

# Neuroscience Information Framework

<http://neuinfo.org>

The Neuroscience Information Framework (NIF), an initiative of the NIH Blueprint for Neuroscience Research, is a semantically-enhanced portal to web-based neuroscience resources: data, materials, and tools. NIF has developed search tools, which expose the contents of federated databases and deep or “hidden” web resources hidden from traditional search engines. NIF is designed to serve the neuroscience research community and is actively looking for resource providers to make their resources accessible through NIF.

# NIF allows you to find information and data from hundreds of neuroscience sources...

The screenshot shows the NIF search interface. At the top, there's a navigation bar with 'ABOUT', 'RESOURCES', and 'DATA' tabs, and a search bar containing the query 'Purkinje Cell'. Below the search bar, it says 'SHOWING 45,792 RESULTS ACROSS 72 DATA SOURCE(S) WITH THE' and a 'Query Expansion' dropdown. A large button labeled 'Show me everything (45,792)' is highlighted with a pink border. To the left, there are category filters: 'Physical Resource or Software Tool (0)', 'Data or Model (229)' (which is selected and highlighted in blue), 'Funding (0)', 'Information (0)', and 'Other (0)'. Below these are 'Categories' and a grid of links like 'Antibody (0)', 'Cell (47)', 'Cell Part (159)', etc. At the bottom, there's a table of search results with columns for 'Model Name', 'Model Concept', 'Software Type', 'Type', 'Neurons', 'Neurotransmitters', and 'Receptors'. One result is expanded to show its details.

Model Name	Model Concept	Software Type	Type	Neurons	Neurotransmitters	Receptors
Controlling KCa channels with different Ca <sup>2+</sup> -buffering models in Purkinje cell (Anwar et al. 2012)	Calcium dynamics	NEURON	Dendrite	Cerebellum purkinje cell		
Parallel STEPS: Large scale stochastic spatial reaction-diffusion simulation. (Chen & De Schutter 2017)	Bursting, Reaction-diffusion, Calcium dynamics, Methods	STEPS		Cerebellum purkinje cell		
Vestibulo-Ocular Reflex model in Matlab (Clopath et al. 2014)	Synaptic Plasticity	MATLAB	Realistic Network	Cerebellum purkinje cell		
Effect of voltage sensitive fluorescent proteins on neuronal excitability (Akeemann et al. 2009)		NEURON	Neuron or other electrically excitable cell	Cerebellum purkinje cell		
Stochastic calcium mechanisms cause dendritic calcium spike variability (Anwar et al. 2013)	Dendritic Action Potentials, Active Dendrites, Calcium dynamics	STEPS (web link to model)	Neuron or other electrically excitable cell, Dendrite	Cerebellum purkinje cell	AMPA	

The screenshot shows the SciCrunch API Docs interface. It has a green header with the title 'SciCrunch API Docs' and a 'Explore' button. Below the header, it says '[ Base url: /api/v1 ] /swagger-docs/swagger.json'. It states 'API endpoints for [scicrunch.org](#), [dknet.org](#) and [neuinfo.org](#). All API calls require the 'key' field to be set with an API key'. Under 'Data services', there are several API endpoints listed with their descriptions:

- GET /dataservices/federation/data/{viewid} search a single data view
- GET /dataservices/federation/search search all data views
- GET /dataservices/federation/facets/{viewid} get facets for a data view
- GET /dataservices/literature/search search the Pubmed literature
- GET /dataservices/literature/pmid retrieve by PMID

**Access information or integrate information into your application or scripts via NIF provided services after registering for an API Key**

Searching a diverse set of resources and making the search results intelligible are major challenges. NIF utilizes many advanced features for information retrieval and integration. Chief among these is the use of a shared vocabulary, InterLex (formerly NeuroLex) and the NIF Standard Ontology, for describing and querying resources. InterLex currently consists of thousands of concepts derived from community-built ontologies and vocabularies and enhanced through the input of neuroscience experts. Through intuitive query interfaces, users can make use of the InterLex vocabularies to expand or refine their search and to perform so-called “concept-based queries.” Through a single interface, users can search across multiple information sources.

# NIF is releasing new terminology tools and services

Term View

Home / Term Dashboard / ILX:0101974

Cerebellum Purkinje cell   
[http://uri.interlex.org/base/ilx\\_0101974](http://uri.interlex.org/base/ilx_0101974)



Log in to suggest term to community

 Back to search results  
 Add new term

Export:   

PreferredId: ILX:0101974 Type: term OWL Equivalent: owl:Class

Principal neuron (projection neuron) of the cerebellar cortex; cell bodies arranged in a single layer; characterized by a pear-shaped cell body, 1 (rarely 2) primary dendrites and an elaborate dendritic tree heavily invested with dendritic spines.

Version: 1

General

Children

Relationships

Annotations

Referenced By

Superclasses:

 Expand list

Cerebellum Purkinje cell

↓

Neuron

↓

Nervous system cell

↓

Cell

↓

Anatomical entity

Synonyms:

Synonym

Type

Purkinje neuron

Purkinje's corpuscles

Cerebellar Purkinje neuron

Purkinje Cell

Purkyne cell

Corpuscles of Purkinje

Existing IDs:

Preferred CURIE

IRI

 NLXWIKI:sao471801888 <http://neurolex.org/wiki/sao471801888>

 ILX:0101974

[http://uri.interlex.org/base/ilx\\_0101974](http://uri.interlex.org/base/ilx_0101974)

InterLex was built on the foundation of NeuroLex (see Larson and Martone 2013). The initial entries in NeuroLex were built from the NIF Standard ontologies which currently has about 60,000 concepts (includes both classes and synonyms) that span gross anatomy, cells, subcellular structures, diseases, functions and techniques. InterLex models terms using primitives of the Web Ontology Language (OWL) and can export directly to a variety of standard ontology formats.

**Access the NIF ontology or integrate the NIF ontology into your application or scripts via NIF provided services after registering for an API Key**

InterLex is a dynamic lexicon of biomedical terms that is being constructed to help improve the way that biomedical scientists communicate about their data, so that information systems can find data more easily and provide more powerful means of integrating data across distributed resources. One of the big roadblocks to data integration is the inconsistent use of terminology in databases and other resources such as the literature. InterLex allows for the association of data values (i.e. the value of a field or text within a field) to terminologies enabling the crowdsourcing of data-terminology mappings within and across communities.

## SciGraph - REST Services

graph : Graph services

Show/Hide | List Operations | Expand Operations | Raw

refine : OpenRefine Reconciliation Services

Show/Hide | List Operations | Expand Operations | Raw

analyzer : Analysis services

Show/Hide | List Operations | Expand Operations | Raw

cypher : Cypher utility services

Show/Hide | List Operations | Expand Operations | Raw

annotations : Annotation services

Show/Hide | List Operations | Expand Operations | Raw

lexical : Lexical services

Show/Hide | List Operations | Expand Operations | Raw

vocabulary : Vocabulary services

Show/Hide | List Operations | Expand Operations | Raw

 /vocabulary/categories

Get all categories

 /vocabulary/search/{term}

Find a concept from a term fragment

 /vocabulary/prefixes

Get all CURIE prefixes

 /vocabulary/suggestions/{term}

Suggest terms

 /vocabulary/id/{id}

Find a concept by its ID

 /vocabulary/autocomplete/{term}

Find a concept by its prefix

 /vocabulary/term/{term}

Find a concept from a term

# NIF assists users in finding scientific resources

The screenshot shows the NIF website interface. At the top, there's a navigation bar with links for ABOUT, RESOURCES (which is currently selected), DATA, LITERATURE, and MY ACCOUNT. Below the navigation is a search bar with the query 'Simulation'. A blue arrow points from the 'Category Graph' sidebar on the left towards the main content area. Another blue arrow points from the 'Resource Details' section at the bottom left towards the 'Related publications' section on the right.

**Resources** [Query options]

Simulation Save this search

ON PAGE 1 SHOWING 20 OUT OF 354 RESULTS FROM 1 SOURCES

Multiscale Object Orientation Simulation Environment

<http://moose.sourceforge.net/>

MOOSE is the Multiscale Object-Oriented Simulation Environment. It is the base and numerical core for large, detailed simulations including Computational Neuroscience and Systems Biology. MOOSE spans the range from single molecules to subcellular networks, from single cells to neuronal networks, and to still larger systems. It is backwards-compatible with GENESIS, and forward compatible with Python and XML-based model definition standards like SBML and MorphML. MOOSE is coordinating with ...[more]

From Current Category

SciCrunch: Registry (354) | Cite This | Edit Source Snippet | View Source Information

MULTI Simulation Coordinator

<http://www.incf.org/programs/modeling/music>

Software that allows large scale neuron simulators to communicate during runtime. It allows exchange of data between different simulators and provides a common interface for them to interact.

**Resource Details** [Q Make another search]

Multiscale Object Orientation Simulation Environment (RRID:SCR\_008031)

<http://moose.sourceforge.net/>

MOOSE is the Multiscale Object-Oriented Simulation Environment. It is the base and numerical core for large, detailed simulations including Computational Neuroscience and Systems Biology. MOOSE spans the range from single molecules to subcellular networks, from single cells to neuronal networks, and to still larger systems. It is backwards-compatible with GENESIS, and forward compatible with Python and XML-based model definition standards like SBML and MorphML. MOOSE is coordinating with ...[more]

INFORMATION RELATIONSHIPS REFERENCED BY ANALYTICS SOURCE

Keywords: cell, computational, molecule, network, neuronal, neuroscience, simulation, subcellular, systems biology

Resource ID: SCR\_008031

Alternate IDs: nif-0000-10307

Website Status: Last checked up

The resource registry within NIF holds the largest collection of scientific resources, such as simulation environments. Resources are manually curated to make sure the information is accurate. Using NLP techniques we also look for literature mentions of resources in full text articles we have access to. This allows the registry to provide information on related resources and suggest other interesting resources.

The screenshot shows the NIF Literature page for the article 'STEPS: Modeling and Simulating Complex Reaction-Diffusion Systems with Python'. The page includes social sharing icons (Facebook, Twitter, LinkedIn), a summary of the article, and sections for INFORMATION, TERMS OF USE, and TOOLS AND RESOURCES. A blue arrow points from the 'Resource Details' section on the left towards the 'Related publications' section on the right.

Home / Literature

STEPS: Modeling and Simulating Complex Reaction-Diffusion Systems with Python.

Wil S J De Schutter E  
Frontiers in neuroinformatics | Jul 22, 2009  
PubMed UC-eLinks

We describe how the use of the Python language improved the user interface of the program STEPS. STEPS is a simulation platform for modeling and stochastic simulation of coupled reaction-diffusion systems with complex 3-dimensional boundary conditions. Setting up such models is a complicated process that consists of many phases. Initial versions of STEPS relied on a static input format that did not cleanly separate these phases, limiting modelers in how they could control the simulation ...[more]

PubMed ID: 19623245

INFORMATION TERMS OF USE TOOLS AND RESOURCES

Research resources used in this publication: None found

Research tools detected in this publication:

- SourceForge
- SBML
- Multiscale Object Orientation Simulation Environment
- CellML

Data used in this publication: None found

Associated grants: None

Related publications:

- STEPS: efficient simulation of stochastic reaction-diffusion models in realistic morphologies. (Hepburn I 2012)
- CHARMM-GUI 10 years for biomolecular modeling and simulation. (Jo S 2017)
- A simple polarizable continuum solvation model for electrolyte solutions. (Lange AW 2011)
- Integrated workflows for spiking neuronal network simulations. (Antolik J 2013)
- JigCell Run Manager (JCR-M): a tool for managing large sets of biochemical model parametrizations. (Palmisano A 2015)

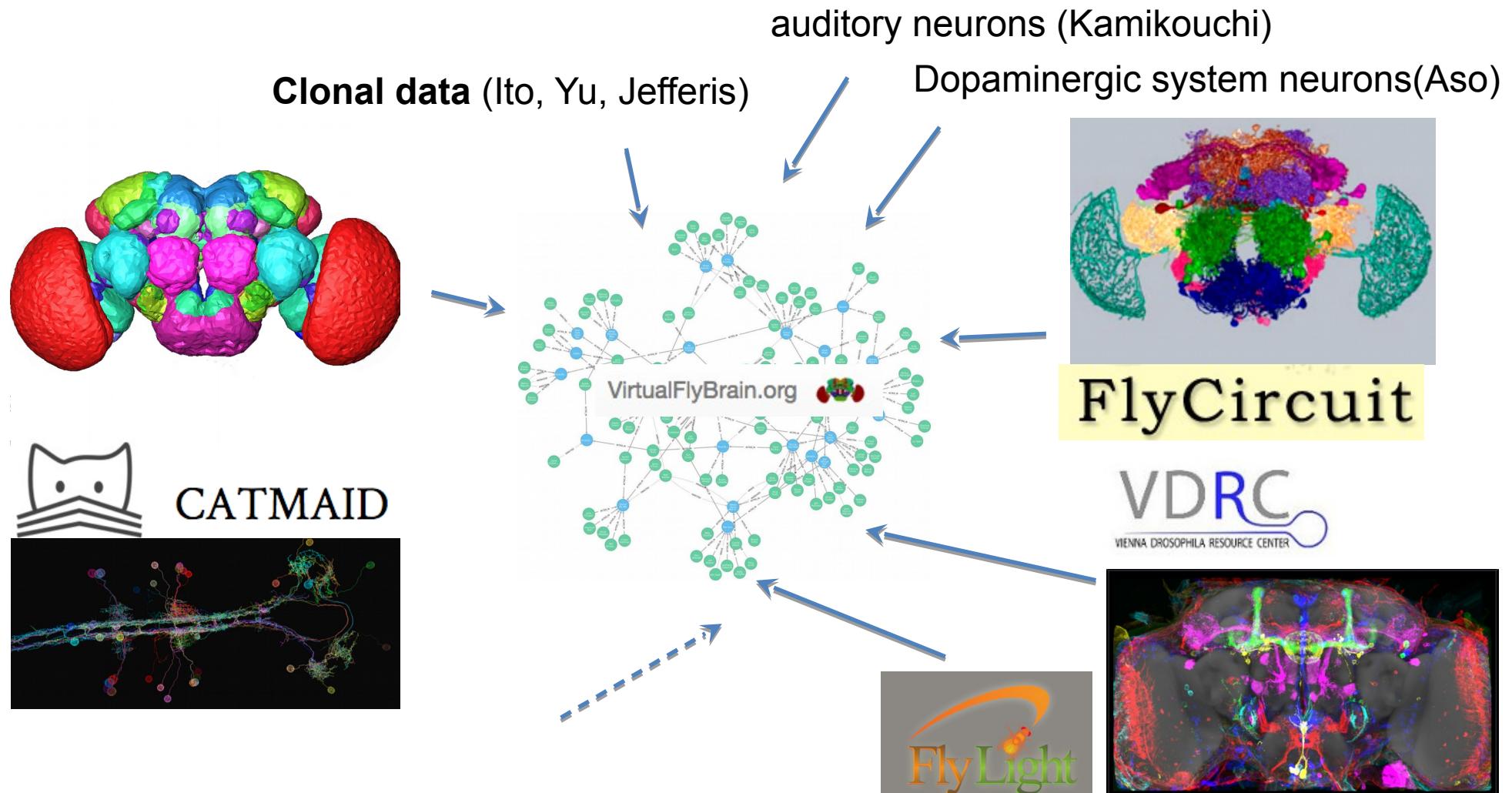
Access resource information or integrate resource information into your application or scripts via NIF provided services after registering for an API Key

# Virtual Fly Brain

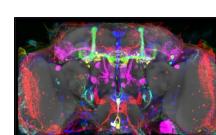
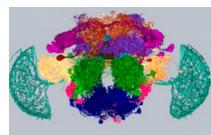
<https://www.virtualflybrain.org>

A data integration hub for *Drosophila* neurobiology, integrating disparate, large-scale datasets and linking them to curated literature and other resources. VFB provides the data to generate circuit hypotheses and identify research tools to test them.

# Combining 3D Anatomy, Light & EM Image Data



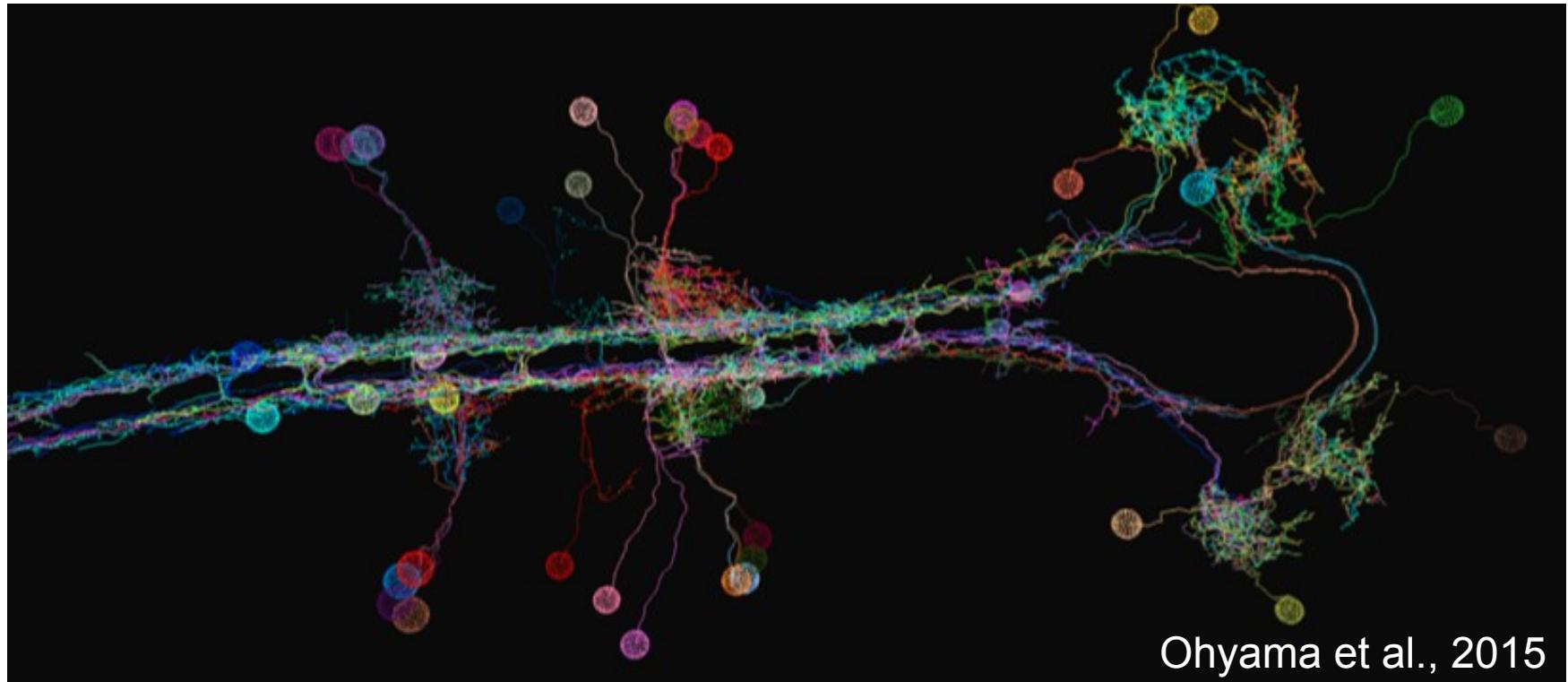
with semantic integration: image annotation



OWL individual  
annotation

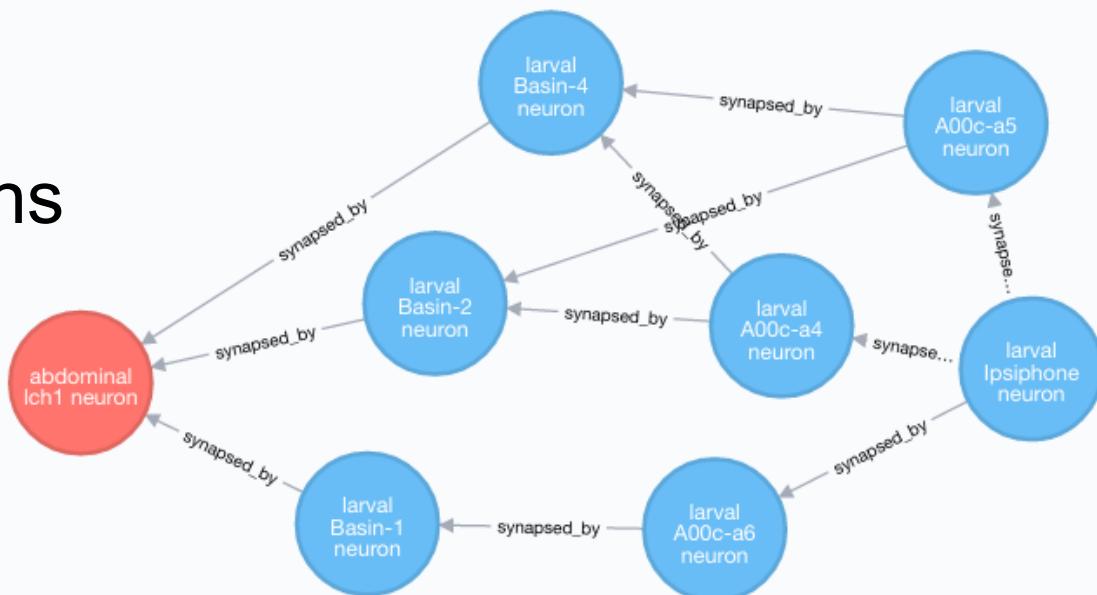
OWL2  
W3C®  
neo4j

# VFB 2 – interactive 3D circuit reconstructions



## Context graphs: Exploring circuit paths

Query: circuit paths from  
**'abdominal vch1 neuron'** to  
**'larval Ipsiphone neuron'**



# Value added by VFB

## OWL-based approach

- › scalable, queryable integration of knowledge and data about *Drosophila* neuroanatomy

## Knowledge curated from the literature

- › context and queryability to bulk data

## Tight integration with FlyBase

- › Expression
- › Phenotypes

## Planned collaboration with EBI

- › integration transcriptomic data

## Nblast

- › find morphologically similar neurons
- › find potential driver lines for a specific neuron

Direct API's to query data.

# HBP Collaboratory

<http://collab.humanbrainproject.eu>

The HBP Collaboratory collects tools from the HBP Platforms in one place and allows you to organize them into your own collaborative workspace or *collab*.

# The HBP Collaboratory is your virtual lab bench

Explore, Work, Collaborate, Organize

- **Explore** the HBP Platform ecosystem
- **Work** with integrated web accessible scientific tools to analyze, visualize and share data.

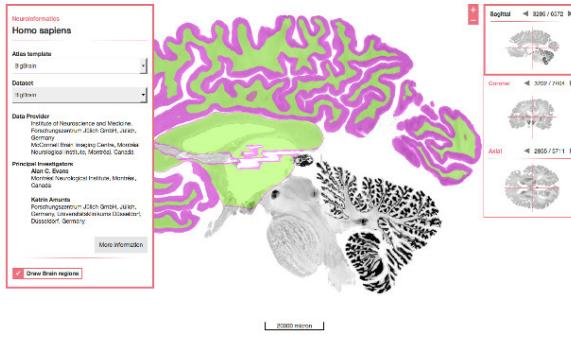
- **Collaborate** by adding team members to your collab to gain insights outside your areas of expertise
- **Organize** your work with tools from the HBP Platforms integrated in the Collaboratory

The screenshot displays the HBP Collaboratory interface, which integrates various scientific tools and platforms. On the left, a navigation sidebar includes links for Getting Started, Software Catalog (which is highlighted), Create a Collab, Platform Collaboratories, HBP Websites, App Development, Roadmap, Co-design Projects, Storage, Team, and Platform Summary. The main workspace shows a list of software libraries, such as Deflect Client Library, AnaRM (Analog Readout Module), Basic software libraries for the I, Logging Framework for UHEI Sc, Low-level Interface for (USB-based), 3DSynapsesSA, SynapseGenerator, and PyNN. A search bar at the top right allows filtering by category (library). Below the workspace, there's a "Circuit Building Pipeline" section with a "requirements installation" sub-section containing a terminal-like interface for running pip commands to install requirements. The bottom right corner shows a user profile and navigation links for Product, Team, Archives, New UI Proposal, HBP Roles, Software Catalog Admin, Meetings, Events, Settings, and Stats.

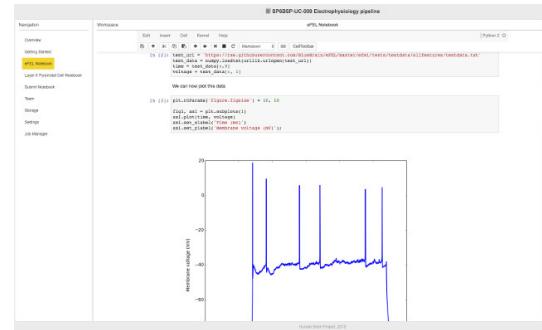
# *Explore* and *Use* the HBP Platform Ecosystem

Federated across Europe, the HBP Platforms provide strategic tools in:

## *Neuroinformatics*



## *Brain Simulation*



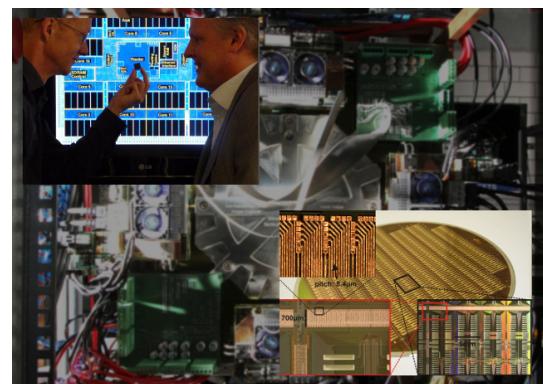
## *Medical Informatics*



## *High Performance Analytics and Computing (HPAC)*



## *Neuromorphic Computing*



## *Neurorobotics*



# Getting Access

To access the HBP Collaboratory you need an **HBP Identity account**.

Information on how to request an account can be found here:

<https://www.humanbrainproject.eu/en/hbp-platforms/getting-access/>

With a basic HBP Identity Account you can access:

- HBP Collaboratory:
- Browse Platform collabs
- Browse HBP Collaboratory public collabs
- Add files to public collabs where the user is a member
- **Create public collabs** and populate them with content
- Create public **Jupyter notebooks** and edit them
- Can be added to private collabs by collab owners

[platform@humanbrainproject.eu](mailto:platform@humanbrainproject.eu)

# NITRC

<https://www.nitrc.org>

Neuroimaging Informatics Tools and Resources Clearinghouse (NITRC) is a free one-stop-shop collaboratory for science researchers that need resources such as neuroimaging analysis software, publicly available data sets, or computing power.

**Browse** by domain **Browse** by software **Browse** by data resources **Browse** by diagnosis **Find neuroimaging tools here:**

Examples: • modeling OR simulation  
• morphology AND animation  
• segmentation NOT Linux  
• "region of interest"

SEARCH Search Builder

**Featured tool/resource:**  
Ultra-high field atlas for DBS planning  
7T T1-w and T2-w average atlas (ANTS) from 12 healthy controls, with manual labelling of deep and mid brain structures.

← 3 of 3 →

**Latest News**

[SPHARM-PDM Toolbox • Jul 3 • no comments]

**SPHARM-PDM Update**

Dear SPHARM-PDM users: I am very glad to announce we have updated the SPHARM-PDM Slicer extension. The new tutorial for this new and improved version can be found here: <https://github.com/bpaniagua/SPHARM-PDM...> SPHARM-PDM...

[CONN : functional connectivity toolbox • Jun 27 • no comments]

**New CONN release and tutorials**

We are happy to announce the latest release of CONN (17f). If you have not had the chance to update CONN recently this is a great time to do so and see what is all the fuzz about the new Quality Assurance plots and measures, increasing BIDS-compatibility...

[NITRC Community • Jun 25 • no comments]

**Join NITRC in Booth 18 at OHBM and for poster 1665**

Please swing by the NITRC Booth #18 at OHBM from June 25-29, 2017 and let us know how things are going! We will also be presenting Poster #1665 Tuesday, June 27, 2017: 12:45 PM-2:45 PM <https://ww5.aievolution.com/hbm1701/inde...>

[NITRC Community • Jun 22 • no comments]

**Join NITRC at OHBM Hackathon June 22-24, 2017**

NITRC will have a project at the OHBM 2017 Hackathon in Vancouver, CANADA. Check out the OHBM Hackathon wiki list of projects here: <https://github.com/ohbm/hackathon2017/wiki>

**Community**

- + General community forum
  - + Funding opportunities
  - + Sustaining NITRC
  - + Submit community news
  - + Submit tool/resource
  - + Publications
  - + Conferences and workshops
  - + Career opportunities
- [20,620 registered users]

**Recently active forums****more forums****NITRC Community: open-discussion**

how to compare different sessions?

[2131 posts, last post 32 minutes ago]

**MRIcron: help**

Best workaround for MNI dimension mismatch?

[77 posts, last post 40 minutes ago]

**CONN : functional connectivity toolbox: help**

Confusing sample ROI-to-ROI results

[5938 posts, last post 3 hours ago]

**Recently updated files****more updates****MASIMatlab**

masimatiab: Abmusclefat\_release

Latest file: 9 hours ago

**MPI-Leipzig Mind-Brain-Body Dataset**

MPIIMBB MRI Data: MPIIMBB MRI Data 1.0

Latest file: 16 hours ago

**Longitudinal neuroimaging hippocampal markers for diagnosing Alzheimer's disease**

longhipsegm: Matlab (mex in win64)

Latest file: Jul 7

**Recently registered****more tools/resources**



## Tools/Resources

## Related Web Pages

[Search NIF](#)

### Narrow your results:

#### ▼ Domain

[Computational Neuroscience \(20\)](#)
[EEG/MEG/ECOG \(6\)](#)
[MR \(5\)](#)
[see all >>](#)

#### ▼ Functionality

[Modeling \(5\)](#)
[Visualization \(2\)](#)
[Quantification \(2\)](#)
[Time Domain Analysis \(1\)](#)
[Connectivity Analysis \(1\)](#)
[Statistical Operation \(1\)](#)
[Tractography \(1\)](#)
[Surface Analysis \(1\)](#)
[Segmentation \(1\)](#)
[Neuronal Characterization \(1\)](#)
[Spatial Transformation \(1\)](#)
[Information Theory \(1\)](#)
[Shape Analysis \(1\)](#)
[Experimental Control \(1\)](#)
[Atlas Application \(1\)](#)

#### ▼ Diagnosis

[Brain Injuries \(1\)](#)

#### ► License

#### ► Development Status

#### ► Programming Language

You searched for:  "neuron"

Search within results:

[Search Builder](#)

Select All /  Unselect All

Sort by:

Results per page:

1 | 2

Showing 1-20 of 31 results

### ▼ NEURON

NEURON is a simulation environment for modeling individual neurons and networks of neurons. It provides tools for conveniently building, managing, and using models in a way that is numerically sound and computationally efficient. It is particularly well-suited to problems that are closely linked to experimental data, especially those that involve cells with complex anatomical and biophysical properties. For a more detailed description see [http://www.neuron.yale.edu/neuron/what\\_i...](http://www.neuron.yale.edu/neuron/what_i...)

Avg. overall:  No Votes

(Show all specifications)

### ▼ Neuron-C

Neuron-C is a simulation language for modeling biophysically realistic neural circuits.

Avg. overall:  No Votes

(Show all specifications)

### ▼ L-Neuron

The L-Neuron program creates anatomically realistic virtual neurons using the formalism of the Lyndenmayer systems to implement sets of neuroanatomical rules discovered by several research groups (and in particular, Hillman's, Tamori's, and Burke's). These rules are local and recursive. The L-Neuron algorithms read in experimental data to generate virtual structures. The experimental data are in the form of statistical distributions (for example, bifurcation angles in Purkinje cells can be represented with a Gaussian distribution, with a certain average and standard deviation). L-Neuron samples the values of the parameters within these statistical distributions in a stochastic (random) fashion during dendritic growth. Therefore, with the same set of parameter distributions, the program can generate an unlimited number of virtual neurons.

Avg. overall:  No Votes

Funding: NIH R01 NS ...

Category: Neuronal Modeling, Simulation (Show all specifications)

### ▼ DONE: Detection of Outlier NEurons

This tool was used by Zawadzki et al. (2012), who reported on a morphology-based approach for the automatic identification of outlier neurons and its application to the NeuroMorpho database. For the analysis, each neuron is represented by a feature vector composed of 20 measurements, which are projected into lower dimensional space with PCA. Bivariate kernel density estimation is then used to obtain a probability distribution for cells. Cells with high probabilities are understood as archetypes, while those with the small probabilities are classified as outliers. Further details about the method and its application in other domains can be found in Costa et al. (2009) and Echtermeyer et al. (2011). References: \* Costa, Rodrigues, Hilgetag, and Kaiser. *Europhysics Letters*, 87, 1 (2009) \* Echtermeyer, Costa, Rodrigues, Kaiser. *PLoS*

Avg. overall:  No Votes



## NITRC Community

[Community Forums](#)

### Recently Active Forums

[Events](#)[News](#)[Funding](#)[Career Opportunities](#)[Documents](#)[Wiki](#)

### Recently Active Forums

Here is the most recent forum post for each tool/resource on NITRC.

Showing 1-15 of 211

Sort by: 1 | 2 | ... | 15 

Latest Post Date	Forum Name	Latest Post Title	Total Posts
Jul 14, 2017	<a href="#">NITRC Community: open-discussion</a>	how to compare different sessions?	2131 posts
Jul 14, 2017	<a href="#">MRIcron: help</a>	Best workaround for MNI dimension mismatch?	77 posts
Jul 14, 2017	<a href="#">CONN : functional connectivity toolbox: help</a>	Confusing sample ROI-to-ROI results	5938 posts
Jul 13, 2017	<a href="#">Signed Differential Mapping: sdm-help-list</a>	homogeneity test	382 posts
Jul 13, 2017	<a href="#">BrainNet Viewer: help</a>	RE: Get Connectivity maps above cortical surf	372 posts
Jul 13, 2017	<a href="#">1000 Functional Connectomes Project: open-discussion</a>	RE: Freesurfer segmentation of CoRR data	296 posts
Jul 13, 2017	<a href="#">MRICroGL: help</a>	RE: Flip L/R (left / right)	24 posts
Jul 13, 2017	<a href="#">dcm2nii: questions</a>	RE: error message upon opening dcm2nii	231 posts
Jul 13, 2017	<a href="#">PANDA: a pipeline tool for diffusion MRI: open-discussion</a>	Problem in installing centos fsl on Ubuntu	297 posts
Jul 11, 2017	<a href="#">CBS High-Res Brain Processing Tools: help</a>	RE: memory with run-cbstools-mac	3 posts
Jul 11, 2017	<a href="#">SPM for fNIRS toolbox: help</a>	how to merge 2 blocks in spm_fnirs	69 posts
Jul 10, 2017	<a href="#">Graph Theory GLM (GTG) MATLAB Toolbox: help</a>	Creating .mat files for input	93 posts
Jul 10, 2017	<a href="#">Surf Ice: help</a>	RE: access violation windows	18 posts
Jul 9, 2017	<a href="#">Vaa3D and Vaa3D-Neuron: help</a>	RE: matlab plugins	1903 posts
Jul 7, 2017	<a href="#">PESTICA &amp; SLOMOCO: physio and motion correction tools: open-discussion</a>	RE: trouble applying to3d after genSMStimeshi	146 posts

Sort by: 1 | 2 | ... | 15