

# Computing resources in Pisa

*Francesca Lizzi*

*Istituto Nazionale di Fisica Nucleare, Pisa, Italy  
Scuola Normale Superiore, Pisa, Italy*

# How to access to computing resources

- The access is made through public login machines, called User Interface (ui).
- Every employee or associate can access to this machines thanks to the AAI infrastructure.
- The use of the infrastructure is made with batch LSF.
- The first login should be made to [setup.pi.infn.it](http://setup.pi.infn.it) to initialize the account.
- In order to access to medical physics exclusive resources, users should be added to `fismed/arianna` group.

# How to use computing resources

- The User Interface machines are made to interface with the whole computing infrastructure of INFN Pisa and they cannot be used to directly compute or execute scripts.
- Once you have logged in the user interface ([localui.pi.infn.it](http://localui.pi.infn.it) or [gridui.pi.infn.it](http://gridui.pi.infn.it)), you can submit jobs using docker.
- To use GPU you need to login to [gridui.pi.infn.it](http://gridui.pi.infn.it)

# Available GPUs and how to use them

- As Medical Physics group, we have:
  1. CPU 32 core Intel(R) Xeon(R) CPU E5-2650 0 @ 2.00GHz
  2. 128 GB RAM
  3. 2x V100 PCIe 16GB
  4. 8x Tesla K80 8GB
- The CUDA installation on this machine follows the docker approach so that it is possible to use only CPU or CPU+GPU.
- Beside hardware, it is possible to choose the software environment:
  1. sl6 - Scientific Linux 6 senza supporto NVidia
  2. cs7 - CentOS 7 senza supporto NVidia
  3. 91\_rtm\_cs7 - CentOS 7 con supporto NVidia runtime ver. 9.1
  4. 91\_dev\_cs7 - CentOS 7 con supporto NVidia sviluppo ver. 9.1
  5. 90\_tfks\_cs7 - CentOS 7 con supporto NVidia runtime ver. 9.0 + Tensorflow + Keras

# How to use GPU/CPU

- To submit an interactive job:  

```
bsub -Is -q gpuari -n 1 -R "select[defined(V100)] rusage[ngpus=1]"  
-a "docker-90_tfks_cs7" /bin/bash
```
- To submit a batch job:  

```
bsub -q gpuari -n 10 -R "select[defined(K80m)] rusage[ngpus=1]"  
-o out.out -e err.err -a "docker-90_tfks_cs7" script-to-be-executed
```
- As a best practice, please save error and output files.
- You can: visualize your active jobs with `bjobs (-q queue name -u user)`, print the output (batch) with `bpeek jobnumber`, kill the job with `bkill...` as any docker job on a lsf system!

# Software and virtualenv

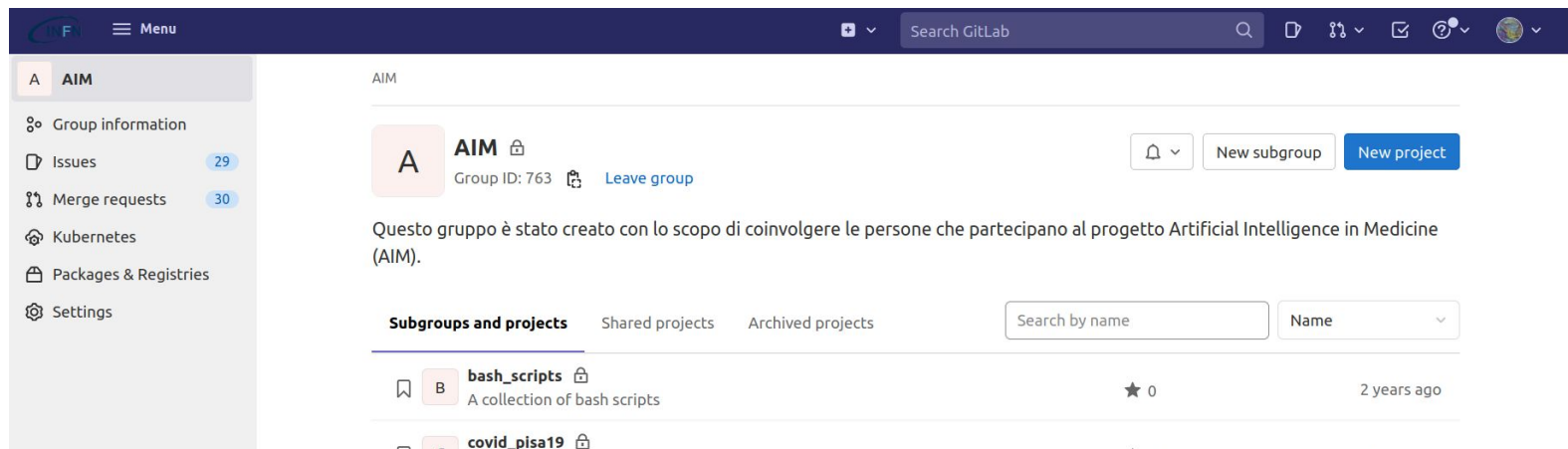
- Machine and deep learning show a strong dependence on software packages and CUDA versions. If you want to use Tensorflow and Keras on GPUs, please note that there are tested build configurations (<https://www.tensorflow.org/install/source?hl=en>)
- You can create your own virtual environment with the desired packages and versions, using Miniconda, which is a free minimal installer for conda (choose the right version).
- Once you have your base environment, you can create the virtual environment you want!!

# Pros and cons

- Drawbacks:
  1. Long queues (PV)
  2. Git issues (PI)
  3. CUDA interfaces in python virtual environments (PI,PV)
  4. Not usable when under maintenance (PI,PV)
  
- Advantages:
  1. Storage (PV,PI)
  2. Batch system (PV,PI)
  3. Sufficiently VRAM for our needs (but not for our dreams!)
  4. Dedicated hardware (PI)
  5. Desktop machines for tests (PV)

# Software repository

- We can use baltig to store the code we develop.
- Baltig is equal to gitlab but it is provided by INFN.
- We can create the nextAIM group and share our code and scripts.
- Goal: have and maintain a repository with useful code for people in the collaboration.



The screenshot displays the GitLab web interface for the 'AIM' group. The top navigation bar includes the GitLab logo, a 'Menu' button, a search bar labeled 'Search GitLab', and various utility icons. The left sidebar shows the 'AIM' group selected, with a list of navigation items: 'Group information', 'Issues' (29), 'Merge requests' (30), 'Kubernetes', 'Packages & Registries', and 'Settings'. The main content area shows the 'AIM' group details, including the group name 'AIM', its ID '763', and a 'Leave group' link. Below this, a description states: 'Questo gruppo è stato creato con lo scopo di coinvolgere le persone che partecipano al progetto Artificial Intelligence in Medicine (AIM)'. There are buttons for 'New subgroup' and 'New project'. A section titled 'Subgroups and projects' lists two items: 'bash\_scripts' (a collection of bash scripts, 0 stars, 2 years old) and 'covid\_pisa19'.

# Conclusion

As WP4 conveners, we plan to:

- Organize tutorials to use computing resources and baltig
- Help in building the shared software repository
- Grant access to machines and computing resources in the collaboration.

Each application and/or software needs specific computing resources, hardware, software, virtual environments and documentation, so that you can write us to discuss how to provide the best configuration for your scopes.

# Thank you for the attention!

[francesca.lizzi@sns.it](mailto:francesca.lizzi@sns.it)  
[ian.postuma@pv.infn.it](mailto:ian.postuma@pv.infn.it)