SpiNNaker Human Brain Project Portal Introduction

This document describes how to use the EBRAINS portal to run PyNN scripts on SpiNNaker machines. It replaces the previous document on how to use the HBP portal to run PyNN scripts.

1. Getting Started

This section describes the current state of the SpiNNaker machine hosted by the HBP Portal and the software stack's limitations.

1.1 SpiNNaker Machine

Before starting to run PyNN scripts on SpiNNaker machines via the portal, be aware that the total SpiNNaker machine capacity is a 10 cabinet machine, comprising 1,036,800 cores, as shown in Figure 1.

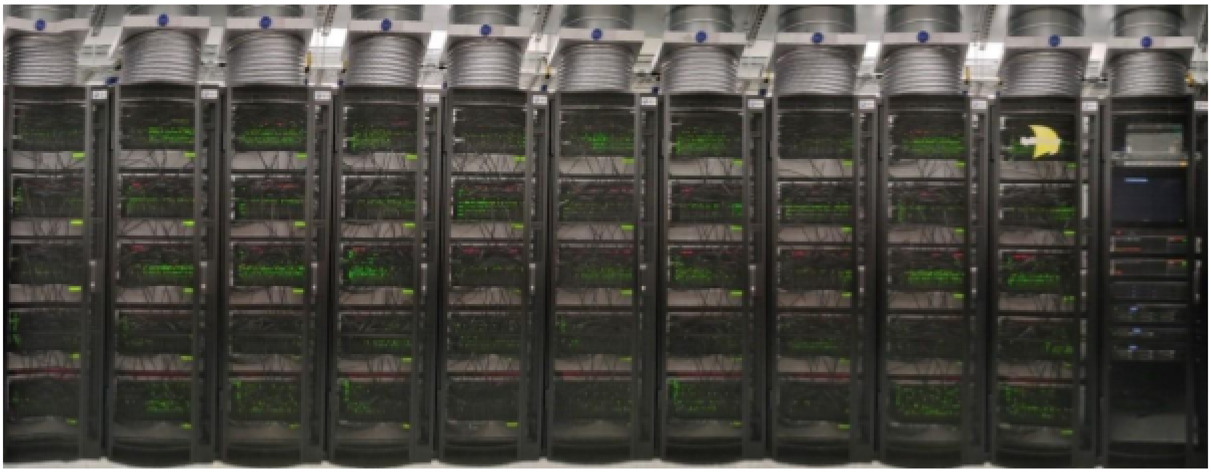


Figure 1: A 10 cabinet machine, wired together (Note: the 11th cabinet in the picture contains servers for handling jobs sent to the machine).

1.2 Software Limitations

To understand how this relates to a PyNN script, be aware that SpiNNaker stores all the data needed to execute a PyNN model within its on-board memory (SDRAM). This SDRAM is limited in size, as each SpiNNaker chip contains only 128MB of memory, split dynamically between the 18 cores (including the operating system core) that reside on the chip. On average, every core has available approximately 8MB to store the neuron parameters as well as the synaptic matrix of the atoms[1] it is executing. Most models, to date, are limited to 256 atoms per core[2], and therefore the connectivity between these 256 atoms and the rest of the simulation must fit within these constraints.

[1] Atoms here represent the atomic element which each core models. In the case of PyNN, these are neurons from a given population.

[2] This limitation may be lifted in the future, but to date, this is due the way that synaptic delays are implemented on SpiNNaker.

Due to these limitations, the maximum possible number of atoms that can be simulated by a PyNN script on the largest SpiNNaker machine available on the HBP portal is 250,675,200. This sounds rather large, but when it is factored in that each atom can only have a maximum incoming fixed number of connections of 8000, and that any more than this will result in a smaller number of neurons per core; therefore a smaller total neurons being simulated.

To make matters worse, currently, if a PyNN Projection between two Populations has delays greater than 16 machine time steps[3] then each core that simulates these neurons will have a delay model attached to it, which in practice reduces the maximum number of simulated neurons by half.

Finally, if the PyNN model includes plastic connections, these require more memory than fixed connections and therefore will further reduce the number of neurons per core. A summary of the rest of the SpiNNaker back end limitations can be found here: http://spinnakermanchester.github.io/spynnaker/6.0.0/SPyNNakerModelsAndLimitations.html

1.3 EBRAINS Portal Limitations

The EBRAINS portal executes its PyNN scripts in a batch mode process. This means certain capabilities supportable by the SpiNNaker software stack (sPyNNaker) are not currently avilable by the EBRAINS portal. These are:

1. Real time visualisation of an executing PyNN script to a standalone visualization kit.
2. Closed loop simulation with real robotics.
3. Closed loop simulation with robots via the virtual robotic environment.

1.4 Script Limitations

This section describes some basic limitations that the PyNN script can experience when running on the EBRAINS Portal.

1. Figures generated by the script must be stored in file format, no figures will be presented to the end user in an interactive mode.
2. A PyNN script running on the SpiNNaker backend needs to adhere to the subset of PyNN that is supported by sPyNNaker[4], a list of what is not implemented can be found here:

http://spinnakermanchester.github.io/spynnaker/6.0.0/SPyNNakerModelsAndLimitations.html

1.5 Recommendations

[3] This is 16 milliseconds in a simulation that runs at 1ms time steps, or 1.6 milliseconds in a simulation running at 0.1 ms time steps

[4] This is the SpiNNaker software stack's front end for simulating PyNN neuron models. See https://www.frontiersin.org/articles/10.3389/fnins.2018.00816/full for more details.

It is recommended that you test your simulation with the sPyNNaker front end in virtual mode before attempting to run it through the EBRAINS portal. Instructions on how to install the sPyNNaker front end can be found here:

http://spinnakermanchester.github.io/spynnaker/6.0.0/PyNNOnSpinnakerInstall.html

and instructions on how to operate the tool chain in virtual mode can be found here:

http://spinnakermanchester.github.io/spynnaker/6.0.0/VirtualMode.html

2. Running a PyNN script on the EBRAINS portal

This section describes how an end user can run a PyNN simulation on the EBRAINS Portal / collaborator, both through the Neuromorphic Computing Job Manager (section 2.2) and through the SpiNNaker Jupyter service (section 2.3). We suggest that if you are testing out PyNN scripts / networks, then you use the Jupyter service to interact with the machine; then, if you wish to run more jobs once you are happy with your network and wish to get some results (e.g. to do parameter sweeps), use the NMC Job Manager to submit scripts.

2.1 Getting an EBRAINS account

To acquire an EBRAINS account, go to https://ebrains.eu/register and follow the instructions.

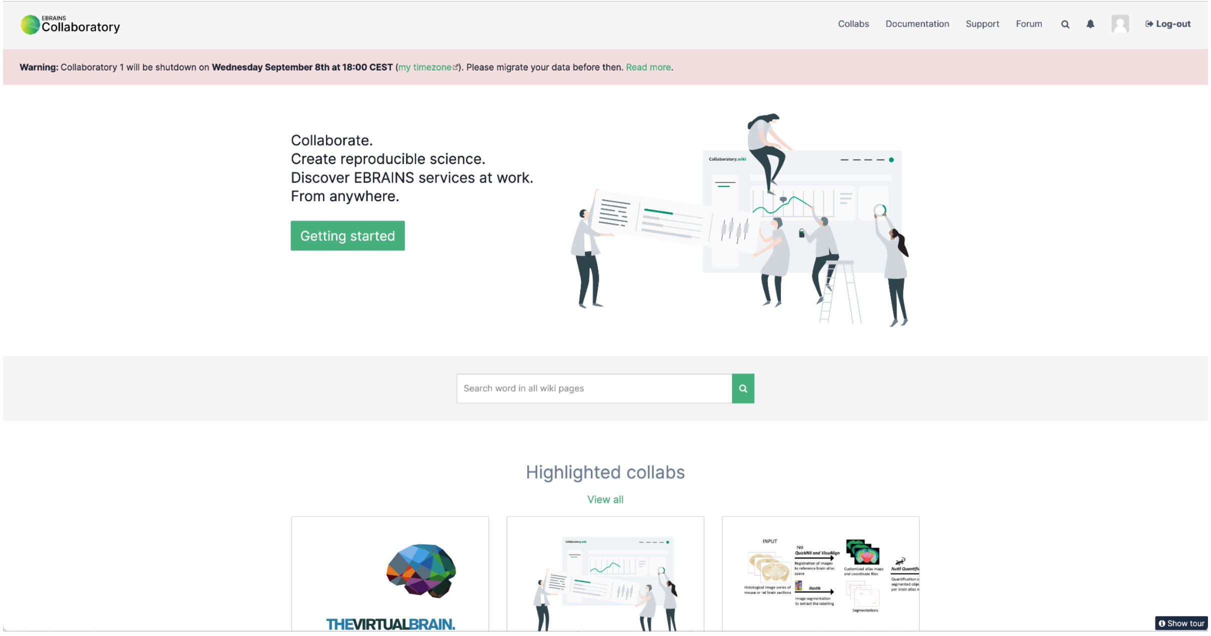
2.2 Creating a Job on the EBRAINS portal/collaboratory.

1. First you must log onto the EBRAINS collaboratory via the link in the top right of the page at:

https://wiki.ebrains.eu/bin/view/Main/

and you may then also find it useful to read the “Getting Started” documentation at

https://wiki.ebrains.eu/bin/view/Collabs/the-collaboratory/Getting%20Started/



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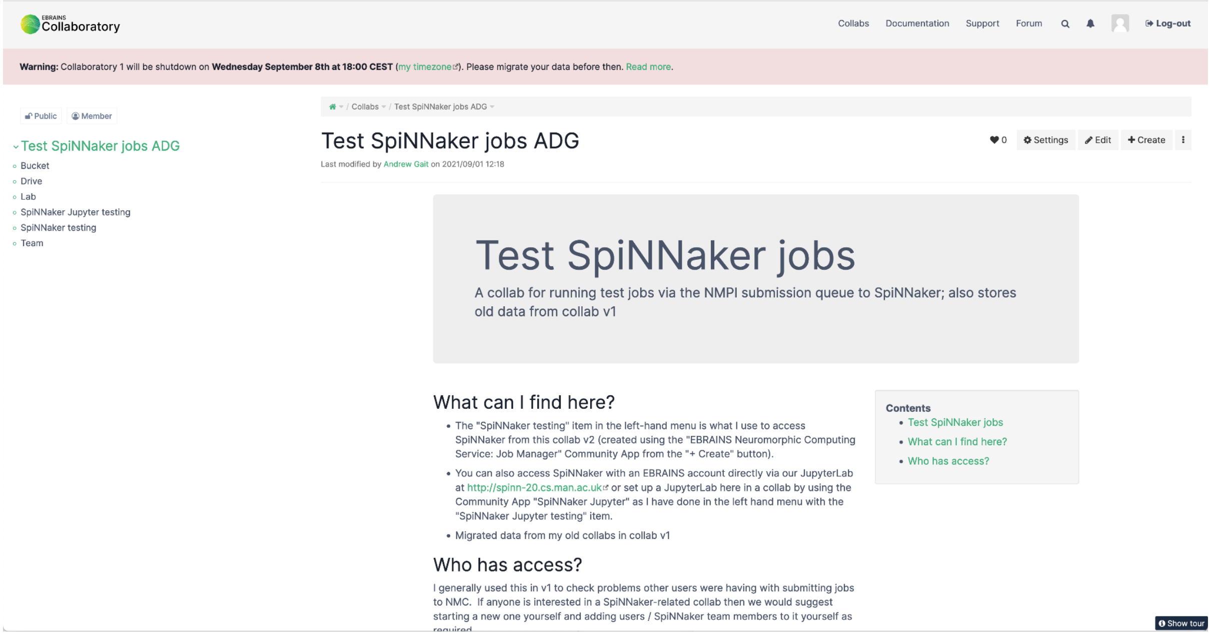
Collaborate.
Create reproducible science.
Discover EBRAINS services at work.
From anywhere.

2. To run jobs, you need to have your own collab; if you don’t yet have one then to do this click on “Collabs” in the top-right menu, and then on the subsequent page click on the “Create a collab” button. On this page, you will be required to give your collab a Title, a Name, a Description, and declare whether it is private or public (note:

making it public makes it easier for others to see and help with your work should you need it).

3. Once you have created your collab you will be able to edit the associated page appropriately. It will look something like the following image (with less menu items on the left-hand menu to start with).



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Test SpiNNaker jobs ADG

Last modified by Andrew Gait on 2021/09/01 12:18

Test SpiNNaker jobs

A collab for running test jobs via the NMPI submission queue to SpiNNaker; also stores old data from collab v1

What can I find here?

- The "SpiNNaker testing" item in the left-hand menu is what I use to access SpiNNaker from this collab v2 (created using the "EBRAINS Neuromorphic Computing Service: Job Manager" Community App from the "+ Create" button).
- You can also access SpiNNaker with an EBRAINS account directly via our JupyterLab at http://spinn-20.cs.man.ac.uk or set up a JupyterLab here in a collab by using the Community App "SpiNNaker Jupyter" as I have done in the left hand menu with the "SpiNNaker Jupyter testing" item.
- Migrated data from my old collabs in collab v1

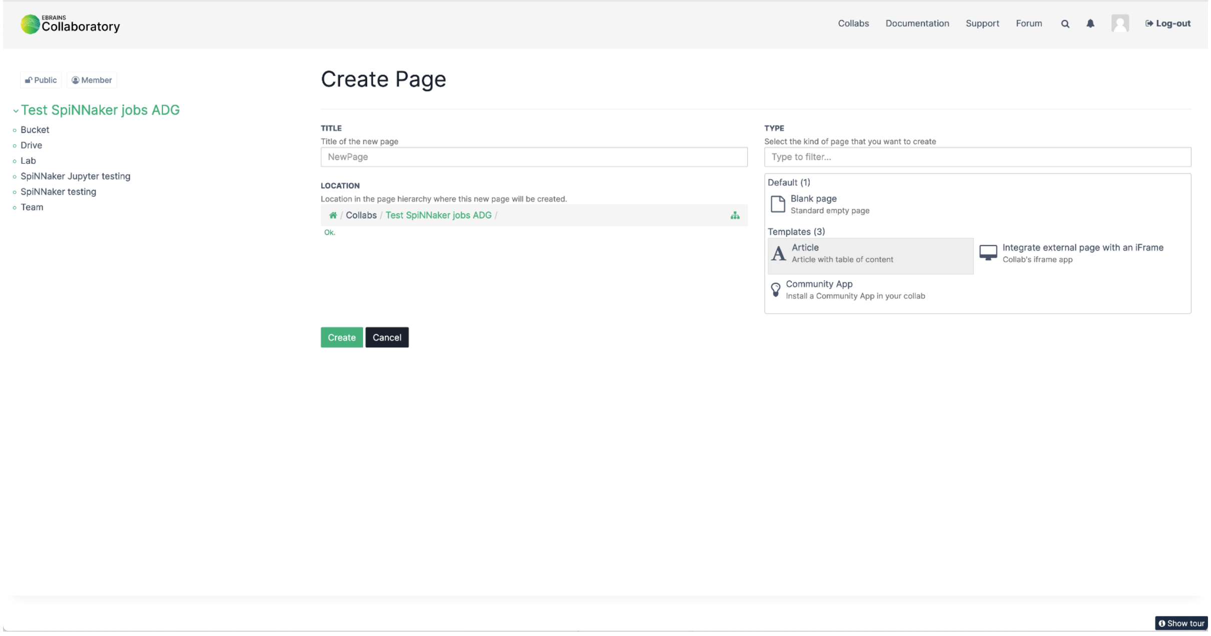
Contents

- Test SpiNNaker jobs
- What can I find here?
- Who has access?

Who has access?

I generally used this in v1 to check problems other users were having with submitting jobs to NMC. If anyone is interested in a SpiNNaker-related collab then we would suggest starting a new one yourself and adding users / SpiNNaker team members to it yourself as required.

4. In this instance, “SpiNNaker testing” links to the portal submission process that we want to use, and “SpiNNaker Jupyter testing” links directly to a Jupyterlab that can be run using your EBRAINS account. To create a portal submission link in this menu, click on the “+ Create” button in the top right to get the following page:



Create Page

TITLE

Title of the new page

NewPage

LOCATION

Location in the page hierarchy where this new page will be created.

/ Collabs / Test SpiNNaker jobs ADG /

Ok.

TYPE

Select the kind of page that you want to create

Type to filter...

Default (1)

Blank page
Standard empty page

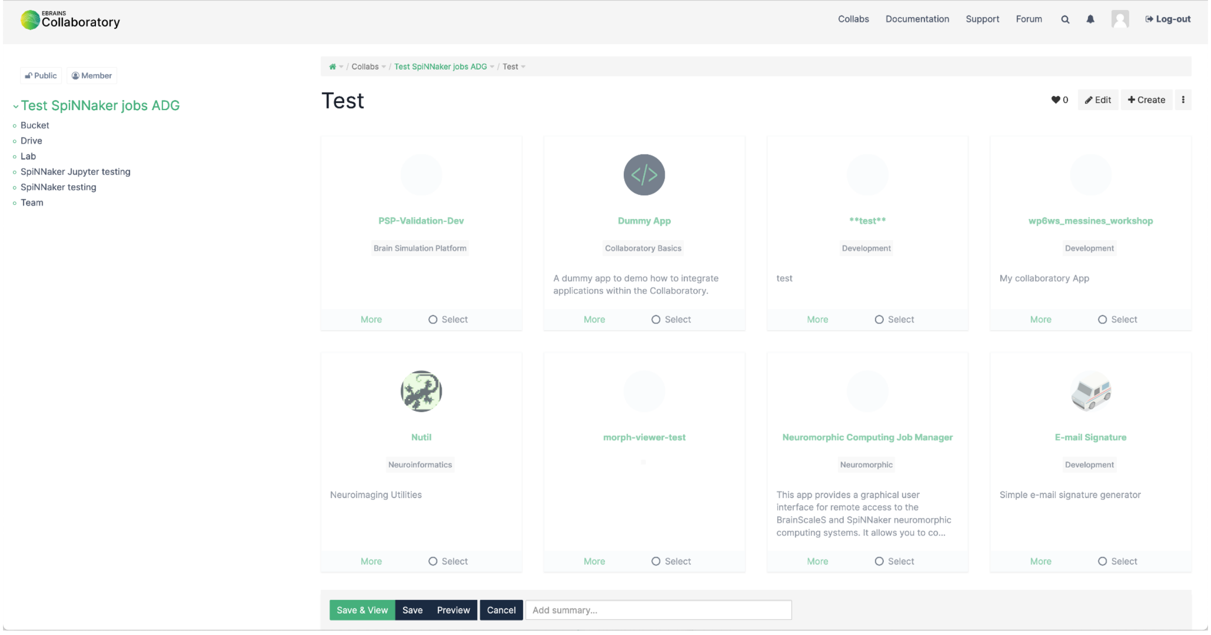
Templates (3)

Article
Article with table of content

Integrate external page with an iFrame
Collab's iframe app

Community App
Install a Community App in your collab

5. Give your new page a Title, then highlight “Community App” and click “Create”



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Test SpiNNaker jobs ADG
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- SpiNNaker Jupyter testing
- SpiNNaker testing
- Team

Collabs / Test SpiNNaker jobs ADG / Test

Test

0 · Edit · Create

PSP-Validation-Dev — Brain Simulation Platform — More · ○ Select

Dummy App — Collaboratory Basics — A dummy app to demo how to integrate applications within the Collaboratory. — More · ○ Select

test — Development — test — More · ○ Select

wp6ws_messines_workshop — Development — My collaboratory App — More · ○ Select

Nutil — Neuroinformatics — Neuroimaging Utilities — More · ○ Select

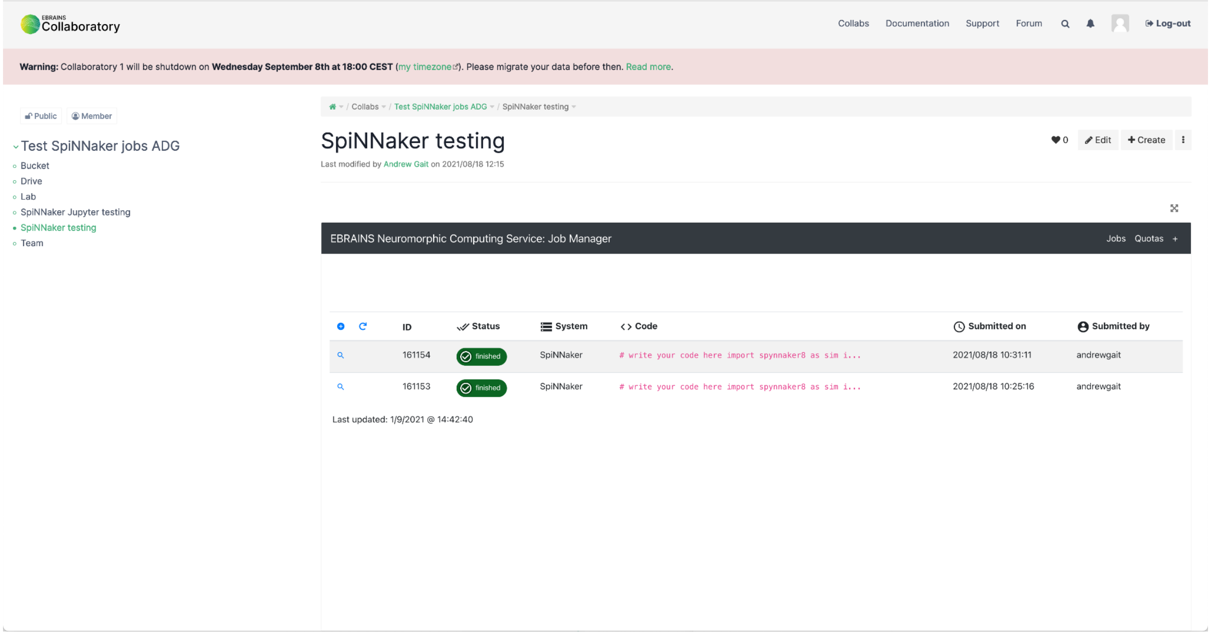
morph-viewer-test — More · ○ Select

Neuromorphic Computing Job Manager — Neuromorphic — This app provides a graphical user interface for remote access to the BrainScaleS and SpiNNaker neuromorphic computing systems. It allows you to co... — More · ○ Select

E-mail Signature — Development — Simple e-mail signature generator — More · ○ Select

Save & View · Save · Preview · Cancel · Add summary...

6. On this Community App screen select the “Neuromorphic Computing Job Manager” and click “Save & View”



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SpiNNaker testing

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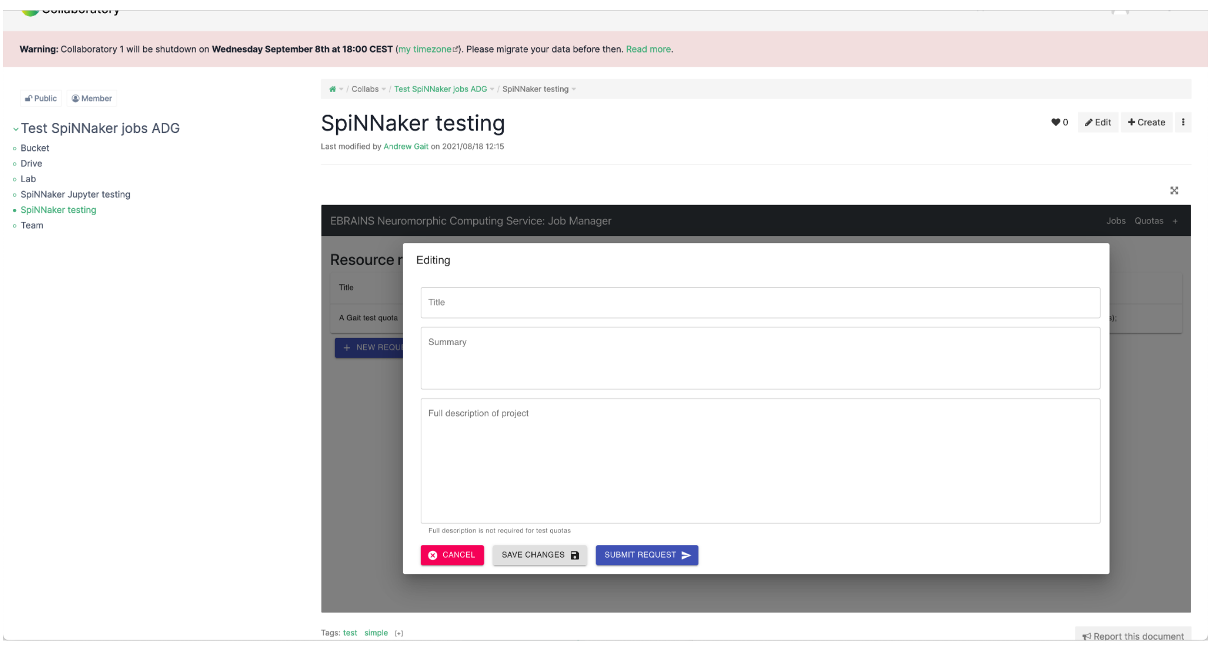
0 · Edit · Create

EBRAINS Neuromorphic Computing Service: Job Manager — Jobs · Quotas · +

ID	Status	System	Code	Submitted on	Submitted by
161154	finished	SpiNNaker	`# write your code here import spynnaker8 as sim i...`	2021/08/18 10:31:11	andrewgait
161153	finished	SpiNNaker	`# write your code here import spynnaker8 as sim i...`	2021/08/18 10:25:16	andrewgait

Last updated: 1/9/2021 @ 14:42:40

7. You should end up with something like this (without the completed jobs). In order to run some jobs using the NMC Job Manager, you will need to request a quota; click on Quotas (on the right of the black bar) and then “New Request” to get to



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SpiNNaker testing

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EBRAINS Neuromorphic Computing Service: Job Manager

Resource r

Title
A Gait test quota

Editing

Title

Summary

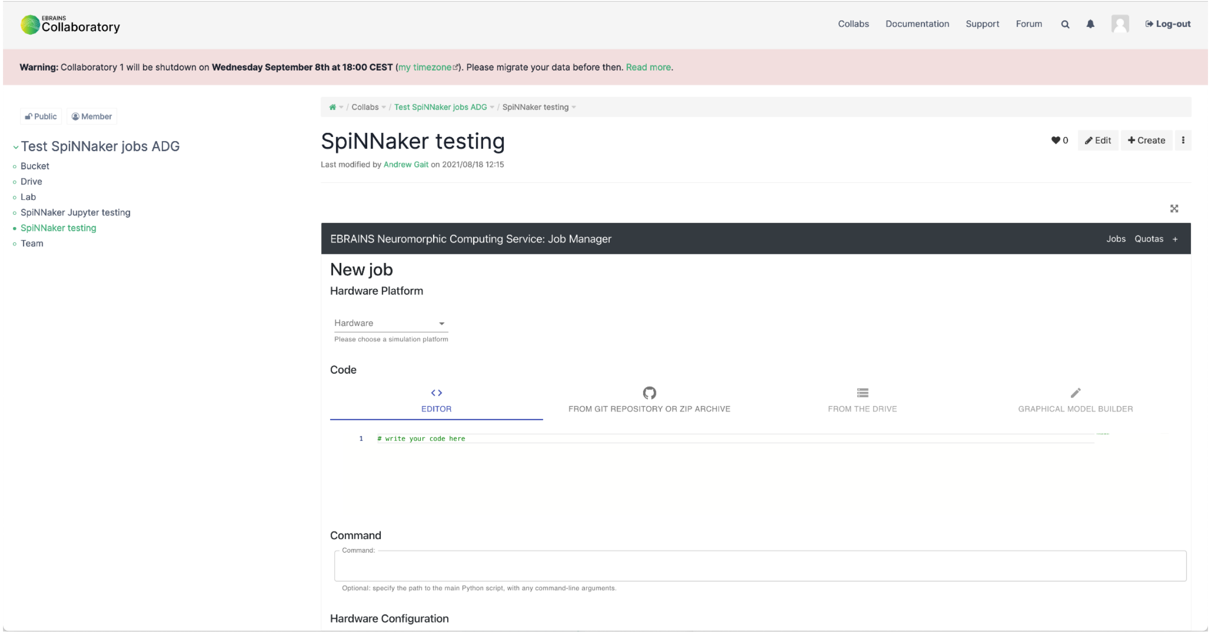
Full description of project

Full description is not required for test quotas

Tags: test simple

where you should fill in the Title & Summary (& Description) accordingly. Once your quota has been approved it will show up when you again click "Quotas".

8. Once your quota has been approved you are now ready to start running jobs. Click on the white plus sign inside a blue circle at the top of the list of jobs, which will take you to the following page:



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EBRAINS Neuromorphic Computing Service: Job Manager

New job

Hardware Platform

Hardware

Please choose a simulation platform

Code

```
1   # write your code here
```

Command

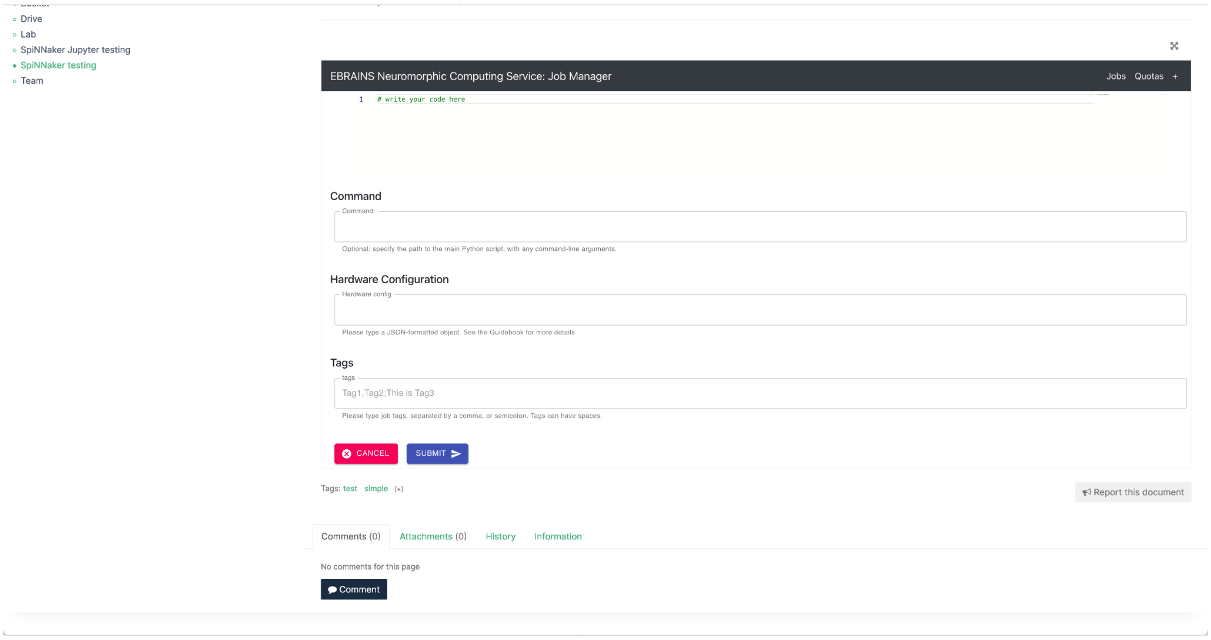
Command:

Optional: specify the path to the main Python script, with any command-line arguments.

Hardware Configuration

9. On this page, under "Hardware Platform" select "SpiNNaker".
10. There are now two ways in which you can submit a PyNN script; either by writing / pasting a script into the editor directly, or directly from a git repository or zip archive file.

11. If you submit a job via a git repository or archive, your script that you wish to run either needs to be called “run.py”, or you need to specify it in the “Command” box along with any (optional) command line arguments.



```
# write your code here
```

Command

Command:

Optional: specify the path to the main Python script, with any command-line arguments.

Hardware Configuration

Hardware config

Please type a JSON-formatted object. See the Guidebook for more details

Tags

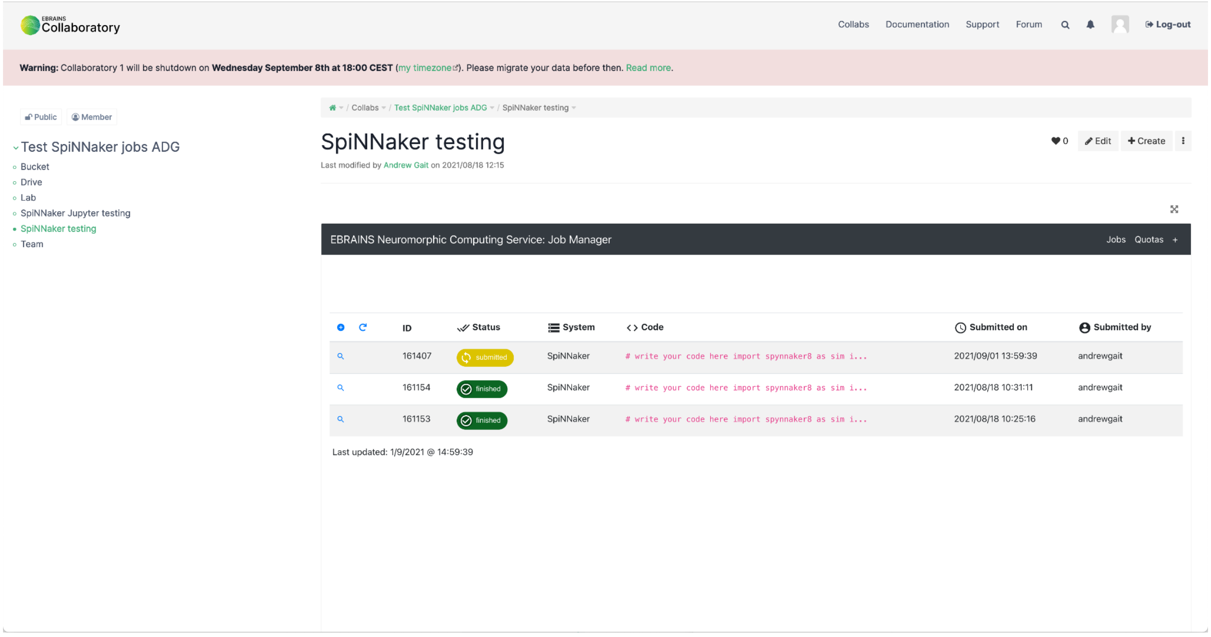
tags: Tag1,Tag2;This is Tag3

Please type job tags, separated by a comma, or semicolon. Tags can have spaces.

Tags: test simple [+]

No comments for this page

12. The “Hardware Configuration” box does not need to be filled in to use the SpiNNaker backend, but gives you some options as to which version of the software you would like to use and whether your script requires any additional installs; for more details see https://electronicvisions.github.io/hbp-sp9-guidebook/using_the_platform.html#hardware-platform-configuration
13. You can additionally put an optional number of tags on your job.
14. Once you are happy with what you have filled in on this page, you can click “Submit”.
15. This will return you to the job list: your Job will start in the “submitted” stage, then “running” stage, then either “finished” or “error”.



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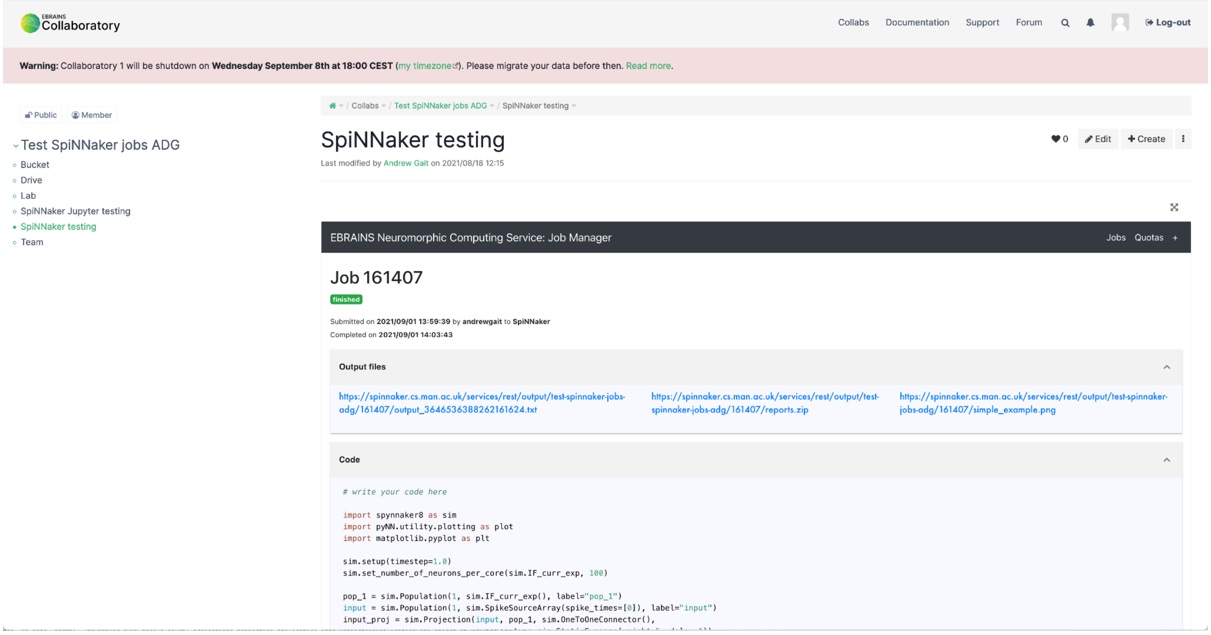
SpiNNaker testing

Last modified by Andrew Gait on 2021/08/18 12:15

	ID	Status	System	Code	Submitted on	Submitted by
	161407	submitted	SpiNNaker	`# write your code here import spynnaker8 as sim i...`	2021/09/01 13:59:39	andrewgait
	161154	finished	SpiNNaker	`# write your code here import spynnaker8 as sim i...`	2021/08/18 10:31:11	andrewgait
	161153	finished	SpiNNaker	`# write your code here import spynnaker8 as sim i...`	2021/08/18 10:25:16	andrewgait

Last updated: 1/9/2021 @ 14:59:39

16. You are able to view more about your job at any stage by clicking on the magnifying glass symbol to the left of the row detailing your job. In particular, while the job is in the “running” state you can see the current state of the log at the bottom of the page.
17. Once your job has reached the finished state, you can then download various files associated with your job:



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SpiNNaker testing

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EBRAINS Neuromorphic Computing Service: Job Manager

Job 161407

Submitted on **2021/09/01 13:59:39** by **andrewgait** to **SpiNNaker**

Completed on **2021/09/01 14:03:43**

Output files

https://spinnaker.cs.man.ac.uk/services/rest/output/test-spinnaker-jobs-adg/161407/output_3646536388262161624.txt

https://spinnaker.cs.man.ac.uk/services/rest/output/test-spinnaker-jobs-adg/161407/reports.zip

https://spinnaker.cs.man.ac.uk/services/rest/output/test-spinnaker-jobs-adg/161407/simple_example.png

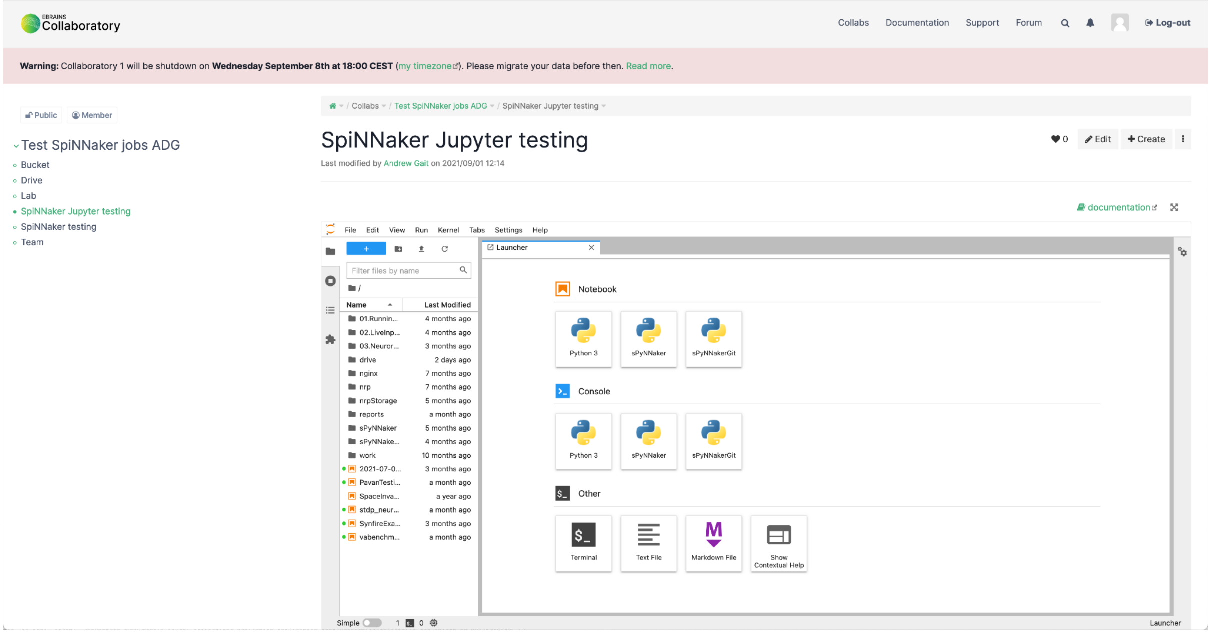
Code

```
# write your code here

import spynnaker8 as sim
import pyNN.utility.plotting as plot
import matplotlib.pyplot as plt

sim.setup(timestep=1.0)
sim.set_number_of_neurons_per_core(sim.IF_curr_exp, 100)

pop_1 = sim.Population(1, sim.IF_curr_exp(), label="pop_1")
input = sim.Population(1, sim.SpikeSourceArray(spike_times=[0]), label="input")
input_proj = sim.Projection(input, pop_1, sim.OneToOneConnector(),
```

Note that compared to a “normal” local run of a PyNN script, in order to plot anything using matplotlib you need to use plt.savefig(filename) rather than plt.show(). Anything plotted in this manner will be saved as one of the files you can download, along with a directory of provenance reporting on your job as well as the output log file of your job. Congratulations, you have now run a PyNN script job via the EBRAINS portal.

2.3 Using the SpiNNaker JupyterLab via EBRAINS

1. It is possible to also use your collab to access SpiNNaker using Jupyter. You may find this an easier and more interactive way to test your PyNN scripts on the machine before running them using the NMC Job Manager described in the previous section. In order to do this, from your collab main page, click on “+ Create”, then from the subsequent page, give what you are creating a “Title”, select “Use Community App”, click “Create”, then on the CommunityApp screen find and highlight the “SpiNNaker Jupyter” app. Once highlighted, click “Save & View”, and this should then log you directly into a SpiNNaker JupyterLab instance as shown in the following image:



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SpiNNaker Jupyter testing

Last modified by Andrew Gait on 2021/09/01 12:14

Name	Last Modified
01.Runnin...	4 months ago
02.LiveInp...	4 months ago
03.Neuror...	3 months ago
drive	2 days ago
nginx	7 months ago
nrp	7 months ago
nrpStorage	5 months ago
reports	a month ago
sPyNNaker	5 months ago
sPyNNake...	4 months ago
work	10 months ago
2021-07-0...	3 months ago
PavanTesti...	a month ago
SpaceInva...	a year ago
stdp_neur...	a month ago
SynfireExa...	3 months ago
vabenchm...	a month ago

For more information about our Jupyter setup see:

http://spinnakermanchester.github.io/common_pages/6.0.0/How_to_use_Jupyter_notebooks_on_SpiNNaker.pdf

Note that you can also use the Jupyter Notebook instance as detailed in the above document by simply doing File - Log Out, then once you log in again from the subsequent screen it will give you the option of using the Notebook or Lab interfaces.