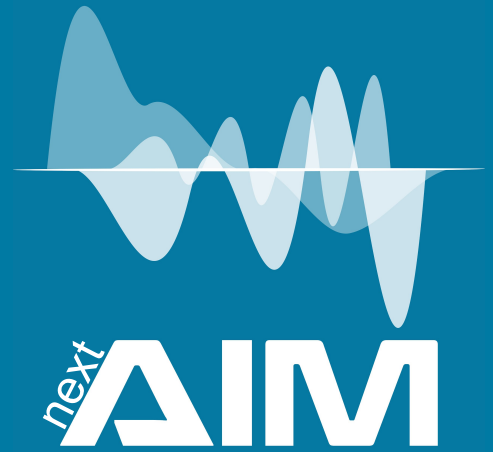


next
Artificial
Intelligence in
Medicine



Status of computing resource usage and SW repository 2024

Francesca Lizzi & Ian Postuma

Computing Resources

<https://baltig.infn.it/nextaim/code>

There is a [wiki](#) containing all the informations on how to connect to and use the available computing resources.

National resources: **AI_INFN**, Recas.

Local resources: Pavia, Pisa.

For those new to **GIT** there is a brief description on how to interact with a git repository.

Mission



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.

Status of the repository upload



Status of the repository upload



Status of the repository upload

Sedi partecipanti	Task	Topic
FE, LNS, NA, PI	T1	Radiomics in Digital Breast Tomosynthesis (DBT)
BO, FE, NA, PI	T2	Super-Resolution in Medical Imaging
BO, CT	T3	Radiomics in prostate cancer
BO, CT	T4	Radiomics and DL in tcMRgFUS
BO, FI, GE, LNS	T5	Nuclear Imaging Quantification and Radiomics
BA, CA, CT, PD, PI	T6	Connectivity in functional MRI and EEG
CA, CT, FE, FI, GE, MI, PI, PV	T7	Radiomics and Deep Learning analysis of CT and patients' data in COVID-19
MI, PI, PV	T8	Radiomics and ML-segmentation on Facio-Scapulo-Humeral dystrophy (FSHD), lung and liver tumor
PV	T9	ML on Imaging data of 10B uptake tracks and dose monitoring by Compton cameras
FI, PI	T10	Artificial intelligence for monitoring RT response in soft-tissue sarcomas
FE, PD	T11	Machine Learning techniques for cardiological applications
FI, PI	T12	Application of NLP techniques to clinical notes towards the automated reading of instrumental data


Code on other repositories





As many of us uses Github to develop their algorithm, here we list the link to reach the code on github:




1. [DNetPro](#) Official implementation of the DNetPRO algorithm published on Scientific Reports by Curti et al. Scientific Reports (WP1 and WP2)
2. [ClearLung](#) Official Implementation of the ClearLung algorithm for radiomic analysis of CT Lung scans.
3. [delta-BIT](#) DELTA-BIT stands for Deep-learning Local TrActography for BraIn Targeting, it comes from the idea to make faster the FSL pipeline for probabilistic tractography.
4. [PVSquared2](#) Machine learning for screening and predicting the best surface modifiers for a rational optimization of efficient perovskite solar cells.
(<https://doi.org/10.1063/5.0214736>)

T1 - Radiomics in Digital Breast Tomosynthesis (DBT)



https://baltig.infn.it/nextaim/dbt_classifier








D **DBT_classifier** 

  Star 0  Fork 0 





 main  dbt_classifier / 


[History](#) [Find file](#) [Edit](#) [Code](#)


 **Minor updates**
Gianfranco Paternò authored 6 months ago 96c528e4 

Name	Last commit	Last update
 utils	Minor updates	6 months ago
 .gitignore	Added gitignore	6 months ago
 DBT_classifier.py	Minor updates	6 months ago
 LICENSE	Initial commit	7 months ago
 README.md	Minor updates	6 months ago
 dataset_creator_DUKE.py	Minor updates	6 months ago
 dataset_patient_folder_cr...	Minor updates	6 months ago

Project information

-  17 Commits
-  1 Branch
-  0 Tags
-  131 KiB Project Storage

 README

 European Union Public License 1.2

- [+ Add CHANGELOG](#)
- [+ Add CONTRIBUTING](#)
- [+ Add Kubernetes cluster](#)
- [+ Set up CI/CD](#)
- [+ Add Wiki](#)
- [+ Configure Integrations](#)

T2 - Super resolution in medical imaging



?

T3 - Radiomics in prostate cancer.

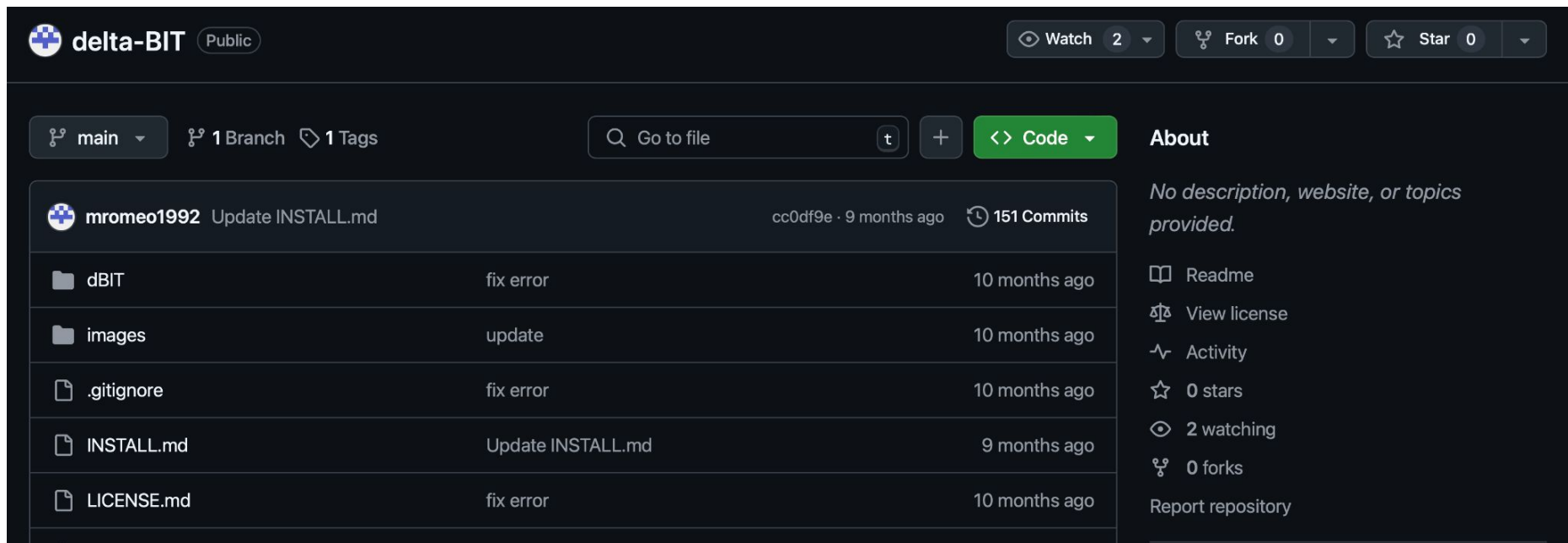


?

T4 - Radiomics and DL in tcMRgFUS



<https://github.com/mromeo1992/delta-BIT>




The screenshot shows the GitHub repository page for **delta-BIT** (Public). The repository is owned by **mromeo1992** and has 2 watchers, 0 forks, and 0 stars. The current branch is **main**, with 1 branch and 1 tag. The repository contains several files and folders:





File/Folder	Commit Message	Commit Hash	Time Ago
dBIT (Folder)	fix error	cc0df9e	10 months ago
images (Folder)	update		10 months ago
.gitignore (File)	fix error		10 months ago
INSTALL.md (File)	Update INSTALL.md		9 months ago
LICENSE.md (File)	fix error		10 months ago


The repository has 151 commits. The **About** section indicates that no description, website, or topics are provided. The repository also includes a Readme, View license, Activity, 0 stars, 2 watching, and 0 forks.



T5 - Nuclear imaging quantification and radiomics








https://baltig.infn.it/nextaim/radiomics_matlab_cnrinfn

R Radiomics_matlab_CNRINFN 





  Star 0  Fork 0 




 main

 **Add new file**
Alessandro Stefano authored 7 months ago 

Name	Last commit	Last update
 DA.m	Upload New File	7 months ago
 feature_selection.m	Upload New File	7 months ago
 license.txt	Upload New File	7 months ago
 main_radiomics.m	Upload New File	7 months ago
 next_AIM.xlsx	Upload New File	7 months ago
 readme.md	Add new file	7 months ago
 train_test.m	Upload New File	7 months ago

Project information

-  7 Commits
-  1 Branch
-  0 Tags
-  1.5 MiB Project Storage


-  README
-  BSD 2-Clause "Simplified" License
-  Wiki
- + [Add CHANGELOG](#)
- + [Add CONTRIBUTING](#)
- + [Add Kubernetes cluster](#)
- + [Set up CI/CD](#)
- + [Configure Integrations](#)

T6 - Connectivity in functional MRI and EEG

https://baltig.infn.it/nextaim/func_abide

F

func_ABIDE



🔔

☆ Star 0

🍴 Fork 0

⋮

🔗 main ▾

func_abide /


+ ▾

History

Find file

Edit ▾

Code ▾



Merge branch 'saponaro-main-patch-99137' into 'main' ⋮

Francesca Lizzi authored 8 months ago

78152f6d

🔄

Name	Last commit	Last update
📁 joint_fusion_DL_model	g	8 months ago
🔥 .gitignore	Update .gitignore	1 year ago
📄 my_abide_library.py	Revert "modifica prima frase"	1 year ago
📄 struct_func.py	programma classificazione	1 year ago

Project information

- 🔗 24 Commits
- 🔗 2 Branches
- 🏷️ 0 Tags
- 📄 83.4 MiB Project Storage

- [+ Add README](#)
- [+ Add LICENSE](#)
- [+ Add CHANGELOG](#)
- [+ Add CONTRIBUTING](#)
- [+ Add Kubernetes cluster](#)

T6 - Connectivity in functional MRI and EEG

<https://baltig.infn.it/nextaim/multimodal-neuroimaging>

M

Multimodal Neuroimaging 🔒

🔔 ▾

☆ Star 0

🍴 Fork 0

⋮

🔗 main ▾

multimodal-neuroimaging /


+ ▾

History

Find file

Edit ▾

Code ▾



added optional save/load flags for filter functions and improved documentation

Gianmarco Tiddia authored 2 months ago

a90aab44

📄

Name	Last commit	Last update
📁 multimodal_neuroimaging	added optional save/load flags for ...	2 months ago
📁 phenotypic_data_informat...	updated notebook with the instruct...	3 months ago
🔗 .gitignore	Removed .DS_Store + Updates in ...	3 months ago
📄 LICENSE	Initial commit	3 months ago
📄 README.md	Updates in README	3 months ago

Project information

- 🔗 43 Commits
- 🔗 5 Branches
- 🏷️ 0 Tags
- 📁 408 KiB Project Storage

- 📄 README
- 🔗 GNU AGPLv3
- + Add CHANGELOG
- + Add CONTRIBUTING
- + Add Kubernetes cluster

T7 - Radiomics and DL of CT and patients data of C19



<https://baltig.infn.it/nextaim/lungquant>


... and UI

ORIGINAL ARTICLE

Open Access



A multicenter evaluation of a deep learning software (LungQuant) for lung parenchyma characterization in COVID-19 pneumonia

Camilla Scapicchio^{1,2*†} , Andrea Chincarini^{3†}, Elena Ballante^{4,5}, Luca Berta^{6,7}, Eleonora Bicci⁸, Chandra Bortolotto^{9,10}, Francesca Brero⁵, Raffaella Fiamma Cabini^{5,11}, Giuseppe Cristofalo¹², Salvatore Claudio Fanni¹³, Maria Evelina Fantacci^{1,2}, Silvia Figini^{4,5}, Massimo Galia¹², Pietro Gemma¹⁴, Emanuele Grassetonio¹², Alessandro Lascialfari⁵, Cristina Lenardi^{7,15}, Alice Lionetti⁹, Francesca Lizzi^{1,2}, Maurizio Marrale^{16,17}, Massimo Midiri¹², Cosimo Nardi⁸, Piernicola Oliva^{18,19}, Noemi Perillo¹⁴, Ian Postuma⁵, Lorenzo Preda^{9,10}, Vieri Rastrelli⁸, Francesco Rizzetto^{20,21}, Nicola Spina¹³, Cinzia Talamonti^{22,23}, Alberto Torresin^{6,7,15}, Angelo Vanzulli^{6,24}, Federica Volpi¹³, Emanuele Neri^{13,25} and Alessandra Retico²

T8 - FSHD, lung and liver tumour

Computer Methods and Programs in Biomedicine 256 (2024) 108399



ELSEVIER

Contents lists available at [ScienceDirect](https://www.sciencedirect.com)

Computer Methods and Programs in Biomedicine

journal homepage: www.sciencedirect.com/journal/computer-methods-and-programs-in-biomedicine



Myo-regressor Deep Informed Neural NetwOrk (Myo-DINO) for fast MR parameters mapping in neuromuscular disorders

Leonardo Barzaghi ^{a,b,c,*}, Francesca Brero ^{c,d}, Raffaella Fiamma Cabini ^{a,c,e}, Matteo Paoletti ^b, Mauro Monforte ^f, Francesca Lizzi ^g, Francesco Santini ^{h,i}, Xeni Deligianni ^{h,i}, Niels Bergsland ^{j,k}, Sabrina Ravaglia ⁿ, Lorenzo Cavagna ^m, Luca Diamanti ⁿ, Chiara Bonizzoni ^b, Alessandro Lascialfari ^{c,d}, Silvia Figini ^{o,p}, Enzo Ricci ^f, Ian Postuma ^{c,d}, Anna Pichiecchio ^{l,b}

T8 - FSHD, lung and liver tumour



<https://github.com/niguardateam/covid-classifier>

The screenshot shows the GitHub repository page for CLEARLUNG. At the top, there are links for 'README' and 'License'. The main content area features a large banner with a blue and white illustration of human lungs on the left. To the right of the illustration, the word 'CLEARLUNG' is written in a large, bold, blue font. Below this, the subtitle 'Clinical Extraction And Radiomics on LUNGs' is displayed in a smaller, blue font. Underneath the banner is a 'Summary' section with the text: 'Welcome to the CLEARLUNG framework! This package provides both clinical and radiomic analysis of lung CT scans. It was developed as a Master Thesis project.'

Contributors 3

- andreasala98** Andrea Sala
- GiuliaZorzi** Giulia Zorzi
- scarrazza** Stefano Carrazza



Languages



- Python 87.4%
- HTML 12.4%
- Shell 0.2%

T9 - 10B uptake measurements and compton cameras


https://baltig.infn.it/nextaim/10b_trackdetection

1 10B_TrackDetection


 ▾
☆ Star 0
 Fork 0
⋮







 master ▾
10b_trackdetection /  ▾

History
Find file
Edit ▾
Code ▾









update
lan Postuma authored just now

f4a71d1e


Name	Last commit	Last update
 CNN	update	just now
 Img_real	update	just now
 Notebooks	update	just now
 Pseudo_tracks	update	just now
 Test_algorithm	update	just now
 TrackDetection	update	just now

Project information

-  1 Commit
-  1 Branch
-  0 Tags
-  44.7 MiB Project Storage

-  README
-  European Union Public License 1.2
- + [Add CHANGELOG](#)
- + [Add CONTRIBUTING](#)
- + [Add Kubernetes cluster](#)
- + [Set up CI/CD](#)
- + [Add Wiki](#)


T10 - AI for monitoring RT response in soft tissue sarcoma



?

T11 - ML for cardiological applications



<https://baltig.infn.it/nextaim/cardiac-mri>

C **Cardiac MRI** 

🔔 ☆ Star 0 🍴 Fork 0 ⋮


🔗 main cardiac-mri / +

History Find file Edit Code


Added README
 zucchett authored 6 months ago
 965990b7 

Name	Last commit	Last update
📁 1_dataExtraction	First commit	6 months ago
📁 2_preprocessing	First commit	6 months ago
📁 3_models	First commit	6 months ago
📄 LICENSE	First commit	6 months ago
📄 README.md	Added README	6 months ago


Project information











- 🔗 3 Commits
- 🔗 1 Branch
- 🏷️ 0 Tags
- 📁 11.9 MiB Project Storage
- 📄 README
- 📄 MIT License
- + Add CHANGELOG
- + Add CONTRIBUTING
- + Add Kubernetes cluster






T12 - NPL application to clinical notes



https://baltig.infn.it/nextaim/nlp_notebooks







NLP_notebooks 


  Star 0  Fork 0 

 main  nlp_notebooks /  

 History  Find file  Edit  Code 





 Merge branch 'main' of baltig.infn.it:nextaim/nlp_notebooks into main
flizzi authored 1 year ago 22238423 


Name	Last commit	Last update
 COVID_19_AOUP	dati per far funzionare il notebook ...	1 year ago
 COVID_USL3	elimino un file che non serve e si p...	1 year ago
 ECOCARDIO	aggiungo i file con i dati di input e i...	1 year ago
 .gitignore	elimino .csv dai file ignorati per pot...	1 year ago
 README.md	readme update	1 year ago
 requirements.txt	notebook fixato per funzionare co...	1 year ago

 README.md

NLP_notebooks

Project information

-  20 Commits
-  1 Branch
-  0 Tags
-  624 KiB Project Storage

 README

- + Add LICENSE
- + Add CHANGELOG
- + Add CONTRIBUTING
- + Add Kubernetes cluster
- + Set up CI/CD
- + Add Wiki
- + Configure Integrations

Created on
July 11, 2023

Thank you for the attention!

francesca.lizzi@sns.it
ian.postuma@pv.infn.it

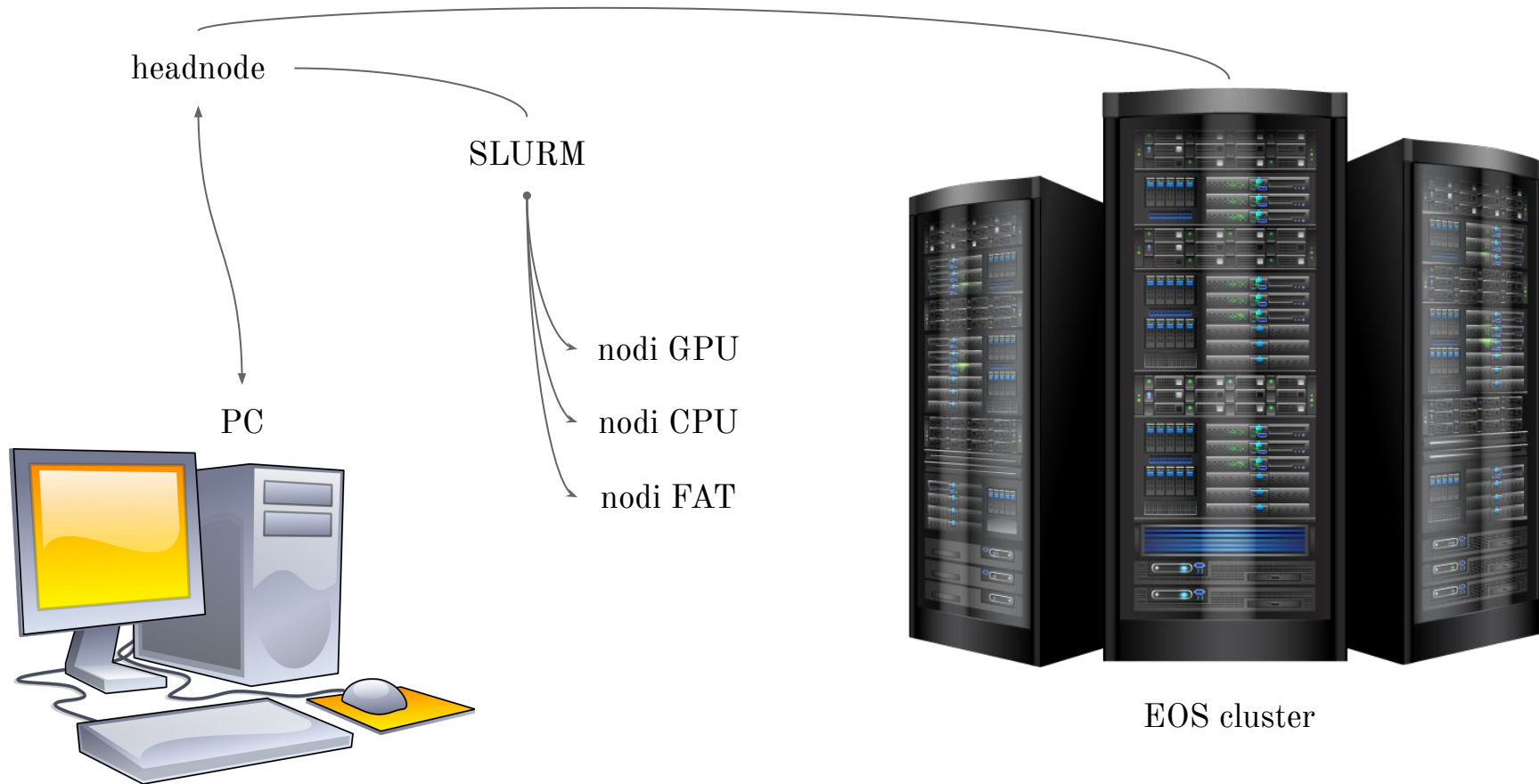
Computing Resources (PV)

- 2 Desktop Workstation
 - WS1: Ubuntu, CPU i9-10850, 1.5TB storage, RTX3060 12GB, 64GB RAM
 - WS2: Linux Mint, CPU AMD FX-8350, 2TB storage, RTX 2070 8GB, 32GB RAM
- 1 remote Server - EOS di UniPv
 - Sistema Linux (CentOs 7)
 - 160 TB di storage
 - 7 nodi FAT (ognuno con 768 GB RAM)
 - 7 nodi GPU (ognuno con 128GB RAM e 2 NVIDIA Tesla V100 da 32GB RAM)
 - 7 nodi standard (ognuno con 128GB RAM)

Accessing Computing Resources (PV)

- 2 Desktop Workstation
 - ssh
 - locally maintained - if needed we can share.
- 1 remote Server - EOS di UniPv
 - there are some restrictions for people outside UniPv
 - registration -> <https://forms.gle/tiH9KDPakGppGz2H8>
 - ssh
 - SLURM batch system

EOS system overview (PV)



Example workflow on EOS batch (PV)

- Create python virtual environment with CONDA
- Write code and update a GIT repository (baltig.infn.it)
- Load the data
- Create a slurm submission file & Train
 - Tell slurm which and how much resources are needed
 - Activate system modules for GPU and CONDA
 - Load the specific virtual environment
 - Execute the python scripts
 - if job terminates badly slurm log files and error outputs are useful
- Use trained network locally

While EOS batch is running (PV)

- Check job status: `squeue -u USERNAME`
- Check job verbosity in slurm log and error files
- Check some output files generated during script execution
- Log into the machine where the job is running
 - Check GPU usage
 - Check CPU usage
 - Check RAM usage
 - Evaluate general state of machine and job

How to access to computing resources (PI)

- 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 to initialize the account.
- In order to access to medical physics exclusive resources, users should be added to `fimed/arianna` group.

How to use computing resources (PI)

- 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 or gridui.pi.infn.it), you can submit jobs using docker.
- To use GPU you need to login to gridui.pi.infn.it

Available GPUs and how to use them (PI)

- 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 (PI)

- 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 (PI)

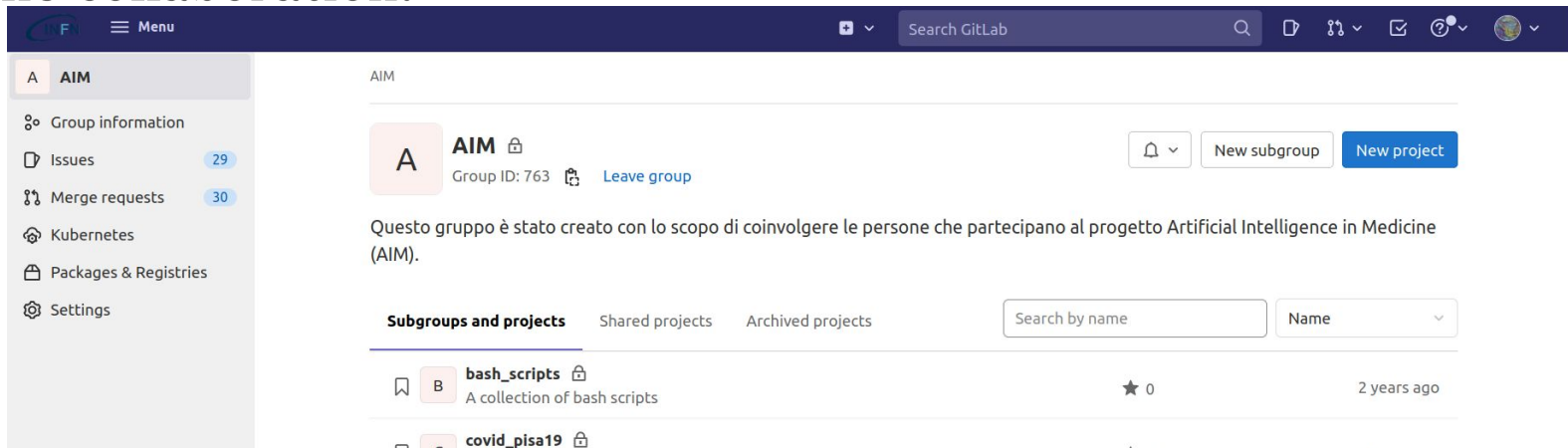
- Machine and deep learning show a strong dependence on software packages and CUDA versions. If you want to use Tensorflow and Keras on GPUs, please note that there are tested build configurations (<https://www.tensorflow.org/install/source?hl=en>)
- You can create your own virtual environment with the 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 shows the GitLab web interface for the 'AIM' group. The top navigation bar includes the INFN logo, a 'Menu' button, and a search bar for GitLab. The left sidebar contains navigation links for 'AIM', 'Group information', 'Issues' (29), 'Merge requests' (30), 'Kubernetes', 'Packages & Registries', and 'Settings'. The main content area displays the 'AIM' group details, including its name, ID (763), and a description in Italian: 'Questo gruppo è stato creato con lo scopo di coinvolgere le persone che partecipano al progetto Artificial Intelligence in Medicine (AIM)'. Below the description, there is a section for 'Subgroups and projects' with a search bar and a dropdown menu. Two subgroups are listed: 'bash_scripts' (A collection of bash scripts, 0 stars, 2 years ago) and 'covid_pisa19'.