

# SpiNNaker Human Brain Project Portal Introduction

This document describes how to use the Human Brain Project (HBP) portal to run PyNN scripts on SpiNNaker machines.

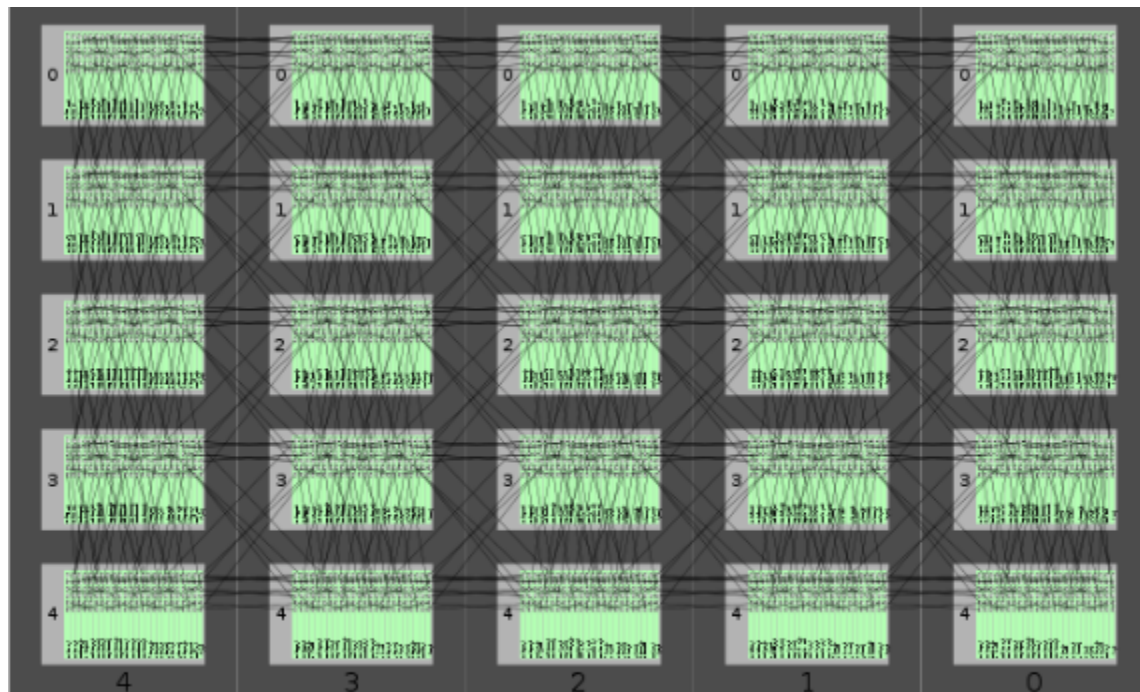
## 1. Getting Started

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

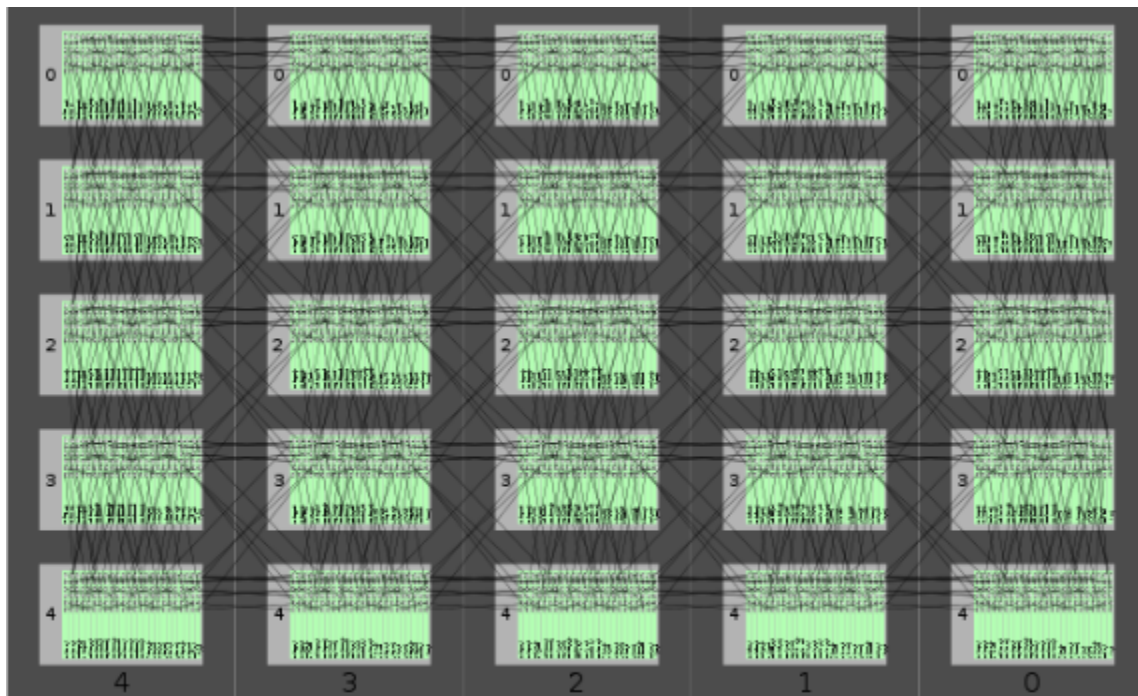
### 1.1 SpiNNaker Machine

Before starting to run PyNN scripts on SpiNNaker machines via the portal, be aware that even though the total SpiNNaker machine capacity currently available via the HBP portal is a 5 cabinet machine, comprising 460,800 cores, as shown in Figure 1 & 2, this, capacity, is not generally available for use without special request; the expectation that most end user's models will not require this level of hardware support. The maximum size machine generally available is a 2 cabinet machine, comprising 184,320 SpiNNaker cores, as shown in Figure 3 & 4.

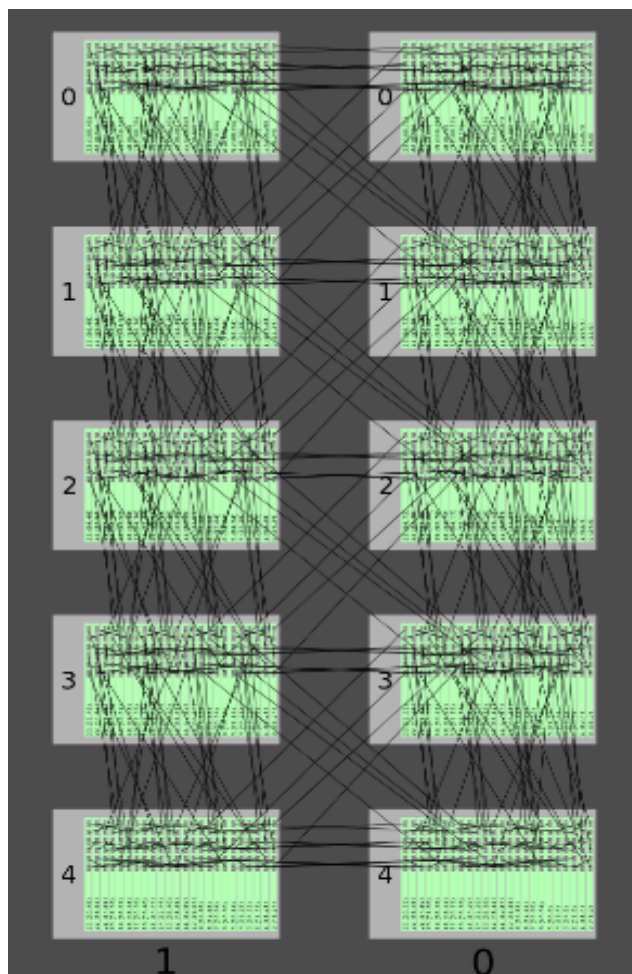
The rest of the SpiNNaker machine (3 cabinets worth) is separated into a number of smaller machines, with differing resources, allowing the opportunity to support multiple jobs in parallel. These machine will consist of XXXXXXXXXXXXXXXXx.



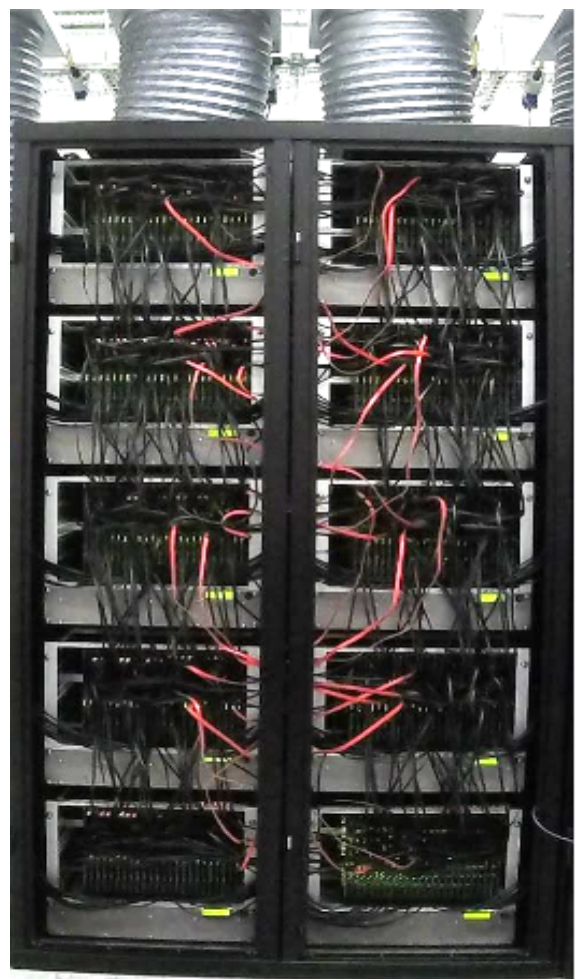
**Figure 1: A 5 cabinet machine, wired together (abstract view).**



**Figure 2: A 5 cabinet machine, wired together (real view).**



**Figure 3: A 2 cabinet machine, wired together (abstract view).**



**Figure 4: A 2 cabinet machine, wired together (real view).**

## 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 120 MBytes of memory, split dynamically between the 16 cores that reside on the chip. On average, every core has available approximately 8 Mbytes to store the neuron parameters as well as the synaptic matrix of the atoms<sup>1</sup> it is executing. Most models, to date, are limited to 256 atoms per core<sup>2</sup>, and therefore the connectivity between these 256 atoms and the rest of the simulation must fit within these rather tight constraints. Figure 5 shows an equation that shows how the amount of space needed by a PyNN model is calculated.

### **Figure 5: the equation for determining the size of SDRAM used by a PyNN model.**

Due to these limitations, the maximum possible number of neurons that can be simulated by a PyNN script on the largest SpiNNaker machine available on the HBP portal is 47,185,920. This sounds rather large, but factor in that each atom needs to have a maximum incoming fixed connections of XXXXXXXX. Any more than this will result in a smaller number of atoms per core, and therefore a smaller total neurons being simulated.

To make matters worse, if the PyNN script has delays greater than 16 machine time steps<sup>3</sup> then each atom will have a delay model attached to it, which in practice reduces the maximum number of atoms simulatable 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 atoms per core. A summary of the rest of the SpiNNaker back end limitations can be found here:

<http://spinnakermanchester.github.io/2015.006.AnotherFineProductFromTheNonsenseFactory/SPyNNakerLimitations.html>

## 1.3 HBP Portal Limitations

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

1. Real time visualisation of an executing PyNN script to a standalone visualization kit.

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<sup>1</sup> Atoms here represents the atomic element which each core models. In the case of PyNN, these are neurons from a given population.

<sup>2</sup> This limitation may be lifted in the future, but to date, this is due the way delay's are implemented on SpiNNaker to date.

<sup>3</sup> 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

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 HBP 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<sup>4</sup>, a list of what is not implemented can be found here:

<http://spinnakermanchester.github.io/2015.006.AnotherFineProductFromTheNonsenseFactory/SPyNNakerLimitations.html>

## 1.5 Recommendations

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

<http://spinnakermanchester.github.io/2015.006.AnotherFineProductFromTheNonsenseFactory/PyNNOnSpinnakerInstall.html>

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

<http://spinnakermanchester.github.io/2015.006.AnotherFineProductFromTheNonsenseFactory/VirtualMode.html>

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<sup>4</sup> This is the spinnaker software stacks front end for simulating PyNN neuron models.



## 2. Running A PyNN script on the HBP portal

This section describes how an end user starts a PyNN simulation on the HBP Portal/collaboratory.

### 2.1 Getting a HBP account

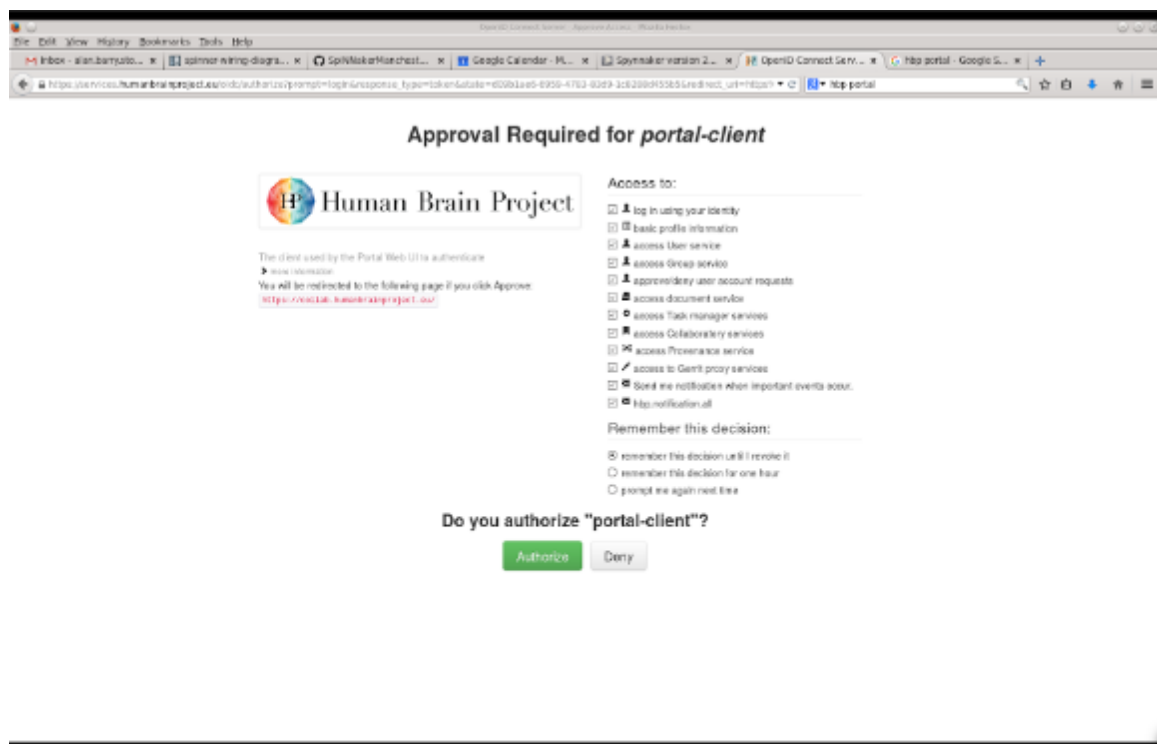
To acquire a HBP account, communicate with the head of your HBP SP which can organise getting account details.

### 2.2 Creating a Job on the HBP portal/collaboratory.

1. First must log onto the HBP portal/collaboratory via the link below:

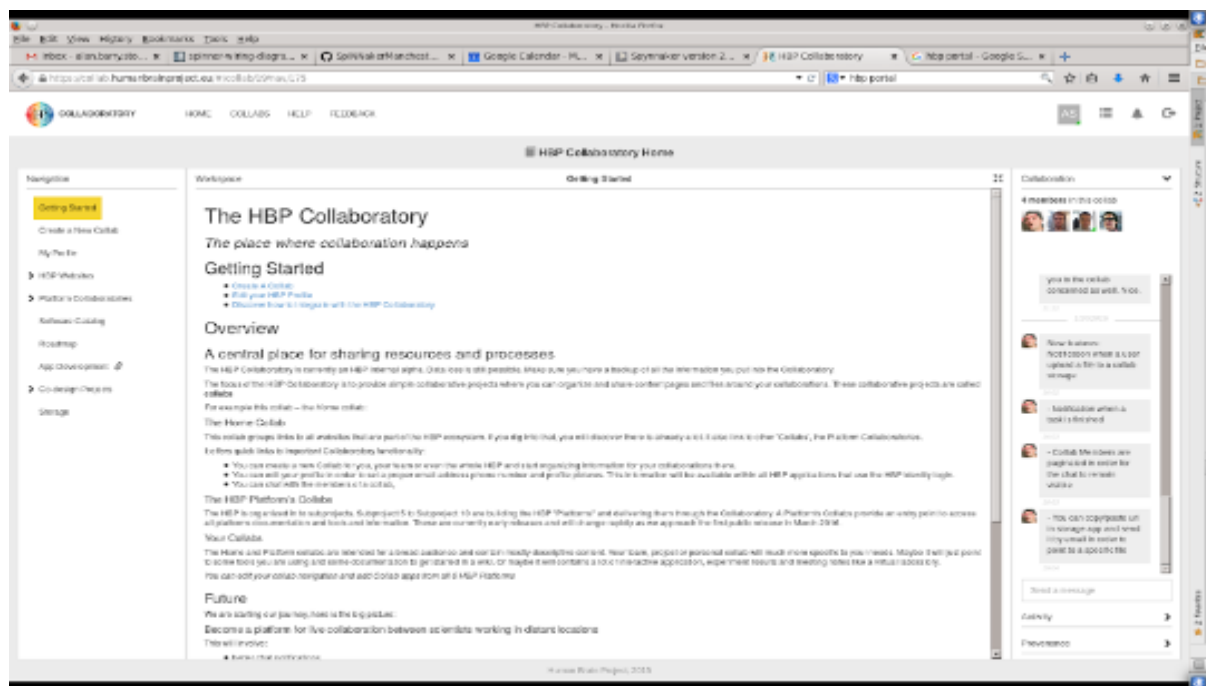
<https://collab.humanbrainproject.eu/>

2. If you have not logged on before, you may be presented with an Approval request by the portal-client, as shown in Figure 6. If you encounter this, we recommend Authorizing this request, as otherwise ??????????????????



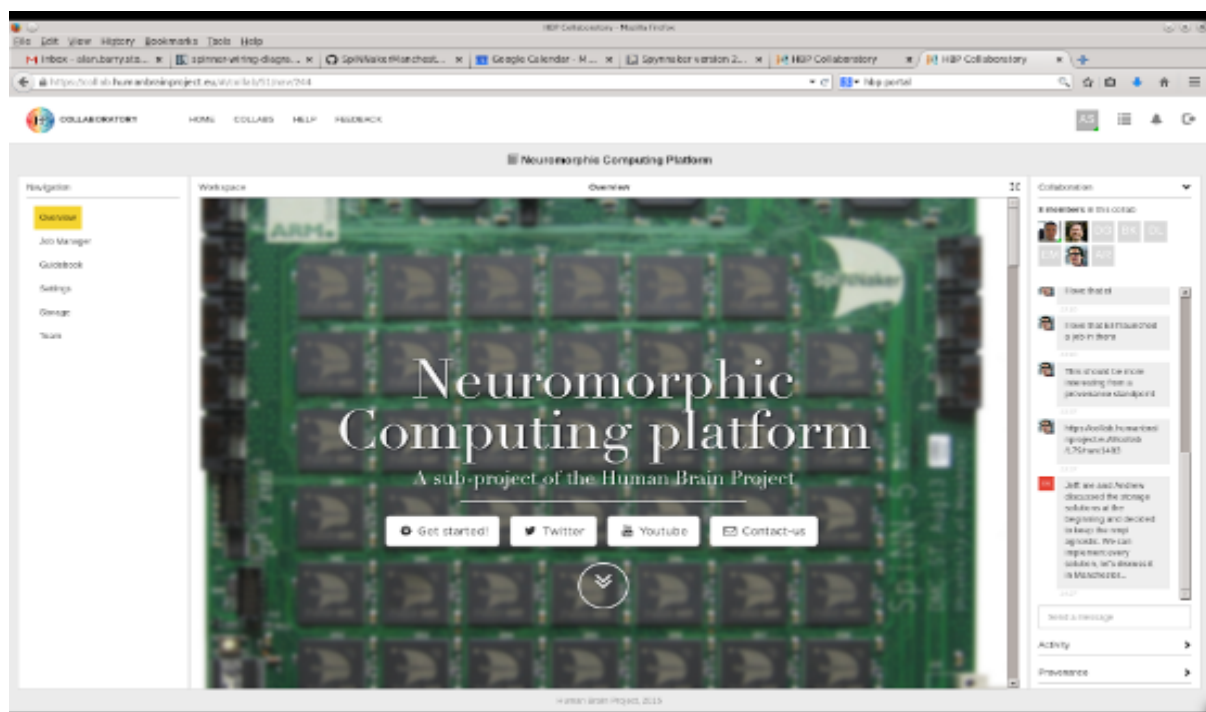
**Figure 6: Approval Request for portal-client**

3. Once you log onto the HBP portal, you should see a screen such as in Figure 7.



**Figure 7: HBP portal/Collaboratory Home Page**

- On the left sidebar, open up the tab called “Platform Collaboratories” (5th one down) and click on “Neuromorphic” (5th one down). You should then see the page shown in Figure 8.



**Figure 8: Neuromorphic Computing Platform Home page**

- From the sidebar, click on Job Manager (second one down). You should then see a page such as Figure 9. This lists all the jobs that have been submitted to the HBP portal to which you have approval to view.

The screenshot shows the HBP portal interface. The top navigation bar includes 'COLLABORATORY', 'HOME', 'COLLAB', 'HELP', and 'FEEDBACK'. The main header is 'Neuromorphic Computing Platform'. The left sidebar has 'Overview', 'Job Manager' (highlighted), 'Dashboard', 'Settings', 'Storage', and 'Team'. The main content area is titled 'Job Manager' and displays a table of submitted jobs.

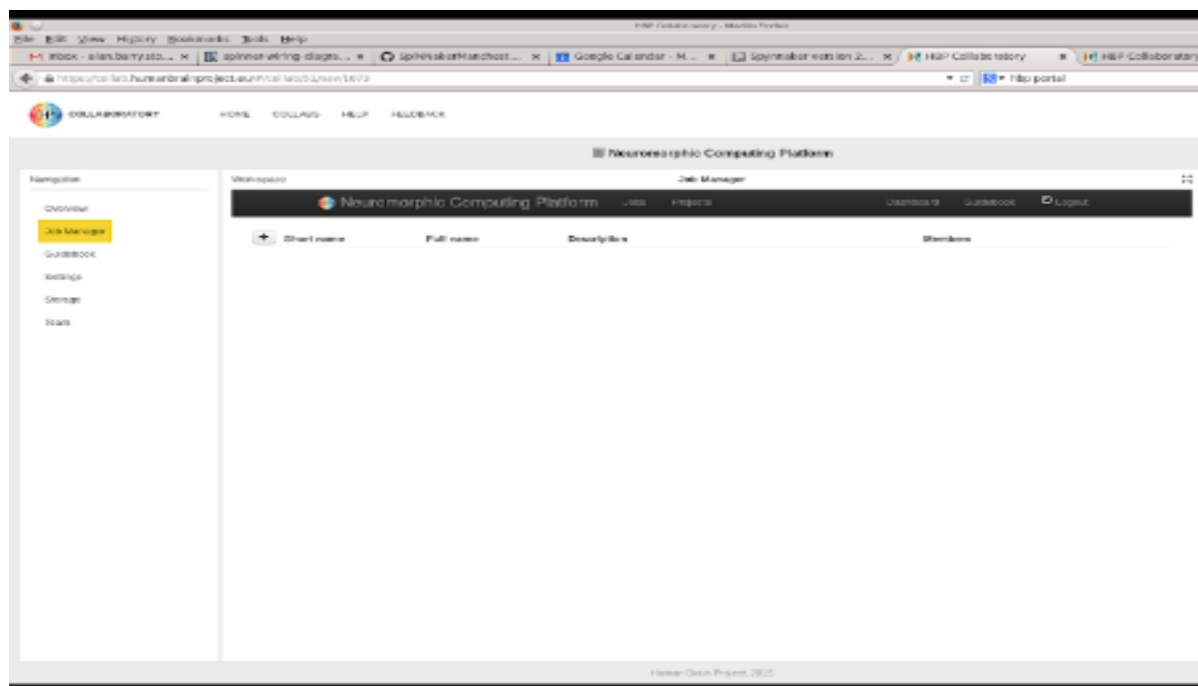
ID	Status	Platform	Date	Project	Submitted on	Submitted by
18076	Failed	NU-MC1	*** RyeTirechab: like example ***	Import: pytk, spik...	2018-10-12 13:43:29	stphs
18077	Failed	NU-MC1	*** RyeTirechab: like example ***	Import: pytk, spik...	2018-10-12 13:48:11	stphs
18078	Failed	NU-MC1	*** RyeTirechab: like example ***	Import: pytk, spik...	2018-10-12 13:48:13	stphs
21008	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-10-31 21:29:04	ruben
21004	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 08:47:02	ruben
21005	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 08:48:02	ruben
21006	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 08:54:00	ruben
21007	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 17:47:00	ruben
21008	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 17:48:02	ruben
21009	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 17:50:00	ruben
21010	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 17:52:17	ruben
21011	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 17:53:28	ruben
21012	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 17:54:00	ruben
21013	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 17:58:02	ruben
21014	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 18:00:00	ruben
21015	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 18:00:45	ruben
21016	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 18:03:29	ruben
21017	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 18:04:44	ruben
21018	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 18:13:23	ruben
21019	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 18:18:42	ruben
21040	Failed	NU-MC1	Import: pytk, spik...	Import: pytk, spik...	2018-11-01 19:22:55	ruben

**Figure 9: Previous submitted Jobs on the HBP portal.**

- If you already have a project created, then go to point 13, otherwise carry on reading.
- If you have not created a project before, above the "Create Job" title is a header, which contains a "project" tab, as shown in Figure 10. Please click on the Projects tab. This will take you to a page as shown in Figure 11.

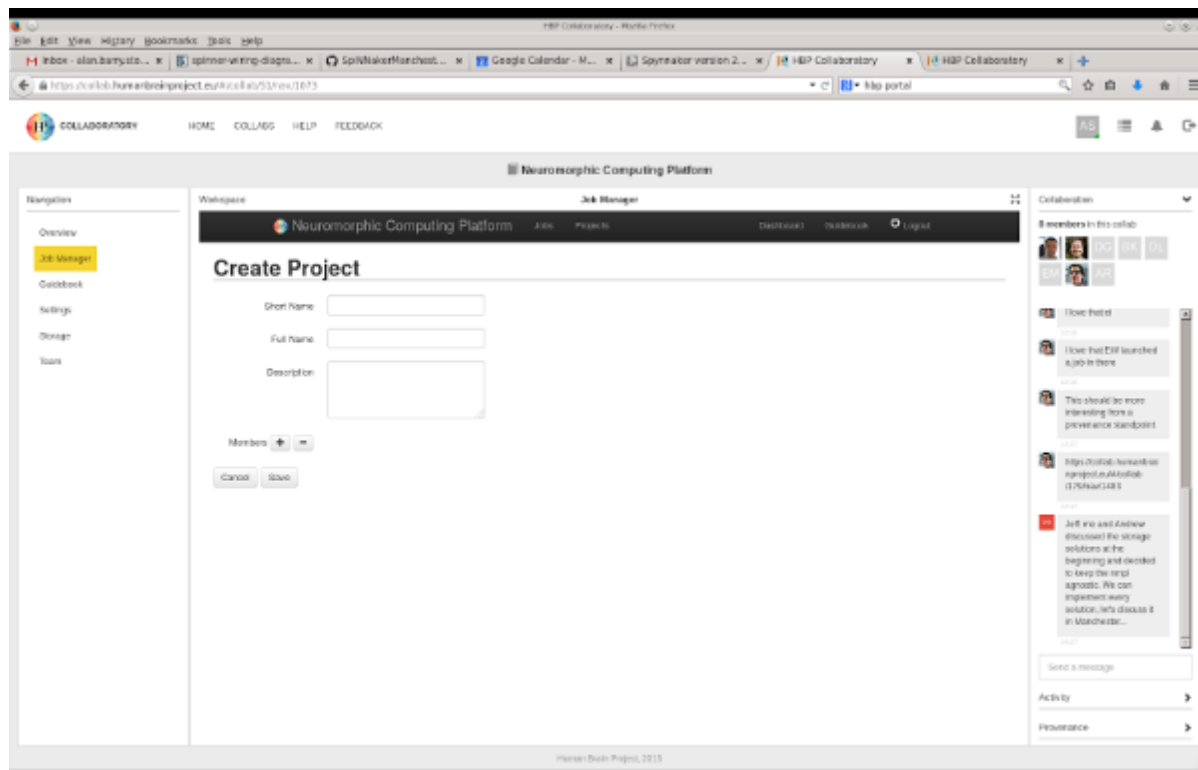


**Figure 10: projects tab**



**Figure 11: Project Listing screen**

8. To create a new project look for the + sign on the left hand side of the column “short name”. Click on this button will result in the screen in Figure 12.



**Figure 12: Create Project page**



9. Fill in the three boxes accordingly.
10. On the members button, click + and add “**uman**” as one of the members, as well as yourself. Click save and you should be sent back to a screen such as the one in Figure 11.
11. You should see that the screen has changed slightly, in that there is now a notification saying “Your project has been created” and the listing should now include an entry which is your project.
12. To get back to the page where you can add new jobs, refresh the job manager page. The easiest way to do this is to click on the overview tab on the left side of the page, and then click on the Job Manager page again. You should get back to the screen as shown in Figure 9.
13. To submit a new job, look for a + sign button (will be located at the top of the list of previously ran jobs) and click it. This will take you into a window such as the one shown in Figure 13.

The screenshot shows the 'Create Job' interface of the Neuromorphic Computing Platform. The left sidebar includes 'Overview' and 'Job Manager'. The main content area is titled 'Create Job' and contains the following fields:

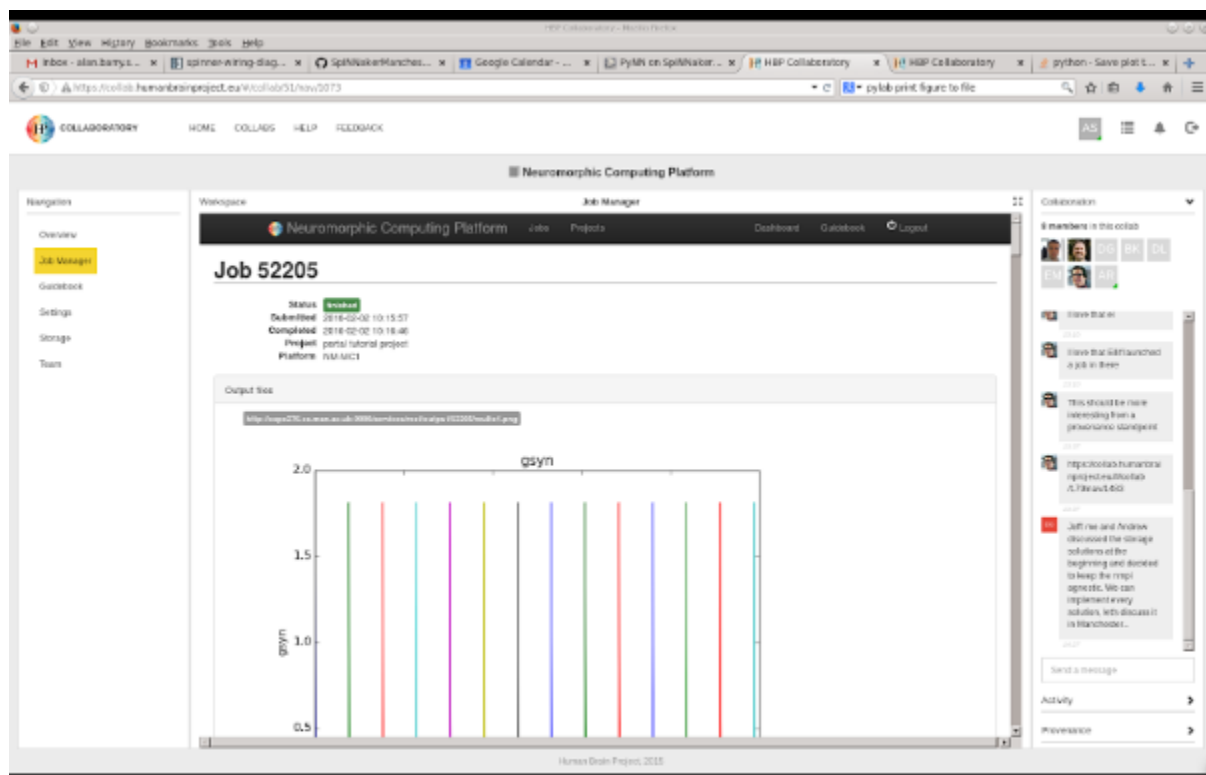
- Project:** A dropdown menu.
- Hardware Platform:** A dropdown menu.
- Description:** A large text input area.
- Hardware Config:** A large text input area.
- Input File:** A button with a plus icon and a file selection interface.
- Buttons:** 'Cancel' and 'Submit' buttons at the bottom.

The right sidebar features a 'Collaboration' section showing 8 members and a chat window with messages.

**Figure 13: Job creation page**

14. Firstly, open the drop down for the Project and select your projects “long title”.
15. To create a job that runs on the SpiNNaker platform you must select NM-MC1 from the “Hardware Platform” field.
16. “Description” can be one of 2 options. These are:
  - A PyNN script that you’re going to run.
  - A URL to a github repository which requires to have a script called run.py within in.
17. “Hardware Config” does not need to be filled in to use the SpiNNaker backend.

18. Click Submit. This has now submitted your job to the HBP portal, and you'll be moved back to the page displayed in Figure 9 but with the notification "Your Job has been submitted. You will receive further updates by email"
19. To get access to the results. Scroll down the page to the bottom, where the most recent jobs have been placed.
20. Your Job will start in the "submitted" stage, then "running" stage, then either "finished" or "error".
21. To get the output from the script, once the script has reached "finished" state, click on the magnifying glass symbol next to your job. You should go to a page like the one shown in Figure 14.



**Figure 14: Script Output Page**

22. A more detailed description of this behaviour for all platforms, and how to use the HBP portal in scripted mode can be found here:

<https://collab.humanbrainproject.eu/#/collab/51/nav/1069>

Congratulations, you have now ran a PyNN script job via the HBP portal.