bash
#SBATCH --ntasks 31 # number of task must be the same as number of processes
launched in background
# fist ARG is $1 in shell
# second arg is $2 ....

YEAR="$1"
MONTH="$2"
for I in {01..31} # work in bash >=4
do
    DAY=${I}
    FILE=/bdd/dataset/truc/${YEAR}/${MONTH}/${DAY}/xx${YEAR}${MONTH}${DAY}.dat
    if [ -r $FILE ];then
        time My_prog $FILE & # launch process in background and continue
    fi
done
wait # Waiting all background processes are finished
```



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- Node architecture
- **SLURM (Job Management)** (<https://documentations.ipsl.fr/spirit/common/slurm.html>)
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 - Practical
 - **Jobs control commands**
 - Jobs monitoring, statistics and best practices



- Information on nodes

`check-cluster`: homemade command that displays the cluster load and status

`sinfo`: display node and partition information

```
user@spiritx1:~$ sinfo -l
```

`pestat` : display job placement on nodes

```
user@spiritx1:~$ pestat -u user -E
```

- Information on job

`scontrol show job <job_id>`: display detailed job information

```
user@spiritx1:~$ scontrol show job xxxxxxxx
```

- Information on partition

`scontrol show partition <partition_name>`: display detailed partition information

```
user@spiritx1:~$ scontrol show partition zen4
```

Job control commands 2/2



- Homemade wrapper command using squeue to display running and pending jobs information :

```
slqueue [-h|--help] [-r|--running] [-i|-b|-p|--pending] [-m|--me] [-u user|--user user]
[-w hostname|--host hostname]
```

```
user@hal:~$ slqueue
```

JobId	State	Partition	Username	Account	Node	CPUs	Memory	Batch	TimeLeft	TimeLimit	Node/Reason
10079	RUNNING	batch	eremenko	lisa	1	4	60G	1	2-01:18:07	3-00:00:00	hal6
10101	RUNNING	interacti	vsambath	lmd	1	4	7.50G	0	9:30:16	10:00:00	hal4

- Cancel job(s):

```
scancel <job_id> [<job_id>]
```

```
user@hal:~$ scancel 10095 10345
```

SLURM job pending reason



“Why my job does not start and stay in pending state”, main reasons:

`slqueue --me --pending`

Resources: there is not enough free resources on cluster to run your job, but you're in first priority

Priority: there is not enough resources on cluster to run your job and you are not in first priority

QOSMaxCpuPerUserLimit: your running jobs hit the max number of CPU permitted for your account

QOSMaxJobsPerUserLimit: your running jobs hit the max number of job permitted for your account

QOSMaxMemoryPerUser: your running jobs hit the max sum of memory permitted for your account

ReqNodeNotAvail, Reserv: there is a reservation on cluster made by admin team for special use or maintenance and with your *TimeLimit* request, your job cannot be finished before the beginning of the reservation. For example you have requested 7 days and we have a maintenance in 3 days with full stop

`scontrol show reservation`

Dependency: you have asked dependency for this job

SLURM job end status



Possible status after job end:

COMPLETED: all seem to be ok

FAILED: non zero error code at the end

TIMEOUT: asked time limit has been reached

CANCELLED: your job has been canceled (by you, admin or job system)



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SLURM jobs monitoring and statistics



Monitoring job during run

Possibility to connect (ssh) to the node only if you have running jobs on this node: top, htop

MEMORY to use with SLURM in top or htop is in RES column (not in VIRT)

MultiThreads program can be identified with CPU more than 100%

PID	USER	PR	NI	VIRT	RES	SHR	S	%CPU	%MEM	TIME+	COMMAND
232285	xxxx	20	0	8093392	7.4g	18428	R	768.1	2.9	2140:47	myjob

NEVER use ssh to a node to do other things than monitoring job

All commands via ssh are shared with your job resources and admin can revoke your account in abusive case

```
sstat -a -j <jobid> # Give near real-time statistics but not easy to read
```

SLURM jobs monitoring and statistics



Statistics for ended job: **jobreports, seff**

```
user@spirit1:~$ jobreports --help

Usage: jobreports [--help] [-c|--color] [-l|--long] [-v|--verylong] [-u user|--user user] [--partition Partition_name] [-d nb_days|-w nb_weeks|-h nb_hours]

--help : print this help

-l or --long : more detail on each job

-v or --verylong : maximum detail on each job

-p or --parsable : fields are delimited by '|'

-c or --color : job efficacy is colored : green good, black ok, red bad

--partition partition_name : select job only in this partition

-h nb_hours or --hour nb_hours : only get jobs since nb_hours ( nb_hours between 1 and 24 )

-d nb_days or --day nb_days : only get jobs since nb_days ( nbdays between 1 and 31 )

-w nb_weeks or --week nb_weeks : only get jobs since nb_weeks ( nb_weeks between 1 and 5 )

-u user or --user user : job for this user
```

Job statistics samples



Good option to start with jobreports -c -l give all your finished jobs on one week:

```
user@spirit1:~$ jobreports -c -l
```

JobID	State	Elapsed	TimeEff	CPUEff	MemEff	Partition	CPUTime	Timelimit	MaxRSS	ReqMem	Nodes	Tasks	CPUS	Start
1497224	TIMEOUT	7-00:00:23	100.0%	---	76.8%	zen4	224-00:12:16	7-00:00:00	92.12G	120Gn	1	1	32	2024-11-11T10:15:17
More than 100% using threads in the core														
1521419	COMPLETED	02:42:50	1.6%	141.8%	24.0%	zen4	03:50:55	7-00:00:00	0.90G	3.75Gc	1	1	1	2024-11-22T22:38:00
Very good job														
1448720	COMPLETED	22:04:00	60.0%	99.9%	66.1%	zen4	44-02:31:52	1-12:45:00	63.48G	96Gn	1	1	48	2024-10-21T21:38:18
Many core low memory on high memory node														
5996075	COMPLETED	1-13:20:30	51.9%	99.5%	35.7%	zen16	74-07:35:40	3-00:00:00	46.46G	130Gn	1	1	48	2024-11-15T03:55:53
Many very short job per day														
6033026	COMPLETED	00:00:05	0.0%	20.0%	0.0%	zen4	00:02.571	03:00:00	0.00G	4Gn	1	1	2	2024-11-26T17:33:34
10 Hours interactive job 100G mem and 4 minutes cpu !!!!														
1507034	TIMEOUT	10:00:01	100.0%	0.1%	0.1%	zen16	04:07.820	10:00:00	0.07G	100Gn	1	1	7	2024-11-15T09:41:59
10G de Ram 3 core ELAPSED > CPUTIME ==> sequential Job														
1521051	COMPLETED	00:36:06	5.0%	24.8%	3.5%	zen4	26:54.589	12:00:00	0.35G	10Gn	1	1	3	2024-11-22T18:51:36



`sreport` is used to get cluster usage on a time period

```
user@spirit1:~$ sreport -t HourPer cluster AccountUtilizationByUser Users=$USER
Start=2021-09-01 End=2025-01-01
-----
Cluster/Account/User Utilization 2021-09-01T00:00:00 - 2024-12-03T06:59:59 (102758400 secs)
Usage reported in CPU Hours/Percentage of Total
-----
Cluster          Account        Login      Proper Name           Used          Energy
-----
spirit          xxxx       aaaaaaa     Dave Null    891 (0.00%)    0 (0.00%)
```



- Do not launch many very short batch < 1 min: launching job has a cost to start, to record statistics
- Sequential high memory job > 4Gb ⇒ always in zen16 partition
- No low memory job and many cores in zen16 partition ⇒ always in zen4
- No long interactive job without effective use ⇒ big resources waste
- Jupyter batch job is often like long interactive job without use: best to connect to <https://jupyter-x.ipsl.fr> or <https://jupyter-su.ipsl.fr>
- Try to limit your job time to a maximum of 24h ⇒ better placement on node

Job best practices 2/2



- No only CPU jobs on Hal GPU nodes ⇒ do CPU jobs on spirit[X] then only GPU job on HAL
- Long low memory job with a high memory end (data recombination) ⇒ launch the end in a different job in zen16 partition with dependency
- High memory job is sometime only memory leak in your code
- Warn with very high I/O job : sample 64 jobs doing `tar xvf` can kill any clustered file system



MERCI - THANK YOU

Institut Pierre Simon Laplace IPSL



Need Help ?

Start to read here: https://documentations.ipsl.fr/spirit/getting_started/support.html

- Documentations :

<https://documentations.ipsl.fr/>

- Email support :

meso-support@ipsl.fr

provide information:

- login
- Cluster name (and nodename if necessary)
- Submission command used for job