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Geppetto is an open source modular platform
to **build neuroscience applications** to **explore**
and **simulate** models and data

What can Geppetto applications do?

- Visualize **neuroscience data** in the browser
 - Computational Neuroscience Models (NeuroML, NEURON, *)
 - Morphologies (SWC, OBJ, Collada, *)
 - Electrophysiology recordings (NWB, HDF5, *)
 - Medical data (MRI, Electromicroscopy via DICOM, NIFTI, DZI, *)
- Run **simulations** from the browser
 - Connect to an external simulator
 - Create your computational experiments, record model variables via the UI
 - Set model parameters
 - Simulate on remote clusters (e.g. San Diego Neuroscience Gateway)

What else can Geppetto applications do?

- Connect your application directly to a Python Kernel
 - Use the **Geppetto Jupyter Backend** to create an application that talks directly to the Python Kernel. Call Python methods and evaluate Python instructions from Javascript.
- Synchronize the user interface with your Python models
 - Edit your models from the user interface or programmatically via an embedded Jupyter Notebook
- Connect to external data sources to provide data and models (e.g. Neo4j, AberOWL, *)
- Simplify the **exploration** of data and models
 - Every model loaded in Geppetto is indexed and easily searchable.
- Facilitates **reproducibility** of workflows
 - The entire user interface works on top of an API layer. Every user action corresponds to an API command easy to inspect and reproduce.





Case Study 1

Open Source Brain

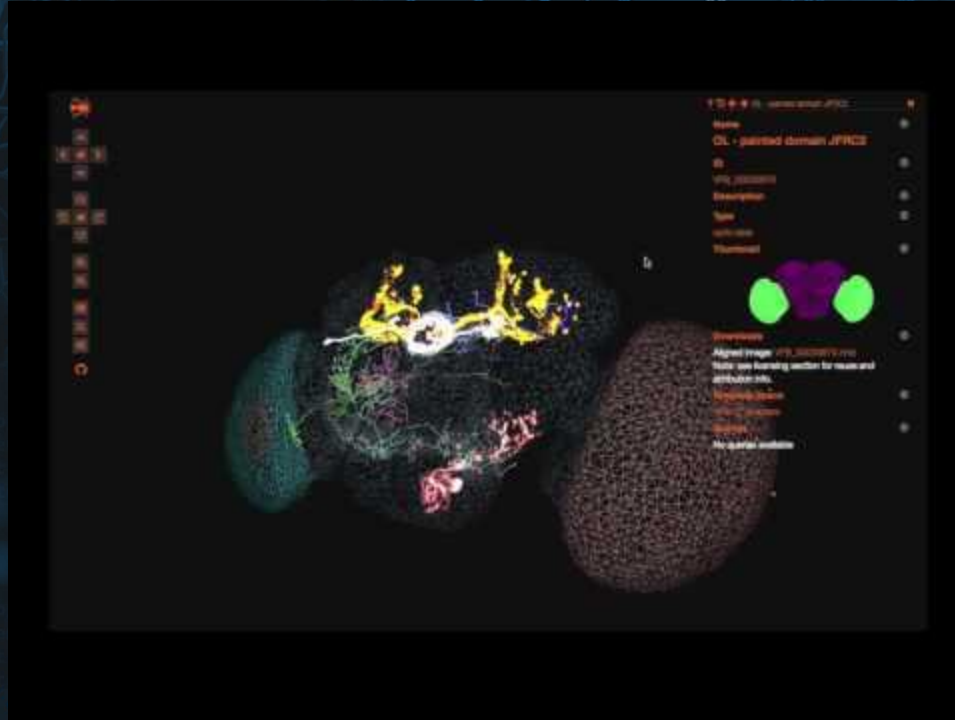
Web based simulation of computational neuroscience models in NeuroML





Case Study 2 Virtual Fly Brain

Exploring the brain of the *Drosophila
Melanogaster*





Case Study 3 NetPyNE UI

Build, simulate and analyse network models

NetPyNE

localhost:8888/geppetto

DEFINE YOUR NETWORKCREATE NETWORK

Populations

Define here the populations of your network

Home

+

Population

Population2

Population3

General

Spatial Distribution

Cell List

The name of your population

Population3

Cell type

?

Cell model

?

Number of cells

?

Cell rules

Define here the rules to set the biophysics and morphology of the cells in your network

Synaptic mechanisms

Define here the synaptic mechanisms available in your network

Connectivity rules

Define here the rules to generate the connections in your network

>_ Console

Python



Geppetto Architecture

- Data/Model agnostic web-based architecture to efficiently lazy load data and stream it in a compressed fashion
- Defines an internal **abstraction** to represent hierarchical models and data
- **Modular backend** to extend supported models, simulators and data source
- Generic and extensible **widgets** framework to expand frontend visualization capabilities
 - [3D CANVAS, PLOT, CONNECTIVITY, STACK VIEWER, MRI VIEWER, BIG IMAGE VIEWER, AUDIO/MOVIE PLAYER, ...]
- Generic and extensible **components** framework to augment user interface
 - [SEARCH, CONTROL PANEL, SIMULATION CONTROLS, EXPERIMENTS CONTROLS, DASHBOARD, BASIC UI CONTROLS, ...]



Is Geppetto a platform or an application?

- **Geppetto is an open-source platform to build neuroscience applications**
- Every Geppetto application can be hosted privately or publicly
- Every Geppetto application can be fully customised
 - **Decide what your interface will look like**
 - Decide what data, models and simulator you want to use
 - Choose only the components and widgets you need

Whether you only need to visualize some surface models or create a system that enables visualization and simulation of integrated data and models Geppetto will save you between two and five years of development.



How to get started?

- Read the paper! <http://paper.geppetto.org>
- **Pick your backend**
 - Java
 - Python Django
 - Jupyter Notebook
- **Build your frontend extension**
 - This is your blank canvas, here you define your **custom user interface and custom workflows**
- Reuse any of the pre-existing 20+ UI components
 - E.g. 3D Viewer, Connectivity Analysis, Plotting widget, MRI Viewer, etc.
- Reuse any of the pre-existing backend modules
 - E.g. NeuroML, NEURON, SWC support, etc.



Open Source, MIT Licensed

20+ Contributors

30 repositories

42 releases

6+ years of development

Automated Travis+Docker+Casper based testing

<http://www.geppetto.org> | paper.geppetto.org |
docs.geppetto.org | live.geppetto.org | git.geppetto.org |
board.geppetto.org | blog.geppetto.org



Applications built with Geppetto so far...

Open Source Brain (University College London)

Virtual Fly Brain (EBI/Uni Cambridge/Edinburgh/MRC)

NetPyNE UI (SUNY)

Patient H.M. (The Brain Observatory)

HNN UI (Brown University)

Scidash (Arizona State University)

NEURON UI (SUNY/Yale)

NWB Explorer

WormSim (OpenWorm)

Advantages

- **Unified platform for computational modeling, visualization and data exploration**
- Reused by multiple groups and projects
 - More users, more testing, more features, less bugs.
 - Open Source features developed for one Geppetto application are available to all Geppetto applications.
- Solutions to common problems are reused and optimised
 - Abstract meta-meta-model definition, streaming of data, scriptable UI, lazy loading, data visualization, data compression, automated unit and UI testing, etc.
- Enterprise architecture for better scalability and robustness
- Growing open source community



Acknowledgements

Core Contributors

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See full list of contributors:
contributors.geppetto.org

Supporting Groups

MetaCell

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NeuroSim Lab and SUNY

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OpenWorm Foundation

JOIN US!

Thanks for your time!

Questions? Get in touch!

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