Human Brain Project

Co-funded by
the European Union

The Brain Simulation Platform

The BSP online:

Url: https://collab.humanbrainproject.eu/#/collab/1655/nav/28538

Twitter: https://twitter.com/hbpbrainsim

Youtube: https://www.youtube.com/watch?v=-PneUEIj-_4

For a free account please contact
bsp-support@humanbrainproject.eu

The Brain Simulation Platform

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Univ. di Palermo, Department of Matematics and Informatics (Visiting Professor, *Cybernetics*)

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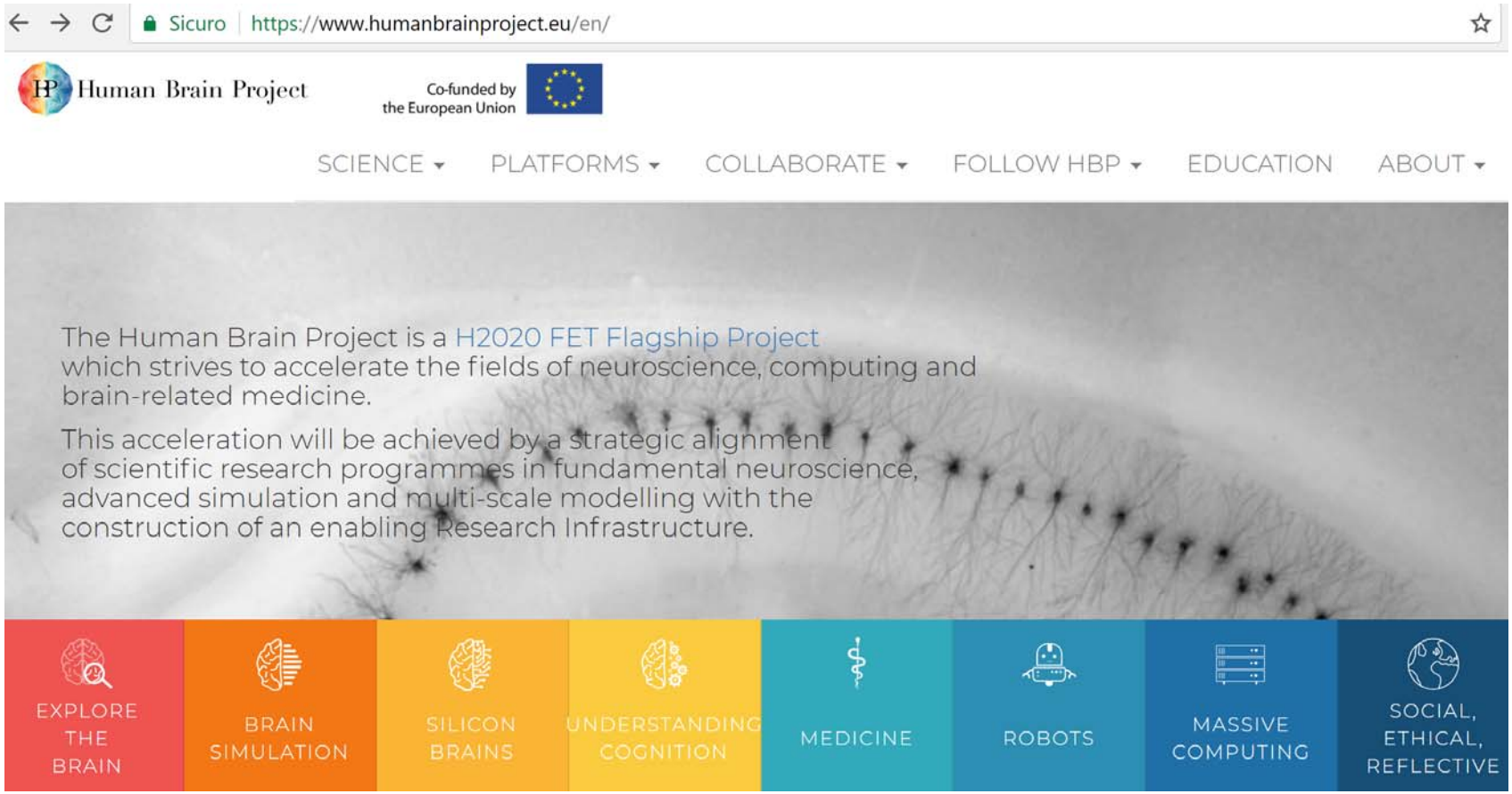
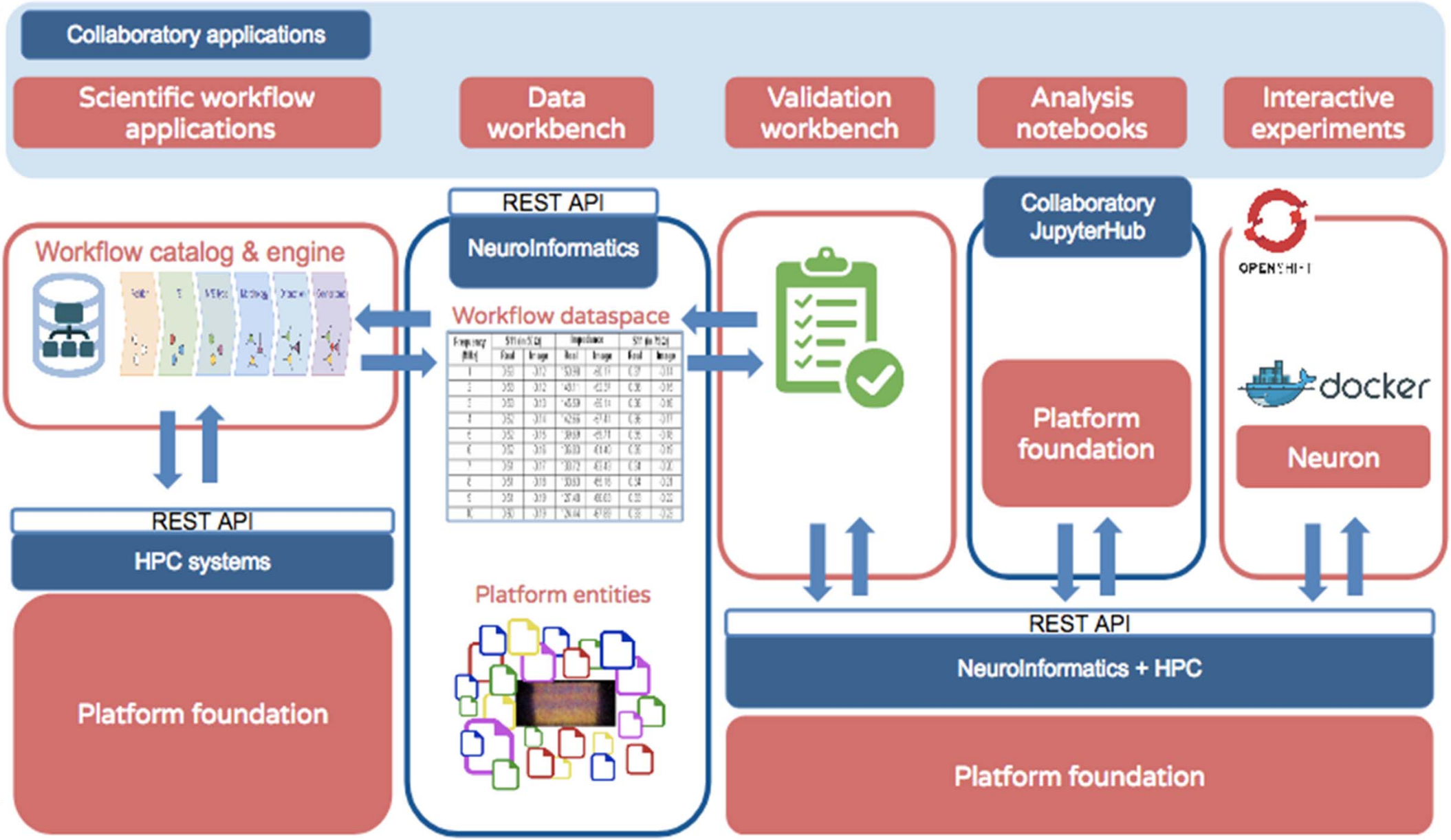
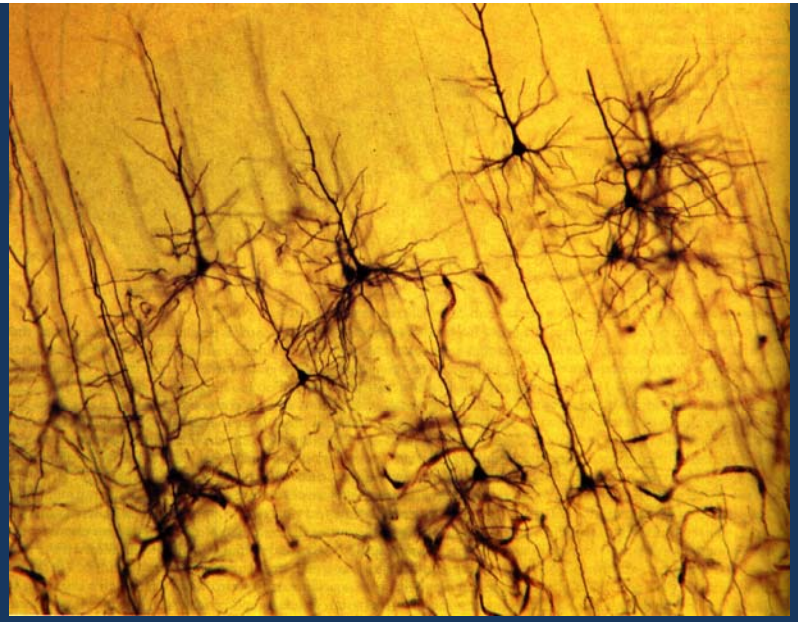
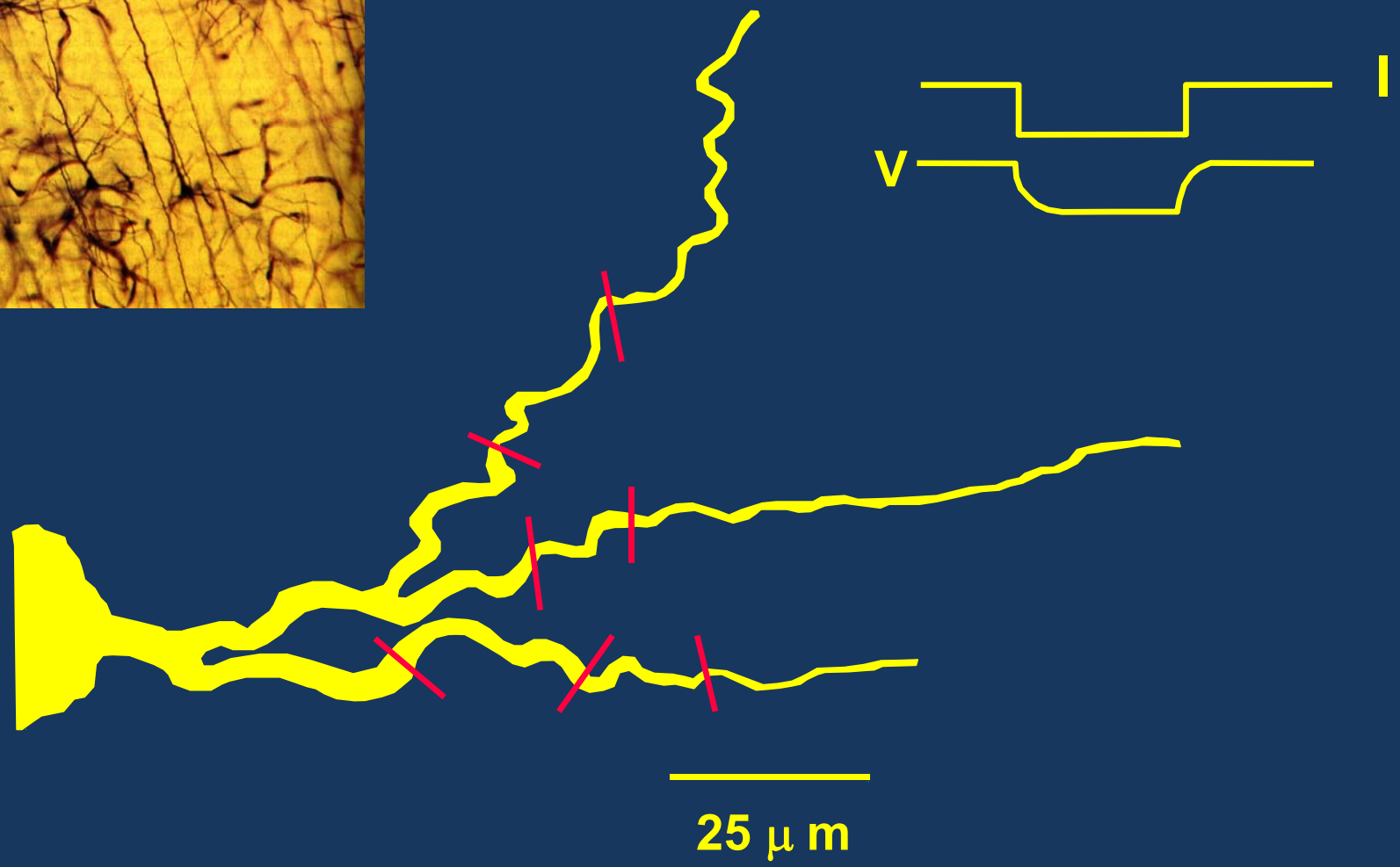

Sicuro
https://www.humanbrainproject.eu/en/
Human Brain Project
Co-funded by the European Union
SCIENCE
PLATFORMS
COLLABORATE
FOLLOW HBP
EDUCATION
ABOUT
The Human Brain Project is a H2020 FET Flagship Project which strives to accelerate the fields of neuroscience, computing and brain-related medicine.
This acceleration will be achieved by a strategic alignment of scientific research programmes in fundamental neuroscience, advanced simulation and multi-scale modelling with the construction of an enabling Research Infrastructure.
EXPLORE THE BRAIN
BRAIN SIMULATION
SILICON BRAINS
UNDERSTANDING COGNITION
MEDICINE
ROBOTS
MASSIVE COMPUTING
SOCIAL, ETHICAL, REFLECTIVE

Architecture



cellular level





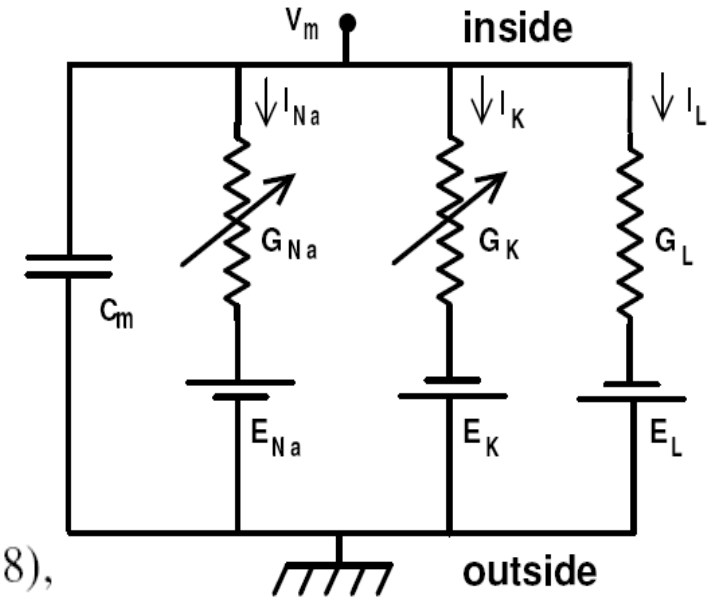
Hodgkin-Huxley equations

$$C\frac{\mathrm{d}V}{\mathrm{d}t} = I_{\mathrm{ext}} - g_{\mathrm{Na}}m^3h(V - V_{\mathrm{Na}}) - g_{\mathrm{K}}n^4(V - V_{\mathrm{K}}) - g_{\mathrm{L}}(V - V_{\mathrm{L}}),$$

$$\frac{dm}{dt} = \alpha_m(V)\,(1-m) - \beta_m(V)\,m,$$

$$\frac{dh}{dt} = \alpha_h(V)\,(1-h) - \beta_h(V)\,h,$$

$$\frac{dn}{dt} = \alpha_n(V)\,(1-n) - \beta_n(V)\,n.$$

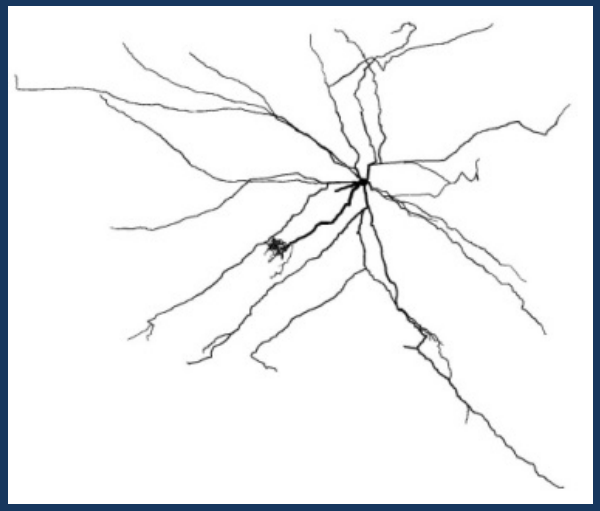


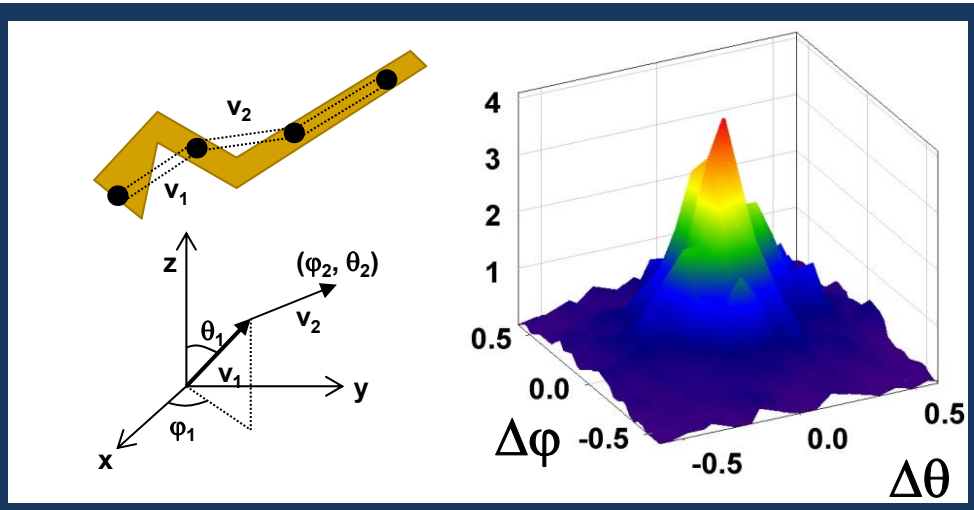
$$\alpha_m = 0.1\frac{-V+25}{\exp((-V+25)/10)-1}, \qquad \beta_m = 4\exp(-V/18),$$

$$\alpha_h = 0.07\exp(-V/20), \qquad \beta_h = \frac{1}{\exp((-V+30)/10)+1},$$

$$\alpha_n = 0.01\frac{-V+10}{\exp((-V+10)/10)-1}, \qquad \beta_n = 0.125\exp(-V/80).$$

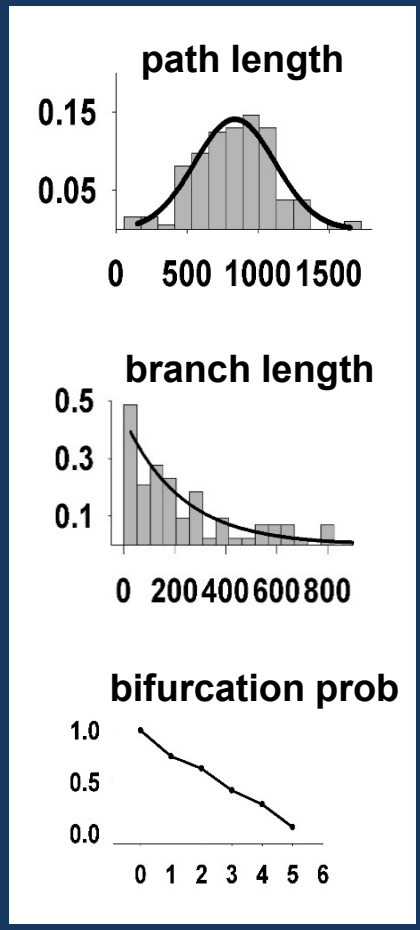
From Igarashi et al., 2012





exp parameters were used to build synthetic morphologies…

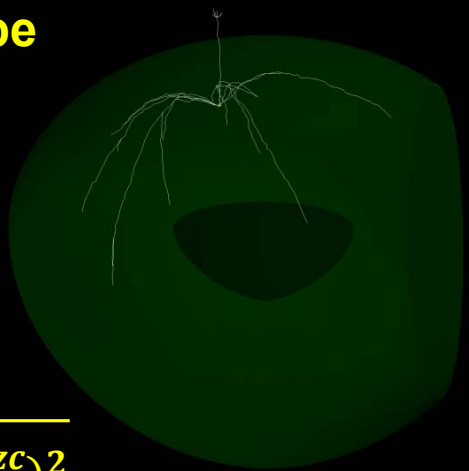
show mitral cells

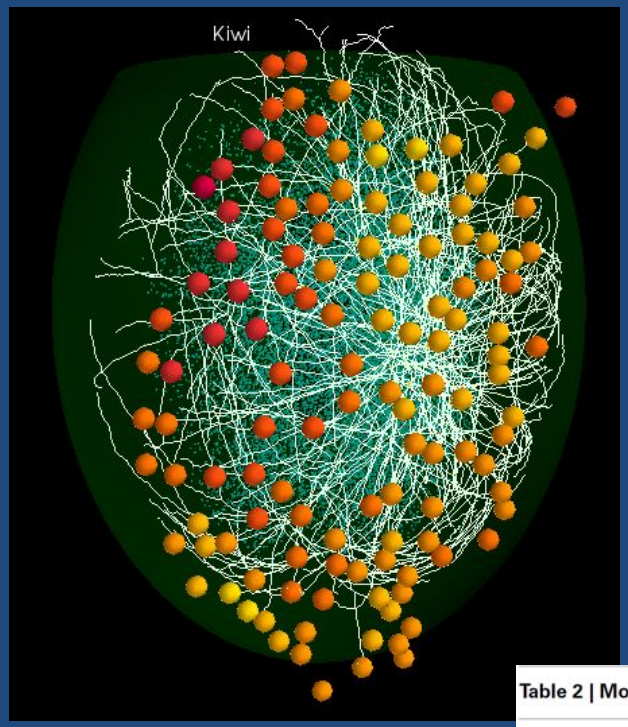


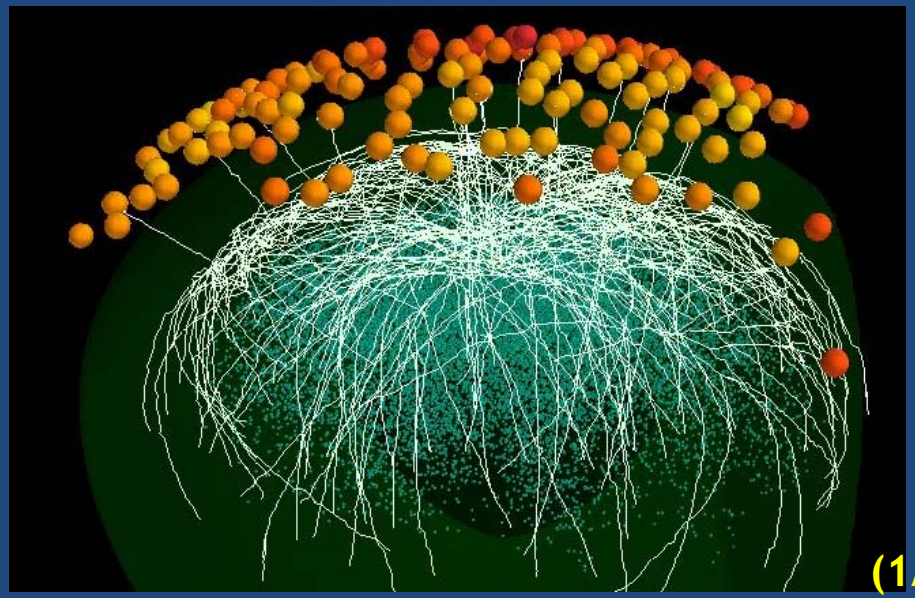
…growing on a bulb-like shape

$$\overrightarrow{v_{i+1}} = \overrightarrow{v_i} + \alpha h(p_i)\vec{u}$$

$$h(p_i) = \sqrt[2]{(\frac{xi-xc}{a})^2+(\frac{yi-yc}{b})^2+(\frac{zi-zc}{c})^2}$$







movie

635 mitral cells,
69000 granule cells,
$7 \cdot 10^5$ synapses
(1/20 of the real system
32,000,000 nonlinear ODEs)

Table 2 | Model parameters and execution times for a typical simulation.

	Seg (min-max)	States (min-max) (v, channels, and syn. gates)	Syn (min-max)
MC ($n = 635$)	380,748 (189–1433)	5,259,735 (2536–20,028)	707,216 (308–2799)
GC ($n = 69013$)	4,344,724 (33–257)	26,892,317 (261–869)	707,216 (1–62)
Total	4,725,472	32,152,052	

	Computation time	Comm. time (spike exchange)	Comm. time (multisplit)	Total run time (2048 procs)
Average (sec)	27,149.35	68.53	555.94	32,552.86
Max (sec)	27,756.25	813.44	1453.96	

CINECA, Bologna

Technical References

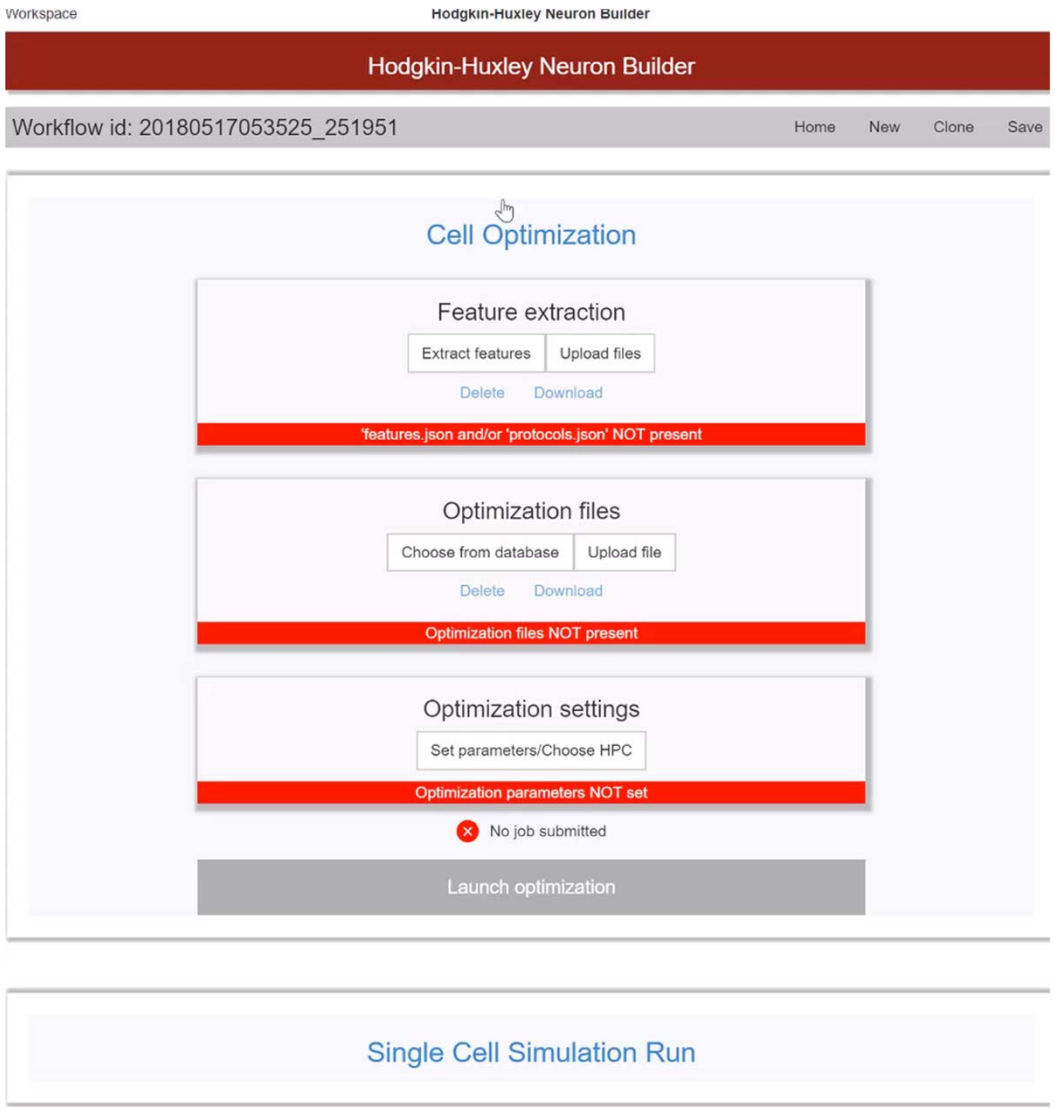
Architecture: 10 BGQ Frame
Model: IBM-BG/Q
Processor Type: IBM PowerA2, 1.6 GHz
Computing Cores: 163840
Computing Nodes: 10240
RAM: 1GByte / core
Internal Network: Network interface with 11 links ->5D Torus
Disk Space: 2PByte of scratch space
Peak Performance: 2PFlop/s

Typical 40 sec of sim. on 2048 processors, fully integrated NEURON+python implementation, $750 \cdot 10^6$ spikes: 9 hours, 10 Gb output, 99% eff.

Brain Simulation Platform v2

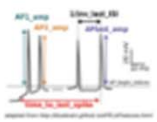
- Released in June 2017
- it delivers an open framework with:
  - Advanced & reproducible model building workflows unique in the field
  - Model Validation Framework;
  - Model Catalog;
  - Intuitive tools and functionality “as a Service”
  - *in silico* experiments;
  - Seamless integration with HPC systems (CINECA, JSC, NSG)
  - MOOC

UC1-UC3: Single cell modeling and in silico microcircuit experimentation



The Collaboratory	**CSCS**
data selection KG, containers, local	**CSCS** **EPFL**
data preproc & analysis custom app BluePyeFE	**EPFL** **CNR**
simulation conf & analysis custom code BluePyOpt	**JSC, CINECA (UNICORE)** **NSG (rest API)**
web tool custom app NaaS	**EPFL**

Use cases: trace analysis

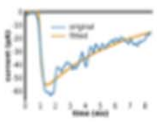


Feature extraction

Extracts electrophysiological features; traces can be from NeuroInformatics Platform or uploaded

Everybody

BETA

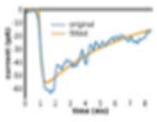


Synaptic events fitting

Fitting synaptic events using data and model in NeuroInformatics Platform

Power users

EXP HPC

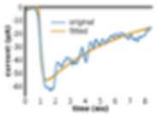


Synaptic events fitting with user model

Fitting synaptic events using data in NeuroInformatics Platform and user's model

Experts

EXP HPC

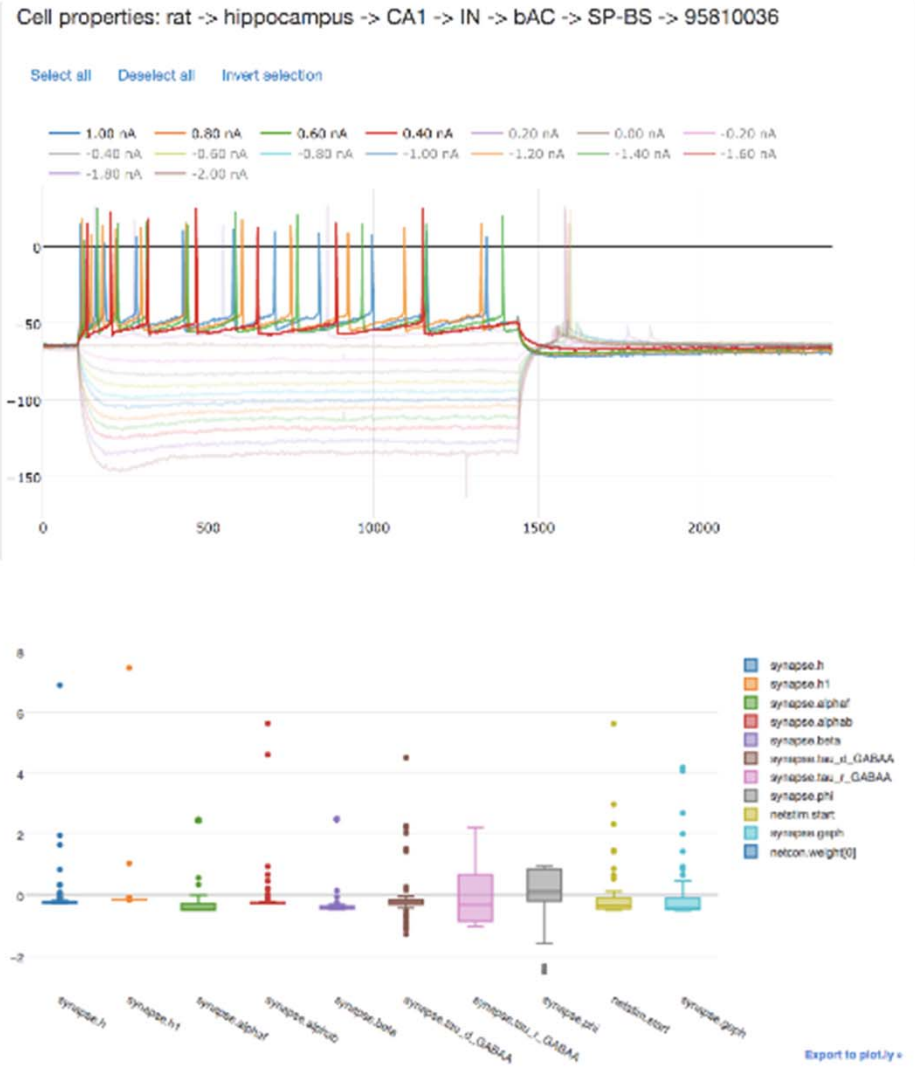


Synaptic events fitting with user data

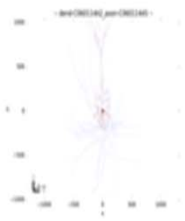
Fitting user's synaptic events data with model from NeuroInformatics Platform

Experts

EXP HPC



Use cases: morphology analysis

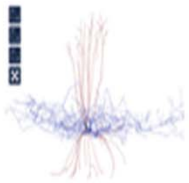


Morphology analysis

Power users

Performs analysis on a morphology with NeuroM

BETA

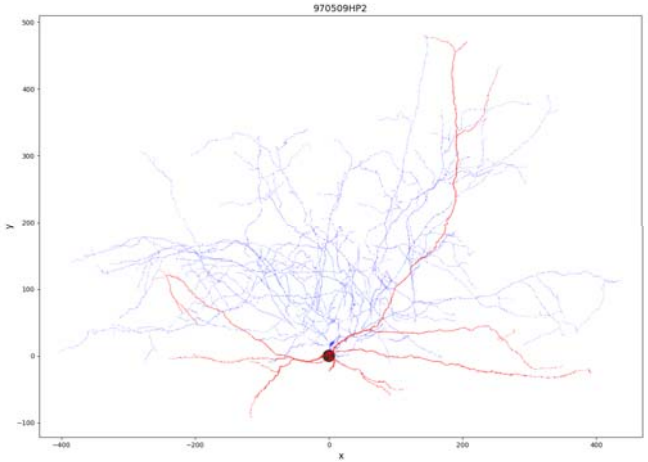


Morphology visualization

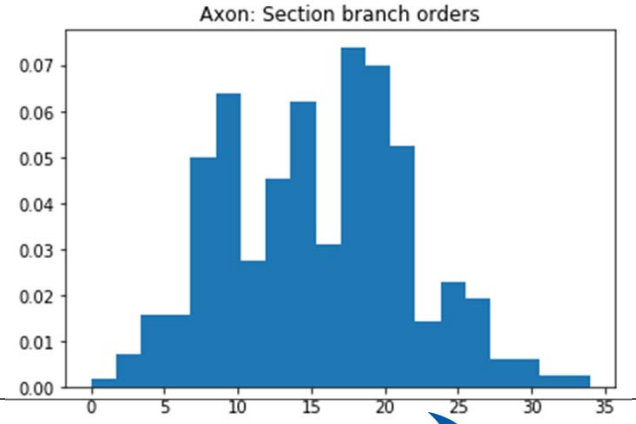
Everybody

Display neuron morphology in 3D

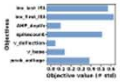
BETA



Component	Feature	Mean	Std
basal_dendrite	local_bifurcation_angles	1.459	0.513
basal_dendrite	neurite_lengths	861.100	404.560
basal_dendrite	neurite_volume_density	0.004	0.005
basal_dendrite	neurite_volumes	758.570	378.123
basal_dendrite	number_of_bifurcations	30.000	0.000
basal_dendrite	number_of_forking_points	30.000	0.000



Use cases: single cell building

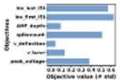


Rebuild an existing single hippocampal cell model

Use the BluePyOpt to re-run an optimization with your choices for the parameters range

Everybody

HPC BYO

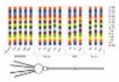


Build your own single hippocampal cell model using HBP data

Use the BluePyOpt to run an optimization choosing from HBP data for morphology, channel kinetics, features, and parameters.

Power users

BETA HPC

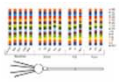


Optimize a cerebellar granule cell model composed by a single section

Using BluePyOpt to optimize a single compartmental cerebellar granule cell. All the parameters, channels and morphology can be modified. This version runs directly on the collaboratory and it is limited to small optimizations

Everybody Power users

HPC

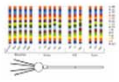


Optimize a cerebellar granule cell multicompartmental model

Using BluePyOpt to optimize a multcompartmental cerebellar granule cell composed by four dendrites, soma and a custom multi segmented axon. All the parameters, channels and morphology can be modified. This version runs directly on the collaboratory and it is limited to small optimizations

Everybody Power users

HPC

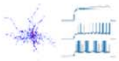


Simulation and validation of a mouse Purkinje cell multicompartmental model

Simulation and validation of a mouse Purkinje cell multicompartmental model obtained from BluePyOpt optimizer. The purpose of this usecase it to extract, simulate and validated a series of physiologically correct Purkinje cells. This notebook runs directly on the Collab and does not require HPC resources

Power users

HPC

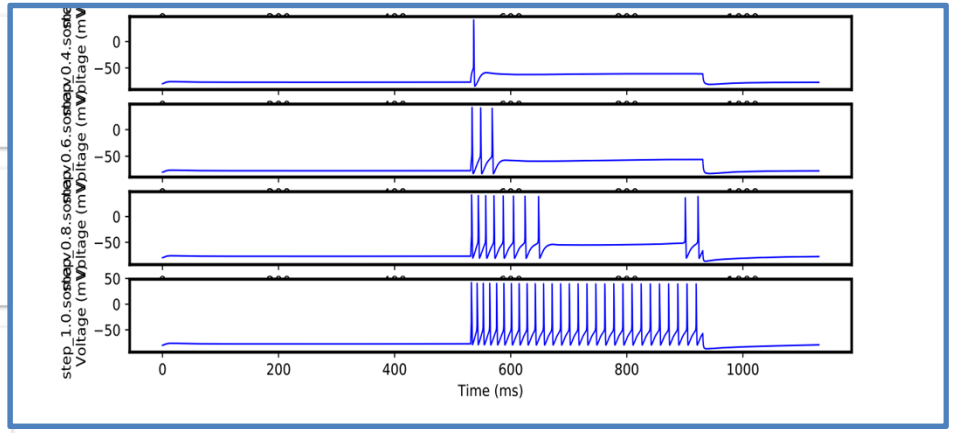


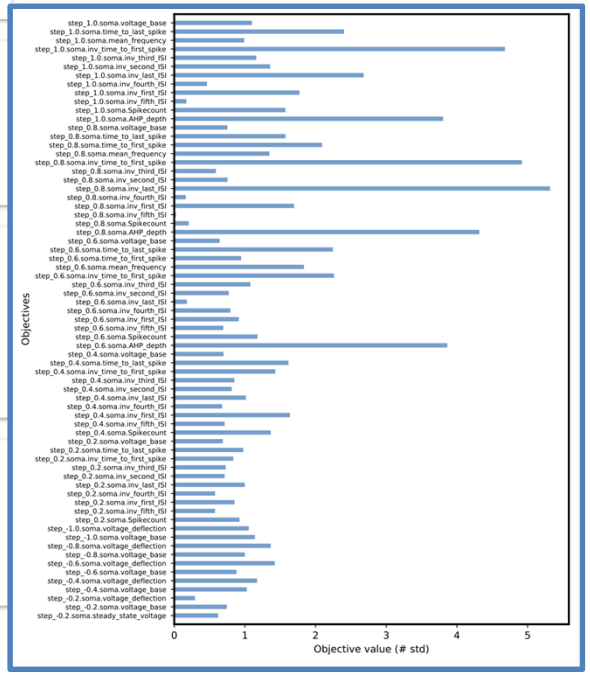
Optimize a striatal fast-spiking interneuron

Fit parameters of a striatal fast-spiking interneuron model to the experimental data. Optimization uses BluePyOpt as well as the realistic morphology, channel kinetics and extracted neurophysiological features. This version runs directly on the collaboratory and it is limited to small optimizations.

Developers

EXP





Use cases: validations

VALIDATION

Validation Framework Demo (Walkthrough)

Demonstrates the use of the validation framework

Everybody

BETA

VALIDATION

Basal Ganglia - BluePyOpt Optimized Model Validation - Multiple HOF

Validates single cell basal ganglia models optimized via BluePyOpt for various features offered by eFEL; models contain multiple hall of fame parameter sets

Everybody

BETA

VALIDATION

Basal Ganglia Morphology Validation

Validates single cell morphologies of MSN and FS cells

Everybody

BETA

VALIDATION

Generic - BluePyOpt Optimized Model Validation

Validates models optimized via BluePyOpt for various features offered by eFEL

Everybody

BETA

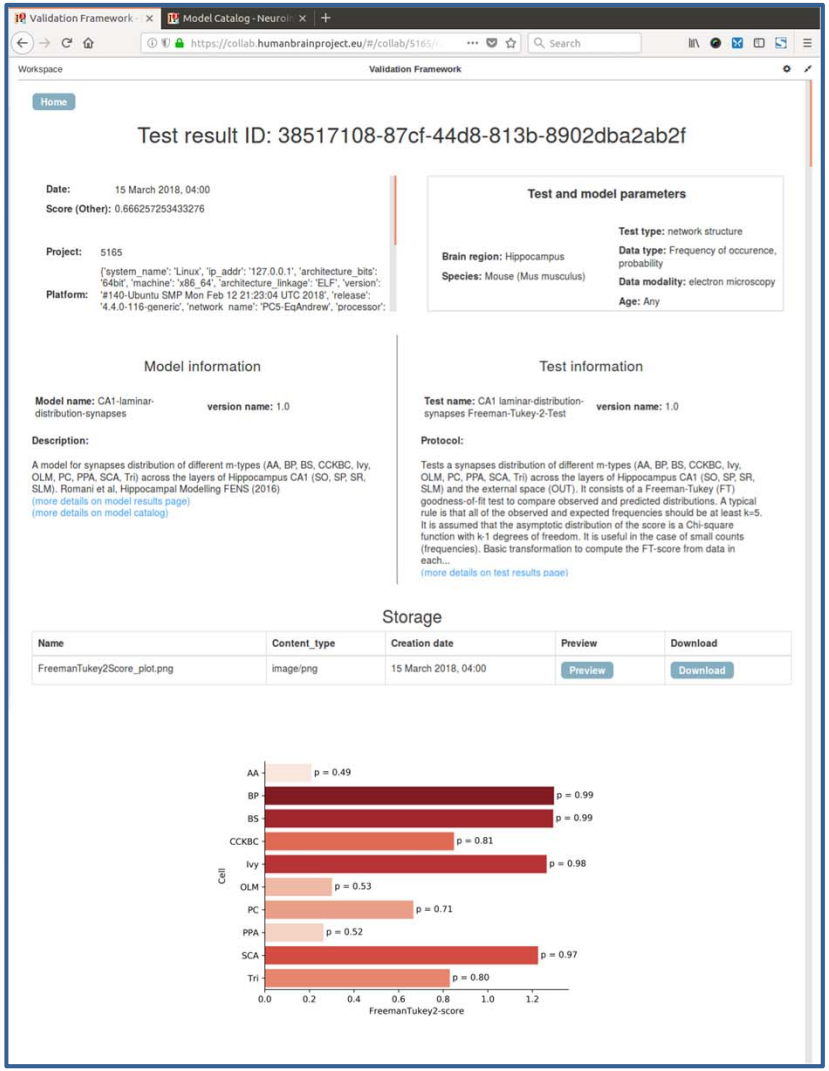
VALIDATION

Hippocampus Single Cell - BluePyOpt Optimized Model Validation

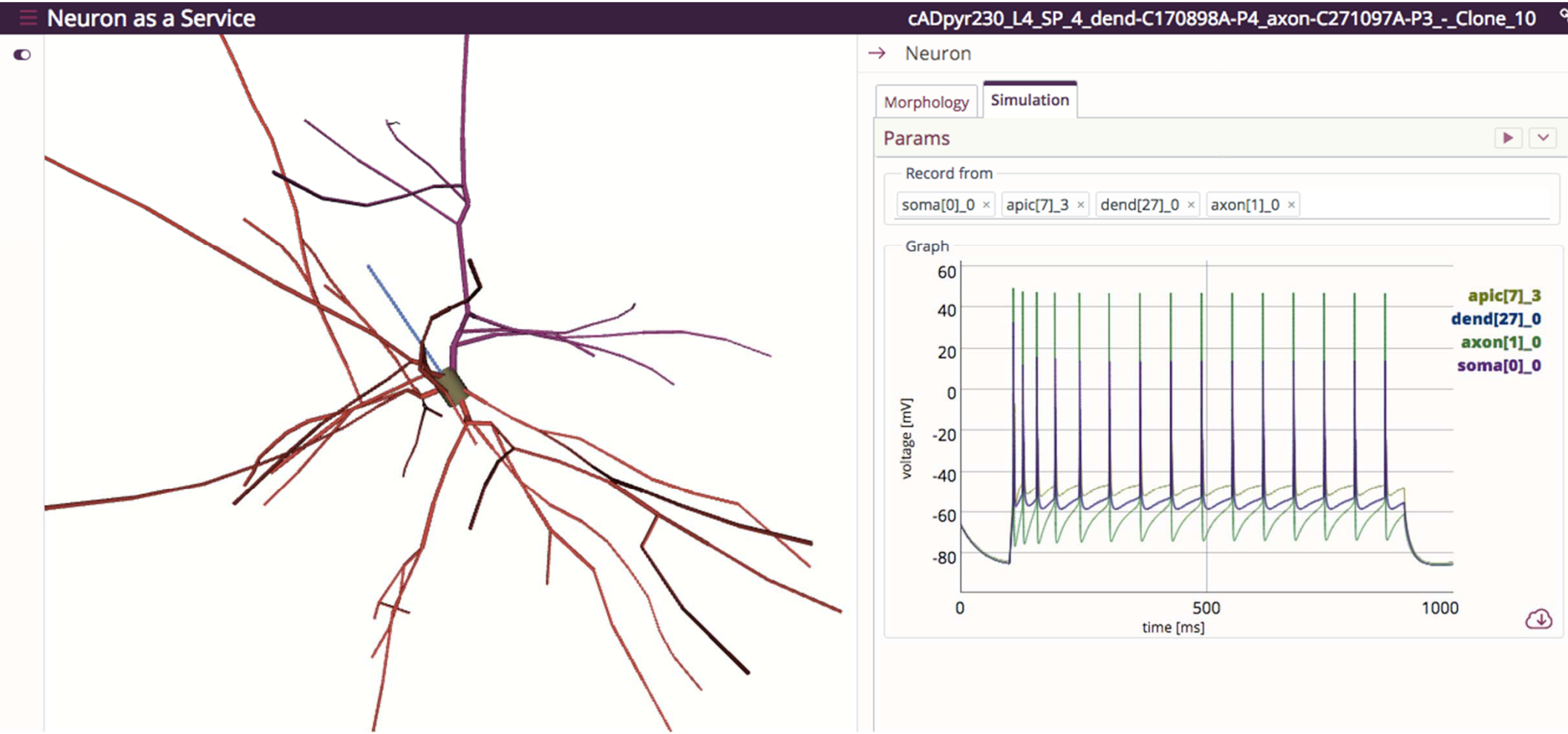
Validates single cell models of Hippocampus optimized via BluePyOpt

Everybody

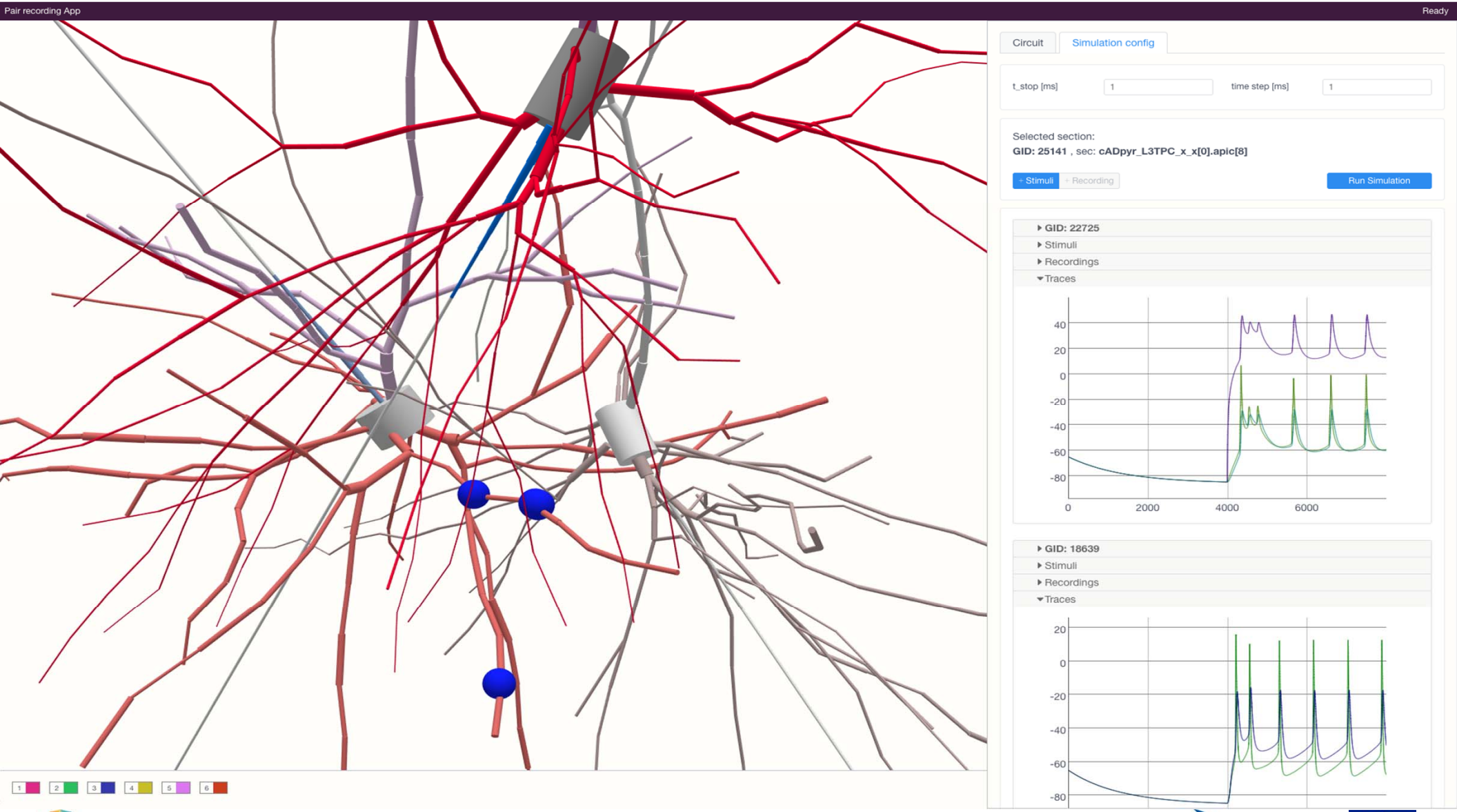
BETA



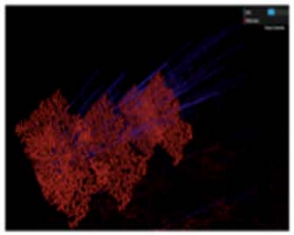
Use cases: single cell experiment



Use cases: small circuit experiment



Use cases: circuit building



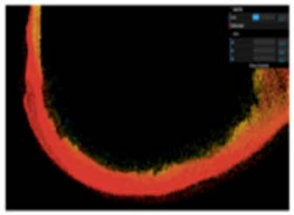
Rat Cerebellum volume

A volume of the cerebellum with detailed neuron model

Credits:

Contributor(s): *Egidio d'Angelo* - egidiougo.dangelo@u

Casellato - claudia.casellato@unipv.it. *Elisa Marenzi* - elis

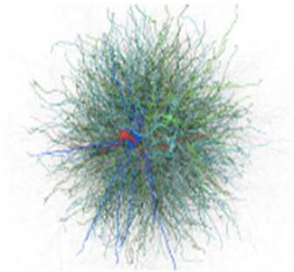


Rat hippocampus CA1

A circuit of detailed neuron models based on the Ascoli

Credits:

Contributor(s): *Armando Romani* - armando.romani@epf

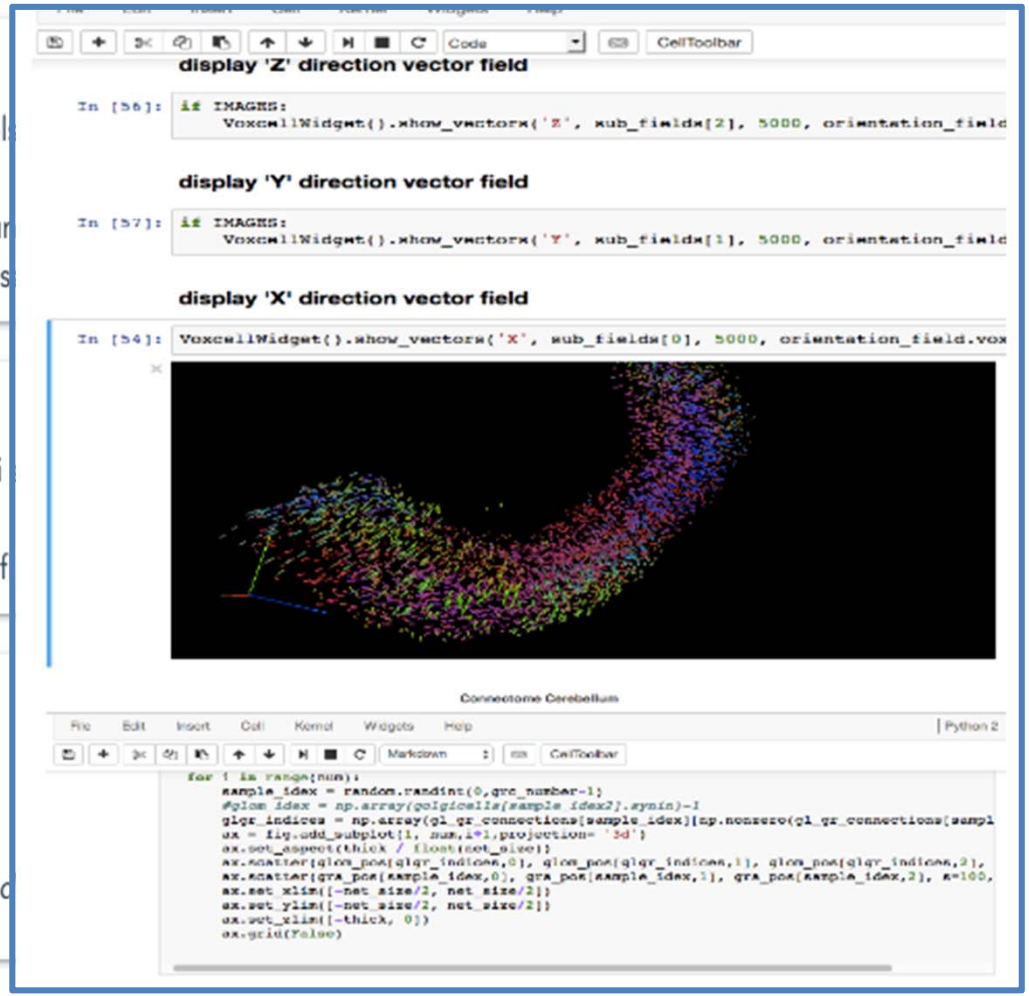


Striatum microcircuitry

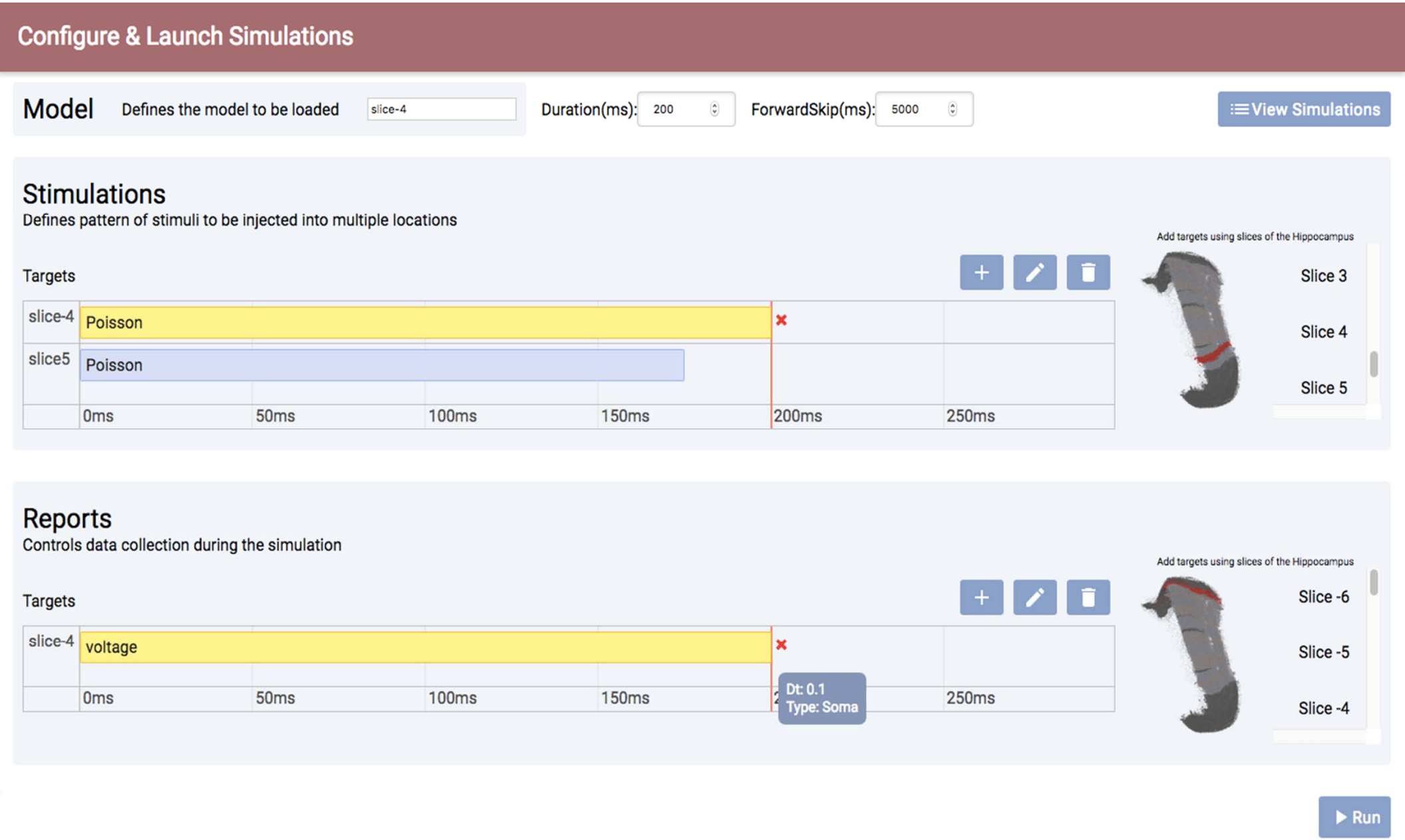
Striatum microcircuitry.

Credits:

Contributor(s): *Johannes Hjorth* - hjorth@kth.se. *Alexand*

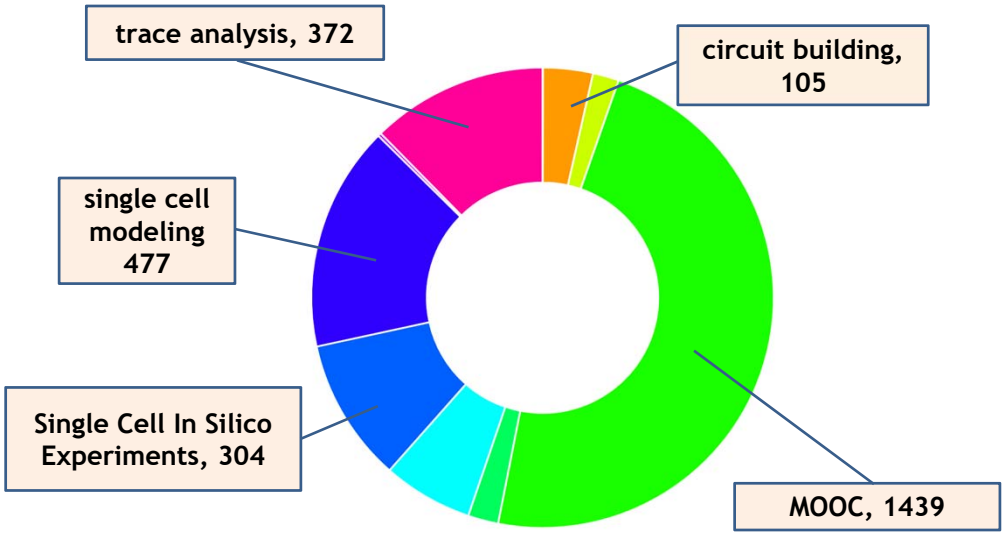


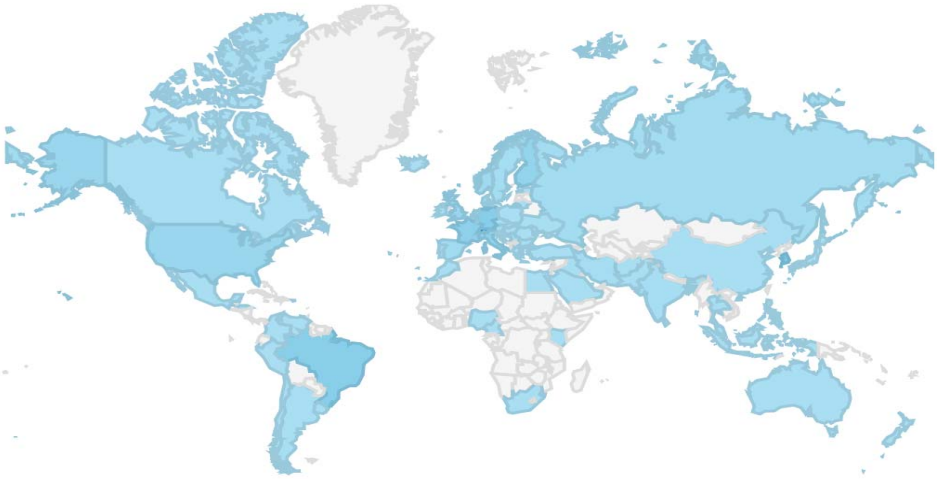
Use cases: brain region experiment



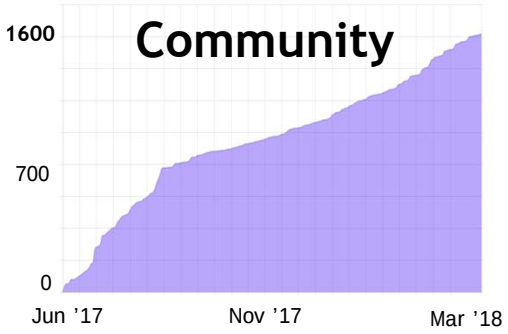
Facts

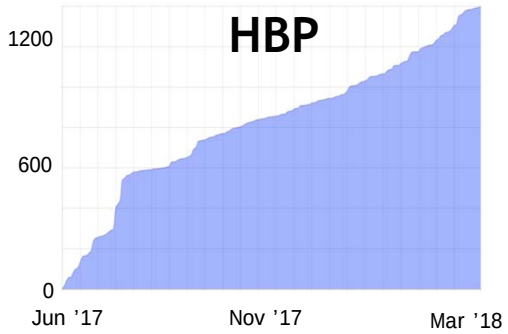
Use cases executed since June 2017





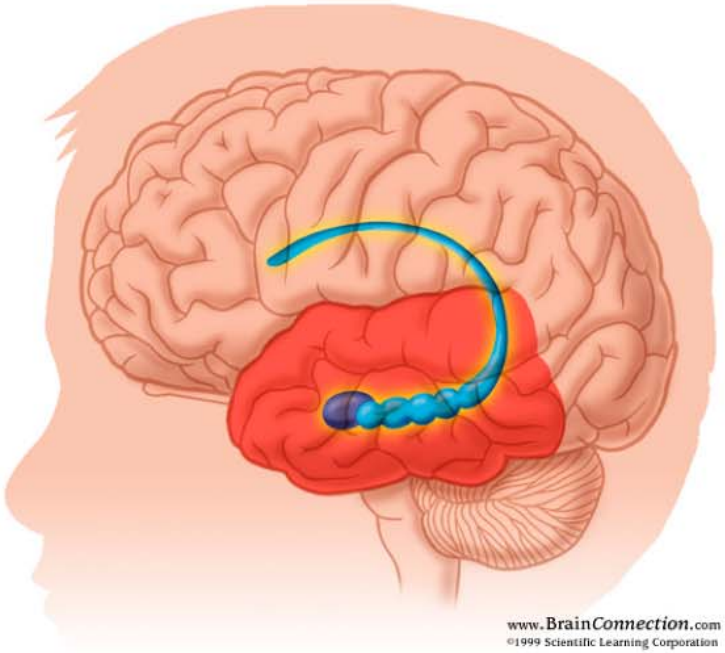
Page views during SGA1

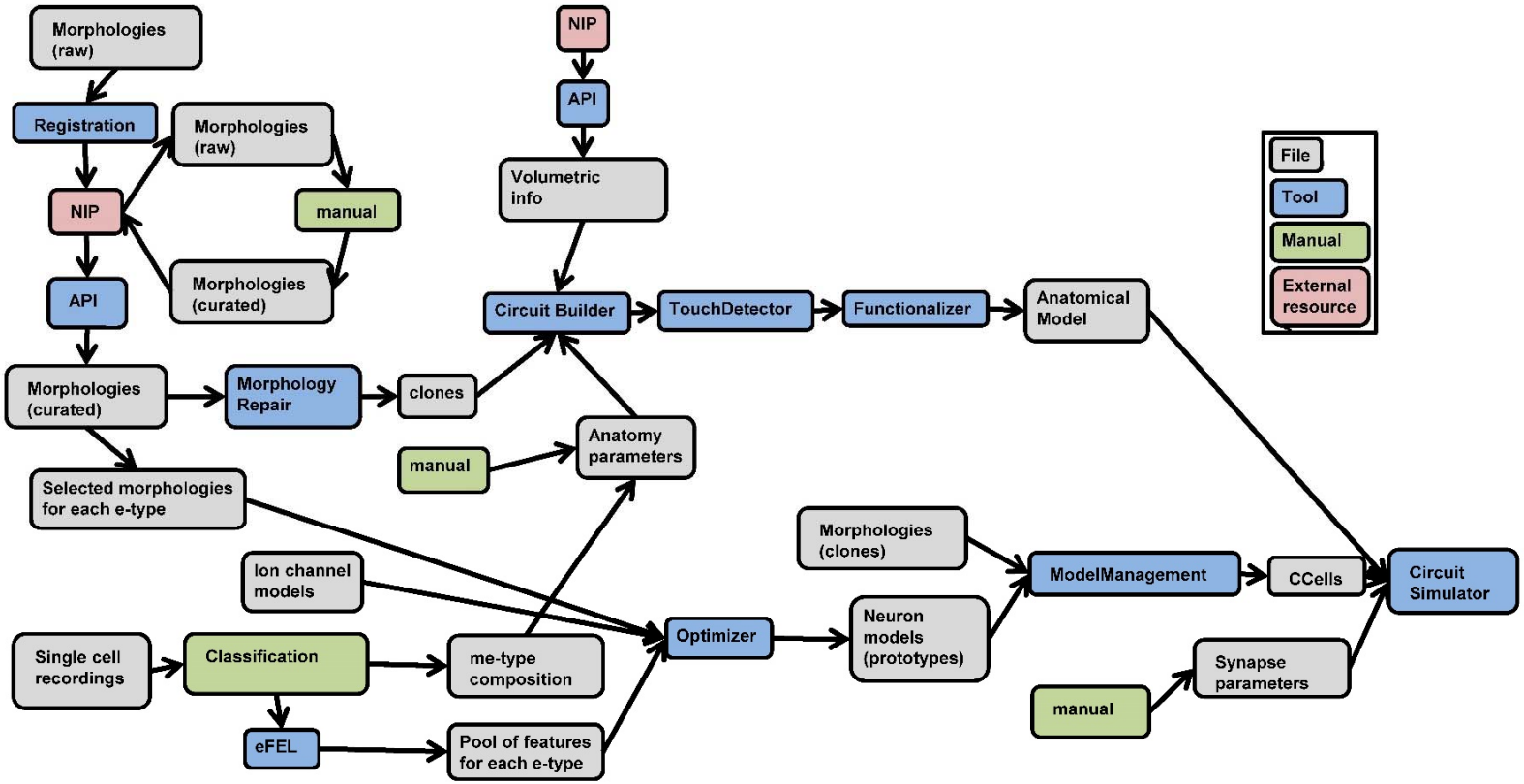




400 active users

A few millions neurons
Strongly involved in higher brain functions (learning, memory, spatial navigation)
Implicated in Alzheimer's disease, temporal lobe epilepsy, cognitive aging, post-traumatic stress disorder, transient global amnesia, schizophrenia, depressive and anxiety disorders.




Morphologies (raw)
Registration
Morphologies (raw)
NIP
manual
Morphologies (curated)
API
Morphologies (curated)
Morphology Repair
clones
manual
Anatomy parameters
Selected morphologies for each e-type
Ion channel models
Single cell recordings
Classification
me-type composition
eFEL
Pool of features for each e-type
NIP
API
Volumetric info
Circuit Builder
TouchDetector
Functionalizer
Anatomical Model
Optimizer
Neuron models (prototypes)
Morphologies (clones)
ModelManagement
CCells
Circuit Simulator
manual
Synapse parameters
File
Tool
Manual
External resource

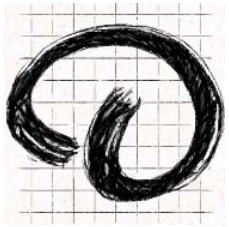
biophysically accurate network

700000 neurons, ~350·10^6 memb seg, 20 ODE/seg
7·10^9 ODEs + synapses
1" of sim time: 5hr on BG/Q using 32000 procs
~8Tb of input, up to ~3Tb of output

The Hippocampus Team

Blue Brain Project

UCL



Romani A, Muller E, Markram H

Thomson A, Mercer A Lange S, Falck J

Káli S, Budd J, Sáray S Tar L, Gulyás A, Freund T

Migliore M, Lupascu C Migliore R, Bologna L, E Giacalone

Neuroinformatics: Jimenez S, Lu H
Morphologies: Ying S, Kanari L, Gonzales MP, Hagens O
Connectome: Reimann M
Synapse physiology: Ecker A, Ramaswamy S
IT: Requelme L, Gevaert M, Dynes J, Courcol JD, Devresse A, King JG, Van Geit W, Vanherpe L, Povolotskiy A
Single cell: Rossert C
Visualization: Antille N, Hernando J, Favreau C

Human Brain Project

Co-funded by
the European Union

Thank You

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