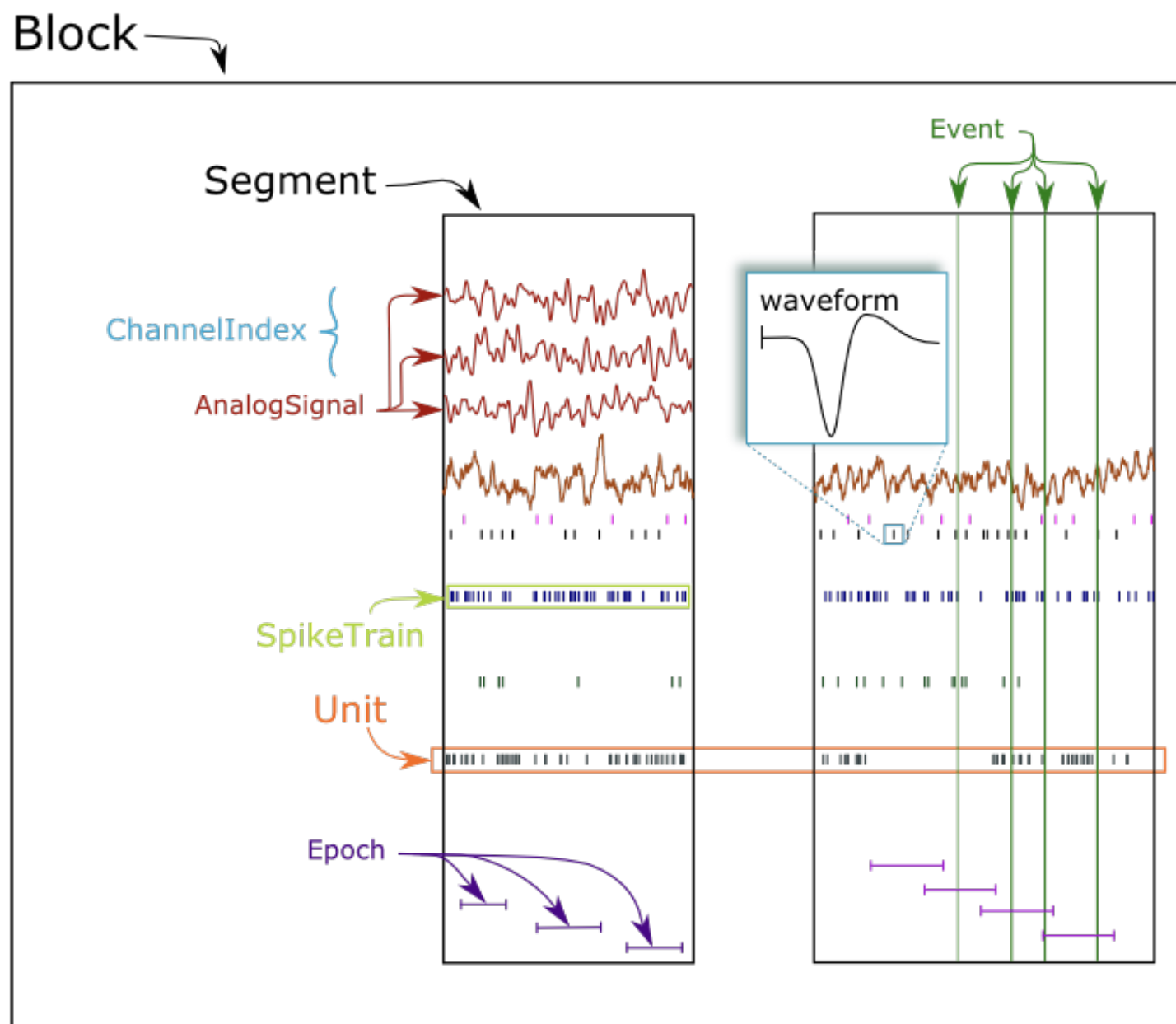
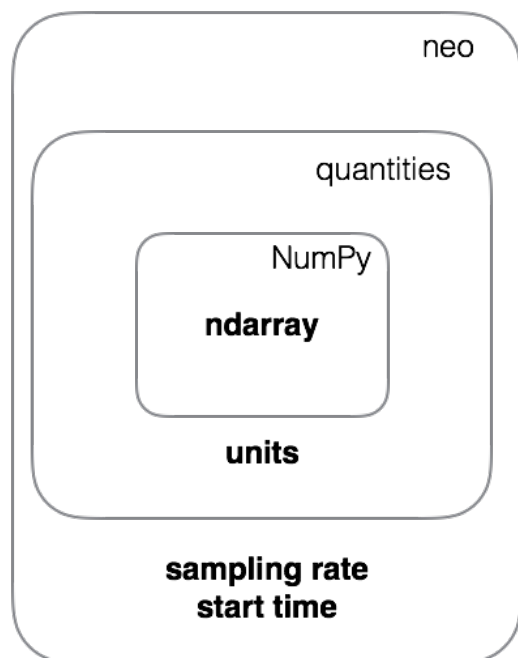
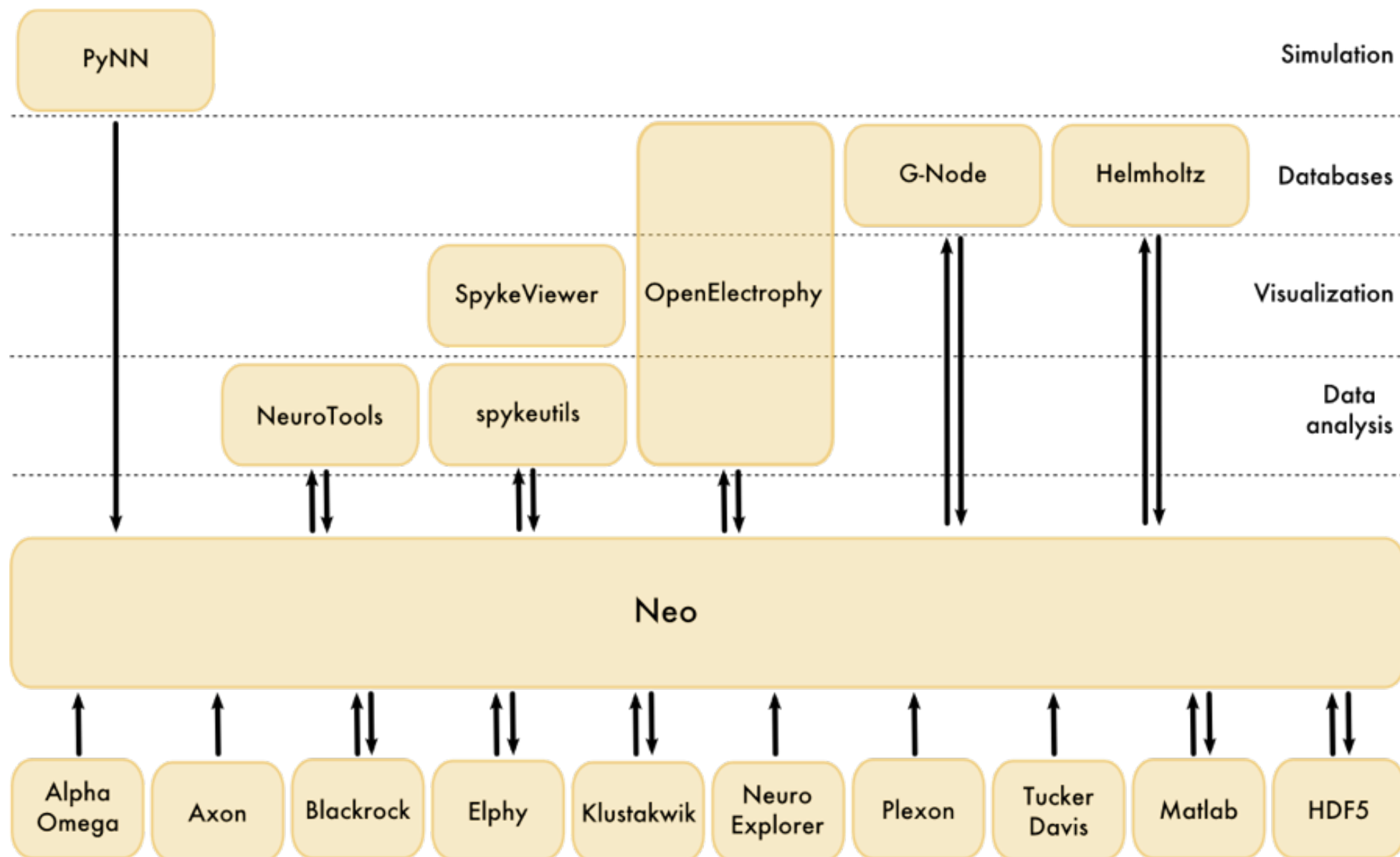




<http://neuralensemble.org/neo/>

Neo is a package for representing electrophysiology data in Python, together with support for reading a wide range of neurophysiology file formats, including Spike2, NeuroExplorer, AlphaOmega, Axon, Blackrock, Plexon, Tdt, and support for writing to a subset of these formats, plus non-proprietary formats including HDF5.





Plans

new, high-performance I/O API supporting fast lazy/partial loading, streaming

support for Neurodata Without Borders format

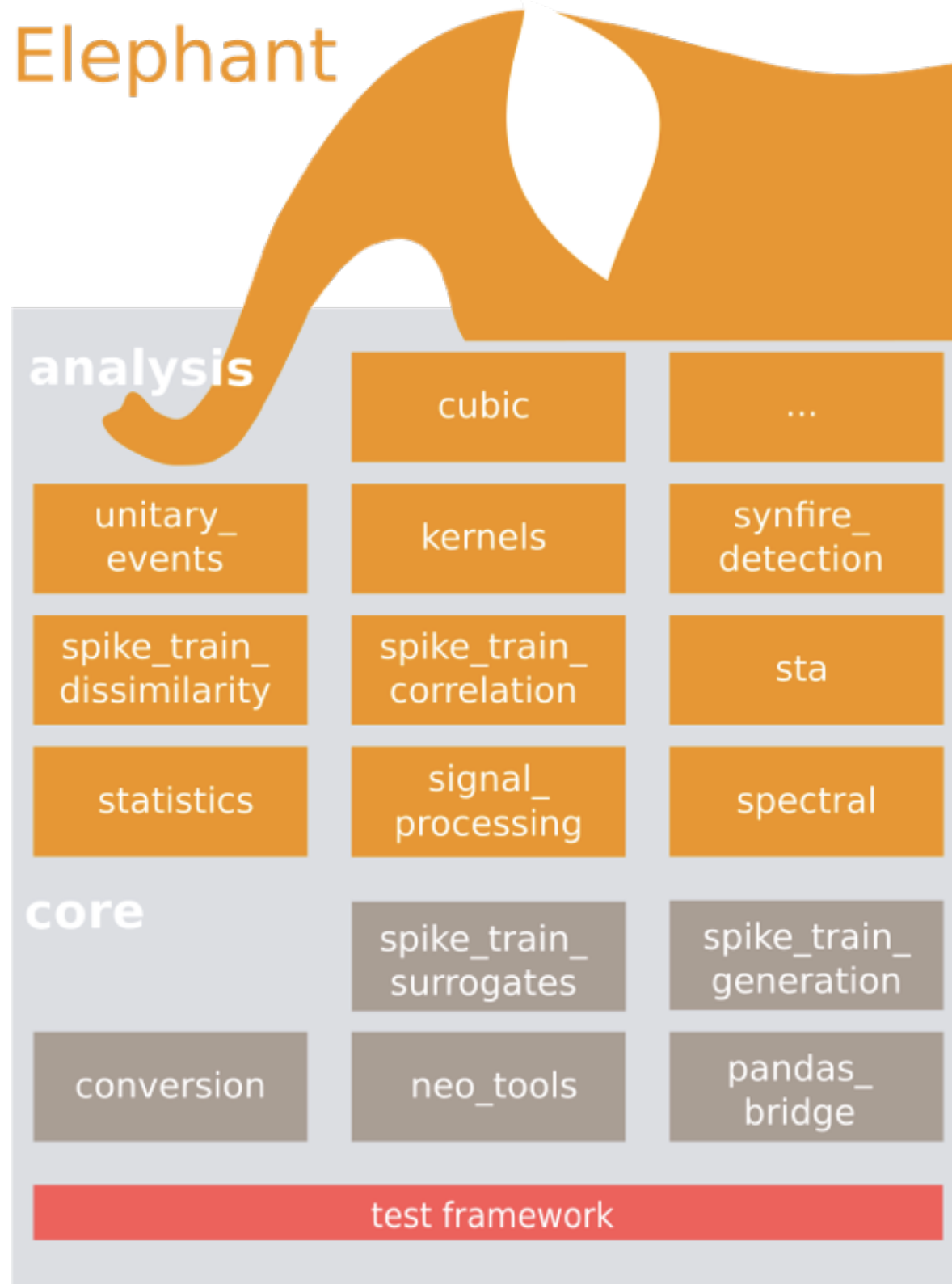
performance improvements



<http://neuralensemble.org/elephant/>

Elephant is an open-source, community centered library for the analysis of electrophysiology data in the Python programming language.

Elephant



Goals:

improve quality of data analysis code in neuroscience
and reduce duplication of effort by:

- developing community Python library of well-tested, well-documented data analysis functions
- encouraging contributions from users
- friendly peer-review of code

Plans:

continued efforts to grow community of contributors

parallelization on clusters, GPUs, supercomputers

NeuronUnit

<http://neuronunit.scidash.org>

NeuronUnit facilitates data-driven validation of neurophysiology models, testing these models for agreement with experimental data. Progress in model development or appropriateness of published models can be evaluated according to performance on these tests.



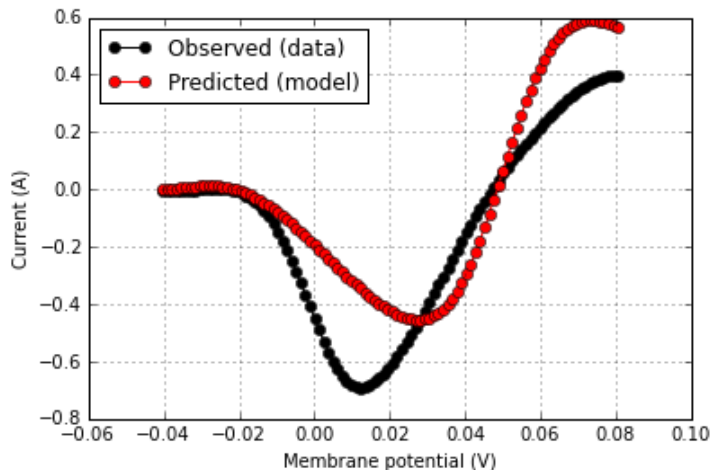
NeuronUnit

Data driven model validation for neuroscience

Write (or reuse) unit tests that each characterize one aspect of model behavior.

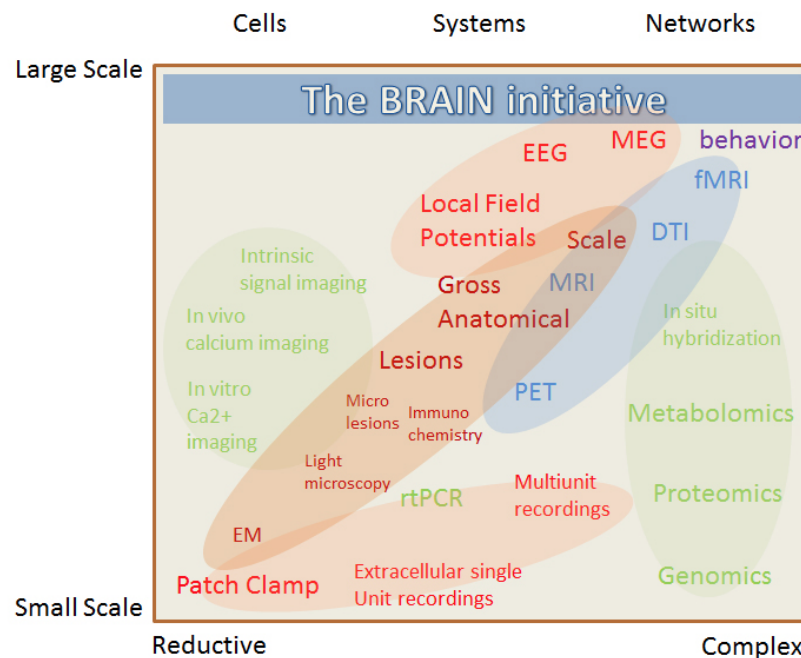
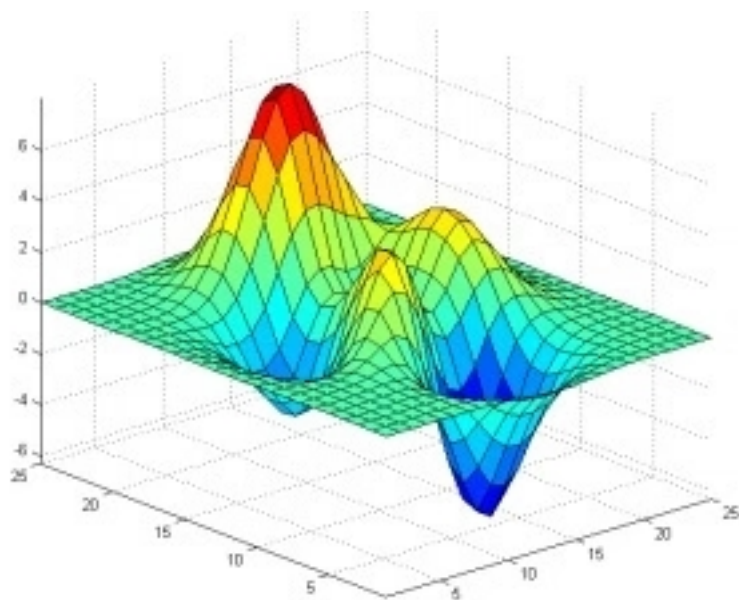
```
my_model = ReducedModel('/path/to/file', backend='NEURON') # Instantiate a reduced neuron model.
my_test = RheobaseTest(observation={'mean': 100*pA, 'std': 5*pA}) # Instantiate a test based on
                                                                # data from the literature or your Lab.
score = my_test.judge() # Runs the test and return a rich score containing test results and more.
```

Visualize model/data
agreement for each test



Examine test performance for different
parameterizations of a model, or different models

	Mean	RheobaseTest	InputResistanceTest	TimeConstantTest
V_rest=-80mV	0.342	Ratio = 1.86	Z = -1.04	Z = -1.49
V_rest=-70mV	0.384	Ratio = 1.00	Z = -0.87	Z = -1.46
V_rest=-60mV	0.356	Ratio = 0.40	Z = -0.53	Z = -1.42
V_rest=-50mV	0.296	Ratio = 0.07	Z = 0.29	Z = -1.29



Optimization of model parameters
using genetic algorithms

Support for models across multiple
scales of neuroscience



Human Brain Project



Model and data integration with
major simulator, data, and
standards providers



Neurodata Without Borders

Neurophysiology format

<http://nwb.org>

A data format designed for storing neurophysiology data and related metadata in a structured manner. It currently stores the data within HDF5 files. A write API is available in Python and Matlab.

NWB features

- Has standard layouts for storing common Neurophysiology data types and metadata
- Ability to link data between files
- Extensible, e.g. allows defining schema for storing new types of data in a standard manner
- Minimal library dependencies
- Human-readable and self-documenting

Overview of NWB format

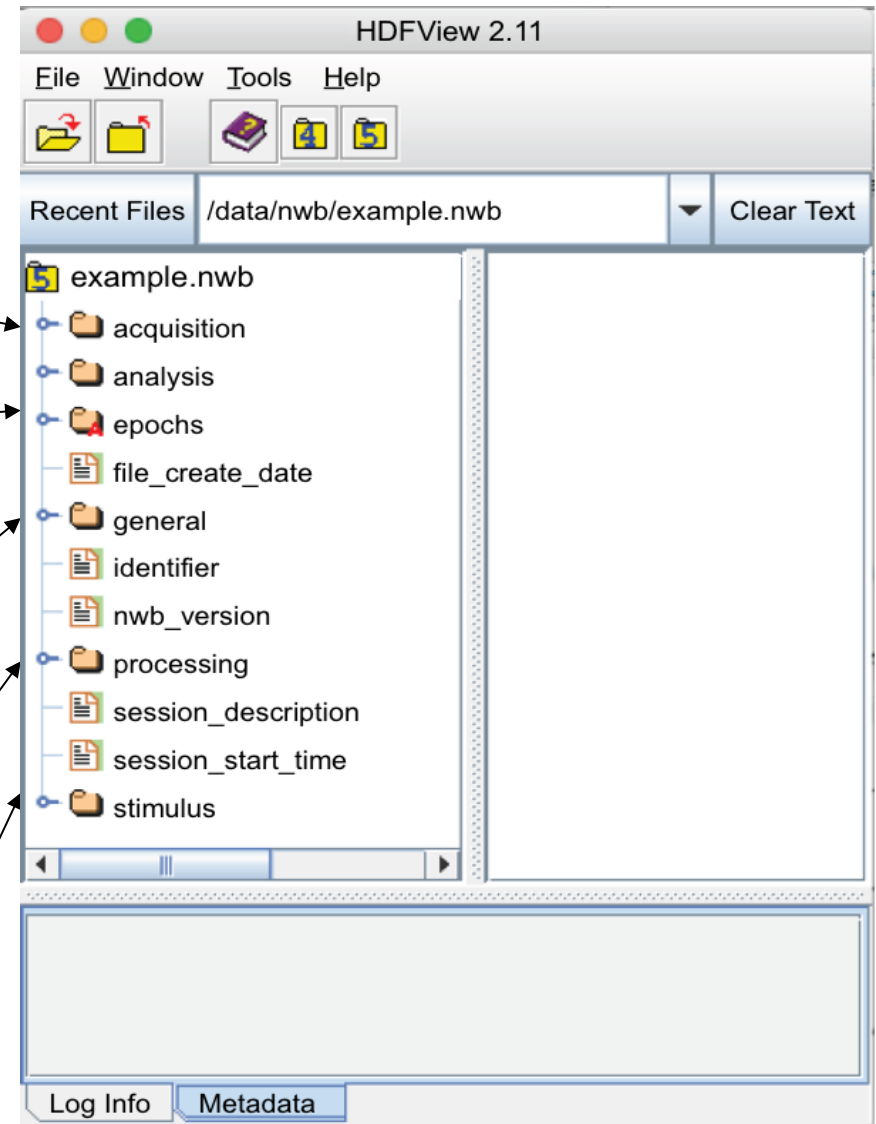
Acquired experimental data
and graphical documentation

Logical intervals that provide
windows into data occurring
during the interval

Metadata, including originating
lab, devices, methods, etc

Intermediate processing of
data, such as spike sorting

Stimuli that were presented
during an experiment



HDFView is a free application for
browsing HDF5 files.

Current work/ future plans

- Develop high-level read and write API
- Extend to store new types of data (e.g. ECoG)
- API features for HPC (High Performance Computing) environments
- Allow using different backends, e.g. other than HDF5
- Formation of governance board to manage the format and related tools
- New version release planned by SfN 2017