

ilifu



ilifu Online Training

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User Training Workshop – Introduction to ilifu

4 April 2023

Topics

- Introduction to the ilifu research facility services
- Directory structure
- Software environment
 - Singularity containers
 - Modules
- Using JupyterHub
- Introduction to Slurm

Getting help

- Support contact

support@ilifu.ac.za

- User documentation

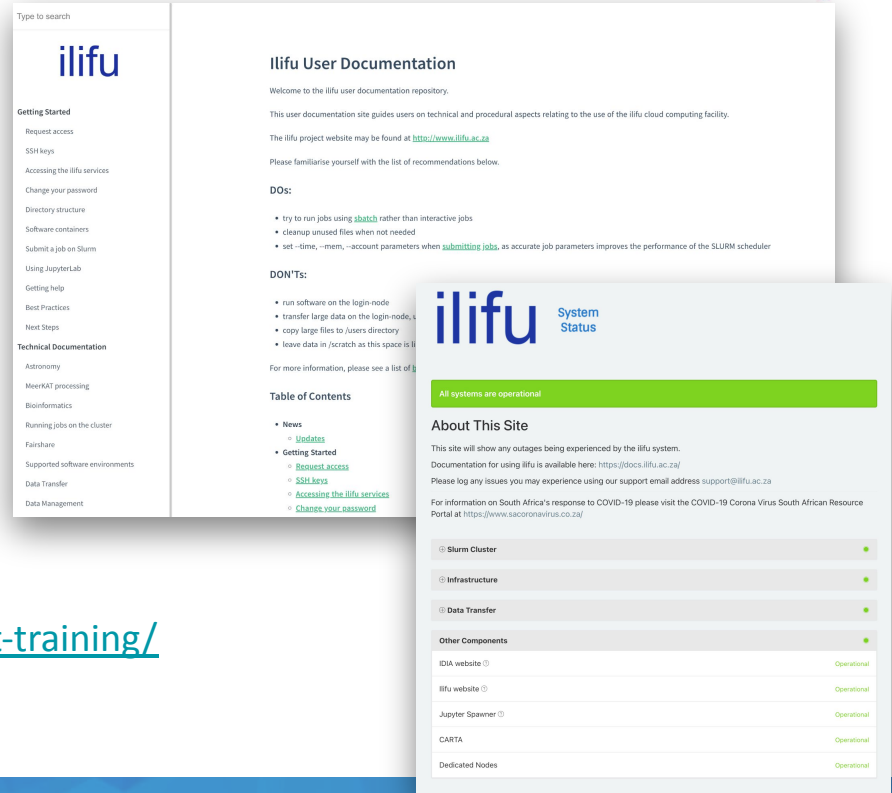
<http://docs.ilifu.ac.za/#/>

- Ilifu System Status

<https://status.ilifu.ac.za/>

- Training videos

<https://www.ilifu.ac.za/latest-training/>



The image shows three overlapping screenshots of the ilifu website. The top-left screenshot is the 'ilifu User Documentation' page, which includes a search bar, a navigation menu with categories like 'Getting Started' and 'Technical Documentation', and a 'Table of Contents' section. The top-right screenshot is the 'ilifu System Status' page, featuring a green banner that says 'All systems are operational' and a list of system components with their status. The bottom screenshot is a 'Training' page with a blue background and the ilifu logo.

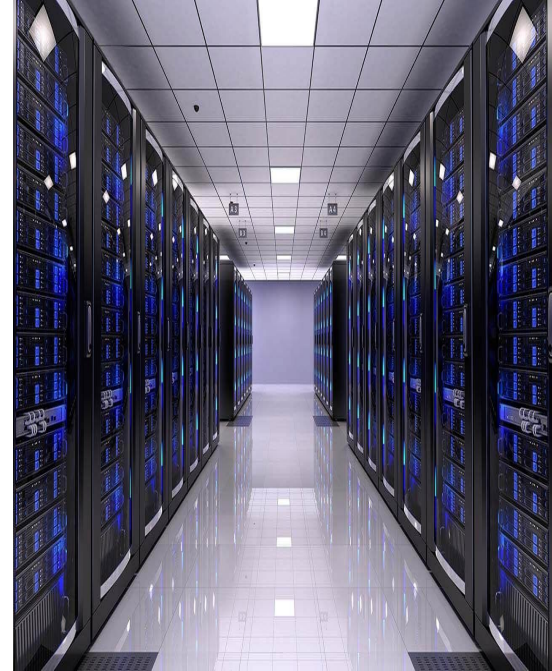
High Performance Computing

Combining power of distributed computers

- Collection of servers (computers)
- Connected by fast local network

Some terminology

- Servers also referred to as nodes
- Group of nodes is a cluster



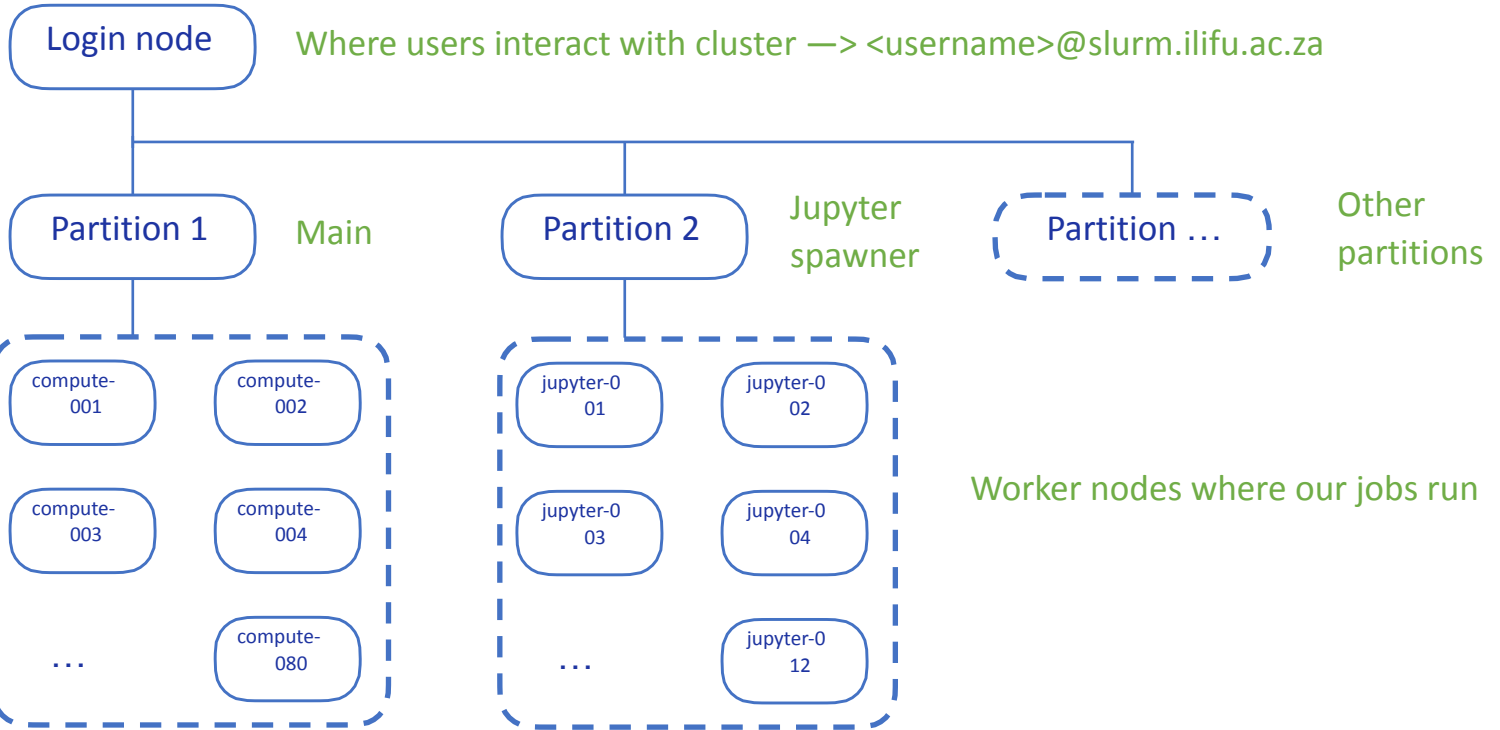
ilifu Research Facility

Cloud-based infrastructure for data-intensive research

Remote access to compute and storage resources:

- Support variety of different scientific projects and requirements
- Flexible compute environment
- Data management: storage, transfer

ilifu Research Facility



Software we use

- Job Scheduler to manage resources - Slurm
- JupyterHub service - development environment
- Containerised software environment - Singularity
- Other services: data transfer, CARTA



Computing environment - interface

ssh - shell terminal

```
* Support: https://ubuntu.com/advantage

System information as of Fri Aug 23 11:36:57 SAST 2019

System load: 0.49      Users logged in: 8
Usage of /: 35.9% of 21.15GB  IP address for ens3: 192.168.100.39
Memory usage: 5%      IP address for ens4: 10.102.26.97
Swap usage: 0%       IP address for ens5: 10.102.28.133
Processes: 396

* Keen to learn Istio? It's included in the single-package MicroK8s.
https://snapcraft.io/microk8s

Get cloud support with Ubuntu Advantage Cloud Guest:
http://www.ubuntu.com/business/services/cloud

* Canonical Livepatch is available for installation.
- Reduce system reboots and improve kernel security. Activate at:
https://ubuntu.com/livepatch

170 packages can be updated.
75 updates are security updates.

Last login: Fri Aug 23 09:08:21 2019 from 196.11.235.232
jeremy@slurm-login:~$ sinfo
PARTITION AVAIL TIMELIMIT NODES STATE NODELIST
Main* up 14-00:00:0 8 mix slwrk-[106-113]
Main* up 14-00:00:0 14 alloc slwrk-[101,104-105,114-124]
Main* up 14-00:00:0 38 idle slwrk-[102-103,125-160]
JupyterSpawnerONLY up infinite 4 mix slwrk-[201-202,205,209]
JupyterSpawnerONLY up infinite 4 alloc slwrk-[206-208,210]
JupyterSpawnerONLY up infinite 2 idle slwrk-[203-204]
jeremy@slurm-login:~$ sbatch compute_job.sh
```

ssh <username>@slurm.ilifu.ac.za

JupyterHub

The screenshot shows a JupyterLab interface with a code editor on the left and a plot on the right. The code editor contains Python code for data analysis and plotting. The plot shows a scatter plot of data points with a circular pattern.

```
test_concurrent | memory_metric | compare_plots | casa_sim_plot | example_notat | Untitled5.ipynb | README.md | layout_mearka
+ + +
Code Jupyter-Casa (local)

Analyze and Image Simulation

In [200]: from simutil import *
In [201]: myutil = simutil()
In [55]: import pylab as pl

myfile = 'sim_exaple_30_dor/sim_exaple_30_dor.meeekat.ms'

if os.path.exists(myfile):
    tb.open(myfile)
    rawdata = tb.geicol('UWV')
    tb.close()

pl.box()

maxbase = max(max(rawdata[0,]),max(rawdata[1,]))
kiam_m = 300/qa.convert(model_specrefval, 'Gs')['value']

pl.plot(rawdata[0,]/kiam_m,rawdata[1,]/kiam_m,'b,')
pl.plot(-rawdata[0,]/kiam_m,-rawdata[1,]/kiam_m,'b,')

ax = pl.gca()
ax.yaxis.LABELPAD = -4
pl.xlabel('v[kilambda]', fontsize='x-small')
pl.ylabel('v[kilambda]', fontsize='x-small')
pl.axis('equal')

Out[55]: (-45.0, 45.0, -30.0, 30.0)
```

The plot on the right shows a scatter plot of data points with a circular pattern. The x-axis is labeled 'X [m]' and the y-axis is labeled 'Y [m]'. The data points are clustered around the origin, forming a circular pattern.

```
README.md
1 # Benchmark
2 A benchmark tool used for performance
3
4 ## Prerequisites
5
6 - Python 2.7
7 - Putil
8
9 ## Running benchmark tool
10
11 ---
12
13 import Benchmark from benchmark
14
15 mybenchmark = Benchmark()
16
17 sn = 'image_script_tclean.py'
18 cp = 'path_to_container/jupyter-casa'
19 desc = 'tclean on jupyter-casa'
20 exec = 'casa --nologger --logtimestid = 'tclean'
21
22 mybenchmark.execute(script_name=sn,
23 mybenchmark.write_to_csv()
24
25
26 See example notebook for detailed i
```

<https://jupyter.ilifu.ac.za>

Computing environment - ssh

Your SSH key

- Used in the SSH (Secure Shell) protocol
- Authentication method for gaining access to encrypted connecting between systems
- Use connection to manage system remotely
- We need your SSH public key so our system knows to let you in

Compute environment - ssh

Generating SSH key

- If you don't already have one
- New compute/formatted existing computer

GitHub docs on key generation:

<https://docs.github.com/en/github/authenticating-to-github/connecting-to-github-with-ssh/generating-a-new-ssh-key-and-adding-it-to-the-ssh-agent>

Directory Structure

Common areas:

- `/users`
 - limited storage shared among all users, for scripts and small files – don't place data here, capping `/users` storage capacity can prevent access to the cluster for all users.
- `/scratch3/users`
 - directory space for processing data, temporary storage only, i.e. use this space during processing, and then clear all files immediately after processing. Remove unnecessary data and move data that you want to keep to project folder.

Remaining storage separated by group: IDIA, CBio, ilifu

Directory Structure

IDIA structure:

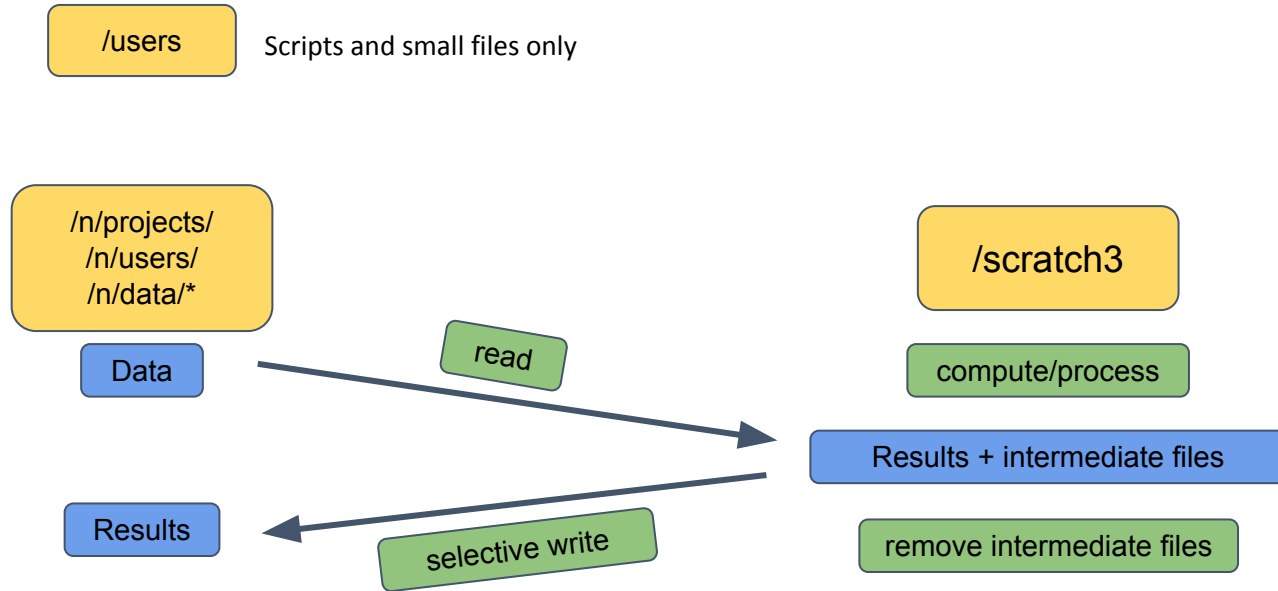
- **/idia/users**
 - user's private work directory, may store data products that are not ready to move to shared project space
- **/idia/projects**
 - project specific directories. These directories are for sharing data and resources within project groups. Raw data associated with a project will also be available from the project folder. Raw data should always be read-only.
- **/idia/software**
 - software containers and the IDIA Pipelines software is stored here

Directory Structure

Similar structure for /cbio and /ilifu groups:

- /cbio/users
- /cbio/projects
- /cbio/soft
- /ilifu/users
- /ilifu/software
- Exception for ilifu projects:
 - /ilifu/astro/projects
 - /ilifu/bio/projects

Directory Structure - Typical workflow



*/n/data generally read-only

Software environment - Singularity containers

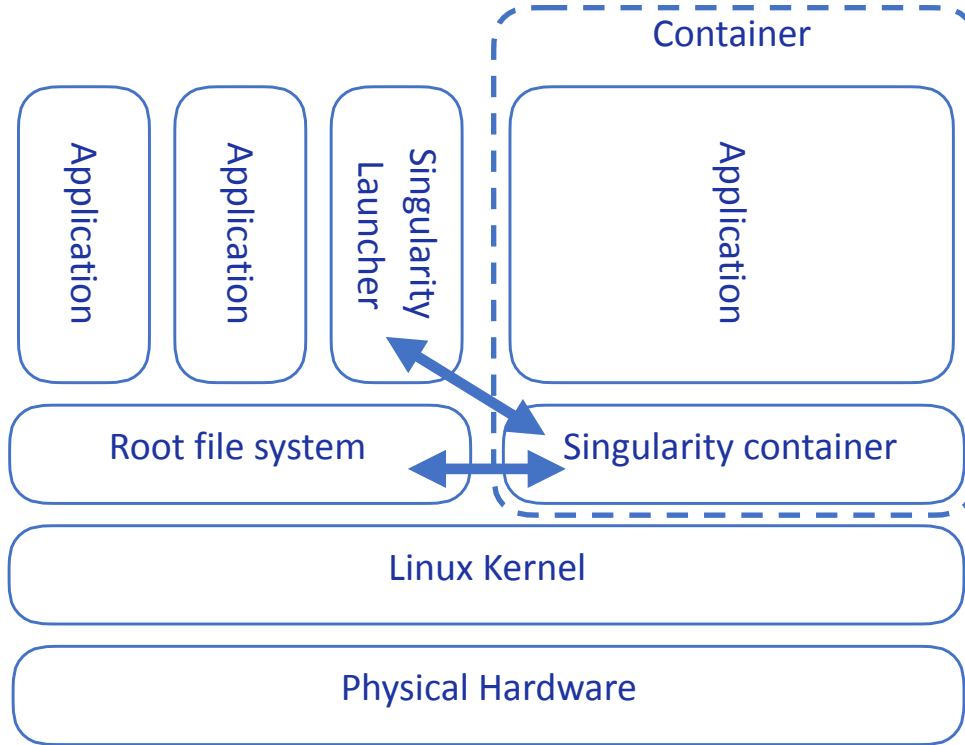
- Encapsulated software environments
- A software stack that contains everything required to run an application/workflow, including files, environments variables, libraries and dependencies
- Containers accessible across platforms and services, allowing sharing of applications environments



<https://sylabs.io/singularity>



Software environment - Singularity containers



Software environment - Singularity containers

Supported Containers:

- CASA 5, CASA 6
- Astronomy container (ASTRO-PY3, ASTRO-PY3.8)
- KERN suite
- GPU Python container
- Project containers:
 - MeerLICHT, LADUMA, HI Intensity mapping
- lots of others



Directories:

- /software
- /idia/software/containers
- /ilifu/software/containers

Software environment - Singularity containers

Open container as an interactive shell:

```
singularity shell /path/to/container
```

Example:

```
$ singularity shell /idia/software/containers/ASTRO-PY3.8.simg
```



Run a script/workflow using a container environment:

```
singularity exec /path/to/container <software> <script/input_parameters>
```

```
$ singularity exec /idia/software/containers/casa-6.simg python myscript.py
```

Software environment - modules

module avail

```
$ module avail
```

```
----- /software/modules/common -----
LAPACK/3.9.0          anaconda3/2020.07      githubcli/2.0.0        mono/6.8.0.123         perlbrew/perlbrew     python/3.10.0
R/RStudio1.2.5042-R4.0.0  anaconda3/2021.05      go/1.16.3              mpich/3.3a2           python/2.7.18         python/3.10.1 (D)
R/RStudio1.2.5042-R4.0.4  anaconda3/2021.11      go/1.17.3              openBLAS/0.3.9       python/3.6.15        ruby/2.6.6
R/3.6.3              cuda/10.0.130_410.48   graphviz/2.49.1        openmpi/2.1.1        python/3.7.7         singularity/2.6.1
R/4.0.0              cuda/10.1.243_418.87.00  homebrew/2.4.13       openmpi/2.1.6        python/3.8.2         singularity/3.7.3
R/4.0.2              cuda/10.2.89_440.33.01  hwloc/1.11.13         openmpi/3.1.6        python/3.8.3         singularity/3.8.3
R/4.0.3              cuda/11.0.2_450.51.05   java/jre-1.8.0_261    openmpi/4.0.3        python/3.8.6         singularity/3.9.0
R/4.1.1              cuda/11.4.2_470.57.02   java/openjdk-14.0.1 (D)  openmpi/4.0.5        python/3.9.0         singularity/3.9.1 (L,D)
anaconda3/login.old    dotnet/5.0.301         julia/1.5.3            openmpi/4.1.0 (D)    python/3.9.4         user_tools
anaconda3/login        drmaa/1.1.1            maven/3.6.3            perl/5.33.0          python/3.9.7

----- /software/modules/astro -----
casa/5.7.0          casa/5.8.0          casa/6.1.2.7-pipeline  casa/6.2          casa/6.4 (D)
casa/5.7.2-4        casa/6.1.0-118-monolithic  casa/6.1.2.7-modular  casa/6.3          pybdsf/1.9.2

----- /software/modules/bio -----
bcbio/bcbio_container  biobambam2/2.0.183  genomestrip/2.00.1958  plink/2.00a2.3  samtools/1.13  vep/singularity
bcbio/1.2.3            canvas/1.40.0.1613  htlib/1.10.2            popgen/0.1      samtools/1.14 (D)  vep/101.0 (D)
bcbio/1.2.9            cd-hit/4.8.2        mafft/7.490             prsice-2/2.3.1d  treePL/homebrew
bcftools/1.10.2        gemini/gemini        mash/2.3                samtools/1.10   vcftools/0.1.16

----- /usr/share/lmod/lmod/modulefiles -----
Core/lmod/6.6  Core/settarg/6.6

Where:
L: Module is loaded
D: Default Module
```

Software environment - modules

- module avail
- module help <module>

```
$ module help python
```

```
----- Module Specific Help for "python/3.10.1" -----  
This module configures Python 3.10.1 for use
```

- module load <module>
- module list
- module purge
- module --help

ilifu

JupyterHub

<https://jupyter.ilifu.ac.za>



ilifu

jupyter
login

Sign in

Username:

jeremy

Password:

.....

Sign In

Session size

Server Options

Nodes Free

as at Tue Mar 8 14:44:01 SAST 2022

83 Minimum

40 Small

18 Medium

7 Large

1 Half-Max

0 Max

0 GPU

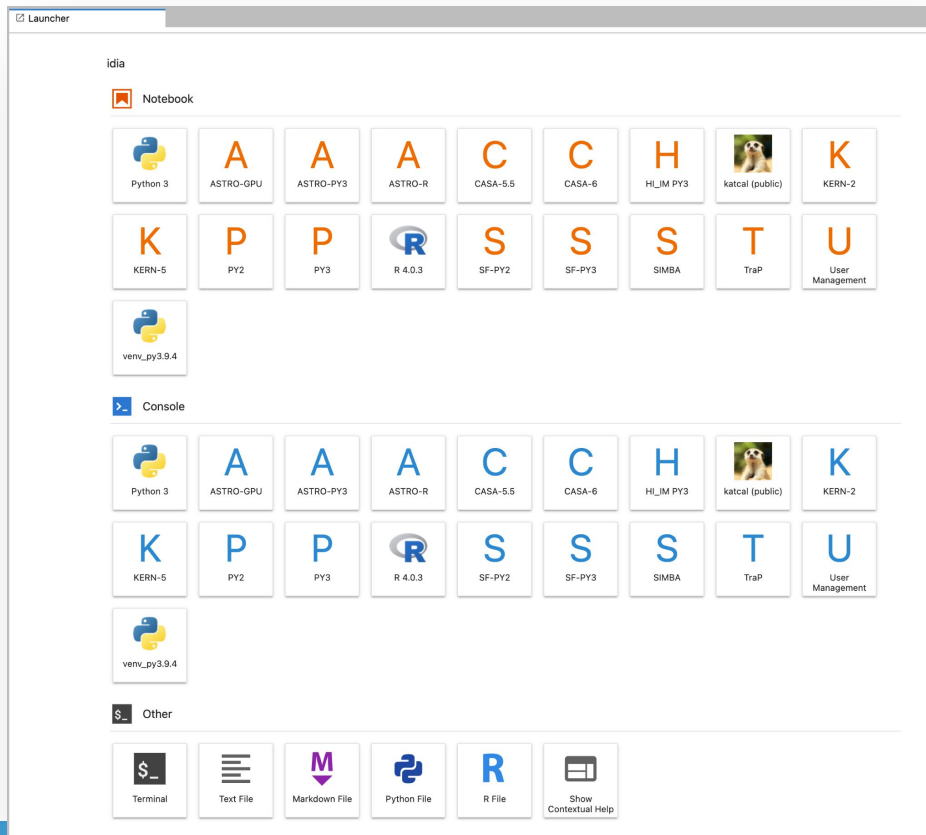
Select a job profile:

Minimum Node - 1 core, 7 GB, 18 hours idle timeout, max 5 days lifespan

Start

JupyterHub

Choose kernel
in launcher



The screenshot shows the JupyterHub Launcher interface. At the top, it says "Launcher". Below that, the environment is identified as "idia".

There are three main sections:

- Notebook:** A grid of 18 kernel options arranged in two rows. The first row contains: Python 3, ASTRO-GPU, ASTRO-PY3, ASTRO-R, CASA-5.5, CASA-6, HI_M PY3, katcal (public), and KERN-2. The second row contains: KERN-5, PY2, PY3, R 4.0.3, SF-PY2, SF-PY3, SIMBA, TraP, and User Management.
- Console:** A grid of 18 kernel options arranged in two rows, identical to the Notebook section.
- Other:** A row of six utility icons: Terminal, Text File, Markdown File, Python File, R File, and Show Contextual Help.

Each kernel option is represented by a square tile with a logo or letter and the kernel name below it. The "Python 3" tile in both sections has a blue Python logo, while others have orange letters or logos.

The logo for 'ilifu' is displayed in a bold, dark blue, lowercase sans-serif font. It is positioned in the upper left corner of the slide, which has a background of a blue geometric pattern of triangles.

Demo

Demo resources https://github.com/ilifu/ilifu_user_training

