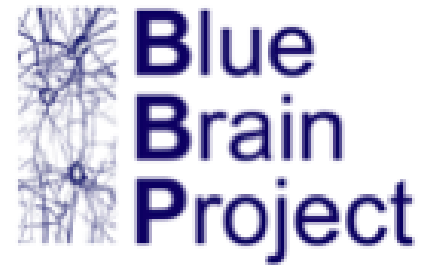


BRAIN MIND INSTITUTE BMI



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The BBP data model, BluePy and friends

HBP CodeJam Workshop #7



Human Brain Project

Eilif Muller

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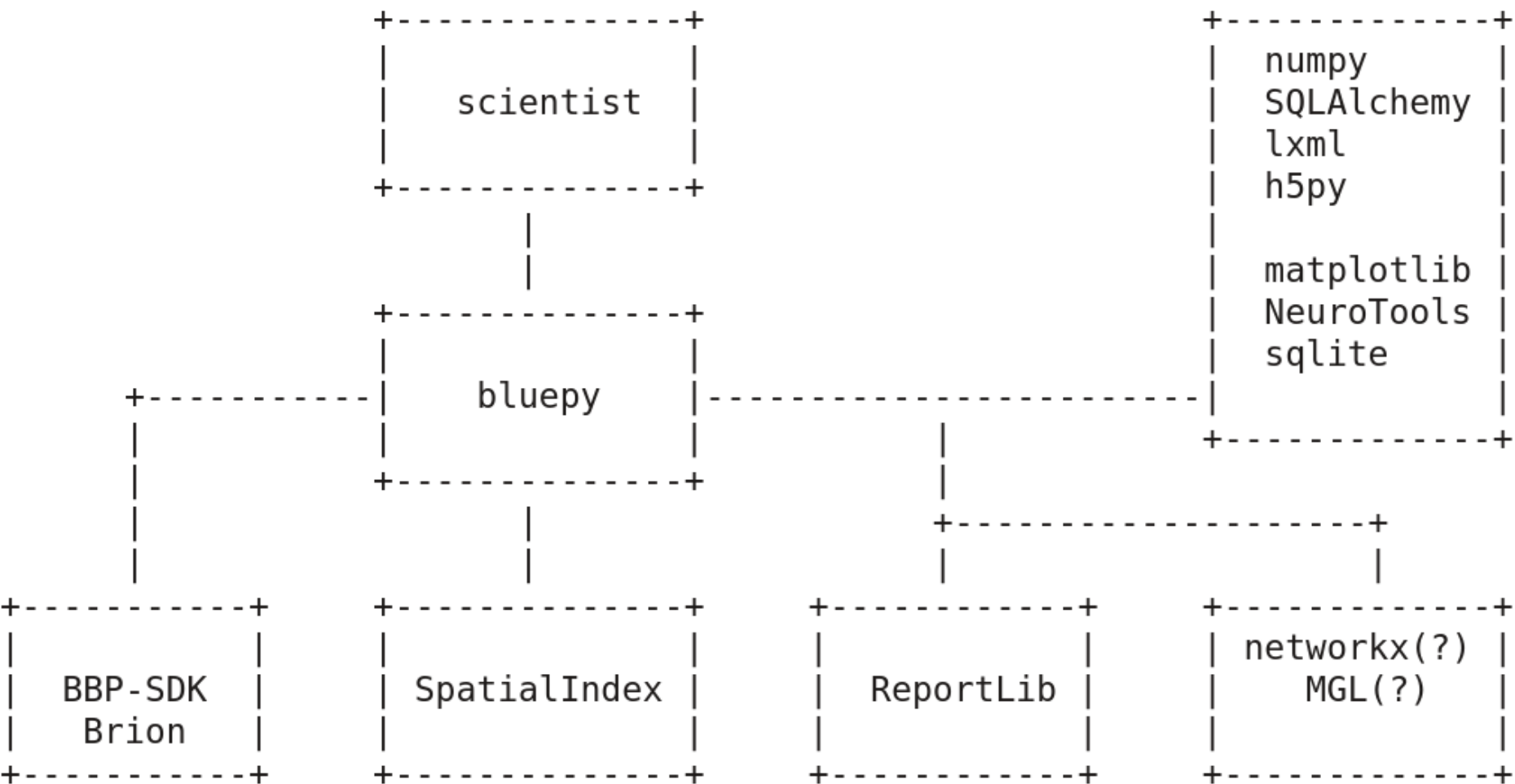
<http://bluebrain.epfl.ch>

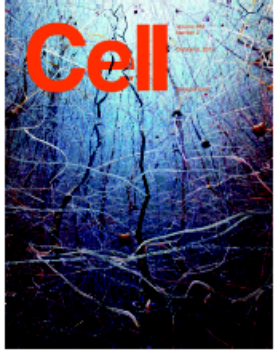


BluePy (pronounced "bloopy") is a scientist targeted productivity layer for scientists to access BBP **production entities**.

Designed to be empowering:

- "One-liners" for scientific needs
- Tools to facilitate automation streamlined

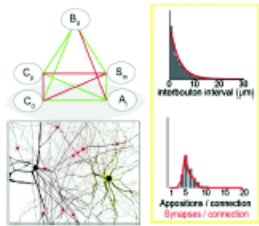




Reconstruction and simulation of neocortical microcircuitry

Markram H, Muller E, Ramaswamy S, Reimann MW, ...
DeFelipe J, Hill SL, Segev I, Schuermann F

Cell 163:2, p456–492, 8 October 2015

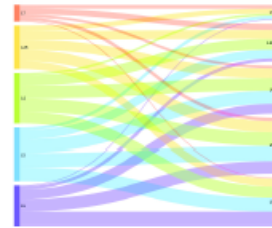


An algorithm to predict the connectome of neural microcircuits

Reimann et al.

Front. Comp. Neurosci., 8 October 2015

<https://github.com/BlueBrain>



The neocortical microcircuit collaboration portal: a resource for rat somatosensory cortex

Ramaswamy S, Courcol J-D, et al.

Frontiers in Neural Circuits, 8 October 2015

<https://bbp.epfl.ch/nmc-portal>

BluePy was the primary API used for above analysis.
Some IPython notebook use-cases ...



- BluePy **is not yet** open-source
- Brion **is** open-source
- Ongoing process to converge with ABI & community on underlying data models
- Intention to release our software ecosystem around such converged data models

bluebrain.github.io/Brion-1.5/index.html

Brion 1.5.0


The Blue Brain C++ I/O library

Main Page Related Pages Classes Files

Brion

- Changelog
- Deprecated List
- Classes
- Files

Brion Documentation



Welcome to Brion, a C++ library for read and write access to Blue Brain data structures, including BlueConfig/CircuitConfig, Circuit, CompartmentReport, Mesh, Morphology, Synapse and Target files.

Brion can be retrieved by cloning the [source code](#).

- Core IO library for accessing BBP data model in C++
- <https://github.com/BlueBrain/Brion>
- <http://bluebrain.github.io/>

Brion includes classes for reading and writing files of the Blue Brain data model.

Fast and low-overhead read access to:

- Circuit descriptors “CircuitConfigs” (brion::Circuit)
- Simulation descriptors “BlueConfigs” (brion::BlueConfig) –
- H5 Synapses data (brion::SynapseSummary, brion::Synapse)
- Groupings of elements (neurons, syns, ...) “Targets” (brion::Target)
- BBP binary meshes (brion::Mesh)
- BBP H5 morphologies and SWC morphologies (brion::Morphology and brion::morphologies)
- Compartment reports (brion::CompartmentReport)
- Spike reports (brion::SpikeReport)

Fast and low-overhead write access to:

- Compartment reports (brion::CompartmentReport)
- BBP binary meshes (brion::Mesh)
- BBP H5 morphologies (brion::Morphology)

BBP Data model - overview

- CircuitConfig
 - start.target “verbatim” defn. of named gid groups
 - nrn.h5 – connectivity and synapse parameters
 - circuit.mvd2 – neuron database
 - Circuit_mvd2.sqlite, SEGMENT_spatial.*, SYNAPSE_spatial.*, nrn_efferent.h5, ...
- BlueConfig
 - out.dat -> CSV: gid, spiketime
 - soma.bbp -> voltages per dt
 - soma.h5 -> voltage trace dataset per gid

Example CircuitConfig – a key-value format

Run Default

```
{
  # URI to the morphology collection entity
  MorphologyPath <...>/release/l2/2012.07.23/morphologies

  # URI to the morpho-electrical model collection entity
  METypePath <...>/release/l2/2012.07.23/ccells
  # URI to the mesh collection entity
  MeshPath <...>/release/l2/2012.07.23/meshes

  # URI to the build recipe entity
  BioName <...>/project/proj1/entities/bionames/SomatosensoryCxS1-v5.r0

  # Circuit specific attributes & paths
  CircuitPath <...>/project/proj1/circuits/SomatosensoryCxS1-v5.r0/01/merged_circuit
  nrnPath ncsFunctionalAllRecipePathways
  TargetFile default_user.target
  CentralHyperColumn 2
}

# Input projection entities defined for this circuit
Projection Thalamocortical_input_VPM
{
  Path ncsThalamocortical_VPM
  Source proj_Thalamocortical_VPM_Source
}
```

circuit.mvd2 – The neuron database

Essentially A CSV file with:

morphology name (string)

database type [not used] (int)

hyperColumn (int)

miniColumn (int)

layer [note that 0 is layer 1, 1 is layer 2, etc.] (int)

morphology type [index into MorphTypes below] (int)

electrophysiology type [index into ElectroTypes below] (int)

neuronCenter[0] (float)

neuronCenter[1] (float)

neuronCenter[2] (float)

neuronRotation[1] (float)

metype (string)

```
sm090317a2_idB 0 0 71 0 3 1 286.965408 1960.801904 83.942752 -144.357745 cNAC187_L1_HA
sm090317a2_idB 0 0 285 0 3 1 468.045056 1966.229605 50.926316 139.318573 cNAC187_L1_HA
sm080905b1 0 0 289 0 3 4 263.596306 1940.176638 31.100535 24.977901 cIR216_L1_HAC_1_sm
C060106F 0 0 297 0 3 0 106.403043 2027.019862 232.607069 66.966942 bNAC219_L1_HAC_1_CO
C280206K 0 0 33 0 5 3 409.051345 1918.453896 130.654939 124.924653 cACint209_L1_SLAC_1
```

Synapses: nrn.h5 – and HDF5 file

Contains a dataset for every gid, with a Nx19 list of its synapses & params:

- 0: Connecting gid: presynaptic for nrn.h5, postsynaptic for nrn_efferent.h5 (int)
- 1: Axonal delay: computed using the distance from AIS to the post synaptic terminal (ms) (float)
- 2: postSection ID (int)
- 3: postSegment ID (int)
- 4: The post distance (in microns) of the synapse from the beginning of the post segment 3D point, or -1 for soma connections (float)
- 5: preSection ID (int)
- 6: preSegment ID (int)
- 7: The pre distance (in microns) of the synapse from the beginning of the pre segment 3D point (float)
- 8: g_{synX} is the conductance of the synapse (nS) (float)
- 9: u_{syn} is the u parameter in the TM model (0-1) (float)
- 10: d_{syn} is the time constant of depression (ms) (float)
- 11: f_{syn} is the time constant of facilitation (ms) (float)
- 12: DTC - Decay Time Constant (milliseconds) (float)
- 13: synapseType, the synapse type Inhibitory < 100 or Excitatory \geq 100 (specific value corresponds to generating recipe)
- 14: The morphology type of the pre neuron. Index corresponds with circuit.mvd2 (int)
- 15-16: BranchOrder of the dendrite, BranchOrder of the axon (int,int)
- 17: ASE Absolute Synaptic Efficacy (Millivolts) (int) (not used)
- 18: Branch Type from the post neuron(0 for soma, 1 for axon and 2 for basal and 3 for apical) (int)

Targets: start.target

ASCII file:

```
Target Cell L1_SLAC
{
a7 a12 a13 a16 a24 a33 a36 a38 a50 a55 a69 a78 a79
}
Target Cell mc1_L6_BPC
{
a51924 a51927 a51941
}
....
```

Simulation descriptors - BlueConfig

- Circuit URI
- Job params
- Define Reporting

```
RunMode LoadBalance
CircuitTarget Slice
Duration 12000
Dt 0.025
ForwardSkip 5000
```

```
Report soma
{
    Target Slice
    Type compartment
    ReportOn v
    Unit mV
    Format Bin
    Dt 0.1
    StartTime 0
    EndTime 20000
}
```

```
Report compartments
{
    Target Slice_5percent_AllComp
    Type compartment
    ReportOn v
    Unit mV
    Format Bin
    Dt 0.25
    StartTime 0
    EndTime 20000
}
```

```
Report I_NonSpecific
{
    Target AllCompartments_mc2
    Type Summation
    ReportOn i_pas ihcn_Ih ihcn_hcn3 icsa_csa
    Unit nA
    Format Bin
    Dt 0.1
    StartTime 0
    EndTime 2000
}
```

- Define stimuli & manipulations

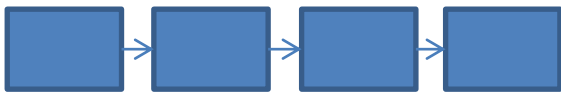
```
Stimulus ThresholdExc
{
    Mode Current
    Pattern Noise
    MeanPercent 88.7711221281
    Variance 0.001
    Delay 0.000000
    Duration 20000.000000
}
```

```
StimulusInject ThresholdIntoExc
{
    Stimulus ThresholdExc
    Target Excitatory
}
```

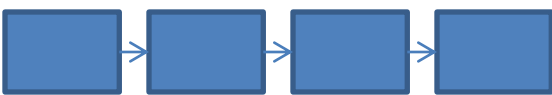
```
# Use adjustments due to Calcium 1.25 mM
Connection scheme_CaUse_ee
{
    Source Excitatory
    Destination Excitatory
    Weight 1.0
    SynapseConfigure %s.Use *= 0.1
}
```

HBP Building Workflows

Morphologies & Electrical models



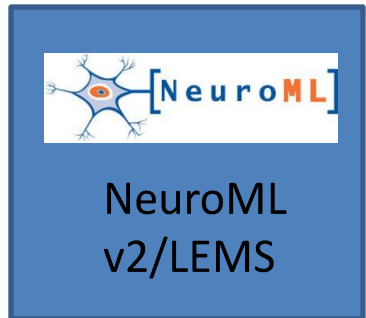
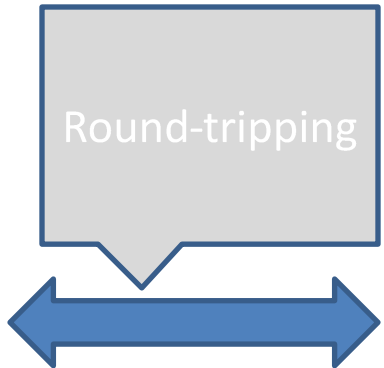
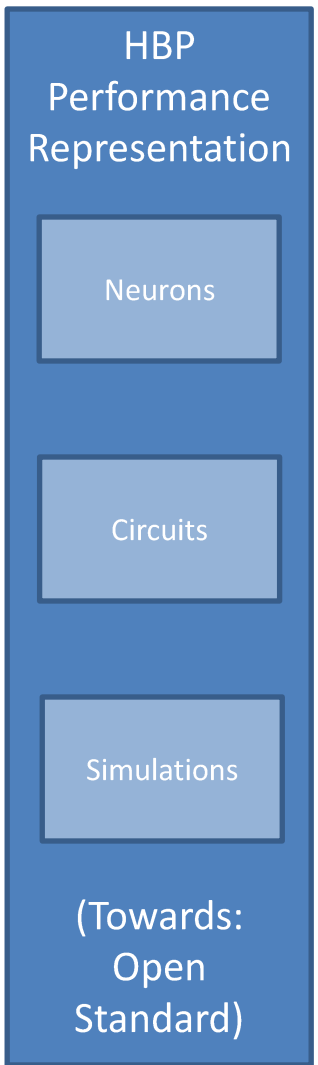
Circuits & Synapses



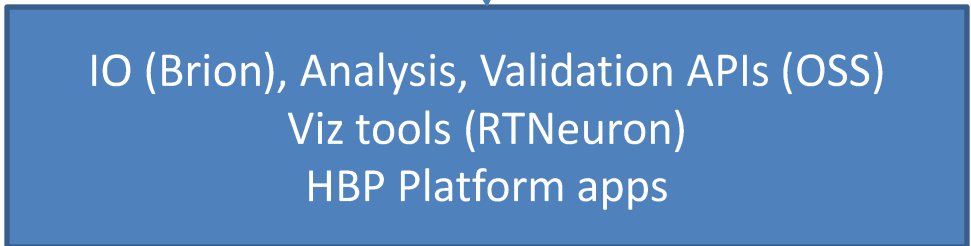
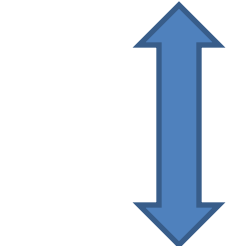
Simplifications

Simulations

STEPS, NEURON, NEST



Curation



Other HBP supported representation formats ... ?

- Relation to validation driven development
 - Validations rely on an analysis API
- Representation of simplified circuits
 - I&F
 - Population density
 - Mean-field

Generality of the BBP data model

- PAVIA example export example
- <https://bbpteam.epfl.ch/project/spaces/display/HWP64/Required+changes+to+BBP+tools>
- Ongoing work in HBP:
 - Cerebellum
 - Hippocampus
 - Basal ganglia

HBP: A first draft model of cerebellar granular layer

Team:

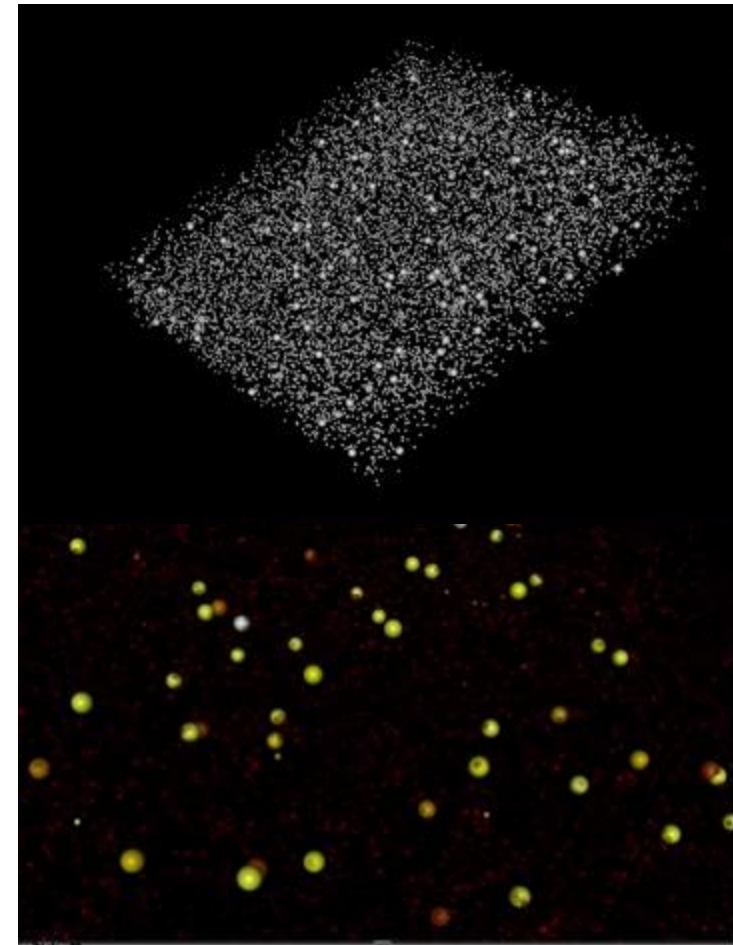
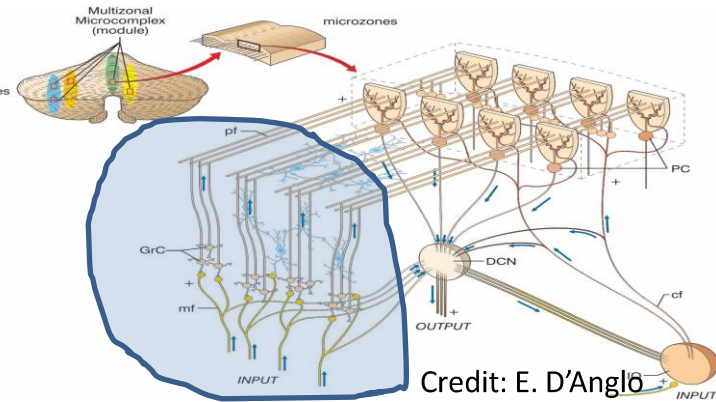
Stefano Masoli, Sergio Solinas, Stefano Casali, Martina Rizza, Werner van Geit, **Egidio D'Angelo**

Reconstruction

- Constructed Cerebellar granular layer model
- Connected **400,000 neurons** in a early draft cerebellar network (**Granule and Golgi Cells**)
- Neuron models optimized using BBP Optimizer framework
- Previous network connectivity (UPavia) ported to BBP circuit representation
- Simulated using BBP framework: **Neurodamus**

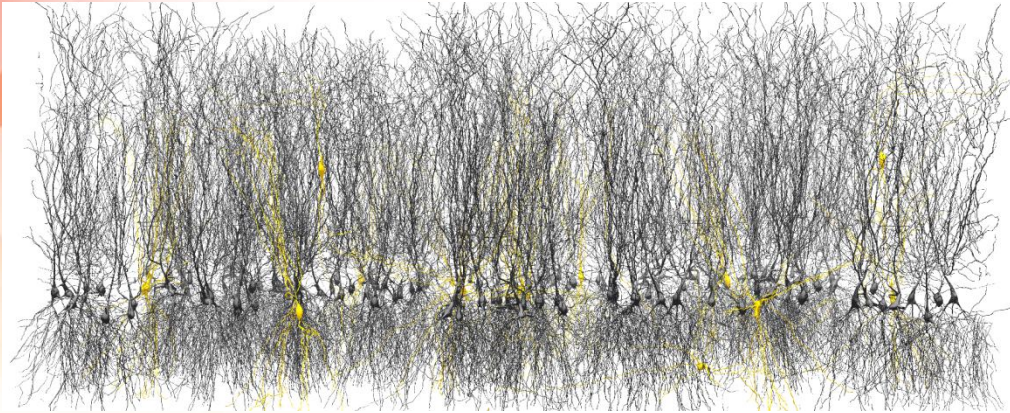
Analysis

- Results analyzed and visualized using **bluepy**, **RTNeuron**.

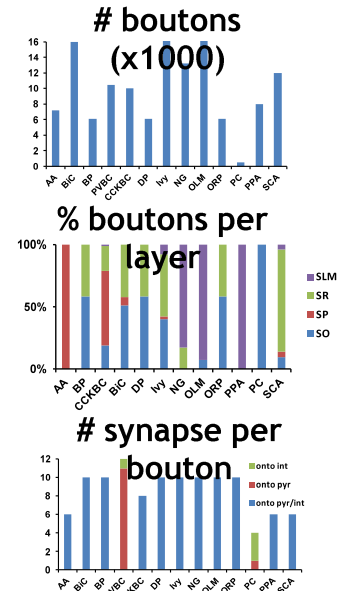
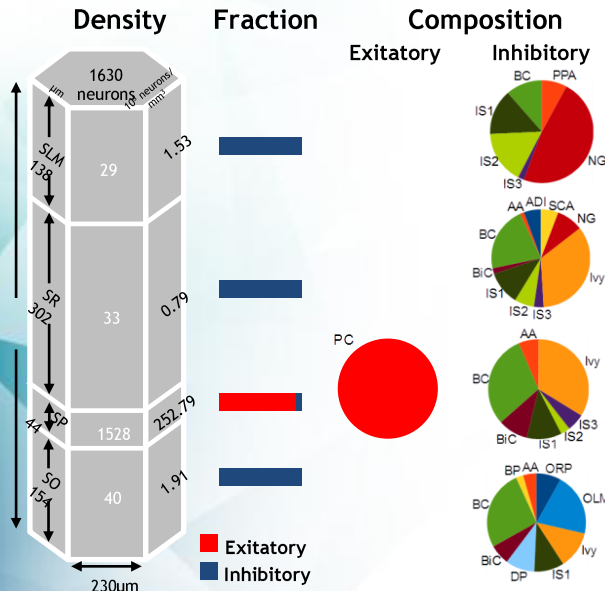
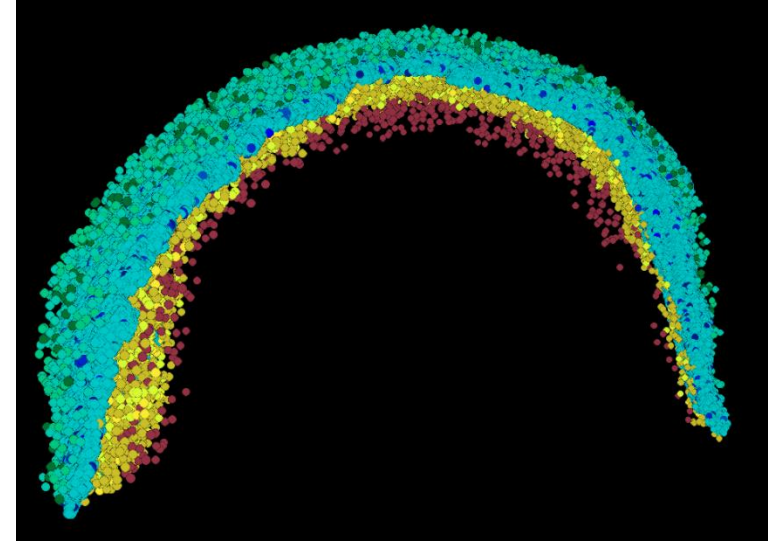


Rendering with RTNeuron

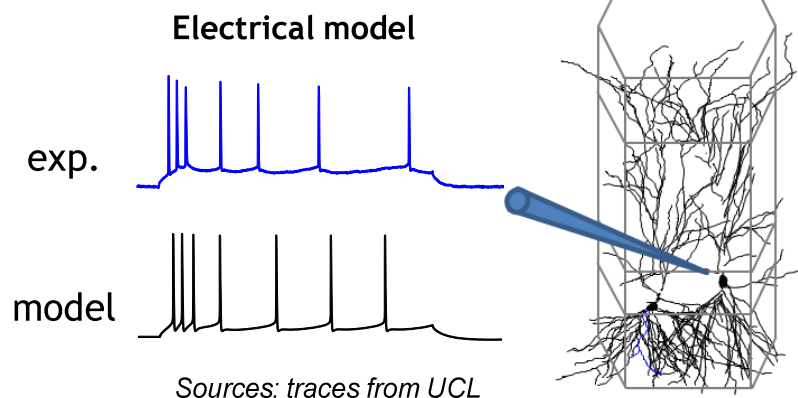
HBP: First draft hippocampal CA1



Sources: morphologies from UCL, IEM



Sources: UCL, Ropireddy et al 2012, Bezaire and Soltesz 2013



Notable future plans: BluePy

- API: make all functions accept interchangeably the ways to express groups of neurons:
 - SQL queries
 - Named “verbatim” targets (deprecate)
 - Gid lists (deprecate)
- Leverage more functionality from Brion (C++ IO lib)
- Converge data model with the community
- Open-source in 2016.
- Support for I&F models

Thoughts for convergence with Allen Brain Inst, and community standards

- NWB for simulation output
- LEMS for channel and synapses
- SWC for morphologies
- NeuroML for neuron biophysics
- Conceptual revision of CircuitConfig & BlueConfig
-> JSON?

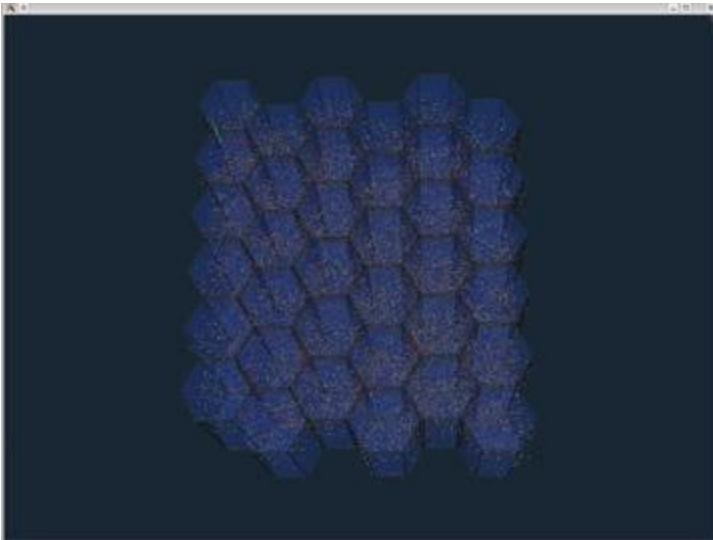
Simplified point-neuron case?

- LEMS for neuron models?
- NeuroML for neuron parameters?

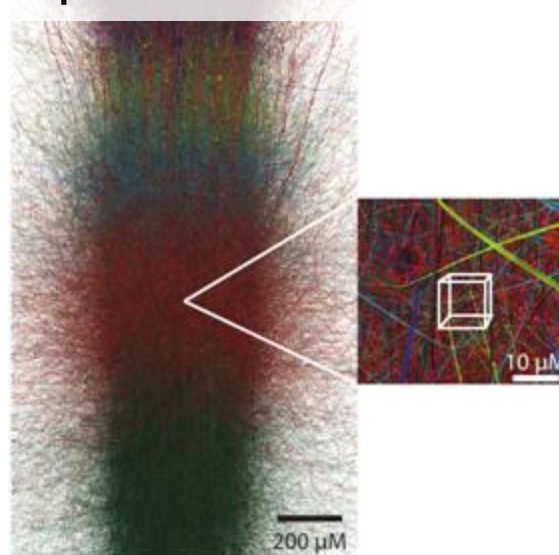
Towards a community ecosystem

- Validation
- Simplification
- Building tools
- Visualization
- Analysis
- Neuroinformatics bridges

RTNeuron



Spatial Indexer



BluePy & Data Model Links

Publically accessible documentation

- <https://developer.humanbrainproject.eu/docs/>
- <https://developer.humanbrainproject.eu/docs/projects/bluepy/0.5.11/index.html>

Accessibility for BBP-EXT members (can be case-by-case granted to HBP members)

Documentation & internal discussion on BBP file formats:

- <https://bbpteam.epfl.ch/project/spaces/display/HWP64/BBP+network+files+format>
- <https://bbpteam.epfl.ch/project/spaces/pages/viewpage.action?spaceKey=HWP64&title=BBP+network+files+format>

Issue tracker

- <https://bbpteam.epfl.ch/project/issues/browse/BLPY>

Data-model Improvement Proposals

- <https://bbpteam.epfl.ch/project/spaces/display/BBPWFA/MVD+version+3+-+Draft+0.0.1>
- <https://bbpteam.epfl.ch/project/spaces/display/BLBLD/New+h5+file+to+support+future+S2F>
- <https://bbpteam.epfl.ch/project/spaces/display/HWP64/Required+changes+to+BBP+tools>

pyNapli

such python
neural analysis
productivity layer.
much **wow**.



Acknowledgements





The BBP team



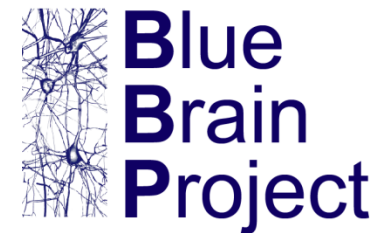
Human Brain Project



Hippocamp Participants



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BBP Platform Team



SP6

Members (WP and Task Leaders)

Data-driven reconstruction of brain models

Henry Markram

Idan Segev
Marc-Oliver Gewaltig
Felix Schürmann

Brain Simulation Platform: integration and operations

Henry Markram

Jeffrey Muller

Brain Simulation Platform: user support and community building

Felix Schürmann

Molecular dynamics simulation

Paolo Carloni

Richard Lavery
Rebecca Wade



Brain simulation engines

Felix Schürmann

Erik De Schutter
Julian Shillcock
Michael Hines
Markus Diesmann
Fabien Delalondre

Brain Simulation Platform: scientific coordination

Felix Schürmann

Initial brain models

Jeanette Hellgren Kotaleski

Antoine Triller
Pierre Magistretti
Alex Thomson
Eilif Muller
Egidio D'Angelo
Sten Grillner



HBP Platform Teams

- SP5 – Neuroinformatics
- SP6 – Brain Simulation
- SP7 – HPC
- SP8 - Medical Informatics
- SP9 – Neuromorphic
- SP10 - Neurorobotics