

Using the Jean Zay AI cluster

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Jean Zay

The super-computer of the future for AI users

1000+ GPUs

Half of the super-computer is for more traditional HPC usages

Specs Hardware

- **HPE SGI 8600** computer with two partitions:
 - **1528 scalar nodes** (CPU only - traditional HPC) **4.9 Pflops**
 - **261 converged nodes** (CPU+GPU - AI+traditional HPC) **9.02 Pflops**
- Each node has:
 - **192 GB** of memory
 - Omni-PAth interconnection network **100 Gb/s** (1 link per scalar node and 4 links per converged node)
 - 4 GPU nVIDIA V100 32 GB (converged nodes)
- In addition: 5 **frontal nodes**, 5 **visualisation nodes**, 4 **large memory nodes** (1 GPU Nvidia V100 and 3 TB of memory per node)
- Spectrum Scale parallel file system (**ex-GPFS**)
- Parallel storage device with **SSD** disks with a capacity of **1 PB**

How to get access

Possible access modes

- **Dynamic access**: individual access, simplified process (≤ 10000 GPU hours).
- **Project access**: group access, more administrative forms.
- **Grand Challenges access** (legacy): **beta testers last summer within the Aramis team**.

Important details:

- Everything is in French: filling the form in English is fine.
- Ask for ≤ 10000 GPU hours and they will be granted easily.
- 5-10 lines is enough for the project description.
- "Directeur structure de recherche": for ICM: Alexis Brice (ask to his assistant).
- "Responsable sécurité informatique": depending on the host institution (for ICM: see with the DSI).

Docs

Jean Zay Hardware:

- <http://www.idris.fr/eng/jean-zay/cpu/jean-zay-cpu-hw-eng.html>

Jean Zay Documentation:

- <http://www.idris.fr/eng/jean-zay>

Users collaborative doc:

- <https://github.com/jean-zay-users/jean-zay-doc>

Environment description

OS:

- RedHat version 7.6

Scheduler:

- Slurm

Modes:

- monoGPU, multiGPU and multiGPU MPI.

Interactive mode is available.

Environment description - storage

\$HOME (config files)

Permanent. Usage: e.g. config files, 3Gb.

\$WORK (quota for the project)

Permanent. Usage: code, databases, 3M inodes, 10Tb

\$SCRATCH (large quota)

Temporary. Usage: output data files, experiments results.

\$STORE (quota for project)

Permanent. Usage: large size but occasional consultation, 100k inodes, 51Tb

\$DSDIR (popular databases)

Environment description - SW

Libraries **ready and optimized**, via **module**:

- Intel compilers, with Intel(R) Math Kernel Library
- PGI compiler
- Python 2/3,
- Tensorflow (1.4, 1.8, 1.13, 1.14, 2.0.0-beta1),
- Pytorch (1.1),
- Caffe (1.0)
- Cuda (10.1.1)
- nccl (2.4.2)
- cudnn (10.1-v7.5.1.10)
- OpenACC
- MPI Cuda
- GPUDirect

You can also install your own libraries via **Conda**.

Environment description - Scheduler

Partitions:

- CPU: two queues - `cpu_p1` et `prepost`.
- GPU: two queues - `gpu_p1` et `prepost`. In the `gpu_p1` queue some nodes are reserved for dev jobs (fast access but limited to 2h).

To be aware:

- Maximal duration of a job (walltime): for batch jobs 20h and for dev jobs 2h (!!).
- Since `last december` a dedicated queue allows to submit long jobs (less than 120 hours).
- Dealing with checkpoints.

Early feedback - Access

- Jean Zay admins try to propose a "lightweight" procedure (compared with HPC traditional procedure).
- FYI:
 - ARAMIS process -> it took more than 1 month to get access (mode "Grand challenge/beta testers").
 - If everything goes well, it could take around 3 weeks to get access to Jean Zay from filling out the first form to be able to ssh to Jean Zay (mode "Dynamic access").
 - It should be possible to get access faster (in particular if signatures can be obtained faster).

Early feedback - Aramis project

- **Goal:** Reproduce experiments to guarantee reproducibility of the results of a publication:
- **What we did:** Train several CNN networks on 3D MRI data.
- **Before using JZ:** It took (on a local cluster) more than 3 months (about 1 month of full cluster usage) to get the results.
- **After using JZ:** All the models were re-trained within a week (about 24h of full cluster usage).
- **Next:** search of hyper-parameters to improve our models.
- **Next:** access to a new database ([UKBIOBANK](#)). More data to re-train our models.

Thanks!

