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Abstract:	The prototype, which is available for use by members of the HBP Consortium, comprises alpha releases of all the key components of the Platform, including the brain builder, the simulators and first draft models of major regions of the mouse brain.		
Keywords:	Platform, App, Collab, Internal Release, Brain Simulation, Brain Building		

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1. The Aim of this Document

This document provides the information needed to access the Brain Simulation Platform v1 - preliminary release for internal Consortium use (Deliverable D6.7.3, Milestone 124).

The documentation on the features in the system currently available is available at web locations specified in links below.

2. How to Access the HBP Brain Simulation Platform

The Brain Simulation Platform v1 is accessed via the HBP Collaboratory.

The HBP Collaboratory URL is:

<https://collab.humanbrainproject.eu/#/collab/161/nav/1389>

The Brain Simulation Platform Collaboratory URL is:

<https://collab.humanbrainproject.eu/#/collab/161/nav/1389>

3. HBP Identity Service login

The HBP Collaboratory uses the HBP Identity Service to log in. To get an HBP Identity Service account, please register for an account at:

<https://services.humanbrainproject.eu/oidc/account/request>.

You will be required to enter the following information:

- First name
- Last name
- An institutional email address
- Birth date
- Gender
- Subproject of your primary HBP contribution
- Institution - Only HBP Consortium members are currently on this list. If your home institution does not appear on the list, please contact support at hbp-platform-support@groupes.epfl.ch.

4. Access to HBP HPC platform

Many of the functionalities provided by the Brain simulation platform require an access to the HPC platform:

For web accessible services and application, you will in most case need to provide a “HPC project” to run a job. You will also need to be granted access to the HPC projects where the data are located:

<https://collab.humanbrainproject.eu/#/collab/264/nav/3304>

For gnu-modules, you will need to login (through SSH for instance) to the HPC facility, and load the gnu-modules in order to access the software:

<https://collab.humanbrainproject.eu/#/collab/161/nav/3171>

5. Platform User Instructions

A screenshot of the Brain Simulation Platform homepage is shown in Annex 2.

The guidebook for the internal release can be found via: Brain Simulation Platform>Platform Functionality>Internal Release V1”.

6. Help and User Feedback

For user help, please contact: bsp-support@humanbrainproject.eu.

To provide user feedback, please contact: bsp-support@humanbrainproject.eu.

Alternatively, users can use the chat function in the Brain Simulation Platform directly, as shown in Figure 3 (see Annex 2).

7. Annexes

- 1) Tools & Features Available in this Platform Release
- 2) Screenshots of Tools & Features Available in this Platform Release

Annex 1: Tools & Functions Available in this Platform Release

Milestone	Milestone Description	Responsible	Tool/Function	Available at *	Keywords
MS111	Software application to fit ion channel densities to reproduce any target electrophysiology, v1	WP6.1 Henry MARKRAM	<ul style="list-style-type: none"> OptimizerFramework 	https://collab.humanbrainproject.eu/#/collab/161/nav/2997 as gnu-module (not open source)	Tool; electrophysiology
			<ul style="list-style-type: none"> Electrophysiology Feature Extraction Library 	https://collab.humanbrainproject.eu/#/collab/161/nav/2996 as open source software	Tool; electrophysiology
			<ul style="list-style-type: none"> ModelManagement 	https://collab.humanbrainproject.eu/#/collab/161/nav/2998 as gnu-module (not open source)	Tool; electrophysiology
MS112	Software to synthesise cellular morphologies, including projecting axons, v1	WP6.1 Henry MARKRAM	<ul style="list-style-type: none"> Morphology utility toolkit 	https://collab.humanbrainproject.eu/#/collab/161/nav/3001 as gnu-module (not open source)	Library; morphology
			<ul style="list-style-type: none"> Morphology repair 	https://collab.humanbrainproject.eu/#/collab/161/nav/3002 as gnu-module (not open source)	Library; morphology
			<ul style="list-style-type: none"> Blue repair SDK 	https://collab.humanbrainproject.eu/#/collab/161/nav/3003 as gnu-module (not open source)	Library; morphology
			<ul style="list-style-type: none"> Axon splicing 	https://collab.humanbrainproject.eu/#/collab/161/nav/3004 as gnu-module (not open source)	Library; morphology
			<ul style="list-style-type: none"> NeuronM 	https://collab.humanbrainproject.eu/#/collab/161/nav/3000 as open source software	Library; morphology; analysis
MS113	Multi-scale cellular simulator (with a range of neuron models from point neurons to detailed neurons) v1	WP6.2 Felix SCHÜRMANN	<ul style="list-style-type: none"> CoreNeuron 	https://collab.humanbrainproject.eu/#/collab/161/nav/2991 as gnu-module	Simulation



MS114	Network Simulator	WP6.2	<ul style="list-style-type: none"> • NEST 	https://collab.humanbrainproject.eu/#/collab/161/nav/2988 as open source software	Simulation
MS116	Drug binding affinities	WP6.3	<ul style="list-style-type: none"> • publication 	http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0135998	Initial Model
MS117	Protein-protein and ligand-protein interactions	WP6.3	<ul style="list-style-type: none"> • SDA 	http://mcm.h-its.org/webSDA as web application	Simulator
MS119	First draft model of somatosensory cortex	WP6.4 Jeanette HELLGREN-KOTALESKI	<ul style="list-style-type: none"> • Draft point neuron model 	Package on HBP Development Computer filesystem	Initial Model
MS120	Advanced methods for automated cellular-level modelling of neurons	WP6.4 Jeanette HELLGREN-KOTALESKI	<ul style="list-style-type: none"> • OptimizerFramework 	https://collab.humanbrainproject.eu/#/collab/161/nav/2997 as open source software	Tool; electrophysiology

MS121	Hippocampus CA1	WP6.4 Jeanette HELLGREN- KOTALESKI	<ul style="list-style-type: none"> Publication 	https://forum.humanbrainproject.eu/t/first-draft-model-of-hippocampus-ca1-microcircuit/86	Initial Model
MS124	Brain Simulation Platform v1 ready for internal release	WP6.5 Felix SCHÜRMANN	<ul style="list-style-type: none"> Brain builder (Function no. 6.1.1.1) 	Due November 2015	
			<ul style="list-style-type: none"> Validations (Function no. 6.1.1.2) 	https://collab.humanbrainproject.eu/#/collab/161/nav/3006 as gnu-module (not open source)	Library; validation
			<ul style="list-style-type: none"> Compound model and model component analysis (Function no. 6.1.1.3) 	Mosaic analysis task https://collab.humanbrainproject.eu/#/collab/161/nav/3048 as webservice https://collab.humanbrainproject.eu/#/collab/161/nav/3164 as webservice	Task; analysis
				Layer analysis task https://collab.humanbrainproject.eu/#/collab/161/nav/3047 as webservice https://collab.humanbrainproject.eu/#/collab/161/nav/3164 as webservice	Task; analysis
				Morphology collage task https://collab.humanbrainproject.eu/#/collab/161/nav/3046 as web service https://collab.humanbrainproject.eu/#/collab/161/nav/3164 as web service	Task; analysis
				Bluepy circuit analysis library https://collab.humanbrainproject.eu/#/collab/161/nav/2986 as gnu-module	Library; analysis

			<ul style="list-style-type: none"> Simulation analysis tools (Function no. 6.1.1.4) 	Post Simulation Analysis Workflow https://collab.humanbrainproject.eu/#/collab/161/nav/2983 as gnu-module	Tool; analysis
				Bluepy simulation analysis library https://collab.humanbrainproject.eu/#/collab/161/nav/2986 as gnu-module	Library; analysis
			<ul style="list-style-type: none"> Collaborative review process (Function no. 6.1.1.5) 	Circuit viewer https://collab.humanbrainproject.eu/#/collab/161/nav/3178 as web application	Viewer; circuit
				Simulation configuration viewer https://collab.humanbrainproject.eu/#/collab/161/nav/3179 as web application	Viewer; simulation
				Circuit validation reports: https://collab.humanbrainproject.eu/#/collab/327/nav/3169 as web application https://collab.humanbrainproject.eu/#/collab/327/nav/3170 as web application	Viewer; validation
				Simulation analysis report https://collab.humanbrainproject.eu/#/collab/327/nav/3232 as web application	Viewer; simulation; analysis

			<ul style="list-style-type: none"> Simulation configure and launch (Function no. 6.1.5.1) 	Cortical microcircuit simulation https://collab.humanbrainproject.eu/#/collab/161/nav/3086 as web service	Task; simulation
				Brunel network simulation https://collab.humanbrainproject.eu/#/collab/161/nav/3087 as web-service	Task; simulation
				Tsodyks synapse simulation https://collab.humanbrainproject.eu/#/collab/161/nav/3088 as web-service	Task; simulation
				Single neuron simulation https://collab.humanbrainproject.eu/#/collab/161/nav/3107 as web-service	Task; simulation
MS124	Brain Simulation Platform v1 ready for internal release - initial models	WP6.4 Jeanette HELLGREN-KOTALESKI	<ul style="list-style-type: none"> Neocortical Neuron Models Neocortical Microcircuit Model 	https://collab.humanbrainproject.eu/#/collab/161/nav/3183	Initial Models
MS128	Guidebook for the use of the Brain Simulation Platform - initial release	WP6.6 Felix SCHÜRMANN	<ul style="list-style-type: none"> Introduction guidebook 	https://collab.humanbrainproject.eu/#/collab/161/nav/3162	Guidebook; support; overview; example

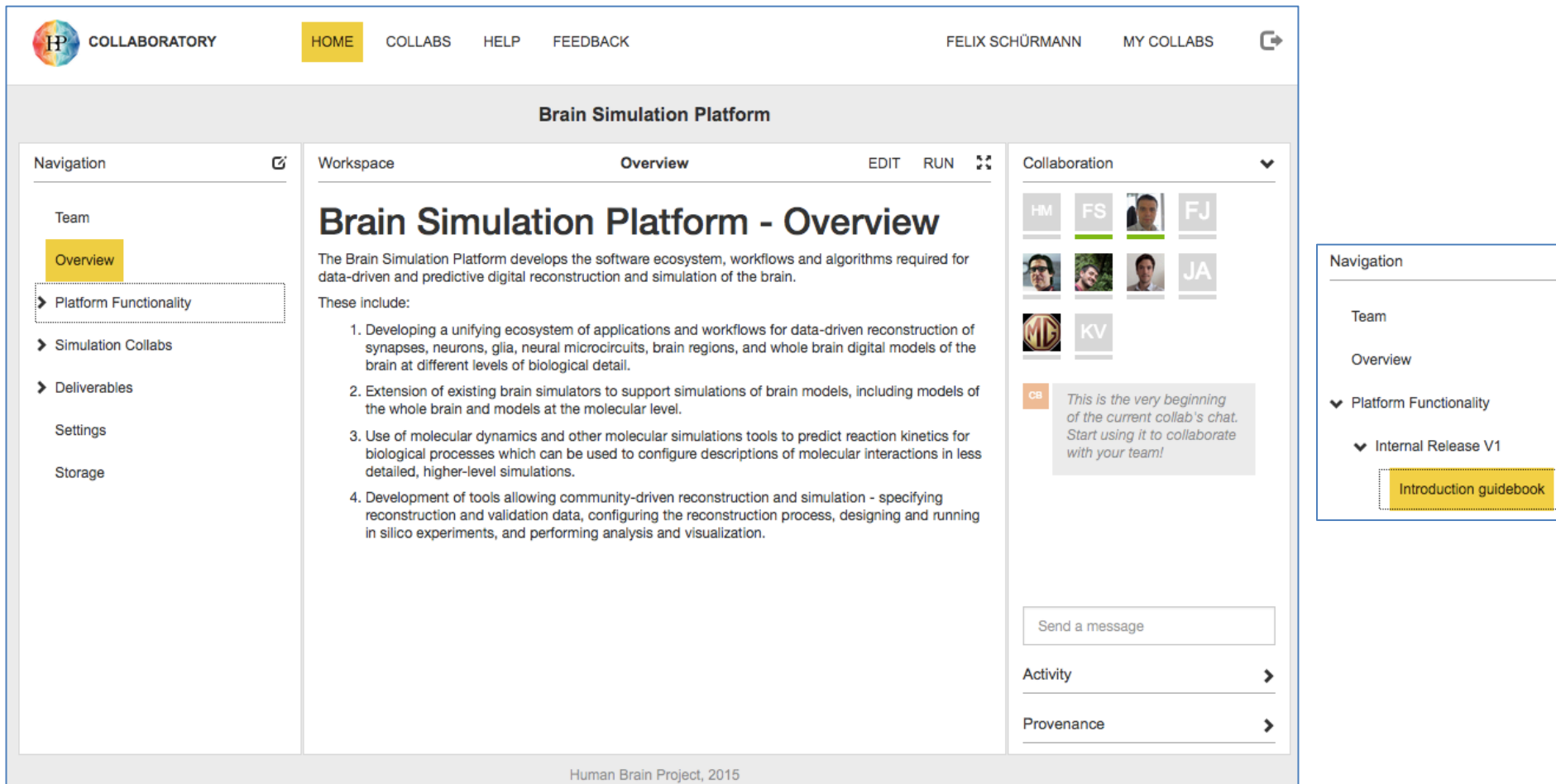
* “as open source software”: available as a open source software

“ as gnu-module” : installed and accessible on the HPC facility as a GNU module.

“as web-service”: accessible through a REST API or through a generated GUI in the collaboratory

“as web-application”: accessible through a GUI in the collaboratory

Annex 2: Screenshots of Tools & Features Available in this Platform Release



The screenshot displays the Brain Simulation Platform interface. The top navigation bar includes the HP Collaboratory logo, a 'HOME' button, and links for 'COLLABS', 'HELP', and 'FEEDBACK'. The user 'FELIX SCHÜRMANN' and 'MY COLLABS' are also visible.

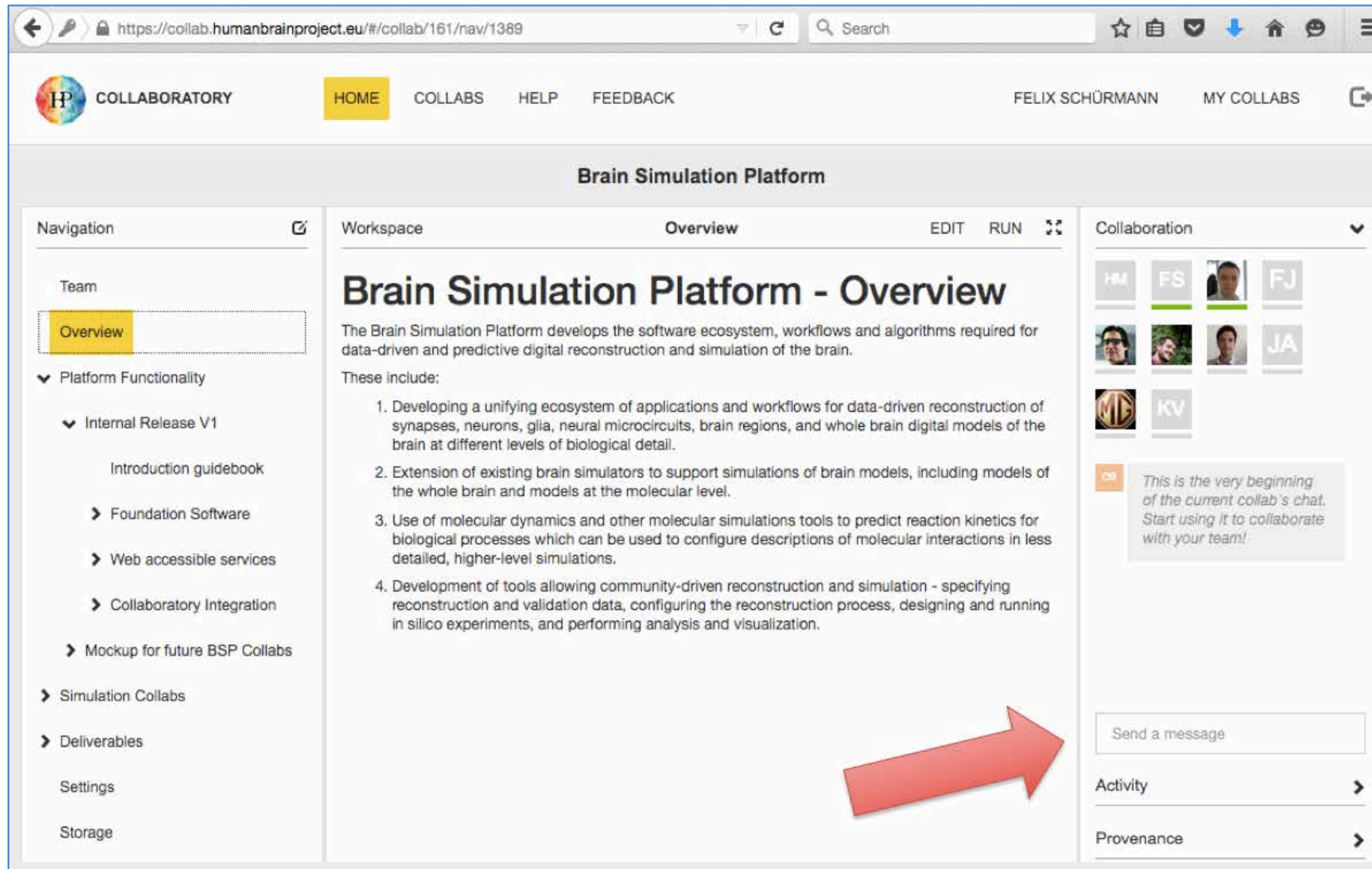
The main content area is titled 'Brain Simulation Platform' and is divided into three sections:

- Navigation:** A sidebar on the left with links for 'Team', 'Overview' (highlighted), 'Platform Functionality', 'Simulation Collabs', 'Deliverables', 'Settings', and 'Storage'.
- Workspace:** The central area titled 'Brain Simulation Platform - Overview'. It contains a description of the platform's purpose and a list of four key features:
 - Developing a unifying ecosystem of applications and workflows for data-driven reconstruction of synapses, neurons, glia, neural microcircuits, brain regions, and whole brain digital models of the brain at different levels of biological detail.
 - Extension of existing brain simulators to support simulations of brain models, including models of the whole brain and models at the molecular level.
 - Use of molecular dynamics and other molecular simulations tools to predict reaction kinetics for biological processes which can be used to configure descriptions of molecular interactions in less detailed, higher-level simulations.
 - Development of tools allowing community-driven reconstruction and simulation - specifying reconstruction and validation data, configuring the reconstruction process, designing and running in silico experiments, and performing analysis and visualization.
- Collaboration:** A sidebar on the right showing a grid of user avatars (HM, FS, FJ, JA, KV, CB) and a chat window with the message: 'This is the very beginning of the current collab's chat. Start using it to collaborate with your team!'.

At the bottom right, a 'Navigation' sidebar is shown, highlighting the 'Introduction guidebook' under the 'Internal Release V1' section.

The footer of the interface reads 'Human Brain Project, 2015'.

Figure 1: Screenshot of the Brain Simulation Platform Homepage (left), and navigation to Guidebook (right)



Navigation

Team

Overview

Platform Functionality

Internal Release V1

Introduction guidebook

Foundation Software

Web accessible services

Collaboratory Integration

Mockup for future BSP Collabs

Simulation Collabs

Deliverables

Settings

Storage

Workspace

Overview

Brain Simulation Platform - Overview

The Brain Simulation Platform develops the software ecosystem, workflows and algorithms required for data-driven and predictive digital reconstruction and simulation of the brain.

These include:

1. Developing a unifying ecosystem of applications and workflows for data-driven reconstruction of synapses, neurons, glia, neural microcircuits, brain regions, and whole brain digital models of the brain at different levels of biological detail.
2. Extension of existing brain simulators to support simulations of brain models, including models of the whole brain and models at the molecular level.
3. Use of molecular dynamics and other molecular simulations tools to predict reaction kinetics for biological processes which can be used to configure descriptions of molecular interactions in less detailed, higher-level simulations.
4. Development of tools allowing community-driven reconstruction and simulation - specifying reconstruction and validation data, configuring the reconstruction process, designing and running in silico experiments, and performing analysis and visualization.

Collaboration

Send a message

Activity

Provenance

Figure 2: Brain Simulation Platform with Chat Function Highlighted

Circuit viewer app

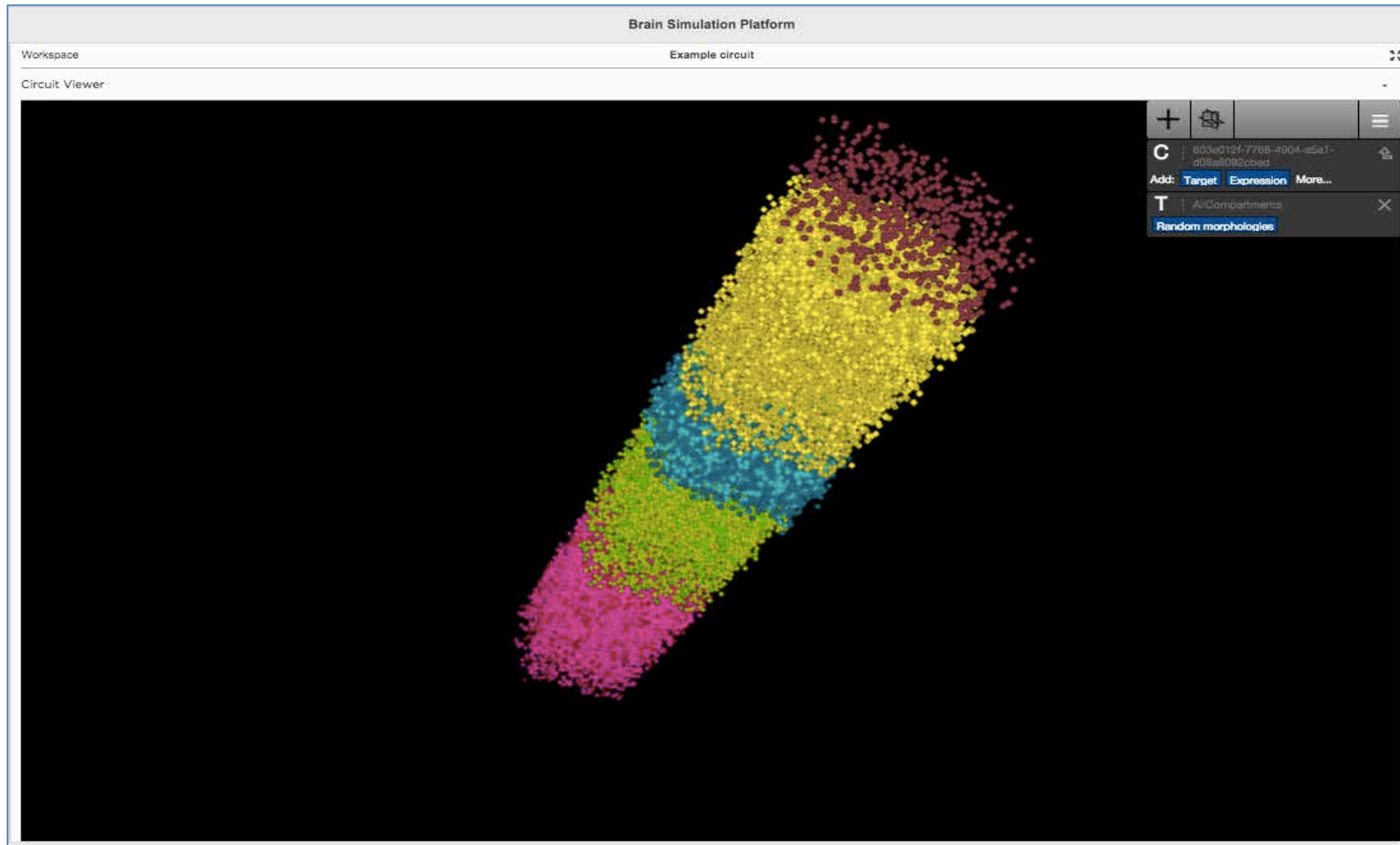


Figure 3: Screenshot of the Circuit Viewer App

Simulation Viewer app

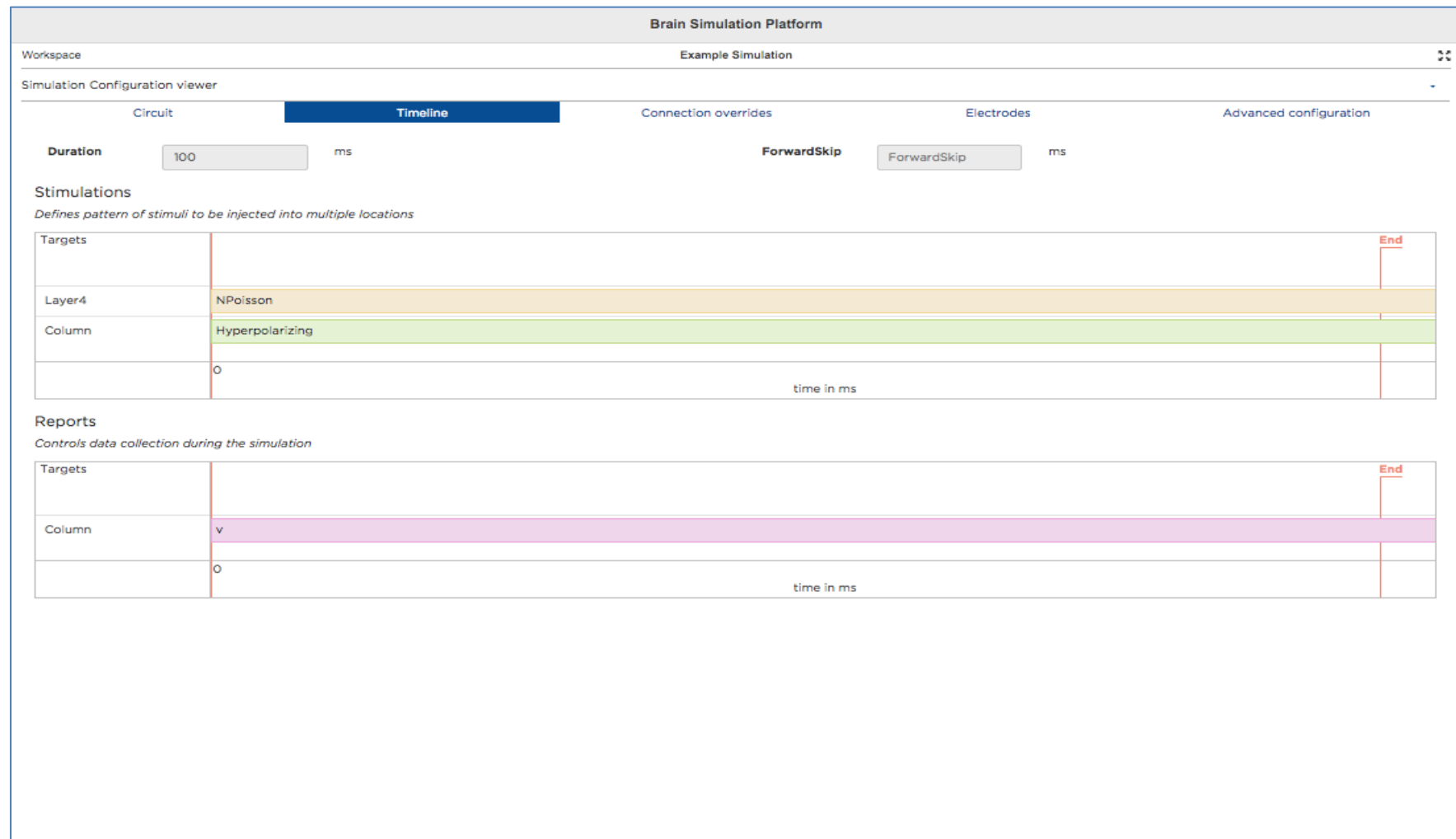


Figure 4: Screenshot of the Simulation Viewer App

Analysis report viewer app

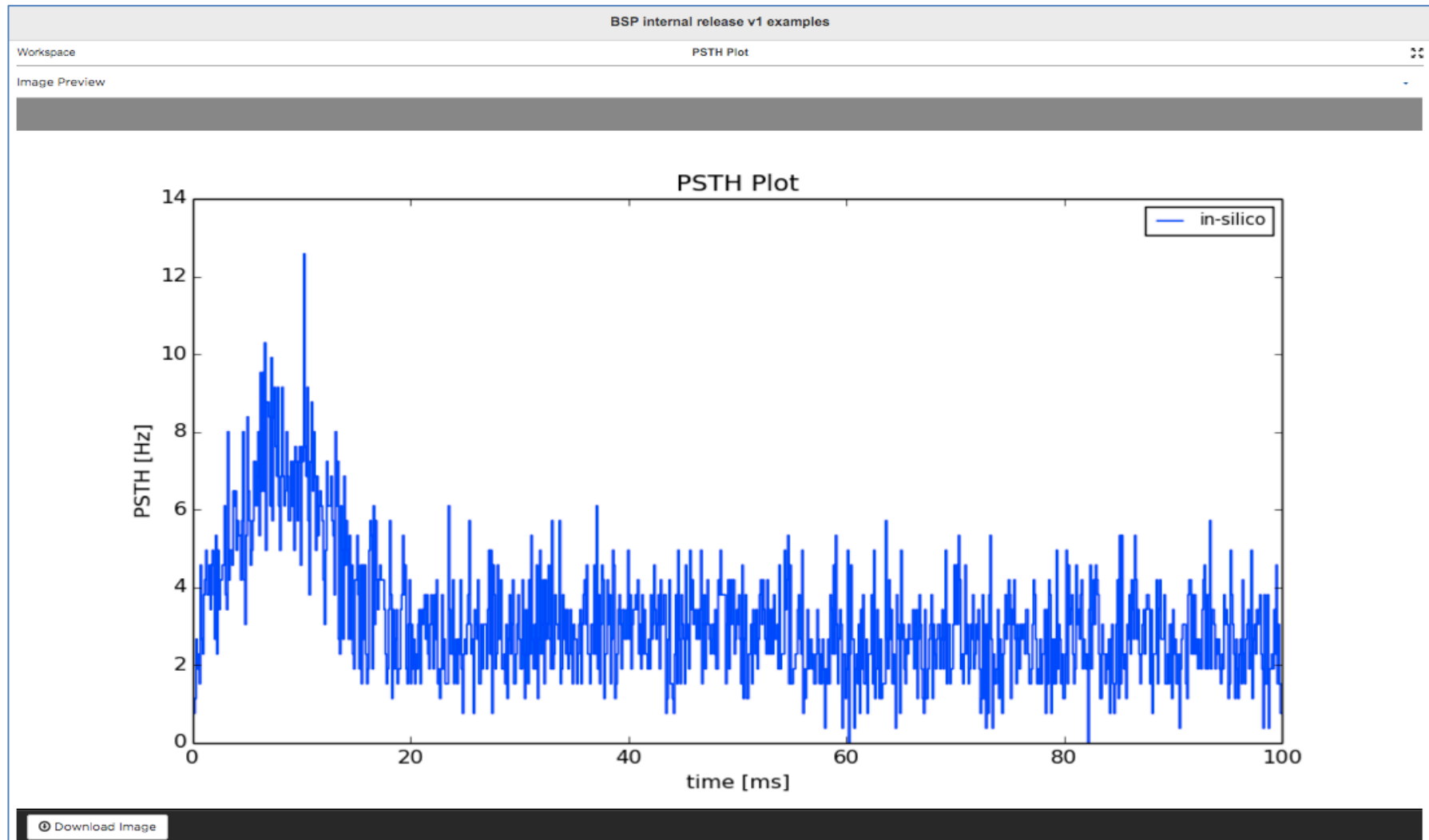


Figure 5: Screenshot of the Analysis Report Viewer App

Validation report viewer app

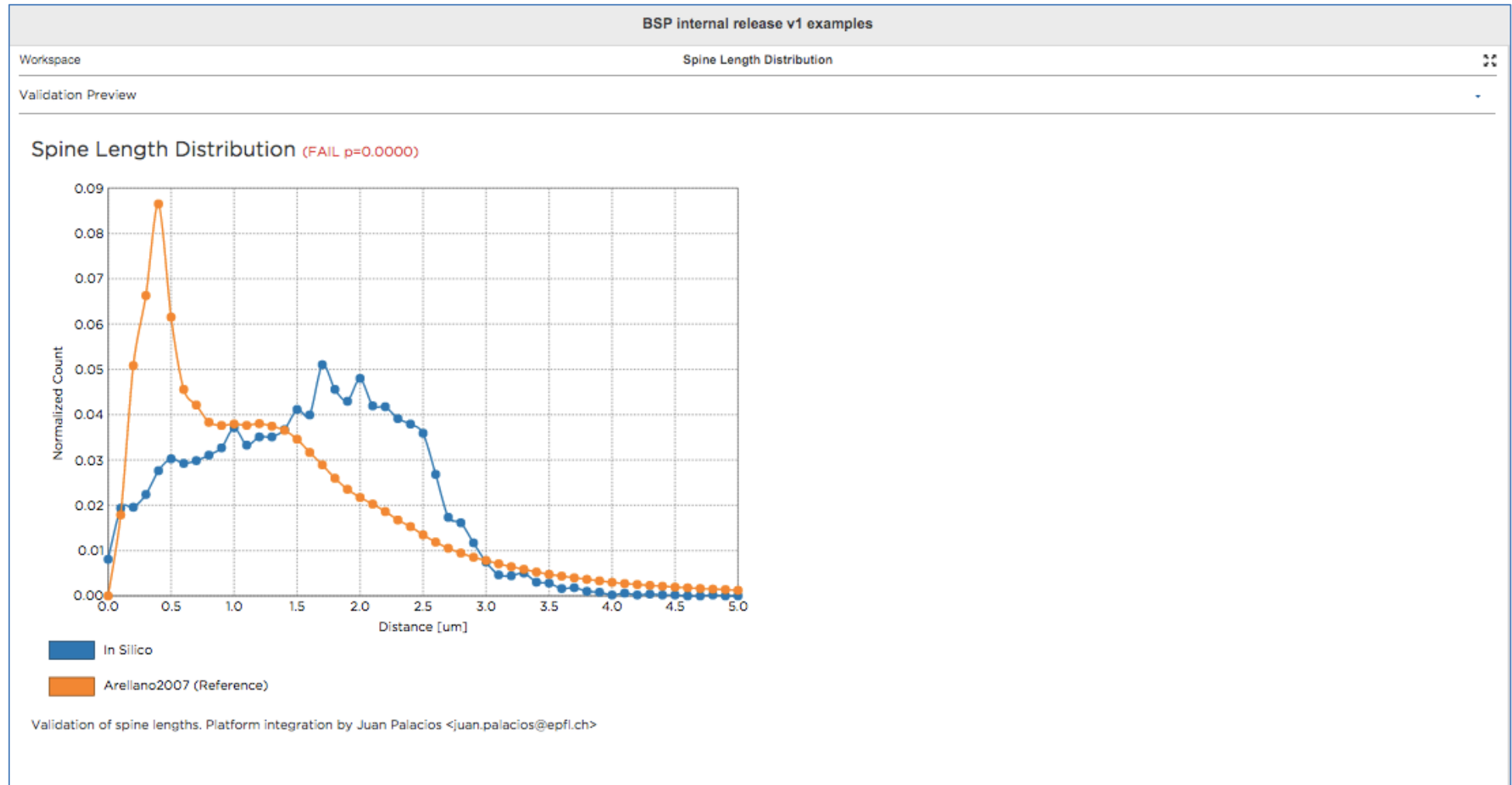


Figure 6: Screenshot of the Validation Report Viewer App

Cortical microcircuit simulation app

Workspace

Cortical microcircuit simulation

microcircuit_task v7 -

Caption: Cortical microcircuit simulation

Description: Multi-layer microcircuit model of early sensory cortex (Potjans & Diesmann 2014), originally implemented in NEST (http://nest-simulator.org). PyNN version modified to run as task in the Collaboratory. Simulation configuration file. For the missing parameters, default values are used. Running the full model, 8 CPU cores and 15360 MB memory should be requested.

Author: NEST Developers

System Name: microcircuit_task

Id: c7d8fe60-6397-11e5-b894-0050569773f6

Creation Date: 2015-09-25

Repository: ssh://bbpcode.epfl.ch/platform/hbp-platform-tasks

Commit: 8f444ae42bfcf4e36b295e88cb372ae1be5eb75

Parameters

configuration_file: URI to application/vnd.juelich.simulation.config

simulation_duration: Double

thalamic_input: Boolean

threads: Long

microcircuit_task v7 -

Multi-layer microcircuit model of early sensory cortex (Potjans, T. C., & Diesmann, M. (2014) Cerebral Cortex 24(3):785-806, code available at <http://www.opensourcebrain.org/projects/potjansdiesmann2014>), originally implemented in NEST (http://nest-simulator.org). PyNN version modified to run as task in the Collaboratory. Simulation parameters are defined in microcircuit.yaml, which needs to be passed as a configuration file. A template can be downloaded from <https://github.com/INM-6/UP-Tasks>. It is possible to provide an empty or partial configuration file. For the missing parameters, default values will be used. After uploading the YAML file, its content type needs to be changed to 'application/vnd.juelich.simulation.config'. Parameters defined in the WUI overwrite values defined in the configuration file. For running the full model, 8 CPU cores and 15360 MB memory should be requested.

written by NEST Developers

Resource auto -

The resource this job should use to run

Job's name microcircuit_task_2015-10-22_12:13:14

This is a name you can give to your job to make it easier to recognize.

configuration_file

YAML file, specifying parameters of the simulation. Point to an empty file to use default parameters.

simulation_duration 12.3

Simulation duration in ms [default=1000].

thalamic_input ☐

If True, a transient thalamic input is applied to the network [default=False].

threads 123

Number of threads NEST uses [default=1]. Needs to be set to the same value as 'CPU cores'.

Output Project

The project this job will output results in.

CPU cores 1

This is the ntasks parameter provided to the slurm launcher.

Memory in MB 2048

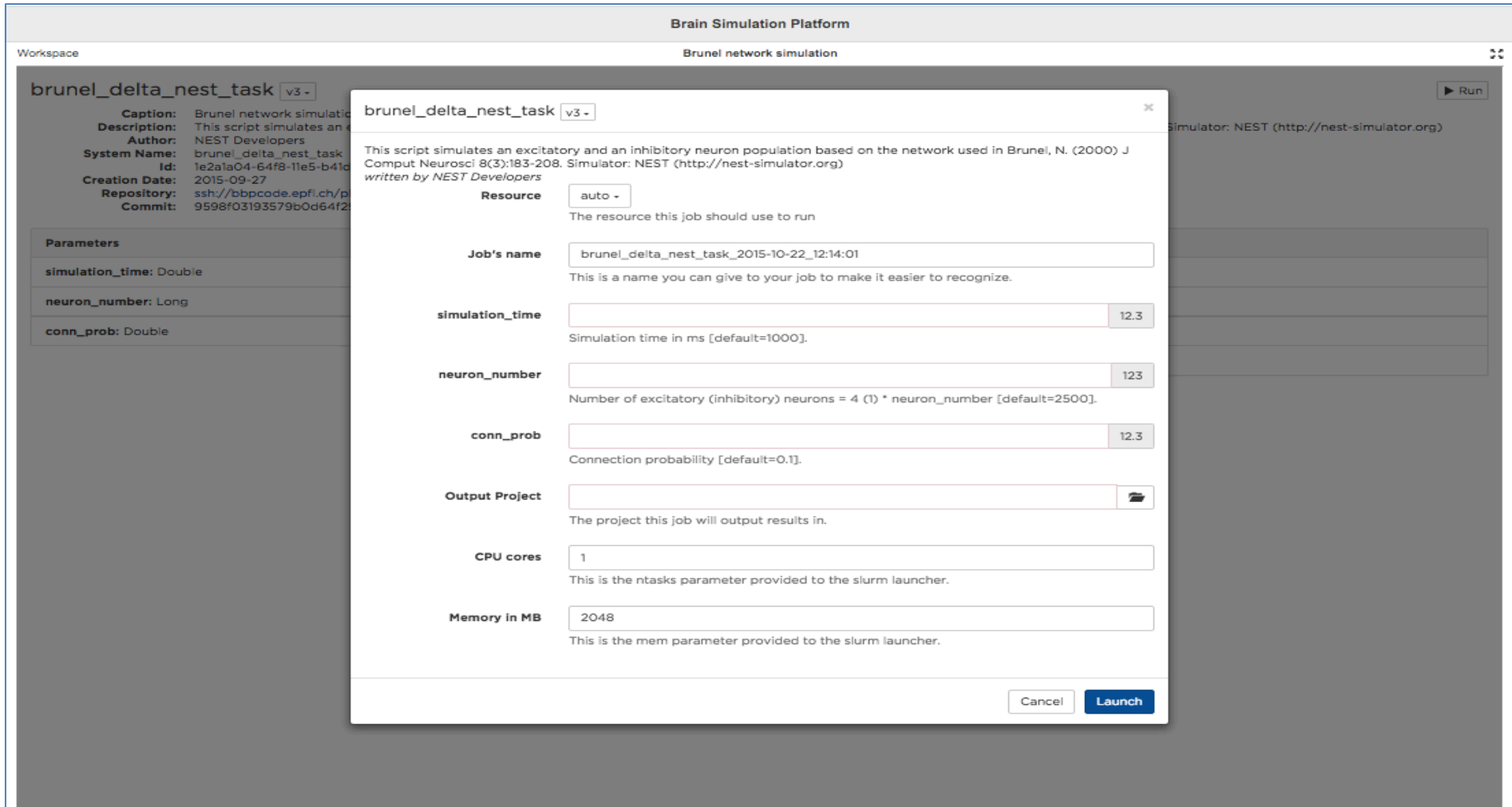
This is the mem parameter provided to the slurm launcher.

Cancel Launch

Run

Figure 7: Screenshot of the Cortical Microcircuit Simulation App

Brunel network simulation app



The screenshot shows the 'Brain Simulation Platform' interface. A 'Workspace' panel on the left displays the 'brunel_delta_nest_task' v3. A 'Launch' dialog box is open, showing the following details:

- Caption:** Brunel network simulation
- Description:** This script simulates an excitatory and an inhibitory neuron population based on the network used in Brunel, N. (2000) J Comput Neurosci 8(3):183-208. Simulator: NEST (<http://nest-simulator.org>)
- Author:** NEST Developers
- System Name:** brunel_delta_nest_task
- Id:** 1e2a1a04-64f8-11e5-b41d-9598f03193579b0d64f2
- Creation Date:** 2015-09-27
- Repository:** <ssh://bbpcode.epfl.ch/p/9598f03193579b0d64f2>
- Commit:** 9598f03193579b0d64f2

Parameters:

- simulation_time:** Double (12.3)
- neuron_number:** Long (123)
- conn_prob:** Double (12.3)

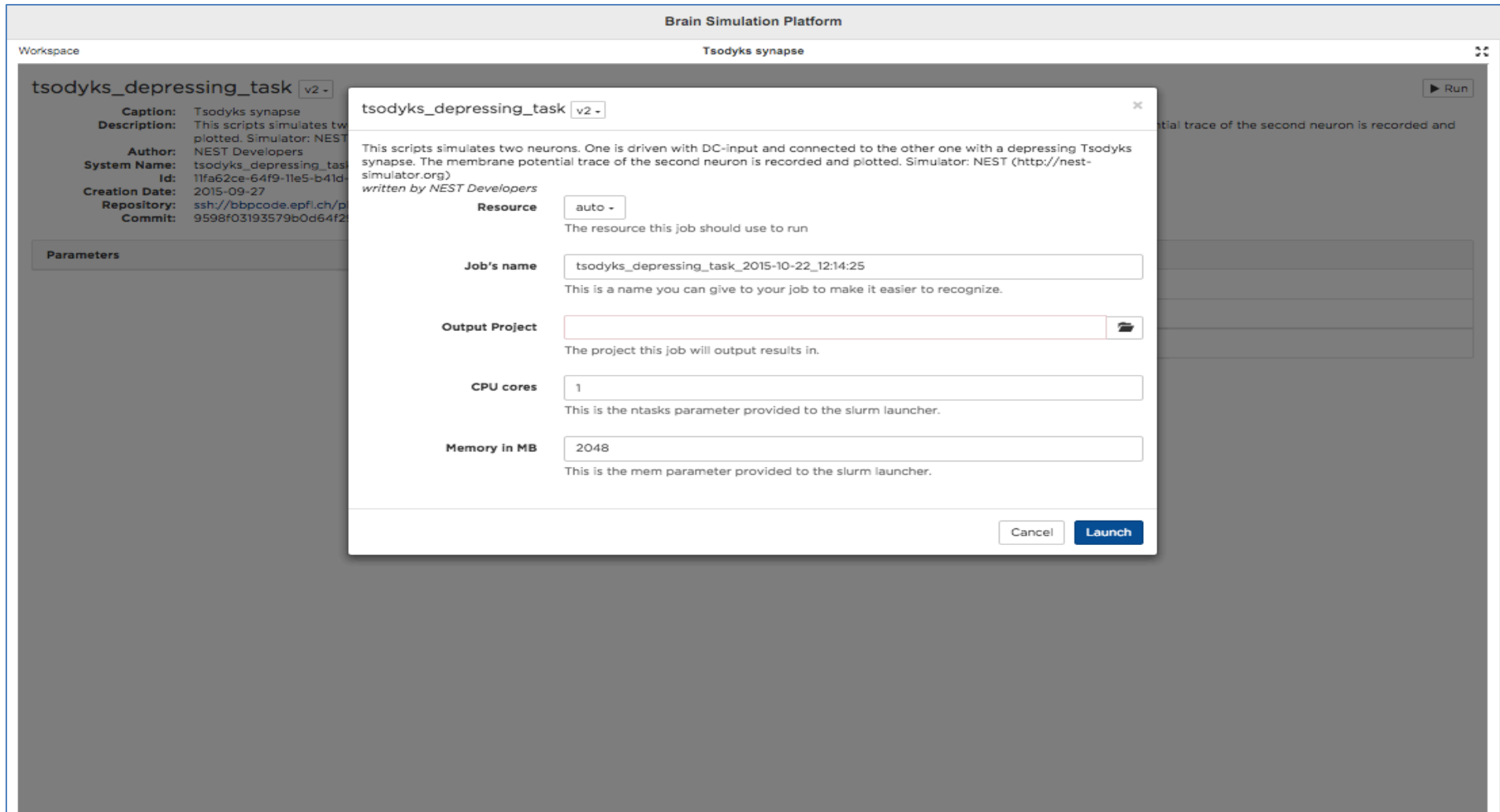
Launch Dialog Fields:

- Resource:** auto - (The resource this job should use to run)
- Job's name:** brunel_delta_nest_task_2015-10-22_12:14:01 (This is a name you can give to your job to make it easier to recognize.)
- simulation_time:** 12.3 (Simulation time in ms [default=1000].)
- neuron_number:** 123 (Number of excitatory (inhibitory) neurons = 4 (1) * neuron_number [default=2500].)
- conn_prob:** 12.3 (Connection probability [default=0.1].)
- Output Project:** (The project this job will output results in.)
- CPU cores:** 1 (This is the ntasks parameter provided to the slurm launcher.)
- Memory in MB:** 2048 (This is the mem parameter provided to the slurm launcher.)

Buttons: Cancel, Launch

Figure 8: Screenshot of the Brunel Network Simulation App

Tsodyks synapse simulation app



The screenshot shows the 'Brain Simulation Platform' interface. In the background, the 'Workspace' displays the 'tsodyks_depressing_task' v2. The task details are as follows:

- Caption:** Tsodyks synapse
- Description:** This scripts simulates two neurons. One is driven with DC-input and connected to the other one with a depressing Tsodyks synapse. The membrane potential trace of the second neuron is recorded and plotted. Simulator: NEST
- Author:** NEST Developers
- System Name:** tsodyks_depressing_task
- Id:** 11fa62ce-64f9-11e5-b41d-000000000000
- Creation Date:** 2015-09-27
- Repository:** ssh://bbpcode.epfl.ch/p
- Commit:** 9598f03193579b0d64f2

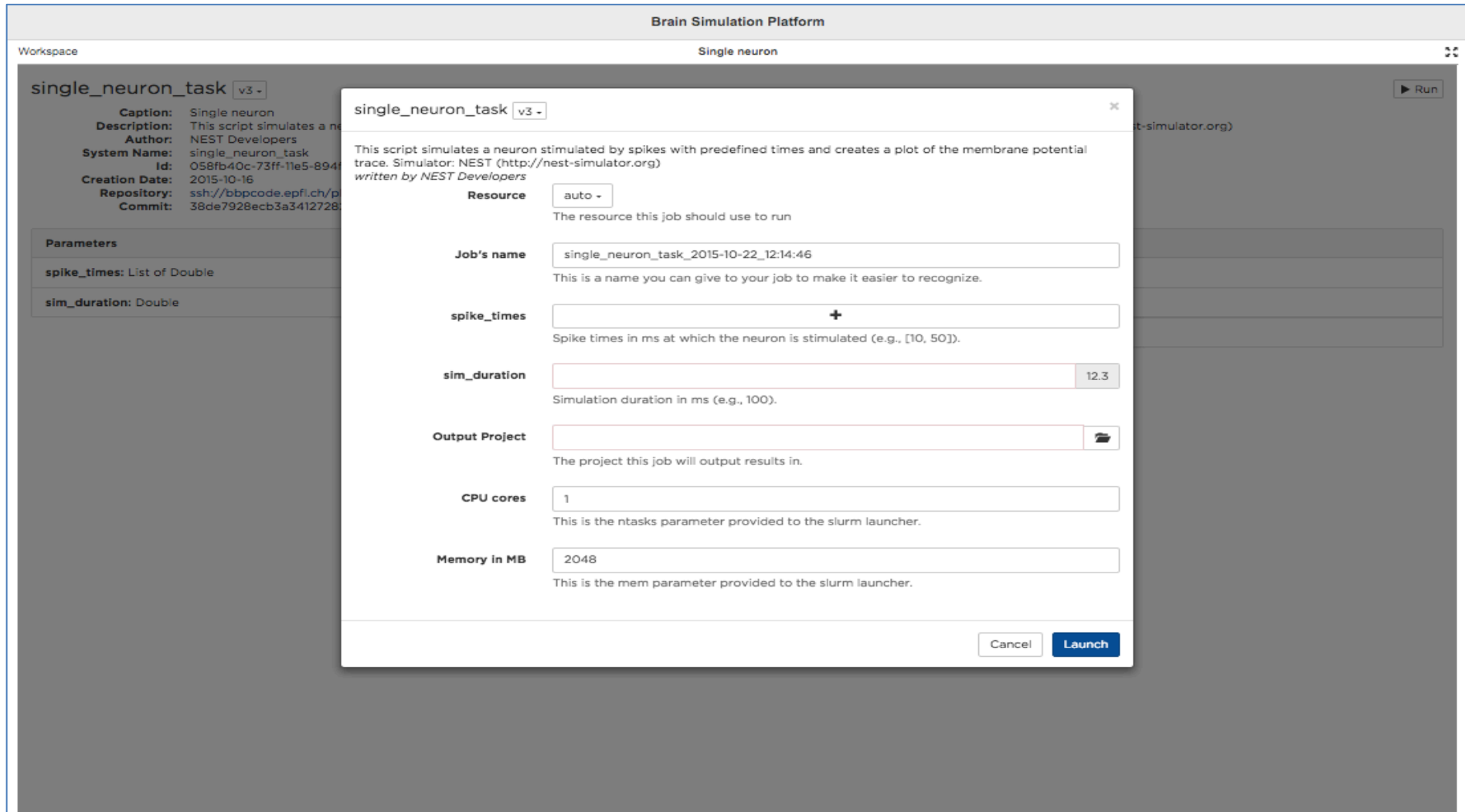
A 'Parameters' section is visible below the details. In the foreground, a 'Launch' dialog box is open for the 'tsodyks_depressing_task' v2. The dialog contains the following fields and options:

- Resource:** auto - (The resource this job should use to run)
- Job's name:** tsodyks_depressing_task_2015-10-22_12:14:25 (This is a name you can give to your job to make it easier to recognize.)
- Output Project:** (The project this job will output results in.)
- CPU cores:** 1 (This is the ntasks parameter provided to the slurm launcher.)
- Memory in MB:** 2048 (This is the mem parameter provided to the slurm launcher.)

At the bottom of the dialog are 'Cancel' and 'Launch' buttons.

Figure 9: Screenshot of the Tsodyks Synaps Simulation App

Single neuron simulation app



The screenshot displays the 'Brain Simulation Platform' interface. A modal window titled 'single_neuron_task v3' is open, showing configuration options for a simulation job. The background workspace shows a 'single_neuron_task' with a 'Run' button.

single_neuron_task v3

Description: This script simulates a neuron stimulated by spikes with predefined times and creates a plot of the membrane potential trace. Simulator: NEST (<http://nest-simulator.org>)
Author: NEST Developers
System Name: single_neuron_task
Id: 058fb40c-73ff-11e5-894d-38de7928ecb3a3412728
Creation Date: 2015-10-16
Repository: [ssh://bbpcode.epfl.ch/p/simulations/single_neuron_task](https://bbpcode.epfl.ch/p/simulations/single_neuron_task)
Commit: 38de7928ecb3a3412728

Parameters

- spike_times:** List of Double
- sim_duration:** Double


Configuration Modal:

Resource: auto -
 The resource this job should use to run

Job's name: single_neuron_task_2015-10-22_12:14:46
 This is a name you can give to your job to make it easier to recognize.

spike_times: +
 Spike times in ms at which the neuron is stimulated (e.g., [10, 50]).

sim_duration: 12.3
 Simulation duration in ms (e.g., 100).

Output Project: 
 The project this job will output results in.

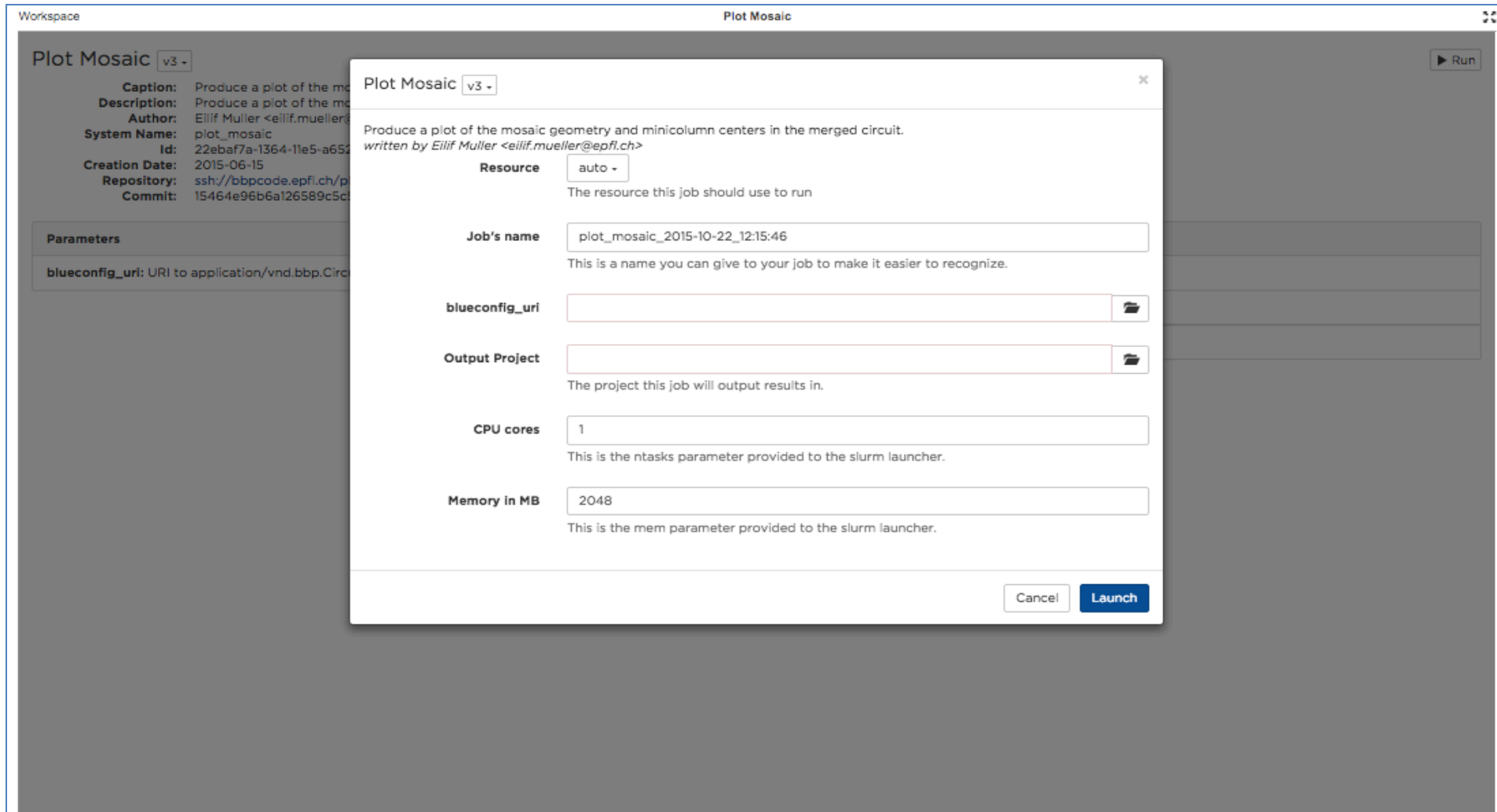
CPU cores: 1
 This is the ntasks parameter provided to the slurm launcher.

Memory in MB: 2048
 This is the mem parameter provided to the slurm launcher.

Buttons: Cancel, Launch

Figure 10: Screenshot of the Single Neuron Simulation App

Circuit mosaic plot analysis app



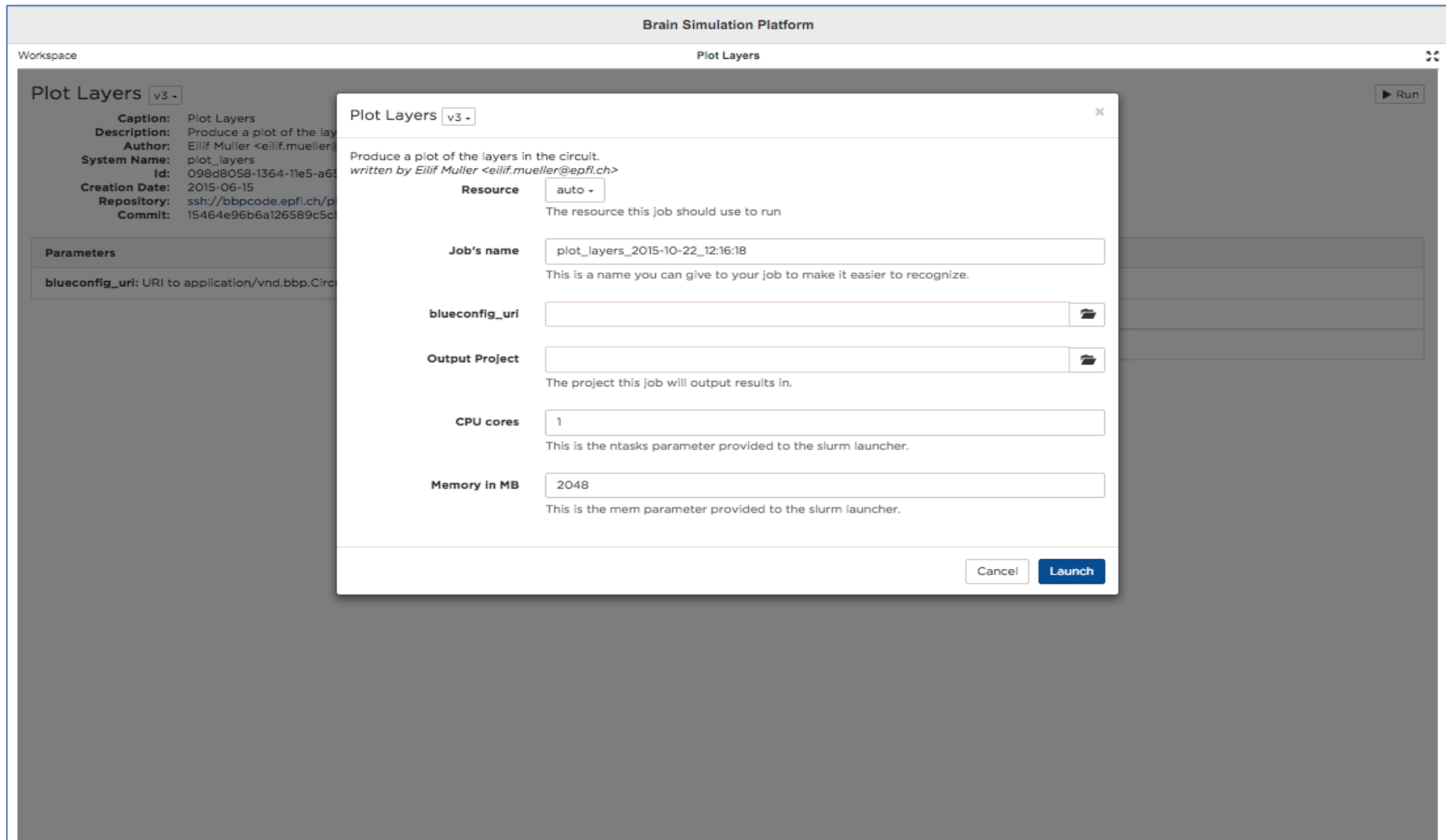
The screenshot shows the 'Plot Mosaic' application interface. A modal dialog box is open, allowing users to configure a job. The background shows a 'Workspace' view with a 'Plot Mosaic v3' entry. The dialog box contains the following fields and options:

- Resource:** A dropdown menu set to 'auto'. Below it, text reads: 'The resource this job should use to run'.
- Job's name:** A text input field containing 'plot_mosaic_2015-10-22_12:15:46'. Below it, text reads: 'This is a name you can give to your job to make it easier to recognize.'
- blueconfig_uri:** An empty text input field with a folder icon on the right.
- Output Project:** An empty text input field with a folder icon on the right. Below it, text reads: 'The project this job will output results in.'
- CPU cores:** A text input field containing '1'. Below it, text reads: 'This is the ntasks parameter provided to the slurm launcher.'
- Memory in MB:** A text input field containing '2048'. Below it, text reads: 'This is the mem parameter provided to the slurm launcher.'

At the bottom right of the dialog box are 'Cancel' and 'Launch' buttons. In the top right corner of the application window, there is a 'Run' button.

Figure 11: Screenshot of the Mosaic Plot Analysis App

Circuit layer plot analysis app



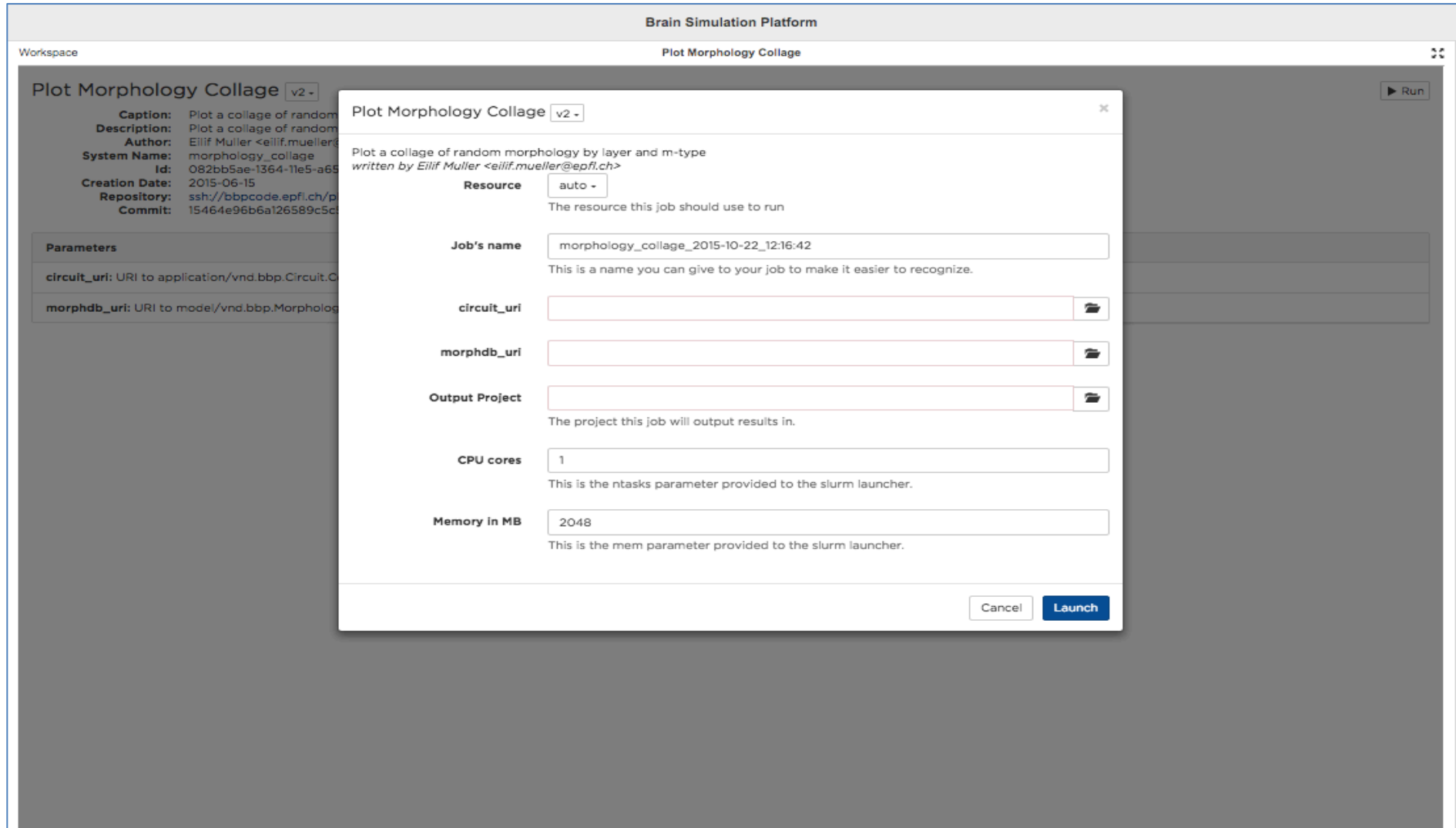
The screenshot shows the 'Brain Simulation Platform' interface. In the background, the 'Plot Layers' app is listed with its metadata: Caption (Plot Layers), Description (Produce a plot of the layers in the circuit), Author (Eilif Muller), System Name (plot_layers), Id (098d8058-1364-11e5-a6b1-15464e96b6a1), Creation Date (2015-06-15), Repository (ssh://bbpcode.epfl.ch/plot_layers), and Commit (15464e96b6a126589c5d). A 'Parameters' section shows 'blueconfig_uri: URI to application/vnd.bbp.Circuit'. Overlaid on this is a configuration window for the 'Plot Layers' app. The window contains the following fields and options:

- Resource:** A dropdown menu set to 'auto'.
- Job's name:** A text field containing 'plot_layers_2015-10-22_12:16:18'.
- blueconfig_uri:** An empty text field with a file icon button.
- Output Project:** An empty text field with a file icon button.
- CPU cores:** A text field containing '1'.
- Memory in MB:** A text field containing '2048'.

At the bottom of the configuration window are 'Cancel' and 'Launch' buttons. A 'Run' button is also visible in the top right corner of the background interface.

Figure 12: Screenshot of the Circuit Layer Plot Analysis App

Circuit morphology collage analysis app



The screenshot shows the 'Brain Simulation Platform' interface. In the background, the 'Workspace' area displays the 'Plot Morphology Collage' app details, including its caption, description, author, system name, ID, creation date, repository, and commit. A 'Parameters' section lists 'circuit_uri' and 'morphdb_uri'. Overlaid on this is a configuration window for the same app. The window contains fields for 'Resource' (set to 'auto'), 'Job's name' (pre-filled with 'morphology_collage_2015-10-22_12:16:42'), 'circuit_uri', 'morphdb_uri', 'Output Project', 'CPU cores' (set to '1'), and 'Memory in MB' (set to '2048'). Each field has a brief description. At the bottom of the window are 'Cancel' and 'Launch' buttons.

Brain Simulation Platform

Workspace

Plot Morphology Collage v2 -

Caption: Plot a collage of random morphology by layer and m-type
Description: Plot a collage of random morphology by layer and m-type
Author: Eilif Muller <eilif.mueller@epfl.ch>
System Name: morphology_collage
Id: 082bb5ae-1364-11e5-a65
Creation Date: 2015-06-15
Repository: ssh://bbpcode.epfl.ch/p
Commit: 15464e96b6a126589c5d

Parameters


circuit_uri: URI to application/vnd.bbp.Circuit.Collage
morphdb_uri: URI to model/vnd.bbp.Morphology.Collage


Plot Morphology Collage v2 -


Plot a collage of random morphology by layer and m-type
 written by Eilif Muller <eilif.mueller@epfl.ch>

Resource: auto -
 The resource this job should use to run

Job's name: morphology_collage_2015-10-22_12:16:42
 This is a name you can give to your job to make it easier to recognize.

circuit_uri: 

morphdb_uri: 

Output Project: 

The project this job will output results in.

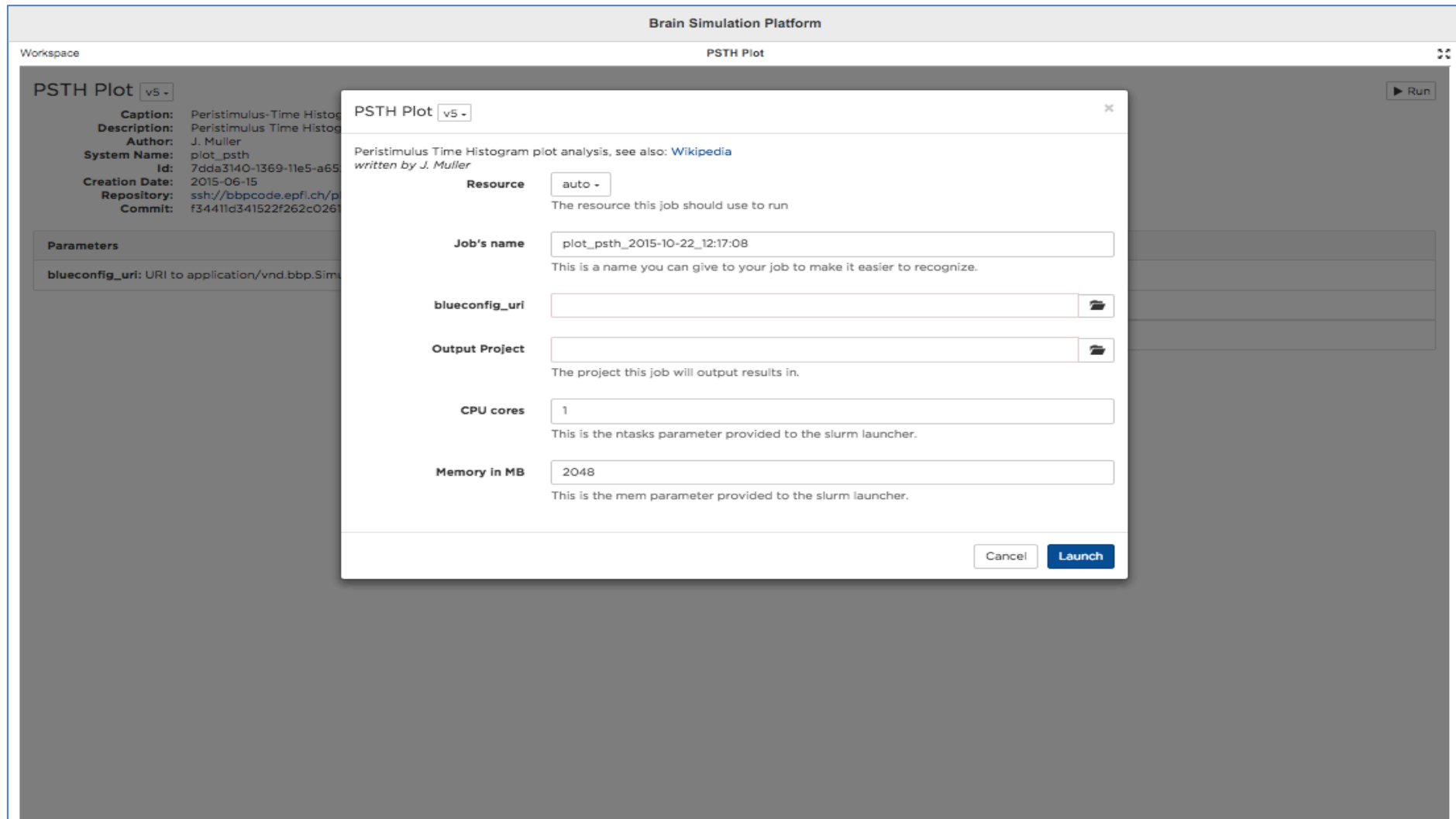
CPU cores: 1
 This is the ntasks parameter provided to the slurm launcher.

Memory in MB: 2048
 This is the mem parameter provided to the slurm launcher.

Cancel Launch

Figure 13: Screenshot of the Circuit Morphology Collage Analysis App

PSTH plot analysis app



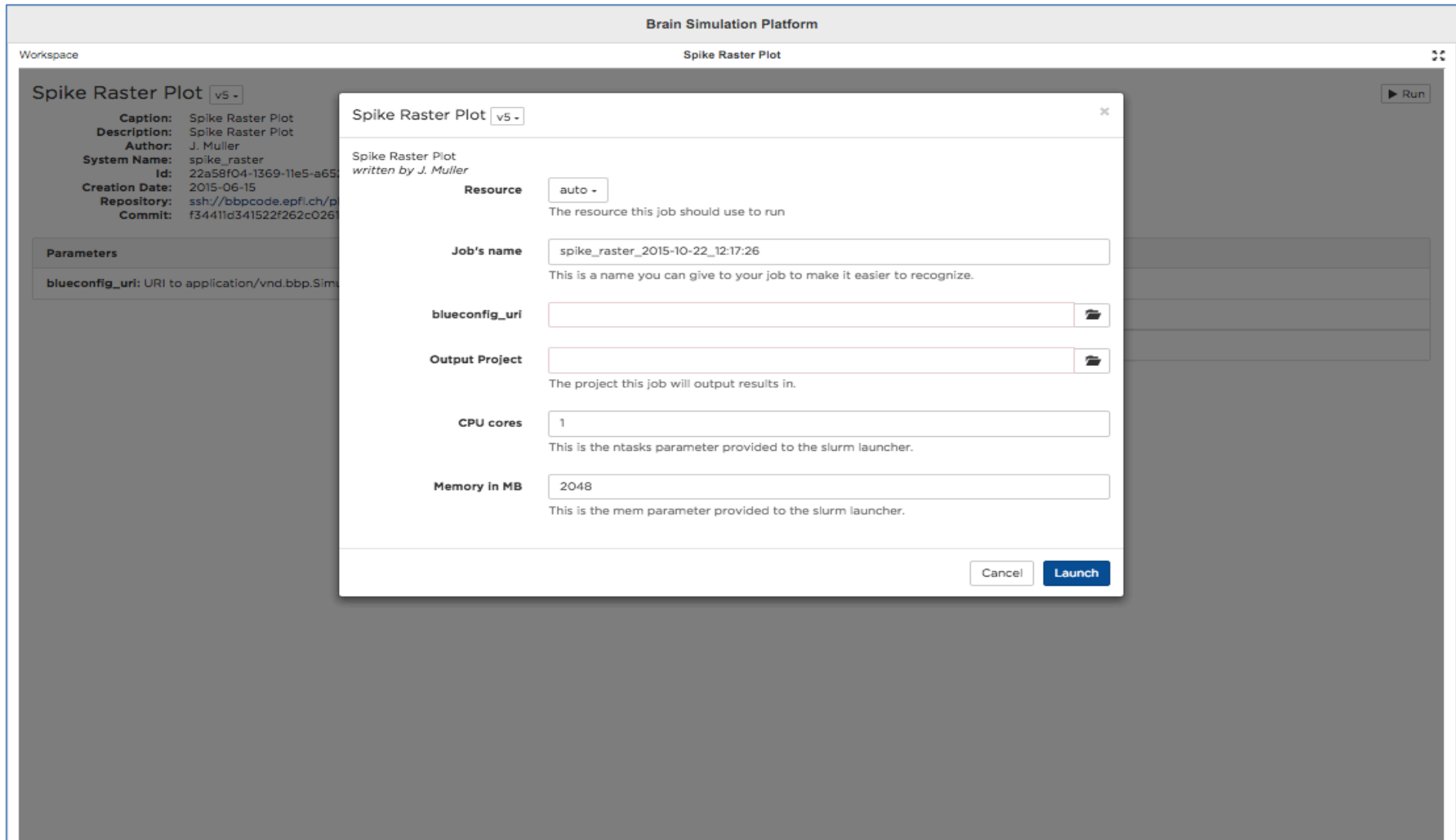
The screenshot shows the 'Brain Simulation Platform' interface with a 'PSTH Plot' app selected. A modal dialog is open for configuring a new job. The background interface includes a 'Workspace' section with metadata for the 'PSTH Plot' app (v5) and a 'Parameters' section with a 'blueconfig_uri' field. The modal dialog contains the following fields:

- Resource:** A dropdown menu set to 'auto'. Description: 'The resource this job should use to run'.
- Job's name:** A text input field containing 'plot_psth_2015-10-22_12:17:08'. Description: 'This is a name you can give to your job to make it easier to recognize'.
- blueconfig_uri:** An empty text input field with a folder icon on the right.
- Output Project:** An empty text input field with a folder icon on the right. Description: 'The project this job will output results in'.
- CPU cores:** A text input field containing '1'. Description: 'This is the ntasks parameter provided to the slurm launcher'.
- Memory in MB:** A text input field containing '2048'. Description: 'This is the mem parameter provided to the slurm launcher'.

At the bottom of the modal are 'Cancel' and 'Launch' buttons. A 'Run' button is also visible in the top right corner of the background interface.

Figure 14: Screenshot of the PSTH Plot Analysis App

Spike raster plot analysis app



The screenshot shows the 'Brain Simulation Platform' interface. In the background, the 'Spike Raster Plot' app is listed with its metadata and parameters. A modal dialog box is open in the foreground, allowing the user to configure and launch the app.

Brain Simulation Platform

Workspace

Spike Raster Plot v5

Metadata:

- Caption:** Spike Raster Plot
- Description:** Spike Raster Plot
- Author:** J. Muller
- System Name:** spike_raster
- Id:** 22a58f04-1369-11e5-a655-f34411d341522f262c0261
- Creation Date:** 2015-06-15
- Repository:** ssh://bbpcode.epfl.ch/p/
- Commit:** f34411d341522f262c0261

Parameters:

- blueconfig_uri:** URI to application/vnd.bbp.Sim


Spike Raster Plot v5 Configuration Dialog:


Spike Raster Plot v5

written by J. Muller

Resource: auto -
The resource this job should use to run

Job's name: spike_raster_2015-10-22_12:17:26
This is a name you can give to your job to make it easier to recognize.

blueconfig_uri: 

Output Project: 

The project this job will output results in.

CPU cores: 1
This is the ntasks parameter provided to the slurm launcher.

Memory in MB: 2048
This is the mem parameter provided to the slurm launcher.

Buttons: Cancel, Launch

Figure 15: Screenshot of the Raster Plot Analysis App

Simulation voltage collage analysis app

Brain Simulation Platform

Workspace Voltage Collage Plot

Voltage Collage Plot v4 -

Caption: Create an analysis plot with a collage of voltage reports.
Description: Create an analysis plot with a collage of voltage reports.
Author: Luis Riquelme
System Name: voltage_collage
Id: 070c6610-2c95-11e5-97e1-000000000000
Creation Date: 2015-07-17
Repository: ssh://bbpcode.epfl.ch/p/voltage_collage
Commit: b6e5b26c7cb7bf9be0ff1

Parameters


simulation_uri: URI to application/vnd.bbp.SimulationReport
report_uri: URI to application/vnd.bbp.VoltageCollageReport
num_cells: Long
num_plots: Long
output_path: String


Voltage Collage Plot v4 -

Create an analysis plot with a collage of voltage reports.
written by Luis Riquelme

Resource auto -
The resource this job should use to run

Job's name voltage_collage_2015-10-22_12:17:44
This is a name you can give to your job to make it easier to recognize.


simulation_uri 

report_uri 

num_cells
number of cells per plot

num_plots
number of voltage plots

output_path

Output Project 
The project this job will output results in.

CPU cores
This is the ntasks parameter provided to the slurm launcher.

Memory in MB
This is the mem parameter provided to the slurm launcher.

Cancel Launch

Run

Figure 16: Screenshot of the Simulation Voltage Collage Analysis App

Circuit cell density per layer validation app

Workspace

Cell Density per Layer v2 -

Caption: Runs the cell densities per layer validation app

Description: Validation of average cell density per layer. This validation takes a 100 by 100 um square centered on the center of the central hypercolumn of a circuit and computes the cell density of each layer within that sample. The data then gets compared with 2 biological datasets, which are used to constrain the model. Constraint 1 source is Sonja's cell count. Constraint 2 is DeFelipe et al. (2011). For both datasets, the animal model was chosen to be as consistent with the simulated bbp column as possible, i.e. P14 to P16 Wistar rat, primary somatosensory area, hindlimb. The statistical comparison (chi-square test) was performed against Sonja's dataset. Platform integration by Juan Palacios

Author: Eilif Muller <eilif.mueller@epfl.ch>

System Name: cell_densities_per_layer

Id: 0ad7da22-14e9-11e5-be3d-7a497411f002550d90a3

Creation Date: 2015-06-17

Repository: ssh://bbpcode.epfl.ch/p/brain-simulation-platform

Commit: 7a497411f002550d90a3

Parameters

circuit_uri: URI to application/vnd.bbp.Circuit.O

pvalue_threshold: Double

Cell Density per Layer v2 -

Validation of average cell density per layer. This validation takes a 100 by 100 um square centered on the center of the central hypercolumn of a circuit and computes the cell density of each layer within that sample. The data then gets compared with 2 biological datasets, which are used to constrain the model. Constraint 1 source is Sonja's cell count. Constraint 2 is DeFelipe et al. (2011). For both datasets, the animal model was chosen to be as consistent with the simulated bbp column as possible, i.e. P14 to P16 Wistar rat, primary somatosensory area, hindlimb. The statistical comparison (chi-square test) was performed against Sonja's dataset. Platform integration by Juan Palacios

written by Eilif Muller <eilif.mueller@epfl.ch>

Resource auto -

The resource this job should use to run

Job's name cell_densities_per_layer_from_mv2_2015-10-22_12:18:11

This is a name you can give to your job to make it easier to recognize.

circuit_uri

pvalue_threshold 12.3

Output Project

The project this job will output results in.

CPU cores 1

This is the ntasks parameter provided to the slurm launcher.

Memory in MB 2048

This is the mem parameter provided to the slurm launcher.

Cancel Launch

Figure 17: Screenshot of the Circuit Cell Density per Layer Validation App

Inhibitory synapses density circuit validation app

Brain Simulation Platform

Workspace Inhibitory Synapses Density Validation

Inhibitory Synapses Density Validation

Caption: Runs the inhibitory synapse density validation.

Description: Validation of average inhibitory synapse density per layer. This validation samples a 10x10x10 um³ cube centered at the center of the central hypercolumn and at the center of each layer. With the help of Farhan's spatial indexer, we can query all the synapses which are located inside the samples. Then we determine the type of each synapse and calculate the density of inhibitory synapses (per layer)... As this second step (aka looping over all the synapses in the volume and checking for their type using BBP-SDK) is very slow, the size of the query was reduced to a 10x10x10 um³ cube for performance reasons (instead of 50x50x50 for the general synapse density validation). The density of inhibitory synapses in each sample is then compared to data originating from 180 um³ EM reconstructions from DeFelipe's lab. In this biological dataset, the animal model was chosen to be as consistent with the simulated bbp column as possible, i.e. P14 to P16 Wistar rat, primary somatosensory area, hindlimb. Platform integration by Juan Palacios

Author: Eilif Muller <eilif.mueller@epfl.ch>

System Name: inhibitory_synapses_density_validation

Id: Oc466e46-14e9-11e5-be33-7a497411f002550d90a3

Creation Date: 2015-06-17

Repository: ssh://bbpcode.epfl.ch/p/

Commit: 7a497411f002550d90a3

Parameters

circuit_url: URI to application/vnd.bbp.Circuit.O


pvalue_threshold: Double

Inhibitory Synapses Density Validation v2


Validation of average inhibitory synapse density per layer. This validation samples a 10x10x10 um³ cube centered at the center of the central hypercolumn and at the center of each layer. With the help of Farhan's spatial indexer, we can query all the synapses which are located inside the samples. Then we determine the type of each synapse and calculate the density of inhibitory synapses (per layer)... As this second step (aka looping over all the synapses in the volume and checking for their type using BBP-SDK) is very slow, the size of the query was reduced to a 10x10x10 um³ cube for performance reasons (instead of 50x50x50 for the general synapse density validation). The density of inhibitory synapses in each sample is then compared to data originating from 180 um³ EM reconstructions from DeFelipe's lab. In this biological dataset, the animal model was chosen to be as consistent with the simulated bbp column as possible, i.e. P14 to P16 Wistar rat, primary somatosensory area, hindlimb. Platform integration by Juan Palacios

Resource: auto -
The resource this job should use to run

Job's name: inhibitory_synapses_density_2015-10-22_12:18:43
This is a name you can give to your job to make it easier to recognize.

circuit_url: 

pvalue_threshold: 12.3

Output Project: 
The project this job will output results in.

CPU cores: 1
This is the ntasks parameter provided to the slurm launcher.

Memory in MB: 2048
This is the mem parameter provided to the slurm launcher.

Cancel Launch

Figure 18: Screenshot of the Inhibitory Synapses Density Circuit App

Circuit GABAergic cells fractions per layer circuit validation app

Brain Simulation Platform

Workspace

GABAergic cell fractions per Layer Validation

Run

GABAergic cell fractions per Layer Validation v2

Caption: Runs the GABAergic cell fractions per layer validation.

Description: Validation of average cell density per layer. This validation takes a 100 by 100 um square centered on the center of the central hypercolumn of a circuit and computes the fraction of GABAergic cells in each layer within that sample. So far, we found 3 datasets against which we can compare our data (Beaulieu 1992, Lefort 2009, Meyer 2011), but none of them is completely matching what is being simulated (wrong animal, wrong age, wrong region... just read the papers), best one is from rat barrel cortex (reference dataset). The statistical comparison (chi-square test) was performed against Meyer's dataset. Platform integration by Juan Palacios

Author: Eilif Muller <eilif.mueller@epfl.ch>

System Name: cell_ratios_per_layer

Id: 0b8a0a76-14e9-11e5-be33-7a497411f002

Creation Date: 2015-06-17

Repository: ssh://bbpcode.epfl.ch/p/brain-simulation-platform

Commit: 7a497411f002550d90a3

Parameters

circuit_uri: URI to application/vnd.bbp.Circuit.Circuit

pvalue_threshold: Double

Resource: auto

The resource this job should use to run

Job's name: cell_ratios_per_layer_2015-10-22_12:18:28

This is a name you can give to your job to make it easier to recognize.

circuit_uri:

pvalue_threshold: 12.3

Output Project:

The project this job will output results in.

CPU cores: 1

This is the ntasks parameter provided to the slurm launcher.

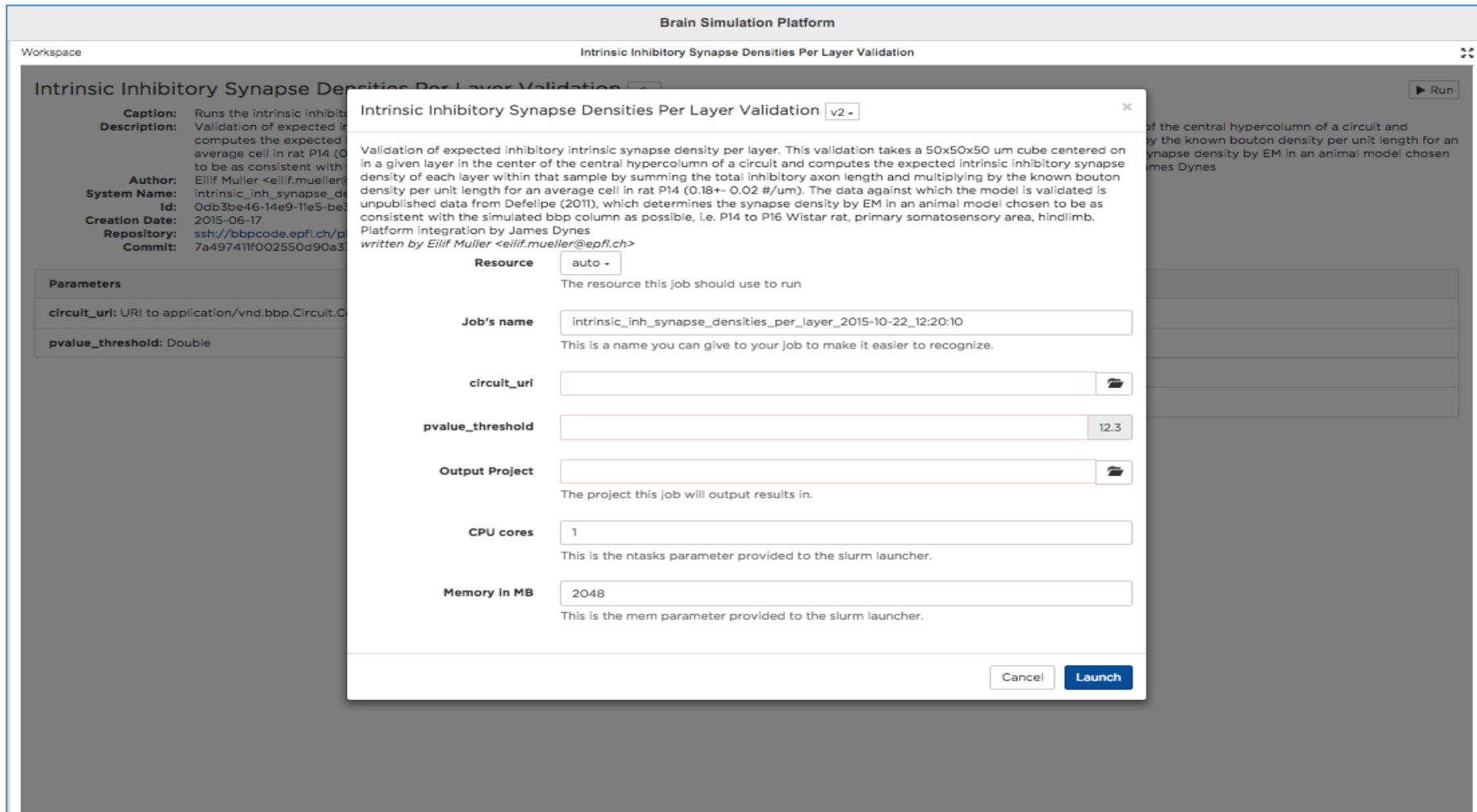
Memory in MB: 2048

This is the mem parameter provided to the slurm launcher.

Cancel **Launch**

Figure 19: Screenshot of the Circuit GABAergic Cells Fractions Per Layer Circuit Validation App

Intrinsic inhibitory synapses density per layer circuit validation app



The screenshot shows the 'Brain Simulation Platform' interface. A modal window titled 'Intrinsic Inhibitory Synapse Densities Per Layer Validation v2' is open, displaying the configuration for a job. The background shows the app's details in the workspace.

App Details (Background):

- Caption:** Runs the intrinsic inhibitory synapse density per layer validation.
- Description:** Validation of expected inhibitory intrinsic synapse density per layer. This validation takes a 50x50x50 um cube centered on a given layer in the center of the central hypercolumn of a circuit and computes the expected intrinsic inhibitory synapse density of each layer within that sample by summing the total inhibitory axon length and multiplying by the known bouton density per unit length for an average cell in rat P14 (0.18+- 0.02 #/um). The data against which the model is validated is unpublished data from Defelipe (2011), which determines the synapse density by EM in an animal model chosen to be as consistent with the simulated bbp column as possible, i.e. P14 to P16 Wistar rat, primary somatosensory area, hindlimb. Platform integration by James Dynes
- Author:** Eilif Muller <eilif.mueller@epfl.ch>
- System Name:** intrinsic_inh_synapse_densities_per_layer_validation
- Id:** 0db3be46-14e9-11e5-bef1-7a497411f002550d90a3
- Creation Date:** 2015-06-17
- Repository:** ssh://bbpcode.epfl.ch/p/
- Commit:** 7a497411f002550d90a3

Parameters:

- circuit_uri:** URI to application/vnd.bbp.Circuit.O
- pvalue_threshold:** Double

Job Configuration (Modal Window):

- Resource:** auto - (The resource this job should use to run)
- Job's name:** intrinsic_inh_synapse_densities_per_layer_2015-10-22_12:20:10 (This is a name you can give to your job to make it easier to recognize.)
- circuit_uri:** (Input field with a file icon)
- pvalue_threshold:** 12.3 (Input field)
- Output Project:** (Input field with a file icon) (The project this job will output results in.)
- CPU cores:** 1 (This is the ntasks parameter provided to the slurm launcher.)
- Memory in MB:** 2048 (This is the mem parameter provided to the slurm launcher.)

Buttons: Cancel, Launch

Figure 20: Screenshot of the Intrinsic Inhibitory Synapses Density Per Layer Circuit Validation App

Somata volume fraction circuit validation app

Brain Simulation Platform

Workspace

Somata Volume Fraction Validation

Caption: Runs the somata volume fraction validation app.

Description: Validation of average fraction of volume occupied by the somata of neurons in each layer. This validation takes a 100 by 100 um square centered on the center of the central hypercolumn of a circuit and computes the cell density of each layer within that sample. For each soma whose center is within the sample, we estimate the volume each soma. A bit of a tricky one... We assumed that the contour of the soma (which is the most detailed geometrical data available) could be rotated along one axis in order to estimate the soma using a pile of cylinders (for more details, please look into the code, there is about two comment lines per code line). This should really, really be seen as the best current estimate, no as a hard core bullet-proof flame-resistant validation... The biological dataset used for comparison is very recent/unpublished data from Javier DeFelipe's lab. The animal model was chosen to be as consistent with the simulated bbp column as possible, i.e. P14 to P16 Wistar rat, primary somatosensory area, hindlimb. Platform integration by Juan Palacios

Author: Eilif Muller <eilif.mueller@epfl.ch>

System Name: somata_volume_fraction

Id: 0e61a09c-14e9-11e5-be3d-7a497411f002550d90a3

Creation Date: 2015-06-17

Repository: ssh://bbpcode.epfl.ch/p/somata_volume_fraction

Commit: 7a497411f002550d90a3

Parameters

circuit_uri: URI to application/vnd.bbp.Circuit.O


pvalue_threshold: Double

Somata Volume Fraction Validation v2


Validation of average fraction of volume occupied by the somata of neurons in each layer. This validation takes a 100 by 100 um square centered on the center of the central hypercolumn of a circuit and computes the cell density of each layer within that sample. For each soma whose center is within the sample, we estimate the volume each soma. A bit of a tricky one... We assumed that the contour of the soma (which is the most detailed geometrical data available) could be rotated along one axis in order to estimate the soma using a pile of cylinders (for more details, please look into the code, there is about two comment lines per code line). This should really, really be seen as the best current estimate, no as a hard core bullet-proof flame-resistant validation... The biological dataset used for comparison is very recent/unpublished data from Javier DeFelipe's lab. The animal model was chosen to be as consistent with the simulated bbp column as possible, i.e. P14 to P16 Wistar rat, primary somatosensory area, hindlimb. Platform integration by Juan Palacios

Resource: auto -
The resource this job should use to run

Job's name: somata_volume_fraction_2015-10-22_12:20:27
This is a name you can give to your job to make it easier to recognize.

circuit_uri: 

pvalue_threshold: 12.3

Output Project: 
The project this job will output results in.

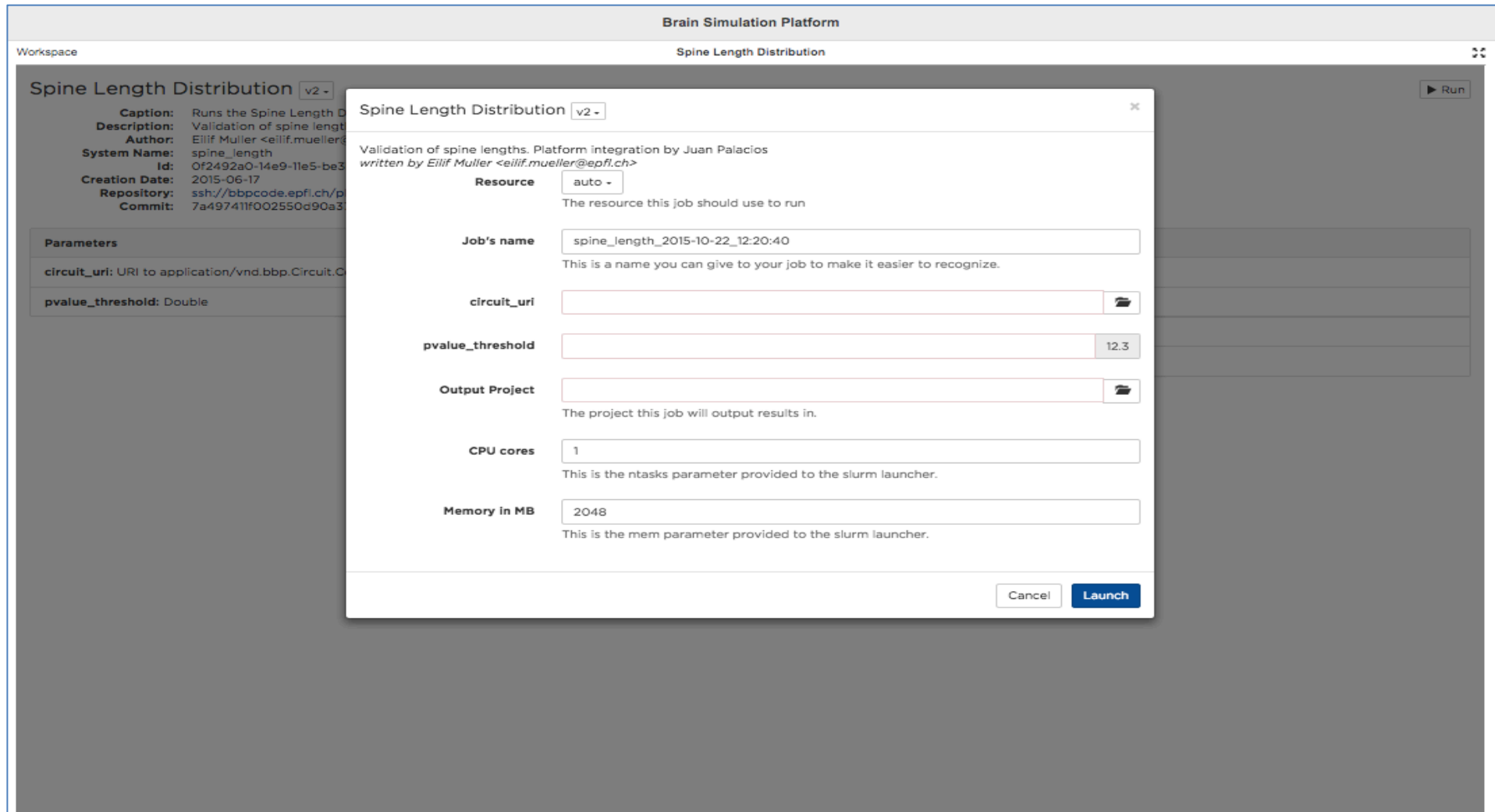
CPU cores: 1
This is the ntasks parameter provided to the slurm launcher.

Memory in MB: 2048
This is the mem parameter provided to the slurm launcher.

Cancel Launch

Figure 21: Screenshot of the Somata Volume Fraction Circuit Validation App

Spine length distribution validation app



The screenshot shows the 'Brain Simulation Platform' interface with a 'Spine Length Distribution' workspace. A modal window is open for configuring a job. The modal contains the following fields and descriptions:

- Resource:** auto - (The resource this job should use to run)
- Job's name:** spine_length_2015-10-22_12:20:40 (This is a name you can give to your job to make it easier to recognize.)
- circuit_uri:** (Empty field with a file icon)
- pvalue_threshold:** 12.3
- Output Project:** (Empty field with a file icon) (The project this job will output results in.)
- CPU cores:** 1 (This is the ntasks parameter provided to the slurm launcher.)
- Memory in MB:** 2048 (This is the mem parameter provided to the slurm launcher.)

At the bottom of the modal are 'Cancel' and 'Launch' buttons. The background workspace shows a 'Spine Length Distribution' v2 - panel with a 'Run' button.

Figure 22: Screenshot of the Spine Length Distribution Validation App

Synapse count circuit validation

Brain Simulation Platform

Workspace

Synapse Count Validation

Synapse Count Validation v2

Caption: Runs the synapse counts

Description: Validation of average incoming synapse counts per neuron for all neuron morphology types. Constraint 1 source is Braitenberg & Schuez (1991), page 196. The data there is for adult mouse, and only a mean is given. A gamma distribution form is assumed with a shape parameter $a=3.0$ to reflect the fact that synapse counts are known to vary widely. The mean given there is reduced by 30% to reflect the fact that in the in-silico model there are no long-range intra- or inter-cortical synapses. Platform integration by James Dynes

Author: Eilif Muller <eilif.mueller@epfl.ch>

System Name: synapse_counts

Id: Ofded46c-14e9-11e5-be3

Creation Date: 2015-06-17

Repository: ssh://bbpcode.epfl.ch/p

Commit: 7a497411f002550d90a3

Parameters

circuit_uri: URI to application/vnd.bbp.Circuit.O

pvalue_threshold: Double

Synapse Count Validation v2

Validation of average incoming synapse counts per neuron for all neuron morphology types. Constraint 1 source is Braitenberg & Schuez (1991), page 196. The data there is for adult mouse, and only a mean is given. A gamma distribution form is assumed with a shape parameter $a=3.0$ to reflect the fact that synapse counts are known to vary widely. The mean given there is reduced by 30% to reflect the fact that in the in-silico model there are no long-range intra- or inter-cortical synapses. Platform integration by James Dynes

written by Eilif Muller <eilif.mueller@epfl.ch>

Resource auto -

The resource this job should use to run

Job's name synapse_counts_2015-10-22_12:21:05

This is a name you can give to your job to make it easier to recognize.

circuit_uri

pvalue_threshold 12.3

Output Project

The project this job will output results in.

CPU cores 1

This is the ntasks parameter provided to the slurm launcher.

Memory in MB 2048

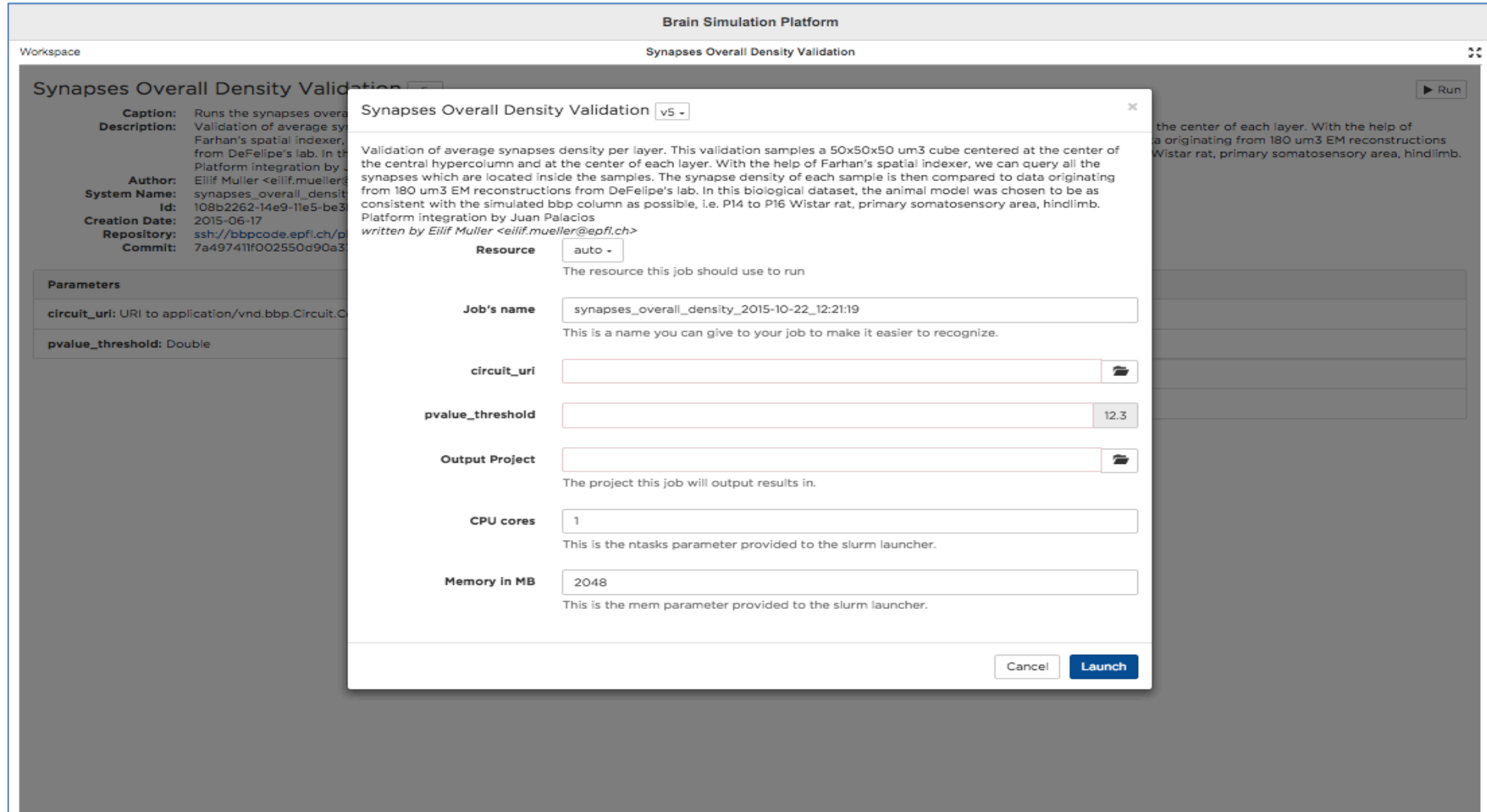
This is the mem parameter provided to the slurm launcher.

Cancel

Launch

Figure 23: Screenshot of the Synapse Count Circuit Validation

Synapse overall density circuit validation app



Brain Simulation Platform

Workspace **Synapses Overall Density Validation**

Synapses Overall Density Validation

Caption: Runs the synapses overall density validation.

Description: Validation of average synapse density per layer. This validation samples a 50x50x50 um³ cube centered at the center of the central hypercolumn and at the center of each layer. With the help of Farhan's spatial indexer, we can query all the synapses which are located inside the samples. The synapse density of each sample is then compared to data originating from 180 um³ EM reconstructions from DeFelipe's lab. In this biological dataset, the animal model was chosen to be as consistent with the simulated bbp column as possible, i.e. P14 to P16 Wistar rat, primary somatosensory area, hindlimb. Platform integration by Juan Palacios

Author: Eilif Muller <eilif.mueller@epfl.ch>

System Name: synapses_overall_density

Id: 108b2262-14e9-11e5-be3d-7a497411f002550d90a3

Creation Date: 2015-06-17

Repository: ssh://bbpcode.epfl.ch/p/synapses_overall_density

Commit: 7a497411f002550d90a3

Parameters

circuit_uri: URI to application/vnd.bbp.Circuit.O

pvalue_threshold: Double

Synapses Overall Density Validation v5

Validation of average synapses density per layer. This validation samples a 50x50x50 um³ cube centered at the center of the central hypercolumn and at the center of each layer. With the help of Farhan's spatial indexer, we can query all the synapses which are located inside the samples. The synapse density of each sample is then compared to data originating from 180 um³ EM reconstructions from DeFelipe's lab. In this biological dataset, the animal model was chosen to be as consistent with the simulated bbp column as possible, i.e. P14 to P16 Wistar rat, primary somatosensory area, hindlimb. Platform integration by Juan Palacios

written by Eilif Muller <eilif.mueller@epfl.ch>

Resource: auto -
The resource this job should use to run

Job's name: synapses_overall_density_2015-10-22_12:21:19
This is a name you can give to your job to make it easier to recognize.

circuit_uri:

pvalue_threshold: 12.3

Output Project:
The project this job will output results in.

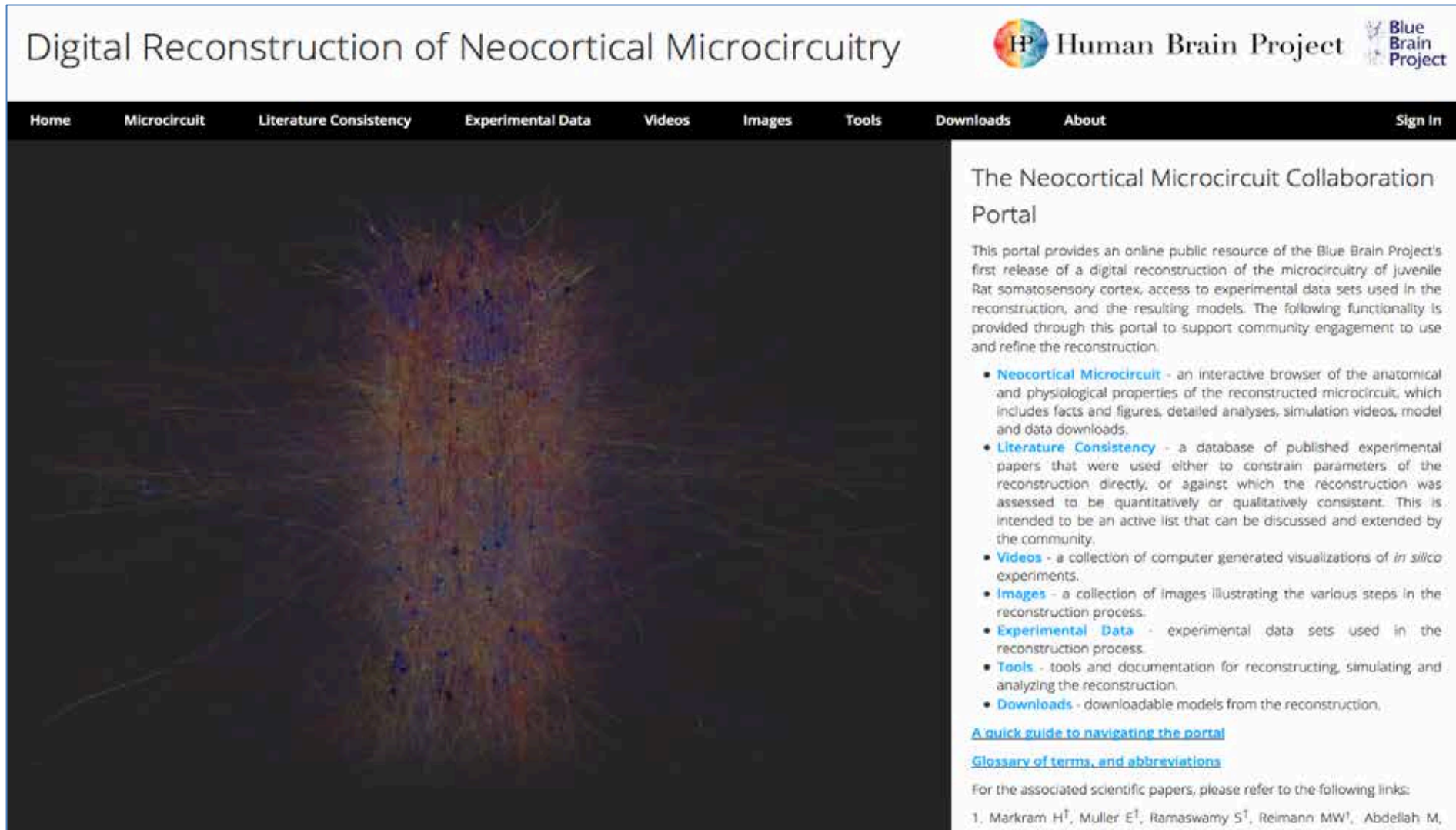
CPU cores: 1
This is the ntasks parameter provided to the slurm launcher.

Memory in MB: 2048
This is the mem parameter provided to the slurm launcher.

Cancel Launch

Figure 24: Screenshot of the Synapse Overall Density Circuit Validation App

NMC Portal



Digital Reconstruction of Neocortical Microcircuitry

Human Brain Project Blue Brain Project

Home Microcircuit Literature Consistency Experimental Data Videos Images Tools Downloads About Sign In

The Neocortical Microcircuit Collaboration Portal

This portal provides an online public resource of the Blue Brain Project's first release of a digital reconstruction of the microcircuitry of juvenile Rat somatosensory cortex, access to experimental data sets used in the reconstruction, and the resulting models. The following functionality is provided through this portal to support community engagement to use and refine the reconstruction.

- **Neocortical Microcircuit** - an interactive browser of the anatomical and physiological properties of the reconstructed microcircuit, which includes facts and figures, detailed analyses, simulation videos, model and data downloads.
- **Literature Consistency** - a database of published experimental papers that were used either to constrain parameters of the reconstruction directly, or against which the reconstruction was assessed to be quantitatively or qualitatively consistent. This is intended to be an active list that can be discussed and extended by the community.
- **Videos** - a collection of computer generated visualizations of *in silico* experiments.
- **Images** - a collection of images illustrating the various steps in the reconstruction process.
- **Experimental Data** - experimental data sets used in the reconstruction process.
- **Tools** - tools and documentation for reconstructing, simulating and analyzing the reconstruction.
- **Downloads** - downloadable models from the reconstruction.

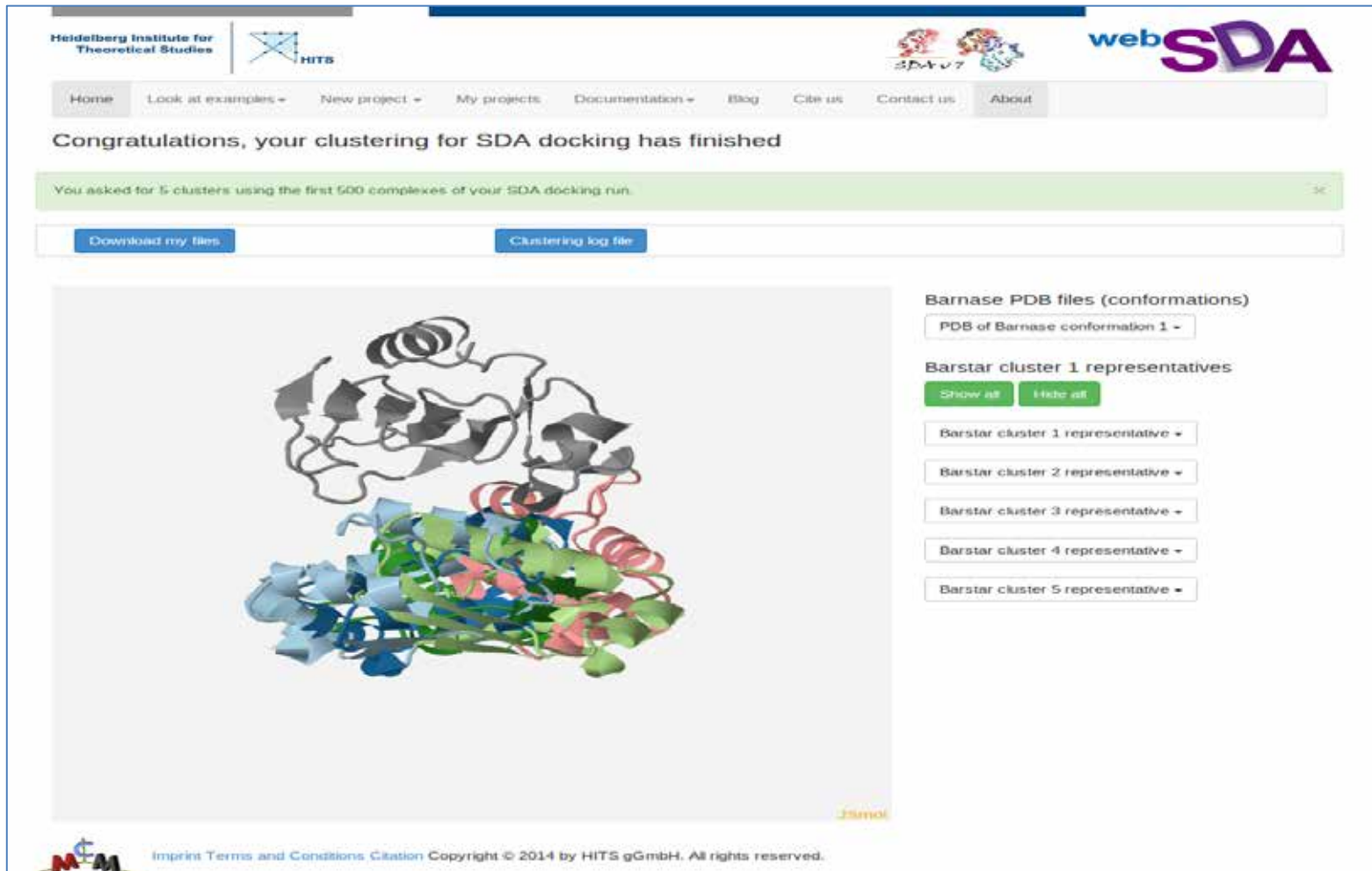
[A quick guide to navigating the portal](#)
[Glossary of terms, and abbreviations](#)

For the associated scientific papers, please refer to the following links:

1. Markram H¹, Muller E¹, Ramaswamy S¹, Reimann MW¹, Abdellah M,

Figure 25: Screenshot of the Neocortical Microcircuit Collaboration Portal

WebSDA



The screenshot displays the WebSDA web application interface. At the top, there is a navigation bar with links: Home, Look at examples, New project, My projects, Documentation, Blog, Cite us, Contact us, and About. The main heading reads "Congratulations, your clustering for SDA docking has finished". Below this, a green message box states: "You asked for 5 clusters using the first 500 complexes of your SDA docking run." Two buttons are provided: "Download my files" and "Clustering log file".

The central part of the interface features a 3D molecular model of a protein-ligand complex. The protein is shown as a grey ribbon structure, and the ligand is represented by a green and blue mesh. To the right of the model, there are sections for "Barnase PDB files (conformations)" with a button "PDB of Barnase conformation 1 -", and "Barstar cluster 1 representatives" with buttons "Show all" and "Hide all". Below these are five buttons labeled "Barstar cluster 1 representative" through "Barstar cluster 5 representative".

At the bottom of the interface, there is a footer with the text: "Imprint Terms and Conditions Citation Copyright © 2014 by HITS gGmbH. All rights reserved." and a small logo.

Figure 26: Screenshot of the WebSDA application