Allen SDK Documentation

Release dev

Allen Institute for Brain Science

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Contents

CHAPTER 1

Install Guide

This guide is a resource for using the Allen SDK package. It is maintained by the Allen Institute for Brain Science.

The Allen SDK was developed and tested with Python 2.7.13 and Python 3.6.4, installed as part of Anaconda Python distribution version 4.3.13. We do not guarantee consistent behavior with other Python versions.

1.1 Quick Start Using Pip

First ensure you have pip installed. It is included with the Anaconda distribution.

```
pip install allensdk
```

To uninstall the SDK:

```
pip uninstall allensdk
```

1.2 Other Distribution Formats

The Allen SDK is also available from the Github source repository.

1.3 Required Dependencies

- NumPy
- SciPy
- matplotlib
- h5py
- pandas

- pynrrd
- Jinja2

1.4 Optional Dependencies

- pytest
- coverage

1.5 Installation with Docker (Optional)

Docker is an open-source technology for building and deploying applications with a consistent environment including required dependencies. The AllenSDK is not distributed as a Docker image, but example Dockerfiles are available.

1. Ensure you have Docker installed.
2. Use Docker to build one of the images.

   Anaconda:

   ```
   docker pull alleninstitute/allensdk
   ```

   Other docker configurations are also available under docker directory in the source repository.

3. Run the docker image:

   ```
   docker run -i -t -p 8888:8888 -v /data:/data alleninstitute/allensdk /bin/bash
   cd allensdk
   make test
   ```

4. Start a Jupyter Notebook:

   ```
   cd allensdk/doc_template/examples_root/examples/nb
   jupyter-notebook --ip=* --no-browser
   ```

CHAPTER 2

Data Resources

The Allen SDK features Python code to support data and model access for the Allen Cell Types Database. Resources for other Allen Brain Atlas data resources will come in future updates.

2.1 Brain Observatory

The Allen Brain Observatory is a database of the visually-evoked functional responses of neurons in mouse visual cortex based on 2-photon fluorescence imaging. Characterized responses include orientation tuning, spatial and temporal frequency tuning, temporal dynamics, and spatial receptive field structure.

The data is organized into experiments and experiment containers. An experiment container represents a group of experiments with the same targeted imaging area, imaging depth, and Cre line. The individual experiments within an experiment container have different stimulus protocols, but cover the same imaging field of view.

Note: Version 1.3 of scipy fixed an error in its 2 sample Kolmogorov-Smirnoff test implementation. The new version produces more accurate p values for small and medium-sized samples. This change impacts speed tuning analysis p values (as returned by *StimulusAnalysis.get_speed_tuning*). If you access precalculated analysis results via *BrainObservatoryCache.get_ophys_experiment_analysis*, you will see values calculated using an older version of scipy's *ks_2samp*. To access values calculated from the new version, install scipy>=1.3.0 in your environment and construct a *StimulusAnalysis* object from a *BrainObservatoryNwbDataSet* (as returned by *BrainObservatoryCache.get_ophys_experiment_data*).

Note: Data collected after September 2016 uses a new session C stimulus designed to better-characterize spatial receptive fields in higher visual areas. The original locally sparse noise stimulus used 4.65 visual degree pixels. Session C2 broke that stimulus into two separate stimulus blocks: one with 4.65 degree pixels and one with 9.3 degree pixels.

Note that the `stimulus_info` module refers to these as *locally_sparse_noise_4deg* and *locally_sparse_noise_8deg*, respectively.

For more information on experimental design and a data overview, please visit the Allen Brain Observatory data portal.

2.1.1 Data Processing

For all data in Allen Brain Observatory, we perform the following processing:

1. Segment cell masks from each experiment's 2-photon fluorescence video
2. Associate cells from experiments belonging to the same experiment container and assign unique IDs
3. Extract each cell's mean fluorescence trace
4. Extract mean fluorescence traces from each cell's surrounding neuropil
5. Demix traces from overlapping ROIs
6. Estimate neuropil-corrected fluorescence traces
7. Compute dF/F
8. Compute stimulus-specific tuning metrics

All traces and masks for segmented cells in an experiment are stored in a Neurodata Without Borders (NWB) file. Stored traces include the raw fluoresence trace, neuropil trace, demixed trace, and dF/F trace. Code for extracting neuropil-corrected fluorescence traces, computing dF/F, and computing tuning metrics is available in the SDK.

New in June 2017: Trace demixing is a new addition as of June 2017. All past data was reprocessed using the new demixing algorithm. We have also developed a new module to better characterize a cell's receptive field. Take a look at the receptive field analysis example notebook

For more information about data processing, please read the technical whitepapers.

2.1.2 Getting Started

The Brain Observatory Jupyter notebook has many code samples to help get started with the available data:

- Download experimental metadata by visual area, imaging depth, and Cre line
- Find cells with specific response properties, like direction tuning
- Download data for an experiment
- Plot raw fluorescences traces, neuropil-corrected traces, and dF/F
- Find the ROI mask for a given cell
- Run neuropil correction
- Get pupil location and size

The code used to analyze and visualize data in the Allen Brain Observatory data portal is available as part of the SDK. Take a look at this Jupyter notebook to find out how to:

- Plot cell's response to its preferred stimulus condition
- Compute a cell's on/off receptive field based on the locally sparse noise stimulus

More detailed documentation is available demonstrating how to:

- Read and visualize the stimulus presentation tables in the NWB files
- Understand the layout of Brain Observatory NWB files

- Map previous cell specimen IDs to current cell specimen IDs

2.1.3 Precomputed Cell Metrics

A large table of precomputed metrics are available for download to support population analysis and filtering. The table below describes all of the metrics in the table. The `get_cell_specimens()` method will download this table as a list of dictionaries which can be converted to a pandas DataFrame as shown in this Jupyter notebook.

Stimulus	Metric	Field Name
drifting gratings	orientation selectivity	osi_dg
	direction selectivity	dsi_dg
	preferred direction	pref_dir_dg
	preferred temporal frequency	pref_tf_dg
	response p value	p_dg
	global ori. selectivity	g_osi_dg
	global dir. selectivity	g_dsi_dg
	response reliability	reliability_dg
	running modulation	run_mod_dg
	running modulation p value	p_run_mod_dg
	pref. condition mean df/f	peak_dff_dg
	TF discrimination index	tfdi_dg
static gratings	orientation selectivity	osi_sg
	preferred orientation	pref_ori_sg
	preferred spatial frequency	pref_sf_sg
	preferred phase	pref_phase_sg
	mean time to peak response	time_to_peak_sg
	response p value	p_sg
	global ori. selectivity	g_osi_sg
	reponse reliability	reliability_sg
	running modulation	run_mod_sg
	running modulation p value	p_run_mod_sg
	pref. condition mean df/f	peak_dff_ns
	SF discrimiation index	sfdi_sg
natural scenes	mean time to peak response	time_to_peak_ns
	preferred scene index	pref_scene_ns
	response p value	p_ns
	image selectivity	image_sel_ns
	running modulation	run_mod_ns
	running modulation p value	p_run_mod_ns
	pref. condition mean df/f	peak_dff_ns
natural movie 1	response reliability (session A)	reliability_nm1_a
	response reliability (session B)	reliability_nm1_b
	response reliability (session C)	reliability_nm1_c
natural movie 2	response reliability	reliability_nm2
natural movie 3	response reliability	reliability_nm3
locally sparse noise	RF area (on subunit)	rf_area_on_lsn
	RF area (off subunit)	rf_area_off_lsn
	RF center (on subunit)	rf_center_on_x, rf_center_on_y
	RF center (off subunit)	rf_center_off_x, rf_center_off_y
	RF chi^2	rf_chi2_lsn
	RF on-off subunit distance	rf_distance_lsn
	RF on-off subunit overlap index	rf_overlap_lsn

2.2 Cell Types

The Allen Cell Types data set is a database of mouse and human neuronal cell types based on multimodal characterization of single cells to enable data-driven approaches to classification and is fully integrated with other Allen Brain Atlas resources. The database currently includes:

- **electrophysiology**: whole cell current clamp recordings made from Cre-positive neurons
- **morphology**: 3D bright-field images of the complete structure of neurons from the visual cortex

This page describes how the SDK can be used to access data in the Cell Types Database. For more information, please visit the Cell Types Database home page and the API documentation.

2.2.1 Examples

The Cell Types Jupyter notebook has many code samples to help get started with analysis:

- Download and plot stimuli and responses from an NWB file for a cell
- Download and plot a cell's morphological reconstruction
- Download and plot precomputed electrophysiology features
- Download precomputed morphology features to a table
- Compute electrophysiology features for a single sweep

2.2.2 Cell Types Cache

The `CellTypesCache` class provides a Python interface for downloading data in the Allen Cell Types Database into well known locations so that you don't have to think about file names and directories. The following example demonstrates how to download meta data for all cells with 3D reconstructions, then download the reconstruction and electrophysiology recordings for one of those cells:

```python
from allensdk.core.cell_types_cache import CellTypesCache

ctc = CellTypesCache(manifest_file='cell_types/manifest.json')

# a list of cell metadata for cells with reconstructions, download if necessary
cells = ctc.get_cells(require_reconstruction=True)

# open the electrophysiology data of one cell, download if necessary
data_set = ctc.get_ephys_data(cells[0]['id'])

# read the reconstruction, download if necessary
reconstruction = ctc.get_reconstruction(cells[0]['id'])
```

`CellTypesCache` takes takes care of knowing if you've already downloaded some files and reads them from disk instead of downloading them again. All data is stored in the same directory as the *manifest_file* argument to the constructor.

2.2.3 Feature Extraction

The `EphysFeatureExtractor` class calculates electrophysiology features from cell recordings. *`extract_cell_features()`* can be used to extract the precise feature values available in the Cell Types Database:

```
from allensdk.core.cell_types_cache import CellTypesCache
from allensdk.ephys.extract_cell_features import extract_cell_features
from collections import defaultdict

# initialize the cache
ctc = CellTypesCache(manifest_file='cell_types/manifest.json')

# pick a cell to analyze
specimen_id = 324257146

# download the ephys data and sweep metadata
data_set = ctc.get_ephys_data(specimen_id)
sweeps = ctc.get_ephys_sweeps(specimen_id)

# group the sweeps by stimulus
sweep_numbers = defaultdict(list)
for sweep in sweeps:
    sweep_numbers[sweep['stimulus_name']].append(sweep['sweep_number'])

# calculate features
cell_features = extract_cell_features(data_set,
                                      sweep_numbers['Ramp'],
                                      sweep_numbers['Short Square'],
                                      sweep_numbers['Long Square'])
```

2.2.4 File Formats

This section provides a short description of the file formats used for Allen Cell Types data.

Morphology SWC Files

Morphological neuron reconstructions are available for download as SWC files. The SWC file format is a white-space delimited text file with a standard set of headers. The file lists a set of 3D neuronal compartments, each of which has:

Column	Data Type	Description
id	string	compartment ID
type	integer	compartment type
x	float	3D compartment position (x)
y	float	3D compartment position (y)
z	float	3D compartment position (z)
radius	float	compartment radius
parent	string	parent compartment ID

Comment lines begin with a '#'. Reconstructions in the Allen Cell Types Database can contain the following compartment types:

Type	Description
0	unknown
1	soma
2	axon
3	basal dendrite
4	apical dendrite

The Allen SDK comes with a `swc` Python module that provides helper functions and classes for manipulating SWC files. Consider the following example:

```python
import allensdk.core.swc as swc

# if you ran the examples above, you will have a reconstruction here
file_name = 'cell_types/specimen_485909730/reconstruction.swc'
morphology = swc.read_swc(file_name)

# subsample the morphology 3x. root, soma, junctions, and the first child of the root␣
↪are preserved.
sparse_morphology = morphology.sparsify(3)

# compartments in the order that they were specified in the file
compartment_list = sparse_morphology.compartment_list

# a dictionary of compartments indexed by compartment id
compartments_by_id = sparse_morphology.compartment_index

# the root soma compartment
soma = morphology.soma

# all compartments are dictionaries of compartment properties
# compartments also keep track of ids of their children
for child in morphology.children_of(soma):
    print(child['x'], child['y'], child['z'], child['radius'])
```

Neurodata Without Borders

The electrophysiology data collected in the Allen Cell Types Database is stored in the Neurodata Without Borders (NWB) file format. This format, created as part of the NWB initiative, is designed to store a variety of neurophysiology data, including data from intra- and extracellular electrophysiology experiments, optophysiology experiments, as well as tracking and stimulus data. It has a defined schema and metadata labeling system designed so software tools can easily access contained data.

The Allen SDK provides a basic Python class for extracting data from Allen Cell Types Database NWB files. These files store data from intracellular patch-clamp recordings. A stimulus current is presented to the cell and the cell's voltage response is recorded. The file stores both stimulus and response for several experimental trials, here called "sweeps." The following code snippet demonstrates how to extract a sweep's stimulus, response, sampling rate, and estimated spike times:

```python
from allensdk.core.nwb_data_set import NwbDataSet

# if you ran the examples above, you will have a NWB file here
file_name = 'cell_types/specimen_485909730/ephys.nwb'
data_set = NwbDataSet(file_name)

sweep_numbers = data_set.get_sweep_numbers()
sweep_number = sweep_numbers[0]
sweep_data = data_set.get_sweep(sweep_number)

# spike times are in seconds relative to the start of the sweep
spike_times = data_set.get_spike_times(sweep_number)

# stimulus is a numpy array in amps
stimulus = sweep_data['stimulus']
```

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```
# response is a numpy array in volts
reponse = sweep_data['response']

# sampling rate is in Hz
sampling_rate = sweep_data['sampling_rate']

# start/stop indices that exclude the experimental test pulse (if applicable)
index_range = sweep_data['index_range']
```

HDF5 Overview

NWB is implemented in HDF5. HDF5 files provide a hierarchical data storage that mirrors the organization of a file system. Just as a file system has directories and files, and HDF5 file has groups and datasets. The best way to understand an HDF5 (and NWB) file is to open a data file in an HDF5 browser. HDFView is the recommended browser from the makers of HDF5.

There are HDF5 manipulation libraries for many languages and platorms. MATLAB and Python in particular have strong HDF5 support.

2.3 Mouse Connectivity

The Allen Mouse Brain Connectivity Atlas consists of high-resolution images of axonal projections targeting different anatomic regions or various cell types using Cre-dependent specimens. Each data set is processed through an informatics data analysis pipeline to obtain spatially mapped quantified projection information.

This page describes how to use the SDK to access experimental projection data and metadata. For more information, please visit the Connectivity Atlas home page and the API documentation

2.3.1 Structure-Level Projection Data

All AAV projection signal in the Allen Mouse Connectivity Atlas has been registered to the expert-annotated Common Coordinate Framework (CCF) and summarized to structures in the adult mouse structure ontology. Most commonly used for analysis are measures of the density of projection signal in all brain areas for every experiment. This data is available for download and is described in more detail on the structure unionizes page.

2.3.2 Voxel-Level Projection Data

The CCF-registered AAV projection signal is also available for download as a set of 3D volumes for each experiment. The following data volumes are available for download:

- **projection density**: sum of detected projection pixels / sum of all pixels in voxel
- **injection_fraction**: fraction of pixels belonging to manually annotated injection site
- **injection_density**: density of detected projection pixels within the manually annotated injection site
- **data_mask**: binary mask indicating if a voxel contains valid data. Only valid voxels should be used for analysis.

2.3.3 Code Examples

The Mouse Connectivity Jupyter notebook has many code samples to help get started with analysis:

- Download experimental metadata by injection structure and transgenic line
- Download projection signal statistics at a structure level
- Build a structure-to-structure matrix of projection signal values
- Download and visualize gridded projection signal volumes

2.3.4 Mouse Connectivity Cache

The *MouseConnectivityCache* class saves all of the data you can download via the `MouseConenctivityApi` in well known locations so that you don't have to think about file names and directories. It also takes care of knowing if you've already downloaded some files and reads them from disk instead of downloading them again. The following example demonstrates how to download meta data for all experiments with injections in the isocortex and download the projetion density volume for one of them:

```
from allensdk.core.mouse_connectivity_cache import MouseConnectivityCache

# tell the cache class what resolution (in microns) of data you want to download
mcc = MouseConnectivityCache(resolution=25)

# use the structure tree class to get information about the isocortex structure
structure_tree = mcc.get_structure_tree()
isocortex_id = structure_tree.get_structures_by_name(['Isocortex'])[0]['id']

# a list of dictionaries containing metadata for non-Cre experiments
experiments = mcc.get_experiments(file_name='non_cre.json',
                                  injection_structure_ids=[isocortex_id])

# download the projection density volume for one of the experiments
pd = mcc.get_projection_density(experiments[0]['id'])
```

2.3.5 File Formats

This section provides a short description of the file formats used for data in the Allen Mouse Connectivity Atlas.

NRRD Files

All of the volumetric data in the connectivity atlas are stored as NRRD (Nearly Raw Raster Data) files. A NRRD file consists of a short ASCII header followed by a binary array of data values.

To read these in Python, we recommend the pynrrd package. Usage is straightforward:

```
import nrrd

file_name = 'mouse_connectivity/experiment_644250774/projection_density_25.nrrd'
data_array, metadata = nrrd.read(file_name)
```

2.4 Reference Space

Allen Institute atlases and data are registered, when possible, to one of several common reference spaces. Working in such a space allows you to easily compare data across subjects and experimental modalities.

This page documents how to use the Allen SDK to interact with a reference space. For more information and a list of reference spaces, see the atlas drawings and ontologies API documentation and the 3D reference models API documentation. For details about the construction of the Common Coordinate Framework space, see the CCFv3 whitepaper.

2.4.1 Structure Tree

Brain structures in our reference spaces are arranged in trees. The leaf nodes of the tree describe the very fine anatomical divisions of the space, while nodes closer to the root correspond to gross divisions. The `StructureTree` class provides an interface for interacting with a structure tree.

To download a structure tree, use the `allensdk.api.queries.ontologies_api.OntologiesApi` class as seen in this example

2.4.2 Annotation Volumes

An annotation volume is a 3d raster image that segments the reference space into structures. Each voxel in the annotation volume is assigned an integer value that describes the finest structure to which that point in space definitely belongs.

To download a nrrd formatted annotation volume at a specified isometric resolution, use the `allensdk.api.queries.mouse_connectivity_api` class. There is an example in the notebook.

2.4.3 ReferenceSpace Class

The `allensdk.core.reference_space.ReferenceSpace` class contains methods for working with our reference spaces. Some use cases might include:

- Building an indicator mask for one or more structures
- Viewing the annotation
- Querying the structure graph

Please see the example notebook for more code samples.

2.5 API Access

The `allensdk.api` package is designed to help retrieve data from the Allen Brain Atlas API. `api` contains methods to help formulate API queries and parse the returned results. There are several pre-made subclasses available that provide pre-made queries specific to certain data sets. Currently there are several subclasses in Allen SDK:

- `CellTypesApi`: data related to the Allen Cell Types Database
- `BiophysicalApi`: data related to biophysical models
- `GlifApi`: data related to GLIF models
- `AnnotatedSectionDataSetsApi`: search for experiments by intensity, density, pattern, and age

- *GridDataApi*: used to download 3-D expression grid data
- *ImageDownloadApi*: download whole or partial two-dimensional images
- *MouseConnectivityApi*: common operations for accessing the Allen Mouse Brain Connectivity Atlas
- *OntologiesApi*: data about neuroanatomical regions of interest
- *ConnectedServices*: schema of Allen Institute Informatics Pipeline services available through the RmaApi
- *RmaApi*: general-purpose HTTP interface to the Allen Institute API data model and services
- *SvgApi*: annotations associated with images as scalable vector graphics (SVG)
- *SynchronizationApi*: data about image alignment
- *TreeSearchApi*: list ancestors or descendents of structure and specimen trees

2.5.1 RMA Database and Service API

One API subclass is the *RmaApi* class. It is intended to simplify constructing an RMA query.

The RmaApi is a base class for much of the allensdk.api.queries package, but it may be used directly to customize queries or to build queries from scratch.

Often a query will simply request a table of data of one type:

```
from allensdk.api.queries.rma_api import RmaApi

rma = RmaApi()

data = rma.model_query('Atlas',
                        criteria="[name$il'*Mouse*']")
```

This will construct the RMA query url, make the query and parse the resulting JSON into an array of Python dicts with the names, ids and other information about the atlases that can be accessed via the API.

Using the criteria, include and other parameter, specific data can be requested.

```
associations = ''.join(['[id$eq1]',
                        'structure_graph(ontology),',
                        'graphic_group_labels'])

atlas_data = rma.model_query('Atlas',
                                include=associations,
                                criteria=associations,
                                only=['atlases.id',
                                    'atlases.name',
                                    'atlases.image_type',
                                    'ontologies.id',
                                    'ontologies.name',
                                    'structure_graphs.id',
                                    'structure_graphs.name',
                                    'graphic_group_labels.id',
                                    'graphic_group_labels.name'])
```

Note that a 'class' name is used for the first parameter. 'Association' names are used to construct the include and criteria parameters nested using parentheses and commas. In the only clause, the 'table' form is used, which is generally a plural lower-case version of the class name. The only clause selects specific 'fields' to be returned. The schema that includes the classes, fields, associations and tables can be accessed in JSON form using:

```
# http://api.brain-map.org/api/v2/data.json
schema = rma.get_schema()
for entry in schema:
    data_description = entry['DataDescription']
    clz = list(data_description.keys())[0]
    info = list(data_description.values())[0]
    fields = info['fields']
    associations = info['associations']
    table = info['table']
    print("class: %s" % (clz))
    print("fields: %s" % (','.join(f['name'] for f in fields)))
    print("associations: %s" % (','.join(a['name'] for a in associations)))
    print("table: %s\n" % (table))
```

2.5.2 Using Pandas to Process Query Results

When it is difficult to get data in exactly the required form using only an RMA query, it may be helpful to perform additional operations on the client side. The pandas library can be useful for this.

Data from the API can be read directly into a pandas Dataframe object.

```
import pandas as pd

structures = pd.DataFrame(
    rma.model_query('Structure',
                    criteria='[graph_id$eq1]',
                    num_rows='all'))
```

Indexing subsets of the data (certain columns, certain rows) is one use of pandas: specifically .loc:

```
names_and_acronyms = structures.loc[:,['name', 'acronym']]
```

and Boolean indexing

```
mea = structures[structures.acronym == 'MEA']
mea_id = mea.iloc[0,:].id
mea_children = structures[structures.parent_structure_id == mea_id]
print(mea_children['name'])
```

Concatenate, merge and join are used to add columns or rows:

When an RMA call contains an include clause, the associated data will be represented as a python dict in a single column. The column may be converted to a proper Dataframe and optionally dropped.

```
criteria_string = "structure_sets[name$eq'Mouse Connectivity - Summary']"
include_string = "ontology"
summary_structures = \
    pd.DataFrame(
        rma.model_query('Structure',
                        criteria=criteria_string,
                        include=include_string,
                        num_rows='all'))
ontologies = \
    pd.DataFrame(
        list(summary_structures.ontology)).drop_duplicates()
flat_structures_dataframe = summary_structures.drop(['ontology'], axis=1)
```

Alternatively, it can be accessed using normal python dict and list operations.

```
print(summary_structures.ontology[0]['name'])
```

Pandas Dataframes can be written to a CSV file using to_csv and read using load_csv.

```
summary_structures[['id',
                    'parent_structure_id',
                    'acronym']].to_csv('summary_structures.csv',
                                       index_label='structure_id')
reread = pd.read_csv('summary_structures.csv')
```

Iteration over a Dataframe of API data can be done in several ways. The .itertuples method is one way to do it.

```
for id, name, parent_structure_id in summary_structures[['name',
                                                          'parent_structure_id']].
↪itertuples():
    print("%d %s %d" % (id, name, parent_structure_id))
```

2.5.3 Caching Queries on Disk

`wrap()` has several parameters for querying the API, saving the results as CSV or JSON and reading the results as a pandas dataframe.

```
from allensdk.api.cache import Cache

cache_writer = Cache()
do_cache=True
structures_from_api = \
    cache_writer.wrap(rma.model_query,
                        path='summary.csv',
                        cache=do_cache,
                        model='Structure',
                        criteria='[graph_id$eq1]',
                        num_rows='all')
```

If you change to_cache to False and run the code again it will read the data from disk rather than executing the query.

2.6 Visual Coding – Neuropixels

The Visual Coding – Neuropixels project uses high-density extracellular electrophysiology (**Ecephys**) probes to record spikes from a wide variety of regions in the mouse brain. Our experiments are designed to study the activity of the visual cortex and thalamus in the context of passive visual stimulation, but these data can be used to address a wide variety of topics.

Spike-sorted data and metadata are available via the AllenSDK as Neurodata Without Borders files. However, if you're using the AllenSDK to interact with the data, no knowledge of the NWB data format is required.

2.6.1 Getting Started

To jump right in, check out the quick start guide (download .ipynb), which will show you how to download the data, align spikes to a visual stimulus, and decode natural images from neural activity patterns. For a quick summary of experimental design and data access, see the cheat sheet.

If you would like more example code, the full example notebook (download .ipynb) covers all of the ways to access data for each experiment.

Additional tutorials are available on the following topics:

1. Data access (download .ipynb)
2. Unit quality metrics (download .ipynb)
3. LFP data analysis (download .ipynb)
4. Receptive field mapping (download .ipynb)

For detailed information about the experimental design, data acquisition, and informatics methods, please refer to our technical whitepaper. AllenSDK API documentation is available here.

A note on terminology: Throughout the SDK, we refer to neurons as "units," because we cannot guarantee that all the spikes assigned to one unit actually originate from a single cell. Unlike in two-photon imaging, where you can visualize each neuron throughout the entire experiment, with electrophysiology we can only "see" a neuron when it fires a spike. If a neuron moves relative to the probe, or if it's far away from the probe, some of its spikes may get mixed together with those from other neurons. Because of this inherent ambiguity, we provide a variety of quality metrics to allow you to find the right units for your analysis. Even highly contaminated units contain potentially valuable information about brain states, so we didn't want to leave them out of the dataset. But certain types of analysis require more stringent quality thresholds, to ensure that all of the included units are well isolated from their neighbors.

2.6.2 Data Processing

_static/neuropixels_data_processing.png

Neuropixels probes contain 374 or 383 channels that continuously detect voltage fluctuations in the surrounding neural tissue. Each channel is split into two separate data streams, or "bands," on the probes. The "spike band" is digitized at 30 kHz, and contains information about action potentials fired by neurons directly adjacent to the probe. The "LFP band" is digitized at 2.5 kHz, and records the low-frequency (<1000 Hz) fluctuations that result from synchronized neural activity over a wider area.

To go from the raw spike-band data to NWB files, we perform the following processing steps:

1. Median-subtraction to remove common-mode noise from the continuous traces
2. High-pass filtering (>150 Hz) and whitening across blocks of 32 channels
3. Spike sorting with Kilosort2, to detect spikes and assign them to individual units
4. Computing the mean waveform for each unit
5. Removing units with artifactual waveforms
6. Computing quality metrics for every unit
7. Computing stimulus-specific tuning metrics

For the LFP band, we:

1. Downsample the signals in space and time (every 4th channel and every 2nd sample)
2. High-pass filter at 0.1 Hz to remove the DC offset from each channel
3. Re-reference to channels outside of the brain to remove common-mode noise

The packaged NWB files contain:

1. Spike times, spike amplitudes, mean waveforms, and quality metrics for every unit
2. Information about the visual stimulus
3. Time series of the mouse's running speed, pupil diameter, and pupil position
4. LFP traces for channels in the brain
5. Experiment metadata

All code for data processing and packaging is available in the ecephys_spike_sorting and the ecephys section of the AllenSDK.

2.6.3 Visual Stimulus Sets

_static/neuropixels_stimulus_sets.png

A central aim of the Visual Coding – Neuropixels project is to measure the impact of visual stimuli on neurons throughout the mouse visual system. To that end, all mice viewed one of two possible stimulus sets, known as “Brain Observatory 1.1” or “Functional Connectivity”. Both stimulus sets began with a Gabor stimulus flashed at 81 different locations on the screen, used to map receptive fields of visually responsive units. Next, the mice were shown brief flashes of light or dark, to measure the temporal dynamics of the visual response.

The remainder of the visual stimulus set either consisted of the same stimuli shown in the two-photon experiments

("Brain Observatory 1.1"), or a subset of those stimuli shown with a higher number of repeats. We also added a dot motion stimulus, to allow us to measure the speed tuning of units across the mouse visual system.

2.6.4 Quality Metrics

`_static/neuropixels_quality_metrics.png`

Every NWB file includes a table of quality metrics, which can be used to assess the completeness, contamination, and stability of units in the recording. By default, we won't show you units below a pre-determined quality threshold; we hide any units that are not present for the whole session (presence_ratio < 0.95), that include many contaminating spikes (isi_violations > 0.5), or are likely missing a large fraction of spikes (amplitude_cutoff > 0.1). However, even contaminated or incomplete units contain information about brain states, and may be of interest to analyze. Therefore, the complete units table can be accessed via special flags in the AllenSDK.

In general, we do not make a distinction between 'single-unit' and 'multi-unit' activity. There is no obvious place to draw a boundary in the overall distributions of quality metrics, and setting a strict cutoff (e.g. isi_violations = 0) will remove a lot of potentially valuable data. We prefer to leave it up to the end user to decide what level of contamination is tolerable. But that means you need to be aware that different units will have different levels of cleanliness.

It should also be noted that all of these metrics assume that the spike waveform is stable throughout the experiment. Given that the probe drifts, on average, about 40 microns over the course of the ~3 hour recordings, this assumption is almost never valid. The resulting changes in waveform shape can cause a unit's quality to fluctuate. If you're unsure about a unit's quality, it can be helpful to plot its spike amplitudes over time. This can make it obvious if it's drifting below threshold, or if it contains spikes from multiple neurons.

Documentation on the various quality metrics can be found in the ecephys_spike_sorting repository.

For a detailed discussion of the appropriate way to apply each of these metrics, please check out this tutorial (download .ipynb)

2.6.5 Precomputed Stimulus Metrics

Tables of precomputed metrics are available for download to support population analysis and filtering. The table below describes all of the available metrics. The `get_unit_analysis_metrics()` method will load this table as a pandas DataFrame.

Stimulus	Metric	Field Name
drifting gratings	preferred orientation	pref_ori_dg
	preferred temporal frequency	pref_tf_dg
	global ori. selectivity	g_osi_dg
	global dir. selectivity	g_dsi_dg
	running modulation	run_mod_dg
	running modulation p-value	p_run_mod_dg
	firing rate	firing_rate_dg
	fano factor	fano_dg
	modulation index	mod_idx_dg
	f1/f0	f1_f0_dg
	lifetime sparseness	lifetime_sparseness_dg
	c50 (contrast tuning stimulus)	c50_dg
static gratings	preferred orientation	pref_ori_sg
	preferred spatial frequency	pref_sf_sg
	preferred phase	pref_phase_sg
	global ori. selectivity	g_osi_sg
	running modulation	run_mod_sg
	running modulation p-value	p_run_mod_sg
	firing rate	firing_rate_sg
	fano factor	fano_sg
	lifetime sparseness	lifetime_sparseness_sg
natural scenes	preferred image index	pref_image_ns
	image selectivity	image_selectivity_ns
	running modulation	run_mod_ns
	running modulation p-value	p_run_mod_ns
	firing rate	firing_rate_ns
	fano factor	fano_factor_ns

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Table 2 – continued from previous page

Stimulus	Metric	Field Name
	lifetime sparseness	lifetime_sparseness_ns
dot motion	preferred speed	pref_speed_dm
	preferred direction	pref_dir_dm
	running modulation	run_mod_dm
	running modulation p-value	p_run_mod_dm
	firing rate	firing_rate_dm
	fano factor	fano_factor_dm
	lifetime sparseness	lifetime_sparseness_dm
full-field flashes	on/off ratio	on_off_ratio_fl
	running modulation	run_mod_fl
	running modulation p-value	p_run_mod_fl
	firing rate	firing_rate_fl
	fano factor	fano_factor_fl
	lifetime sparseness	lifetime_sparseness_fl
gabors	RF area	area_rf
	RF elevation	elevation_rf
	RF azimuth	azimuth_rf
	RF p-value	p_value_rf
	running modulation	run_mod_rf
	running modulation p-value	p_run_mod_rf
	firing rate	firing_rate_rf
	fano factor	fano_factor_rf
	lifetime sparseness	lifetime_sparseness_rf

CHAPTER 3

Models

The Allen SDK currently focuses on models generated from electrophysiology data in the Allen Cell Types Database. There are two classes of models available for download: biophysical models and generalize leaky integrate-and-fire models.

3.1 Generalized LIF Models

The Allen Cell Types Database contains Generalized Leaky Integrate and Fire (GLIF) models that simulate the firing behavior of neurons at five levels of complexity. Review the GLIF technical white paper for details on these models and how their parameters were optimized.

The Allen SDK GLIF simulation module is an explicit time-stepping simulator that evolves a neuron's simulated voltage over the course of an input current stimulus. The module also tracks the neuron's simulated spike threshold and registers action potentials whenever voltage surpasses threshold. Action potentials initiate reset rules that update voltage, threshold, and (optionally) trigger afterspike currents.

The GLIF simulator in this package has a modular architecture that enables users to choose from a number of dynamics and reset rules that update the simulation's voltage, spike threshold, and afterspike currents during the simulation. The GLIF package contains a built-in set of rules, however developers can plug in custom rule implementations provided they follow a simple argument specification scheme.

The Allen SDK GLIF simulator was developed and tested with Python 2.7.9, installed as part of Anaconda Python distribution version 2.1.0.

The rest of this page provides examples demonstrating how to download models, examples of simulating these models, and general GLIF model documentation.

Note: the GLIF simulator module is still under heavy development and may change significantly in the future.

3.1.1 Downloading GLIF Models

There are two ways to download files necessary to run a GLIF model. The first way is to visit http://celltypes.brain-map.org and find cells that have GLIF models available for download. The electrophysiology details page for a cell has a neuronal model download link. Specifically:

1. Click 'More Options +' and filter for GLIF models.
2. Click the electrophysiology thumbnail for a cell on the right hand panel.
3. Choose a GLIF model from the 'Show model responses' dropdown.
4. Scroll down to the model response click 'Download model'.

One such link (for a simple LIF neuronal model, ID 566302806), would look like this:

```
http://api.brain-map.org/neuronal_model/download/566302806
```

This link returns .zip archive containing the neuron configuration file and sweep metadata required to simulate the model with stimuli applied to the cell. Specifically, the .zip archive will contain:

- **472423251_neuron_config.json**: JSON config file for the GLIF model
- **ephys_sweeps.json**: JSON with metadata for sweeps presented to the cell
- **neuronal_model.json**: JSON with general metadata for the cell

If you would like to reproduce the model traces seen in the Cell Types Database, you can download an NWB file containing both the stimulus and cell response traces via a 'Download data' link on the cell's electrophysiology page. See the NWB description section for more details on the NWB file format.

You can also download all of these files, including the cell's NWB file, using the *GlifApi* class:

```
from allensdk.api.queries.glif_api import GlifApi
from allensdk.core.cell_types_cache import CellTypesCache
import allensdk.core.json_utilities as json_utilities

neuronal_model_id = 566302806

# download model metadata
glif_api = GlifApi()
nm = glif_api.get_neuronal_models_by_id([neuronal_model_id])[0]

# download the model configuration file
nc = glif_api.get_neuron_configs([neuronal_model_id])[neuronal_model_id]
neuron_config = glif_api.get_neuron_configs([neuronal_model_id])
json_utilities.write('neuron_config.json', neuron_config)

# download information about the cell
ctc = CellTypesCache()
ctc.get_ephys_data(nm['specimen_id'], file_name='stimulus.nwb')
ctc.get_ephys_sweeps(nm['specimen_id'], file_name='ephys_sweeps.json')
```

3.1.2 Running a GLIF Simulation

To run a GLIF simulation, the most important file you you need is the `neuron_config` JSON file. You can use this file to instantiate a simulator and feed in your own stimulus:

```
import allensdk.core.json_utilities as json_utilities
from allensdk.model.glif.glif_neuron import GlifNeuron

# initialize the neuron
neuron_config = json_utilities.read('neuron_config.json')['566302806']
neuron = GlifNeuron.from_dict(neuron_config)

# make a short square pulse. stimulus units should be in Amps.
stimulus = [ 0.0 ] * 100 + [ 10e-9 ] * 100 + [ 0.0 ] * 100

# important! set the neuron's dt value for your stimulus in seconds
neuron.dt = 5e-6

# simulate the neuron
output = neuron.run(stimulus)

voltage = output['voltage']
threshold = output['threshold']
spike_times = output['interpolated_spike_times']
```

Note: The GLIF simulator does not simulate during action potentials. Instead it inserts `NaN` values for a fixed number of time steps when voltage surpasses threshold. The simulator skips `neuron.spike_cut_length` time steps after voltage surpasses threshold.

To reproduce the model's traces displayed on the Allen Cell Types Database web page, the Allen SDK provides the `allensdk.core.model.glif.simulate_neuron` module for simulating all sweeps presented to a cell and storing them in the NWB format:

```
import allensdk.core.json_utilities as json_utilities

from allensdk.model.glif.glif_neuron import GlifNeuron
from allensdk.model.glif.simulate_neuron import simulate_neuron

neuron_config = json_utilities.read('neuron_config.json')['566302806']
ephys_sweeps = json_utilities.read('ephys_sweeps.json')
ephys_file_name = 'stimulus.nwb'

neuron = GlifNeuron.from_dict(neuron_config)

sweep_numbers = [ s['sweep_number'] for s in ephys_sweeps if s['stimulus_units'] ==
↪'Amps' ]
sweep_numbers = sweep_numbers[:1] # for the sake of a speedy example, just run the␣
↪first one
simulate_neuron(neuron, sweep_numbers, ephys_file_name, ephys_file_name, 0.05)
```

Warning: These stimuli are sampled at a very high resolution (200kHz), and a given cell can have many sweeps. This process can take over an hour.

The `simulate_neuron` function call simulates all sweeps in the NWB file. Because the same NWB file is being used for both input and output, the cell's response traces will be overwritten as stimuli are simulated. `simulate_neuron` optionally accepts a value which will be used to overwrite these `NaN` values generated during action potentials (in this case 0.05 Volts).

If you would like to run a single sweep instead of all sweeps, try the following:

```python
import allensdk.core.json_utilities as json_utilities
from allensdk.model.glif.glif_neuron import GlifNeuron
from allensdk.core.nwb_data_set import NwbDataSet

neuron_config = json_utilities.read('neuron_config.json')['566302806']
ephys_sweeps = json_utilities.read('ephys_sweeps.json')
ephys_file_name = 'stimulus.nwb'

# pull out the stimulus for the current-clamp first sweep
ephys_sweep = next( s for s in ephys_sweeps
                    if s['stimulus_units'] == 'Amps' )
ds = NwbDataSet(ephys_file_name)
data = ds.get_sweep(ephys_sweep['sweep_number'])
stimulus = data['stimulus']

# initialize the neuron
# important! update the neuron's dt for your stimulus
neuron = GlifNeuron.from_dict(neuron_config)
neuron.dt = 1.0 / data['sampling_rate']

# simulate the neuron
output = neuron.run(stimulus)

voltage = output['voltage']
threshold = output['threshold']
spike_times = output['interpolated_spike_times']
```

Note: The `dt` value provided in the downloadable GLIF neuron configuration files does not correspond to the sampling rate of the original stimulus. Stimuli were subsampled and filtered for parameter optimization. Be sure to overwrite the neuron's `dt` with the correct sampling rate.

If you would like to plot the outputs of this simulation using numpy and matplotlib, try:

```python
import numpy as np
import matplotlib.pyplot as plt

voltage = output['voltage']
threshold = output['threshold']
interpolated_spike_times = output['interpolated_spike_times']
spike_times = output['interpolated_spike_times']
interpolated_spike_voltages = output['interpolated_spike_voltage']
interpolated_spike_thresholds = output['interpolated_spike_threshold']
grid_spike_indices = output['spike_time_steps']
grid_spike_times = output['grid_spike_times']
after_spike_currents = output['AScurrents']

# create a time array for plotting
time = np.arange(len(stimulus))*neuron.dt

plt.figure(figsize=(10, 10))

# plot stimulus
plt.subplot(3,1,1)
plt.plot(time, stimulus)
plt.xlabel('time (s)')
```

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```
plt.ylabel('current (A)')
plt.title('Stimulus')

# plot model output
plt.subplot(3,1,2)
plt.plot(time,  voltage, label='voltage')
plt.plot(time,  threshold, label='threshold')

if grid_spike_indices is not None:
    plt.plot(interpolated_spike_times, interpolated_spike_voltages, 'x',
             label='interpolated spike')

    plt.plot((grid_spike_indices-1)*neuron.dt, voltage[grid_spike_indices-1], '.',
             label='last step before spike')

plt.xlabel('time (s)')
plt.ylabel('voltage (V)')
plt.legend(loc=3)
plt.title('Model Response')

# plot after spike currents
plt.subplot(3,1,3)
for ii in range(np.shape(after_spike_currents)[1]):
    plt.plot(time, after_spike_currents[:,ii])
plt.xlabel('time (s)')
plt.ylabel('current (A)')
plt.title('After Spike Currents')

plt.tight_layout()
plt.show()
```

Note: There both interpolated spike times and grid spike times. The grid spike is the first time step where the voltage is higher than the threshold. Note that if you try to plot the voltage at the grid spike indices the output will be `NaN`. The interpolated spike is the calculated intersection of the threshold and voltage between the time steps.

3.1.3 GLIF Configuration

Instances of the *GlifNeuron* class require many parameters for initialization. Fixed neuron parameters are stored directly as properties on the class instance:

Parameter	Description	Units	Type
El	resting potential	Volts	float
dt	time duration of each simulation step	seconds	float
R_input	input resistance	Ohms	float
C	capacitance	Farads	float
asc_vector	afterspike current coefficients	Amps	np.array
spike_cut_length	spike duration	time steps	int
th_inf	instantaneous threshold	Volts	float
th_adapt	adapted threshold	Volts	float

Some of these fixed parameters were optimized to fit Allen Cell Types Database electrophysiology data. Optimized coefficients for these parameters are stored by name in the `neuron.coeffs` dictionary. For more details on which parameters were optimized, please see the technical white paper.

The `GlifNeuron` class has six methods that can be customized: three rules for updating voltage, threshold, and afterspike currents during the simulation; and three rules for updating those values when a spike is detected (voltage surpasses threshold).

Method Type	Description
voltage_dynamics_method	Update simulation voltage for the next time step.
threshold_dynamics_method	Update simulation threshold for the next time step.
AScurrent_dynamics_method	Update afterspike current coefficients for the next time step.
voltage_reset_method	Reset simulation voltage after a spike occurs.
threshold_reset_method	Reset simulation threshold after a spike occurs.
AScurrent_reset_method	Reset afterspike current coefficients after a spike occurs.

The GLIF neuron configuration files available from the Allen Brain Atlas API use built-in methods, however you can supply your own custom method if you like:

```
# define your own custom voltage reset rule
# this one linearly scales the input voltage
def custom_voltage_reset_rule(neuron, voltage_t0, custom_param_a, custom_param_b):
    return custom_param_a * voltage_t0 + custom_param_b

# initialize a neuron from a neuron config file
neuron_config = json_utilities.read('neuron_config.json')['566302806']
neuron = GlifNeuron.from_dict(neuron_config)

# configure a new method and overwrite the neuron's old method
method = neuron.configure_method('custom', custom_voltage_reset_rule,
                                 { 'custom_param_a': 0.1, 'custom_param_b': 0.0 })
neuron.voltage_reset_method = method

output = neuron.run(stimulus)
```

Notice that the function is allowed to take custom parameters (here `custom_param_a` and `custom_param_b`), which are configured on method initialization from a dictionary. For more details, see the documentation for the `GlifNeuron` and `GlifNeuronMethod` classes.

3.1.4 Built-in Dynamics Rules

The job of a dynamics rule is to describe how the simulator should update the voltage, spike threshold, and afterspike currents of the simulator at a given simulation time step.

Voltage Dynamics Rules

These methods update the output voltage of the simulation. They all expect a voltage, afterspike current vector, and current injection value to be passed in by the GlifNeuron. All other function parameters must be fixed using the GlifNeuronMethod class. They all return an updated voltage value.

`allensdk.model.glif.glif_neuron_methods.dynamics_voltage_linear_forward_euler()`

Threshold Dynamics Rules

These methods update the spike threshold of the simulation. They all expect the current threshold and voltage values of the simulation to be passed in by the GlifNeuron. All other function parameters must be fixed using the GlifNeuronMethod class. They all return an updated threshold value.

`allensdk.model.glif.glif_neuron_methods.dynamics_threshold_three_components_exact()`

allensdk.model.glif.glif_neuron_methods.dynamics_threshold_spike_component()

allensdk.model.glif.glif_neuron_methods.dynamics_threshold_inf()

Afterspike Current Dynamics Rules

These methods expect current afterspike current coefficients, current time step, and time steps of all previous spikes to be passed in by the GlifNeuron. All other function parameters must be fixed using the GlifNeuronMethod class. They all return an updated afterspike current array.

allensdk.model.glif.glif_neuron_methods.dynamics_AScurrent_exp()

allensdk.model.glif.glif_neuron_methods.dynamics_AScurrent_none()

3.1.5 Built-in Reset Rules

The job of a reset rule is to describe how the simulator should update the voltage, spike threshold, and afterspike currents of the simulator after the simulator has detected that the simulated voltage has surpassed threshold.

Voltage Reset Rules

These methods update the output voltage of the simulation after voltage has surpassed threshold. They all expect a voltageto be passed in by the GlifNeuron. All other function parameters must be fixed using the GlifNeuronMethod class. They all return an updated voltage value.

allensdk.model.glif.glif_neuron_methods.reset_voltage_zero()

allensdk.model.glif.glif_neuron_methods.reset_voltage_v_before()

Threshold Reset Rules

These methods update the spike threshold of the simulation after a spike has been detected. They all expect the current threshold and the reset voltage value of the simulation to be passed in by the GlifNeuron. All other function parameters must be fixed using the GlifNeuronMethod class. They all return an updated threshold value.

allensdk.model.glif.glif_neuron_methods.reset_threshold_inf()

allensdk.model.glif.glif_neuron_methods.reset_threshold_three_components()

Afterspike Reset Reset Rules

These methods expect current afterspike current coefficients to be passed in by the GlifNeuron. All other function parameters must be fixed using the GlifNeuronMethod class. They all return an updated afterspike current array.

allensdk.model.glif.glif_neuron_methods.reset_AScurrent_none()

allensdk.model.glif.glif_neuron_methods.reset_AScurrent_sum()

3.2 Biophysical Models

The Allen Cell Types Database contains biophysical models that characterize the firing behavior of neurons measured in slices through current injection by a somatic whole-cell patch clamp electrode. These models contain a set of 10 active conductances placed at the soma and use the reconstructed 3D morphologies of the modeled neurons. The biophysical modeling technical white paper contains details on the specific construction of these models and the optimization of the model parameters to match the experimentally-recorded firing behaviors.

The biophysical models are run with the NEURON simulation environment. The Allen SDK package contains libraries that assist in downloading and setting up the models available on the Allen Institute web site for users to run using NEURON. The examples and scripts provided run on Linux using the bash shell.

3.2.1 Prerequisites

You must have NEURON with the Python interpreter enabled and the Allen SDK installed.

The Allen Institute perisomatic biophysical models were generated using NEURON version v7.4.rel-1370. Instructions for compiling NEURON with the Python interpreter are available from the NEURON team under the heading Installation with Python as an alternative interpreter. The Allen SDK is compatible with Python version 2.7.9, included in the Anaconda 2.1.0 distribution.

Instructions for optional Docker installation are also available.

Note: Building and installing NEURON with the Python wrapper enabled is not always easy. This page targets users that have a background in NEURON usage and installation.

3.2.2 Downloading Biophysical Models

There are two ways to download files necessary to run a biophysical model. The first way is to visit http://celltypes.brain-map.org and find cells that have biophysical models available for download. The electrophysiology details page for a cell has a neuronal model download link. Specifically:

1. Click 'More Options+'
2. Check 'Models -> Biophysical - perisomatic' or 'Biophysical - all active'
3. Use the Filters, Cell Location and Cell Feature Filters to narrow your results.
4. Click on a Cell Summary to view the Mouse Experiment Electrophysiology.
5. Click the "download data" link to download the NWB stimulus and response file.
6. Click "show model response" and select 'Biophysical - perisomatic' or 'Biophysical - all active'.
7. Scroll down and click the 'Biophysical - perisomatic' or 'Biophysical - all active' "download model" link.

This may be also be done programmatically. The neuronal model id can be found to the left of the corresponding 'Biophysical - perisomatic' or 'Biophysical - all active' "download model" link.

```python
from allensdk.api.queries.biophysical_api import \
    BiophysicalApi

bp = BiophysicalApi()
bp.cache_stimulus = True # change to False to not download the large stimulus NWB file
neuronal_model_id = 472451419    # get this from the web site as above
bp.cache_data(neuronal_model_id, working_directory='neuronal_model')
```

More help can be found in the online help for the Allen Cell Types Database web application.

3.2.3 Directory Structure

The structure of the directory created looks like this. It includes stimulus files, model parameters, morphology, cellular mechanisms and application configuration.

```
neuronal_model
|-- manifest.json
|-- 472451419_fit.json
|-- Nr5a1-Cre_Ai14_IVSCC_-169248.04.02.01.nwb
|-- Nr5a1-Cre_Ai14_IVSCC_-169248.04.02.01_403165543_m.swc
|-- modfiles
|    |--CaDynamics.mod
|    |--Ca_HVA.mod
|    |--Ca_LVA.mod
|    |--Ih.mod
|    `--...etc.
|
|--x86_64
`---work
```

3.2.4 Running the Simulation (Linux shell prompt)

All of the sweeps available from the web site are included in manifest.json and will be run by default. This can take some time.

```
cd neuronal_model
nrnivmodl ./modfiles   # compile the model (only needs to be done once)
python -m allensdk.model.biophysical.runner manifest.json
```

3.2.5 Selecting a Specific Sweep

The sweeps are listed in manifest.json. You can remove all of the sweep numbers that you do not want run.

3.2.6 Simulation Main Loop

The top level script is in the `run()` method of the `allensdk.model.biophysical.runner` module. The implementation of the method is discussed here step-by-step:

First configure NEURON based on the configuration file, which was read in from the command line at the very bottom of the script.

`run()`:

```
# configure NEURON -- this will infer model type (perisomatic vs. all-active)
utils = Utils.create_utils(description)
h = utils.h
```

The next step is to get the path of the morphology file and pass it to NEURON.

```
# configure model
manifest = description.manifest
morphology_path = description.manifest.get_path('MORPHOLOGY')
utils.generate_morphology(morphology_path.encode('ascii', 'ignore'))
utils.load_cell_parameters()
```

Then read the stimulus and recording configuration and configure NEURON

```
# configure stimulus and recording
stimulus_path = description.manifest.get_path('stimulus_path')
nwb_out_path = manifest.get_path("output")
output = NwbDataSet(nwb_out_path)
run_params = description.data['runs'][0]
sweeps = run_params['sweeps']
junction_potential = description.data['fitting'][0]['junction_potential']
mV = 1.0e-3
```

Loop through the stimulus sweeps and write the output.

```
# run sweeps
for sweep in sweeps:
    utils.setup_iclamp(stimulus_path, sweep=sweep)
    vec = utils.record_values()

    h.finitialize()
    h.run()

    # write to an NWB File
    output_data = (numpy.array(vec['v']) - junction_potential) * mV
    output.set_sweep(sweep, None, output_data)
```

3.2.7 Customization

Much of the code in the perisomatic simulation is not core Allen SDK code. The runner.py script largely reads the configuration file and calls into methods in the *Utils* class. Utils is a subclass of the *HocUtils* class, which provides access to objects in the NEURON package. The various methods called by the runner.script are implemented here, including: *generate_morphology()*, *load_cell_parameters()*, *setup_iclamp()*, *read_stimulus()* and *record_values()*.

Utils:

```
from allensdk.model.biophys_sim.neuron.hoc_utils import HocUtils

.....

class Utils(HocUtils):
.....

    def __init__(self, description):
        super(Utils, self).__init__(description)
....
```

To create a biophysical model using your own software or data, simply model your directory structure on one of the downloaded simulations or one of the examples below. Add your own runner.py and utils.py module to the simulation directory.

Compile the .mod files using NEURON's nrnivmodl command (Linux shell):

```
nrnivmodl modfiles
```

Then call your runner script directly, passing in the manifest file to your script:

```
python runner.py manifest.json
```

The output from your simulation and any intermediate files will go in the work directory.

3.2.8 Examples

A minimal example (`simple_example.tgz`) and a multicell example (`multicell_example.tgz`) are available to download as a starting point for your own projects.

Each example provides its own utils.py file along with a main script (Linux shell) and supporting configuration files.

simple_example.tgz:

```
tar xvzf simple_example.tgz
cd simple
nrnivmodl modfiles
python simple.py
```

multicell_example.tgz:

```
tar xvzf multicell_example.tgz
cd multicell
nrnivmodl modfiles
python multi.py
python multicell_diff.py
```

3.2.9 Exporting Output to Text Format or Image

This is an example of using the AllenSDK to save a response voltage to other formats.

```
from allensdk.core.dat_utilities import \
    DatUtilities
from allensdk.core.nwb_data_set import \
    NwbDataSet
import numpy as np
import matplotlib
matplotlib.use("Agg")
import matplotlib.pyplot as plt

nwb_file = '313862020.nwb'
sweep_number = 52
dat_file = '313862020_%d.dat' % (sweep_number)

nwb = NwbDataSet(nwb_file)
sweep = nwb.get_sweep(sweep_number)

# read v and t as numpy arrays
v = sweep['response']
dt = 1.0e3 / sweep['sampling_rate']
num_samples = len(v)
t = np.arange(num_samples) * dt

# save as text file
data = np.transpose(np.vstack((t, v)))
with open (dat_file, "w") as f:
    np.savetxt(f, data)

# save image using matplotlib
fig, ax = plt.subplots(nrows=1, ncols=1)
ax.plot(t, v)
```

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```
ax.set_title("Sweep %s" % (sweep_number))
fig.savefig('out.png')
```

3.2.10 Model Description Files

Basic Structure

A model description file is simply a JSON object with several sections at the top level and an array of JSON objects within each section.

```
 {
    "cell_section": [
        {
          "name": "cell 1",
          "shape": "pyramidal"
          "position": [ 0.1, 0.2, 0.3 ]
        },
        {
          "name": "cell 2",
          "shape": "glial",
          "position": [ 0.1, 0.2, 0.3 ]
        }
    ],
    "extra": [
       { "what": "wood",
         "who": "woodchuck"
       }
    ]
}
```

Even if a section contains no objects or only one object the array brackets must be present.

Objects Within Sections

While no restrictions are enforced on what kinds of objects are stored in a section, some rules of thumb make the file easier to work with.

1. All objects within a section are the same structure. Common operations on a section are to display it as a table, iterate over it, load from or write to a spreadsheet or csv file. These operations are all easier if the section is fairly homogeneous.
2. Objects are not deeply nested. While some shallow nesting is often useful, deep nesting such as a tree structure is not recommended. It makes interoperability with other tools and data formats more difficult.
3. Arrays are allowed, though they should not be deeply nested either.
4. Object member values should be literals. Do not use pickled classes, for example.

Comment Lines

The JSON specification does not allow comments. However, the Allen SDK library applies a preprocessing stage to remove C++-style comments, so they can be used in description files.

Multi-line comments should be surrounded by /* */ and single-line comments start with //. Commented description files will not be recognized by strict json parsers unless the comments are stripped.

commented.json:

```
{
   /*
    *  multi-line comment
    */
   "section1": [
       {
          "name": "simon"  // single line comment
       }]
   }
```

Split Description Files by Section

A model description can be split into multiple files by putting some sections in one file and other sections into another file. This can be useful if you want to put a topology of cells and connections in one file and experimental conditions and stimulus in another file. The resulting structure in memory will behave the same way as if the files were not split. This allows a small experiment to be described in a single file and large experiments to be more modular.

cells.json:

```
{
   "cell_section": [
       {
         "name": "cell 1",
         "shape": "pyramidal"
         "position": [ 0.1, 0.2, 0.3 ]
       },
       {
         "name": "cell 2",
         "shape": "glial",
         "position": [ 0.1, 0.2, 0.3 ]
       }
   ]
}
```

extras.json:

```
{
    "extra": [
       {
         "what": "wood",
         "who": "woodchuck"
       }
    ]
}
```

Split Sections Between Description Files

If two description files containing the same sections are combined, the resulting description will contain objects from both files. This feature allows sub-networks to be described in separate files. The sub-networks can then be composed into a larger network with an additional description of the interconnections.

network1.json:

```
/* A self-contained sub-network */
{
    "cells": [
        { "name": "cell1" },
        { "name": "cell2" }
    ],
    /* intra-network connections /*
    "connections": [
        { "source": "cell1", "target" : "cell2" }
    ]
}
```

network2.json:

```
/* Another self-contained sub-network */
{
    "cells": [
        { "name": "cell3" },
        { "name": "cell4" }
    ],
    "connections": [
        { "source": "cell3", "target" : "cell4" }
    ]
}
```

interconnect.json:

```
{
    // the additional connections needed to
    // connect the network1 and network2
    // into a ring topology.
    "connections": [
       { "source": "cell2", "target": "cell3" },
       { "source": "cell4", "target": "cell1" }
    ]
}
```

3.2.11 Resource Manifest

JSON has many advantages. It is widely supported, readable and easy to parse and edit. As data sets get larger or specialized those advantages diminish. Large or complex models and experiments generally need more than a single model description file to completely describe an experiment. A manifest file is a way to describe all of the resources needed within the Allen SDK description format itself.

The manifest section is named "manifest" by default, though it is configurable. The objects in the manifest section each specify a directory, file, or file pattern. Files and directories may be organized in a parent-child relationship.

A Simple Manifest

This is a simple manifest file that specifies the BASEDIR directory using ".", meaning the current directory:

```
{
    "manifest": [
```

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```
        {   "key": "BASEDIR",
            "type": "dir",
            "spec": "."
        }
    ] }
}
```

Parent Child Relationships

Adding the optional "parent_key" member to a manifest object creates a parent-child relation. In this case WORKDIR will be found in "./work":

```
{
    "manifest": [
        {   "key": "BASEDIR",
            "type": "dir",
            "spec": "."
        },
        {   "key": "WORKDIR",
            "type": "dir",
            "spec": "/work",
            "parent_key": "BASEDIR"
        }
    ] }
}
```

File Spec Patterns

Files can be specified using the type "file" instead of "dir". If a sequence of many files is needed, the spec may contain patterns to indicate where the sequence number (%d) or string (%s) will be interpolated:

```
{
    "manifest": [
        {   "key": "BASEDIR",
            "type": "dir",
            "spec": "."
        },
        {
            "key": "voltage_out_cell_path",
            "type": "file",
            "spec": "v_out-cell-%d.dat",
            "parent_key": "BASEDIR"
        }
    ] }
}
```

Split Manifest Files

Manifest files can be split like any description file. This allows the specification of a general directory structure in a shared file and specific files in a separate configuration (i.e. stimulus and working directory)

Extensions

To date, manifest description files have not been used to reference URLs that provide model data, but it is a planned future use case.

3.2.12 Further Reading

- NEURON
- Python
- JSON

CHAPTER 4

Examples

Take a look at the table below for a list of SDK example notebooks and scripts.

Description	Link
Introduction to the Mouse Connectivity Atlas	Jupyter notebook (download .ipynb)
Introduction to the Cell Types Database	Jupyter notebook (download .ipynb)
Introduction to the Brain Observatory	Jupyter notebook (download .ipynb)
Brain Observatory Stimulus Manipulation	Jupyter notebook (download .ipynb)
Brain Observatory Tuning Analysis	Jupyter notebook (download .ipynb)
Brain Observatory Receptive Field Analysis	Jupyter notebook (download .ipynb)
Brain Observatory Cell Specimen ID Mapping	Jupyter notebook (download .ipynb)
Brain Observatory Monitor	Jupyter notebook (download .ipynb)
Dynamic Brain Workshop 2015 experiment detail	Jupyter notebook (download .ipynb)
Stimulating a biophysical model with a square pulse	Jupyter notebook (download .ipynb)
Using a Reference Space	Jupyter notebook (download .ipynb)
Downloading Images	Jupyter notebook (download .ipynb)
Visual Coding Neuropixels Quick Start	Jupyter notebook (download .ipynb)
Visual Coding Neuropixels Reference	Jupyter notebook (download .ipynb)

CHAPTER 5

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CHAPTER 6

allensdk package

6.1 Subpackages

6.1.1 allensdk.api package

Subpackages

allensdk.api.queries package

Submodules

allensdk.api.queries.annotated_section_data_sets_api module

class `allensdk.api.queries.annotated_section_data_sets_api.`**`AnnotatedSectionDataSetsApi`**(*base_*

Bases: *`allensdk.api.queries.rma_api.RmaApi`*

See: Searching Annotated SectionDataSets

`get_annotated_section_data_sets`(*self*, *structures*, *intensity_values=None*, *density_values=None*, *pattern_values=None*, *age_names=None*)

For a list of target structures, find the SectionDataSet that matches the parameters for intensity_values, density_values, pattern_values, and Age.

Parameters

structure_graph_id [dict of integers] what to retrieve

intensity_values [array of strings, optional] 'High','Low', 'Medium' (default)

density_values [array of strings, optional] 'High', 'Low'

pattern_values [array of strings, optional] 'Full'

age_names [array of strings, options] for example 'E11.5', '13.5'

Returns

data [dict] The parsed JSON repsonse message.

Notes

This method uses the non-RMA Annotated SectionDataSet endpoint.

get_annotated_section_data_sets_via_rma(*self*, *structures*, *intensity_values=None*, *density_values=None*, *pattern_values=None*, *age_names=None*)

For a list of target structures, find the SectionDataSet that matches the parameters for intensity_values, density_values, pattern_values, and Age.

Parameters

structure_graph_id [dict of integers] what to retrieve

intensity_values [array of strings, optional] intensity values, 'High','Low', 'Medium' (default)

density_values [array of strings, optional] density values, 'High', 'Low'

pattern_values [array of strings, optional] pattern values, 'Full'

age_names [array of strings, options] for example 'E11.5', '13.5'

Returns

data [dict] The parsed JSON response message.

Notes

This method uses the RMA endpoint to search annotated SectionDataSet data.

get_compound_annotated_section_data_sets(*self*, *queries*, *fmt='json'*)

Find the SectionDataSet that matches several annotated_section_data_sets queries linked together with a Boolean 'and' or 'or'.

Parameters

queries [array of dicts] dicts with args like build_query

fmt [string, optional] 'json' or 'xml'

Returns

data [dict] The parsed JSON repsonse message.

allensdk.api.queries.biophysical_api module

class allensdk.api.queries.biophysical_api.**BiophysicalApi**(*base_uri=None*)

Bases: *allensdk.api.queries.rma_template.RmaTemplate*

BIOPHYSICAL_MODEL_TYPE_IDS = (491455321, 329230710)

build_rma(*self*, *neuronal_model_id*, *fmt='json'*)

Construct a query to find all files related to a neuronal model.

Parameters

neuronal_model_id [integer or string representation] key of experiment to retrieve.

fmt [string, optional] json (default) or xml

Returns

string RMA query url.

`cache_data` (*self*, *neuronal_model_id*, *working_directory=None*)
Take a an experiment id, query the Api RMA to get well-known-files download the files, and store them in the working directory.

Parameters

neuronal_model_id [int or string representation] found in the neuronal_model table in the api

working_directory [string] Absolute path name where the downloaded well-known files will be stored.

`create_manifest` (*self*, *fit_path=”*, *model_type=”*, *stimulus_filename=”*, *swc_morphology_path=”*, *marker_path=”*, *sweeps=[]*)
Generate a json configuration file with parameters for a a biophysical experiment.

Parameters

fit_path [string] filename of a json configuration file with cell parameters.

stimulus_filename [string] path to an NWB file with input currents.

swc_morphology_path [string] file in SWC format.

sweeps [array of integers] which sweeps in the stimulus file are to be used.

`get_neuronal_models` (*self*, *specimen_ids*, *num_rows='all'*, *count=False*, *model_type_ids=None*, ***kwargs*)
Fetch all of the biophysically detailed model records associated with a particular specimen_id

Parameters

specimen_ids [list] One or more integer ids identifying specimen records.

num_rows [int, optional] how many records to retrieve. Default is ‘all’.

count [bool, optional] If True, return a count of the lines found by the query. Default is False.

model_type_ids [list, optional] One or more integer ids identifying categories of neuronal model. Defaults to all-active and perisomatic biophysical_models.

Returns

List of dict Each element is a biophysical model record, containing a unique integer id, the id of the associated specimen, and the id of the model type to which this model belongs.

`get_well_known_file_ids` (*self*, *neuronal_model_id*)
Query the current RMA endpoint with a neuronal_model id to get the corresponding well known file ids.

Returns

list A list of well known file id strings.

`is_well_known_file_type` (*self*, *wkf*, *name*)
Check if a structure has the expected name.

Parameters

wkf [dict] A well-known-file structure with nested type information.

name [string] The expected type name

See also:

read_json where this helper function is used.

read_json (*self*, *json_parsed_data*)
Get the list of well_known_file ids from a response body containing nested sample,microarray_slides,well_known_files.

Parameters

json_parsed_data [dict] Response from the Allen Institute Api RMA.

Returns

list of strings Well known file ids.

rma_templates = {'model_queries': [{'name': 'models_by_specimen', 'description': 's

allensdk.api.queries.brain_observatory_api module

class allensdk.api.queries.brain_observatory_api.**BrainObservatoryApi** (*base_uri=None*, *datacube_uri=None*)
Bases: *allensdk.api.queries.rma_template.RmaTemplate*

CELL_MAPPING_ID = 590985414

NWB_FILE_TYPE = 'NWBOphys'

OPHYS_ANALYSIS_FILE_TYPE = 'OphysExperimentCellRoiMetricsFile'

OPHYS_EVENTS_FILE_TYPE = 'ObservatoryEventsFile'

dataframe_query (*self*, *data*, *filters*, *primary_key*)
Given a list of dictionary records and a list of filter dictionaries, filter the records using Pandas and return the filtered set of records.

Parameters

data: list of dicts List of dictionaries

filters: list of dicts Each dictionary describes a filtering operation on a field in the dictionary. The general form is { 'field': <field>, 'op': <operation>, 'value': <filter_value(s)> }. For example, you can apply a threshold on the "osi_dg" column with something like this: { 'field': 'osi_dg', 'op': '>', 'value': 1.0 }. See _QUERY_TEMPLATES for a full list of operators.

dataframe_query_string (*self*, *filters*)
Convert a list of cell metric filter dictionaries into a Pandas query string.

filter_cell_specimens (*self*, *cell_specimens*, *ids=None*, *experiment_container_ids=None*, *include_failed=False*, *filters=None*)
Filter a list of cell specimen records returned from the get_cell_metrics method according some of their properties.

Parameters

cell_specimens: list of dicts List of records returned by the get_cell_metrics method.

ids: list of integers Return only records for cells with cell specimen ids in this list

experiment_container_ids: list of integers Return only records for cells that belong to experiment container ids in this list

include_failed: bool Whether to include cells from failed experiment containers

filters: list of dicts Custom query used to reproduce filter sets created in the Allen Brain Observatory web application. The general form is a list of dictionaries each of which describes a filtering operation based on a metric. For more information, see dataframe_query.

filter_experiment_containers(*self*, *containers*, *ids=None*, *targeted_structures=None*, *imaging_depths=None*, *cre_lines=None*, *reporter_lines=None*, *transgenic_lines=None*, *include_failed=False*, *simple=False*)

filter_experiments_and_containers(*self*, *objs*, *ids=None*, *targeted_structures=None*, *imaging_depths=None*, *cre_lines=None*, *reporter_lines=None*, *transgenic_lines=None*, *include_failed=False*)

filter_ophys_experiments(*self*, *experiments*, *ids=None*, *experiment_container_ids=None*, *targeted_structures=None*, *imaging_depths=None*, *cre_lines=None*, *reporter_lines=None*, *transgenic_lines=None*, *stimuli=None*, *session_types=None*, *include_failed=False*, *require_eye_tracking=False*, *simple=False*)

get_cell_metrics(*self*, *cell_specimen_ids=None*, **args*, ***kwargs*)
Get cell metrics by id

Parameters

cell_metrics_ids [integer or list of integers, optional] only select specific cell metric records.

Returns

dict [cell metric metadata]

get_cell_specimen_id_mapping(*self*, *file_name*, *mapping_table_id=None*)
Download mapping table from old to new cell specimen IDs.

The mapping table is a CSV file that maps cell specimen ids that have changed between processing runs of the Brain Observatory pipeline.

Parameters

file_name [string] Filename to save locally.

mapping_table_id [integer] ID of the mapping table file. Defaults to the most recent mapping table.

Returns

pandas.DataFrame Mapping table as a DataFrame.

get_column_definitions(*self*, *api_class_name=None*)
Get column definitions

Parameters

api_class_names [string or list of strings, optional] only select specific column definition records.

Returns

dict [column definition metadata]

get_experiment_container_metrics(*self*, *experiment_container_metric_ids=None*)
Get experiment container metrics by id

Parameters

isi_experiment_ids [integer or list of integers, optional] only select specific experiments.

Returns

dict [isi experiment metadata]

`get_experiment_containers`(*self*, *experiment_container_ids=None*)
Get experiment container by id

Parameters

experiment_container_ids [integer or list of integers, optional] only select specific experiment containers.

Returns

dict [experiment container metadata]

`get_isi_experiments`(*self*, *isi_experiment_ids=None*)
Get ISI Experiments by id

Parameters

isi_experiment_ids [integer or list of integers, optional] only select specific experiments.

Returns

dict [isi experiment metadata]

`get_ophys_experiments`(*self*, *ophys_experiment_ids=None*)
Get OPhys Experiments by id

Parameters

ophys_experiment_ids [integer or list of integers, optional] only select specific experiments.

Returns

dict [ophys experiment metadata]

`get_stimulus_mappings`(*self*, *stimulus_mapping_ids=None*)
Get stimulus mappings by id

Parameters

stimulus_mapping_ids [integer or list of integers, optional] only select specific stimulus mapping records.

Returns

dict [stimulus mapping metadata]

`list_column_definition_class_names`(*self*)
Get column definitions

Returns

list [api class name strings]

`list_isi_experiments`(*self*, *isi_ids=None*)
List ISI experiments available through the Allen Institute API

Parameters

neuronal_model_ids [integer or list of integers, optional] only select specific isi experiments.

Returns

dict [neuronal model metadata]

rma_templates = {'brain_observatory_queries': [{'name': 'list_isi_experiments', 'des

save_ophys_experiment_analysis_data (*self*, *ophys_experiment_id*, *file_name*)

save_ophys_experiment_data (*self*, *ophys_experiment_id*, *file_name*)

save_ophys_experiment_event_data (*self*, *ophys_experiment_id*, *file_name*)

save_ophys_experiment_eye_gaze_data (*self*, *ophys_experiment_id: int*, *ophys_session_id: int*, *file_name: str*)

simplify_experiment_containers (*self*, *containers*)

simplify_ophys_experiments (*self*, *exps*)

allensdk.api.queries.brain_observatory_api.**find_container_tags** (*container*)
Custom logic for extracting tags from donor conditions. Filtering out tissuecyte tags.

allensdk.api.queries.brain_observatory_api.**find_experiment_acquisition_age** (*exp*)

allensdk.api.queries.brain_observatory_api.**find_specimen_cre_line** (*specimen*)

allensdk.api.queries.brain_observatory_api.**find_specimen_reporter_line** (*specimen*)

allensdk.api.queries.brain_observatory_api.**find_specimen_transgenic_lines** (*specimen*)

allensdk.api.queries.cell_types_api module

class allensdk.api.queries.cell_types_api.**CellTypesApi** (*base_uri=None*)
Bases: *allensdk.api.queries.rma_api.RmaApi*

HUMAN = 'Homo Sapiens'

MARKER_FILE_TYPE = '3DNeuronMarker'

MOUSE = 'Mus musculus'

NWB_FILE_TYPE = 'NWBDownload'

SWC_FILE_TYPE = '3DNeuronReconstruction'

filter_cells (*self*, *cells*, *require_morphology*, *require_reconstruction*, *reporter_status*, *species*)
Filter a list of cell specimens to those that optionally have morphologies or have morphological reconstructions.

Parameters

cells: list List of cell metadata dictionaries to be filtered

require_morphology: boolean Filter out cells that have no morphological images.

require_reconstruction: boolean Filter out cells that have no morphological reconstructions.

reporter_status: list Filter for cells that have a particular cell reporter status

species: list Filter for cells that belong to one or more species. If None, return all. Must be one of [CellTypesApi.MOUSE, CellTypesApi.HUMAN].

filter_cells_api (*self*, *cells*, *require_morphology=False*, *require_reconstruction=False*, *reporter_status=None*, *species=None*, *simple=True*)

get_cell(*self*, *id*)
Query the API for a one cells in the Cell Types Database.

Returns

list Meta data for one cell.

get_ephys_features(*self*)
Query the API for the full table of EphysFeatures for all cells.

get_ephys_sweeps(*self*, *specimen_id*)
Query the API for a list of sweeps for a particular cell in the Cell Types Database.

Parameters

specimen_id: int Specimen ID of a cell.

Returns

list: List of sweep dictionaries belonging to a cell

get_morphology_features(*self*)
Query the API for the full table of morphology features for all cells

Notes

by default the tags column is removed because it isn't useful

list_cells(*self*, *id=None*, *require_morphology=False*, *require_reconstruction=False*, *reporter_status=None*, *species=None*)
Query the API for a list of all cells in the Cell Types Database.

Parameters

id: int ID of a cell. If not provided returns all matching cells.

require_morphology: boolean Only return cells that have morphology images.

require_reconstruction: boolean Only return cells that have morphological reconstructions.

reporter_status: list Return cells that have a particular cell reporter status.

species: list Filter for cells that belong to one or more species. If None, return all. Must be one of [CellTypesApi.MOUSE, CellTypesApi.HUMAN].

Returns

list Meta data for all cells.

list_cells_api(*self*, *id=None*, *require_morphology=False*, *require_reconstruction=False*, *reporter_status=None*, *species=None*)

save_ephys_data(*self*, *specimen_id*, *file_name*)
Save the electrophysology recordings for a cell as an NWB file.

Parameters

specimen_id: int ID of the specimen, from the Specimens database model in the Allen Institute API.

file_name: str Path to save the NWB file.

save_reconstruction(*self*, *specimen_id*, *file_name*)
Save the morphological reconstruction of a cell as an SWC file.

Parameters

specimen_id: int ID of the specimen, from the Specimens database model in the Allen Institute API.

file_name: str Path to save the SWC file.

save_reconstruction_markers(*self*, *specimen_id*, *file_name*)

Save the marker file for the morphological reconstruction of a cell. These are comma-delimited files indicating points of interest in a reconstruction (truncation points, early tracing termination, etc).

Parameters

specimen_id: int ID of the specimen, from the Specimens database model in the Allen Institute API.

file_name: str Path to save the marker file.

simplify_cells_api(*self*, *cells*)

allensdk.api.queries.connected_services module

class allensdk.api.queries.connected_services.**ConnectedServices**

Bases: `object`

A class representing a schema of informatics web services.

Notes

See Connected Services and Pipes for a human-readable list of services and parameters.

The URL format is documented at Service Pipelines.

Connected Services only include API services that are accessed via the RMA endpoint using an rma::services stage.

ARRAY = 'array'

BOOLEAN = 'boolean'

FLOAT = 'float'

INTEGER = 'integer'

STRING = 'string'

build_url(*self*, *service_name*, *kwargs*)

Create a single stage RMA url from a service name and parameters.

classmethod schema()

Dictionary of service names and parameters.

Notes

See Connected Services and Pipes for a human-readable list of connected services and their parameters.

allensdk.api.queries.glif_api module

class allensdk.api.queries.glif_api.**GlifApi**(*base_uri=None*)

Bases: *allensdk.api.queries.rma_template.RmaTemplate*

GLIF_TYPES = [395310498, 395310469, 395310475, 395310479, 471355161]

NWB_FILE_TYPE = None

cache_stimulus_file(*self, output_file_name*)

DEPRECATED Download the NWB file for the current neuronal model and save it to a file.

Parameters

output_file_name: string File name to store the NWB file.

get_ephys_sweeps(*self*)

DEPRECATED Retrieve ephys sweep information out of downloaded metadata for a neuronal model

Returns

list A list of sweeps metadata dictionaries

get_neuron_config(*self, output_file_name=None*)

DEPRECATED Retrieve a model configuration file from the API, optionally save it to disk, and return the contents of that file as a dictionary.

Parameters

output_file_name: string File name to store the neuron configuration (optional).

get_neuron_configs(*self, neuronal_model_ids=None*)

get_neuronal_model(*self, neuronal_model_id*)

DEPRECATED Query the current RMA endpoint with a neuronal_model id to get the corresponding well known files and meta data.

Returns

dict A dictionary containing

get_neuronal_model_templates(*self*)

get_neuronal_models(*self, ephys_experiment_ids=None*)

get_neuronal_models_by_id(*self, neuronal_model_ids=None*)

list_neuronal_models(*self*)

DEPRECATED Query the API for a list of all GLIF neuronal models.

Returns

list Meta data for all GLIF neuronal models.

rma_templates = {'glif_queries': [{'name': 'neuronal_model_templates', 'description'

allensdk.api.queries.grid_data_api module

class allensdk.api.queries.grid_data_api.**GridDataApi**(*resolution=None, base_uri=None*)

Bases: *allensdk.api.queries.rma_api.RmaApi*

HTTP Client for the Allen 3-D Expression Grid Data Service.

See: Downloading 3-D Expression Grid Data

DATA_MASK = 'data_mask'

DENSITY = 'density'

ENERGY = 'energy'

INJECTION_DENSITY = 'injection_density'

INJECTION_ENERGY = 'injection_energy'

INJECTION_FRACTION = 'injection_fraction'

INTENSITY = 'intensity'

PROJECTION_DENSITY = 'projection_density'

PROJECTION_ENERGY = 'projection_energy'

download_alignment3d(*self*, *section_data_set_id*, *num_rows='all'*, *count=False*, ***kwargs*)

Download the parameters of the 3D affine tranformation mapping this section data set's image-space stack to CCF-space (or vice-versa).

Parameters

section_data_set_id [int] download the parameters for this data set.

Returns

dict : parameters of this section data set's alignment3d

download_deformation_field(*self*, *section_data_set_id*, *header_path=None*, *voxel_path=None*, *voxel_type='DeformationFieldVoxels'*, *header_type='DeformationFieldHeader'*)

Download the local alignment parameters for this dataset. This a 3D vector image (3 components) describing a deformable local mapping from CCF voxels to this section data set's affine-aligned image stack.

Parameters

section_data_set_id [int]

Download the deformation field for this data set

header_path [str, optional] If supplied, the deformation field header will be downloaded to this path.

voxel_path [str, optiona] If supplied, the deformation field voxels will be downloaded to this path.

voxel_type [str] WellKnownFileType of this dataset's data file

header_type [str] WellKnownFileType of this dataset's header file

download_expression_grid_data(*self*, *section_data_set_id*, *include=None*, *path=None*)

Download in zipped metaimage format.

Parameters

section_data_set_id [integer] What to download.

include [list of strings, optional] Image volumes. 'energy' (default), 'density', 'intensity'.

path [string, optional] File name to save as.

Returns

file [3-D expression grid data packaged into a compressed archive file (.zip).]

download_gene_expression_grid_data(*self*, *section_data_set_id*, *volume_type*, *path*)
Download a metaimage file containing registered gene expression grid data

Parameters

section_data_set_id [int] Download data from this experiment

volume_type [str] Download this type of data (options are GridDataApi.ENERGY, GridDataApi.DENSITY, GridDataApi.INTENSITY)

path [str] Download to this path

download_projection_grid_data(*self*, *section_data_set_id*, *image=None*, *resolution=None*, *save_file_path=None*)
Download in NRRD format.

Parameters

section_data_set_id [integer] What to download.

image [list of strings, optional] Image volume. 'projection_density', 'projection_energy', 'injection_fraction', 'injection_density', 'injection_energy', 'data_mask'.

resolution [integer, optional] in microns. 10, 25, 50, or 100 (default).

save_file_path [string, optional] File name to save as.

Notes

See Downloading 3-D Projection Grid Data for additional documentation.

allensdk.api.queries.image_download_api module

class allensdk.api.queries.image_download_api.**ImageDownloadApi**(*base_uri=None*)
Bases: *allensdk.api.queries.rma_template.RmaTemplate*

HTTP Client to download whole or partial two-dimensional images from the Allen Institute with the SectionImage, AtlasImage and ProjectionImage Download Services.

See Downloading an Image for more documentation.

COLORMAPS = {'aba': 8, 'aibsmap_alt': 9, 'blue': 6, 'colormap': 10, 'expression':

atlas_image_query(*self*, *atlas_id*, *image_type_name=None*)
List atlas images belonging to a specified atlas

Parameters

atlas_id [integer, optional] Find images from this atlas.

image_type_name [string, optional] Restrict response to images of this type. If not provided, the query will get it from the atlas id.

Returns

list of dict : Each element is an AtlasImage record.

Notes

See Downloading Atlas Images and Graphics for additional documentation. `allensdk.api.queries.ontologies_api.OntologiesApi.get_atlases()` can also be used to list atlases along with their ids.

download_atlas_image(*self*, *atlas_image_id*, *file_path=None*, ***kwargs*)

download_image(*self*, *image_id*, *file_path=None*, *endpoint=None*, ***kwargs*)

Download whole or partial two-dimensional images from the Allen Institute with the SectionImage or AtlasImage service.

Parameters

image_id [integer] SubImage to download.

file_path [string, optional] where to put it, defaults to image_id.jpg

downsample [int, optional] Number of times to downsample the original image.

quality [int, optional] jpeg quality of the returned image, 0 to 100 (default)

expression [boolean, optional] Request the expression mask for the SectionImage.

view [string, optional] 'expression', 'projection', 'tumor_feature_annotation' or 'tumor_feature_boundary'

top [int, optional] Index of the topmost row of the region of interest.

left :int, optional Index of the leftmost column of the region of interest.

width [int, optional] Number of columns in the output image.

height [int, optional] Number of rows in the output image.

range [list of ints, optional] Filter to specify the RGB channels. low,high,low,high,low,high

colormap [list of floats, optional] Filter to specify the RGB channels. [lower_threshold,colormap] gain 0-1, colormap id is a string from ImageDownloadApi.COLORMAPS

rgb [list of floats, optional] Filter to specify the RGB channels. [red,green,blue] 0-1

contrast [list of floats, optional] Filter to specify contrast parameters. [gain,bias] 0-1

annotation [boolean, optional] Request the annotated AtlasImage

atlas [int, optional] Specify the desired Atlas' annotations.

projection [boolean, optional] Request projection for the specified image.

downsample_dimensions [boolean, optional] Indicates if the width and height should be adjusted to account for downsampling.

Returns

None the file is downloaded and saved to the path.

Notes

By default, an unfiltered full-sized image with the highest quality is returned as a download if no parameters are provided.

'downsample=1' halves the number of pixels of the original image both horizontally and vertically. range_list = kwargs.get('range', None)

Specifying 'downsample=2' quarters the height and width values.

Quality must be an integer from 0, for the lowest quality, up to as high as 100. If it is not specified, it defaults to the highest quality.

Top is specified in full-resolution (largest tier) pixel coordinates. SectionImage.y is the default value.

Left is specified in full-resolution (largest tier) pixel coordinates. SectionImage.x is the default value.

Width is specified in tier-resolution (desired tier) pixel coordinates. SectionImage.width is the default value. It is automatically adjusted when downsampled.

Height is specified in tier-resolution (desired tier) pixel coordinates. SectionImage.height is the default value. It is automatically adjusted when downsampled.

The range parameter consists of 6 comma delimited integers that define the lower (0) and upper (4095) bound for each channel in red-green-blue order (i.e. "range=0,1500,0,1000,0,4095"). The default range values can be determined by referring to the following fields on the Equalization model associated with the SectionDataSet: red_lower, red_uppper, green_lower, green_upper, blue_lower, blue_upper. For more information, see the Image Controls section of the Allen Mouse Brain Connectivity Atlas: Projection Dataset help topic. See: 'Image Download Service '<http://help.brain-map.org/display/api/Downloading+an+Image>_

download_projection_image(*self*, *projection_image_id*, *file_path=None*, ***kwargs*)

download_section_image(*self*, *section_image_id*, *file_path=None*, ***kwargs*)

get_section_data_sets_by_product(*self*, *product_ids*, *include_failed=False*, *num_rows='all'*, *count=False*, ***kwargs*)

List all of the section data sets produced as part of one or more products

Parameters

product_ids [list of int] Integer specifiers for Allen Institute products. A product is a set of related data.

include_failed [bool, optional] If True, find both failed and passed datasets. Default is False

num_rows [int, optional] how many records to retrieve. Default is 'all'.

count [bool, optional] If True, return a count of the lines found by the query. Default is False.

Returns

list of dict : Each returned element is a section data set record.

Notes

See http://api.brain-map.org/api/v2/data/query.json?criteria=model::Product for a list of products.

get_section_image_ranges(*self*, *section_image_ids*, *num_rows='all'*, *count=False*, *as_lists=True*, ***kwargs*)

Section images from the Mouse Connectivity Atlas are displayed on connectivity.brain-map.org after having been linearly windowed and leveled. This method obtains parameters defining channelwise upper and lower bounds of the windows used for one or more images.

Parameters

section_image_ids [list of int] Each element is a unique identifier for a section image.

num_rows [int, optional] how many records to retrieve. Default is 'all'.

count [bool, optional] If True, return a count of the lines found by the query. Default is False.

as_lists [bool, optional] If True, return the window parameters in a list, rather than a dict (this is the format of the range parameter on ImageDownloadApi.download_image). Default is False.

Returns

list of dict or list of list : For each section image id provided, return the window bounds for each channel.

`rma_templates = {'image_queries': [{'name': 'section_image_ranges', 'description':`

`section_image_query`(*self*, *section_data_set_id*, *num_rows='all'*, *count=False*, ***kwargs*)
List section images belonging to a specified section data set

Parameters

atlas_id [integer, optional] Find images from this section data set.

num_rows [int] how many records to retrieve. Default is 'all'

count [bool] If True, return a count of the lines found by the query.

Returns

list of dict : Each element is an SectionImage record.

Notes

The SectionDataSet model is used to represent single experiments which produce an array of images. This includes Mouse Connectivity and Mouse Brain Atlas experiments, among other projects. You may see references to the ids of experiments from those projects. These are the same as section data set ids.

allensdk.api.queries.mouse_atlas_api module

class `allensdk.api.queries.mouse_atlas_api.`**`MouseAtlasApi`**(*base_uri=None*)
Bases: *`allensdk.api.queries.reference_space_api.ReferenceSpaceApi`*, *`allensdk.api.queries.grid_data_api.GridDataApi`*

Downloads Mouse Brain Atlas grid data, reference volumes, and metadata.

`DEVMOUSE_ATLAS_PRODUCTS = (3,)`

`HUMAN_ORGANISM = (1,)`

`MOUSE_ATLAS_PRODUCTS = (1,)`

`MOUSE_ORGANISM = (2,)`

`download_expression_density`(*self*, *path*, *experiment_id*)

`download_expression_energy`(*self*, *path*, *experiment_id*)

`download_expression_intensity`(*self*, *path*, *experiment_id*)

`get_genes`(*self*, *organism_ids=None*, *chromosome_ids=None*, ***kwargs*)
Download a list of genes

Parameters

organism_ids [list of int, optional] Filter genes to those appearing in these organisms. Defaults to mouse (2).

chromosome_ids [list of int, optional] Filter genes to those appearing on these chromosomes. Defaults to all.

Returns

list of dict: Each element is a gene record, with a nested chromosome record (also a dict).

get_section_data_sets (*self*, *gene_ids=None*, *product_ids=None*, ***kwargs*)
Download a list of section data sets (experiments) from the Mouse Brain Atlas project.

Parameters

gene_ids [list of int, optional] Filter results based on the genes whose expression was characterized in each experiment. Default is all.

product_ids [list of int, optional] Filter results to a subset of products. Default is the Mouse Brain Atlas.

Returns

list of dict : Each element is a section data set record, with one or more gene records nested in a list.

allensdk.api.queries.mouse_connectivity_api module

class allensdk.api.queries.mouse_connectivity_api.**MouseConnectivityApi** (*base_uri=None*)
Bases: *allensdk.api.queries.reference_space_api.ReferenceSpaceApi*, *allensdk.api.queries.grid_data_api.GridDataApi*

HTTP Client for the Allen Mouse Brain Connectivity Atlas.

See: Mouse Connectivity API

PRODUCT_IDS = [5, 31]

build_reference_aligned_image_channel_volumes_url (*self*, *data_set_id*)
Construct url to download the red, green, and blue channels aligned to the 25um adult mouse brain reference space volume.

Parameters

data_set_id [integerallensdk.api.queries] aka attachable_id

Notes

See: Reference-aligned Image Channel Volumes for additional documentation.

calculate_injection_centroid (*self*, *injection_density*, *injection_fraction*, *resolution=25*)
Compute the centroid of an injection site.

Parameters

injection_density: np.ndarray The injection density volume of an experiment

injection_fraction: np.ndarray The injection fraction volume of an experiment

download_data_mask (*self*, *path*, *experiment_id*, *resolution*)

download_injection_density (*self*, *path*, *experiment_id*, *resolution*)

download_injection_fraction(*self*, *path*, *experiment_id*, *resolution*)

download_projection_density(*self*, *path*, *experiment_id*, *resolution*)

download_reference_aligned_image_channel_volumes(*self*, *data_set_id*, *save_file_path=None*)

Returns

The well known file is downloaded

experiment_correlation_search(*self*, ***kwargs*)

Select a seed experiment and a domain over which the similarity comparison is to be made.

Parameters

row [integer] SectionDataSet.id to correlate against.

structures [list of integers or strings, optional] Integer Structure.id or String Structure.acronym.

hemisphere [string, optional] Use 'right' or 'left'. Defaults to both hemispheres.

transgenic_lines [list of integers or strings, optional] Integer TransgenicLine.id or String TransgenicLine.name. Specify ID 0 to exclude all TransgenicLines.

injection_structures [list of integers or strings, optional] Integer Structure.id or String Structure.acronym.

primary_structure_only [boolean, optional]

product_ids [list of integers, optional] Integer Product.id

start_row [integer, optional] For paging purposes. Defaults to 0.

num_rows [integer, optional] For paging purposes. Defaults to 2000.

Notes

See Correlation Search and service::mouse_connectivity_correlation.

experiment_injection_coordinate_search(*self*, ***kwargs*)

User specifies a seed location within the 3D reference space. The service returns a rank list of experiments by distance of its injection site to the specified seed location.

Parameters

seed_point [list of floats] The coordinates of a point in 3-D SectionDataSet space.

transgenic_lines [list of integers or strings, optional] Integer TransgenicLine.id or String TransgenicLine.name. Specify ID 0 to exclude all TransgenicLines.

injection_structures [list of integers or strings, optional] Integer Structure.id or String Structure.acronym.

primary_structure_only [boolean, optional]

product_ids [list of integers, optional] Integer Product.id

start_row [integer, optional] For paging purposes. Defaults to 0.

num_rows [integer, optional] For paging purposes. Defaults to 2000.

Notes

See Injection Coordinate Search and service::mouse_connectivity_injection_coordinate.

experiment_source_search(*self*, ***kwargs*)

Search over the whole projection signal statistics dataset to find experiments with specific projection profiles.

Parameters

injection_structures [list of integers or strings] Integer Structure.id or String Structure.acronym.

target_domain [list of integers or strings, optional] Integer Structure.id or String Structure.acronym.

injection_hemisphere [string, optional] 'right' or 'left', Defaults to both hemispheres.

target_hemisphere [string, optional] 'right' or 'left', Defaults to both hemispheres.

transgenic_lines [list of integers or strings, optional] Integer TransgenicLine.id or String TransgenicLine.name. Specify ID 0 to exclude all TransgenicLines.

injection_domain [list of integers or strings, optional] Integer Structure.id or String Structure.acronym.

primary_structure_only [boolean, optional]

product_ids [list of integers, optional] Integer Product.id

start_row [integer, optional] For paging purposes. Defaults to 0.

num_rows [integer, optional] For paging purposes. Defaults to 2000.

Notes

See Source Search, Target Search, and service::mouse_connectivity_injection_structure.

experiment_spatial_search(*self*, ***kwargs*)

Displays all SectionDataSets with projection signal density >= 0.1 at the seed point. This service also returns the path along the most dense pixels from the seed point to the center of each injection site..

Parameters

seed_point [list of floats] The coordinates of a point in 3-D SectionDataSet space.

transgenic_lines [list of integers or strings, optional] Integer TransgenicLine.id or String TransgenicLine.name. Specify ID 0 to exclude all TransgenicLines.

section_data_sets [list of integers, optional] Ids to filter the results.

injection_structures [list of integers or strings, optional] Integer Structure.id or String Structure.acronym.

primary_structure_only [boolean, optional]

product_ids [list of integers, optional] Integer Product.id

start_row [integer, optional] For paging purposes. Defaults to 0.

num_rows [integer, optional] For paging purposes. Defaults to 2000.

Notes

See Spatial Search and service::mouse_connectivity_target_spatial.

get_experiment_detail(*self*, *experiment_id*)
Retrieve the experiments data.

get_experiments(*self*, *structure_ids*, ***kwargs*)
Fetch experiment metadata from the Mouse Brain Connectivity Atlas.

Parameters

structure_ids [integer or list, optional] injection structure

Returns

url [string] The constructed URL

get_experiments_api(*self*)
Fetch experiment metadata from the Mouse Brain Connectivity Atlas via the ApiConnectivity table.

Returns

url [string] The constructed URL

get_manual_injection_summary(*self*, *experiment_id*)
Retrieve manual injection summary.

get_projection_image_info(*self*, *experiment_id*, *section_number*)
Fetch meta-information of one projection image.

Parameters

experiment_id [integer]

section_number [integer]

Notes

See: image examples under Experimental Overview and Metadata for additional documentation. Download the image using `allensdk.api.queries.image_download_api.ImageDownloadApi.download_section_image()`

get_reference_aligned_image_channel_volumes_url(*self*, *data_set_id*)
Retrieve the download link for a specific data set. Notes —– See Reference-aligned Image Channel Volumes for additional documentation.

get_structure_unionizes(*self*, *experiment_ids*, *is_injection=None*, *structure_name=None*, *structure_ids=None*, *hemisphere_ids=None*, *normalized_projection_volume_limit=None*, *include=None*, *debug=None*, *order=None*)

allensdk.api.queries.ontologies_api module

class allensdk.api.queries.ontologies_api.**OntologiesApi**(*base_uri=None*)
Bases: `allensdk.api.queries.rma_template.RmaTemplate`

See: Atlas Drawings and Ontologies

get_atlases(*self*)

get_atlases_table(*self*, *atlas_ids=None*, *brief=True*)

List Atlases available through the API with associated ontologies and structure graphs.

Parameters

atlas_ids [integer or list of integers, optional] only select specific atlases

brief [boolean, optional] True (default) requests only name and id fields.

Returns

dict [atlas metadata]

Notes

This query is based on the table of available Atlases. See also: Class: Atlas

get_structure_graphs(*self*)

get_structure_sets(*self*, *structure_set_ids=None*)

get_structures(*self*, *structure_graph_ids=None*, *structure_graph_names=None*, *structure_set_ids=None*, *structure_set_names=None*, *order=['structures.graph_order']*, *num_rows='all'*, *count=False*, ***kwargs*)

Retrieve data about anatomical structures.

Parameters

structure_graph_ids [int or list of ints, optional] database keys to get all structures in particular graphs

structure_graph_names [string or list of strings, optional] list of graph names to narrow the query

structure_set_ids [int or list of ints, optional] database keys to get all structures in a particular set

structure_set_names [string or list of strings, optional] list of set names to narrow the query.

order [list of strings] list of RMA order clauses for sorting

num_rows [int] how many records to retrieve

Returns

dict the parsed json response containing data from the API

Notes

Only one of the methods of limiting the query should be used at a time.

get_structures_with_sets(*self*, *structure_graph_ids*, *order=['structures.graph_order']*, *num_rows='all'*, *count=False*, ***kwargs*)

Download structures along with the sets to which they belong.

Parameters

structure_graph_ids [int or list of int] Only fetch structure records from these graphs.

order [list of strings] list of RMA order clauses for sorting

num_rows [int] how many records to retrieve

Returns

dict the parsed json response containing data from the API

rma_templates = {'ontology_queries': [{'name': 'structures_by_graph_ids', 'descripti

unpack_structure_set_ancestors (*self*, *structure_dataframe*)
Convert a slash-separated structure_id_path field to a list.

Parameters

structure_dataframe [DataFrame] structure data from the API

Returns

None A new column is added to the dataframe containing the ancestor list.

allensdk.api.queries.reference_space_api module

class allensdk.api.queries.reference_space_api.**ReferenceSpaceApi** (*base_uri=None*)
Bases: *allensdk.api.queries.rma_api.RmaApi*

ARA_NISSL = 'ara_nissl'

AVERAGE_TEMPLATE = 'average_template'

CCF_2015 = 'annotation/ccf_2015'

CCF_2016 = 'annotation/ccf_2016'

CCF_2017 = 'annotation/ccf_2017'

CCF_VERSION_DEFAULT = 'annotation/ccf_2017'

DEVMOUSE_2012 = 'annotation/devmouse_2012'

MOUSE_2011 = 'annotation/mouse_2011'

VOXEL_RESOLUTION_100_MICRONS = 100

VOXEL_RESOLUTION_10_MICRONS = 10

VOXEL_RESOLUTION_25_MICRONS = 25

VOXEL_RESOLUTION_50_MICRONS = 50

build_volumetric_data_download_url (*self*, *data_path*, *file_name*, *voxel_resolution=None*, *release=None*, *coordinate_framework=None*)
Construct url to download 3D reference model in NRRD format.

Parameters

data_path [string] 'average_template', 'ara_nissl', 'annotation/ccf_{year}', 'annotation/mouse_2011', or 'annotation/devmouse_2012'

voxel_resolution [int] 10, 25, 50 or 100

coordinate_framework [string] 'mouse_ccf' (default) or 'mouse_annotation'

Notes

See: 3-D Reference Models for additional documentation.

download_annotation_volume (*self*, *ccf_version*, *resolution*, *file_name*)
Download the annotation volume at a particular resolution.

Parameters

ccf_version: string Which reference space version to download. Defaults to "annotation/ccf_2017"

resolution: int Desired resolution to download in microns. Must be 10, 25, 50, or 100.

file_name: string Where to save the annotation volume.

Note: the parameters must be used as positional parameters, not keywords

`download_mouse_atlas_volume`(*self*, *age*, *volume_type*, *file_name*)

Download a reference volume (annotation, grid annotation, atlas volume) from the mouse brain atlas project

Parameters

age [str] Specify a mouse age for which to download the reference volume

volume_type [str] Specify the type of volume to download

file_name [str] Specify the path to the downloaded volume

`download_structure_mask`(*self*, *structure_id*, *ccf_version*, *resolution*, *file_name*)

Download an indicator mask for a specific structure.

Parameters

structure_id [int] Unique identifier for the annotated structure

ccf_version [string] Which reference space version to download. Defaults to "annotation/ccf_2017"

resolution [int] Desired resolution to download in microns. Must be 10, 25, 50, or 100.

file_name [string] Where to save the downloaded mask.

`download_structure_mesh`(*self*, *structure_id*, *ccf_version*, *file_name*)

Download a Wavefront obj file containing a triangulated 3d mesh built from an annotated structure.

Parameters

structure_id [int] Unique identifier for the annotated structure

ccf_version [string] Which reference space version to download. Defaults to "annotation/ccf_2017"

file_name [string] Where to save the downloaded mask.

`download_template_volume`(*self*, *resolution*, *file_name*)

Download the registration template volume at a particular resolution.

Parameters

resolution: int Desired resolution to download in microns. Must be 10, 25, 50, or 100.

file_name: string Where to save the registration template volume.

`download_volumetric_data`(*self*, *data_path*, *file_name*, *voxel_resolution=None*, *save_file_path=None*, *release=None*, *coordinate_framework=None*)

Download 3D reference model in NRRD format.

Parameters

data_path [string] 'average_template', 'ara_nissl', 'annotation/ccf_{year}', 'annotation/mouse_2011', or 'annotation/devmouse_2012'

file_name [string] server-side file name. 'annotation_10.nrrd' for example.

voxel_resolution [int] 10, 25, 50 or 100

coordinate_framework [string] ‘mouse_ccf’ (default) or ‘mouse_annotation’

Notes

See: 3-D Reference Models for additional documentation.

allensdk.api.queries.rma_api module

class allensdk.api.queries.rma_api.**RmaApi**(*base_uri=None*)

Bases: *allensdk.api.api.Api*

See: RESTful Model Access (RMA)

ALL = 'all'

COUNT = 'count'

CRITERIA = 'rma::criteria'

DEBUG = 'debug'

EQ = '$eq'

EXCEPT = 'except'

EXCPT = 'excpt'

FALSE = 'false'

INCLUDE = 'rma::include'

IS = '$is'

MODEL = 'model::'

NUM_ROWS = 'num_rows'

ONLY = 'only'

OPTIONS = 'rma::options'

ORDER = 'order'

PIPE = 'pipe::'

PREVIEW = 'preview'

SERVICE = 'service::'

START_ROW = 'start_row'

TABULAR = 'tabular'

TRUE = 'true'

build_query_url(*self*, *stage_clauses*, *fmt='json'*)

Combine one or more RMA query stages into a single RMA query.

Parameters

stage_clauses [list of strings] subqueries

fmt [string, optional] json (default), xml, or csv

Returns

string complete RMA url

`build_schema_query`(*self*, *clazz=None*, *fmt='json'*)
Build the URL that will fetch the data schema.

Parameters

clazz [string, optional] Name of a specific class or None (default).

fmt [string, optional] json (default) or xml

Returns

url [string] The constructed URL

Notes

If a class is specified, only the schema information for that class will be requested, otherwise the url requests the entire schema.

`debug_clause`(*self*, *debug_value=None*)
Construct a debug clause for use in an rma::options clause. Parameters ——— debug_value : string or boolean

True, False, None (default) or 'preview'

Returns

clause [string] The query clause for inclusion in an RMA query URL.

Notes

True will request debugging information in the response. False will request no debugging information. None will return an empty clause. 'preview' will request debugging information without the query being run.

`filter`(*self*, *key*, *value*)
serialize a single RMA query filter clause.

Parameters

key [string] keys for narrowing a query.

value [string] value for narrowing a query.

Returns

string a single filter clause for an RMA query string.

`filters`(*self*, *filters*)
serialize RMA query filter clauses.

Parameters

filters [dict] keys and values for narrowing a query.

Returns

string filter clause for an RMA query string.

`get_schema`(*self*, *clazz=None*)
Retrieve schema information.

model_query (*self*, **args*, ***kwargs*)
Construct and execute a model stage of an RMA query string.

Parameters

model [string] The top level data type

filters [dict] key, value comparisons applied to the top-level model to narrow the results.

criteria [string] raw RMA criteria clause to choose what object are returned

include [string] raw RMA include clause to return associated objects

only [list of strings, optional] to be joined into an rma::options only filter to limit what data is returned

except [list of strings, optional] to be joined into an rma::options except filter to limit what data is returned

excpt [list of strings, optional] synonym for except parameter to avoid a reserved word conflict.

tabular [list of string, optional] return columns as a tabular data structure rather than a nested tree.

count [boolean, optional] False to skip the extra database count query.

debug [string, optional] 'true', 'false' or 'preview'

num_rows [int or string, optional] how many database rows are returned (may not correspond directly to JSON tree structure)

start_row [int or string, optional] which database row is start of returned data (may not correspond directly to JSON tree structure)

Notes

See RMA Path Syntax for a brief overview of the normalized RMA syntax. Normalized RMA syntax differs from the legacy syntax used in much of the RMA documentation. Using the &debug=true option with an RMA URL will include debugging information in the response, including the normalized query.

model_stage (*self*, *model*, ***kwargs*)
Construct a model stage of an RMA query string.

Parameters

model [string] The top level data type

filters [dict] key, value comparisons applied to the top-level model to narrow the results.

criteria [string] raw RMA criteria clause to choose what object are returned

include [string] raw RMA include clause to return associated objects

only [list of strings, optional] to be joined into an rma::options only filter to limit what data is returned

except [list of strings, optional] to be joined into an rma::options except filter to limit what data is returned

tabular [list of string, optional] return columns as a tabular data structure rather than a nested tree.

count [boolean, optional] False to skip the extra database count query.

debug [string, optional] 'true', 'false' or 'preview'

num_rows [int or string, optional] how many database rows are returned (may not correspond directly to JSON tree structure)

start_row [int or string, optional] which database row is start of returned data (may not correspond directly to JSON tree structure)

Notes

See RMA Path Syntax for a brief overview of the normalized RMA syntax. Normalized RMA syntax differs from the legacy syntax used in much of the RMA documentation. Using the &debug=true option with an RMA URL will include debugging information in the response, including the normalized query.

only_except_tabular_clause(*self*, *filter_type*, *attribute_list*)
Construct a clause to filter which attributes are returned for use in an rma::options clause.

Parameters

filter_type [string] 'only', 'except', or 'tabular'

attribute_list [list of strings] for example ['acronym', 'products.name', 'structure.id']

Returns

clause [string] The query clause for inclusion in an RMA query URL.

Notes

The title of tabular columns can be set by adding '+as+<title>' to the attribute. The tabular filter type requests a response that is row-oriented rather than a nested structure. Because of this, the tabular option can mask the lazy query behavior of an rma::include clause. The tabular option does not mask the inner-join behavior of an rma::include clause. The tabular filter is required for .csv format RMA requests.

options_clause(*self*, ***kwargs*)
build rma:: options clause.

Parameters

only [list of strings, optional]

except [list of strings, optional]

tabular [list of string, optional]

count [boolean, optional]

debug [string, optional] 'true', 'false' or 'preview'

num_rows [int or string, optional]

start_row [int or string, optional]

order_clause(*self*, *order_list=None*)
Construct a debug clause for use in an rma::options clause.

Parameters

order_list [list of strings] for example ['acronym', 'products.name+asc', 'structure.id+desc']

Returns

clause [string] The query clause for inclusion in an RMA query URL.

Notes

Optionally adding '+asc' (default) or '+desc' after an attribute will change the sort order.

pipe_stage(*self*, *pipe_name*, *parameters*)
Connect model and service stages via their JSON responses.

Notes

See: Service Pipelines and Connected Services and Pipes

quote_string(*self*, *the_string*)
Wrap a clause in single quotes.

Parameters

the_string [string] a clause to be included in an rma query that needs to be quoted

Returns

string input wrapped in single quotes

service_query(*self*, **args*, ***kwargs*)
Construct and Execute a single-stage RMA query to send a request to a connected service.

Parameters

service_name [string] Name of a documented connected service.

parameters [dict] key-value pairs as in the online documentation.

Notes

See: Service Pipelines and Connected Services and Pipes

service_stage(*self*, *service_name*, *parameters=None*)
Construct an RMA query fragment to send a request to a connected service.

Parameters

service_name [string] Name of a documented connected service.

parameters [dict] key-value pairs as in the online documentation.

Notes

See: Service Pipelines and Connected Services and Pipes

tuple_filters(*self*, *filters*)
Construct an RMA filter clause.

Notes

See RMA Path Syntax - Square Brackets for Filters for additional documentation.

allensdk.api.queries.rma_pager module

class allensdk.api.queries.rma_pager.**RmaPager**

Bases: object

static pager(*fn*, **args*, ***kwargs*)

allensdk.api.queries.rma_pager.**pageable**(*total_rows=None*, *num_rows=None*)

allensdk.api.queries.rma_template module

class allensdk.api.queries.rma_template.**RmaTemplate**(*base_uri=None*, *query_manifest=None*)

Bases: *allensdk.api.queries.rma_api.RmaApi*

See: Atlas Drawings and Ontologies

template_query(*self*, *template_name*, *entry_name*, ***kwargs*)

to_filter_rhs(*self*, *rhs*)

allensdk.api.queries.svg_api module

class allensdk.api.queries.svg_api.**SvgApi**(*base_uri=None*)

Bases: *allensdk.api.api.Api*

build_query(*self*, *section_image_id*, *groups=None*, *download=False*)

Build the URL that will fetch meta data for the specified structure.

Parameters

section_image_id [integer] Key of the object to be retrieved.

groups [array of integers] Keys of the group labels to filter the svg types that are returned.

Returns

url [string] The constructed URL

download_svg(*self*, *section_image_id*, *groups=None*, *file_path=None*)

Download the svg file

get_svg(*self*, *section_image_id*, *groups=None*)

Get the svg document.

allensdk.api.queries.synchronization_api module

class allensdk.api.queries.synchronization_api.**SynchronizationApi**(*base_uri=None*)

Bases: *allensdk.api.api.Api*

HTTP client for image synchronization services uses the image alignment results from the Informatics Data Processing Pipeline. Note: all locations on SectionImages are reported in pixel coordinates and all locations in 3-D ReferenceSpaces are reported in microns.

See Image to Image Synchronization for additional documentation.

get_image_to_atlas(*self*, *section_image_id*, *x*, *y*, *atlas_id*)

For a specified Atlas, find the closest annotated SectionImage and (x,y) location as defined by a seed SectionImage and seed (x,y) location.

Parameters

section_image_id [integer] Seed for spatial sync.

x [float] Pixel coordinate of the seed location in the seed SectionImage.

y [float] Pixel coordinate of the seed location in the seed SectionImage.

atlas_id [int] Target Atlas for image sync.

Returns

dict The parsed json response

`get_image_to_image`(*self*, *section_image_id*, *x*, *y*, *section_data_set_ids*)
For a list of target SectionDataSets, find the closest SectionImage and (x,y) location as defined by a seed SectionImage and seed (x,y) pixel location.

Parameters

section_image_id [integer] Seed for spatial sync.

x [float] Pixel coordinate of the seed location in the seed SectionImage.

y [float] Pixel coordinate of the seed location in the seed SectionImage.

section_data_set_ids [list of integers] Target SectionDataSet IDs for image sync.

Returns

dict The parsed json response

`get_image_to_image_2d`(*self*, *section_image_id*, *x*, *y*, *section_image_ids*)
For a list of target SectionImages, find the closest (x,y) location as defined by a seed SectionImage and seed (x,y) location.

Parameters

section_image_id [integer] Seed for image sync.

x [float] Pixel coordinate of the seed location in the seed SectionImage.

y [float] Pixel coordinate of the seed location in the seed SectionImage.

section_image_ids [list of ints] Target SectionImage IDs for image sync.

Returns

dict The parsed json response

`get_image_to_reference`(*self*, *section_image_id*, *x*, *y*)
For a specified SectionImage and (x,y) location, return the (x,y,z) location in the ReferenceSpace of the associated SectionDataSet.

Parameters

section_image_id [integer] Seed for image sync.

x [float] Pixel coordinate on the specified SectionImage.

y [float] Pixel coordinate on the specified SectionImage.

Returns

dict The parsed json response

`get_reference_to_image`(*self*, *reference_space_id*, *x*, *y*, *z*, *section_data_set_ids*)
For a list of target SectionDataSets, find the closest SectionImage and (x,y) location as defined by a (x,y,z) location in a specified ReferenceSpace.

Parameters

reference_space_id [integer] Seed for spatial sync.

x [float] Coordinate (in microns) of the seed location in the seed ReferenceSpace.

y [float] Coordinate (in microns) of the seed location in the seed ReferenceSpace.

z [float] Coordinate (in microns) of the seed location in the seed ReferenceSpace.

section_data_set_ids [list of ints] Target SectionDataSets IDs for image sync.

Returns

dict The parsed json response

`get_structure_to_image`(*self*, *section_data_set_id*, *structure_ids*)
For a list of target structures, find the closest SectionImage and (x,y) location as defined by the centroid of each Structure.

Parameters

section_data_set_id [integer] primary key

structure_ids [list of integers] primary key

Returns

dict The parsed json response

allensdk.api.queries.tree_search_api module

class `allensdk.api.queries.tree_search_api.`**`TreeSearchApi`**(*base_uri=None*)
Bases: *`allensdk.api.api.Api`*

See Searching a Specimen or Structure Tree for additional documentation.

`get_tree`(*self*, *kind*, *db_id*, *ancestors=None*, *descendants=None*)
Fetch meta data for the specified structure or specimen.

Parameters

kind [string] ‘Structure’ or ‘Specimen’

db_id [integer] The id of the structure or specimen to search.

ancestors [boolean, optional] whether to include ancestors in the response (defaults to False)

descendants [boolean, optional] whether to include descendants in the response (defaults to False)

Returns

dict parsed json response data

Module contents

Submodules

allensdk.api.api module

class `allensdk.api.api.`**`Api`**(*api_base_url_string=None*)
Bases: `object`

`cleanup_truncated_file`(*self*, *file_path*)
Helper for removing files.

Parameters

file_path [string] Absolute path including the file name to remove.

`construct_well_known_file_download_url`(*self*, *well_known_file_id*)
Join data api endpoint and id.

Parameters

well_known_file_id [integer or string representing an integer] well known file id

Returns

string the well-known-file download url for the current api api server

See also:

`retrieve_file_over_http` Can be used to retrieve the file from the url.

`default_api_url = 'http://api.brain-map.org'`

`do_query`(*self*, *url_builder_fn*, *json_traversal_fn*, **args*, ***kwargs*)
Bundle an query url construction function with a corresponding response json traversal function.

Parameters

url_builder_fn [function] A function that takes parameters and returns an rma url.

json_traversal_fn [function] A function that takes a json-parsed python data structure and returns data from it.

post [boolean, optional kwarg] True does an HTTP POST, False (default) does a GET

args [arguments] Arguments to be passed to the url builder function.

kwargs [keyword arguments] Keyword arguments to be passed to the rma builder function.

Returns

any type The data extracted from the json response.

Examples

A simple Api subclass example.

`do_rma_query`(*self*, *rma_builder_fn*, *json_traversal_fn*, **args*, ***kwargs*)
Bundle an RMA query url construction function with a corresponding response json traversal function.

..note:: Deprecated in AllenSDK 0.9.2 *do_rma_query* will be removed in AllenSDK 1.0, it is replaced by *do_query* because the latter is more general.

Parameters

rma_builder_fn [function] A function that takes parameters and returns an rma url.

json_traversal_fn [function] A function that takes a json-parsed python data structure and returns data from it.

args [arguments] Arguments to be passed to the rma builder function.

kwargs [keyword arguments] Keyword arguments to be passed to the rma builder function.

Returns

any type The data extracted from the json response.

Examples

A simple Api subclass example.

`download_url = 'http://download.alleninstitute.org'`

`json_msg_query` (*self*, *url*, *dataframe=False*)

Common case where the url is fully constructed and the response data is stored in the 'msg' field.

Parameters

url [string] Where to get the data in json form

dataframe [boolean] True converts to a pandas dataframe, False (default) doesn't

Returns

dict or DataFrame returned data; type depends on dataframe option

`load_api_schema` (*self*)

Download the RMA schema from the current RMA endpoint

Returns

dict the parsed json schema message

Notes

This information and other Allen Brain Atlas Data Portal Data Model documentation is also available as a Class Hierarchy and Class List.

`read_data` (*self*, *parsed_json*)

Return the message data from the parsed query.

Parameters

parsed_json [dict] A python structure corresponding to the JSON data returned from the API.

Notes

See API Response Formats - Response Envelope for additional documentation.

`retrieve_file_over_http` (*self*, *url*, *file_path*, *zipped=False*)

Get a file from the data api and save it.

Parameters

url [string] Url[R099781a1d33c-1]_ from which to get the file.

file_path [string] Absolute path including the file name to save.

zipped [bool, optional] If true, assume that the response is a zipped directory and attempt to extract contained files into the directory containing file_path. Default is False.

See also:

construct_well_known_file_download_url Can be used to construct the url.

References

[1]

retrieve_parsed_json_over_http(*self*, *url*, *post=False*)
Get the document and put it in a Python data structure

Parameters

url [string] Full API query url.

post [boolean] True does an HTTP POST, False (default) encodes the URL and does a GET

Returns

dict Result document as parsed by the JSON library.

retrieve_xml_over_http(*self*, *url*)
Get the document and put it in a Python data structure

Parameters

url [string] Full API query url.

Returns

string Unparsed xml string.

set_api_urls(*self*, *api_base_url_string*)
Set the internal RMA and well known file download endpoint urls based on a api server endpoint.

Parameters

api_base_url_string [string] url of the api to point to

set_default_working_directory(*self*, *working_directory*)
Set the working directory where files will be saved.

Parameters

working_directory [string] the absolute path string of the working directory.

allensdk.api.api.**stream_file_over_http**(*url*, *file_path*, *timeout=(9.05, 31.1)*)
Supply an http get request and stream the response to a file.

Parameters

url [str] Send the request to this url

file_path [str] Stream the response to this path

timeout [float or tuple of float, optional] Specify a timeout for the request. If a tuple, specify seperate connect and read timeouts.

allensdk.api.api.**stream_zip_directory_over_http**(*url*, *directory*, *members=None*, *timeout=(9.05, 31.1)*)
Supply an http get request and stream the response to a file.

Parameters

url [str] Send the request to this url

directory [str] Extract the response to this directory

members [list of str, optional] Extract only these files

timeout [float or tuple of float, optional] Specify a timeout for the request. If a tuple, specify seperate connect and read timeouts.

allensdk.api.cache module

class `allensdk.api.cache.`**`Cache`**(*manifest=None*, *cache=True*, *version=None*, ***kwargs*)

Bases: `object`

`add_manifest_paths`(*self*, *manifest_builder*)

Add cache-class specific paths to the manifest. In derived classes, should call super.

`build_manifest`(*self*, *file_name*)

Creation of default path specifications.

Parameters

file_name [string] where to save it

static `cache_csv`()

static `cache_csv_dataframe`()

static `cache_csv_json`()

static `cache_json`()

static `cache_json_dataframe`()

static `cacher`(*fn*, **args*, ***kwargs*)

make an rma query, save it and return the dataframe.

Parameters

fn [function reference] makes the actual query using kwargs.

path [string] where to save the data

strategy [string or None, optional] 'create' always generates the data, 'file' loads from disk, 'lazy' queries the server if no file exists, None generates the data and bypasses all caching behavior

pre [function] df|json->df|json, takes one data argument and returns filtered version, None for pass-through

post [function] df|json->?, takes one data argument and returns Object

reader [function, optional] path -> data, default NOP

writer [function, optional] path, data -> None, default NOP

kwargs [objects] passed through to the query function

Returns

Object or None data type depends on fn, reader and/or post methods.

static `csv_writer`(*pth*, *gen*)

`get_cache_path`(*self*, *file_name*, *manifest_key*, **args*)

Helper method for accessing path specs from manifest keys.

Parameters

file_name [string]

manifest_key [string]

args [ordered parameters]

Returns

string or None path

static json_remove_keys(*data*, *keys*)

static json_rename_columns(*data*, *new_old_name_tuples=None*)
Convenience method to rename columns in a pandas dataframe.

Parameters

data [dataframe] edited in place.

new_old_name_tuples [list of string tuples (new, old)]

load_csv(*self*, *path*, *rename=None*, *index=None*)
Read a csv file as a pandas dataframe.

Parameters

rename [list of string tuples (new old), optional] columns to rename

index [string, optional] post-rename column to use as the row label.

load_json(*self*, *path*, *rename=None*, *index=None*)
Read a json file as a pandas dataframe.

Parameters

rename [list of string tuples (new old), optional] columns to rename

index [string, optional] post-rename column to use as the row label.

load_manifest(*self*, *file_name*, *version=None*)
Read a keyed collection of path specifications.

Parameters

file_name [string] path to the manifest file

Returns

Manifest

manifest_dataframe(*self*)
Convenience method to view manifest as a pandas dataframe.

static nocache_dataframe()

static nocache_json()

static pathfinder(*file_name_position*, *secondary_file_name_position=None*, *path_keyword=None*)
helper method to find path argument in legacy methods written prior to the @cacheable decorator. Do not use for new @cacheable methods.

Parameters

file_name_position [integer] zero indexed position in the decorated method args where file path may be found.

secondary_file_name_position [integer] zero indexed position in the decorated method args where tha file path may be found.

path_keyword [string] kwarg that may have the file path.

Notes

This method is only intended to provide backward-compatibility for some methods that otherwise do not follow the path conventions of the @cacheable decorator.

static remove_keys(*data*, *keys=None*)
DataFrame version

static rename_columns(*data*, *new_old_name_tuples=None*)
Convenience method to rename columns in a pandas dataframe.

Parameters

data [dataframe] edited in place.

new_old_name_tuples [list of string tuples (new, old)]

wrap(*self*, *fn*, *path*, *cache*, *save_as_json=True*, *return_dataframe=False*, *index=None*, *rename=None*, ***kwargs*)
make an rma query, save it and return the dataframe.

Parameters

fn [function reference] makes the actual query using kwargs.

path [string] where to save the data

cache [boolean] True will make the query, False just loads from disk

save_as_json [boolean, optional] True (default) will save data as json, False as csv

return_dataframe [boolean, optional] True will cast the return value to a pandas dataframe, False (default) will not

index [string, optional] column to use as the pandas index

rename [list of string tuples, optional] (new, old) columns to rename

kwargs [objects] passed through to the query function

Returns

dict or DataFrame data type depends on return_dataframe option.

Notes

Column renaming happens after the file is reloaded for json

allensdk.api.cache.**cacheable**(*strategy=None*, *pre=None*, *writer=None*, *reader=None*, *post=None*, *pathfinder=None*)
decorator for rma queries, save it and return the dataframe.

Parameters

fn [function reference] makes the actual query using kwargs.

path [string] where to save the data

strategy [string or None, optional] 'create' always gets the data from the source (server or generated), 'file' loads from disk, 'lazy' creates the data and saves to file if no file exists, None queries the server and bypasses all caching behavior

pre [function] df|json->df|json, takes one data argument and returns filtered version, None for pass-through

post [function] df|json->?, takes one data argument and returns Object

reader [function, optional] path -> data, default NOP

writer [function, optional] path, data -> None, default NOP

kwargs [objects] passed through to the query function

Returns

dict or DataFrame data type depends on dataframe option.

Notes

Column renaming happens after the file is reloaded for json

`allensdk.api.cache.`**`get_default_manifest_file`**(*cache_name*)

`allensdk.api.cache.`**`memoize`**(*f*)

Creates an unbound cache of function calls and results. Note that arguments of different types are not cached separately (so f(3.0) and f(3) are not treated as distinct calls)

Arguments to the cached function must be hashable.

View the cache size with f.cache_size(). Clear the cache with f.cache_clear(). Access the underlying function with f.__wrapped__.

allensdk.api.caching_utilities module

`allensdk.api.caching_utilities.`**`call_caching`**(*fetch: Callable[[], ~Q], write: Callable[[~Q], NoneType], read: Union[Callable[[], ~P], NoneType] = None, pre_write: Union[Callable[[~Q], ~Q], NoneType] = None, cleanup: Union[Callable[[], NoneType], NoneType] = None, lazy: bool = True, num_tries: int = 1, failure_message: str = ”*) → Union[~P, NoneType]

Access data, caching on a local store for future accesses.

Parameters

fetch : Function which pulls data from a remote/expensive source.

write : Function which stores data in a local/inexpensive store.

read : Function which pulls data from a local/inexpensive store.

pre_write : Function applied to obtained data after fetching, but before writing.

cleanup : Function for fixing a failed fetch. e.g. unlinking a partially downloaded file. Exceptions raised by cleanup are not themselves handled

lazy : If True, attempt to read the data from the local/inexpensive store before fetching it. If False, forcibly fetch from the remote/expensive store.

num_tries : How many fetches to attempt before (re)raising an exception. A fetch is failed if reading the result raises an exception.

failure_message : Provides additional context in the event of a failed download. Emitted when retrying, and when a fetch failure occurs after tries are exhausted

Returns

The result of calling read

allensdk.api.caching_utilities.**one_file_call_caching**(*path: Union[pathlib.Path, str], fetch: Callable[[], ~Q], write: Callable[[Union[pathlib.Path, str], ~Q], NoneType], read: Union[Callable[[Union[pathlib.Path, str]], ~P], NoneType] = None, pre_write: Union[Callable[[~Q], ~Q], NoneType] = None, cleanup: Union[Callable[[], NoneType], NoneType] = None, lazy: bool = True, num_tries: int = 1, failure_message: str = ''*) → Union[~P, NoneType]

A call_caching variant where the local store is a single file. See call_caching for complete documentation.

Parameters

path : Path at which the data will be stored

Module contents

Subclasses of allensdk.api.api.Api to implement specific queries to the Allen Brain Atlas Data Portal.

6.1.2 allensdk.brain_observatory package

Subpackages

allensdk.brain_observatory.behavior package

Subpackages

allensdk.brain_observatory.behavior.behavior_ophys_api package

Submodules

allensdk.brain_observatory.behavior.behavior_ophys_api.behavior_ophys_nwb_api module

Module contents

class allensdk.brain_observatory.behavior.behavior_ophys_api.**BehaviorOphysApiBase**

Bases: object

get_average_projection(*self*)

get_cell_specimen_table(*self*)

get_corrected_fluorescence_traces(*self*)

get_dff_traces(*self*)

get_licks(*self*)

get_max_projection(*self*)

get_metadata(*self*)

get_motion_correction(*self*)

get_ophys_experiment_id(*self*) → int

get_ophys_timestamps(*self*)

get_rewards(*self*)

get_running_data_df(*self*)

get_running_speed(*self*)

get_segmentation_mask_image(*self*)

get_stimulus_presentations(*self*)

get_stimulus_templates(*self*)

get_stimulus_timestamps(*self*)

get_task_parameters(*self*)

get_trials(*self*)

allensdk.brain_observatory.behavior.internal package

Submodules

allensdk.brain_observatory.behavior.internal.behavior_base module

class `allensdk.brain_observatory.behavior.internal.behavior_base.`**BehaviorBase**

Bases: `abc.ABC`

Abstract base class implementing required methods for interacting with behavior session data.

Child classes should be instantiated with a fetch API that implements these methods.

get_licks(*self*) → pandas.core.frame.DataFrame

Get lick data from pkl file.

Returns

np.ndarray A dataframe containing lick timestamps.

get_rewards(*self*) → pandas.core.frame.DataFrame

Get reward data from pkl file.

Returns

pd.DataFrame A dataframe containing timestamps of delivered rewards.

get_running_data_df(*self*) → pandas.core.frame.DataFrame

Get running speed data.

Returns

pd.DataFrame Dataframe containing various signals used to compute running speed.

get_running_speed(*self*) → allensdk.brain_observatory.running_speed.RunningSpeed
Get running speed using timestamps from self.get_stimulus_timestamps.

NOTE: Do not correct for monitor delay.

Returns

RunningSpeed (NamedTuple with two fields)

timestamps [np.ndarray] Timestamps of running speed data samples

values [np.ndarray] Running speed of the experimental subject (in cm / s).

get_stimulus_presentations(*self*) → pandas.core.frame.DataFrame
Get stimulus presentation data.

NOTE: Uses timestamps that do not account for monitor delay.

Returns

pd.DataFrame Table whose rows are stimulus presentations (i.e. a given image, for a given duration, typically 250 ms) and whose columns are presentation characteristics.

get_stimulus_templates(*self*) → Dict[str, numpy.ndarray]
Get stimulus templates (movies, scenes) for behavior session.

Returns

Dict[str, np.ndarray] A dictionary containing the stimulus images presented during the session. Keys are data set names, and values are 3D numpy arrays.

get_stimulus_timestamps(*self*) → numpy.ndarray
Get stimulus timestamps from pkl file.

NOTE: Located with behavior_session_id

Returns

np.ndarray Timestamps associated with stimulus presentations on the monitor that do no account for monitor delay.

get_task_parameters(*self*) → dict
Get task parameters from pkl file.

Returns

dict A dictionary containing parameters used to define the task runtime behavior.

get_trials(*self*) → pandas.core.frame.DataFrame
Get trials from pkl file

Returns

pd.DataFrame A dataframe containing behavioral trial start/stop times, and trial data

allensdk.brain_observatory.behavior.internal.behavior_ophys_base module

class allensdk.brain_observatory.behavior.internal.behavior_ophys_base.**BehaviorOphysBase**
Bases: *allensdk.brain_observatory.behavior.internal.behavior_base.BehaviorBase*

Abstract base class implementing required methods for interacting with behavior+ophys session data.

Child classes should be instantiated with a fetch API that implements these methods. Both fetch API and session object should inherit from this base.

get_average_projection(*self*) → allensdk.brain_observatory.behavior.image_api.Image
Get an image whose values are the average obtained values at each pixel of the ophys movie over time.

Returns

allensdk.brain_observatory.behavior.image_api.Image: Array-like interface to avg projection image data and metadata.

get_cell_specimen_table(*self*) → pandas.core.frame.DataFrame
Get a cell specimen dataframe containing ROI information about cells identified in an ophys experiment.

Returns

pd.DataFrame Cell ROI information organized into a dataframe. Index is the cell ROI IDs.

get_corrected_fluorescence_traces(*self*) → pandas.core.frame.DataFrame
Get motion-corrected fluorescence traces.

Returns

pd.DataFrame Motion-corrected fluorescence traces organized into a dataframe. Index is the cell ROI IDs.

get_dff_traces(*self*) → pandas.core.frame.DataFrame
Get a table of delta fluorescence over fluorescence traces.

Returns

pd.DataFrame The traces of dff (normalized fluorescence) organized into a dataframe. Index is the cell ROI IDs.

get_max_projection(*self*) → allensdk.brain_observatory.behavior.image_api.Image
Get an image whose values are the maximum obtained values at each pixel of the ophys movie over time.

Returns

allensdk.brain_observatory.behavior.image_api.Image: Array-like interface to max projection image data and metadata.

get_metadata(*self*) → dict
Get behavior+ophys session metadata.

Returns

dict A dictionary of session-specific metadata.

get_motion_correction(*self*) → pandas.core.frame.DataFrame
Get motion correction trace data.

Returns

pd.DataFrame A dataframe containing trace data used during motion correction computation.

get_ophys_timestamps(*self*) → numpy.ndarray
Get optical physiology frame timestamps.

Returns

np.ndarray Timestamps associated with frames captured by the microscope.

get_raw_stimulus_timestamps(*self*) → numpy.ndarray
Get raw stimulus timestamps.

Returns

np.ndarray Timestamps associated with stimulus presentations on the monitor without accounting for monitor delay.

get_stimulus_presentations(*self*) → pandas.core.frame.DataFrame
Get stimulus presentation data.

NOTE: Uses monitor delay corrected stimulus timestamps.

Returns

pd.DataFrame Table whose rows are stimulus presentations (i.e. a given image, for a given duration, typically 250 ms) and whose columns are presentation characteristics.

get_stimulus_timestamps(*self*) → numpy.ndarray
Get stimulus timestamps.

Returns

np.ndarray Timestamps associated with stimulus presentations on the monitor after accounting for monitor delay.

allensdk.brain_observatory.behavior.internal.behavior_project_base module

Module contents

allensdk.brain_observatory.behavior.sync package

Submodules

allensdk.brain_observatory.behavior.sync.process_sync module

allensdk.brain_observatory.behavior.sync.process_sync.**calculate_delay**(*sync_data*, *stim_vsync_fall*, *sample_frequency*)

allensdk.brain_observatory.behavior.sync.process_sync.**filter_digital**(*rising*, *falling*, *threshold=0.0001*)

Removes short transients from digital signal.

Rising and falling should be same length and units in seconds.

Kwargs: threshold (float): transient width

Module contents

Created on Sunday July 15 2018

@author: marinag

allensdk.brain_observatory.behavior.sync.**get_stimulus_rebase_function**(*data*, *stimulus_timestamps_no_monitor_d*

allensdk.brain_observatory.behavior.sync.**get_sync_data**(*sync_path*)

allensdk.brain_observatory.behavior.write_nwb package

Module contents

Submodules

allensdk.brain_observatory.behavior.behavior_data_session module

allensdk.brain_observatory.behavior.behavior_ophys_analysis module

allensdk.brain_observatory.behavior.behavior_ophys_session module

allensdk.brain_observatory.behavior.behavior_project_cache module

allensdk.brain_observatory.behavior.behavior_project_lims_api module

allensdk.brain_observatory.behavior.criteria module

Functions for calculating mtrain state transitions. If criteria are met, return true. Otherwise, return false.

`allensdk.brain_observatory.behavior.criteria.`**`consistency_is_key`**`(`*session_summary*`)`

need some way to judge consistency of various parameters

- dprime
- num trials
- hit rate
- fa rate
- lick timing

`allensdk.brain_observatory.behavior.criteria.`**`consistent_behavior_within_session`**`(`*session_summa*

need some way to measure consistent performance within a session

- compare peak to overall dprime?
- variance in rolling window dprime?

`allensdk.brain_observatory.behavior.criteria.`**`meets_engagement_criteria`**`(`*session_summary*`)`

Returns true if engagement criteria were met for the past 3 days, else false. Args:

> session_summary (pd.DataFrame): Pandas dataframe with daily values for ‘dprime_peak’ and ‘num_engaged_trials’, ordered ascending by training day, for at least 3 days. If dataframe is not properly ordered, criterion may not be correctly calculated. This function does not sort the data to preserve prior behavior (sorting column was not required by mtrain function) The mtrain implementation created the required columns if they didn’t exist, so a more informative error is raised here to assist end-users in debugging.

Returns: bool: True if criterion is met, False otherwise

`allensdk.brain_observatory.behavior.criteria.`**`mostly_useful`**`(`*trials*`)`

Returns True if fewer than half the trial time on the last day were aborted trials.

> Args: trials (pd.DataFrame): Pandas dataframe with columns ‘training_day’, ‘trial_type’, and ‘trial_length’.

Returns: bool: True if criterion is met, False otherwise

`allensdk.brain_observatory.behavior.criteria.`**`n_complete`**`(`*threshold*, *count*`)`

For compatibility with original API. If count >= threshold, return True. Otherwise return False. Args:

threshold (numeric): Threshold for the count to meet. count (numeric): The count to compare to the threshold.

Returns: True if count >= threshold, otherwise False.

`allensdk.brain_observatory.behavior.criteria.`**`no_response_bias`**`(`*session_summary*`)`

the mouse meets this criterion if their last session exhibited a response bias between 10% and 90%

Args: session_summary (pd.DataFrame): Pandas dataframe with daily values for 'response_bias', ordered ascending by training day, for at least 1 day. If dataframe is not properly ordered, criterion may not be correctly calculated. This function does not sort the data to preserve prior behavior (sorting column was not required by mtrain function). The mtrain implementation created the required columns if they didn't exist, so a more informative error is raised here to assist end-users in debugging.

Returns: bool: True if criterion is met, False otherwise

`allensdk.brain_observatory.behavior.criteria.`**`summer_over`**`(`*trials*`)`

Returns true if the maximum value of 'training_day' in the trials dataframe is >= 40, else false.

`allensdk.brain_observatory.behavior.criteria.`**`two_out_of_three_aint_bad`**`(`*session_summary*`)`

Returns true if 2 of the last 3 days showed a peak d-prime above 2.

Args: session_summary (pd.DataFrame): Pandas dataframe with daily values for 'dprime_peak', ordered ascending by training day, for at least the past 3 days. If dataframe is not properly ordered, criterion may not be correctly calculated. This function does not sort the data to preserve prior behavior (sorting column was not required by mtrain function). The mtrain implementation created the required columns if they didn't exist, so a more informative error is raised here to assist end-users in debugging.

Returns: bool: True if criterion is met, False otherwise

`allensdk.brain_observatory.behavior.criteria.`**`whole_lotta_trials`**`(`*session_summary*`)`

Mouse meets this criterion if the last session has more than 300 trials. Args:

session_summary (pd.DataFrame): Pandas dataframe with daily values for 'num_contingent_trials', ordered ascending by training day, for at least 1 day. If dataframe is not properly ordered, criterion may not be correctly calculated. This function does not sort the data to preserve prior behavior (sorting column was not required by mtrain function). The mtrain implementation created the required columns if they didn't exist, so a more informative error is raised here to assist end-users in debugging.

Returns: bool: True if criterion is met, False otherwise

`allensdk.brain_observatory.behavior.criteria.`**`yesterday_was_good`**`(`*session_summary*`)`

Returns true if the last day showed a peak d-prime above 2 Args:

session_summary (pd.DataFrame): Pandas dataframe with daily values for 'dprime_peak', ordered ascending by training day, for at least 1 day. If dataframe is not properly ordered, criterion may not be correctly calculated. This function does not sort the data to preserve prior behavior (sorting column was not required by mtrain function). The mtrain implementation created the required columns if they didn't exist, so a more informative error is raised here to assist end-users in debugging.

Returns: bool: True if criterion is met, False otherwise

allensdk.brain_observatory.behavior.dprime module

allensdk.brain_observatory.behavior.dprime.**get_catch_responses**(*correct_reject=None, false_alarm=None, aborted=None*)

allensdk.brain_observatory.behavior.dprime.**get_dprime**(*hit_rate, fa_rate, sliding_window=100*)

calculates the d-prime for a given hit rate and false alarm rate https://en.wikipedia.org/wiki/Sensitivity_index Parameters ——— hit_rate : float

rate of hits in the True class

fa_rate [float] rate of false alarms in the False class

limits [tuple, optional] limits on extreme values, which distort. default: (0.01,0.99)

d_prime

allensdk.brain_observatory.behavior.dprime.**get_false_alarm_rate**(*correct_reject=None, false_alarm=None, aborted=None, sliding_window=100*)

allensdk.brain_observatory.behavior.dprime.**get_go_responses**(*hit=None, miss=None, aborted=None*)

allensdk.brain_observatory.behavior.dprime.**get_hit_rate**(*hit=None, miss=None, aborted=None, sliding_window=100*)

allensdk.brain_observatory.behavior.dprime.**get_rolling_dprime**(*rolling_hit_rate, rolling_fa_rate, sliding_window=100*)

allensdk.brain_observatory.behavior.dprime.**get_trial_count_corrected_false_alarm_rate**(*correc false_a aborte slid- ing_wi*

allensdk.brain_observatory.behavior.dprime.**get_trial_count_corrected_hit_rate**(*hit=None, miss=None, aborted=None, sliding_window=100*)

allensdk.brain_observatory.behavior.dprime.**trial_number_limit**(*p, N*)

allensdk.brain_observatory.behavior.image_api module

class allensdk.brain_observatory.behavior.image_api.**Image**

Bases: `tuple`

Describes a 2D Image

data [np.ndarray] Image data points

spacing [tuple] Spacing describes the physical size of each pixel

unit [str] Physical unit of the spacing (currently constrained to be isotropic)

data
Alias for field number 0

spacing
Alias for field number 1

unit
Alias for field number 2

class allensdk.brain_observatory.behavior.image_api.**ImageApi**
Bases: object

static deserialize(*img*)

static serialize(*data*, *spacing*, *unit*)

allensdk.brain_observatory.behavior.metadata_processing module

allensdk.brain_observatory.behavior.metadata_processing.**get_task_parameters**(*data*)

allensdk.brain_observatory.behavior.mtrain module

allensdk.brain_observatory.behavior.rewards_processing module

allensdk.brain_observatory.behavior.rewards_processing.**get_rewards**(*data*, *stimulus_rebase_function*)

allensdk.brain_observatory.behavior.running_processing module

allensdk.brain_observatory.behavior.running_processing.**calc_deriv**(*x*, *time*)

allensdk.brain_observatory.behavior.running_processing.**deg_to_dist**(*speed_deg_per_s*)
takes speed in degrees per second converts to radians multiplies by radius (in cm) to get linear speed in cm/s

allensdk.brain_observatory.behavior.running_processing.**get_running_df**(*data*, *time*)

allensdk.brain_observatory.behavior.schemas module

allensdk.brain_observatory.behavior.session_metrics module

allensdk.brain_observatory.behavior.session_metrics.**num_contingent_trials**(*session_trials*)
Returns the number of "go" and "catch" trials in a training session dataframe. Args:

session_trials (pandas.DataFrame): a pandas.DataFrame describing behavior training trials, with the string column "trial_type" describing the type of trial.

Returns (int): Number of "go" and "catch" trials `allensdk.brain_observatory.behavior.session_metrics.`**`response_bias`**`(`*trials*, *detect_col*, *trial_types=('go', 'catch')*`)`

Calculate the response bias for a subset of trial types from a behavioral training dataframe. Args:

trials (pandas.DataFrame): Dataframe containing trial-level information from a behavioral training session. Required columns: "trial_type", *detect_col*.

detect_col (str): Name of column containing boolean or numeric codings (0/1) for whether or not the mouse had a response.

trial_types (iterable<str>): Iterable containing string trial types to check for the response bias. Trials of types not included in this iterable will be ignored. Default=("go", "catch")

Return: The response bias (or average value of the *detect_col*) for trials in *trial_types*.

allensdk.brain_observatory.behavior.stimulus_processing module

`allensdk.brain_observatory.behavior.stimulus_processing.`**`convert_filepath_caseinsensitive`**`(`*fil*

`allensdk.brain_observatory.behavior.stimulus_processing.`**`get_images_dict`**`(`*pkl*`)`

`allensdk.brain_observatory.behavior.stimulus_processing.`**`get_stimulus_metadata`**`(`*pkl*`)`

`allensdk.brain_observatory.behavior.stimulus_processing.`**`get_stimulus_presentations`**`(`*data*, *stimulus_timesta*

`allensdk.brain_observatory.behavior.stimulus_processing.`**`get_stimulus_templates`**`(`*pkl*`)`

`allensdk.brain_observatory.behavior.stimulus_processing.`**`get_visual_stimuli_df`**`(`*data*, *time*`)`

`allensdk.brain_observatory.behavior.stimulus_processing.`**`load_pickle`**`(`*pstream*`)`

`allensdk.brain_observatory.behavior.stimulus_processing.`**`unpack_change_log`**`(`*change*`)`

allensdk.brain_observatory.behavior.trial_masks module

`allensdk.brain_observatory.behavior.trial_masks.`**`contingent_trials`**`(`*trials*`)`

GO & CATCH trials only

Parameters

trials [pandas DataFrame] dataframe of trials

Returns

mask [pandas Series of booleans, indexed to trials DataFrame]

`allensdk.brain_observatory.behavior.trial_masks.`**`reward_rate`**`(`*trials*, *thresh=2.0*`)`

masks trials where the reward rate (per minute) is below some threshold.

This de facto omits trials in which the animal was not licking for extended periods or periods when they were licking indiscriminantly.

Parameters

trials [pandas DataFrame] dataframe of trials

thresh [float, optional] threshold under which trials will not be included, default: 2.0

Returns

mask [pandas Series of booleans, indexed to trials DataFrame]

`allensdk.brain_observatory.behavior.trial_masks.`**`trial_types`**(*trials*, *trial_types*)
only include trials of certain trial types

Parameters

trials [pandas DataFrame] dataframe of trials

trial_types [list or other iterator]

Returns

mask [pandas Series of booleans, indexed to trials DataFrame]

allensdk.brain_observatory.behavior.trials_processing module

`allensdk.brain_observatory.behavior.trials_processing.`**`calculate_reward_rate`**(*response_latency=No start-time=None, win-dow=0.75, trial_window=25, ini-tial_trials=10*)

`allensdk.brain_observatory.behavior.trials_processing.`**`categorize_one_trial`**(*tr*)

`allensdk.brain_observatory.behavior.trials_processing.`**`colormap`**(*trial_type*, *response_type*)

`allensdk.brain_observatory.behavior.trials_processing.`**`create_extended_trials`**(*trials=None*, *meta-data=None*, *time=None*, *licks=None*)

`allensdk.brain_observatory.behavior.trials_processing.`**`data_to_licks`**(*data*, *time*)

`allensdk.brain_observatory.behavior.trials_processing.`**`data_to_metadata`**(*data*, *time*)

`allensdk.brain_observatory.behavior.trials_processing.`**`find_licks`**(*reward_times*, *licks*, *win-dow=3.5*)

`allensdk.brain_observatory.behavior.trials_processing.`**`get_change_time_frame_response_latenc`**

`allensdk.brain_observatory.behavior.trials_processing.`**`get_even_sampling`**(*data*)
Get status of even_sampling

Parameters

data: Mapping foraging2 experiment output data

Returns

bool: True if even_sampling is enabled allensdk.brain_observatory.behavior.trials_processing.**get_extended_trials**(*data*, *time=None*)

allensdk.brain_observatory.behavior.trials_processing.**get_image_info_from_trial**(*trial_log*, *ti*)

allensdk.brain_observatory.behavior.trials_processing.**get_mouse_id**(*exp_data*)

allensdk.brain_observatory.behavior.trials_processing.**get_ori_info_from_trial**(*trial_log*, *ti*)

allensdk.brain_observatory.behavior.trials_processing.**get_params**(*exp_data*)

allensdk.brain_observatory.behavior.trials_processing.**get_response_latency**(*change_event*, *trial*)

allensdk.brain_observatory.behavior.trials_processing.**get_response_type**(*trials*)

allensdk.brain_observatory.behavior.trials_processing.**get_stimulus_attr_changes**(*stim_dict*, *change_frame*, *first_frame*, *last_frame*)

Notes

- assumes only two stimuli are ever shown
- converts attr_names to lowercase
- gets the net attr changes from the start of a trial to the end of a trial

allensdk.brain_observatory.behavior.trials_processing.**get_time**(*exp_data*)

allensdk.brain_observatory.behavior.trials_processing.**get_trial_image_names**(*trial*, *stimuli*)

allensdk.brain_observatory.behavior.trials_processing.**get_trial_lick_times**(*lick_times*, *start_time*, *stop_time*)

extract lick times in time range

allensdk.brain_observatory.behavior.trials_processing.**get_trial_reward_time**(*rebased_reward_time*
start_time, *stop_time*)

extract reward times in time range

allensdk.brain_observatory.behavior.trials_processing.**get_trial_timing**(*event_dict*, *stimulus_presentations_df*, *licks*, *go*, *catch*, *auto_rewarded*, *hit*, *false_alarm*)

extract trial timing data

content of trial log depends on trial type depends on trial type and response type go, catch, auto_rewarded, hit, false_alarm must be passed as booleans to disambiguate trial and response type

on *go* or *auto_rewarded* trials, extract the stimulus_changed time on *catch* trials, extract the sham_change time on *hit* trials, extract the response time from the *hit* entry in event_dict on *false_alarm* trials, extract the response time from the *false_alarm* entry in event_dict

`allensdk.brain_observatory.behavior.trials_processing.`**`get_trials`**(*data*, *licks_df*, *rewards_df*, *stimulus_presentations_df*, *rebase*)

`allensdk.brain_observatory.behavior.trials_processing.`**`get_trials_v0`**(*data*, *time*)

`allensdk.brain_observatory.behavior.trials_processing.`**`local_time`**(*iso_timestamp*, *timezone=None*)

`allensdk.brain_observatory.behavior.trials_processing.`**`resolve_initial_image`**(*stimuli*, *start_frame*)

Attempts to resolve the initial image for a given start_frame for a trial

Parameters

stimuli: Mapping foraging2 shape stimuli mapping

start_frame: int start frame of the trial

Returns

initial_image_category_name: str stimulus category of initial image

initial_image_group: str group name of the initial image

initial_image_name: str name of the initial image

`allensdk.brain_observatory.behavior.trials_processing.`**`trial_data_from_log`**(*trial*)

Infer trial logic from trial log. Returns a dictionary.

- reward volume: volume of water delivered on the trial, in mL

Each of the following values is boolean:

Trial category values are mutually exclusive * go: trial was a go trial (trial with a stimulus change) * catch: trial was a catch trial (trial with a sham stimulus change)

stimulus_change/sham_change are mutually exclusive * stimulus_change: did the stimulus change (True on 'go' trials) * sham_change: stimulus did not change, but response was evaluated (True on 'catch' trials)

Each trial can be one (and only one) of the following: * hit (stimulus changed, animal responded in response window) * miss (stimulus changed, animal did not respond in response window) * false_alarm (stimulus did not change, animal responded in response window) * correct_reject (stimulus did not change, animal did not respond in response window) * aborted (animal responded before change time) * auto_rewarded (reward was automatically delivered following the change. This will bias the animals choice and should not be categorized as hit/miss)

`allensdk.brain_observatory.behavior.trials_processing.`**`validate_trial_condition_exclusivity`**

ensure that only one of N possible mutually exclusive trial conditions is True

allensdk.brain_observatory.behavior.validation module

Module contents

allensdk.brain_observatory.ecephys package

Subpackages

allensdk.brain_observatory.ecephys.align_timestamps package

Submodules

allensdk.brain_observatory.ecephys.align_timestamps.barcode module

`allensdk.brain_observatory.ecephys.align_timestamps.barcode.`**`extract_barcodes_from_times`**`(`*on_ off_ in- ter_ bar bar cod nbi*

Read barcodes from timestamped rising and falling edges.

Parameters

on_times [numpy.ndarray] Timestamps of rising edges on the barcode line

off_times [numpy.ndarray] Timestamps of falling edges on the barcode line

inter_barcode_interval [numeric, optional] Minimun duration of time between barcodes.

bar_duration [numeric, optional] A value slightly shorter than the expected duration of each bar

barcode_duration_ceiling [numeric, optional] The maximum duration of a single barcode

nbits [int, optional] The bit-depth of each barcode

Returns

barcode_start_times [list of numeric] For each detected barcode, the time at which that barcode started

barcodes [list of int] For each detected barcode, the value of that barcode as an integer.

Notes

ignores first code in prod (ok, but not intended) ignores first on pulse (intended - this is needed to identify that a barcode is starting)

`allensdk.brain_observatory.ecephys.align_timestamps.barcode.`**`find_matching_index`**`(`*master_barcode probe_barcodes align- ment_type='sta*

Given a set of barcodes for the master clock and the probe clock, find the indices of a matching set, either starting from the beginning or the end of the list.

Parameters

master_barcodes [np.ndarray] barcode values on the master line. One per barcode

probe_barcodes [np.ndarray] barcode values on the probe line. One per barcode

alignment_type [string] ‘start’ or ‘end’

Returns

master_barcode_index [int] matching index for master barcodes (None if not found)

probe_barcode_index [int] matching index for probe barcodes (None if not found)

`allensdk.brain_observatory.ecephys.align_timestamps.barcode.`**`get_probe_time_offset`**(*master_time mas- ter_barcodes probe_times probe_barco acq_start_in lo- cal_probe_r*

Time offset between master clock and recording probes. For converting probe time to master clock.

Parameters

master_times [np.ndarray] start times of barcodes (according to the master clock) on the master line. One per barcode.

master_barcodes [np.ndarray] barcode values on the master line. One per barcode

probe_times [np.ndarray] start times (according to the probe clock) of barcodes on the probe line. One per barcode

probe_barcodes [np.ndarray] barcode values on the probe_line. One per barcode

acq_start_index [int] sample index of probe acquisition start time

local_probe_rate [float] the probe’s apparent sampling rate

Returns

total_time_shift [float] Time at which the probe started acquisition, assessed on the master clock. If < 0, the probe started earlier than the master line.

probe_rate [float] The probe’s sampling rate, assessed on the master clock

master_endpoints [iterable] Defines the start and end times of the sync interval on the master clock

`allensdk.brain_observatory.ecephys.align_timestamps.barcode.`**`linear_transform_from_interval`**

Find a scale and translation which aligns two 1d segments

Parameters

master [iterable] Pair of floats defining the master interval. Order is [start, end].

probe [iterable] Pair of floats defining the probe interval. Order is [start, end].

Returns

scale [float] Scale factor. If > 1.0, the probe clock is running fast compared to the master clock. If < 1.0, the probe clock is running slow.

translation [float] If > 0, the probe clock started before the master clock. If > 0, after.

Notes

solves (master + translation) * scale = probe for scale and translation

`allensdk.brain_observatory.ecephys.align_timestamps.barcode.`**`match_barcodes`**(*master_times*, *master_barcodes*, *probe_times*, *probe_barcodes*)

Given sequences of barcode values and (local) times on a probe line and a master line, find the time points on each clock corresponding to the first and last shared barcode.

If there's only one probe barcode, only the first matching timepoint is returned.

Parameters

master_times [np.ndarray] start times of barcodes (according to the master clock) on the master line. One per barcode.

master_barcodes [np.ndarray] barcode values on the master line. One per barcode

probe_times [np.ndarray] start times (according to the probe clock) of barcodes on the probe line. One per barcode

probe_barcodes [np.ndarray] barcode values on the probe_line. One per barcode

Returns

probe_interval [np.ndarray] Start and end times of the matched interval according to the probe_clock.

master_interval [np.ndarray] Start and end times of the matched interval according to the master clock

allensdk.brain_observatory.ecephys.align_timestamps.barcode_sync_dataset module

`class` `allensdk.brain_observatory.ecephys.align_timestamps.barcode_sync_dataset.`**`BarcodeSyncD`**

Bases: *`allensdk.brain_observatory.ecephys.file_io.ecephys_sync_dataset.EcephysSyncDataset`*

`barcode_line`

Obtain the index of the barcode line for this dataset.

`extract_barcodes`(*self*, ***barcode_kwargs*)

Read barcodes and their times from this dataset's barcode line.

Parameters

****barcode_kwargs :** Will be passed to .barcode.extract_barcodes_from_times

Returns

times [np.ndarray] The start times of each detected barcode.

codes [np.ndarray] The values of each detected barcode

`get_barcode_table`(*self*, ***barcode_kwargs*)

A convenience method for getting barcode times and codes in a dictionary.

Notes

This method is deprecated!

allensdk.brain_observatory.ecephys.align_timestamps.channel_states module

`allensdk.brain_observatory.ecephys.align_timestamps.channel_states.`**`extract_barcodes_from_st`**

Obtain barcodes from timestamped rising/falling edges.

Parameters

channel_states [numpy.ndarray] Rising and falling edges, denoted 1 and -1

timestamps [numpy.ndarray] Sample index of each event.

sampling_rate [numeric] Samples / second

****barcode_kwargs :** Additional parameters describing the barcodes.

`allensdk.brain_observatory.ecephys.align_timestamps.channel_states.`**`extract_splits_from_stat`**

Obtain barcodes from timestamped rising/falling edges.

Parameters

channel_states [numpy.ndarray] Rising and falling edges, denoted 1 and -1

timestamps [numpy.ndarray] Sample index of each event.

sampling_rate [numeric] Samples / second

****barcode_kwargs :** Additional parameters describing the barcodes.

allensdk.brain_observatory.ecephys.align_timestamps.probe_synchronizer module

`class` `allensdk.brain_observatory.ecephys.align_timestamps.probe_synchronizer.`**`ProbeSynchroni`**

Bases: `object`

`classmethod compute`(*master_barcode_times*, *master_barcodes*, *probe_barcode_times*, *probe_barcodes*, *min_time*, *max_time*, *probe_start_index*, *local_probe_sampling_rate*)

Compute a transform from probe samples to master times by aligning barcodes.

Parameters

master_barcode_times [np.ndarray] start times of barcodes (according to the master clock) on the master line. One per barcode.

master_barcodes [np.ndarray] barcode values on the master line. One per barcode

probe_barcode_times [np.ndarray] start times (according to the probe clock) of barcodes on the probe line. One per barcode

probe_barcodes [np.ndarray] barcode values on the probe_line. One per barcode

min_time [Float] time (in seconds) of first barcode to align

max_time [Float] time (in seconds) of last barcode to align

probe_start_index [int] sample index of probe acquisition start time

local_probe_sampling_rate [float] the probe's apparent sampling rate

Returns

ProbeSynchronizer : When called, applies the transform computed here to samples on the probe clock.

`sampling_rate_scale`
The ratio of the probe's sampling rate assessed on the global clock to the probe's locally assessed sampling rate.

Module contents

allensdk.brain_observatory.ecephys.copy_utility package

Module contents

allensdk.brain_observatory.ecephys.current_source_density package

Module contents

allensdk.brain_observatory.ecephys.ecephys_project_api package

Subpackages

allensdk.brain_observatory.ecephys.ecephys_project_api.warehouse_patches package

Module contents

Submodules

allensdk.brain_observatory.ecephys.ecephys_project_api.ecephys_project_api module

class `allensdk.brain_observatory.ecephys.ecephys_project_api.ecephys_project_api.`**`EcephysPro`**
Bases: `object`

`get_channels`(*self*, *channel_ids: Union[~ArrayLike, NoneType] = None*, *probe_ids: Union[~ArrayLike, NoneType] = None*, *session_ids: Union[~ArrayLike, NoneType] = None*, *published_at: Union[str, NoneType] = None*)

`get_isi_experiments`(*self*, **args*, ***kwargs*)

`get_natural_movie_template`(*self*, *number*) → Iterable

get_natural_scene_template(*self*, *number*) → Iterable

get_probe_lfp_data(*self*, *probe_id: int*) → Iterable

get_probes(*self*, *probe_ids: Union[~ArrayLike*, *NoneType] = None*, *session_ids: Union[~ArrayLike*, *NoneType] = None*, *published_at: Union[str*, *NoneType] = None*)

get_session_data(*self*, *session_id: int*) → Iterable

get_sessions(*self*, *session_ids: Union[~ArrayLike*, *NoneType] = None*, *published_at: Union[str*, *NoneType] = None*)

get_unit_analysis_metrics(*self*, *unit_ids: Union[~ArrayLike*, *NoneType] = None*, *ecephys_session_ids: Union[~ArrayLike*, *NoneType] = None*, *session_types: Union[~ArrayLike*, *NoneType] = None*) → pandas.core.frame.DataFrame

get_units(*self*, *unit_ids: Union[~ArrayLike*, *NoneType] = None*, *channel_ids: Union[~ArrayLike*, *NoneType] = None*, *probe_ids: Union[~ArrayLike*, *NoneType] = None*, *session_ids: Union[~ArrayLike*, *NoneType] = None*, *published_at: Union[str*, *NoneType] = None*)

allensdk.brain_observatory.ecephys.ecephys_project_api.ecephys_project_fixed_api module

allensdk.brain_observatory.ecephys.ecephys_project_api.ecephys_project_lims_api module

allensdk.brain_observatory.ecephys.ecephys_project_api.ecephys_project_warehouse_api module

allensdk.brain_observatory.ecephys.ecephys_project_api.http_engine module

allensdk.brain_observatory.ecephys.ecephys_project_api.rma_engine module

allensdk.brain_observatory.ecephys.ecephys_project_api.utilities module

Module contents

allensdk.brain_observatory.ecephys.ecephys_session_api package

Submodules

allensdk.brain_observatory.ecephys.ecephys_session_api.ecephys_nwb1_session_api module

allensdk.brain_observatory.ecephys.ecephys_session_api.ecephys_nwb_session_api module

allensdk.brain_observatory.ecephys.ecephys_session_api.ecephys_session_api module

Module contents

allensdk.brain_observatory.ecephys.file_io package

Submodules

allensdk.brain_observatory.ecephys.file_io.continuous_file module

class allensdk.brain_observatory.ecephys.file_io.continuous_file.**ContinuousFile**(*data_path*, *timestamps_path*, *total_num_chann* *dtype=<class 'numpy.int16'>*

Bases: `object`

Represents a continuous (.dat) file, and its associated timestamps

get_lfp_channel_order(*self*)
Returns the channel ordering for LFP data extracted from NPX files.

None

load(*self*, *memmap=False*, *memmap_thresh=10000000000.0*)
Reads lfp data and timestamps from the filesystem

memmap [bool, optional] If True, the returned data array will be a memory map of the file on disk. Default is True.

memmap_thresh [float, optional] Files above this size in bytes will be memory-mapped, regardless of memmap setting

allensdk.brain_observatory.ecephys.file_io.ecephys_sync_dataset module

class allensdk.brain_observatory.ecephys.file_io.ecephys_sync_dataset.**EcephysSyncDataset**
Bases: *allensdk.brain_observatory.sync_dataset.Dataset*

extract_frame_times(*self*, *strategy*, *photodiode_cycle=60*, *frame_keys=('frames', 'stim_vsync')*, *photodiode_keys=('photodiode', 'stim_photodiode')*)

extract_frame_times_from_photodiode(*self*, *photodiode_cycle=60*, *frame_keys=('frames', 'stim_vsync')*, *photodiode_keys=('photodiode', 'stim_photodiode')*)

extract_frame_times_from_vsyncs(*self*, *photodiode_cycle=60*, *frame_keys=('frames', 'stim_vsync')*, *photodiode_keys=('photodiode', 'stim_photodiode')*)

extract_led_times(*self*, *keys=('LED_sync', 'opto_trial')*, *fallback_line=18*)

classmethod factory(*path*)
Build a new SyncDataset.

Parameters

path [str] Filesystem path to the h5 file containing sync information to be loaded.

sample_frequency

allensdk.brain_observatory.ecephys.file_io.stim_file module

class allensdk.brain_observatory.ecephys.file_io.stim_file.**CamStimOnePickleStimFile**(*data*, ***kwargs*

Bases: `object`

angular_wheel_rotation
Extract the total rotation of the running wheel on each frame.

angular_wheel_velocity
Extract the mean angular velocity of the running wheel (degrees / s) for each frame.

classmethod factory(*path*, ***kwargs*)

frames_per_second
Framerate of stimulus presentation

pre_blank_sec
Time (s) before initial stimulus presentation

stimuli
List of dictionaries containing information about individual stimuli

vin

vsig
Running speed signal voltage

Module contents

allensdk.brain_observatory.ecephys.lfp_subsampling package

Submodules

allensdk.brain_observatory.ecephys.lfp_subsampling.subsampling module

allensdk.brain_observatory.ecephys.lfp_subsampling.subsampling.**remove_lfp_noise**(*lfp*, *surface_channel*, *channel_numbers*, *channel_max=384*, *channel_limit=380*)

Subtract mean of channels out of brain to remove noise

lfp [numpy.ndarray] 2D array of LFP values (time x channels)

surface_channel [int] Surface channel (relative to original probe)

channel_numbers [numpy.ndarray] Channel numbers in 'lfp' array (relative to original probe)

Returns:

lfp_noise_removed [numpy.ndarray] New 2D array of LFP values

allensdk.brain_observatory.ecephys.lfp_subsampling.subsampling.**remove_lfp_offset**(*lfp*, *sampling_frequen*
cutoff_frequency, *filter_order*)

High-pass filters LFP data to remove offset

lfp [numpy.ndarray] 2D array of LFP values (time x channels)

sampling_frequency [float] Sampling frequency in Hz

cutoff_frequency [float] Cutoff frequency for highpass filter

filter_order [int] Butterworth filter order

Returns:

lfp_filtered [numpy.ndarray] New 2D array of LFP values

`allensdk.brain_observatory.ecephys.lfp_subsampling.subsampling.`**`select_channels`**(*total_channels, surface_channel, surface_padding, start_channel_of chan- nel_stride, chan- nel_order, noisy_channels= dtype=float64), re- move_noisy_char ref- er- ence_channels=a dtype=float64), re- move_references*

Selects a subset of channels for spatial downsampling

total_channels [int] Number of channels in the original data file

surface_channel [int] Index of channel at brain surface

surface_padding [int] Number of channels above surface to save

start_channel_offset [int] First channel to save

channel_stride [int] Number of channels to skip in output

channel_order [np.ndarray] Actual order of LFP channels (needed to account for the bug in NPX extraction)

noisy_channels [numpy.ndarray] Array indicating noisy channels

remove_noisy_channels [bool] Flag to remove noisy channels

reference_channels [numpy.ndarray] Array indicating refence channels

remove_references [bool] Flag to remove reference channels

`allensdk.brain_observatory.ecephys.lfp_subsampling.subsampling.`**`subsample_lfp`**(*lfp_raw, selected_channels, subsampling_factor*)

Subsamples LFP data

lfp_raw [numpy.ndarray] 2D array of LFP values (time x channels)

selected_channels [numpy.ndarray] Indices of channels to select (spatial subsampling)

downsampling_factor [int] Factor by which to subsample in time

Returns:

lfp_subsampled [numpy.ndarray] New 2D array of LFP values

`allensdk.brain_observatory.ecephys.lfp_subsampling.subsampling.`**`subsample_timestamps`**(*timestamp sub- sam- pling_fac*

Subsamples an array of timestamps

timestamps [numpy.ndarray] 1D array of timestamp values

downsampling_factor [int] Factor by which to subsample the timestamps

Returns:

timestamps_sub [numpy.ndarray] New 1D array of timestamps

Module contents

allensdk.brain_observatory.ecephys.nwb package

Module contents

allensdk.brain_observatory.ecephys.optotagging_table package

Module contents

allensdk.brain_observatory.ecephys.stimulus_analysis package

Submodules

allensdk.brain_observatory.ecephys.stimulus_analysis.dot_motion module

allensdk.brain_observatory.ecephys.stimulus_analysis.drifting_gratings module

allensdk.brain_observatory.ecephys.stimulus_analysis.flashes module

allensdk.brain_observatory.ecephys.stimulus_analysis.natural_movies module

allensdk.brain_observatory.ecephys.stimulus_analysis.natural_scenes module

allensdk.brain_observatory.ecephys.stimulus_analysis.receptive_field_mapping module

allensdk.brain_observatory.ecephys.stimulus_analysis.static_gratings module

allensdk.brain_observatory.ecephys.stimulus_analysis.stimulus_analysis module

Module contents

allensdk.brain_observatory.ecephys.stimulus_table package

Subpackages

allensdk.brain_observatory.ecephys.stimulus_table.visualization package

Submodules

allensdk.brain_observatory.ecephys.stimulus_table.visualization.view_blocks module

Module contents

Submodules

allensdk.brain_observatory.ecephys.stimulus_table.ephys_pre_spikes module

Created on Fri Dec 16 15:11:23 2016

@author: Xiaoxuan Jia

`allensdk.brain_observatory.ecephys.stimulus_table.ephys_pre_spikes.`**`apply_display_sequence`**`(`*s*
f
s
e
d
b

Adjust raw sweep frames for a stimulus based on the display sequence for that stimulus.

Parameters

sweep_frames_table [pd.DataFrame] Each row is a sweep. Has two columns, 'start' and 'end', which describe (in frames) when that sweep began and ended.

frame_display_sequence [np.ndarray] 2D array. Rows are display intervals. The 0th column is the start frame of that interval, the 1st the end frame.

Returns

sweep_frames_table [pd.DataFrame] As above, but start and end frames have been adjusted based on the display sequence.

Notes

The frame values in the raw sweep_frames_table are given in 0-indexed offsets from the start of display for this stimulus. This domain only takes into account frames which are part of a display interval for that stimulus, so the frame ids need to be adjusted to lie on the global frame sequence.

allensdk.brain_observatory.ecephys.stimulus_table.ephys_pre_spikes.**apply_frame_times**(*stimulus frame_t frames_ ex- tra_fran map_co 'End'*))

Converts sweep times from frames to seconds.

Parameters

stimulus_table [pd.DataFrame] Rows are sweeps. Columns are stimulus parameters as well as start and end frames for each sweep.

frame_times [numpy.ndarrray] Gives the time in seconds at which each frame (indices) began.

frames_per_second [numeric, optional] If provided, and extra_frame_time is True, will be used to calculcate the extra_frame_time.

extra_frame_time [float, optional] If provided, an additional frame time will be appended. The time will be incremented by extra_frame_time from the previous last frame time, to denote the time at which the last frame ended. If False, no extra time will be appended. If None (default), the increment will be 1.0/fps.

map_columns [tuple of str, optional] Which columns to replace with times. Defaults to 'Start' and 'End

Returns

stimulus_table [pd.DataFrame] As above, but with map_columns values converted to seconds from frames.

allensdk.brain_observatory.ecephys.stimulus_table.ephys_pre_spikes.**assign_sweep_values**(*stim_ swee on=' drop tmp_*

Left joins a stimulus table to a sweep table in order to associate epochs in time with stimulus characteristics.

Parameters

stim_table [pd.DataFrame] Each row is a stimulus epoch, with start and end times and a foreign key onto a particular sweep.

sweep_table [pd.DataFrame] Each row is a sweep. Should have columns in common with the stim_table - the resulting table will use values from the sweep_table.

on [str, optional] Column on which to join.

drop [bool, optional] If True (default), the join column (argument on) will be dropped from the output.

tmp_suffix [str, optional] Will be used to identify overlapping columns. Should not appear in the name of any column in either dataframe.

allensdk.brain_observatory.ecephys.stimulus_table.ephys_pre_spikes.**build_stimuluswise_table**

Construct a table of sweeps, including their times on the experiment-global clock and the values of each relevant parameter.

Parameters

stimulus [dict] Describes presentation of a stimulus on a particular experiment. Has a number of fields, of which we are using:

stim_path [str] windows file path to the stimulus data

sweep_frames [list of lists] rows are sweeps, columns are start and end frames of that sweep (in the stimulus-specific frame domain). C-order.

sweep_order [list of int] indices are frames, values are the sweep on that frame

display_sequence [list of list]

rows are intervals in which the stimulus was displayed. Columns are start and end times (s, global) of the display. C-order.

dimnames [list of str] Names of parameters for this stimulus (such as "Contrast")

sweep_table [list of tuple] Each element is a tuple of parameter values (1 per dimname) describing a single sweep.

seconds_to_frames [function] Converts experiment seconds to frames

start_key [str, optional] key to use for start frame indices. Defaults to 'Start'

end_key [str, optional] key to use for end frame indices. Defaults to 'End'

name_key [str, optional] key to use for stimulus name annotations. Defaults to 'stimulus_name'

block_key [str, optional] key to use for the 0-index position of this stimulus block

get_stimulus_name [function | dict -> str, optional] extracts stimulus name from the stimulus dictionary. Default is read_stimulus_name_from_path

Returns

list of pandas.DataFrame : Each table corresponds to an entry in the display sequence. Rows are sweeps, columns are stimulus parameter values as well as "Start" and "End".

allensdk.brain_observatory.ecephys.stimulus_table.ephys_pre_spikes.**create_stim_table**(*stimuli*, *stim-u-lus_tabl spon-ta-neous_a sort_key block_ke in-dex_key*

Build a full stimulus table

Parameters

stimuli [list of dict] Each element is a stimulus dictionary, as provided by the stim.pkl file.

stimulus_tabler [function] A function which takes a single stimulus dictionary as its argument and returns a stimulus table dataframe.

spontaneous_activity_tabler [function] A function which takes a list of stimulus tables as arguments and returns a list of 0 or more tables describing spontaneous activity sweeps.

sort_key [str, optional] Sort the final stimulus table in ascending order by this key. Defaults to 'Start'.

Returns

stim_table_full [pandas.DataFrame] Each row is a sweep. Has columns describing (in frames) the start and end times of each sweep. Other columns describe the values of stimulus parameters on those sweeps.

allensdk.brain_observatory.ecephys.stimulus_table.ephys_pre_spikes.**make_spontaneous_activit**

Fills in frame gaps in a set of stimulus tables. Suitable for use as the spontaneous_activity_tabler in create_stim_table.

Parameters

stimulus_tables [list of pd.DataFrame] Input tables - should have start_key and end_key columns.

start_key [str, optional] Column name for the start of a sweep. Defaults to 'Start'.

end_key [str, optional] Column name for the end of a sweep. Defaults to 'End'.

duration_threshold [numeric or None] If not None (default is 0), remove spontaneous activity sweeps whose duration is less than this threshold.

Returns

list : Either empty, or contains a single pd.DataFrame. The rows of the dataframe are spontenous activity sweeps.

allensdk.brain_observatory.ecephys.stimulus_table.ephys_pre_spikes.**read_stimulus_name_from_**

Obtains a human-readable stimulus name by looking at the filename of the 'stim_path' item.

Parameters

stimulus [dict] must contain a 'stim_path' item.

Returns

str : name of stimulus

`allensdk.brain_observatory.ecephys.stimulus_table.ephys_pre_spikes.`**`split_column`**(*table*, *col- umn*, *new_columns*, *drop_old=True*

Divides a dataframe column into multiple columns.

Parameters

table [pandas.DataFrame] Columns will be drawn from and assigned to this dataframe. This dataframe will NOT be modified inplace.

column [str] This column will be split.

new_columns [dict, mapping strings to functions] Each key will be the name of a new column, while its value (a function) will be used to build the new column's values. The functions should map from a single value of the original column to a single value of the new column.

drop_old [bool, optional] If True, the original column will be dropped from the table.

Returns

table [pd.DataFrame] The modified table

allensdk.brain_observatory.ecephys.stimulus_table.naming_utilities module

`allensdk.brain_observatory.ecephys.stimulus_table.naming_utilities.`**`add_number_to_shuffled_m`**

`allensdk.brain_observatory.ecephys.stimulus_table.naming_utilities.`**`collapse_columns`**(*table*)

merge, where possible, columns that describe the same parameter. This is pretty conservative - it only matches columns by capitalization and it only overrides nans.

`allensdk.brain_observatory.ecephys.stimulus_table.naming_utilities.`**`drop_empty_columns`**(*table*)

Remove from the stimulus table columns whose values are all nan

`allensdk.brain_observatory.ecephys.stimulus_table.naming_utilities.`**`map_column_names`**(*table*, *name_ma* *ig- nore_case* allensdk.brain_observatory.ecephys.stimulus_table.naming_utilities.**map_stimulus_names**(*table*, *name_* *stim_c*

Applies a mappting to the stimulus names in a stimulus table

Parameters

table [pd.DataFrame] the input stimulus table

name_map [dict, optional] rename the stimuli according to this mapping

stim_colname: str, optional look in this column for stimulus names

allensdk.brain_observatory.ecephys.stimulus_table.naming_utilities.**standardize_movie_numbe**

Natural movie stimuli in visual coding are numbered using words, like “natural_movie_two” rather than “natural_movie_2”. This function ensures that all of the natural movie stimuli in an experiment are named by that convention.

Parameters

table [pd.DataFrame] the incoming stimulus table

movie_re [re.Pattern, optional] regex that matches movie stimulus names

numeral_re [re.Pattern, optional] regex that extracts movie numbers from stimulus names

digit_names [dict, optional] map from numerals to english words

stim_colname [str, optional] the name of the dataframe column that contains stimulus names

Returns

table [pd.DataFrame] the stimulus table with movie numerals having been mapped to english words

allensdk.brain_observatory.ecephys.stimulus_table.output_validation module

`allensdk.brain_observatory.ecephys.stimulus_table.output_validation.`**`validate_epoch_duratio`**

`allensdk.brain_observatory.ecephys.stimulus_table.output_validation.`**`validate_epoch_order`**(*ta*
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`allensdk.brain_observatory.ecephys.stimulus_table.output_validation.`**`validate_max_spontaneo`**

allensdk.brain_observatory.ecephys.stimulus_table.stimulus_parameter_extraction module

`allensdk.brain_observatory.ecephys.stimulus_table.stimulus_parameter_extraction.`**`extract_co`**

Parameters which are not set as sweep_params in the stimulus script (usually because they are not varied during the course of the session) are not output in an easily machine-readable format. This function attempts to recover them by parsing the string repr of the stimulus.

Parameters

stim_repr [str]

The repr of the camstim stimulus object. Served up per-stimulus in the stim pickle.

repr_params_re [re.Pattern] Extracts attributes as "="-seperated strings

array_re [re.Pattern] Extracts list reprs from numpy array reprs.

Returns

repr_params [dict] dictionary of paramater keys and values extracted from the stim repr. Where possible, the values are converted to native Python types.

`allensdk.brain_observatory.ecephys.stimulus_table.stimulus_parameter_extraction.`**`extract_st`** allensdk.brain_observatory.ecephys.stimulus_table.stimulus_parameter_extraction.**parse_stim_**

Read the string representation of a psychopy stimulus and extract stimulus parameters.

Parameters

stim_repr [str]

drop_params [tuple]

repr_params_re [re.Pattern]

array_re [re.Pattern]

Returns

dict : maps extracted parameter names to values

Module contents

allensdk.brain_observatory.ecephys.visualization package

Module contents

allensdk.brain_observatory.ecephys.visualization.**plot_mean_waveforms**(*mean_waveforms*, *unit_ids*, *peak_channels*)

Utility for plotting mean waveforms on each unit's peak channel

Parameters

mean_waveforms [dictionary] Maps unit ids to channelwise averege spike waveforms for those units

unit_ids [array-like] unique integer identifiers for units to be included `allensdk.brain_observatory.ecephys.visualization.`**`plot_spike_counts`**(*data_array*, *time_coords*, *cbar_label*, *title*, *xlabel='time relative to stimulus onset (s)'*, *ylabel='unit'*, *xtick_step=20*)

Utility for making a simple spike counts plot.

Parameters

data_array [xarray.DataArray] 2D data array unitwise values per time bin. See EcephysSession.sweepwise_spike_counts

`allensdk.brain_observatory.ecephys.visualization.`**`raster_plot`**(*spike_times*, *figsize=(8, 8)*, *cmap=<matplotlib.colors.ListedColormap object at 0x7f2b1ad8e198>*, *title='spike raster'*, *cycle_colors=False*)

allensdk.brain_observatory.ecephys.write_nwb package

Module contents

Submodules

allensdk.brain_observatory.ecephys.ecephys_project_cache module

allensdk.brain_observatory.ecephys.ecephys_session module

allensdk.brain_observatory.ecephys.stimulus_sync module

`allensdk.brain_observatory.ecephys.stimulus_sync.`**`allocate_by_vsync`**(*vs_diff*, *index*, *starts*, *ends*, *frame_duration*, *irregularity*, *cycle*)

`allensdk.brain_observatory.ecephys.stimulus_sync.`**`assign_to_last`**(*index*, *starts*, *ends*, *frame_duration*, *irregularity*, *cycle*) `allensdk.brain_observatory.ecephys.stimulus_sync.`**`compute_frame_times`**(*photodiode_times, frame_duration, num_frames, cycle, irregular_interval_policy=<function assign_to_last at 0x7f2ae0ef2ae8>*)

`allensdk.brain_observatory.ecephys.stimulus_sync.`**`correct_on_off_effects`**(*pd_times*)

Notes

This cannot (without additional info) determine whether an assymmetric offset is odd-long or even-long.

`allensdk.brain_observatory.ecephys.stimulus_sync.`**`estimate_frame_duration`**(*pd_times, cycle=60*)

`allensdk.brain_observatory.ecephys.stimulus_sync.`**`fix_unexpected_edges`**(*pd_times, ndevs=10, cycle=60, max_frame_offset=4*)

`allensdk.brain_observatory.ecephys.stimulus_sync.`**`flag_unexpected_edges`**(*pd_times, ndevs=10*)

`allensdk.brain_observatory.ecephys.stimulus_sync.`**`trim_border_pulses`**(*pd_times, vs_times, frame_interval=0.0166666666666, num_frames=5*)

`allensdk.brain_observatory.ecephys.stimulus_sync.`**`trimmed_stats`**(*data, pctiles=(10, 90)*)

Module contents

`allensdk.brain_observatory.ecephys.`**`get_unit_filter_value`**(*key, pop=True, replace_none=True, **source*)

allensdk.brain_observatory.extract_running_speed package

Module contents

allensdk.brain_observatory.gaze_mapping package

Module contents

allensdk.brain_observatory.nwb package

Submodules

allensdk.brain_observatory.nwb.metadata module

allensdk.brain_observatory.nwb.nwb_api module

allensdk.brain_observatory.nwb.schemas module

Module contents

allensdk.brain_observatory.ophys package

Subpackages

allensdk.brain_observatory.ophys.trace_extraction package

Module contents

Module contents

allensdk.brain_observatory.receptive_field_analysis package

Submodules

allensdk.brain_observatory.receptive_field_analysis.chisquarerf module

`allensdk.brain_observatory.receptive_field_analysis.chisquarerf.`**`NLL_to_pvalue`**(*NLLs*, *log_base=10.0*)

`allensdk.brain_observatory.receptive_field_analysis.chisquarerf.`**`build_trial_matrix`**(*LSN_templ* *num_trials* *on_off_lum* *0)*)

Construct indicator arrays for on/off pixels across trials.

Parameters

LSN_template [np.ndarray] Dimensions are (nTrials, nYPixels, nXPixels). Luminance values per pixel and trial. The size of the first dimension may be larger than the num_trials argument (in which case only the first num_trials slices will be used) but may not be smaller.

num_trials [int] The number of trials (left-justified) to build indicators for.

on_off_luminance [array-like, optional] The zeroth element is the luminance value of a pixel when on, the first when off. Defaults are [255, 0].

Returns

trial_mat [np.ndarray] Dimensions are (nYPixels, nXPixels, {on, off}, nTrials). Boolean values indicate that a pixel was on/off on a particular trial.

`allensdk.brain_observatory.receptive_field_analysis.chisquarerf.`**`chi_square_binary`**(*events*, *LSN_templa* allensdk.brain_observatory.receptive_field_analysis.chisquarerf.**chi_square_within_mask**(*exclu event tri- als_p*

Determine if cells respond preferentially to on/off pixels in a mask using a chi2 test.

Parameters

exclusion_mask [np.ndarray] Dimensions are (nYPixels, nXPixels, {on, off}). Integer indicator for INCLUSION (!) of a pixel within the testing region.

events_per_pixel [np.ndarray] Dimensions are (nCells, nYPixels, nXPixels, {on, off}). Integer values are response counts by cell to on/off luminance at each pixel.

trials_per_pixel [np.ndarray] Dimensions are (nYPixels, nXPixels, {on, off}). Integer values are counts of trials where a pixel is on/off.

Returns

p_vals [np.ndarray] One-dimensional, of length nCells. Float values are p-values for the hypothesis that a given cell has a receptive field within the exclusion mask.

chi [np.ndarray] Dimensions are (nCells, nYPixels, nXPixels, {on, off}). Values (float) are squared residual event counts divided by expected event counts.

allensdk.brain_observatory.receptive_field_analysis.chisquarerf.**deinterpolate_RF**(*rf_map*, *x_pnts*, *y_pnts*, *deg_per_pnt*)

Downsample an image

Parameters

rf_map [np.ndarray] Input image

x_pnts [np.ndarray] Count of sample points along the first (column) axis

y_pnts [np.ndarray] Count of sample points along the zeroth (row) axis

deg_per_pnt [numeric] scale factor

Returns

sampled_yx [np.ndarray] Downsampled image

allensdk.brain_observatory.receptive_field_analysis.chisquarerf.**get_disc_masks**(*LSN_template*, *ra- dius=3*, *on_luminance=2 off_luminance=0*

Obtain an indicator mask surrounding each pixel. The mask is a square, excluding pixels which are coactive on any trial with the main pixel.

Parameters

LSN_template [np.ndarray] Dimensions are (nTrials, nYPixels, nXPixels). Luminance values per pixel and trial.

radius [int] The base mask will be a box whose sides are 2 * radius + 1 in length.

on_luminance [int, optional] The value of the luminance for on trials. Default is 255

off_luminance [int, optional] The value of the luminance for off trials. Default is 0

Returns

masks [np.ndarray] Dimensions are (nYPixels, nXPixels, nYPixels, nXPixels). The first 2 dimensions describe the pixel from which the mask was computed. The last 2 serve as the dimensions of the mask images themselves. Masks are binary arrays of type float, with 1 indicating inside, 0 outside.

`allensdk.brain_observatory.receptive_field_analysis.chisquarerf.`**`get_events_per_pixel`**`(`*respons*
trial_ma

Obtain a matrix linking cellular responses to pixel activity.

Parameters

responses_np [np.ndarray] Dimensions are (nTrials, nCells). Boolean values indicate presence/absence of a response on a given trial.

trial_matrix [np.ndarray] Dimensions are (nYPixels, nXPixels, {on, off}, nTrials). Boolean values indicate that a pixel was on/off on a particular trial.

Returns

events_per_pixel [np.ndarray] Dimensions are (nCells, nYPixels, nXPixels, {on, off}). Values for each cell, pixel, and on/off state are the sum of events for that cell across all trials where the pixel was in the on/off state.

`allensdk.brain_observatory.receptive_field_analysis.chisquarerf.`**`get_expected_events_by_pixe`**

Calculate expected number of events per pixel

Parameters

exclusion_mask [np.ndarray] Dimensions are (nYPixels, nXPixels, {on, off}). Integer indicator for INCLUSION (!) of a pixel within the testing region.

events_per_pixel [np.ndarray] Dimensions are (nCells, nYPixels, nXPixels, {on, off}). Integer values are response counts by cell to on/off luminance at each pixel.

trials_per_pixel [np.ndarray] Dimensions are (nYPixels, nXPixels, {on, off}). Integer values are counts of trials where a pixel is on/off.

Returns

np.ndarray : Dimensions (nCells, nYPixels, nXPixels, {on, off}). Float values are pixelwise counts of events expected if events are evenly distributed in mask across trials.

`allensdk.brain_observatory.receptive_field_analysis.chisquarerf.`**`get_peak_significance`**`(`*chi_sq*
LSN_t
al-
pha=0

`allensdk.brain_observatory.receptive_field_analysis.chisquarerf.`**`interpolate_RF`**`(`*rf_map*,
deg_per_pnt`)`

Upsample an image

Parameters

rf_map [np.ndarray] Input image

deg_per_pnt [numeric] scale factor

Returns

interpolated [np.ndarray] Upsampled image `allensdk.brain_observatory.receptive_field_analysis.chisquarerf.`**`locate_median`**(*y*, *x*)

`allensdk.brain_observatory.receptive_field_analysis.chisquarerf.`**`pvalue_to_NLL`**(*p_values*, *max_NLL=10.0*)

`allensdk.brain_observatory.receptive_field_analysis.chisquarerf.`**`smooth_STA`**(*STA*, *gauss_std=0.75*, *total_degrees=64*)

Smooth an image by convolution with a gaussian kernel

Parameters

STA [np.ndarray] Input image

gauss_std [numeric, optional] Standard deviation of the gaussian kernel. Will be applied to the upsampled image, so units are visual degrees. Default is 0.75

total_degrees [int, optional] Size in visual degrees of the input image along its zeroth (row) axis. Used to set the scale factor for up/downsampling.

Returns

STA_smoothed [np.ndarray] Smoothed image

allensdk.brain_observatory.receptive_field_analysis.eventdetection module

`allensdk.brain_observatory.receptive_field_analysis.eventdetection.`**`detect_events`**(*data*, *cell_index*, *stimulus*, *debug_plots=Fa*

allensdk.brain_observatory.receptive_field_analysis.fit_parameters module

`allensdk.brain_observatory.receptive_field_analysis.fit_parameters.`**`add_to_fit_parameters_di`**

`allensdk.brain_observatory.receptive_field_analysis.fit_parameters.`**`compute_distance`**(*center_on*, *center_off*)

`allensdk.brain_observatory.receptive_field_analysis.fit_parameters.`**`compute_overlap`**(*data_fitted_*, *data_fitted_*

`allensdk.brain_observatory.receptive_field_analysis.fit_parameters.`**`get_gaussian_fit_single_`**

allensdk.brain_observatory.receptive_field_analysis.fitgaussian2D module

`exception` `allensdk.brain_observatory.receptive_field_analysis.fitgaussian2D.`**`GaussianFitErro`**

Bases: `RuntimeError`

`allensdk.brain_observatory.receptive_field_analysis.fitgaussian2D.`**`fitgaussian2D`**(*data*)

Fit a 2D gaussian to an image

Parameters

data [np.ndarray] input image

Returns

p2 [list] height row mean column mean row standard deviation column standard deviation rotation

Notes

see gaussian2D for details about output values

`allensdk.brain_observatory.receptive_field_analysis.fitgaussian2D.`**`gaussian2D`**(*height*, *center_x*, *center_y*, *width_x*, *width_y*, *rotation*)

Build a function which evaluates a scaled 2d gaussian pdf

Parameters

height [float] scale factor

center_x [float] first coordinate of mean

center_y [float] second coordinate of mean

width_x [float] standard deviation along x axis

width_y [float] standard deviation along y axis

rotation [float] degrees clockwise by which to rotate the gaussian

Returns

rotgauss: fn parameters are x and y positions (row/column semantics are set by your inputs to this function). Return value is the scaled gaussian pdf evaluated at the argued point.

`allensdk.brain_observatory.receptive_field_analysis.fitgaussian2D.`**`moments2`**(*data*)

Treating input image data as an independent multivariate gaussian, estimate mean and standard deviations

Parameters

data [np.ndarray] 2d numpy array.

Returns

height [float] The maximum observed value in the data

y [float] Mean row index

x [float] Mean column index

width_y [float] The standard deviation along the mean row

width_x [float] The standard deviation along the mean column

None : This function returns an instance of None.

Notes

uses original method from website for finding center

allensdk.brain_observatory.receptive_field_analysis.postprocessing module

allensdk.brain_observatory.receptive_field_analysis.postprocessing.**get_gaussian_fit**(*rf*)

allensdk.brain_observatory.receptive_field_analysis.postprocessing.**run_postprocessing**(*data*, *rf*)

allensdk.brain_observatory.receptive_field_analysis.receptive_field module

allensdk.brain_observatory.receptive_field_analysis.receptive_field.**compute_receptive_fielc**

allensdk.brain_observatory.receptive_field_analysis.receptive_field.**compute_receptive_fielc**

allensdk.brain_observatory.receptive_field_analysis.receptive_field.**events_to_pvalues_no_fc**

allensdk.brain_observatory.receptive_field_analysis.receptive_field.**get_attribute_dict**(*rf*)

allensdk.brain_observatory.receptive_field_analysis.receptive_field.**print_summary**(*rf*)

allensdk.brain_observatory.receptive_field_analysis.receptive_field.**read_h5_group**(*g*)

allensdk.brain_observatory.receptive_field_analysis.receptive_field.**read_receptive_field_fr**

allensdk.brain_observatory.receptive_field_analysis.receptive_field.**write_receptive_field_t**

allensdk.brain_observatory.receptive_field_analysis.tools module

allensdk.brain_observatory.receptive_field_analysis.tools.**dict_generator**(*indict*, *pre=None*)

allensdk.brain_observatory.receptive_field_analysis.tools.**list_of_dicts_to_dict_of_lists**(*lis* allensdk.brain_observatory.receptive_field_analysis.tools.**read_h5_group**(*g*)

allensdk.brain_observatory.receptive_field_analysis.utilities module

allensdk.brain_observatory.receptive_field_analysis.utilities.**convolve**(*img*, *sigma=4*)

2D Gaussian convolution

allensdk.brain_observatory.receptive_field_analysis.utilities.**get_A**(*data*, *stimulus*)

allensdk.brain_observatory.receptive_field_analysis.utilities.**get_A_blur**(*data*, *stimulus*)

allensdk.brain_observatory.receptive_field_analysis.utilities.**get_attribute_dict**(*rf*)

allensdk.brain_observatory.receptive_field_analysis.utilities.**get_components**(*receptive_field_data*

allensdk.brain_observatory.receptive_field_analysis.utilities.**get_shuffle_matrix**(*data*, *event_vector*, *A*, *number_of_shuffle* *response_detect*

allensdk.brain_observatory.receptive_field_analysis.utilities.**get_sparse_noise_epoch_mask_**

allensdk.brain_observatory.receptive_field_analysis.utilities.**smooth**(*x*, *window_len=11*, *window='hanning'*, *mode='valid'*)

smooth the data using a window with requested size.

This method is based on the convolution of a scaled window with the signal. The signal is prepared by introducing reflected copies of the signal (with the window size) in both ends so that transient parts are minimized in the begining and end part of the output signal.

input: x: the input signal window_len: the dimension of the smoothing window; should be an odd integer window: the type of window from 'flat', 'hanning', 'hamming', 'bartlett', 'blackman'

flat window will produce a moving average smoothing.

output: the smoothed signal

example:

t=linspace(-2,2,0.1) x=sin(t)+randn(len(t))*0.1 y=smooth(x)

see also:

numpy.hanning, numpy.hamming, numpy.bartlett, numpy.blackman, numpy.convolve scipy.signal.lfilter

TODO: the window parameter could be the window itself if an array instead of a string NOTE: length(output) != length(input), to correct this: return y[(window_len/2-1):-(window_len/2)] instead of just y.

`allensdk.brain_observatory.receptive_field_analysis.utilities.`**`upsample_image_to_degrees`**`(`*img*

allensdk.brain_observatory.receptive_field_analysis.visualization module

`allensdk.brain_observatory.receptive_field_analysis.visualization.`**`plot_chi_square_summary`**`(`*r*
a
a
a

`allensdk.brain_observatory.receptive_field_analysis.visualization.`**`plot_ellipses`**`(`*gaussian_fit_di*
ax=None,
show=True,
close=True,
save_file_name
color='b'`)`

Example Usage: oeid, cell_index, stimulus = 512176430, 12, 'locally_sparse_noise' brain_observatory_cache = BrainObservatoryCache() data_set = brain_observatory_cache.get_ophys_experiment_data(oeid) lsn = LocallySparseNoise(data_set, stimulus) result = compute_receptive_field_with_postprocessing(data_set, cell_index, stimulus, alpha=.05, number_of_shuffles=5000) plot_ellipses(result['off']['gaussian_fit'], color='r')

`allensdk.brain_observatory.receptive_field_analysis.visualization.`**`plot_fields`**`(`*on_data*,
off_data,
on_axes,
off_axes,
cbar_axes=None,
clim=None,
cmap='magma'`)`

`allensdk.brain_observatory.receptive_field_analysis.visualization.`**`plot_gaussian_fit`**`(`*rf_data*,
ax_on,
ax_off,
ax_cbar=
cmap='m

`allensdk.brain_observatory.receptive_field_analysis.visualization.`**`plot_mask`**`(`*rf_data*,
ax_on,
ax_off,
ax_cbar=None,
cmap='magma'`)`

`allensdk.brain_observatory.receptive_field_analysis.visualization.`**`plot_msr_summary`**`(`*lsn*,
cell_index,
ax_on,
ax_off,
ax_cbar=N
cmap=Non

`allensdk.brain_observatory.receptive_field_analysis.visualization.`**`plot_p_values`**`(`*rf_data*,
ax_on,
ax_off,
ax_cbar=None,
cmap='magma

allensdk.brain_observatory.receptive_field_analysis.visualization.**plot_receptive_field_data**

allensdk.brain_observatory.receptive_field_analysis.visualization.**plot_rts_blur_summary**(*rf_*
*ax_*
*ax_*
*ax_*
cma

allensdk.brain_observatory.receptive_field_analysis.visualization.**plot_rts_summary**(*rf_data, ax_on, ax_off, ax_cbar=N cmap='ma*

allensdk.brain_observatory.receptive_field_analysis.visualization.**pvalue_to_NLL**(*p_values, max_NLL=10.0*

Module contents

allensdk.brain_observatory.sync_utilities package

Module contents

allensdk.brain_observatory.sync_utilities.**get_synchronized_frame_times**(*session_sync_file: pathlib.Path, sync_line_label_keys: Tuple[str, ...]*) → pandas.core.series.Series

Get experimental frame times from an experiment session sync file.

Parameters

session_sync_file [Path] Path to an ephys session sync file. The sync file contains rising/falling edges from a daq system which indicates when certain events occur (so they can be related to each other).

sync_line_label_keys [Tuple[str, . . .]] Line label keys to get times for. See class attributes of allensdk.brain_observatory.sync_dataset.Dataset for a listing of possible keys.

Returns

pd.Series An array of times when frames for the eye tracking camera were acquired.

allensdk.brain_observatory.sync_utilities.**trim_discontiguous_times**(*times, threshold=100*)

allensdk.brain_observatory.visualization package

Module contents

`allensdk.brain_observatory.visualization.`**`plot_running_speed`**(*timestamps, values, start_index=0, stop_index=None, step=1, ylabel='running speed (cm/s)', xlabel='time (s)', title=None*)

Make a simple plot of a running speed trace

Parameters

timestamps [numpy.ndarray] Times at which running speed samples were collected

values [numpy.ndarray] Running speed values (by default: linear cm / s with negative values indicating backwards movement)

Submodules

allensdk.brain_observatory.argschema_utilities module

allensdk.brain_observatory.brain_observatory_exceptions module

exception `allensdk.brain_observatory.brain_observatory_exceptions.`**`BrainObservatoryAnalysisE`**

Bases: `Exception`

exception `allensdk.brain_observatory.brain_observatory_exceptions.`**`EpochSeparationException`**

Bases: `Exception`

exception `allensdk.brain_observatory.brain_observatory_exceptions.`**`MissingStimulusException`**

Bases: `Exception`

exception `allensdk.brain_observatory.brain_observatory_exceptions.`**`NoEyeTrackingException`**

Bases: `Exception`

allensdk.brain_observatory.brain_observatory_plotting module

`allensdk.brain_observatory.brain_observatory_plotting.`**`plot_drifting_grating_traces`**(*dg, save_dir*)

saves figures with a Ori X TF grid of mean resposes

`allensdk.brain_observatory.brain_observatory_plotting.`**`plot_lsn_traces`**(*lsn, save_dir, suffix=''*)

`allensdk.brain_observatory.brain_observatory_plotting.`**`plot_ns_traces`**(*nsa, save_dir*)

`allensdk.brain_observatory.brain_observatory_plotting.`**`plot_running_a`**(*dg, nm1, nm3, save_dir*) allensdk.brain_observatory.brain_observatory_plotting.**plot_sg_traces**(*sg, save_dir*)

allensdk.brain_observatory.chisquare_categorical module

Created on Wed Jun 5 15:52:22 2019

@author: dan

allensdk.brain_observatory.chisquare_categorical.**advance_combination**(*curr_combination, options_per_column*)

allensdk.brain_observatory.chisquare_categorical.**chisq_from_stim_table**(*stim_table, columns, mean_sweep_events, num_shuffles=1000, verbose=False*)

allensdk.brain_observatory.chisquare_categorical.**compute_chi**(*observed, expected*)

allensdk.brain_observatory.chisquare_categorical.**compute_chi_shuffle**(*mean_sweep_events, sweep_categories, num_shuffles=1000*)

allensdk.brain_observatory.chisquare_categorical.**compute_expected**(*mean_sweep_events, sweep_conditions*)

allensdk.brain_observatory.chisquare_categorical.**compute_observed**(*mean_sweep_events, sweep_conditions*)

allensdk.brain_observatory.chisquare_categorical.**make_category_dummy**(*sweep_categories*)

allensdk.brain_observatory.chisquare_categorical.**stim_table_to_categories**(*stim_table, columns, verbose=False*)

allensdk.brain_observatory.circle_plots module

class allensdk.brain_observatory.circle_plots.**CoronaPlotter**(*angle_start=270, plot_scale=1.2, inner_radius=0.3, *args, **kwargs*)

Bases: *allensdk.brain_observatory.circle_plots.PolarPlotter*

infer_dims(*self, category_data*)

plot(*self, category_data, data=None, clim=None, cmap=<matplotlib.colors.LinearSegmentedColormap object at 0x7f2b050d0ef0>*)

set_dims(*self, categories*)

show_arrow(*self, color=None*)

show_circle(*self, color=None*)

class allensdk.brain_observatory.circle_plots.**FanPlotter**(*group_scale=0.9, *args, **kwargs*)

Bases: *allensdk.brain_observatory.circle_plots.PolarPlotter*

static for_drifting_gratings()

static for_static_gratings()

infer_dims(*self*, *r_data*, *angle_data*, *group_data*)

plot(*self*, *r_data*, *angle_data*, *group_data=None*, *data=None*, *cmap=<matplotlib.colors.LinearSegmentedColormap object at 0x7f2b050d0ef0>*, *clim=None*, *rmap=None*, *rlim=None*, *axis_color=None*, *label_color=None*)

set_dims(*self*, *rs*, *angles*, *groups*)

show_angle_labels(*self*, *angles=None*, *labels=None*, *color=None*, *offset=0.05*, *fontdict=None*)

show_axes(*self*, *angles=None*, *radii=None*, *closed=False*, *color=None*)

show_group_labels(*self*, *groups=None*, *color=None*, *fontdict=None*)

show_r_labels(*self*, *radii=None*, *labels=None*, *color=None*, *offset=0.1*, *fontdict=None*)

class allensdk.brain_observatory.circle_plots.**PolarPlotter**(*direction=-1*, *angle_start=0*, *circle_scale=1.1*, *inner_radius=None*, *plot_center=(0.0, 0.0)*, *plot_scale=0.9*)

Bases: `object`

DIR_CCW = 1

DIR_CW = -1

finalize(*self*)

class allensdk.brain_observatory.circle_plots.**TrackPlotter**(*direction=-1*, *angle_start=270.0*, *inner_radius=0.45*, *ring_length=None*, **args*, ***kwargs*)

Bases: *allensdk.brain_observatory.circle_plots.PolarPlotter*

plot(*self*, *data*, *clim=None*, *cmap=<matplotlib.colors.LinearSegmentedColormap object at 0x7f2b050d0ef0>*, *mean_cmap=<matplotlib.colors.LinearSegmentedColormap object at 0x7f2ae0f6f208>*, *norm=None*)

show_arrow(*self*, *color=None*)

allensdk.brain_observatory.circle_plots.**add_angle_labels**(*ax*, *angles*, *labels*, *radius*, *color=None*, *fontdict=None*, *offset=0.05*)

allensdk.brain_observatory.circle_plots.**add_arrow**(*ax*, *radius*, *start_angle*, *end_angle*, *color=None*, *width=18.0*)

allensdk.brain_observatory.circle_plots.**angle_lines**(*angles*, *inner_radius*, *outer_radius*)

allensdk.brain_observatory.circle_plots.**build_hex_pack**(*n*)

allensdk.brain_observatory.circle_plots.**hex_pack**(*radius*, *n*)

allensdk.brain_observatory.circle_plots.**make_pincushion_plot**(*data*, *trials*, *on*, *nrows*, *ncols*, *clim=None*, *color_map=None*, *radius=None*) allensdk.brain_observatory.circle_plots.**polar_line_circles**(*radii*, *theta*, *start_r=0*)

allensdk.brain_observatory.circle_plots.**polar_linspace**(*radius*, *start_angle*, *stop_angle*, *num*, *endpoint=False*, *degrees=True*)
Evenly distributed list of x,y coordinates from an input range of angles and a radius in polar coordinates.

allensdk.brain_observatory.circle_plots.**polar_to_xy**(*angles*, *radius*)
Convert an array of angles (in radians) and a radius in polar coordinates to an array of x,y coordinates.

allensdk.brain_observatory.circle_plots.**radial_arcs**(*rs*, *start_theta*, *end_theta*)

allensdk.brain_observatory.circle_plots.**radial_circles**(*rs*)

allensdk.brain_observatory.circle_plots.**reset_hex_pack**()

allensdk.brain_observatory.circle_plots.**rings_in_hex_pack**(*ct*)

allensdk.brain_observatory.circle_plots.**spiral_trials**(*radii*, *x=0.0*, *y=0.0*)

allensdk.brain_observatory.circle_plots.**spiral_trials_polar**(*r*, *theta*, *radii*, *offset=None*)

allensdk.brain_observatory.circle_plots.**wedge_ring**(*N*, *inner_radius*, *outer_radius*, *start=0*, *stop=360*)

allensdk.brain_observatory.demixer module

allensdk.brain_observatory.demixer.**demix_time_dep_masks**(*raw_traces*, *stack*, *masks*)

Parameters

- **raw_traces** – extracted traces
- **stack** – movie (same length as traces)
- **masks** – binary roi masks

Returns demixed traces

allensdk.brain_observatory.demixer.**find_negative_baselines**(*trace*)

allensdk.brain_observatory.demixer.**find_negative_transients_threshold**(*trace*, *window=500*, *length=10*, *std_devs=3*)

allensdk.brain_observatory.demixer.**find_zero_baselines**(*traces*)

allensdk.brain_observatory.demixer.**plot_negative_baselines**(*raw_traces*, *demix_traces*, *mask_array*, *roi_ids_mask*, *plot_dir*, *ext='png'*)

allensdk.brain_observatory.demixer.**plot_negative_transients**(*raw_traces*, *demix_traces*, *valid_roi*, *mask_array*, *roi_ids_mask*, *plot_dir*, *ext='png'*) allensdk.brain_observatory.demixer.**plot_overlap_masks_lengthOne**(*roi_ind*, *masks*, *savefile=None*, *weighted=False*)

allensdk.brain_observatory.demixer.**plot_traces**(*raw_trace*, *demix_trace*, *roi_id*, *roi_ind*, *save_file*)

allensdk.brain_observatory.demixer.**plot_transients**(*roi_ind*, *t_trans*, *masks*, *traces*, *demix_traces*, *savefile*)

allensdk.brain_observatory.demixer.**rolling_window**(*trace*, *window=500*)

Parameters

- **trace** –
- **window** –

Returns

allensdk.brain_observatory.dff module

allensdk.brain_observatory.dff.**calculate_dff**(*traces*, *dff_computation_cb=None*, *save_plot_dir=None*)

Apply dF/F computation to a set of traces.

The default computation method is `compute_dff_windowed_median()` using default window parameters.

Parameters

traces [np.ndarray] 2D array of traces to be analyzed.

dff_computation_cb [function] Function that takes traces as an argument and returns an array of the same shape that is the calculated dF/F.

save_plot_dir [str] Directory to save dF/F plots to. By default no plots are saved.

Returns

dff [np.ndarray] 2D array of dF/F traces.

allensdk.brain_observatory.dff.**compute_dff_windowed_median**(*traces*, *median_kernel_long=5401*, *median_kernel_short=101*, *noise_stds=None*, *n_small_baseline_frames=None*, ***kwargs*)

Compute dF/F of a set of traces with median filter detrending.

The operation is basically:

T_long = windowed_median(T) # long timescale kernel

T_dff1 = (T - T_long) / elementwise_max(T_long, noise_std(T))

T_short = windowed_median(T_dff1) # short timescale kernel

T_dff = T_dff1 - elementwise_min(T_short, 2.5*noise_std(T_dff1))

Parameters

traces [np.ndarray] 2D array of traces to be analyzed.

median_kernel_long [int] Window size to use for long timescale median detrending.

median_kernel_short [int] Window size to use for short timescale median detrending.

noise_stds [list] List that will contain noise_std(T_dff1) for each trace. The value for each trace will be appended to the list if provided.

n_small_baseline_frames [list] List that will contain the number of frames for each trace where the long-timescale median window is less than noise_std(T). The value for each trace will be appended to the list if provided.

kwargs: Additional keyword arguments are passed to `noise_std()` .

Returns

dff [np.ndarray] 2D array of dF/F traces.

`allensdk.brain_observatory.dff.`**`compute_dff_windowed_mode`**(*traces*, *mode_kernelsize=5400*, *mean_kernelsize=3000*)

Compute dF/F of a set of traces using a low-pass windowed-mode operator.

The operation is basically:

T_mm = windowed_mean(windowed_mode(T))

T_dff = (T - T_mm) / T_mm

Parameters

traces [np.ndarray] 2D array of traces to be analyzed.

mode_kernelsize [int] Window size to use for windowed_mode.

mean_kernelsize [int] Window size to use for windowed_mean.

Returns

dff [np.ndarray] 2D array of dF/F traces.

`allensdk.brain_observatory.dff.`**`main`**()

`allensdk.brain_observatory.dff.`**`movingaverage`**(*x*, *kernelsize*, *y*)

Compute the windowed average of an array.

Parameters

x [np.ndarray] Array to be analyzed

kernelsize [int] Size of the moving window

y [np.ndarray] Output array to store the results

`allensdk.brain_observatory.dff.`**`movingmode_fast`**(*x*, *kernelsize*, *y*)

Compute the windowed mode of an array. A running mode is initialized with a histogram of values over the initial kernelsize/2 values. The mode is then updated as the kernel moves by adding and subtracting values from the histogram.

Parameters

x [np.ndarray] Array to be analyzed

kernelsize [int] Size of the moving window

y [np.ndarray] Output array to store the results `allensdk.brain_observatory.dff.`**`noise_std`**(*x*, *noise_kernel_length=31*, *positive_peak_scale=1.5*, *outlier_std_scale=2.5*)

Robust estimate of the standard deviation of the trace noise.

`allensdk.brain_observatory.dff.`**`plot_onetrace`**(*dff*, *fc*)

Debug plotting function

`allensdk.brain_observatory.dff.`**`robust_std`**(*x*)

Robust estimate of standard deviation.

Estimate of the standard deviation using the median absolute deviation of x.

allensdk.brain_observatory.drifting_gratings module

`class` `allensdk.brain_observatory.drifting_gratings.`**`DriftingGratings`**(*data_set*, ***kwargs*)

Bases: *`allensdk.brain_observatory.stimulus_analysis.StimulusAnalysis`*

Perform tuning analysis specific to drifting gratings stimulus.

Parameters

data_set: BrainObservatoryNwbDataSet object

`static from_analysis_file`(*data_set*, *analysis_file*)

`get_noise_correlation`(*self*, *corr='spearman'*)

`get_peak`(*self*)

Computes metrics related to each cell's peak response condition.

Returns

Pandas data frame containing the following columns (_dg suffix is

for drifting grating):

- ori_dg (orientation)
- tf_dg (temporal frequency)
- reliability_dg
- osi_dg (orientation selectivity index)
- dsi_dg (direction selectivity index)
- peak_dff_dg (peak dF/F)
- ptest_dg
- p_run_dg
- run_modulation_dg
- cv_dg (circular variance)

`get_representational_similarity`(*self*, *corr='spearman'*)

`get_response`(*self*)

Computes the mean response for each cell to each stimulus condition. Return is a (# orientations, # temporal frequencies, # cells, 3) np.ndarray. The final dimension contains the mean response to the condition (index 0), standard error of the mean of the response to the condition (index 1), and the number of trials with a significant response (p < 0.05) to that condition (index 2).

Returns

Numpy array storing mean responses.

`get_signal_correlation`(*self*, *corr='spearman'*)

`number_ori`

`number_tf`

`open_star_plot`(*self*, *cell_specimen_id=None*, *include_labels=False*, *cell_index=None*)

`orivals`

`plot_direction_selectivity`(*self*, *si_range=[0, 1.5]*, *n_hist_bins=50*, *color='#ccccdd'*, *p_value_max=0.05*, *peak_dff_min=3*)

`plot_orientation_selectivity`(*self*, *si_range=[0, 1.5]*, *n_hist_bins=50*, *color='#ccccdd'*, *p_value_max=0.05*, *peak_dff_min=3*)

`plot_preferred_direction`(*self*, *include_labels=False*, *si_range=[0, 1.5]*, *color='#ccccdd'*, *p_value_max=0.05*, *peak_dff_min=3*)

`plot_preferred_temporal_frequency`(*self*, *si_range=[0, 1.5]*, *color='#ccccdd'*, *p_value_max=0.05*, *peak_dff_min=3*)

`populate_stimulus_table`(*self*)

Implemented by subclasses.

`reshape_response_array`(*self*)

Returns response array in cells x stim x repetition for noise correlations

`tfvals`

allensdk.brain_observatory.findlevel module

`allensdk.brain_observatory.findlevel.`**`findlevel`**(*inwave*, *threshold*, *direction='both'*)

allensdk.brain_observatory.locally_sparse_noise module

class `allensdk.brain_observatory.locally_sparse_noise.`**`LocallySparseNoise`**(*data_set*, *stimulus=None*, ***kwargs*)

Bases: *`allensdk.brain_observatory.stimulus_analysis.StimulusAnalysis`*

Perform tuning analysis specific to the locally sparse noise stimulus.

Parameters

data_set: BrainObservatoryNwbDataSet object

stimulus: string Name of locally sparse noise stimulus. See brain_observatory.stimulus_info.

nrows: int Number of rows in the stimulus template

ncol: int Number of columns in the stimulus template

`LSN`

`LSN_GREY = 127`

`LSN_OFF = 0`

LSN_OFF_SCREEN = 64

LSN_ON = 255

LSN_mask

cell_index_receptive_field_analysis_data

extralength

static from_analysis_file(*data_set*, *analysis_file*, *stimulus*)

get_mean_response(*self*)

get_peak(*self*)
Implemented by subclasses.

get_receptive_field(*self*)
Calculates receptive fields for each cell

get_receptive_field_analysis_data(*self*)
Calculates receptive fields for each cell

get_receptive_field_attribute_df(*self*)

interlength

mean_response

static merge_mean_response(*rc1*, *rc2*)
Move out of this class, to session analysis

open_pincushion_plot(*self*, *on*, *cell_specimen_id=None*, *color_map=None*, *cell_index=None*)

plot_cell_receptive_field(*self*, *on*, *cell_specimen_id=None*, *color_map=None*, *clim=None*, *mask=None*, *cell_index=None*, *scalebar=True*)

plot_population_receptive_field(*self*, *color_map='RdPu'*, *clim=None*, *mask=None*, *scalebar=True*)

plot_receptive_field_analysis_data(*self*, *cell_index*, ***kwargs*)

populate_stimulus_table(*self*)
Implemented by subclasses.

static read_cell_index_receptive_field_analysis(*file_handle*, *prefix*, *path=None*)

receptive_field

static save_cell_index_receptive_field_analysis(*cell_index_receptive_field_analysis_data*, *new_nwb*, *prefix*)

sort_trials(*self*)

sweeplength

allensdk.brain_observatory.natural_movie module

class allensdk.brain_observatory.natural_movie.**NaturalMovie**(*data_set*, *movie_name*, ***kwargs*)

Bases: *allensdk.brain_observatory.stimulus_analysis.StimulusAnalysis*

Perform tuning analysis specific to natural movie stimulus.

Parameters

data_set: BrainObservatoryNwbDataSet object

movie_name: string

one of [stimulus_info.NATURAL_MOVIE_ONE, stimulus_info.NATURAL_MOVIE_TWO, stimulus_info.NATURAL_MOVIE_THREE]

static from_analysis_file (*data_set*, *analysis_file*, *movie_name*)

get_peak (*self*)
Computes properties of the peak response condition for each cell.

Returns

Pandas data frame with the below fields. A suffix of "nm1", "nm2" or "nm3" is appended to the field name

on which of three movie clips was presented.

- peak_nm1 (frame with peak response)
- response_variability_nm1

get_sweep_response (*self*)
Returns the dF/F response for each cell

Returns

Numpy array

open_track_plot (*self*, *cell_specimen_id=None*, *cell_index=None*)

populate_stimulus_table (*self*)
Implemented by subclasses.

sweep_response

sweeplength

allensdk.brain_observatory.natural_scenes module

class allensdk.brain_observatory.natural_scenes.**NaturalScenes** (*data_set*, ***kwargs*)
Bases: *allensdk.brain_observatory.stimulus_analysis.StimulusAnalysis*

Perform tuning analysis specific to natural scenes stimulus.

Parameters

data_set: BrainObservatoryNwbDataSet object

extralength

static from_analysis_file (*data_set*, *analysis_file*)

get_noise_correlation (*self*, *corr='spearman'*)

get_peak (*self*)
Computes metrics about peak response condition for each cell.

Returns

Pandas data frame with the following fields ('_ns' suffix is for

natural scene):

- scene_ns (scene number)

- reliability_ns
- peak_dff_ns (peak dF/F)
- ptest_ns
- p_run_ns
- run_modulation_ns
- time_to_peak_ns

get_representational_similarity(*self*, *corr='spearman'*)

get_response(*self*)
Computes the mean response for each cell to each stimulus condition. Return is a (# scenes, # cells, 3) np.ndarray. The final dimension contains the mean response to the condition (index 0), standard error of the mean of the response to the condition (index 1), and the number of trials with a significant ($p < 0.05$) response to that condition (index 2).

Returns

Numpy array storing mean responses.

get_signal_correlation(*self*, *corr='spearman'*)

interlength

number_scenes

open_corona_plot(*self*, *cell_specimen_id=None*, *cell_index=None*)

plot_time_to_peak(*self*, *p_value_max=0.05*, *color_map=<matplotlib.colors.LinearSegmentedColormap object at 0x7f2ae1005400>*)

populate_stimulus_table(*self*)
Implemented by subclasses.

reshape_response_array(*self*)

Returns response array in cells x stim x repetition for noise correlations

sweeplength

allensdk.brain_observatory.observatory_plots module

class allensdk.brain_observatory.observatory_plots.**DimensionPatchHandler**(*vals*, *start_color*, *end_color*, **args*, ***kwargs*)

Bases: object

dim_color(*self*, *index*)

legend_artist(*self*, *legend*, *orig_handle*, *fontsize*, *handlebox*)

allensdk.brain_observatory.observatory_plots.**figure_in_px**(*w*, *h*, *file_name*, *dpi=96.0*, *transparent=False*)

allensdk.brain_observatory.observatory_plots.**finalize_no_axes**(*pad=0.0*)

allensdk.brain_observatory.observatory_plots.**finalize_no_labels**(*pad=0.3*, *legend=False*) allensdk.brain_observatory.observatory_plots.**finalize_with_axes**(*pad=0.3*)

allensdk.brain_observatory.observatory_plots.**float_label**(*n*)

allensdk.brain_observatory.observatory_plots.**plot_cell_correlation**(*sig_corrs, labels, colors, scale=15*)

allensdk.brain_observatory.observatory_plots.**plot_combined_speed**(*binned_resp_vis, binned_dx_vis, binned_resp_sp, binned_dx_sp, evoked_color, spont_color*)

allensdk.brain_observatory.observatory_plots.**plot_condition_histogram**(*vals, bins, color='#ccccdd'*)

allensdk.brain_observatory.observatory_plots.**plot_mask_outline**(*mask, ax, color='k'*)

allensdk.brain_observatory.observatory_plots.**plot_pupil_location**(*xy_deg, s=1, c=None, cmap=<matplotlib.colors.LinearSegm object at 0x7f2ae10053c8>, edgecolor='', include_labels=True*)

allensdk.brain_observatory.observatory_plots.**plot_radial_histogram**(*angles, counts, all_angles=None, include_labels=False, offset=180.0, direction=-1, closed=False, color='#ccccdd'*)

allensdk.brain_observatory.observatory_plots.**plot_receptive_field**(*rf, color_map=None, clim=None, mask=None, outline_color='#cccccc', scalebar=True*) allensdk.brain_observatory.observatory_plots.**plot_representational_similarity**(*rs, dims=None, dim_labels=None, colors=None, dim_order=None, labels=True*)

allensdk.brain_observatory.observatory_plots.**plot_selectivity_cumulative_histogram**(*sis, xlabel, si_range=[1.5], n_hist_bins color='#cc*

allensdk.brain_observatory.observatory_plots.**plot_speed**(*binned_resp, binned_dx, num_bins, color*)

allensdk.brain_observatory.observatory_plots.**plot_time_to_peak**(*msrs, ttps, t_start, t_end, stim_start, stim_end, cmap*)

allensdk.brain_observatory.observatory_plots.**population_correlation_scatter**(*sig_corrs, noise_corrs, labels, colors, scale=15*)

allensdk.brain_observatory.r_neuropil module

class allensdk.brain_observatory.r_neuropil.**NeuropilSubtract**(*lam=0.05, dt=1.0, folds=4*)

Bases: `object`

TODO: docs

estimate_error(*self, r*)
Estimate error values for a given r for each fold and return the mean.

fit(*self, r_range=[0.0, 2.0], iterations=3, dr=0.1, dr_factor=0.1*)
Estimate error values for a range of r values. Identify a new r range around the minimum error values and repeat multiple times. TODO: docs

fit_block_coordinate_desc(*self, r_init=5.0, min_delta_r=1e-08*)

set_F(*self, F_M, F_N*)
Break the F_M and F_N traces into the number of folds specified in the class constructor and normalize each fold of F_M and R_N relative to F_N.

allensdk.brain_observatory.r_neuropil.**ab_from_T**(*T, lam, dt*)

allensdk.brain_observatory.r_neuropil.**ab_from_diagonals**(*mat_dict*)
Constructs value for scipy.linalg.solve_banded

Parameters

mat_dict: dictionary of diagonals keyed by offsets

Returns

ab: value for scipy.linalg.solve_banded

`allensdk.brain_observatory.r_neuropil.`**`alpha_filter`**(*A=1.0*, *alpha=0.05*, *beta=0.25*, *T=100*)

`allensdk.brain_observatory.r_neuropil.`**`error_calc`**(*F_M*, *F_N*, *F_C*, *r*)

`allensdk.brain_observatory.r_neuropil.`**`error_calc_outlier`**(*F_M*, *F_N*, *F_C*, *r*)

`allensdk.brain_observatory.r_neuropil.`**`estimate_contamination_ratios`**(*F_M*, *F_N*, *lam=0.05*, *folds=4*, *iterations=3*, *r_range=[0.0, 2.0]*, *dr=0.1*, *dr_factor=0.1*)

Calculates neuropil contamination of ROI

Parameters

F_M: ROI trace F_N: Neuropil trace

Returns

dictionary: key-value pairs

- 'r': the contamination ratio – corrected trace = M - r*N
- 'err': RMS error
- 'min_error': minimum error
- 'bounds_error': boolean. True if error or R are outside tolerance

`allensdk.brain_observatory.r_neuropil.`**`get_diagonals_from_sparse`**(*mat*)

Returns a dictionary of diagonals keyed by offsets

Parameters

mat: scipy.sparse matrix

Returns

dictionary: diagonals keyed by offsets

`allensdk.brain_observatory.r_neuropil.`**`normalize_F`**(*F_M*, *F_N*)

`allensdk.brain_observatory.r_neuropil.`**`synthesize_F`**(*T*, *af1*, *af2*, *p1=0.05*, *p2=0.1*)

Build a synthetic F_C, F_M, F_N, and r of length T TODO: docs

`allensdk.brain_observatory.r_neuropil.`**`validate_with_synthetic_F`**(*T*, *N*)

Compute N synthetic traces of length T with known values of r, then estimate r. TODO: docs

allensdk.brain_observatory.roi_masks module

class allensdk.brain_observatory.roi_masks.**Mask**(*image_w*, *image_h*, *label*, *mask_group*)

Bases: object

Abstract class to represent image segmentation mask. Its two main subclasses are RoiMask and NeuropilMask. The former represents the mask of a region of interest (ROI), such as a cell observed in 2-photon imaging. The latter represents the neuropil around that cell, and is useful when subtracting the neuropil signal from the measured ROI signal.

This class should not be instantiated directly.

Parameters

image_w: integer Width of image that ROI resides in

image_h: integer Height of image that ROI resides in

label: text User-defined text label to identify mask

mask_group: integer User-defined number to help put masks into different categories

get_mask_plane(*self*)

Returns mask content on full-size image plane

Returns

numpy 2D array [img_rows][img_cols]

init_by_pixels(*self*, *border*, *pix_list*)

Initialize mask using a list of mask pixels

Parameters

border: float[4] Coordinates defining useable area of image. See create_roi_mask()

pix_list: integer[][2] List of pixel coordinates (x,y) that define the mask

overlaps_motion_border

class allensdk.brain_observatory.roi_masks.**NeuropilMask**(*w*, *h*, *label*, *mask_group*)

Bases: *allensdk.brain_observatory.roi_masks.Mask*

init_by_mask(*self*, *border*, *array*)

Initialize mask using spatial mask

Parameters

border: float[4] Border widths on the [right, left, down, up] sides. The resulting neuropil mask will not include pixels falling into a border.

array: integer[image height][image width] Image-sized array that describes the mask. Active parts of the mask should have values >0. Background pixels must be zero

class allensdk.brain_observatory.roi_masks.**RoiMask**(*image_w*, *image_h*, *label*, *mask_group*)

Bases: *allensdk.brain_observatory.roi_masks.Mask*

init_by_mask(*self*, *border*, *array*)

Initialize mask using spatial mask

Parameters

border: float[4] Coordinates defining useable area of image. See create_roi_mask().

roi_mask: integer[image height][image width] Image-sized array that describes the mask. Active parts of the mask should have values >0. Background pixels must be zero

allensdk.brain_observatory.roi_masks.**calculate_roi_and_neuropil_traces**(*movie_h5*, *roi_mask_list*, *motion_border*)

get roi and neuropil masks

allensdk.brain_observatory.roi_masks.**calculate_traces**(*stack*, *mask_list*, *block_size=1000*)

Calculates the average response of the specified masks in the image stack

Parameters

stack: float[image height][image width] Image stack that masks are applied to

mask_list: list<Mask> List of masks

Returns

float[number masks][number frames] This is the average response for each Mask in each image frame

allensdk.brain_observatory.roi_masks.**create_neuropil_mask**(*roi*, *border*, *combined_binary_mask*, *label=None*)

Conveninece function to create and initializes a Neuropil mask. Neuropil masks are defined as the region around an ROI, up to 13 pixels out, that does not include other ROIs

Parameters

roi: RoiMask object The ROI that the neuropil masks will be based on

border: float[4] Border widths on the [right, left, down, up] sides. The resulting neuropil mask will not include pixels falling into a border.

combined_binary_mask List of pixel coordinates (x,y) that define the mask

combined_binary_mask: integer[image_h][image_w] Image-sized array that shows the position of all ROIs in the image. ROI masks should have a value of one. Background pixels must be zero. In other words, ithe combined_binary_mask is a bitmap union of all ROI masks

label: text User-defined text label to identify the mask

Returns

NeuropilMask object

allensdk.brain_observatory.roi_masks.**create_roi_mask**(*image_w*, *image_h*, *border*, *pix_list=None*, *roi_mask=None*, *label=None*, *mask_group=-1*)

Conveninece function to create and initializes an RoiMask

Parameters

image_w: integer Width of image that ROI resides in

image_h: integer Height of image that ROI resides in

border: float[4] Coordinates defining useable area of image. If the entire image is usable, and masks are valid anywhere in the image, this should be [0, 0, 0, 0]. The following constants help describe the array order:

RIGHT_SHIFT = 0

LEFT_SHIFT = 1

DOWN_SHIFT = 2

UP_SHIFT = 3

When parts of the image are unusable, for example due motion correction shifting of different image frames, the border array should store the usable image area

pix_list: integer[][2] List of pixel coordinates (x,y) that define the mask

roi_mask: integer[image_h][image_w] Image-sized array that describes the mask. Active parts of the mask should have values >0. Background pixels must be zero

label: text User-defined text label to identify mask

mask_group: integer User-defined number to help put masks into different categories

Returns

RoiMask object

`allensdk.brain_observatory.roi_masks.`**`create_roi_mask_array`**(*rois*)

Create full image mask array from list of RoiMasks.

Parameters

rois: list<RoiMask> List of roi masks.

Returns

np.ndarray: NxWxH array Boolean array of of len(rois) image masks.

`allensdk.brain_observatory.roi_masks.`**`validate_mask`**(*mask*)

Check a given roi or neuropil mask for (a subset of) disqualifying problems.

allensdk.brain_observatory.running_speed module

`class` `allensdk.brain_observatory.running_speed.`**`RunningSpeed`**

Bases: `tuple`

Describes the rate at which an experimental subject ran during a session.

values [np.ndarray] running speed (cm/s) at each sample point

timestamps [np.ndarray] The time at which each sample was collected (s).

`timestamps`

Alias for field number 0

`values`

Alias for field number 1

allensdk.brain_observatory.session_analysis module

class `allensdk.brain_observatory.session_analysis.`**`SessionAnalysis`**(*nwb_path*, *save_path*)

Bases: `object`

Run all of the stimulus-specific analyses associated with a single experiment session.

Parameters

nwb_path: string, path to NWB file

save_path: string, path to HDF5 file to store outputs. Recommended NOT to modify the NWB file.

`append_experiment_metrics`(*self*, *metrics*)
Extract stimulus-agnostic metrics from an experiment into a dictionary

`append_metadata`(*self*, *df*)
Append the metadata fields from the NWB file as columns to a pd.DataFrame

`append_metrics_drifting_grating`(*self*, *metrics*, *dg*)
Extract metrics from the DriftingGratings peak response table into a dictionary.

`append_metrics_locally_sparse_noise`(*self*, *metrics*, *lsn*)
Extract metrics from the LocallySparseNoise peak response table into a dictionary.

`append_metrics_natural_movie_one`(*self*, *metrics*, *nma*)
Extract metrics from the NaturalMovie(stimulus_info.NATURAL_MOVIE_ONE) peak response table into a dictionary.

`append_metrics_natural_movie_three`(*self*, *metrics*, *nma*)
Extract metrics from the NaturalMovie(stimulus_info.NATURAL_MOVIE_THREE) peak response table into a dictionary.

`append_metrics_natural_movie_two`(*self*, *metrics*, *nma*)
Extract metrics from the NaturalMovie(stimulus_info.NATURAL_MOVIE_TWO) peak response table into a dictionary.

`append_metrics_natural_scene`(*self*, *metrics*, *ns*)
Extract metrics from the NaturalScenes peak response table into a dictionary.

`append_metrics_static_grating`(*self*, *metrics*, *sg*)
Extract metrics from the StaticGratings peak response table into a dictionary.

`save_session_a`(*self*, *dg*, *nm1*, *nm3*, *peak*)
Save the output of session A analysis to self.save_path.

Parameters

dg: DriftingGratings instance

nm1: NaturalMovie instance This NaturalMovie instance should have been created with movie_name = stimulus_info.NATURAL_MOVIE_ONE

nm3: NaturalMovie instance This NaturalMovie instance should have been created with movie_name = stimulus_info.NATURAL_MOVIE_THREE

peak: pd.DataFrame The combined peak response property table created in self.session_a().

`save_session_b`(*self*, *sg*, *nm1*, *ns*, *peak*)
Save the output of session B analysis to self.save_path.

Parameters

sg: StaticGratings instance

nm1: NaturalMovie instance This NaturalMovie instance should have been created with movie_name = stimulus_info.NATURAL_MOVIE_ONE

ns: NaturalScenes instance

peak: pd.DataFrame The combined peak response property table created in self.session_b().

save_session_c (*self*, *lsn*, *nm1*, *nm2*, *peak*)
Save the output of session C analysis to self.save_path.

Parameters

lsn: LocallySparseNoise instance

nm1: NaturalMovie instance This NaturalMovie instance should have been created with movie_name = stimulus_info.NATURAL_MOVIE_ONE

nm2: NaturalMovie instance This NaturalMovie instance should have been created with movie_name = stimulus_info.NATURAL_MOVIE_TWO

peak: pd.DataFrame The combined peak response property table created in self.session_c().

save_session_c2 (*self*, *lsn4*, *lsn8*, *nm1*, *nm2*, *peak*)
Save the output of session C2 analysis to self.save_path.

Parameters

lsn4: LocallySparseNoise instance This LocallySparseNoise instance should have been created with self.stimulus = stimulus_info.LOCALLY_SPARSE_NOISE_4DEG.

lsn8: LocallySparseNoise instance This LocallySparseNoise instance should have been created with self.stimulus = stimulus_info.LOCALLY_SPARSE_NOISE_8DEG.

nm1: NaturalMovie instance This NaturalMovie instance should have been created with movie_name = stimulus_info.NATURAL_MOVIE_ONE

nm2: NaturalMovie instance This NaturalMovie instance should have been created with movie_name = stimulus_info.NATURAL_MOVIE_TWO

peak: pd.DataFrame The combined peak response property table created in self.session_c2().

session_a (*self*, *plot_flag=False*, *save_flag=True*)
Run stimulus-specific analysis for natural movie one, natural movie three, and drifting gratings. The input NWB be for a stimulus_info.THREE_SESSION_A experiment.

Parameters

plot_flag: bool Whether to generate brain_observatory_plotting work plots after running analysis.

save_flag: bool Whether to save the output of analysis to self.save_path upon completion.

session_b (*self*, *plot_flag=False*, *save_flag=True*)
Run stimulus-specific analysis for natural scenes, static gratings, and natural movie one. The input NWB be for a stimulus_info.THREE_SESSION_B experiment.

Parameters

plot_flag: bool Whether to generate brain_observatory_plotting work plots after running analysis.

save_flag: bool Whether to save the output of analysis to self.save_path upon completion.

session_c(*self*, *plot_flag=False*, *save_flag=True*)
Run stimulus-specific analysis for natural movie one, natural movie two, and locally sparse noise. The input NWB be for a stimulus_info.THREE_SESSION_C experiment.

Parameters

plot_flag: bool Whether to generate brain_observatory_plotting work plots after running analysis.

save_flag: bool Whether to save the output of analysis to self.save_path upon completion.

session_c2(*self*, *plot_flag=False*, *save_flag=True*)
Run stimulus-specific analysis for locally sparse noise (4 deg.), locally sparse noise (8 deg.), natural movie one, and natural movie two. The input NWB be for a stimulus_info.THREE_SESSION_C2 experiment.

Parameters

plot_flag: bool Whether to generate brain_observatory_plotting work plots after running analysis.

save_flag: bool Whether to save the output of analysis to self.save_path upon completion.

verify_roi_lists_equal(*self*, *roi1*, *roi2*)
TODO: replace this with simpler numpy comparisons

allensdk.brain_observatory.session_analysis.**main**()

allensdk.brain_observatory.session_analysis.**multi_dataframe_merge**(*dfs*)
merge a number of pd.DataFrames into a single dataframe on their index columns. If any columns are duplicated, prefer the first occuring instance of the column

allensdk.brain_observatory.session_analysis.**run_session_analysis**(*nwb_path*, *save_path*, *plot_flag=False*, *save_flag=True*)
Inspect an NWB file to determine which experiment session was run and compute all stimulus-specific analyses.

Parameters

nwb_path: string Path to NWB file.

save_path: string path to save results. Recommended NOT to use NWB file.

plot_flag: bool Whether to save brain_observatory_plotting work plots.

save_flag: bool Whether to save results to save_path.

allensdk.brain_observatory.static_gratings module

class allensdk.brain_observatory.static_gratings.**StaticGratings**(*data_set*, ***kwargs*)
Bases: *allensdk.brain_observatory.stimulus_analysis.StimulusAnalysis*

Perform tuning analysis specific to static gratings stimulus.

Parameters

data_set: BrainObservatoryNwbDataSet object

`extralength`

`static from_analysis_file`(*data_set*, *analysis_file*)

`get_noise_correlation`(*self*, *corr='spearman'*)

`get_peak`(*self*)
Computes metrics related to each cell's peak response condition.

Returns

Panda data frame with the following fields (_sg suffix is

for static grating):

- ori_sg (orientation)
- sf_sg (spatial frequency)
- phase_sg
- response_variability_sg
- osi_sg (orientation selectivity index)
- peak_dff_sg (peak dF/F)
- ptest_sg
- time_to_peak_sg

`get_representational_similarity`(*self*, *corr='spearman'*)

`get_response`(*self*)
Computes the mean response for each cell to each stimulus condition. Return is a (# orientations, # spatial frequencies, # phasees, # cells, 3) np.ndarray. The final dimension contains the mean response to the condition (index 0), standard error of the mean of the response to the condition (index 1), and the number of trials with a significant response ($p < 0.05$) to that condition (index 2).

Returns

Numpy array storing mean responses.

`get_signal_correlation`(*self*, *corr='spearman'*)

`interlength`

`number_ori`

`number_phase`

`number_sf`

`open_fan_plot`(*self*, *cell_specimen_id=None*, *include_labels=False*, *cell_index=None*)

`orivals`

`phasevals`

`plot_orientation_selectivity`(*self*, *si_range=[0, 1.5]*, *n_hist_bins=50*, *color='#ccccdd'*, *p_value_max=0.05*, *peak_dff_min=3*)

`plot_preferred_orientation`(*self*, *include_labels=False*, *si_range=[0, 1.5]*, *color='#ccccdd'*, *p_value_max=0.05*, *peak_dff_min=3*)

plot_preferred_spatial_frequency(*self, si_range=[0, 1.5], color='#ccccdd', p_value_max=0.05, peak_dff_min=3*)

plot_time_to_peak(*self, p_value_max=0.05, color_map=<matplotlib.colors.LinearSegmentedColormap object at 0x7f2ae1005400>*)

populate_stimulus_table(*self*)
Implemented by subclasses.

reshape_response_array(*self*)

Returns response array in cells x stim conditions x repetition for noise correlations

this is a re-organization of the mean sweep response table

sfvals

sweeplength

allensdk.brain_observatory.stimulus_analysis module

class `allensdk.brain_observatory.stimulus_analysis.`**StimulusAnalysis**(*data_set*)
Bases: `object`

Base class for all response analysis code. Subclasses are responsible for computing metrics and traces relevant to a particular stimulus. The base class contains methods for organizing sweep responses row of a stimulus stable (get_sweep_response). Subclasses implement the get_response method, computes the mean sweep response to all sweeps for a each stimulus condition.

Parameters

data_set: BrainObservatoryNwbDataSet instance

speed_tuning: boolean, deprecated Whether or not to compute speed tuning histograms

acquisition_rate

binned_cells_sp

binned_cells_vis

binned_dx_sp

binned_dx_vis

cell_id

celltraces

dfftraces

dxcm

dxtime

get_fluorescence(*self*)

get_peak(*self*)
Implemented by subclasses.

get_response(*self*)
Implemented by subclasses.

get_speed_tuning(*self, binsize*)
Calculates speed tuning, spontaneous versus visually driven. The return is a 5-tuple of speed and dF/F histograms.

binned_dx_sp: (bins,2) np.ndarray of running speeds binned during spontaneous activity stimulus. The first bin contains all speeds below 1 cm/s. Dimension 0 is mean running speed in the bin. Dimension 1 is the standard error of the mean.

binned_cells_sp: (bins,2) np.ndarray of fluorescence during spontaneous activity stimulus. First bin contains all data for speeds below 1 cm/s. Dimension 0 is mean fluorescence in the bin. Dimension 1 is the standard error of the mean.

binned_dx_vis: (bins,2) np.ndarray of running speeds outside of spontaneous activity stimulus. The first bin contains all speeds below 1 cm/s. Dimension 0 is mean running speed in the bin. Dimension 1 is the standard error of the mean.

binned_cells_vis: np.ndarray of fluorescence outside of spontaneous activity stimulu. First bin contains all data for speeds below 1 cm/s. Dimension 0 is mean fluorescence in the bin. Dimension 1 is the standard error of the mean.

peak_run: pd.DataFrame of speed-related properties of a cell.

Returns

tuple: binned_dx_sp, binned_cells_sp, binned_dx_vis, binned_cells_vis, peak_run

`get_sweep_response` (*self*)

Calculates the response to each sweep in the stimulus table for each cell and the mean response. The return is a 3-tuple of:

- sweep_response: pd.DataFrame of response dF/F traces organized by cell (column) and sweep (row)
- mean_sweep_response: mean values of the traces returned in sweep_response
- pval: p value from 1-way ANOVA comparing response during sweep to response prior to sweep

Returns

3-tuple: sweep_response, mean_sweep_response, pval

`mean_sweep_response`

`numbercells`

`peak`

`peak_run`

`plot_representational_similarity` (*self*, *repsim*, *stimulus=False*)

`plot_running_speed_histogram` (*self*, *xlim=None*, *nbins=None*)

`plot_speed_tuning` (*self*, *cell_specimen_id=None*, *cell_index=None*, *evoked_color='#b30000'*, *spontaneous_color='#0000b3'*)

`populate_stimulus_table` (*self*)

Implemented by subclasses.

`pval`

`response`

`roi_id`

`row_from_cell_id` (*self*, *csid=None*, *idx=None*)

`stim_table`

`sweep_response`

timestamps

allensdk.brain_observatory.stimulus_analysis.**nonraising_ks_2samp**(*data1*, *data2*, ***kwargs*)

scipy.stats.ks_2samp now raises a ValueError if one of the input arrays is of length 0. Previously it signaled this case by returning nans. This function restores the prior behavior.

allensdk.brain_observatory.stimulus_info module

class allensdk.brain_observatory.stimulus_info.**BinaryIntervalSearchTree**(*search_list*)

Bases: `object`

add(*self*, *input_list*, *tmp=None*)

static from_df(*input_df*)

search(*self*, *fi*, *tmp=None*)

class allensdk.brain_observatory.stimulus_info.**BrainObservatoryMonitor**(*experiment_geometry=None*

Bases: `allensdk.brain_observatory.stimulus_info.Monitor`

http://help.brain-map.org/display/observatory/Documentation?preview=/10616846/10813485/VisualCoding_VisualStimuli.pdf https://www.cnet.com/products/asus-pa248q/specs/

grating_to_screen(*self*, *phase*, *spatial_frequency*, *orientation*, ***kwargs*)

lsn_image_to_screen(*self*, *img*, ***kwargs*)

pixels_to_visual_degrees(*self*, *n*, ***kwargs*)

visual_degrees_to_pixels(*self*, *vd*, ***kwargs*)

warp_image(*self*, *img*, ***kwargs*)

class allensdk.brain_observatory.stimulus_info.**ExperimentGeometry**(*distance*, *mon_height_cm*, *mon_width_cm*, *mon_res*, *eyepoint*)

Bases: `object`

generate_warp_coordinates(*self*)

warp_coordinates

class allensdk.brain_observatory.stimulus_info.**Monitor**(*n_pixels_r*, *n_pixels_c*, *panel_size*, *spatial_unit*)

Bases: `object`

aspect_ratio

get_mask(*self*)

grating_to_screen(*self*, *phase*, *spatial_frequency*, *orientation*, *distance_from_monitor*, *p2p_amp=256*, *baseline=127*, *translation=(0, 0)*)

height

lsn_image_to_screen(*self*, *img*, *stimulus_type*, *origin='lower'*, *background_color=127*, *translation=(0, 0)*)

map_stimulus(*self*, *source_stimulus_coordinate*, *source_stimulus_type*, *target_stimulus_type*)

mask

natural_movie_image_to_screen (*self*, *img*, *origin='lower'*, *translation=(0, 0)*)

natural_scene_image_to_screen (*self*, *img*, *origin='lower'*, *translation=(0, 0)*)

panel_size

pixel_size

pixels_to_visual_degrees (*self*, *n*, *distance_from_monitor*, *small_angle_approximation=True*)

set_spatial_unit (*self*, *new_unit*)

show_image (*self*, *img*, *ax=None*, *show=True*, *mask=False*, *warp=False*, *origin='lower'*)

spatial_frequency_to_pix_per_cycle (*self*, *spatial_frequency*, *distance_from_monitor*)

visual_degrees_to_pixels (*self*, *vd*, *distance_from_monitor*, *small_angle_approximation=True*)

width

class allensdk.brain_observatory.stimulus_info.**StimulusSearch** (*nwb_dataset*)
Bases: object

search (*self*, *fi*)

allensdk.brain_observatory.stimulus_info.**all_stimuli** ()
Return a list of all stimuli in the data set

allensdk.brain_observatory.stimulus_info.**get_spatial_grating** (*height=None*, *aspect_ratio=None*, *ori=None*, *pix_per_cycle=None*, *phase=None*, *p2p_amp=2*, *baseline=0*)

allensdk.brain_observatory.stimulus_info.**get_spatio_temporal_grating** (*t*, *temporal_frequency=None*, ***kwargs*)

allensdk.brain_observatory.stimulus_info.**lsn_coordinate_to_monitor_coordinate** (*lsn_coordinate*, *monitor_shape*, *stimulus_type*)

allensdk.brain_observatory.stimulus_info.**make_display_mask** (*display_shape=(1920, 1200)*)
Build a display-shaped mask that indicates which pixels are on screen after warping the stimulus.

allensdk.brain_observatory.stimulus_info.**map_monitor_coordinate_to_stimulus_coordinate** (*moni mon- i- tor_s stim- u- lus_t* allensdk.brain_observatory.stimulus_info.**map_monitor_coordinate_to_template_coordinate**(*moni mon- i- tor_s tem- plate*

allensdk.brain_observatory.stimulus_info.**map_stimulus**(*source_stimulus_coordinate*, *source_stimulus_type*, *target_stimulus_type*, *monitor_shape*)

allensdk.brain_observatory.stimulus_info.**map_stimulus_coordinate_to_monitor_coordinate**(*temp mon- i- tor_s stim- u- lus_t*

allensdk.brain_observatory.stimulus_info.**map_template_coordinate_to_monitor_coordinate**(*temp mon- i- tor_s tem- plate*

allensdk.brain_observatory.stimulus_info.**mask_stimulus_template**(*template_display_coords*, *template_shape*, *display_mask=None*, *threshold=1.0*)

Build a mask for a stimulus template of a given shape and display coordinates that indicates which part of the template is on screen after warping.

Parameters

template_display_coords: list list of (x,y) display coordinates

template_shape: tuple (width,height) of the display template

display_mask: np.ndarray boolean 2D mask indicating which display coordinates are on screen after warping.

threshold: float Fraction of pixels associated with a template display coordinate that should remain on screen to count as belonging to the mask.

Returns

tuple: (template mask, pixel fraction)

allensdk.brain_observatory.stimulus_info.**monitor_coordinate_to_lsn_coordinate**(*monitor_coordinat*, *monitor_shape*, *stimulus_type*) `allensdk.brain_observatory.stimulus_info.`**`monitor_coordinate_to_natural_movie_coordinate`**`(`*mon mon i- tor_*

`allensdk.brain_observatory.stimulus_info.`**`natural_movie_coordinate_to_monitor_coordinate`**`(`*natu mon i- tor_*

`allensdk.brain_observatory.stimulus_info.`**`natural_scene_coordinate_to_monitor_coordinate`**`(`*natu mon i- tor_*

`allensdk.brain_observatory.stimulus_info.`**`rotate`**`(`*X*, *Y*, *theta*`)`

`allensdk.brain_observatory.stimulus_info.`**`sessions_with_stimulus`**`(`*stimulus*`)`

Return the names of the sessions that contain a given stimulus.

`allensdk.brain_observatory.stimulus_info.`**`stimuli_in_session`**`(`*session*, *allow_unknown=True*`)`

Return a list what stimuli are available in a given session.

Parameters

session: string Must be one of: [stimulus_info.THREE_SESSION_A, stimulus_info.THREE_SESSION_B, stimulus_info.THREE_SESSION_C, stimulus_info.THREE_SESSION_C2]

`allensdk.brain_observatory.stimulus_info.`**`translate_image_and_fill`**`(`*img*, *translation=(0, 0)*`)`

`allensdk.brain_observatory.stimulus_info.`**`warp_stimulus_coords`**`(`*vertices*, *distance=15.0*, *mon_height_cm=32.5*, *mon_width_cm=51.0*, *mon_res=(1920, 1200)*, *eyepoint=(0.5, 0.5)*`)`

For a list of screen vertices, provides a corresponding list of texture coordinates.

Parameters

vertices: numpy.ndarray [[x0,y0], [x1,y1], …] A set of vertices to convert to texture positions.

distance: float distance from the monitor in cm.

mon_height_cm: float monitor height in cm

mon_width_cm: float monitor width in cm

mon_res: tuple monitor resolution (x,y)

eyepoint: tuple

Returns

np.ndarray x,y coordinates shaped like the input that describe what pixel coordinates are displayed an the input coordinates after warping the stimulus.

allensdk.brain_observatory.sync_dataset module

dataset.py

Dataset object for loading and unpacking an HDF5 dataset generated by sync.py

@author: derricw

Allen Institute for Brain Science

Dependencies

numpy http://www.numpy.org/ h5py http://www.h5py.org/

class allensdk.brain_observatory.sync_dataset.**Dataset**(*path*)
Bases: object

A sync dataset. Contains methods for loading and parsing the binary data.

Parameters

path [str] Path to HDF5 file.

Examples

```
>>> dset = Dataset('my_h5_file.h5')
>>> logger.info(dset.meta_data)
>>> dset.stats()
>>> dset.close()
```

```
>>> with Dataset('my_h5_file.h5') as d:
...     logger.info(dset.meta_data)
...     dset.stats()
```

BEHAVIOR_TRACKING_KEYS = ('cam1_exposure',)

EYE_TRACKING_KEYS = ('cam2_exposure', 'eyetracking')

FRAME_KEYS = ('frames', 'stim_vsync')

OPTOGENETIC_STIMULATION_KEYS = ('LED_sync', 'opto_trial')

PHOTODIODE_KEYS = ('photodiode', 'stim_photodiode')

analog_meta_data

close(*self*)
Closes the dataset.

duty_cycle(*self*, *line*)
Doesn't work right now. Freezes python for some reason.

Returns the duty cycle of a line.

frequency(*self*, *line*, *edge='rising'*)
Returns the average frequency of a line.

get_all_bits(*self*)
Returns the data for all bits.

get_all_events (*self*)
Returns all counter values and their cooresponding IO state.

get_all_times (*self*, *units='samples'*)
Returns all counter values.

Parameters

units [str] Return times in 'samples' or 'seconds'

get_analog_channel (*self*, *channel*, *start_time=0.0*, *stop_time=None*, *downsample=1*)

Returns the data from the specified analog channel between the timepoints.

Args: channel (int, str): desired channel index or label start_time (Optional[float]): start time in seconds stop_time (Optional[float]): stop time in seconds downsample (Optional[int]): downsample factor

Returns: ndarray: slice of data for specified channel

Raises: KeyError: no analog data present

get_analog_meta (*self*)
Returns the metadata for the analog data.

get_bit (*self*, *bit*)
Returns the values for a specific bit.

Parameters

bit [int] Bit to return.

get_bit_changes (*self*, *bit*)

Returns the first derivative of a specific bit. Data points are 1 on rising edges and 255 on falling edges.

Parameters

bit [int] Bit for which to return changes.

get_edges (*self*, *kind*, *keys*, *units='seconds'*)
Utility function for extracting edge times from a line

get_events_by_bit (*self*, *bit*, *units='samples'*)

Returns all counter values for transitions (both rising and falling) for a specific bit.

Parameters

bit [int] Bit for which to return events.

get_events_by_line (*self*, *line*, *units='samples'*)

Returns all counter values for transitions (both rising and falling) for a specific line.

Parameters

line [str] Line for which to return events.

get_falling_edges (*self*, *line*, *units='samples'*)

Returns the counter values for the falling edges for a specific bit or line.

Parameters

line [str] Line for which to return edges.

get_line (*self*, *line*)
Returns the values for a specific line.

Parameters

line [str] Line to return.

get_line_changes (*self*, *line*)

Returns the first derivative of a specific line. Data points are 1 on rising edges and 255 on falling edges.

Parameters

line [(str)] Line name for which to return changes.

get_nearest (*self*, *source*, *target*, *source_edge='rising'*, *target_edge='rising'*, *direction='previous'*, *units='indices'*)

For all values of the source line, finds the nearest edge from the target line.

By default, returns the indices of the target edges.

Args: source (str, int): desired source line target (str, int): desired target line source_edge [Optional(str)]: “rising” or “falling” source edges target_edge [Optional(str): “rising” or “falling” target edges direction (str): “previous” or “next”. Whether to prefer the

previous edge or the following edge.

units (str): “indices”

get_rising_edges (*self*, *line*, *units='samples'*)

Returns the counter values for the rizing edges for a specific bit or line.

Parameters

line [str] Line for which to return edges.

line_stats (*self*, *line*, *print_results=True*)
Quick-and-dirty analysis of a bit.

##TODO: Split this up into smaller functions.

load (*self*, *path*)
Loads an hdf5 sync dataset.

Parameters

path [str] Path to hdf5 file.

period (*self*, *line*, *edge='rising'*)
Returns a dictionary with avg, min, max, and st of period for a line.

plot_all (*self*, *start_time*, *stop_time*, *auto_show=True*)
Plot all active bits.

Yikes. Come up with a better way to show this.

plot_bit (*self*, *bit*, *start_time=0.0*, *end_time=None*, *auto_show=True*, *axes=None*, *name=''*)
Plots a specific bit at a specific time period.

plot_bits (*self*, *bits*, *start_time=0.0*, *end_time=None*, *auto_show=True*)
Plots a list of bits.

plot_line (*self*, *line*, *start_time=0.0*, *end_time=None*, *auto_show=True*)
Plots a specific line at a specific time period.

plot_lines (*self*, *lines*, *start_time=0.0*, *end_time=None*, *auto_show=True*)
Plots specific lines at a specific time period.

sample_freq

stats (*self*)

Quick-and-dirty analysis of all bits. Prints a few things about each bit where events are found.

allensdk.brain_observatory.sync_dataset.**get_bit** (*uint_array*, *bit*)
Returns a bool array for a specific bit in a uint ndarray.

Parameters

uint_array [(numpy.ndarray)] The array to extract bits from.

bit [(int)] The bit to extract.

allensdk.brain_observatory.sync_dataset.**unpack_uint32** (*uint32_array*, *endian='L'*)
Unpacks an array of 32-bit unsigned integers into bits.

Default is least significant bit first.

***Not currently used by sync dataset because get_bit is better and does** basically the same thing. I'm just leaving it in because it could potentially account for endianness and possibly have other uses in the future.

Module contents

class allensdk.brain_observatory.**JSONEncoder** (***, *skipkeys=False*, *ensure_ascii=True*, *check_circular=True*, *allow_nan=True*, *sort_keys=False*, *indent=None*, *separators=None*, *default=None*)
Bases: `json.encoder.JSONEncoder`

default (*self*, *o*)
Implement this method in a subclass such that it returns a serializable object for `o`, or calls the base implementation (to raise a `TypeError`).

For example, to support arbitrary iterators, you could implement default like this:

```python
def default(self, o):
    try:
        iterable = iter(o)
    except TypeError:
        pass
    else:
        return list(iterable)
    # Let the base class default method raise the TypeError
    return JSONEncoder.default(self, o)
```

allensdk.brain_observatory.**dict_to_indexed_array** (*dc*, *order=None*)
Given a dictionary and an ordered arr, build a concatenation of the dictionary's values and an index describing how that concatenation can be unpacked

allensdk.brain_observatory.**hook** (*json_dict*)

6.1.3 allensdk.config package

Subpackages

allensdk.config.app package

Submodules

allensdk.config.app.application_config module

class `allensdk.config.app.application_config.`**`ApplicationConfig`**(*defaults*, *name='app'*, *halp='Run application.'*, *default_log_config=None*)

Bases: `object`

Convenience class that handles of application configuration from environment variables, .conf files and the command line using Python standard libraries and formats.

`apply_configuration_from_command_line`(*self*, *parsed_args*)
Read application configuration variables from the command line.

Unassigned variables are left unchanged if previously assigned, set to their default values, or None if no default is specified at init time. Assigned variables will overwrite the previous value.

see: https://docs.python.org/2/howto/argparse.html

Parameters

parsed_args [dict] the arguments as parsed from the command line.

`apply_configuration_from_environment`(*self*)
Read application configuration variables from the environment.

The variable names are upper case and have a prefix defined by the application.

See: https://docs.python.org/2/library/os.html

`apply_configuration_from_file`(*self*, *config_file_path*)
Read application configuration variables from a .conf file.

Unassigned variables are set to their default values or None if no default is specified at init time. The variables are found in a section named by the application.

Parameters

config_file_path [string] path to to an INI (.conf) or JSON format application config file.

Returns

see: https://docs.python.org/2/library/configparser.html

`create_argparser`(*self*)
Initialization for the command-line parsing stage.

An application specific prefix is applied to argument names.

Parameters

prog [string] Application specific prefix for argument names.

description [string] A brief 'help' description of the application.

Returns

argParse.ArgumentParser The initialized argument parser object.

Notes

Defaults are set at the first environment reading. Command line args only override them when present

`from_json_file`(*self*, *json_path*)

Read an application configuration from a JSON format file.

Parameters

json_path [string] Path to the JSON file.

Returns

string An application configuration in INI format

`from_json_string`(*self*, *json_string*)

Read a configuration from a JSON format string.

Parameters

json_string [string] A JSON-formatted string containing an application configuration.

Returns

string An application configuration in INI format

`load`(*self*, *command_line_args*, *disable_existing_loggers=True*)

Load application configuration options, first from the environment, then from the configuration file, then from the command line.

Each stage of loading can override the previous stage.

Parameters

command_line_args [dict] Parameters passed to the application.

disable_existing_loggers [boolean] Reset the logging system or not.

Returns

fileConfig Configuration object with all levels applied

`parse_command_line_args`(*self*, *args*)

Simply call the internal argparser object.

Parameters

args [array] Parameters passed to the application.

Returns

Namespace Parsed paramenters.

`to_config_string`(*self*, *description*)

Create a configuration string from a dict.

Parameters

description [dict] Configuration options for an application.

Returns

string Equivalent configuration as an INI format string

Notes

The Python configparser library natively supports this functionality in Python 3.

Module contents

allensdk.config.app is a package that assists in configuring application software, as opposed to domain-specific configuration.

allensdk.config.model package

Subpackages

allensdk.config.model.formats package

Submodules

allensdk.config.model.formats.hdf5_util module

class `allensdk.config.model.formats.hdf5_util.`**`Hdf5Util`**
Bases: `object`

`read`(*self*, *file_path*)

`write`(*self*, *file_path*, *m*)

allensdk.config.model.formats.json_description_parser module

class `allensdk.config.model.formats.json_description_parser.`**`JsonDescriptionParser`**
Bases: *`allensdk.config.model.description_parser.DescriptionParser`*

`log = <Logger allensdk.config.model.formats.json_description_parser (WARNING)>`

`read`(*self*, *file_path*, *description=None*, *section=None*, ***kwargs*)
Parse a complete or partial configuration.

Parameters

json_string [string] Input to parse.

description [Description, optional] Where to put the parsed configuration. If None a new one is created.

section [string, optional] Where to put the parsed configuration within the description.

Returns

Description The input description with parsed configuration added.

Section is only specified for "bare" objects that are to be added to a section array.

`read_string`(*self*, *json_string*, *description=None*, *section=None*, ***kwargs*)
Parse a complete or partial configuration.

Parameters

json_string [string] Input to parse.

description [Description, optional] Where to put the parsed configuration. If None a new one is created.

section [string, optional] Where to put the parsed configuration within the description.

Returns

Description The input description with parsed configuration added.

Section is only specified for "bare" objects that are to be added to a section array.

write (*self*, *filename*, *description*)
Write the description to a JSON file.

Parameters

description [Description] Object to write.

write_string (*self*, *description*)
Write the description to a JSON string.

Parameters

description [Description] Object to write.

Returns

string JSON serialization of the input.

allensdk.config.model.formats.pycfg_description_parser module

class allensdk.config.model.formats.pycfg_description_parser.**PycfgDescriptionParser**
Bases: *allensdk.config.model.description_parser.DescriptionParser*

log = <Logger allensdk.config.model.formats.pycfg_description_parser (WARNING)>

read (*self*, *pycfg_file_path*, *description=None*, *section=None*, ***kwargs*)
Read a serialized description from a Python (.pycfg) file.

Parameters

filename [string] Name of the .pycfg file.

Returns

Description Configuration object.

read_string (*self*, *python_string*, *description=None*, *section=None*, ***kwargs*)
Read a serialized description from a Python (.pycfg) string.

Parameters

python_string [string] Python string with a serialized description.

Returns

Description Configuration object.

write (*self*, *filename*, *description*)
Write the description to a Python (.pycfg) file.

Parameters

filename [string] Name of the file to write.

`write_string`(*self*, *description*)

Write the description to a pretty-printed Python string.

Parameters

description [Description] Configuration object to write.

Module contents

Submodules

allensdk.config.model.description module

class `allensdk.config.model.description.`**`Description`**

Bases: `object`

`fix_unary_sections`(*self*, *section_names=None*)

Wrap section contents that don't have the proper array surrounding them in an array.

Parameters

section_names [list of strings, optional] Keys of sections that might not be in array form.

`is_empty`(*self*)

Check if anything is in the object.

Returns

boolean true if self.data is missing or empty

`unpack`(*self*, *data*, *section=None*)

Read the manifest and other stand-alone configuration structure, or insert a configuration object into a section of an existing configuration.

Parameters

data [dict] A configuration object including top level sections, or an configuration object to be placed within a section.

section [string, optional.] If this is present, place data within an existing section array.

`unpack_manifest`(*self*, *data*)

Pull the manifest configuration section into a separate place.

Parameters

data [dict] A configuration structure that still has a manifest section.

`update_data`(*self*, *data*, *section=None*)

Merge configuration data possibly from multiple files.

Parameters

data [dict] Configuration structure to add.

section [string, optional] What configuration section to read it into if the file does not specify.

allensdk.config.model.description_parser module

class allensdk.config.model.description_parser.**DescriptionParser**

Bases: object

log = <Logger allensdk.config.model.description_parser (WARNING)>

parser_for_extension (*self*, *filename*)

Choose a subclass that can read the format.

Parameters

filename [string] For the extension.

Returns

DescriptionParser Appropriate subclass.

read (*self*, *file_path*, *description=None*, *section=None*, ***kwargs*)

Parse data needed for a simulation.

Parameters

description [dict] Configuration from parsing previous files.

section [string, optional] What configuration section to read it into if the file does not specify.

read_string (*self*, *data_string*, *description=None*, *section=None*, *header=None*)

Parse data needed for a simulation from a string.

write (*self*, *filename*, *description*)

Save the configuration.

Parameters

filename [string] Name of the file to write.

Module contents

Submodules

allensdk.config.manifest module

class allensdk.config.manifest.**Manifest** (*config=None*, *relative_base_dir='.'*, *version=None*)

Bases: object

Manages the location of external files referenced in an Allen SDK configuration

DIR = 'dir'

DIRNAME = 'dir_name'

FILE = 'file'

VERSION = 'manifest_version'

add_file (*self*, *file_key*, *file_name*, *dir_key=None*, *path_format=None*)

Insert a new file entry.

Parameters

file_key [string] Reference to the entry.

file_name [string] Subtitutions of the %s, %d style allowed.

dir_key [string] Reference to the parent directory entry.

path_format [string, optional] File type for further parsing.

add_path (*self*, *key*, *path*, *path_type='dir'*, *absolute=True*, *path_format=None*, *parent_key=None*)
Insert a new entry.

Parameters

key [string] Identifier for referencing the entry.

path [string] Specification for a path using %s, %d style substitution.

path_type [string enumeration] 'dir' (default) or 'file'

absolute [boolean] Is the spec relative to the process current directory.

path_format [string, optional] Indicate a known file type for further parsing.

parent_key [string] Refer to another entry.

add_paths (*self*, *path_info*)
add information about paths stored in the manifest.

Parameters

path_info [dict] Information about the new paths

as_dataframe (*self*)

check_dir (*self*, *path_key*, *do_exit=False*)
Verify a directories existence or optionally exit.

Parameters

path_key [string] Reference to the entry.

do_exit [boolean] What to do if the directory is not present.

create_dir (*self*, *path_key*)
Make a directory for an entry.

Parameters

path_key [string] Reference to the entry.

get_format (*self*, *path_key*)
Retrieve the type of a path entry.

Parameters

path_key [string] reference to the entry

Returns

string File type.

get_path (*self*, *path_key*, **args*)
Retrieve an entry with substitutions.

Parameters

path_key [string] Refer to the entry to retrieve.

args [any types, optional] arguments to be substituted into the path spec for %s, %d, etc.

Returns

string Path with parent structure and substitutions applied.

load_config(*self*, *config*, *version=None*)
Load paths into the manifest from an Allen SDK config section.

Parameters

config [Config] Manifest section of an Allen SDK config.

log = <Logger allensdk.config.manifest (WARNING)>

resolve_paths(*self*, *description_dict*, *suffix='_key'*)
Walk input items and expand those that refer to a manifest entry.

Parameters

description_dict [dict] Any entries with key names ending in suffix will be expanded.

suffix [string] Indicates the entries to be expanded.

classmethod safe_make_parent_dirs(*file_name*)
Create a parent directories for file.

Parameters

file_name [string]

Returns

leftmost [string] most rootward directory created

classmethod safe_mkdir(*directory*)
Create path if not already there.

Parameters

directory [string] create it if it doesn't exist

Returns

leftmost [string] most rootward directory created

exception allensdk.config.manifest.**ManifestVersionError**(*message*, *version*, *found_version*)
Bases: `Exception`

outdated

allensdk.config.manifest_builder module

class allensdk.config.manifest_builder.**ManifestBuilder**
Bases: `object`

add_path(*self*, *key*, *spec*, *typename='dir'*, *parent_key=None*, *format=None*)

add_section(*self*, *name*, *contents*)

as_dataframe(*self*)

df_columns = ['key', 'parent_key', 'spec', 'type', 'format']

from_dataframe(*self*, *df*)

get_config(*self*)

get_manifest(*self*)

set_version(*self*, *value*)

write_json_file(*self*, *path*, *overwrite=False*)

write_json_string(*self*)

Module contents

allensdk.config.**enable_console_log**(*level=None*)
configure allensdk logging to output to the console.

Parameters

level [int] logging level 0-50 (logging.INFO, logging.DEBUG, etc.)

Notes

See: Logging Cookbook

6.1.4 allensdk.core package

Subpackages

allensdk.core.lazy_property package

Submodules

allensdk.core.lazy_property.lazy_property module

class allensdk.core.lazy_property.lazy_property.**LazyProperty**(*api_method*, *wrappers=()*, **args*, ***kwargs*)

Bases: object

calculate(*self*)

allensdk.core.lazy_property.lazy_property_mixin module

class allensdk.core.lazy_property.lazy_property_mixin.**LazyPropertyMixin**

Bases: object

LazyProperty

Module contents

Submodules

allensdk.core.brain_observatory_cache module

allensdk.core.brain_observatory_nwb_data_set module

class allensdk.core.brain_observatory_nwb_data_set.**BrainObservatoryNwbDataSet**(*nwb_file*)
Bases: object

FILE_METADATA_MAPPING = {'age': 'general/subject/age', 'device_string': 'general/dev

MOTION_CORRECTION_DATASETS = ['MotionCorrection/2p_image_series/xy_translations', 'Mot

PIPELINE_DATASET = 'brain_observatory_pipeline'

STIMULUS_TABLE_TYPES = {'abstract_feature_series': ['drifting_gratings', 'static_grat

SUPPORTED_PIPELINE_VERSION = '3.0'

get_cell_specimen_ids(*self*)
Returns an array of cell IDs for all cells in the file

Returns

cell specimen IDs: list

get_cell_specimen_indices(*self*, *cell_specimen_ids*)
Given a list of cell specimen ids, return their index based on their order in this file.

Parameters

cell_specimen_ids: list of cell specimen ids

get_corrected_fluorescence_traces(*self*, *cell_specimen_ids=None*)
Returns an array of demixed and neuropil-corrected fluorescence traces for all ROIs and the timestamps for each datapoint

Parameters

cell_specimen_ids: list or array (optional) List of cell IDs to return traces for. If this is None (default) then all are returned

Returns

timestamps: 2D numpy array Timestamp for each fluorescence sample

traces: 2D numpy array Corrected fluorescence traces for each cell

get_demixed_traces(*self*, *cell_specimen_ids=None*)
Returns an array of demixed fluorescence traces for all ROIs and the timestamps for each datapoint

Parameters

cell_specimen_ids: list or array (optional) List of cell IDs to return traces for. If this is None (default) then all are returned

Returns

timestamps: 2D numpy array Timestamp for each fluorescence sample

traces: 2D numpy array Demixed fluorescence traces for each cell

get_dff_traces(*self*, *cell_specimen_ids=None*)
Returns an array of dF/F traces for all ROIs and the timestamps for each datapoint

Parameters

cell_specimen_ids: list or array (optional) List of cell IDs to return data for. If this is None (default) then all are returned

Returns

timestamps: 2D numpy array Timestamp for each fluorescence sample

dF/F: 2D numpy array dF/F values for each cell

get_fluorescence_timestamps(*self*)
Returns an array of timestamps in seconds for the fluorescence traces

get_fluorescence_traces(*self*, *cell_specimen_ids=None*)
Returns an array of fluorescence traces for all ROI and the timestamps for each datapoint

Parameters

cell_specimen_ids: list or array (optional) List of cell IDs to return traces for. If this is None (default) then all are returned

Returns

timestamps: 2D numpy array Timestamp for each fluorescence sample

traces: 2D numpy array Fluorescence traces for each cell

get_locally_sparse_noise_stimulus_template(*self*, *stimulus*, *mask_off_screen=True*)
Return an array of the stimulus template for the specified stimulus.

Parameters

stimulus: string

Which locally sparse noise stimulus to retrieve. Must be one of:
stimulus_info.LOCALLY_SPARSE_NOISE stimulus_info.LOCALLY_SPARSE_NOISE_4DEG stimulus_info.LOCALLY_SPARSE_NOISE_8DEG

mask_off_screen: boolean Set off-screen regions of the stimulus to LocallySparseNoise.LSN_OFF_SCREEN.

Returns

tuple: (template, off-screen mask)

get_max_projection(*self*)
Returns the maximum projection image for the 2P movie.

Returns

max projection: np.ndarray

get_metadata(*self*)
Returns a dictionary of meta data associated with each experiment, including Cre line, specimen number, visual area imaged, imaging depth

Returns

metadata: dictionary

get_motion_correction(*self*)
Returns a Panda DataFrame containing the x- and y- translation of each image used for image alignment

get_neuropil_r(*self*, *cell_specimen_ids=None*)
Returns a scalar value of r for neuropil correction of flourescence traces

Parameters

cell_specimen_ids: list or array (optional) List of cell IDs to return traces for. If this is None (default) then results for all are returned

Returns

r: 1D numpy array, len(r)=len(cell_specimen_ids) Scalar for neuropil subtraction for each cell

get_neuropil_traces(*self*, *cell_specimen_ids=None*)
Returns an array of neuropil fluorescence traces for all ROIs and the timestamps for each datapoint

Parameters

cell_specimen_ids: list or array (optional) List of cell IDs to return traces for. If this is None (default) then all are returned

Returns

timestamps: 2D numpy array Timestamp for each fluorescence sample

traces: 2D numpy array Neuropil fluorescence traces for each cell

get_pupil_location(*self*, *as_spherical=True*)
Returns the x, y pupil location.

Parameters

as_spherical [bool] Whether to return the location as spherical (default) or not. If true, the result is altitude and azimuth in degrees, otherwise it is x, y in centimeters. (0,0) is the center of the monitor.

Returns

(timestamps, location) Timestamps is an (Nx1) array of timestamps in seconds. Location is an (Nx2) array of spatial location.

get_pupil_size(*self*)
Returns the pupil area in pixels.

Returns

(timestamps, areas) Timestamps is an (Nx1) array of timestamps in seconds. Areas is an (Nx1) array of pupil areas in pixels.

get_roi_ids(*self*)
Returns an array of IDs for all ROIs in the file

Returns

ROI IDs: list

get_roi_mask(*self*, *cell_specimen_ids=None*)
Returns an array of all the ROI masks

Parameters

cell specimen IDs: list or array (optional) List of cell IDs to return traces for. If this is None (default) then all are returned

Returns

List of ROI_Mask objects

get_roi_mask_array(*self*, *cell_specimen_ids=None*)
Return a numpy array containing all of the ROI masks for requested cells. If cell_specimen_ids is omitted, return all masks.

Parameters

cell_specimen_ids: list List of cell specimen ids. Default None.

Returns

np.ndarray: NxWxH array, where N is number of cells

`get_running_speed`(*self*)
Returns the mouse running speed in cm/s

`get_session_type`(*self*)
Returns the type of experimental session, presently one of the following: three_session_A, three_session_B, three_session_C

Returns

session type: string

`get_stimulus`(*self*, *frame_ind*)

`get_stimulus_epoch_table`(*self*)
Returns a pandas dataframe that summarizes the stimulus epoch duration for each acquisition time index in the experiment

Parameters

None

Returns

timestamps: 2D numpy array Timestamp for each fluorescence sample

traces: 2D numpy array Fluorescence traces for each cell

`get_stimulus_table`(*self*, *stimulus_name*)
Return a stimulus table given a stimulus name

Notes

For more information, see: http://help.brain-map.org/display/observatory/Documentation?preview=/10616846/10813485/VisualCoding_VisualStimuli.pdf

`get_stimulus_template`(*self*, *stimulus_name*)
Return an array of the stimulus template for the specified stimulus.

Parameters

stimulus_name: string Must be one of the strings returned by list_stimuli().

Returns

stimulus table: pd.DataFrame

`list_stimuli`(*self*)
Return a list of the stimuli presented in the experiment.

Returns

stimuli: list of strings

`number_of_cells`
Number of cells in the experiment

`save_analysis_arrays`(*self*, **datasets*)

`save_analysis_dataframes`(*self*, **tables*)

`stimulus_search`

allensdk.core.brain_observatory_nwb_data_set.**align_running_speed**(*dxcm*, *dxtime*, *timestamps*)

If running speed timestamps differ from fluorescence timestamps, adjust by inserting NaNs to running speed.

Returns

tuple: dxcm, dxtime

allensdk.core.brain_observatory_nwb_data_set.**get_epoch_mask_list**(*st*, *threshold*, *max_cuts=2*)

Convenience function to cut a stim table into multiple epochs

Parameters

- **st** – input stimtable
- **threshold** – threshold on the max duration of a subepoch
- **max_cuts** – maximum number of allowed epochs to cut into

Returns epoch_mask_list, a list of indices that define the start and end of sub-epochs

allensdk.core.cache_method_utilities module

class allensdk.core.cache_method_utilities.**CachedInstanceMethodMixin**

Bases: object

cache_clear(*self*)

Calls *cache_clear* method on all bound methods in this instance (where valid). Intended to clear calls cached with the *memoize* decorator. Note that this will also clear functions decorated with *lru_cache* and *lfu_cache* in this class (or any other function with *cache_clear* attribute).

allensdk.core.cell_types_cache module

class allensdk.core.cell_types_cache.**CellTypesCache**(*cache=True*, *manifest_file=None*, *base_uri=None*)

Bases: *allensdk.api.cache.Cache*

Cache class for storing and accessing data from the Cell Types Database. By default, this class will cache any downloaded metadata or files in well known locations defined in a manifest file. This behavior can be disabled.

Parameters

cache: boolean Whether the class should save results of API queries to locations specified in the manifest file. Queries for files (as opposed to metadata) must have a file location. If caching is disabled, those locations must be specified in the function call (e.g. get_ephys_data(file_name='file.nwb')).

manifest_file: string File name of the manifest to be read. Default is "cell_types_manifest.json".

Attributes

api: CellTypesApi instance The object used for making API queries related to the Cell Types Database

CELLS_KEY = 'CELLS'

EPHYS_DATA_KEY = 'EPHYS_DATA'

EPHYS_FEATURES_KEY = 'EPHYS_FEATURES'

EPHYS_SWEEPS_KEY = 'EPHYS_SWEEPS'

MANIFEST_VERSION = '1.1'

MARKER_KEY = 'MARKER'

MORPHOLOGY_FEATURES_KEY = 'MORPHOLOGY_FEATURES'

RECONSTRUCTION_KEY = 'RECONSTRUCTION'

build_manifest(*self*, *file_name*)
Construct a manifest for this Cache class and save it in a file.

Parameters

file_name: string File location to save the manifest.

get_all_features(*self*, *dataframe=False*, *require_reconstruction=True*)
Download morphology and electrophysiology features for all cells and merge them into a single table.

Parameters

dataframe: boolean Return the output as a Pandas DataFrame. If False, return a list of dictionaries.

require_reconstruction: boolean Only return ephys and morphology features for cells that have reconstructions. Default True.

get_cells(*self*, *file_name=None*, *require_morphology=False*, *require_reconstruction=False*, *reporter_status=None*, *species=None*, *simple=True*)
Download metadata for all cells in the database and optionally return a subset filtered by whether or not they have a morphology or reconstruction.

Parameters

file_name: string File name to save/read the cell metadata as JSON. If file_name is None, the file_name will be pulled out of the manifest. If caching is disabled, no file will be saved. Default is None.

require_morphology: boolean Filter out cells that have no morphological images.

require_reconstruction: boolean Filter out cells that have no morphological reconstructions.

reporter_status: list Filter for cells that have one or more cell reporter statuses.

species: list Filter for cells that belong to one or more species. If None, return all. Must be one of [CellTypesApi.MOUSE, CellTypesApi.HUMAN].

get_ephys_data(*self*, *specimen_id*, *file_name=None*)
Download electrophysiology traces for a single cell in the database.

Parameters

specimen_id: int The ID of a cell specimen to download.

file_name: string File name to save/read the ephys features metadata as CSV. If file_name is None, the file_name will be pulled out of the manifest. If caching is disabled, no file will be saved. Default is None.

Returns

NwbDataSet A class instance with helper methods for retrieving stimulus and response traces out of an NWB file.

get_ephys_features(*self*, *dataframe=False*, *file_name=None*)
Download electrophysiology features for all cells in the database.

Parameters

file_name: string File name to save/read the ephys features metadata as CSV. If file_name is None, the file_name will be pulled out of the manifest. If caching is disabled, no file will be saved. Default is None.

dataframe: boolean Return the output as a Pandas DataFrame. If False, return a list of dictionaries.

`get_ephys_sweeps`(*self*, *specimen_id*, *file_name=None*)
Download sweep metadata for a single cell specimen.

Parameters

specimen_id: int ID of a cell.

`get_morphology_features`(*self*, *dataframe=False*, *file_name=None*)
Download morphology features for all cells with reconstructions in the database.

Parameters

file_name: string File name to save/read the ephys features metadata as CSV. If file_name is None, the file_name will be pulled out of the manifest. If caching is disabled, no file will be saved. Default is None.

dataframe: boolean Return the output as a Pandas DataFrame. If False, return a list of dictionaries.

`get_reconstruction`(*self*, *specimen_id*, *file_name=None*)
Download and open a reconstruction for a single cell in the database.

Parameters

specimen_id: int The ID of a cell specimen to download.

file_name: string File name to save/read the reconstruction SWC. If file_name is None, the file_name will be pulled out of the manifest. If caching is disabled, no file will be saved. Default is None.

Returns

Morphology A class instance with methods for accessing morphology compartments.

`get_reconstruction_markers`(*self*, *specimen_id*, *file_name=None*)
Download and open a reconstruction marker file for a single cell in the database.

Parameters

specimen_id: int The ID of a cell specimen to download.

file_name: string File name to save/read the reconstruction marker. If file_name is None, the file_name will be pulled out of the manifest. If caching is disabled, no file will be saved. Default is None.

Returns

Morphology A class instance with methods for accessing morphology compartments.

class `allensdk.core.cell_types_cache.`**`ReporterStatus`**
Bases: `object`

Valid strings for filtering by cell reporter status.

`INDETERMINATE = None`

`NA = None`

NEGATIVE = 'negative'

POSITIVE = 'positive'

allensdk.core.dat_utilities module

class allensdk.core.dat_utilities.**DatUtilities**

Bases: object

classmethod save_voltage(*output_path*, *v*, *t*)

Save a single voltage output result into a simple text format.

The output file is one t v pair per line.

Parameters

output_path [string] file name for output

v [numpy array] voltage

t [numpy array] time

allensdk.core.exceptions module

exception allensdk.core.exceptions.**DataFrameIndexError**(*msg*, *caught_exception=None*)

Bases: LookupError

More verbose method for accessing invalid rows or columns in a dataframe. Should be used when an index error is thrown on a dataframe.

exception allensdk.core.exceptions.**DataFrameKeyError**(*msg*, *caught_exception=None*)

Bases: LookupError

More verbose method for accessing invalid rows or columns in a dataframe. Should be used when a keyerror is thrown on a dataframe.

exception allensdk.core.exceptions.**MissingDataError**

Bases: ValueError

allensdk.core.h5_utilities module

allensdk.core.h5_utilities.**decode_bytes**(*bytes_dataset*, *encoding='UTF-8'*)

Convert the elements of a dataset of bytes to str

allensdk.core.h5_utilities.**h5_object_matcher_relname_in**(*relnames*, *h5_object_name*, *h5_object*)

Asks if an h5 object's relative name (the final section of its absolute name) is contained within a provided array

Parameters

relnames [array-like] Relative names against which to match

h5_object_name [str] Full name (path from origin) of h5 object

h5_object [h5py.Group, h5py.Dataset] Check this object's relative name

Returns

bool : whether the match succeeded

h5_object [h5py.group, h5py.Dataset] the argued object

`allensdk.core.h5_utilities.`**`keyed_locate_h5_objects`**(*matcher_cbs*, *h5_file*, *start_node=None*)
Traverse an h5 file and build up a dictionary mapping supplied keys to located objects

`allensdk.core.h5_utilities.`**`load_datasets_by_relnames`**(*relnames*, *h5_file*, *start_node*)
A convenience function for finding and loading into memory one or more datasets from an h5 file

`allensdk.core.h5_utilities.`**`locate_h5_objects`**(*matcher_cb*, *h5_file*, *start_node=None*)
Traverse an h5 file and return objects matching supplied criteria

`allensdk.core.h5_utilities.`**`traverse_h5_file`**(*callback*, *h5_file*, *start_node=None*)
Traverse an h5 file and apply a callback to each node

allensdk.core.json_utilities module

class `allensdk.core.json_utilities.`**`JsonComments`**
Bases: `object`

classmethod read_file(*file_name*)

classmethod read_string(*json_string*)

classmethod remove_comments(*json_string*)
Strip single and multiline javascript-style comments.

Parameters

json [string] Json string with javascript-style comments.

Returns

string Copy of the input with comments removed.

Note: A JSON decoder MAY accept and ignore comments.

classmethod remove_multiline_comments(*json_string*)
Rebuild input without substrings matching /. . . /.

Parameters

json_string [string] may or may not contain multiline comments.

Returns

string Copy of the input without the comments.

`allensdk.core.json_utilities.`**`json_handler`**(*obj*)
Used by write_json convert a few non-standard types to things that the json package can handle.

`allensdk.core.json_utilities.`**`read`**(*file_name*)
Shortcut reading JSON from a file.

`allensdk.core.json_utilities.`**`read_url`**(*url*, *method='POST'*)

`allensdk.core.json_utilities.`**`read_url_get`**(*url*)
Transform a JSON contained in a file into an equivalent nested python dict.

Parameters

url [string] where to get the json.

Returns

dict Python version of the input

Note: if the input is a bare array or literal, for example,

the output will be of the corresponding type.

`allensdk.core.json_utilities.`**`read_url_post`**(*url*)

Transform a JSON contained in a file into an equivalent nested python dict.

Parameters

url [string] where to get the json.

Returns

dict Python version of the input

Note: if the input is a bare array or literal, for example,

the output will be of the corresponding type.

`allensdk.core.json_utilities.`**`write`**(*file_name*, *obj*)

Shortcut for writing JSON to a file. This also takes care of serializing numpy and data types.

`allensdk.core.json_utilities.`**`write_string`**(*obj*)

Shortcut for writing JSON to a string. This also takes care of serializing numpy and data types.

allensdk.core.mouse_connectivity_cache module

`class` `allensdk.core.mouse_connectivity_cache.`**`MouseConnectivityCache`**(*resolution=None*, *cache=True*, *manifest_file=None*, *ccf_version=None*, *base_uri=None*, *version=None*)

Bases: `allensdk.core.reference_space_cache.ReferenceSpaceCache`

Cache class for storing and accessing data related to the adult mouse Connectivity Atlas. By default, this class will cache any downloaded metadata or files in well known locations defined in a manifest file. This behavior can be disabled.

Parameters

resolution: int Resolution of grid data to be downloaded when accessing projection volume, the annotation volume, and the annotation volume. Must be one of (10, 25, 50, 100). Default is 25.

ccf_version: string Desired version of the Common Coordinate Framework. This affects the annotation volume (get_annotation_volume) and structure masks (get_structure_mask). Must be one of (MouseConnectivityApi.CCF_2015, MouseConnectivityApi.CCF_2016). Default: MouseConnectivityApi.CCF_2016

cache: boolean Whether the class should save results of API queries to locations specified in the manifest file. Queries for files (as opposed to metadata) must have a file location. If caching is disabled, those locations must be specified in the function call (e.g. get_projection_density(file_name='file.nrrd')).

manifest_file: string File name of the manifest to be read. Default is "mouse_connectivity_manifest.json".

Attributes

resolution: int Resolution of grid data to be downloaded when accessing projection volume, the annotation volume, and the annotation volume. Must be one of (10, 25, 50, 100). Default is 25.

api: MouseConnectivityApi instance Used internally to make API queries.

ALIGNMENT3D_KEY = 'ALIGNMENT3D'

DATA_MASK_KEY = 'DATA_MASK'

DEFAULT_STRUCTURE_SET_IDS = (167587189,)

DEFORMATION_FIELD_HEADER_KEY = 'DEFORMATION_FIELD_HEADER'

DEFORMATION_FIELD_VOXEL_KEY = 'DEFORMATION_FIELD_VOXELS'

DFMFLD_RESOLUTIONS = (25,)

EXPERIMENTS_KEY = 'EXPERIMENTS'

INJECTION_DENSITY_KEY = 'INJECTION_DENSITY'

INJECTION_FRACTION_KEY = 'INJECTION_FRACTION'

MANIFEST_VERSION = 1.3

PROJECTION_DENSITY_KEY = 'PROJECTION_DENSITY'

STRUCTURE_UNIONIZES_KEY = 'STRUCTURE_UNIONIZES'

SUMMARY_STRUCTURE_SET_ID = 167587189

add_manifest_paths (*self*, *manifest_builder*)
Construct a manifest for this Cache class and save it in a file.

Parameters

file_name: string File location to save the manifest.

default_structure_ids

filter_experiments (*self*, *experiments*, *cre=None*, *injection_structure_ids=None*)
Take a list of experiments and filter them by cre status and injection structure.

Parameters

cre: boolean or list If True, return only cre-positive experiments. If False, return only cre-negative experiments. If None, return all experients. If list, return all experiments with cre line names in the supplied list. Default None.

injection_structure_ids: list Only return experiments that were injected in the structures provided here. If None, return all experiments. Default None.

filter_structure_unionizes (*self*, *unionizes*, *is_injection=None*, *structure_ids=None*, *include_descendants=False*, *hemisphere_ids=None*)
Take a list of unionzes and return a subset of records filtered by injection status, structure, and hemisphere.

Parameters

is_injection: boolean If True, only return unionize records that disregard non-injection pixels. If False, only return unionize records that disregard injection pixels. If None, return all records. Default None.

structure_ids: list Only return unionize records for a set of structures. If None, return all records. Default None.

include_descendants: boolean Include all descendant records for specified structures. Default False.

hemisphere_ids: list Only return unionize records that disregard pixels outside of a hemisphere. or set of hemispheres. Left = 1, Right = 2, Both = 3. If None, include all records [1, 2, 3]. Default None.

get_affine_parameters(*self*, *section_data_set_id*, *direction='trv'*, *file_name=None*)
Extract the parameters of the 3D affine tranformation mapping this section data set's image-space stack to CCF-space (or vice-versa).

Parameters

section_data_set_id [int] download the parameters for this data set.

direction [str, optional]

Valid options are:

trv ["transform from reference to volume". Maps CCF points to image space points. If you are] resampling data into CCF, this is the direction you want.

tvr : "transform from volume to reference". Maps image space points to CCF points.

file_name [str] If provided, store the downloaded file here.

Returns

alignment [numpy.ndarray]

4 X 3 matrix. In order to transform a point [X_1, X_2, X_3] run np.dot([X_1, X_2, X_3, 1], alignment). In

to build a SimpleITK affine transform run: transform = sitk.AffineTransform(3) transform.SetParameters(alignment.flatten())

get_data_mask(*self*, *experiment_id*, *file_name=None*)
Read a data mask volume for a single experiment. Download it first if it doesn't exist. Data mask is a binary mask of voxels that have valid data. Only use valid data in analysis!

Parameters

experiment_id: int ID of the experiment to download/read. This corresponds to section_data_set_id in the API.

file_name: string File name to store the template volume. If it already exists, it will be read from this file. If file_name is None, the file_name will be pulled out of the manifest. Default is None.

get_deformation_field(*self*, *section_data_set_id*, *header_path=None*, *voxel_path=None*)
Extract the local alignment parameters for this dataset. This a 3D vector image (3 components) describing a deformable local mapping from CCF voxels to this section data set's affine-aligned image stack.

Parameters

section_data_set_id [int]

Download the deformation field for this data set

header_path [str, optional] If supplied, the deformation field header will be downloaded to this path.

voxel_path [str, optiona] If supplied, the deformation field voxels will be downloaded to this path.

Returns

numpy.ndarray : 3D X 3 component vector array (origin 0, 0, 0; 25-micron isometric resolution) defining a deformable transformation from CCF-space to affine-transformed image space.

get_experiment_structure_unionizes(*self*, *experiment_id*, *file_name=None*, *is_injection=None*, *structure_ids=None*, *include_descendants=False*, *hemisphere_ids=None*)

Retrieve the structure unionize data for a specific experiment. Filter by structure, injection status, and hemisphere.

Parameters

experiment_id: int ID of the experiment of interest. Corresponds to section_data_set_id in the API.

file_name: string File name to save/read the experiments list. If file_name is None, the file_name will be pulled out of the manifest. If caching is disabled, no file will be saved. Default is None.

is_injection: boolean If True, only return unionize records that disregard non-injection pixels. If False, only return unionize records that disregard injection pixels. If None, return all records. Default None.

structure_ids: list Only return unionize records for a specific set of structures. If None, return all records. Default None.

include_descendants: boolean Include all descendant records for specified structures. Default False.

hemisphere_ids: list Only return unionize records that disregard pixels outside of a hemisphere. or set of hemispheres. Left = 1, Right = 2, Both = 3. If None, include all records [1, 2, 3]. Default None.

get_experiments(*self*, *dataframe=False*, *file_name=None*, *cre=None*, *injection_structure_ids=None*)

Read a list of experiments that match certain criteria. If caching is enabled, this will save the whole (unfiltered) list of experiments to a file.

Parameters

dataframe: boolean Return the list of experiments as a Pandas DataFrame. If False, return a list of dictionaries. Default False.

file_name: string File name to save/read the structures table. If file_name is None, the file_name will be pulled out of the manifest. If caching is disabled, no file will be saved. Default is None.

cre: boolean or list If True, return only cre-positive experiments. If False, return only cre-negative experiments. If None, return all experients. If list, return all experiments with cre line names in the supplied list. Default None.

injection_structure_ids: list Only return experiments that were injected in the structures provided here. If None, return all experiments. Default None.

get_injection_density(*self*, *experiment_id*, *file_name=None*)

Read an injection density volume for a single experiment. Download it first if it doesn't exist. Injection density is the proportion of projecting pixels in a grid voxel only including pixels that are part of the injection site in [0,1].

Parameters

experiment_id: int ID of the experiment to download/read. This corresponds to section_data_set_id in the API.

file_name: string File name to store the template volume. If it already exists, it will be read from this file. If file_name is None, the file_name will be pulled out of the manifest. Default is None.

`get_injection_fraction`(*self*, *experiment_id*, *file_name=None*)

Read an injection fraction volume for a single experiment. Download it first if it doesn't exist. Injection fraction is the proportion of pixels in the injection site in a grid voxel in [0,1].

Parameters

experiment_id: int ID of the experiment to download/read. This corresponds to section_data_set_id in the API.

file_name: string File name to store the template volume. If it already exists, it will be read from this file. If file_name is None, the file_name will be pulled out of the manifest. Default is None.

`get_projection_density`(*self*, *experiment_id*, *file_name=None*)

Read a projection density volume for a single experiment. Download it first if it doesn't exist. Projection density is the proportion of of projecting pixels in a grid voxel in [0,1].

Parameters

experiment_id: int ID of the experiment to download/read. This corresponds to section_data_set_id in the API.

file_name: string File name to store the template volume. If it already exists, it will be read from this file. If file_name is None, the file_name will be pulled out of the manifest. Default is None.

`get_projection_matrix`(*self*, *experiment_ids*, *projection_structure_ids=None*, *hemisphere_ids=None*, *parameter='projection_volume'*, *dataframe=False*)

`get_structure_unionizes`(*self*, *experiment_ids*, *is_injection=None*, *structure_ids=None*, *include_descendants=False*, *hemisphere_ids=None*)

Get structure unionizes for a set of experiment IDs. Filter the results by injection status, structure, and hemisphere.

Parameters

experiment_ids: list List of experiment IDs. Corresponds to section_data_set_id in the API.

is_injection: boolean If True, only return unionize records that disregard non-injection pixels. If False, only return unionize records that disregard injection pixels. If None, return all records. Default None.

structure_ids: list Only return unionize records for a specific set of structures. If None, return all records. Default None.

include_descendants: boolean Include all descendant records for specified structures. Default False.

hemisphere_ids: list Only return unionize records that disregard pixels outside of a hemisphere. or set of hemispheres. Left = 1, Right = 2, Both = 3. If None, include all records [1, 2, 3]. Default None.

`rank_structures`(*self*, *experiment_ids*, *is_injection*, *structure_ids=None*, *hemisphere_ids=None*, *rank_on='normalized_projection_volume'*, *n=5*, *threshold=0.01*)

Produces one or more (per experiment) ranked lists of brain structures, using a specified data field.

Parameters

experiment_ids [list of int] Obtain injection_structures for these experiments.

is_injection [boolean] Use data from only injection (or non-injection) unionizes.

structure_ids [list of int, optional] Consider only these structures. It is a good idea to make sure that these structures are not spatially overlapping; otherwise your results will contain redundant information. Defaults to the summary structures - a brain-wide list of nonoverlapping mid-level structures.

hemisphere_ids [list of int, optional] Consider only these hemispheres (1: left, 2: right, 3: both). Like with structures, you might get redundant results if you select overlapping options. Defaults to [1, 2].

rank_on [str, optional] Rank unionize data using this field (descending). Defaults to normalized_projection_volume.

n [int, optional] Return only the top n structures.

threshold [float, optional] Consider only records whose data value - specified by the rank_on parameter - exceeds this value.

Returns

list : Each element (1 for each input experiment) is a list of dictionaries. The dictionaries describe the top injection structures in descending order. They are specified by their structure and hemisphere id fields and additionally report the value specified by the rank_on parameter.

allensdk.core.nwb_data_set module

class `allensdk.core.nwb_data_set.`**`NwbDataSet`**(*file_name*, *spike_time_key=None*)

Bases: `object`

A very simple interface for exracting electrophysiology data from an NWB file.

`DEPRECATED_SPIKE_TIMES = 'aibs_spike_times'`

`SPIKE_TIMES = 'spike_times'`

`fill_sweep_responses`(*self*, *fill_value=0.0*, *sweep_numbers=None*, *extend_experiment=False*)

Fill sweep response arrays with a single value.

Parameters

fill_value: float Value used to fill sweep response array

sweep_numbers: list List of integer sweep numbers to be filled (default all sweeps)

extend_experiment: bool If True, extend experiment epoch length to the end of the sweep (undo any truncation)

`get_experiment_sweep_numbers`(*self*)

Get all of the sweep numbers for experiment epochs in the file, not including test sweeps.

`get_pipeline_version`(*self*)

Returns the AI pipeline version number, stored in the metadata field 'generated_by'. If that field is missing, version 0.0 is returned.

Returns

int tuple: (major, minor)

get_spike_times(*self*, *sweep_number*, *key=None*)
Return any spike times stored in the NWB file for a sweep.

Parameters

sweep_number: int index to access

key [string] label where the spike times are stored (default NwbDataSet.SPIKE_TIMES)

Returns

list list of spike times in seconds relative to the start of the sweep

get_sweep(*self*, *sweep_number*)
Retrieve the stimulus, response, index_range, and sampling rate for a particular sweep. This method hides the NWB file's distinction between a "Sweep" and an "Experiment". An experiment is a subset of of a sweep that excludes the initial test pulse. It also excludes any erroneous response data at the end of the sweep (usually for ramp sweeps, where recording was terminated mid-stimulus).

Some sweeps do not have an experiment, so full data arrays are returned. Sweeps that have an experiment return full data arrays (include the test pulse) with any erroneous data trimmed from the back of the sweep.

Parameters

sweep_number: int

Returns

dict A dictionary with 'stimulus', 'response', 'index_range', and 'sampling_rate' elements. The index range is a 2-tuple where the first element indicates the end of the test pulse and the second index is the end of valid response data.

get_sweep_metadata(*self*, *sweep_number*)
Retrieve the sweep level metadata associated with each sweep. Includes information on stimulus parameters like its name and amplitude as well as recording quality metadata, like access resistance and seal quality.

Parameters

sweep_number: int

Returns

dict A dictionary with 'aibs_stimulus_amplitude_pa', 'aibs_stimulus_name', 'gain', 'initial_access_resistance', 'seal' elements. These specific fields are ones encoded in the original AIBS in vitro .nwb files.

get_sweep_numbers(*self*)
Get all of the sweep numbers in the file, including test sweeps.

set_spike_times(*self*, *sweep_number*, *spike_times*, *key=None*)
Set or overwrite the spikes times for a sweep.

Parameters

sweep_number [int] index to access

key [string] where the times are stored (default NwbDataSet.SPIKE_TIME)

spike_times: np.array array of spike times in seconds

set_sweep(*self*, *sweep_number*, *stimulus*, *response*)
Overwrite the stimulus or response of an NWB file. If the supplied arrays are shorter than stored arrays, they are padded with zeros to match the original data size.

Parameters

sweep_number: int

stimulus: np.array Overwrite the stimulus with this array. If None, stimulus is unchanged.

response: np.array Overwrite the response with this array. If None, response is unchanged.

allensdk.core.obj_utilities module

`allensdk.core.obj_utilities.`**`parse_obj`**`(`*lines*`)`

Parse a wavefront obj file into a triplet of vertices, normals, and faces. This parser is specific to obj files generated from our annotation volumes

Parameters

lines [list of str] Lines of input obj file

Returns

vertices [np.ndarray] Dimensions are (nSamples, nCoordinates=3). Locations in the reference space of vertices

vertex_normals [np.ndarray] Dimensions are (nSample, nElements=3). Vectors normal to vertices.

face_vertices [np.ndarray] Dimensions are (sample, nVertices=3). References are given in indices (0-indexed here, but 1-indexed in the file) of vertices that make up each face.

face_normals [np.ndarray] Dimensions are (sample, nNormals=3). References are given in indices (0-indexed here, but 1-indexed in the file) of vertex normals that make up each face.

Notes

This parser is specialized to the obj files that the Allen Institute for Brain Science generates from our own structure annotations.

`allensdk.core.obj_utilities.`**`read_obj`**`(`*path*`)`

allensdk.core.ontology module

`class` `allensdk.core.ontology.`**`Ontology`**`(`*df*`)`

Bases: `object`

Note: Deprecated from 0.12.5 *Ontology* has been replaced by *StructureTree*.

`get_child_ids``(`*self*, *structure_ids*`)`

Find the set of ids that are immediate children of one or more structures.

Parameters

structure_ids: iterable Any iterable type that contains structure ids that can be cast to integers.

Returns

set Set of child structure ids

get_children (*self*, *structure_ids*)
Find the set of structures that are immediate children of one or more structures.

Parameters

structure_ids: iterable Any iterable type that contains structure ids that can be cast to integers.

Returns

pandas.DataFrame Set of child structures

get_descendant_ids (*self*, *structure_ids*)
Find the set of the ids of structures that are descendants of one or more structures. The returned set will include the input structure ids.

Parameters

structure_ids: iterable Any iterable type that contains structure ids that can be cast to integers.

Returns

set Set of descendant structure ids.

get_descendants (*self*, *structure_ids*)
Find the set of structures that are descendants of one or more structures. The returned set will include the input structures.

Parameters

structure_ids: iterable Any iterable type that contains structure ids that can be cast to integers.

Returns

pandas.DataFrame Set of descendant structures.

structure_descends_from (*self*, *child_id*, *parent_id*)
Return whether one structure id is a descendant of another structure id.

allensdk.core.ophys_experiment_session_id_mapping module

allensdk.core.reference_space module

class allensdk.core.reference_space.**ReferenceSpace** (*structure_tree*, *annotation*, *resolution*)
Bases: object

static check_and_write (*base_dir*, *structure_id*, *fn*)
A many_structure_masks callback that writes the mask to a nrrd file if the file does not already exist.

check_coverage (*self*, *structure_ids*, *domain_mask*)
Determines whether a spatial domain is completely covered by structures in a set.

Parameters

structure_ids [list of int] Specifies the set of structures to check.

domain_mask [numpy ndarray] Same shape as annotation. 1 inside the mask, 0 out. Specifies spatial domain.

Returns

numpy ndarray : 1 where voxels are missing from the candidate, 0 where the candidate exceeds the domain

direct_voxel_counts(*self*)
Determines the number of voxels directly assigned to one or more structures.

Returns

dict : Keys are structure ids, values are the number of voxels directly assigned to those structures.

direct_voxel_map

downsample(*self*, *target_resolution*)
Obtain a smaller reference space by downsampling

Parameters

target_resolution [tuple of numeric] Resolution in microns of the output space.

interpolator [string] Method used to interpolate the volume. Currently only 'nearest' is supported

Returns

ReferenceSpace : A new ReferenceSpace with the same structure tree and a downsampled annotation.

export_itksnap_labels(*self*, *id_type=<class 'numpy.uint16'>*, *label_description_kwargs=None*)
Produces itksnap labels, remapping large ids if needed.

Parameters

id_type [np.integer, optional] Used to determine the type of the output annotation and whether ids need to be remapped to smaller values.

label_description_kwargs [dict, optional] Keyword arguments passed to StructureTree.export_label_description

Returns

np.ndarray : Annotation volume, remapped if needed

pd.DataFrame label_description dataframe

get_slice_image(*self*, *axis*, *position*, *cmap=None*)
Produce a AxBx3 RGB image from a slice in the annotation

Parameters

axis [int] Along which to slice the annotation volume. 0 is coronal, 1 is horizontal, and 2 is sagittal.

position [int] In microns. Take the slice from this far along the specified axis.

cmap [dict, optional] Keys are structure ids, values are rgb triplets. Defaults to structure rgb_triplets.

Returns

np.ndarray : RGB image array.

Notes

If you assign a custom colormap, make sure that you take care of the background in addition to the structures.

`make_structure_mask`(*self*, *structure_ids*, *direct_only=False*)
Return an indicator array for one or more structures

Parameters

structure_ids [list of int] Make a mask that indicates the union of these structures' voxels

direct_only [bool, optional] If True, only include voxels directly assigned to a structure in the mask. Otherwise include voxels assigned to descendants.

Returns

numpy ndarray : Same shape as annotation. 1 inside mask, 0 outside.

`many_structure_masks`(*self*, *structure_ids*, *output_cb=None*, *direct_only=False*)
Build one or more structure masks and do something with them

Parameters

structure_ids [list of int] Specify structures to be masked

output_cb [function, optional] Must have the following signature: output_cb(structure_id, fn). On each requested id, fn will be curried to make a mask for that id. Defaults to returning the structure id and mask.

direct_only [bool, optional] If True, only include voxels directly assigned to a structure in the mask. Otherwise include voxels assigned to descendants.

Yields

Return values of output_cb called on each structure_id, structure_mask

pair.

Notes

output_cb is called on every yield, so any side-effects (such as writing to a file) will be carried out regardless of what you do with the return values. You do actually have to iterate through the output, though.

`remove_unassigned`(*self*, *update_self=True*)
Obtains a structure tree consisting only of structures that have at least one voxel in the annotation.

Parameters

update_self [bool, optional] If True, the contained structure tree will be replaced,

Returns

list of dict : elements are filtered structures

`static return_mask_cb`(*structure_id*, *fn*)
A basic callback for many_structure_masks

`total_voxel_counts`(*self*)
Determines the number of voxels assigned to a structure or its descendants

Returns

dict : Keys are structure ids, values are the number of voxels assigned to structures' descendants.

total_voxel_map

validate_structures (*self*, *structure_ids*, *domain_mask*)
Determines whether a set of structures produces an exact and nonoverlapping tiling of a spatial domain

Parameters

structure_ids [list of int] Specifies the set of structures to check.

domain_mask [numpy ndarray] Same shape as annotation. 1 inside the mask, 0 out. Specifies spatial domain.

Returns

set : Ids of structures that are the ancestors of other structures in the supplied set.

numpy ndarray : Indicator for missing voxels.

write_itksnap_labels (*self*, *annotation_path*, *label_path*, ***kwargs*)
Generate a label file (nrrd) and a label_description file (csv) for use with ITKSnap

Parameters

annotation_path [str] write generated label file here

label_path [str] write generated label_description file here

****kwargs :** will be passed to self.export_itksnap_labels

allensdk.core.reference_space_cache module

class allensdk.core.reference_space_cache.**ReferenceSpaceCache** (*resolution*, *reference_space_key*, ***kwargs*)

Bases: *allensdk.api.cache.Cache*

ANNOTATION_KEY = 'ANNOTATION'

MANIFEST_VERSION = 1.2

REFERENCE_SPACE_VERSION_KEY = 'REFERENCE_SPACE_VERSION'

STRUCTURES_KEY = 'STRUCTURES'

STRUCTURE_MASK_KEY = 'STRUCTURE_MASK'

STRUCTURE_MESH_KEY = 'STRUCTURE_MESH'

STRUCTURE_TREE_KEY = 'STRUCTURE_TREE'

TEMPLATE_KEY = 'TEMPLATE'

add_manifest_paths (*self*, *manifest_builder*)
Construct a manifest for this Cache class and save it in a file.

Parameters

file_name: string File location to save the manifest.

get_annotation_volume (*self*, *file_name=None*)
Read the annotation volume. Download it first if it doesn't exist.

Parameters

file_name: string File name to store the annotation volume. If it already exists, it will be read from this file. If file_name is None, the file_name will be pulled out of the manifest. Default is None.

get_reference_space(*self*, *structure_file_name=None*, *annotation_file_name=None*)
Build a ReferenceSpace from this cache's annotation volume and structure tree. The ReferenceSpace does operations that relate brain structures to spatial domains.

Parameters

structure_file_name: string File name to save/read the structures table. If file_name is None, the file_name will be pulled out of the manifest. If caching is disabled, no file will be saved. Default is None.

annotation_file_name: string File name to store the annotation volume. If it already exists, it will be read from this file. If file_name is None, the file_name will be pulled out of the manifest. Default is None.

get_structure_mask(*self*, *structure_id*, *file_name=None*, *annotation_file_name=None*)
Read a 3D numpy array shaped like the annotation volume that has non-zero values where voxels belong to a particular structure. This will take care of identifying substructures.

Parameters

structure_id: int ID of a structure.

file_name: string File name to store the structure mask. If it already exists, it will be read from this file. If file_name is None, the file_name will be pulled out of the manifest. Default is None.

annotation_file_name: string File name to store the annotation volume. If it already exists, it will be read from this file. If file_name is None, the file_name will be pulled out of the manifest. Default is None.

Notes

This method downloads structure masks from the Allen Institute. To make your own locally, see ReferenceSpace.many_structure_masks.

get_structure_mesh(*self*, *structure_id*, *file_name=None*)
Obtain a 3D mesh specifying the surface of an annotated structure.

Parameters

structure_id: int ID of a structure.

file_name: string File name to store the structure mesh. If it already exists, it will be read from this file. If file_name is None, the file_name will be pulled out of the manifest. Default is None.

Returns

vertices [np.ndarray] Dimensions are (nSamples, nCoordinates=3). Locations in the reference space of vertices

vertex_normals [np.ndarray] Dimensions are (nSample, nElements=3). Vectors normal to vertices.

face_vertices [np.ndarray] Dimensions are (sample, nVertices=3). References are given in indices (0-indexed here, but 1-indexed in the file) of vertices that make up each face.

face_normals [np.ndarray] Dimensions are (sample, nNormals=3). References are given in indices (0-indexed here, but 1-indexed in the file) of vertex normals that make up each face.

Notes

These meshes are meant for 3D visualization and as such have been smoothed. If you are interested in performing quantative analyses, we recommend that you use the structure masks instead.

get_structure_tree(*self*, *file_name=None*, *structure_graph_id=1*)
Read the list of adult mouse structures and return an StructureTree instance.

Parameters

file_name: string File name to save/read the structures table. If file_name is None, the file_name will be pulled out of the manifest. If caching is disabled, no file will be saved. Default is None.

structure_graph_id: int Build a tree using structure only from the identified structure graph.

get_template_volume(*self*, *file_name=None*)
Read the template volume. Download it first if it doesn't exist.

Parameters

file_name: string File name to store the template volume. If it already exists, it will be read from this file. If file_name is None, the file_name will be pulled out of the manifest. Default is None.

classmethod validate_structure_id(*structure_id*)

classmethod validate_structure_ids(*structure_ids*)

allensdk.core.simple_tree module

class allensdk.core.simple_tree.**SimpleTree**(*nodes*, *node_id_cb*, *parent_id_cb*)
Bases: `object`

ancestor_ids(*self*, *node_ids*)
Obtain the ids of one or more nodes' ancestors

Parameters

node_ids [list of hashable] Items are ids of nodes whose ancestors you wish to find.

Returns

list of list of hashable : Items are lists of input nodes' ancestors' ids.

Notes

Given the tree: A -> B -> C

‘-> D

The ancestors of C are [C, B, A]. The ancestors of A are [A]. The ancestors of D are [D, A]

ancestors(*self*, *node_ids*)
Get one or mode nodes' ancestor nodes

Parameters

node_ids [list of hashable] Items are ids of nodes whose ancestors will be found.

Returns

list of list of dict : Items are lists of ancestor nodes corresponding to argued ids.

child_ids (*self*, *node_ids*)
Obtain the ids of one or more nodes' children

Parameters

node_ids [list of hashable] Items are ids of nodes whose children you wish to find.

Returns

list of list of hashable : Items are lists of input nodes' children's ids.

children (*self*, *node_ids*)
Get one or mode nodes' child nodes

Parameters

node_ids [list of hashable] Items are ids of nodes whose children will be found.

Returns

list of list of dict : Items are lists of child nodes corresponding to argued ids.

descendant_ids (*self*, *node_ids*)
Obtain the ids of one or more nodes' descendants

Parameters

node_ids [list of hashable] Items are ids of nodes whose descendants you wish to find.

Returns

list of list of hashable : Items are lists of input nodes' descendants' ids.

Notes

Given the tree: A -> B -> C

'-> D

The descendants of A are [B, C, D]. The descendants of C are [].

descendants (*self*, *node_ids*)
Get one or mode nodes' descendant nodes

Parameters

node_ids [list of hashable] Items are ids of nodes whose descendants will be found.

Returns

list of list of dict : Items are lists of descendant nodes corresponding to argued ids.

filter_nodes (*self*, *criterion*)
Obtain a list of nodes filtered by some criterion

Parameters

criterion [function | node dict => bool] Only nodes for which criterion returns true will be returned.

Returns

list of dict : Items are node dictionaries that passed the filter.

`node` (*self*, *node_ids=None*)

`node_ids` (*self*)
Obtain the node ids of each node in the tree

Returns

list : elements are node ids

`nodes` (*self*, *node_ids=None*)
Get one or more nodes' full dictionaries from their ids.

Parameters

node_ids [list of hashable] Items are ids of nodes to be returned. Default is all.

Returns

list of dict : Items are nodes corresponding to argued ids.

`nodes_by_property` (*self*, *key*, *values*, *to_fn=None*)
Get nodes by a specified property

Parameters

key [hashable or function] The property used for lookup. Should be unique. If a function, will be invoked on each node.

values [list] Select matching elements from the lookup.

to_fn [function, optional] Defines the outputs, on a per-node basis. Defaults to returning the whole node.

Returns

list : outputs, 1 for each input value.

`parent` (*self*, *node_ids*)

`parent_id` (*self*, *node_ids*)

`parent_ids` (*self*, *node_ids*)
Obtain the ids of one or more nodes' parents

Parameters

node_ids [list of hashable] Items are ids of nodes whose parents you wish to find.

Returns

list of hashable : Items are ids of input nodes' parents in order.

`parents` (*self*, *node_ids*)
Get one or mode nodes' parent nodes

Parameters

node_ids [list of hashable] Items are ids of nodes whose parents will be found.

Returns

list of dict : Items are parents of nodes corresponding to argued ids.

`value_map` (*self*, *from_fn*, *to_fn*)
Obtain a look-up table relating a pair of node properties across nodes

Parameters

from_fn [function | node dict => hashable value] The keys of the output dictionary will be obtained by calling from_fn on each node. Should be unique.

to_fn [function | node_dict => value] The values of the output function will be obtained by calling to_fn on each node.

Returns

dict : Maps the node property defined by from_fn to the node property defined by to_fn across nodes.

allensdk.core.sitk_utilities module

`allensdk.core.sitk_utilities.`**`fix_array_dimensions`**(*array*, *ncomponents=1*)
Convenience function that reorders ndarray dimensions for io with SimpleITK

Parameters

array [np.ndarray] The array to be reordered

ncomponents [int, optional] Number of components per pixel, default 1.

Returns

np.ndarray : Reordered array

`allensdk.core.sitk_utilities.`**`get_sitk_image_information`**(*image*)
Extract information about a SimpleITK image

Parameters

image [sitk.Image] Extract information about this image.

Returns

dict : Extracted information. Includes spacing, origin, size, direction, and number of components per pixel

`allensdk.core.sitk_utilities.`**`read_ndarray_with_sitk`**(*path*)
Read a numpy array from a file using SimpleITK

Parameters

path [str] Read from this path

Returns

image [np.ndarray] Obtained array

information [dict] Additional information about the array

`allensdk.core.sitk_utilities.`**`set_sitk_image_information`**(*image*, *information*)
Set information on a SimpleITK image

Parameters

image [sitk.Image] Set information on this image.

information [dict] Stores information to be set. Supports spacing, origin, direction. Also checks (but cannot set) size and number of components per pixel

`allensdk.core.sitk_utilities.`**`write_ndarray_with_sitk`**(*array*, *path*, ***information*)
Write a numpy array to a file using SimpleITK

Parameters

array [np.ndarray] Array to be written.

path [str] Write to here

****information** [dict] Contains additional information to be stored in the image file. See set_sitk_image_information for more information.

allensdk.core.structure_tree module

class allensdk.core.structure_tree.**StructureTree**(*nodes*)

Bases: *allensdk.core.simple_tree.SimpleTree*

static clean_structures(*structures*, *whitelist=None*, *data_transforms=None*, *renames=None*)

Convert structures_with_sets query results into a form that can be used to construct a StructureTree

Parameters

structures [list of dict] Each element describes a structure. Should have a structure id path field (str values) and a structure_sets field (list of dict).

whitelist [list of str, optional] Only these fields will be included in the final structure record. Default is the output of StructureTree.whitelist.

data_transforms [dict, optional] Keys are str field names. Values are functions which will be applied to the data associated with those fields. Default is to map colors from hex to rgb and convert the structure id path to a list of int.

renames [dict, optional] Controls the field names that appear in the output structure records. Default is to map 'color_hex_triplet' to 'rgb_triplet'.

Returns

list of dict : structures, after conversion of structure_id_path and structure_sets

static collect_sets(*structure*)

Structure sets may be specified by full records or id. This method collects all of the structure set records/ids in a structure record and replaces them with a single list of id records.

static data_transforms()

export_label_description(*self*, *alphas=None*, *exclude_label_vis=None*, *exclude_mesh_vis=None*, *label_key='acronym'*)

Produces an itksnap label_description table from this structure tree

Parameters

alphas [dict, optional] Maps structure ids to alpha levels. Optional - will only use provided ids.

exclude_label_vis [list, optional] The structures denoted by these ids will not be visible in ITKSnap.

exclude_mesh_vis [list, optional] The structures denoted by these ids will not have visible meshes in ITKSnap.

label_key: str, optional Use this column for display labels.

Returns

pd.DataFrame : Contains data needed for loading as an ITKSnap label description file.

get_ancestor_id_map(*self*)
Get a dictionary mapping structure ids to ancestor ids across all nodes.

Returns

dict : Keys are structure ids. Values are lists of ancestor ids.

get_colormap(*self*)
Get a dictionary mapping structure ids to colors across all nodes.

Returns

dict : Keys are structure ids. Values are RGB lists of integers.

get_id_acronym_map(*self*)
Get a dictionary mapping structure acronyms to ids across all nodes.

Returns

dict : Keys are structure acronyms. Values are structure ids.

get_name_map(*self*)
Get a dictionary mapping structure ids to names across all nodes.

Returns

dict : Keys are structure ids. Values are structure name strings.

get_structure_sets(*self*)
Lists all unique structure sets that are assigned to at least one structure in the tree.

Returns

list of int : Elements are ids of structure sets.

get_structures_by_acronym(*self*, *acronyms*)
Obtain a list of brain structures from their acronyms

Parameters

names [list of str] Get structures corresponding to these acronyms.

Returns

list of dict : Each item describes a structure.

get_structures_by_id(*self*, *structure_ids*)
Obtain a list of brain structures from their structure ids

Parameters

structure_ids [list of int] Get structures corresponding to these ids.

Returns

list of dict : Each item describes a structure.

get_structures_by_name(*self*, *names*)
Obtain a list of brain structures from their names,

Parameters

names [list of str] Get structures corresponding to these names.

Returns

list of dict : Each item describes a structure.

get_structures_by_set_id(*self*, *structure_set_ids*)
Obtain a list of brain structures from by the sets that contain them.

Parameters

structure_set_ids [list of int] Get structures belonging to these structure sets.

Returns

list of dict : Each item describes a structure.

has_overlaps(*self*, *structure_ids*)
Determine if a list of structures contains structures along with their ancestors

Parameters

structure_ids [list of int] Check this set of structures for overlaps

Returns

set : Ids of structures that are the ancestors of other structures in the supplied set.

static hex_to_rgb(*hex_color*)
Convert a hexadecimal color string to a uint8 triplet

Parameters

hex_color [string] Must be 6 characters long, unless it is 7 long and the first character is #. If hex_color is a triplet of int, it will be returned unchanged.

Returns

list of int : 3 characters long - 1 per two characters in the input string.

static path_to_list(*path*)
Structure id paths are sometimes formatted as "/"-seperated strings. This method converts them to a list of integers, if needed.

static renames()

structure_descends_from(*self*, *child_id*, *parent_id*)
Tests whether one structure descends from another.

Parameters

child_id [int] Id of the putative child structure.

parent_id [int] Id of the putative parent structure.

Returns

bool : True if the structure specified by child_id is a descendant of the one specified by parent_id. Otherwise False.

static whitelist()

allensdk.core.swc module

class allensdk.core.swc.**Compartment**(**args*, ***kwargs*)
Bases: `dict`

A dictionary class storing information about a single morphology node

print_node(*self*)
print out compartment information with field names

class `allensdk.core.swc.`**`Marker`**(**args*, ***kwargs*)

Bases: `dict`

Simple dictionary class for handling reconstruction marker objects.

`CUT_DENDRITE = 10`

`NO_RECONSTRUCTION = 20`

`SPACING = [0.1144, 0.1144, 0.28]`

class `allensdk.core.swc.`**`Morphology`**(*compartment_list=None*, *compartment_index=None*)

Bases: `object`

Keep track of the list of compartments in a morphology and provide a few helper methods (soma, tree information, pruning, etc).

`APICAL_DENDRITE = 4`

`AXON = 2`

`BASAL_DENDRITE = 3`

`DENDRITE = 3`

`NODE_TYPES = [1, 2, 3, 3, 4]`

`SOMA = 1`

`append`(*self*, *node_list*)

Add additional nodes to this Morphology. Those nodes must originate from another morphology object.

Parameters

node_list: list of Morphology nodes

`apply_affine`(*self*, *aff*, *scale=None*)

Apply an affine transform to all compartments in this morphology. Node radius is adjusted as well.

Format of the affine matrix is:

[x0 y0 z0] [tx] [x1 y1 z1] [ty] [x2 y2 z2] [tz]

where the left 3x3 the matrix defines the affine rotation and scaling, and the right column is the translation vector.

The matrix must be collapsed and stored in a list as follows:

[x0 y0, z0, x1, y1, z1, x2, y2, z2, tx, ty, tz]

Parameters

aff: 3x4 array of floats (python 2D list, or numpy 2D array) the transformation matrix

`change_parent`(*self*, *child*, *parent*)

Change the parent of a node. The child node is adjusted to point to the new parent, the child is taken off of the previous parent's child list, and it is added to the new parent's child list.

Parameters

child: integer or Morphology Object The ID of the child node, or the child node itself

parent: integer or Morphology Object The ID of the parent node, or the parent node itself

Returns

Nothing

`children_of` (*self*, *seg*)
Returns a list of the children of the specified node

Parameters

seg: integer or Morphology Object The ID of the parent node, or the parent node itself

Returns

A list of the child morphology objects. If the ID of the parent

node is invalid, None is returned.

`compartment_index`
Return the compartment index. This is a property to ensure that the compartment list and compartment index are in sync.

`compartment_index_by_type` (*self*, *compartment_type*)
Return an dictionary of compartments indexed by id that all have a particular compartment type.

Parameters

compartment_type: int Desired compartment type

Returns

A dictionary of Morphology Objects, indexed by ID

`compartment_list`
Return the compartment list. This is a property to ensure that the compartment list and compartment index are in sync.

`compartment_list_by_type` (*self*, *compartment_type*)
Return an list of all compartments having the specified compartment type.

Parameters

compartment_type: int Desired compartment type

Returns

A list of of Morphology Objects

`convert_type` (*self*, *old_type*, *new_type*)
Converts all compartments from one type to another. Nodes of the original type are not affected so this procedure can also be used as a merge procedure.

Parameters

old_type: enum The compartment type to be changed. Use one of the following constants: SOMA, AXON, DENDRITE, BASAL_DENDRITE, or APICAL_DENDRITE

new_type: enum The target compartment type. Use one of the following constants: SOMA, AXON, DENDRITE, BASAL_DENDRITE, or APICAL_DENDRITE

`delete_tree` (*self*, *n*)
Delete tree, and all of its compartments, from the morphology.

Parameters

n: Integer The tree number to delete

find(*self*, *x*, *y*, *z*, *dist*, *node_type=None*)
Returns a list of Morphology Objects located within 'dist' of coordinate (x,y,z). If node_type is specified, the search will be constrained to return only nodes of that type.

Parameters

x, y, z: float The x,y,z coordinates from which to search around

dist: float The search radius

node_type: enum (optional) One of the following constants: SOMA, AXON, DENDRITE, BASAL_DENDRITE or APICAL_DENDRITE

Returns

A list of all Morphology Objects matching the search criteria

node(*self*, *n*)
Returns the morphology node having the specified ID.

Parameters

n: integer ID of desired node

Returns

A morphology object having the specified ID, or None if such a

node doesn't exist

num_nodes
Return the number of compartments in the morphology.

num_trees
Return the number of trees in the morphology. A tree is defined as everything following from a single root compartment.

parent_of(*self*, *seg*)
Returns parent of the specified node.

Parameters

seg: integer or Morphology Object The ID of the child node, or the child node itself

Returns

A morphology object, or None if no parent exists or if the

specified node ID doesn't exist

root
[deprecated] Returns root node of soma, if present. Use 'soma' instead of 'root'

save(*self*, *file_name*)
Write this morphology out to an SWC file

Parameters

file_name: string desired name of your SWC file

soma
Returns root node of soma, if present

sparsify(*self*, *modulo*, *compress_ids=False*)
Return a new Morphology object that has a given number of non-leaf, non-root nodes removed. IDs can be reassigned so as to be continuous.

Parameters

modulo: int keep 1 out of every modulo nodes.

compress_ids: boolean Reassign ids so that ids are continuous (no missing id numbers).

Returns

Morphology A new morphology instance

`strip_all_other_types` (*self*, *node_type*, *keep_soma=True*)
Strips everything from the morphology except for the specified type. Parent and child relationships are updated accordingly, creating new roots when necessary.

Parameters

node_type: enum The compartment type to keep in the morphology. Use one of the following constants: SOMA, AXON, DENDRITE, BASAL_DENDRITE, or APICAL_DENDRITE

keep_soma: Boolean (optional) True (default) if soma nodes should remain in the morpyhology, and False if the soma should also be stripped

`strip_type` (*self*, *node_type*)
Strips all compartments of the specified type from the morphology. Parent and child relationships are updated accordingly, creating new roots when necessary.

Parameters

node_type: enum The compartment type to strip from the morphology. Use one of the following constants: SOMA, AXON, DENDRITE, BASAL_DENDRITE, or APICAL_DENDRITE

`stumpify_axon` (*self*, *count=10*)
Remove all axon compartments except the first ‘count’ nodes, as counted from the connected axon root.

Parameters

count: Integer The length of the axon ‘stump’, in number of compartments

`tree` (*self*, *n*)
Returns a list of all Morphology Nodes within the specified tree. A tree is defined as a fully connected graph of nodes. Each tree has exactly one root.

Parameters

n: integer ID of desired tree

Returns

A list of all morphology objects in the specified tree, or None

if the tree doesn’t exist

`write` (*self*, *file_name*)

`allensdk.core.swc.`**`read_marker_file`** (*file_name*)
read in a marker file and return a list of dictionaries

`allensdk.core.swc.`**`read_swc`** (*file_name*, *columns='NOT_USED'*, *numeric_columns='NOT_USED'*)
Read in an SWC file and return a Morphology object.

Parameters

file_name: string SWC file name.

Returns

Morphology A Morphology instance.

allensdk.core.typing module

class allensdk.core.typing.**SupportsStr**

Bases: `typing._Protocol`

Classes that support the __str__ method

Module contents

6.1.5 allensdk.ephys package

Submodules

allensdk.ephys.ephys_extractor module

class allensdk.ephys.ephys_extractor.**EphysCellFeatureExtractor**(*ramps_ext*, *short_squares_ext*, *long_squares_ext*, *subthresh_min_amp=-100*)

Bases: `object`

SAG_TARGET = -100.0

SUBTHRESH_MAX_AMP = 0

as_dict(*self*)

Create dict of cell features.

cell_features(*self*)

long_squares_features(*self*, *option=None*)

long_squares_stim_amps(*self*, *option=None*)

process(*self*, *keys=None*)

Processes features. Can take a specific key (or set of keys) to do a subset of processing.

ramps_features(*self*, *all=False*)

short_squares_features(*self*)

class `allensdk.ephys.ephys_extractor.`**`EphysSweepFeatureExtractor`**(*t=None*, *v=None*, *i=None*, *start=None*, *end=None*, *filter=10.0*, *dv_cutoff=20.0*, *max_interval=0.005*, *min_height=2.0*, *min_peak=-30.0*, *thresh_frac=0.05*, *baseline_interval=0.1*, *baseline_detect_thresh=0.3*, *id=None*)

Bases: `object`

Feature calculation for a sweep (voltage and/or current time series).

`as_dict`(*self*)
Create dict of features and spikes.

`burst_metrics`(*self*)
Find bursts and return max "burstiness" index (normalized max rate in burst vs out).

Returns

max_burstiness_index [max "burstiness" index across detected bursts]

num_bursts [number of bursts detected]

`delay_metrics`(*self*)
Calculates ratio of latency to dominant time constant of rise before spike

Returns

delay_ratio [ratio of latency to tau (higher means more delay)]

tau [dominant time constant of rise before spike]

`estimate_sag`(*self*, *peak_width=0.005*)
Calculate the sag in a hyperpolarizing voltage response.

Parameters

peak_width [window width to get more robust peak estimate in sec (default 0.005)]

Returns

sag [fraction that membrane potential relaxes back to baseline]

`estimate_time_constant`(*self*)
Calculate the membrane time constant by fitting the voltage response with a single exponential.

Returns

tau [membrane time constant in seconds]

`is_spike_feature_affected_by_clipping`(*self*, *key*)

`pause_metrics`(*self*)
Estimate average number of pauses and average fraction of time spent in a pause

Attempts to detect pauses with a variety of conditions and averages results together.

Pauses that are consistently detected contribute more to estimates.

Returns

avg_n_pauses [average number of pauses detected across conditions]

avg_pause_frac [average fraction of interval (between start and end) spent in a pause]

max_reliability [max fraction of times most reliable pause was detected given weights tested]

n_max_rel_pauses [number of pauses detected with *max_reliability*]

`process_new_spike_feature`(*self*, *feature_name*, *feature_func*, *affected_by_clipping=False*)
Add new spike-level feature calculation function

The function should take this sweep extractor as its argument. Its results can be accessed by calling the method spike_feature(<feature_name>).

`process_new_sweep_feature`(*self*, *feature_name*, *feature_func*)
Add new sweep-level feature calculation function

The function should take this sweep extractor as its argument. Its results can be accessed by calling the method sweep_feature(<feature_name>).

`process_spikes`(*self*)
Perform spike-related feature analysis

`set_stimulus_amplitude_calculator`(*self*, *function*)

`spike_feature`(*self*, *key*, *include_clipped=False*, *force_exclude_clipped=False*)
Get specified feature for every spike.

Parameters

key [feature name]

include_clipped: return values for every identified spike, even when clipping means they will be incorrect/u

Returns

spike_feature_values [ndarray of features for each spike]

`spike_feature_keys`(*self*)
Get list of every available spike feature.

`spikes`(*self*)
Get all features for each spike as a list of records.

`stimulus_amplitude`(*self*)

`sweep_feature`(*self*, *key*, *allow_missing=False*)
Get sweep-level feature (*key*).

Parameters

key [name of sweep-level feature]

allow_missing [return np.nan if key is missing for sweep (default False)]

Returns

sweep_feature [sweep-level feature value]

sweep_feature_keys(*self*)
Get list of every available sweep-level feature.

voltage_deflection(*self*, *deflect_type=None*)
Measure deflection (min or max, between start and end if specified).

Parameters

deflect_type [measure minimal ('min') or maximal ('max') voltage deflection] If not specified, it will check to see if the current (i) is positive or negative between start and end, then choose 'max' or 'min', respectively If the current is not defined, it will default to 'min'.

Returns

deflect_v [peak]

deflect_index [index of peak deflection]

class allensdk.ephys.ephys_extractor.**EphysSweepSetFeatureExtractor**(*t_set=None*, *v_set=None*, *i_set=None*, *start=None*, *end=None*, *filter=10.0*, *dv_cutoff=20.0*, *max_interval=0.005*, *min_height=2.0*, *min_peak=-30.0*, *thresh_frac=0.05*, *baseline_interval=0.1*, *baseline_detect_thresh=0.3*, *id_set=None*)

Bases: `object`

classmethod from_sweeps(*sweep_list*)
Initialize EphysSweepSetFeatureExtractor object with a list of pre-existing sweep feature extractor objects.

process_spikes(*self*)
Analyze spike features for all sweeps.

spike_feature_averages(*self*, *key*)
Get nparray of average spike-level feature (*key*) for all sweeps

sweep_features(*self*, *key*, *allow_missing=False*)
Get nparray of sweep-level feature (*key*) for all sweeps

Parameters

key [name of sweep-level feature]

allow_missing [return np.nan if key is missing for sweep (default False)]

Returns

sweep_feature [nparray of sweep-level feature values]

sweeps(*self*)
Get list of EphysSweepFeatureExtractor objects.

allensdk.ephys.ephys_extractor.**cell_extractor_for_nwb**(*dataset*, *ramps*, *short_squares*, *long_squares*, *subthresh_min_amp=-100*)
Initialize EphysCellFeatureExtractor object from NWB data set

Parameters

dataset [NwbDataSet]

ramps [list of sweep numbers of ramp sweeps]

short_squares [list of sweep numbers of short square sweeps]

long_squares [list of sweep numbers of long square sweeps]

allensdk.ephys.ephys_extractor.**extractor_for_nwb_sweeps**(*dataset*, *sweep_numbers*, *fixed_start=None*, *fixed_end=None*, *dv_cutoff=20.0*, *thresh_frac=0.05*)

allensdk.ephys.ephys_extractor.**fit_fi_slope**(*ext*)
Fit the rate and stimulus amplitude to a line and return the slope of the fit.

allensdk.ephys.ephys_extractor.**input_resistance**(*ext*)
Estimate input resistance in MOhms, assuming all sweeps in passed extractor are hyperpolarizing responses.

allensdk.ephys.ephys_extractor.**membrane_time_constant**(*ext*)
Average the membrane time constant values estimated from each sweep in passed extractor.

allensdk.ephys.ephys_extractor.**reset_long_squares_start**(*when*)

allensdk.ephys.ephys_features module

exception allensdk.ephys.ephys_features.**FeatureError**
Bases: Exception

Generic Python-exception-derived object raised by feature detection functions.

allensdk.ephys.ephys_features.**adaptation_index**(*isis*)
Calculate adaptation index of *isis*.

allensdk.ephys.ephys_features.**analyze_trough_details**(*v*, *t*, *spike_indexes*, *peak_indexes*, *clipped=None*, *end=None*, *filter=10.0*, *heavy_filter=1.0*, *term_frac=0.01*, *adp_thresh=0.5*, *tol=0.5*, *flat_interval=0.002*, *adp_max_delta_t=0.005*, *adp_max_delta_v=10.0*, *dvdt=None*)
Analyze trough to determine if an ADP exists and whether the reset is a 'detour' or 'direct'

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

spike_indexes [numpy array of spike indexes]

peak_indexes [numpy array of spike peak indexes]

end [end of time window (optional)]

filter [cutoff frequency for 4-pole low-pass Bessel filter in kHz (default 1)]

heavy_filter [lower cutoff frequency for 4-pole low-pass Bessel filter in kHz (default 1)]

thresh_frac [fraction of average upstroke for threshold calculation (optional, default 0.05)]

adp_thresh: minimum dV/dt in V/s to exceed to be considered to have an ADP (optional, default 1.5)

tol [tolerance for evaluating whether Vm drops appreciably further after end of spike (default 1.0 mV)]

flat_interval: if the trace is flat for this duration, stop looking for an ADP (default 0.002 s)

adp_max_delta_t: max possible ADP delta t (default 0.005 s)

adp_max_delta_v: max possible ADP delta v (default 10 mV)

dvdt [pre-calculated time-derivative of voltage (optional)]

Returns

isi_types [numpy array of isi reset types (direct or detour)]

fast_trough_indexes [numpy array of indexes at the start of the trough (i.e. end of the spike)]

adp_indexes [numpy array of adp indexes (np.nan if there was no ADP in that ISI]

slow_trough_indexes [numpy array of indexes at the minimum of the slow phase of the trough] (if there wasn't just a fast phase)

`allensdk.ephys.ephys_features.`**`average_rate`**(*t*, *spikes*, *start*, *end*)

Calculate average firing rate during interval between *start* and *end*.

Parameters

t [numpy array of times in seconds]

spikes [numpy array of spike indexes]

start [start of time window for spike detection]

end [end of time window for spike detection]

Returns

avg_rate [average firing rate in spikes/sec]

`allensdk.ephys.ephys_features.`**`average_voltage`**(*v*, *t*, *start=None*, *end=None*)

Calculate average voltage between start and end.

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

start [start of time window for spike detection (optional, default None)]

end [end of time window for spike detection (optional, default None)]

Returns

v_avg [average voltage]

allensdk.ephys.ephys_features.**calculate_dvdt**(*v*, *t*, *filter=None*)

Low-pass filters (if requested) and differentiates voltage by time.

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

filter [cutoff frequency for 4-pole low-pass Bessel filter in kHz (optional, default None)]

Returns

dvdt [numpy array of time-derivative of voltage (V/s = mV/ms)]

allensdk.ephys.ephys_features.**check_thresholds_and_peaks**(*v*, *t*, *spike_indexes*, *peak_indexes*, *upstroke_indexes*, *end=None*, *max_interval=0.005*, *thresh_frac=0.05*, *filter=10.0*, *dvdt=None*, *tol=1.0*)

Validate thresholds and peaks for set of spikes

Check that peaks and thresholds for consecutive spikes do not overlap Spikes with overlapping thresholds and peaks will be merged.

Check that peaks and thresholds for a given spike are not too far apart.

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

spike_indexes [numpy array of spike indexes]

peak_indexes [numpy array of indexes of spike peaks]

upstroke_indexes [numpy array of indexes of spike upstrokes]

max_interval [maximum allowed time between start of spike and time of peak in sec (default 0.005)]

thresh_frac [fraction of average upstroke for threshold calculation (optional, default 0.05)]

filter [cutoff frequency for 4-pole low-pass Bessel filter in kHz (optional, default 10)]

dvdt [pre-calculated time-derivative of voltage (optional)]

tol [tolerance for returning to threshold in mV (optional, default 1)]

Returns

spike_indexes [numpy array of modified spike indexes]

peak_indexes [numpy array of modified spike peak indexes]

upstroke_indexes [numpy array of modified spike upstroke indexes]

clipped [numpy array of clipped status of spikes]

allensdk.ephys.ephys_features.**detect_bursts**(*isis*, *isi_types*, *fast_tr_v*, *fast_tr_t*, *slow_tr_v*, *slow_tr_t*, *thr_v*, *tol=0.5*, *pause_cost=1.0*)

Detect bursts in spike train.

Parameters

isis [numpy array of n interspike intervals]

isi_types [numpy array of n interspike interval types]

fast_tr_v [numpy array of fast trough voltages for the n + 1 spikes of the train]

fast_tr_t [numpy array of fast trough times for the n + 1 spikes of the train]

slow_tr_v [numpy array of slow trough voltages for the n + 1 spikes of the train]

slow_tr_t [numpy array of slow trough times for the n + 1 spikes of the train]

thr_v [numpy array of threshold voltages for the n + 1 spikes of the train]

tol [tolerance for the difference in slow trough voltages and thresholds (default 0.5 mV)] Used to identify "delay" interspike intervals that occur within a burst

Returns

bursts [list of bursts] Each item in list is a tuple of the form (burst_index, start, end) where *burst_index* is a comparison index between the highest instantaneous rate within the burst vs the highest instantaneous rate outside the burst. *start* is the index of the first ISI of the burst, and *end* is the ISI index immediately following the burst.

`allensdk.ephys.ephys_features.`**`detect_pauses`**(*isis*, *isi_types*, *cost_weight=1.0*)

Determine which ISIs are "pauses" in ongoing firing.

Pauses are unusually long ISIs with a "detour reset" among "direct resets".

Parameters

isis [numpy array of interspike intervals]

isi_types [numpy array of interspike interval types ('direct' or 'detour')]

cost_weight [weight for cost function for calling an ISI a pause] Higher cost weights lead to fewer ISIs identified as pauses. The cost function also depends on the difference between the duration of the "pause" ISIs and the average duration and standard deviation of "non-pause" ISIs.

Returns

pauses [numpy array of indices corresponding to pauses in *isis*]

`allensdk.ephys.ephys_features.`**`detect_putative_spikes`**(*v*, *t*, *start=None*, *end=None*, *filter=10.0*, *dv_cutoff=20.0*)

Perform initial detection of spikes and return their indexes.

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

start [start of time window for spike detection (optional)]

end [end of time window for spike detection (optional)]

filter [cutoff frequency for 4-pole low-pass Bessel filter in kHz (optional, default 10)]

dv_cutoff [minimum dV/dt to qualify as a spike in V/s (optional, default 20)]

dvdt [pre-calculated time-derivative of voltage (optional)]

Returns

putative_spikes [numpy array of preliminary spike indexes] allensdk.ephys.ephys_features.**estimate_adjusted_detection_parameters**(*v_set*, *t_set*, *interval_start*, *interval_end*, *filter=10*)

Estimate adjusted values for spike detection by analyzing a period when the voltage changes quickly but passively (due to strong current stimulation), which can result in spurious spike detection results.

Parameters

v_set [list of numpy arrays of voltage time series in mV]

t_set [list of numpy arrays of times in seconds]

interval_start [start of analysis interval (sec)]

interval_end [end of analysis interval (sec)]

Returns

new_dv_cutoff [adjusted dv/dt cutoff (V/s)]

new_thresh_frac [adjusted fraction of avg upstroke to find threshold]

allensdk.ephys.ephys_features.**filter_putative_spikes**(*v*, *t*, *spike_indexes*, *peak_indexes*, *min_height=2.0*, *min_peak=-30.0*, *filter=10.0*, *dvdt=None*)

Filter out events that are unlikely to be spikes based on:

- Voltage failing to go down between peak and the next spike's threshold
- Height (threshold to peak)
- Absolute peak level

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

spike_indexes [numpy array of preliminary spike indexes]

peak_indexes [numpy array of indexes of spike peaks]

min_height [minimum acceptable height from threshold to peak in mV (optional, default 2)]

min_peak [minimum acceptable absolute peak level in mV (optional, default -30)]

filter [cutoff frequency for 4-pole low-pass Bessel filter in kHz (optional, default 10)]

dvdt [pre-calculated time-derivative of voltage (optional)]

Returns

spike_indexes [numpy array of threshold indexes]

peak_indexes [numpy array of peak indexes] `allensdk.ephys.ephys_features.`**`find_downstroke_indexes`**(*v*, *t*, *peak_indexes*, *trough_indexes*, *clipped=None*, *filter=10.0*, *dvdt=None*)

Find indexes of minimum voltage (troughs) between spikes.

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

peak_indexes [numpy array of spike peak indexes]

trough_indexes [numpy array of threshold indexes]

clipped: boolean array - False if spike not clipped by edge of window

filter [cutoff frequency for 4-pole low-pass Bessel filter in kHz (optional, default 10)]

dvdt [pre-calculated time-derivative of voltage (optional)]

Returns

downstroke_indexes [numpy array of downstroke indexes]

`allensdk.ephys.ephys_features.`**`find_peak_indexes`**(*v*, *t*, *spike_indexes*, *end=None*)

Find indexes of spike peaks.

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

spike_indexes [numpy array of preliminary spike indexes]

end [end of time window for spike detection (optional)]

`allensdk.ephys.ephys_features.`**`find_time_index`**(*t*, *t_0*)

Find the index value of a given time (t_0) in a time series (t).

`allensdk.ephys.ephys_features.`**`find_trough_indexes`**(*v*, *t*, *spike_indexes*, *peak_indexes*, *clipped=None*, *end=None*)

Find indexes of minimum voltage (trough) between spikes.

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

spike_indexes [numpy array of spike indexes]

peak_indexes [numpy array of spike peak indexes]

end [end of time window (optional)]

Returns

trough_indexes [numpy array of threshold indexes]

`allensdk.ephys.ephys_features.`**`find_upstroke_indexes`**(*v*, *t*, *spike_indexes*, *peak_indexes*, *filter=10.0*, *dvdt=None*)

Find indexes of maximum upstroke of spike.

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

spike_indexes [numpy array of preliminary spike indexes]

peak_indexes [numpy array of indexes of spike peaks]

filter [cutoff frequency for 4-pole low-pass Bessel filter in kHz (optional, default 10)]

dvdt [pre-calculated time-derivative of voltage (optional)]

Returns

upstroke_indexes [numpy array of upstroke indexes]

`allensdk.ephys.ephys_features.`**`find_widths`**(*v*, *t*, *spike_indexes*, *peak_indexes*, *trough_indexes*, *clipped=None*)

Find widths at half-height for spikes.

Widths are only returned when heights are defined

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

spike_indexes [numpy array of spike indexes]

peak_indexes [numpy array of spike peak indexes]

trough_indexes [numpy array of trough indexes]

Returns

widths [numpy array of spike widths in sec]

`allensdk.ephys.ephys_features.`**`fit_membrane_time_constant`**(*v*, *t*, *start*, *end*, *min_rsme=0.0001*)

Fit an exponential to estimate membrane time constant between start and end

Parameters

v [numpy array of voltages in mV]

t [numpy array of times in seconds]

start [start of time window for exponential fit]

end [end of time window for exponential fit]

min_rsme: minimal acceptable root mean square error (default 1e-4)

Returns

a, inv_tau, y0 [Coeffients of equation y0 + a * exp(-inv_tau * x)]

returns np.nan for values if fit fails

`allensdk.ephys.ephys_features.`**`fit_prespike_time_constant`**(*v*, *t*, *start*, *spike_time*, *dv_limit=-0.001*, *tau_limit=0.3*)

Finds the dominant time constant of the pre-spike rise in voltage

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

start [start of voltage rise (seconds)]

spike_time [time of first spike (seconds)]

dv_limit [dV/dt cutoff (default -0.001)] Shortens fit window if rate of voltage drop exceeds this limit

tau_limit [upper bound for slow time constant (seconds, default 0.3)] If the slower time constant of a double-exponential fit is twice that of the faster and exceeds this limit, the faster one will be considered the dominant one

Returns

tau [dominant time constant (seconds)]

`allensdk.ephys.ephys_features.`**`get_isis`**(*t*, *spikes*)
Find interspike intervals in sec between spikes (as indexes).

`allensdk.ephys.ephys_features.`**`has_fixed_dt`**(*t*)
Check that all time intervals are identical.

`allensdk.ephys.ephys_features.`**`latency`**(*t*, *spikes*, *start*)
Calculate time to the first spike.

`allensdk.ephys.ephys_features.`**`norm_diff`**(*a*)
Calculate average of (a[i] - a[i+1]) / (a[i] + a[i+1]).

`allensdk.ephys.ephys_features.`**`norm_sq_diff`**(*a*)
Calculate average of (a[i] - a[i+1])^2 / (a[i] + a[i+1])^2.

`allensdk.ephys.ephys_features.`**`refine_threshold_indexes`**(*v*, *t*, *upstroke_indexes*, *thresh_frac=0.05*, *filter=10.0*, *dvdt=None*)
Refine threshold detection of previously-found spikes.

Parameters

v [numpy array of voltage time series in mV]

t [numpy array of times in seconds]

upstroke_indexes [numpy array of indexes of spike upstrokes (for threshold target calculation)]

thresh_frac [fraction of average upstroke for threshold calculation (optional, default 0.05)]

filter [cutoff frequency for 4-pole low-pass Bessel filter in kHz (optional, default 10)]

dvdt [pre-calculated time-derivative of voltage (optional)]

Returns

threshold_indexes [numpy array of threshold indexes]

allensdk.ephys.extract_cell_features module

`allensdk.ephys.extract_cell_features.`**`extract_cell_features`**(*data_set*, *ramp_sweep_numbers*, *short_square_sweep_numbers*, *long_square_sweep_numbers*, *subthresh_min_amp=None*)

`allensdk.ephys.extract_cell_features.`**`extract_sweep_features`**(*data_set*, *sweeps_by_type*)

allensdk.ephys.extract_cell_features.**get_ramp_stim_characteristics**(*i*, *t*)
Identify the start time and start index of a ramp sweep.

allensdk.ephys.extract_cell_features.**get_square_stim_characteristics**(*i*, *t*, *no_test_pulse=False*)
Identify the start time, duration, amplitude, start index, and end index of a square stimulus. This assumes that there is a test pulse followed by the stimulus square.

allensdk.ephys.extract_cell_features.**get_stim_characteristics**(*i*, *t*, *no_test_pulse=False*)
Identify the start time, duration, amplitude, start index, and end index of a general stimulus. This assumes that there is a test pulse followed by the stimulus square.

allensdk.ephys.extract_cell_features.**mean_features_spike_zero**(*sweeps*)
Compute mean feature values for the first spike in list of extractors

allensdk.ephys.feature_extractor module

class allensdk.ephys.feature_extractor.**EphysFeatureExtractor**
Bases: `object`

adaptation_index(*self*, *spikes*, *stim_end*)

calculate_trough(*self*, *spike*, *v*, *curr*, *t*, *next_idx*)

isicv(*self*, *spikes*)

process_instance(*self*, *name*, *v*, *curr*, *t*, *onset*, *dur*, *stim_name*)

push_summary(*self*, *new_summary*)

score_feature_set(*self*, *set_num*)

summarize(*self*, *summary*)

class allensdk.ephys.feature_extractor.**EphysFeatures**(*name*)
Bases: `object`

clone(*self*, *param_dict*)

print_out(*self*)

Module contents

6.1.6 allensdk.internal package

Subpackages

allensdk.internal.api package

Subpackages

allensdk.internal.api.queries package

Submodules

allensdk.internal.api.queries.biophysical_module_api module

allensdk.internal.api.queries.biophysical_module_reader module

allensdk.internal.api.queries.grid_data_api_prerelease module

allensdk.internal.api.queries.mouse_connectivity_api_prerelease module

allensdk.internal.api.queries.optimize_config_reader module

allensdk.internal.api.queries.pre_release module

Module contents

Submodules

allensdk.internal.api.api_prerelease module

allensdk.internal.api.behavior_data_lims_api module

allensdk.internal.api.behavior_lims_api module

allensdk.internal.api.behavior_ophys_api module

allensdk.internal.api.lims_api module

allensdk.internal.api.mtrain_api module

allensdk.internal.api.ophys_lims_api module

Module contents

allensdk.internal.brain_observatory package

Subpackages

allensdk.internal.brain_observatory.resources package

Module contents

Submodules

allensdk.internal.brain_observatory.annotated_region_metrics module

Module for calculating annotated region metrics from ISI data `allensdk.internal.brain_observatory.annotated_region_metrics.`**`create_region_mask`**(*image_shape*, *x*, *y*, *width*, *height*, *mask*)

Create mask for region on retinotopic map

Parameters

image_shape [tuple] (height, width) of retinotopic map

x [int] x offset of region mask within retinotopic map

y [int] y offset of region mask within retinotopic map

width [int] width of region mask

height [int] height of region mask

mask [list] region mask as a list of lists

Returns

numpy.ndarray Region mask

`allensdk.internal.brain_observatory.annotated_region_metrics.`**`eccentricity`**(*az*, *alt*, *az_center*, *alt_center*)

Compute eccentricity

Parameters

az [numpy.ndarray] Azimuth retinotopic map

alt [numpy.ndarray] Altitude retinotopic map

az_center [float] Azimuth value to use as center of eccentricity map

alt_center [float] Altitude value to use as center of eccentricity map

Returns

numpy.ndarray Eccentricity map

`allensdk.internal.brain_observatory.annotated_region_metrics.`**`get_metrics`**(*altitude_phase*, *azimuth_phase*, *x=None*, *y=None*, *width=None*, *height=None*, *mask=None*, *altitude_scale=0.322*, *azimuth_scale=0.383*)

Calculate annotated region metrics

`allensdk.internal.brain_observatory.annotated_region_metrics.`**`retinotopy_metric`**(*mask*, *isi_map*)

Compute retinotopic metrics for a responding area

Parameters

mask [numpy.ndarray] Mask representing the area over which to calculate metrics

isi_map [numpy.ndarray] Retinotopic map

Returns

(float, float, float, float) tuple min, max, range, bias of retinotopic map over masked region

allensdk.internal.brain_observatory.demix_report module

`allensdk.internal.brain_observatory.demix_report.`**`background_trace`**(*trace*, *save_dir*, *data_set=None*)

`allensdk.internal.brain_observatory.demix_report.`**`compute_correlations`**(*dm*, *movie_path*, *movie_dataset*)

`allensdk.internal.brain_observatory.demix_report.`**`compute_correlations_without_masks`**(*dm*)

`allensdk.internal.brain_observatory.demix_report.`**`compute_non_overlap_masks`**(*dm*)

`allensdk.internal.brain_observatory.demix_report.`**`compute_non_overlap_traces`**(*dm*, *movie_path*, *movie_dataset*)

`allensdk.internal.brain_observatory.demix_report.`**`correlation_report`**(*dm*, *save_dir*, *without_masks=True*)

parameters: dm: [DeMix object] without_masks: boolean

`allensdk.internal.brain_observatory.demix_report.`**`plot_masks`**(*dm*, *save_dir*, *movie_file*, *movie_dataset*, *window=150*, *add_background=True*)

allensdk.internal.brain_observatory.demixer module

`allensdk.internal.brain_observatory.demixer.`**`demix_time_dep_masks`**(*raw_traces*, *stack*, *masks*)

Parameters

- **`raw_traces`** – extracted traces
- **`stack`** – movie (same length as traces)
- **`masks`** – binary roi masks

Returns demixed traces

`allensdk.internal.brain_observatory.demixer.`**`find_negative_baselines`**(*trace*) allensdk.internal.brain_observatory.demixer.**find_negative_transients_threshold**(*trace*, *window=500*, *length=10*, *std_devs=3*)

allensdk.internal.brain_observatory.demixer.**find_zero_baselines**(*traces*)

allensdk.internal.brain_observatory.demixer.**identify_valid_masks**(*mask_array*)

allensdk.internal.brain_observatory.demixer.**plot_negative_baselines**(*raw_traces*, *demix_traces*, *mask_array*, *roi_ids_mask*, *plot_dir*, *ext='png'*)

allensdk.internal.brain_observatory.demixer.**plot_negative_transients**(*raw_traces*, *demix_traces*, *valid_roi*, *mask_array*, *roi_ids_mask*, *plot_dir*, *ext='png'*)

allensdk.internal.brain_observatory.demixer.**plot_overlap_masks_lengthOne**(*roi_ind*, *masks*, *savefile=None*, *weighted=False*)

allensdk.internal.brain_observatory.demixer.**plot_traces**(*raw_trace*, *demix_trace*, *roi_id*, *roi_ind*, *save_file*)

allensdk.internal.brain_observatory.demixer.**plot_transients**(*roi_ind*, *t_trans*, *masks*, *traces*, *demix_traces*, *savefile*)

allensdk.internal.brain_observatory.demixer.**rolling_window**(*trace*, *window=500*)

Parameters

- **trace** –
- **window** –

Returns

allensdk.internal.brain_observatory.eye_calibration module

class allensdk.internal.brain_observatory.eye_calibration.**EyeCalibration**(*monitor_position=array([8.62, 3.16]), monitor_rotations=array([0., 0., 0.]), led_position=array([25.8 - 6.12, 3.21]), camera_position=array([13., 0., 0.]), camera_rotations=array([0., 0., 0.22863813]), eye_radius=0.1682, cm_per_pixel=0.0010199*

Bases: object

Class for performing eye-tracking calibration.

Provides methods for estimating the position of the pupil in 3D space and projecting the gaze onto the monitor in both 3D space and monitor space given the experimental geometry.

Parameters

monitor_position [numpy.ndarray] [x,y,z] position of monitor in cm.

monitor_rotations [numpy.ndarray] [x,y,z] rotations of monitor in radians.

led_position [numpy.ndarray] [x,y,z] position of LED in cm.

camera_position [numpy.ndarray] [x,y,z] position of camera in cm.

camera_rotations [numpy.ndarray] [x,y,z] rotations for camera in radians. X and Y must be 0.

eye_radius [float] Radius of the eye in cm.

cm_per_pixel [float] Pixel size of eye-tracking camera.

compute_area(*self, pupil_parameters*)

Compute the area of the pupil.

Assume the pupil is a circle, and that as it moves off-axis with the camera the observed ellipse major axis remains the diameter of the circle.

Parameters

pupil_parameters [numpy.ndarray] [nx5] array of pupil parameters.

Returns

numpy.ndarray [nx1] array of pupil areas in estimated pixels.

static cr_position_in_mouse_eye_coordinates(*led_position*, *eye_radius*)

Determine the 3D position of the corneal reflection.

The eye is modeled as a spherical mirror, so the reflection appears to be half the radius of the eye from the origin along the eye-LED axis.

Parameters

led_position [numpy.ndarray] [x,y,z] position of the LED in eye coordinates.

eye_radius [float] Radius of the eye in centimeters.

Returns

numpy.ndarray [x,y,z] location of the corneal reflection in eye coordinates.

pupil_position_in_mouse_eye_coordinates(*self*, *pupil_parameters*, *cr_parameters*)

Compute the 3D pupil position in mouse eye coordinates.

Parameters

pupil_parameters [numpy.ndarray] Array of pupil parameters for each eye tracking frame.

cr_paramaeters [numpy.ndarray] Array of corneal reflection parameters for each eye tracking frame.

Returns

numpy.ndarray Pupil position estimates in eye coordinates.

pupil_position_on_monitor_in_cm(*self*, *pupil_parameters*, *cr_parameters*)

Compute the pupil position on the monitor in cm.

Parameters

pupil_parameters [numpy.ndarray] Array of pupil parameters for each eye tracking frame.

cr_paramaeters [numpy.ndarray] Array of corneal reflection parameters for each eye tracking frame.

Returns

numpy.ndarray Pupil position estimates in eye coordinates.

pupil_position_on_monitor_in_degrees(*self*, *pupil_parameters*, *cr_parameters*)

Get pupil position on monitor measured in visual degrees.

Parameters

pupil_parameters [numpy.ndarray] Array of pupil parameters for each eye tracking frame.

cr_paramaeters [numpy.ndarray] Array of corneal reflection parameters for each eye tracking frame.

Returns

numpy.ndarray Pupil position estimate in visual degrees.

allensdk.internal.brain_observatory.eye_calibration.**base_object_to_eye_rotation_matrix**(*objec*

Rotation matrix to rotate base object frame to eye coordinates.

By convention, any other object's coordinate frame before rotations is set with positive Z pointing from the object's position back to the origin of the eye coordinate system, with X parallel to the eye X-Y plane.

Parameters

object_position [np.ndarray] [x, y, z] position of object in eye coordinates.

Returns

numpy.ndarray [3x3] rotation matrix.

`allensdk.internal.brain_observatory.eye_calibration.`**`object_norm_eye_coordinates`**(*object_position x_rotation*, *y_rotation*, *z_rotation*)

Get the normal vector for the object plane in eye coordinates.

Parameters

object_position [numpy.ndarray] [x, y, z] location of the object in eye coordinates.

x_rotation [float] Rotation about the x-axis in radians.

y_rotation [float] Rotation about the y-axis in radians.

z_rotation [float] Rotation about the z-axis in radians.

Returns

numpy.ndarray Endpoint of the object plane vector in eye coordinates.

`allensdk.internal.brain_observatory.eye_calibration.`**`object_rotation_matrix`**(*x_rotation*, *y_rotation*, *z_rotation*)

Rotation matrix in object coordinate frame.

The rotation matrix for rotating the object coordinate frame from the initial position. This is done by rotating around x, then around y', then around z''.

Parameters

x_rotation [float] Rotation about x axis in radians.

y_rotation [float] Rotation about y axis in radians.

z_rotation [float] Rotation about z axis in radians.

Returns

numpy.ndarray [3x3] rotation matrix.

`allensdk.internal.brain_observatory.eye_calibration.`**`project_to_plane`**(*plane_normal*, *plane_point*, *points*)

Project from the origin through points onto a plane.

Parameters

plane_normal [numpy.ndarray] [x, y, z] normal unit vector to the plane.

plane_point [numpy.ndarray] [x, y, z] point on the plane.

points [numpy.ndarray] [nx3] points in space through which to project.

Returns

numpy.ndarray [nx3] points projected on the plane.

allensdk.internal.brain_observatory.fit_ellipse module

class allensdk.internal.brain_observatory.fit_ellipse.**FitEllipse**(*min_points*, *max_iter*, *threshold*, *num_close*)

Bases: object

choose_inliers(*self*, *candidate_points*)

fit_ellipse(*self*, *inlier_points*)

outlier_cost(*self*, *outlier_points*, *params*)

ransac_fit(*self*, *candidate_points*)

allensdk.internal.brain_observatory.fit_ellipse.**ellipse_angle_of_rotation**(*a*)

allensdk.internal.brain_observatory.fit_ellipse.**ellipse_angle_of_rotation2**(*a*)

allensdk.internal.brain_observatory.fit_ellipse.**ellipse_axis_length**(*a*)

allensdk.internal.brain_observatory.fit_ellipse.**ellipse_center**(*a*)

allensdk.internal.brain_observatory.fit_ellipse.**fit_ellipse**(*candidate_points*)

allensdk.internal.brain_observatory.fit_ellipse.**rotate_vector**(*y*, *x*, *theta*)

allensdk.internal.brain_observatory.fit_ellipse.**test_fit**()

allensdk.internal.brain_observatory.frame_stream module

class allensdk.internal.brain_observatory.frame_stream.**CvInputStream**(*movie_path*, *num_frames=None*, *block_size=1*, *cache_frames=False*)

Bases: object

close(*self*)

open(*self*)

class allensdk.internal.brain_observatory.frame_stream.**FfmpegInputStream**(*movie_path*, *frame_shape*, *ffmpeg_bin='ffmpeg'*, *num_frames=None*, *block_size=1*, *cache_frames=False*, *process_frame_cb=None*)

Bases: *allensdk.internal.brain_observatory.frame_stream.FrameInputStream*

close(*self*)

create_images(*self*, *output_directory*, *image_type*)

open(*self*)

class allensdk.internal.brain_observatory.frame_stream.**FfmpegOutputStream**(*frame_shape*, *ffmpeg_bin='ffmpeg'*, *block_size=1*)

Bases: *allensdk.internal.brain_observatory.frame_stream.FrameOutputStream*

close(*self*)

open(*self*, *movie_path*)

class allensdk.internal.brain_observatory.frame_stream.**FrameInputStream**(*movie_path*, *num_frames=None*, *block_size=1*, *cache_frames=False*, *process_frame_cb=None*)

Bases: object

close(*self*)

create_images(*self*, *output_directory*, *image_type*)

open(*self*)

class allensdk.internal.brain_observatory.frame_stream.**FrameOutputStream**(*block_size=1*)

Bases: object

close(*self*)

open(*self*, *movie_path*)

write(*self*, *frame*)

class allensdk.internal.brain_observatory.frame_stream.**ImageOutputStream**(*block_size=1*)

Bases: *allensdk.internal.brain_observatory.frame_stream.FrameOutputStream*

allensdk.internal.brain_observatory.itracker module

allensdk.internal.brain_observatory.itracker_utils module

allensdk.internal.brain_observatory.itracker_utils.**default_ray**(*n*)

allensdk.internal.brain_observatory.itracker_utils.**eccentricity**(*a1*, *a2*)

allensdk.internal.brain_observatory.itracker_utils.**filter_bad_params**(*params*, *frame_width*, *frame_height*)

Replace positions outside image with nan

allensdk.internal.brain_observatory.itracker_utils.**generate_rays**(*image_array*, *seed_pixel*)

allensdk.internal.brain_observatory.itracker_utils.**initial_cr_point**(*image_array*, *bbox=None*)

bbox is a tuple of (xmin, xmax, ymin, ymax)

allensdk.internal.brain_observatory.itracker_utils.**initial_pupil_point**(*image_array*, *bbox=None*)

bbox is a tuple of (xmin, xmax, ymin, ymax)

allensdk.internal.brain_observatory.itracker_utils.**medfilt_custom**(*x*, *kernel_size=3*)

This median filter returns 'nan' whenever any value in the kernal width is 'nan' and the median otherwise allensdk.internal.brain_observatory.itracker_utils.**median_absolute_deviation**(*a*, *consistency_constant=1.4*

Calculate the median absolute deviation of a univariate dataset.

Parameters

a [numpy.ndarray] Sample data.

consistency_constant [float] Constant to make the MAD a consistent estimator of the population standard deviation (1.4826 for a normal distribution).

Returns

float Median absolute deviation of the data.

allensdk.internal.brain_observatory.itracker_utils.**post_process_cr**(*cr_params*)

This will replace questionable values of the CR x and y position with 'nan'

1) threshold ellipse area by 99th percentile area distribution
2) median filter using custom median filter
3) remove deviations from discontinuous jumps

The 'nan' values likely represent obscured CRs, secondary reflections, merges with the secondary reflection, or visual distortions due to the whisker or deformations of the eye

allensdk.internal.brain_observatory.itracker_utils.**post_process_pupil**(*pupil_params*)

Filter pupil parameters to replace outliers with nan

Parameters

pupil_params [numpy.ndarray] (Nx5) array of pupil parameters [x, y, angle, axis1, axis2].

Returns

numpy.ndarray Pupil parameters with outliers replaced with nan

allensdk.internal.brain_observatory.itracker_utils.**rotate_ray**(*ray*, *theta*)

allensdk.internal.brain_observatory.itracker_utils.**sobel_grad**(*image_array*)

allensdk.internal.brain_observatory.mask_set module

class allensdk.internal.brain_observatory.mask_set.**MaskSet**(*masks*)

Bases: object

close(*self*, *mask_idxs*, *max_dist*)

close_sets(*self*, *set_size*, *max_dist*)

count

detect_duplicates(*self*, *overlap_threshold*)

detect_unions(*self*, *set_size=2*, *max_dist=10*, *threshold=0.7*)

distance(*self*, *mask_idxs*)

intersection(*self*, *mask_idxs*)

intersection_size(*self*, *mask_idxs*)

mask(*self*, *mask_idx*)

mask_is_union_of_set (*self*, *mask_idx*, *set_idxs*, *threshold*)

overlap_fraction (*self*, *idx0*, *idx1*)

size (*self*, *mask_idx*)

union (*self*, *mask_idxs*)

union_size (*self*, *mask_idxs*)

allensdk.internal.brain_observatory.mask_set.**bb_dist** (*bbs*)

allensdk.internal.brain_observatory.mask_set.**make_bbs** (*masks*)

allensdk.internal.brain_observatory.ophys_session_decomposition module

allensdk.internal.brain_observatory.ophys_session_decomposition.**export_frame_to_hdf5** (*raw_file data_hd aux- il- iary_hd frame_n com- pres- sion='g com- pres- sion_op*

Export a frame from raw to hdf5.

Data with the channel_description *data* is stored in the data_hdf5_filename, while any other data is stored in the auxiliary_hdf5_filename

allensdk.internal.brain_observatory.ophys_session_decomposition.**load_frame** (*raw_filename*, *json_meta*, *use_memmap=False*)

Load a frame of a multi-frame raw file.

allensdk.internal.brain_observatory.ophys_session_decomposition.**open_view_on_binary** (*file_like*, *dtype=<c 'numpy.u mode='r' off- set=0, shape=No or- der='C', strides=N*

Open a view into a memory-mapped binary file.

Parameters

file_like [{string, file object}] File to open.

dtype [numpy.dtype] Numpy dtype to open the memory-mapped array as.

mode [string] Mode to open the file in.

offset [integer] Offset (in bytes) into the file at which to start the memory map.

shape [{tuple, list}] Shape of the array.

order [{"C", "F"}] C or Fortran ordering.

strides [{tuple, list}] Strides along each axis for reading the array.

Returns

numpy.memmap Strided view into memory-mapped array.

`allensdk.internal.brain_observatory.ophys_session_decomposition.`**`read_strided`**(*filename*, *dtype*, *offset*, *shape*, *strides*)

Load a frame without memory-mapping.

allensdk.internal.brain_observatory.roi_filter module

`class` `allensdk.internal.brain_observatory.roi_filter.`**`ROIClassifier`**(*model_data=None*)

Bases: `object`

Wrapper for machine learning classifier.

Provides an underlying classifier model implementing *fit*, *score*, and *predict*. Tracks additional information for constructing the feature array from input datastreams, as well as training data used and cross validation scores generated.

Parameters

model_data [dictionary] Dictionary of classifier properties *sklearn_version*: Version of sklearn used for training. *model*: Underlying classifier. *training_features*: Feature set used to train model. *training_labels*: Label set used to train model. *trimmed_features*: Features to remove from input data. *structure_ids*: Structure ID set used for training. *drivers*: Driver set used for training. *reporters*: Reporter set used for training. *other_appended_labels*: Labels appended outside model. *cross_validation_scores*: Cross validation if generated.

`create_feature_array`(*self*, *object_data*, *depth*, *structure_id*, *drivers*, *reporters*)

Creates feature array from input data.

See also:

`create_feature_array` Create a feature array given model and inputs

`cross_validate`(*self*, *features*, *labels*, *n_folds=5*, *n_jobs=1*)

Generate cross-validation scores for the classifier.

Parameters

features [pandas.DataFrame] Set of features for classification.

labels [pandas.DataFrame] Set of ground truth labels for training and evaluation.

n_folds [int] Number of folds for K-Fold cross-validation.

n_jobjs [int] Number of CPUs to use.

Returns

numpy.ndarray *n_folds* cross-validation scores.

fit (*self*, *features*, *labels*)
Fit model to data.

Parameters

features [pandas.DataFrame] Training feature set.

labels [pandas.DataFrame] Training labels.

static from_file (*filename*)
Load an ROIClassifier from file.

get_labels (*self*, *object_data*, *depth*, *structure_id*, *drivers*, *reporters*)
Generate labels from input data.

See also:

ROIClassifier.create_feature_array

label_names
Return label names for the classifier.

model_data
The classifier properties as a dictionary.

predict (*self*, *features*)
Generate classification labels given features.

save (*self*, *filename*)
Save the classifier to file by pickling.

score (*self*, *features*, *labels*)
Calculate classifier score on data.

allensdk.internal.brain_observatory.roi_filter.**apply_labels** (*rois*, *label_array*, *label_names*)
Apply labels to rois.

Parameters

rois [list] List of RoiMask objects sorted to *label_array* order.

label_array [numpy.ndarray] Label array output from classifier.

label_names [list] Names to apply to columns of *label_array*.

Returns

list List of ROIs with labels appended.

allensdk.internal.brain_observatory.roi_filter.**create_feature_array** (*model_data*, *object_data*, *depth*, *structure_id*, *drivers*, *reporters*)
Create feature array from input data.

This creates the feature array with column ordering matching what the classifier was trained on.

Parameters

model_data [dictionary] Dictionary containing information about the machine learning model and training set.

object_data [pandas.DataFrame] Object list data.

depth [float] Imaging depth of the experiment.

structure_id [string] Targeted structure id.

drivers [list] List of drivers for the mouse.

reporters [list] List of reporters for the mouse.

`allensdk.internal.brain_observatory.roi_filter.`**`get_unexpected_features`**(*model_data*, *object_data*, *structure_id*, *drivers*, *reporters*)

Get list of incoming features that weren't in traning data.

Parameters

model_data [dictionary] Dictionary containing information about the machine learning model and training set.

object_data [pandas.DataFrame] Object list data.

structure_id [string] Targeted structure id.

drivers [list] List of drivers for the mouse.

reporters [list] List of reporters for the mouse.

`allensdk.internal.brain_observatory.roi_filter.`**`label_unions_and_duplicates`**(*rois*, *overlap_threshold*)

Detect unions and duplicates and label ROIs.

`allensdk.internal.brain_observatory.roi_filter.`**`mean_gray_to_sigma`**(*meanInt0*, *snpoffsetstdv*)

Calculate intensity variation used in prior code.

Parameters

meanInt0 [pandas.Series] Array of intensity averages.

snpoffsetstdv [pandas.Series] Array of soma-neuropil standard deviations.

Returns

pandas.Series meanInt0/snpoffsetstdv, preventing Inf (returns as 0).

allensdk.internal.brain_observatory.roi_filter_utils module

`allensdk.internal.brain_observatory.roi_filter_utils.`**`CRITERIA`**()

`class` `allensdk.internal.brain_observatory.roi_filter_utils.`**`TrainingLabelClassifier`**(*criteria*)

Bases: `object`

Very basic threshold_based classifier.

Has a decision function that is just the number of distinct criteria met by the classifier. Criteria are defined as a list of strings used with pandas.DataFrame.eval.

Parameters

criteria [list] List of evaluation strings.

decision_function(*self*, *X*)
Get the distance from the decision boundary.

Parameters

X [array-like] Features for each ROI.

Returns

T [array-like] Distance for each sample from the decision boundary.

class allensdk.internal.brain_observatory.roi_filter_utils.**TrainingMultiLabelClassifier**(*crit*
Bases: object

Multilabel classifier using groups of TrainingLabelClassifiers.

This was used to generate labeling for training the original SVM for classification.

Parameters

criteria [dictionary] Label names and criteria for each label.

get_eXcluded(*self*, *X*)
Get the calculated value of the eXcluded column.

This is useful for comparison with the original classifier implementation.

Parameters

X [pandas.DataFrame] Object features from the object list file.

Returns

numpy.ndarray Calculated eXcluded score from the classifier.

label_data(*self*, *X*, *as_columns=True*)
Generate labels for each row in X.

Parameters

X [pandas.DataFrame] Object features from the object list file.

Returns

numpy.ndarray Array of label codes representing the combination of labels found for each row.

allensdk.internal.brain_observatory.roi_filter_utils.**calculate_max_border**(*motion_df*, *max_shift*)
Calculate motion boundary from frame offsets.

When the motion correction algorithm fails to find sufficient matches, it generates very large frame offsets. The use of *max_shift* avoids filtering too many cells due to the large offsets, with the tradeoff that those frames will be noise.

Parameters

motion_df [pandas.DataFrame] Dataframe containing the x, y offsets from motion correction.

max_shift [float] Maximum shift to allow when considering motion correction. Any larger shifts are considered outliers.

Returns

list [right_shift, left_shift, down_shift, up_shift]

`allensdk.internal.brain_observatory.roi_filter_utils.`**`get_indices_by_distance`**(*object_list_points*, *mask_points*)

Find indices of nearest neighbor matches.

Require a distance of 0 (perfect match) and a unique match between masks and object_list entries.

`allensdk.internal.brain_observatory.roi_filter_utils.`**`get_rois`**(*segmentation_stack*, *border=None*)

Extract a list of rois from the segmentation data array.

Parameters

segmentation_stack [numpy.ndarray] The array from the maxInt_masks file showing the object masks.

border [list] [right_shift, left_shift, down_shift, up_shift] bounding box determined from motion correction.

Returns

list List of RoiMask objects.

`allensdk.internal.brain_observatory.roi_filter_utils.`**`order_rois_by_object_list`**(*object_data*, *rois*)

Reorder rois by matching bounding boxes to object list.

Parameters

object_data [pandas.DataFrame] Object list data.

rois [list] List of RoiMasks.

Returns

list The list of rois reordered to index the same as object_data.

allensdk.internal.brain_observatory.run_itracker module

allensdk.internal.brain_observatory.time_sync module

`class` `allensdk.internal.brain_observatory.time_sync.`**`OphysTimeAligner`**(*sync_file*, *scanner=None*, *dff_file=None*, *stimulus_pkl=None*, *eye_video=None*, *behavior_video=None*, *long_stim_threshold=0.2*)

Bases: `object`

`behavior_video_timestamps`

`corrected_behavior_video_timestamps`

corrected_eye_video_timestamps

corrected_ophys_timestamps

corrected_stim_timestamps

dataset

eye_video_timestamps

ophys_timestamps
Get the timestamps for the ophys data.

stim_timestamps

allensdk.internal.brain_observatory.time_sync.**corrected_video_timestamps**(*video_name*, *timestamps*, *data_length*)

allensdk.internal.brain_observatory.time_sync.**get_alignment_array**(*ref*, *other*, *int_method=<ufunc 'floor'>*)
Generate an alignment array

allensdk.internal.brain_observatory.time_sync.**get_keys**(*sync_dset*)
Get the correct lookup for line labels.

This method is fragile, but not all old data contains the full list of keys.

allensdk.internal.brain_observatory.time_sync.**get_ophys_data_length**(*filename*)

allensdk.internal.brain_observatory.time_sync.**get_photodiode_events**(*sync_dset*, *photodiode_key*)
Returns the photodiode events with the start/stop indicators and the window init flash stripped off.

allensdk.internal.brain_observatory.time_sync.**get_real_photodiode_events**(*sync_dset*, *photodiode_key*, *anomaly_threshold=0.5*)
Gets the photodiode events with the anomalies removed.

allensdk.internal.brain_observatory.time_sync.**get_stim_data_length**(*filename: str*) → int
Get stimulus data length from .pkl file.

Parameters

filename [str] Path of stimulus data .pkl file.

Returns

int Stimulus data length.

allensdk.internal.brain_observatory.time_sync.**get_video_length**(*filename*) allensdk.internal.brain_observatory.time_sync.**monitor_delay**(*sync_dset, stim_times, photodiode_key, transition_frame_interval=60, max_monitor_delay=0.07, assumed_delay=0.0351*)

Calculate monitor delay.

Module contents

allensdk.internal.core package

Submodules

allensdk.internal.core.lims_pipeline_module module

class allensdk.internal.core.lims_pipeline_module.**PipelineModule**(*description=”, parser=None*)

Bases: object

args

input_data(*self*)

write_output_data(*self, data*)

allensdk.internal.core.lims_pipeline_module.**default_argument_parser**(*description=”*)

allensdk.internal.core.lims_pipeline_module.**run_module**(*module, input_data, storage_directory, optional_args=None, python='/shared/utils.x86_64/python-2.7/bin/python', sdk_path='/shared/bioapps/infoapps/lims2_modules/ local=False, pbs=None*)

allensdk.internal.core.lims_utilities module

allensdk.internal.core.lims_utilities.**append_well_known_file**(*wkfs, path, wkf_type_id=None, content_type=None*)

allensdk.internal.core.lims_utilities.**connect**(*user='limsreader', host='limsdb2', database='lims2', password='limsro', port=5432*)

allensdk.internal.core.lims_utilities.**convert_from_titan_linux**(*file_name*)

allensdk.internal.core.lims_utilities.**get_input_json**(*object_id, object_class, strategy_class, host='lims2', **kwargs*)

allensdk.internal.core.lims_utilities.**get_well_known_file_by_name**(*wkfs, filename*) allensdk.internal.core.lims_utilities.**get_well_known_file_by_type**(*wkfs*, *wkf_type_id*)

allensdk.internal.core.lims_utilities.**get_well_known_files_by_name**(*wkfs*, *filename*)

allensdk.internal.core.lims_utilities.**get_well_known_files_by_type**(*wkfs*, *wkf_type_id*)

allensdk.internal.core.lims_utilities.**linux_to_windows**(*file_name*)

allensdk.internal.core.lims_utilities.**query**(*query*, *user='limsreader'*, *host='limsdb2'*, *database='lims2'*, *password='limsro'*, *port=5432*)

allensdk.internal.core.lims_utilities.**safe_system_path**(*file_name*)

allensdk.internal.core.lims_utilities.**select**(*cursor*, *query*)

allensdk.internal.core.mouse_connectivity_cache_prerelease module

allensdk.internal.core.simpletree module

class allensdk.internal.core.simpletree.**SimpleTree**(*nodes*, *node_id_cb*, *parent_id_cb*)

Bases: object

ancestor_ids(*self*, *nid*)

ancestors(*self*, *nid*)

child_ids(*self*, *nid*)

children(*self*, *nid*)

descendant_ids(*self*, *nid*)

descendants(*self*, *nid*)

node(*self*, *nid*)

node_ids(*self*)

nodes(*self*, *nids=None*)

parent(*self*, *nid*)

parent_id(*self*, *nid*)

allensdk.internal.core.swc module

class allensdk.internal.core.swc.**Marker**(**args*, ***kwargs*)

Bases: dict

Simple dictionary class for handling reconstruction marker objects.

CUT_DENDRITE = 10

NO_RECONSTRUCTION = 20

SPACING = [0.1144, 0.1144, 0.28]

allensdk.internal.core.swc.**read_marker_file**(*file_name*)

read in a marker file and return a list of dictionaries `allensdk.internal.core.swc.`**`read_swc`**(*file_name*)

Read in an SWC file and return a Morphology object.

Parameters

file_name: string SWC file name.

Returns

Morphology A Morphology instance.

Module contents

allensdk.internal.ephys package

Submodules

allensdk.internal.ephys.core_feature_extract module

`allensdk.internal.ephys.core_feature_extract.`**`extract_data`**(*data*, *nwb_file*)

`allensdk.internal.ephys.core_feature_extract.`**`filter_sweeps`**(*sweeps*, *types=None*, *passed_only=True*, *iclamp_only=True*)

`allensdk.internal.ephys.core_feature_extract.`**`filtered_sweep_numbers`**(*sweeps*, *types=None*, *passed_only=True*, *iclamp_only=True*)

`allensdk.internal.ephys.core_feature_extract.`**`find_coarse_long_square_amp_delta`**(*sweeps*, *decimals=0*)

Find the delta between amplitudes of coarse long square sweeps. Includes failed sweeps.

`allensdk.internal.ephys.core_feature_extract.`**`find_stim_start`**(*stim*, *idx0=0*)

Find the index of the first nonzero positive or negative jump in an array.

Parameters

stim: np.ndarray Array to be searched

idx0: int Start searching with this index (default: 0).

Returns

int

`allensdk.internal.ephys.core_feature_extract.`**`find_sweep_stim_start`**(*data_set*, *sweep_number*)

`allensdk.internal.ephys.core_feature_extract.`**`generate_output_cell_features`**(*cell_features*, *sweep_features*, *sweep_index*)

`allensdk.internal.ephys.core_feature_extract.`**`nan_get`**(*obj*, *key*)

Return a value from a dictionary. If it does not exist, return None. If it is NaN, return None allensdk.internal.ephys.core_feature_extract.**save_qc_figures**(*qc_fig_dir*, *nwb_file*, *output_data*, *plot_cell_figures*)

allensdk.internal.ephys.core_feature_extract.**update_output_sweep_features**(*cell_features*, *sweep_features*, *sweep_index*)

allensdk.internal.ephys.plot_qc_figures module

allensdk.internal.ephys.plot_qc_figures.**exp_curve**(*x*, *a*, *inv_tau*, *y0*)
Function used for tau curve fitting

allensdk.internal.ephys.plot_qc_figures.**get_features**(*sweep_features*, *sweep_number*)

allensdk.internal.ephys.plot_qc_figures.**get_spikes**(*sweep_features*, *sweep_number*)

allensdk.internal.ephys.plot_qc_figures.**get_time_string**()

allensdk.internal.ephys.plot_qc_figures.**load_experiment**(*file_name*, *sweep_number*)

allensdk.internal.ephys.plot_qc_figures.**main**()

allensdk.internal.ephys.plot_qc_figures.**make_cell_html**(*image_files*, *ephys_roi_result*, *file_name*, *relative_sweep_link*)

allensdk.internal.ephys.plot_qc_figures.**make_cell_page**(*nwb_file*, *ephys_roi_result*, *working_dir*, *save_cell_plots=True*)

allensdk.internal.ephys.plot_qc_figures.**make_sweep_html**(*sweep_files*, *file_name*)

allensdk.internal.ephys.plot_qc_figures.**make_sweep_page**(*nwb_file*, *ephys_roi_result*, *working_dir*)

allensdk.internal.ephys.plot_qc_figures.**mask_nulls**(*data*)

allensdk.internal.ephys.plot_qc_figures.**plot_cell_figures**(*nwb_file*, *ephys_roi_result*, *image_dir*, *sizes*)

allensdk.internal.ephys.plot_qc_figures.**plot_fi_curve_figures**(*nwb_file*, *cell_features*, *lims_features*, *sweep_features*, *image_dir*, *sizes*, *cell_image_files*)

allensdk.internal.ephys.plot_qc_figures.**plot_hero_figures**(*nwb_file*, *cell_features*, *lims_features*, *sweep_features*, *image_dir*, *sizes*, *cell_image_files*)

allensdk.internal.ephys.plot_qc_figures.**plot_images**(*ephys_roi_result*, *image_dir*, *sizes*, *image_sets*) allensdk.internal.ephys.plot_qc_figures.**plot_instantaneous_threshold_thumbnail**(*nwb_file*, *sweep_numbers*, *cell_features*, *lims_features*, *sweep_features*, *color='red'*)

allensdk.internal.ephys.plot_qc_figures.**plot_long_square_summary**(*nwb_file*, *cell_features*, *lims_features*, *sweep_features*)

allensdk.internal.ephys.plot_qc_figures.**plot_ramp_figures**(*nwb_file*, *cell_specimen*, *cell_features*, *lims_features*, *sweep_features*, *image_dir*, *sizes*, *cell_image_files*)

allensdk.internal.ephys.plot_qc_figures.**plot_rheo_figures**(*nwb_file*, *cell_features*, *lims_features*, *sweep_features*, *image_dir*, *sizes*, *cell_image_files*)

allensdk.internal.ephys.plot_qc_figures.**plot_sag_figures**(*nwb_file*, *cell_features*, *lims_features*, *sweep_features*, *image_dir*, *sizes*, *cell_image_files*)

allensdk.internal.ephys.plot_qc_figures.**plot_short_square_figures**(*nwb_file*, *cell_features*, *lims_features*, *sweep_features*, *image_dir*, *sizes*, *cell_image_files*)

allensdk.internal.ephys.plot_qc_figures.**plot_single_ap_values**(*nwb_file*, *sweep_numbers*, *lims_features*, *sweep_features*, *cell_features*, *type_name*)

allensdk.internal.ephys.plot_qc_figures.**plot_subthreshold_long_square_figures**(*nwb_file*, *cell_features*, *lims_features*, *sweep_features*, *image_dir*, *sizes*, *cell_image_files*)

allensdk.internal.ephys.plot_qc_figures.**plot_sweep_figures**(*nwb_file*, *ephys_roi_result*, *image_dir*, *sizes*) `allensdk.internal.ephys.plot_qc_figures.`**`plot_sweep_set_summary`**(*nwb_file, highlight_sweep_number, sweep_numbers, highlight_color='#0779BE', background_color='#dddddd'*)

`allensdk.internal.ephys.plot_qc_figures.`**`plot_sweep_value_figures`**(*cell_specimen, image_dir, sizes, cell_image_files*)

`allensdk.internal.ephys.plot_qc_figures.`**`save_figure`**(*fig, image_name, image_set_name, image_dir, sizes, image_sets, scalew=1, scaleh=1, ext='jpg'*)

allensdk.internal.ephys.plot_qc_figures3 module

`allensdk.internal.ephys.plot_qc_figures3.`**`exp_curve`**(*x, a, inv_tau, y0*)

Function used for tau curve fitting

`allensdk.internal.ephys.plot_qc_figures3.`**`get_features`**(*sweep_features, sweep_number*)

`allensdk.internal.ephys.plot_qc_figures3.`**`get_spikes`**(*sweep_features, sweep_number*)

`allensdk.internal.ephys.plot_qc_figures3.`**`get_time_string`**()

`allensdk.internal.ephys.plot_qc_figures3.`**`load_experiment`**(*file_name, sweep_number*)

`allensdk.internal.ephys.plot_qc_figures3.`**`make_cell_html`**(*image_files, file_name, relative_sweep_link, specimen_info, fields*)

`allensdk.internal.ephys.plot_qc_figures3.`**`make_cell_page`**(*nwb_file, cell_features, rheo_features, sweep_features, sweep_info, well_known_files, specimen_info, working_dir, fields_to_show, save_cell_plots=True*)

nwb_file: name of nwb file (string)

cell_features:

rheo_features: dict containing extracted features from rheobase sweep

sweep_features:

sweep_info:

well_known_files: LIMS-output information containing graphics file names

working_dir:

save_cell_plots:

`allensdk.internal.ephys.plot_qc_figures3.`**`make_sweep_html`**(*sweep_files, file_name*) allensdk.internal.ephys.plot_qc_figures3.**make_sweep_page**(*nwb_file*, *working_dir*, *sweep_data*)

allensdk.internal.ephys.plot_qc_figures3.**mask_nulls**(*data*)

allensdk.internal.ephys.plot_qc_figures3.**plot_cell_figures**(*nwb_file*, *cell_features*, *sweep_features*, *rheo_features*, *image_dir*, *sweep_info*, *sizes*)

allensdk.internal.ephys.plot_qc_figures3.**plot_fi_curve_figures**(*nwb_file*, *cell_features*, *rheo_features*, *sweep_features*, *image_dir*, *sizes*, *cell_image_files*)

allensdk.internal.ephys.plot_qc_figures3.**plot_hero_figures**(*nwb_file*, *cell_features*, *rheo_features*, *sweep_features*, *image_dir*, *sizes*, *cell_image_files*)

allensdk.internal.ephys.plot_qc_figures3.**plot_images**(*well_known_files*, *image_dir*, *sizes*, *image_sets*)

allensdk.internal.ephys.plot_qc_figures3.**plot_instantaneous_threshold_thumbnail**(*nwb_file*, *sweep_numbers*, *cell_features*, *rheo_features*, *sweep_features*, *color='red'*)

allensdk.internal.ephys.plot_qc_figures3.**plot_long_square_summary**(*nwb_file*, *cell_features*, *rheo_features*, *sweep_features*)

allensdk.internal.ephys.plot_qc_figures3.**plot_ramp_figures**(*nwb_file*, *sweep_info*, *cell_features*, *rheo_features*, *sweep_features*, *image_dir*, *sizes*, *cell_image_files*)

allensdk.internal.ephys.plot_qc_figures3.**plot_rheo_figures**(*nwb_file*, *cell_features*, *rheo_features*, *sweep_features*, *image_dir*, *sizes*, *cell_image_files*)

allensdk.internal.ephys.plot_qc_figures3.**plot_sag_figures**(*nwb_file*, *cell_features*, *rheo_features*, *sweep_features*, *image_dir*, *sizes*, *cell_image_files*) allensdk.internal.ephys.plot_qc_figures3.**plot_short_square_figures**(*nwb_file, cell_features, rheo_features, sweep_features, image_dir, sizes, cell_image_files*)

allensdk.internal.ephys.plot_qc_figures3.**plot_single_ap_values**(*nwb_file, sweep_numbers, rheo_features, sweep_features, cell_features, type_name*)

allensdk.internal.ephys.plot_qc_figures3.**plot_subthreshold_long_square_figures**(*nwb_file, cell_features, rheo_features, sweep_features, image_dir, sizes, cell_image_files*)

allensdk.internal.ephys.plot_qc_figures3.**plot_sweep_figures**(*nwb_file, sweep_data, image_dir, sizes*)

allensdk.internal.ephys.plot_qc_figures3.**plot_sweep_set_summary**(*nwb_file, highlight_sweep_number, sweep_numbers, highlight_color='#0779BE', background_color='#dddddd'*)

allensdk.internal.ephys.plot_qc_figures3.**plot_sweep_value_figures**(*sweep_info, image_dir, sizes, cell_image_files*)

allensdk.internal.ephys.plot_qc_figures3.**save_figure**(*fig, image_name, image_set_name, image_dir, sizes, image_sets, scalew=1, scaleh=1, ext='jpg'*)

Module contents

allensdk.internal.model package

Subpackages

allensdk.internal.model.biophysical package

Subpackages

allensdk.internal.model.biophysical.fits package

Subpackages

allensdk.internal.model.biophysical.fits.fit_styles package

Module contents

Module contents

allensdk.internal.model.biophysical.passive_fitting package

Subpackages

allensdk.internal.model.biophysical.passive_fitting.passive package

Module contents

Submodules

allensdk.internal.model.biophysical.passive_fitting.neuron_passive_fit module

allensdk.internal.model.biophysical.passive_fitting.neuron_passive_fit.**arg_parser**()

allensdk.internal.model.biophysical.passive_fitting.neuron_passive_fit.**main**()

allensdk.internal.model.biophysical.passive_fitting.neuron_passive_fit.**process_inputs**(*parser*

allensdk.internal.model.biophysical.passive_fitting.neuron_passive_fit2 module

allensdk.internal.model.biophysical.passive_fitting.neuron_passive_fit2.**main**()

allensdk.internal.model.biophysical.passive_fitting.neuron_passive_fit_elec module

allensdk.internal.model.biophysical.passive_fitting.neuron_passive_fit_elec.**main**()

allensdk.internal.model.biophysical.passive_fitting.neuron_utils module

allensdk.internal.model.biophysical.passive_fitting.neuron_utils.**get_h**()

allensdk.internal.model.biophysical.passive_fitting.neuron_utils.**load_morphology**(*filename*)

allensdk.internal.model.biophysical.passive_fitting.neuron_utils.**parse_neuron_output**(*output_*

allensdk.internal.model.biophysical.passive_fitting.neuron_utils.**read_neuron_fit_stdout**(*func*

allensdk.internal.model.biophysical.passive_fitting.output_grabber module

class allensdk.internal.model.biophysical.passive_fitting.output_grabber.**OutputGrabber**(*strea*
threa

Bases: object

Class used to grab standard output or another stream.

escape_char = '\x08'

readOutput(*self*)
Read the stream data (one byte at a time) and save the text in *capturedtext*.

start(*self*)
Start capturing the stream data.

stop(*self*)
Stop capturing the stream data and save the text in *capturedtext*.

allensdk.internal.model.biophysical.passive_fitting.preprocess module

allensdk.internal.model.biophysical.passive_fitting.preprocess.**get_cap_check_indices**(*i*)

allensdk.internal.model.biophysical.passive_fitting.preprocess.**get_passive_fit_data**(*cap_chec*
data_set)

allensdk.internal.model.biophysical.passive_fitting.preprocess.**main**()

Module contents

Submodules

allensdk.internal.model.biophysical.biophysical_archiver module

class allensdk.internal.model.biophysical.biophysical_archiver.**BiophysicalArchiver**(*archive_di*

Bases: object

archive_cell(*self*, *ephys_result_id*, *specimen_id*, *template*, *neuronal_model_id*)

get_cells(*self*)

get_neuronal_models(*self*, *specimen_ids*)

get_stimulus_file(*self*, *neuronal_model_id*)

get_template_names(*self*)

allensdk.internal.model.biophysical.check_fi_shift module

allensdk.internal.model.biophysical.check_fi_shift.**calculate_fi_curves**(*data_set*,
sweeps)

allensdk.internal.model.biophysical.check_fi_shift.**estimate_fi_shift**(*data_set*,
sweeps)

allensdk.internal.model.biophysical.deap_utils module

class allensdk.internal.model.biophysical.deap_utils.**Utils**(*description*)

Bases: *allensdk.model.biophys_sim.neuron.hoc_utils.HocUtils*

actual_parameters_from_normalized(*self, params*)

calculate_feature_errors(*self, t_ms, v, i*)

generate_morphology(*self, morph_filename*)

insert_iclamp(*self*)

load_cell_parameters(*self*)

normalize_actual_parameters(*self, params*)

record_values(*self*)

set_actual_parameters(*self, params*)

set_iclamp_params(*self, amp, delay, dur*)

set_normalized_parameters(*self, params*)

allensdk.internal.model.biophysical.ephys_utils module

allensdk.internal.model.biophysical.ephys_utils.**get_step_stim_characteristics**(*i, t*)

allensdk.internal.model.biophysical.ephys_utils.**get_sweep_v_i_t_from_set**(*data_set, sweep_number*)

allensdk.internal.model.biophysical.ephys_utils.**get_sweeps_of_type**(*sweep_type, sweeps*)

allensdk.internal.model.biophysical.fit_stage_1 module

allensdk.internal.model.biophysical.fit_stage_2 module

allensdk.internal.model.biophysical.make_deap_fit_json module

class allensdk.internal.model.biophysical.make_deap_fit_json.**Report**(*top_level_description, fit_type*)

Bases: object

best_fit_value(*self*)

check_org_selections_for_noise_block(*self*)

gather_from_seeds(*self*)

generate_fit_file(*self*)

make_fit_json_file(*self*)

setup_model(*self*)

allensdk.internal.model.biophysical.neuron_parallel module

allensdk.internal.model.biophysical.optimize module

allensdk.internal.model.biophysical.run_optimize module

allensdk.internal.model.biophysical.run_optimize_workflow module

allensdk.internal.model.biophysical.run_passive_fit module

`allensdk.internal.model.biophysical.run_passive_fit.`**`main`**(*limit*, *manifest_path*)

`allensdk.internal.model.biophysical.run_passive_fit.`**`run_passive_fit`**(*description*)

allensdk.internal.model.biophysical.run_simulate_lims module

`class` `allensdk.internal.model.biophysical.run_simulate_lims.`**`RunSimulateLims`**(*input_json*, *output_json*)

Bases: *allensdk.model.biophysical.run_simulate.RunSimulate*

`copy_local`(*self*)

`generate_manifest_lims`(*self*, *lims_data_path*, *manifest_path*)

`generate_manifest_rma`(*self*, *neuronal_model_run_id*, *manifest_path*, *api_url=None*)

`allensdk.internal.model.biophysical.run_simulate_lims.`**`main`**(*command*, *lims_strategy_json*, *lims_response_json*)

Entry point for module. :param command: select behavior, nrnivmodl or simulate :type command: string :param lims_strategy_json: path to json file output from lims. :type lims_strategy_json: string :param lims_response_json: path to json file returned to lims. :type lims_response_json: string

allensdk.internal.model.biophysical.run_simulate_workflow module

Module contents

allensdk.internal.model.glif package

Submodules

allensdk.internal.model.glif.ASGLM module

`allensdk.internal.model.glif.ASGLM.`**`ASGLM_pairwise`**(*ks_int*, *I_stim*, *voltage*, *spike_ind*, *cinit*, *tauinit*, *SCL*, *dt*, *resting_potential*, *SHORT_RUN=False*, *MAKE_PLOT=False*, *SHOW_PLOT=False*, *BLOCK=False*)

Calculate the resistance and amplitude of the afterspike currents for Parameters ———-

ks_int: list initial possible k's (k=1/tau, where tau is the time constant of the exponential decay)

I_stim: list of arrays input stimulus traces of sweeps

voltage: list of arrays voltage of cell as a result of I_stim

spike_ind: list of arrays each array contains the index of the spikes

cinit: float membrane capacitance

tauinit: float time constant of membrane

SCL: float number of indicies that should be cut after a spike

dt: float size of time step of injected current

Returns

allensdk.internal.model.glif.MLIN module

`allensdk.internal.model.glif.MLIN.`**`MLIN`**(*voltage*, *current*, *res*, *cap*, *dt*, *MAKE_PLOT=False*, *SHOW_PLOT=False*, *BLOCK=False*, *PUBLICATION_PLOT=False*)

voltage, current input:

voltage: numpy array of voltage with test pulse cut out current: numpy array of stimulus with test pulse cut out

`allensdk.internal.model.glif.MLIN.`**`autocorr`**(*x*)

`allensdk.internal.model.glif.MLIN.`**`exp_decay`**(*time*, *amp*, *tau*)

`allensdk.internal.model.glif.MLIN.`**`expsymm_cdf`**(*v*, *dv*)

`allensdk.internal.model.glif.MLIN.`**`expsymm_pdf`**(*v*, *dv*)

`allensdk.internal.model.glif.MLIN.`**`find_bin_center`**(*edges*)

allensdk.internal.model.glif.are_two_lists_of_arrays_the_same module

`allensdk.internal.model.glif.are_two_lists_of_arrays_the_same.`**`are_two_lists_of_arrays_the_s`**

returns False if to lists of arrays are different. otherwise the function returns True.

allensdk.internal.model.glif.configure_model module

allensdk.internal.model.glif.error_functions module

`allensdk.internal.model.glif.error_functions.`**`MLIN_list_error`**(*param_guess*, *experiment*, *input_data*)

allensdk.internal.model.glif.find_spikes module

`allensdk.internal.model.glif.find_spikes.`**`align_and_cut_spikes`**(*voltage_list*, *current_list*, *dt*, *spike_window=None*)

This function aligns the spikes to some criteria and returns a current and voltage trace of of the spike over a time window. Also returns zero crossing,and threshold in reference to the aligned spikes.

`allensdk.internal.model.glif.find_spikes.`**`find_spikes_list`**`(`*voltage_list*, *dt*`)`

`allensdk.internal.model.glif.find_spikes.`**`find_spikes_list_old`**`(`*voltage_list*, *dt*`)`

`allensdk.internal.model.glif.find_spikes.`**`find_spikes_old`**`(`*v*, *dt*`)`

`allensdk.internal.model.glif.find_spikes.`**`find_spikes_ssq_list`**`(`*voltage_list*, *dt*, *dv_cutoff*, *thresh_frac*`)`

allensdk.internal.model.glif.find_sweeps module

`exception` `allensdk.internal.model.glif.find_sweeps.`**`MissingSweepException`**

Bases: `Exception`

`allensdk.internal.model.glif.find_sweeps.`**`find_long_square_sweeps`**`(`*sweeps*`)`

`allensdk.internal.model.glif.find_sweeps.`**`find_noise_sweeps`**`(`*sweeps*`)`

Find 1) the noise1 sweeps 2) the noise2 sweeps 4) all noise sweeps

`allensdk.internal.model.glif.find_sweeps.`**`find_ramp_sweeps`**`(`*sweeps*`)`

Find 1) all ramp sweeps

2) all subthreshold ramps

3) all superthreshold ramps

`allensdk.internal.model.glif.find_sweeps.`**`find_ramp_to_rheo_sweeps`**`(`*sweeps*`)`

`allensdk.internal.model.glif.find_sweeps.`**`find_ranked_sweep`**`(`*sweep_list*, *key*, *reverse=False*`)`

`allensdk.internal.model.glif.find_sweeps.`**`find_short_square_sweeps`**`(`*sweeps*`)`

Find 1) all of the subthreshold short square sweeps

2) all of the superthreshold short square sweeps

3) the subthresholds short square sweep with maximum stimulus amplitude

`allensdk.internal.model.glif.find_sweeps.`**`find_sweeps`**`(`*sweep_list*`)`

`allensdk.internal.model.glif.find_sweeps.`**`get_sweep_numbers`**`(`*sweep_list*`)`

`allensdk.internal.model.glif.find_sweeps.`**`get_sweeps_by_name`**`(`*sweeps*, *sweep_type*`)`

`allensdk.internal.model.glif.find_sweeps.`**`main`**`()`

`allensdk.internal.model.glif.find_sweeps.`**`organize_sweeps_by_name`**`(`*sweeps*, *name*`)`

`allensdk.internal.model.glif.find_sweeps.`**`parse_arguments`**`()`

allensdk.internal.model.glif.glif_experiment module

class allensdk.internal.model.glif.glif_experiment.**GlifExperiment**(*neuron*, *dt*, *stim_list*, *resp_list*, *spike_time_steps*, *grid_spike_times*, *grid_spike_voltages*, *param_fit_names*, ***kwargs*)

Bases: object

neuron_parameter_count(*self*)

run(*self*, *param_guess*)

This code will run the loaded neuron model in reference to the target neuron spikes. inputs:

self: is the instance of the neuron model and parameters alone with the values of the target spikes.
NOTE the values in each array of the self.gridSpikeIndexTarge_list and the self.interpolated_spike_times are in reference to the time start of of the stim in each induvidual array (not the universal time)

param_guess: array of scalars of the values that will be inserted into the mapping function below.

returns:

voltage_list: list of array of voltage values. NOTE: IF THE MODEL NEURON SPIKES BEFORE THE TARG
NOT BE CALCULATED THEREFORE THE RESULTING VECTOR WILL NOT BE AS LONG AS THE TARGET AND ALSO WILL NOT MAKE SENSE WITH THE STIMULUS UNLESS YOU CUT IT AND OUTPUT IT TOO.

grid_spike_times_list: interpolated_spike_time_list: an array of the actual times of the spikes. NOTE: THESE TIMES ARE CALCULATED BY ADDING THE

TIME OF THE INDIVIDUAL SPIKE TO THE TIME OF THE LAST SPIKE.

gridISIFromLastTargSpike_list: list of arrays of spike times of the model in reference to the last target (biologi
spike (not in reference to sweep start)

interpolatedISIFromLastTargSpike_list: list of arrays of spike times of the model in reference to the last target
spike (not in reference to sweep start)

voltageOfModelAtGridBioSpike_list: list of arrays of scalars that contain the voltage of the model neuron when the target or bio neuron spikes. theshOfModelAtGridBioSpike_list: list of arrays of scalars that contain the threshold of the model neuron when the target or bio neuron spikes.

run_base_model(*self*, *param_guess*)

This code will run the loaded neuron model. inputs:

self: is the instance of the neuron model and parameters alone with the values of the target spikes.
NOTE the values in each array of the self.gridSpikeIndexTarge_list and the self.interpolated_spike_times are in reference to the time start of of the stim in each induvidual array (not the universal time)

param_guess: array of scalars of the values that will be inserted into the mapping function below.

returns:

voltage_list: list of array of voltage values. NOTE: IF THE MODEL NEURON SPIKES BEFORE THE TARG
NOT BE CALCULATED THEREFORE THE RESULTING VECTOR WILL NOT BE AS LONG AS THE TARGET AND ALSO WILL NOT MAKE SENSE WITH THE STIMULUS UNLESS YOU CUT IT AND OUTPUT IT TOO.

gridTime_list: interpolatedTime_list: an array of the actual times of the spikes. NOTE: THESE TIMES ARE CALCULATED BY ADDING THE

TIME OF THE INDIVIDUAL SPIKE TO THE TIME OF THE LAST SPIKE.

grid_ISI_list: list of arrays of spike times of the model in reference to the last target (biological)
spike (not in reference to sweep start)

interpolated_ISI_list: list of arrays of spike times of the model in reference to the last target (biological)
spike (not in reference to sweep start)

grid_spike_voltage_list: list of arrays of scalars that contain the voltage of the model neuron when the target or bio neuron spikes. grid_spike_threshold_list: list of arrays of scalars that contain the threshold of the model neuron when the target or bio neuron spikes.

set_neuron_parameters (*self*, *param_guess*)
Maps the parameter guesses to the coefficients of the model. input:

param_guess is vector of values. It is assumed that the length will be

allensdk.internal.model.glif.glif_optimizer module

class allensdk.internal.model.glif.glif_optimizer.**GlifOptimizer** (*experiment*, *dt*, *outer_iterations*, *inner_iterations*, *sigma_outer*, *sigma_inner*, *param_fit_names*, *stim*, *xtol*, *ftol*, *internal_iterations*, *bessel*, *error_function=None*, *error_function_data=None*, *init_params=None*)

Bases: object

evaluate (*self*, *x*, *dt_multiplier=100*)

initiate_unique_seed (*self*, *seed=None*)

randomize_parameter_values (*self*, *values*, *sigma*)

run_many (*self*, *iteration_finished_callback=None*, *seed=None*)

run_once (*self*, *param0*)
@param param0: a list of the initial guesses for the optimizer @return: tuple including parameters that optimize function and value - see fmin docs

run_once_bound(*self*, *low_bound*, *high_bound*)

@param low_bound: a scalar initial guess for the optimizer @param high_bound: a scalar high bound for the optimizer @return: tuple including parameters that optimize function and value - see fmin docs

to_dict(*self*)

allensdk.internal.model.glif.glif_optimizer_neuron module

exception allensdk.internal.model.glif.glif_optimizer_neuron.**GlifBadInitializationExceptio**

Bases: Exception

Exception raised when voltage is above threshold at the beginning of a sweep. i.e. probably caused by the optimizer.

exception allensdk.internal.model.glif.glif_optimizer_neuron.**GlifNeuronException**(*message*, *data*)

Bases: Exception

Exception for catching simulation errors and reporting intermediate data.

class allensdk.internal.model.glif.glif_optimizer_neuron.**GlifOptimizerNeuron**(**args*, ***kwargs*)

Bases: *allensdk.model.glif.glif_neuron.GlifNeuron*

Contains methods for running the neuron model in a "forced-spike" paradigm used during optimization.

TYPE = 'GLIF'

classmethod from_dict(*d*)

classmethod from_dict_legacy(*d*)

run_until_biological_spike(*self*, *voltage_t0*, *threshold_t0*, *AScurrents_t0*, *stimulus*, *response*, *start_index*, *after_end_index*, *bio_spike_time_steps*)

Run the neuron simulation over a segment of a stimulus given initial conditions for use in the "forced spike" optimization paradigm. [Note: the section of stimulus is meant to be between two biological neuron spikes. Thus the stimulus is during the interspike interval (ISI)]. The model is simulated until either the model spikes or the end of the segment is reached. If the model does not spike, a spike time is extrapolated past the end of the simulation segment.

This function also returns the initial conditions for the subsequent stimulus segment. In the forced spike paradigm there are several ways

Parameters

voltage_t0 [float] the current voltage of the neuron

threshold_t0 [float] the current spike threshold level of the neuron

AScurrents_t0 [np.ndarray] the current state of the afterspike currents in the neuron

stimulus [np.ndarray] the full stimulus array (not just the segment of data being simulated)

response [np.ndarray] the full response array (not just the segment of data being simulated)

start_index [int] index of global stimulus at which to start simulation

after_end_index [int] index of global stimulus *after* the last index to be simulated

bio_spike_time_steps [list] time steps of input spikes

Returns

dict

a dictionary containing: 'voltage': simulated voltage value 'threshold': simulated threshold values 'AScurrent_matrix': afterspike current values during the simulation 'grid_model_spike_time': model spike time (in units of dt) 'interpolated_model_spike_time': model spike time (in units of dt) interpolated between time steps 'voltage_t0': reset voltage value to be used in subsequent simulation interval 'threshold_t0': reset threshold value to be used in subsequent simulation interval 'AScurrents_t0': reset afterspike current value to be used in subsequent simulation interval 'grid_bio_spike_model_voltage': model voltage at the time of the input spike 'grid_bio_spike_model_threshold': model threshold at the time of the input spike

`run_with_biological_spikes`(*self*, *stimulus*, *response*, *bio_spike_time_steps*)

Run the neuron simulation over a stimulus, but do not allow the model to spike on its own. Rather, force the simulation to spike and reset at a given set of spike indices. Dynamics rules are applied between spikes regardless of the simulated voltage and threshold values. Reset rules are applied only at input spike times. This is used during optimization to force the model to follow the spikes of biological data. The model is optimized in this way so that history effects due to spiking can be adequately modeled. For example, every time the model spikes a new set of afterspike currents will be initiated. To ensure that afterspike currents can be optimized, we force them to be initiated at the time of the biological spike.

Parameters

stimulus [np.ndarray] vector of scalar current values

respones [np.ndarray] vector of scalar voltage values

bio_spike_time_steps [list] spike time step indices

Returns

dict

a dictionary containing: 'voltage': simulated voltage values, 'threshold': simulated threshold values, 'AScurrent_matrix': afterspike currents during the simulation, 'grid_model_spike_times': spike times of the model aligned to the simulation grid (when it would have spiked), 'interpolated_model_spike_times': spike times of the model linearly interpolated between time steps, 'grid_ISI': interspike interval between grid model spike times, 'interpolated_ISI': interspike interval between interpolated model spike times, 'grid_bio_spike_model_voltage': voltage of the model at biological/input spike times, 'grid_bio_spike_model_threshold': voltage of the model at biological/input spike times interpolated between time steps

`to_dict`(*self*)

Convert the neuron to a serializable dictionary.

`allensdk.internal.model.glif.glif_optimizer_neuron.`**`extrapolate_model_spike_from_endpoints`**(

`allensdk.internal.model.glif.glif_optimizer_neuron.`**`extrapolate_model_spike_from_endpoints_s`**

`allensdk.internal.model.glif.glif_optimizer_neuron.`**`extrapolate_spike_time`**(*dt*, *num_time_steps*, *threshold_t0*, *threshold_t1*, *voltage_t0*, *voltage_t1*)

Given two voltage and threshold values and an interval between them, extrapolate a spike time by intersecting lines the thresholds and voltages.

`allensdk.internal.model.glif.glif_optimizer_neuron.`**`extrapolate_spike_voltage`**(*dt*, *num_time_steps*, *threshold_t0*, *threshold_t1*, *voltage_t0*, *voltage_t1*)

Given two voltage and threshold values and an interval between them, extrapolate a spike time by intersecting lines the thresholds and voltages.

`allensdk.internal.model.glif.glif_optimizer_neuron.`**`find_first_model_spike`**(*voltage*, *threshold*, *voltage_t1*, *threshold_t1*, *dt*)

`allensdk.internal.model.glif.glif_optimizer_neuron.`**`interpolate_spike_voltage`**(*dt*, *time_step*, *threshold_t0*, *threshold_t1*, *voltage_t0*, *voltage_t1*)

Given two voltage and threshold values, the dt between them and the initial time step, interpolate a spike time within the dt interval by intersecting the two lines.

allensdk.internal.model.glif.optimize_neuron module

`allensdk.internal.model.glif.optimize_neuron.`**`get_optimize_sweep_numbers`**(*sweep_index*)

`allensdk.internal.model.glif.optimize_neuron.`**`main`**()

`allensdk.internal.model.glif.optimize_neuron.`**`optimize_neuron`**(*model_config*, *sweep_index*, *nwb_file*, *save_callback=None*)

Optimizes a neuron. 1. Loads optimizer and neuron configuration data. 2. Loads the voltage trace sweeps that will be optimized 3. Configures the experiment and optimizer 4. Runs the optimizer 5. TODO: where is data saved

Parameters

model_config [dictionary] contains values of neuron and optimizer parameters

sweep_index [list of integers] indices (as labeled in the data configuration file) of sweeps that will be optimized

save_callback [module] saves output

allensdk.internal.model.glif.plotting module

Written by Corinne Teeter 3-31-14

`allensdk.internal.model.glif.plotting.`**`checkPreprocess`**(*originalStim_list*, *processedStim_list*, *originalVoltage_list*, *processedVoltage_list*, *config*, *blockME=False*)

`allensdk.internal.model.glif.plotting.`**`checkSpikeCutting`**(*originalStim_list*, *cutStim_list*, *originalVoltage_list*, *cutVoltage_list*, *allindOfNonSpiking_list*, *config*, *blockME=False*)

`allensdk.internal.model.glif.plotting.`**`plotLineRegress1`**(*slope*, *intercept*, *r*, *xlim*)

`allensdk.internal.model.glif.plotting.`**`plotLineRegressRed`**(*slope*, *intercept*, *r*, *xlim*)

`allensdk.internal.model.glif.plotting.`**`plotSpikes`**(*voltage_list*, *spike_ind_list*, *dt*, *blockME=False*, *method=False*)

allensdk.internal.model.glif.preprocess_neuron module

`exception` `allensdk.internal.model.glif.preprocess_neuron.`**`MissingSpikeException`**

Bases: `Exception`

`allensdk.internal.model.glif.preprocess_neuron.`**`estimate_dv_cutoff`**(*voltage_list*, *dt*, *start_t*, *end_t*) `allensdk.internal.model.glif.preprocess_neuron.`**`find_first_spike_voltage`**`(`*voltage*, *dt*, *ssq=False*, *MAKE_PLOT=False*, *SHOW_PLOT=False*, *BLOCK=False*, *dv_cutoff=20.0*, *thresh_frac=0.05*`)`

calculate voltage at threshold of first spike Parameters ——– voltage: numpy array

voltage trace

dt: float sampling time step

ssq: Boolean whether there is or is not a subrathreshold short square pulse (note that if thes

MAKE_PLOT: Boolean specifies whether or not a plot should be made

SHOW_PLOT: Boolean specifies if a visualization should be made

BLOCK: Boolean if a plot is made this specifies weather to stop the code until the plot is closed

dv_cutoff: float specifies cut off of the derivative of the voltage

thresh_frac: float variable that goes into feature extractor

Returns

:float voltage of threshold of first spike

`allensdk.internal.model.glif.preprocess_neuron.`**`main`**`()`

`allensdk.internal.model.glif.preprocess_neuron.`**`preprocess_neuron`**`(`*nwb_file*, *sweep_list*, *cell_properties=None*, *dt=None*, *cut=None*, *bessel=None*, *save_figure_path=None*`)`

`allensdk.internal.model.glif.preprocess_neuron.`**`tag_plot`**`(`*tag*, *fs=9*`)`

allensdk.internal.model.glif.rc module

`allensdk.internal.model.glif.rc.`**`least_squares_RCEl_calc_tested`**`(`*voltage_list*, *current_list*, *dt*`)`

Calculate resistance, capacitance and resting potential by performing least squares on current and voltage.

Parameters

voltage_list: list of arrays voltage responses for several sweep repeats

current_list: list of arrays current injections for several sweep repeats

dt: float time step size in voltage and current traces

Returns

r_list: list of floats each value corresponds to the resistance of a sweep

c_list: list of floats each value corresponds to the capacitance of a sweep

el_list: list of floats each value corresponds to the resting potential of a sweep

allensdk.internal.model.glif.spike_cutting module

allensdk.internal.model.glif.spike_cutting.**calc_spike_cut_and_v_reset_via_expvar_residuals**

This function calculates where the spike should be cut based on explained variance. The goal is to find a model where the voltage after a spike maximally explains the voltage before a spike. This will also specify the voltage reset rule inputs:

spike_determination_method: string specifing the method used to find threshold all_current_list: list of current (list of current traces injected into neuron) all_voltage_list: list of voltages (list of voltage trace)

The change is that if the slope is greater than one or intercept is greater than zero it forces it. Regardless of required force the residuals are used.

allensdk.internal.model.glif.spike_cutting.**plotLineRegress1**(*slope*, *intercept*, *r*, *xlim*)

allensdk.internal.model.glif.spike_cutting.**plotLineRegressRed**(*slope*, *intercept*, *r*, *xlim*)

allensdk.internal.model.glif.threshold_adaptation module

allensdk.internal.model.glif.threshold_adaptation.**calc_spike_component_of_threshold_from_mu**

Calculate the spike components of the threshold by fitting a decaying exponential function to data to threshold versus time since last spike in the multiblip data. The exponential is forced to decay to the local th_inf (calculated as the mean all of the threshold values of the first spikes in each individual triblip stimulus). For each multiblip stimulus in a stimulus set if there is more than one spike the difference in voltages from the first and second spike are plotted versus the separation in time. Note that this algorithm should only be implemented on multiblips sweeps where the neuron spike on the first and second blip. Since there is no easy way to do this, this erroneous data should not be provided to this algorithm (i.e is should be visually checked and eliminated the preprocessor should hold back this data manually for now.)

#TODO: check to see if this is still true. Notes: The standard SDK spike detection algorithm does not work with the multiblip stimulus due to artifacts when the stimulus turns on and off. Please see the find_multiblip_spikes module for more information.

Input:

multi_SS: dictionary contains multiblip information such as current and stimulus

dt: float time step in seconds

Returns:

const_to_add_to_thresh_for_reset: float amplitude of the exponential fit otherwise known as a_spike. Note that this is without any spike cutting

decay_const: float decay constant of exponential. Note the function fit is a negative exponential which will mean this value will either have to be negated when it is used or the functions used will have to have to include the negative.

thresh_inf: float

`allensdk.internal.model.glif.threshold_adaptation.`**`exp_fit_c`**(*t*, *a1*, *k1*, *const*)

`allensdk.internal.model.glif.threshold_adaptation.`**`exp_force_c`**(*t_const*, *a1*, *k1*)

`allensdk.internal.model.glif.threshold_adaptation.`**`fit_avoltage_bvoltage`**(*x*, *v_trace_list*, *El_list*, *spike_cut_length*, *all_spikeInd_list*, *th_inf*, *dt*, *a_spike*, *b_spike*, *fake=False*)

This is a version of fit_avoltage_bvoltage_debug that does not require the th_trace, v_component_of_thresh_trace, and spike_component_of_thresh_trace needed for debugging. A test should be run to make sure the same output comes out from this and the debug function

This function returns the squared error for the difference between the 'known' voltage component of the threshold obtained from the biological neuron and the voltage component of the threshold of the model obtained with the input parameters (so that the minimum can be searched for via fmin). The overall threshold is the sum of threshold infinity the spike component of the threshold and the voltage component of the threshold. Therefore threshold infinity and the spike component of the threshold must be subtracted from the threshold of the neuron in order to isolate the voltage component of the threshold. In the evaluation of the model the actual voltage of the neuron is used so that any errors in the other components of the model will not influence the fits here (for example, if a afterspike current was estimated incorrectly)

Notes: * The spike component of the threshold is subtracted from the

voltage which means that the voltage component of the threshold should only be added to rules.

- **b_spike was fit using a negative value in the function therefore the negative is placed in the** equation.
- **values in this function are in 'real' voltage as opposed to voltage** relative to resting potential.
- **current injection during the spike is not taken into account. This seems reasonable as the** ion channels are open during this time and injected current may not greatly influence the neuron.

x: numpy array x[0]=a_voltage input, x[1] is b_voltage_input, x[2] is th_inf

v_trace_list: list of numpy arrays voltage traces (v_trace, El, and th_inf must be in the same frame of reference)

El_list: list of floats reversal potential (v_trace, El, and th_inf must be in the same frame of reference)

spike_cut_length: int number of indicies removed after initiation of a spike

all_spikeInd_list: list of numpy arrays indicies of spike trains

th_inf: float threshold infinity (v_trace, El, and th_inf must be in the same frame of reference)

dt: float size of time step (SI units)

a_spike: float amplitude of spike component of threshold.

b_spike: float decay constant in spike component of the threshold

fake: Boolean if True makes uses the voltage value of spike step-1 because there is not a voltage value at the spike step because it is set to nan in the simulator.

allensdk.internal.model.glif.threshold_adaptation.**fit_avoltage_bvoltage_th**(*x*, *v_trace_list*, *El_list*, *spike_cut_length*, *all_spikeInd_list*, *dt*, *a_spike*, *b_spike*, *fake=False*)

This is a version of fit_avoltage_bvoltage_th_debug that does not require the th_trace, v_component_of_thresh_trace, and spike_component_of_thresh_trace needed for debugging. A test should be run to make sure the same output comes out from this and the debug function

This function returns the squared error for the difference between the 'known' voltage component of the threshold obtained from the biological neuron and the voltage component of the threshold of the model obtained with the input parameters (so that the minimum can be searched for via fmin). The overall threshold is the sum of threshold infinity the spike component of the threshold and the voltage component of the threshold. Therefore threshold infinity and the spike component of the threshold must be subtracted from the threshold of the neuron in order to isolate the voltage component of the threshold. In the evaluation of the model the actual voltage of the neuron is used so that any errors in the other components of the model will not influence the fits here (for example, if a afterspike current was estimated incorrectly)

Notes: * The spike component of the threshold is subtracted from the

voltage which means that the voltage component of the threshold should only be added to rules.

- **b_spike was fit using a negative value in the function therefore the negative is placed in the** equation.
- **values in this function are in 'real' voltage as opposed to voltage** relative to resting potential.
- **current injection during the spike is not taken into account. This seems reasonable as the** ion channels are open during this time and injected current may not greatly influence the neuron.

x: numpy array x[0]=a_voltage input, x[1] is b_voltage_input, x[2] is th_inf

v_trace_list: list of numpy arrays voltage traces (v_trace, El, and th_inf must be in the same frame of reference)

El_list: list of floats reversal potential (v_trace, El, and th_inf must be in the same frame of reference)

spike_cut_length: int number of indicies removed after initiation of a spike

all_spikeInd_list: list of numpy arrays indicies of spike trains

dt: float size of time step (SI units)

a_spike: float amplitude of spike component of threshold.

b_spike: float decay constant in spike component of the threshold

fake: Boolean if True makes uses the voltage value of spike step-1 because there is not a voltage value at the spike step because it is set to nan in the simulator.

`allensdk.internal.model.glif.threshold_adaptation.`**`get_peaks`**(*voltage*, *aboveValue=0*)

This function was written by Corinne Teeter and calculates the action potential peaks of a voltage equation" inputs

voltage: numpy array of voltages aboveValue: scalar voltage value over which voltage is considered a spike.

outputs: peakInd: array of indicies of peaks

Module contents

Submodules

allensdk.internal.model.AIC module

`allensdk.internal.model.AIC.`**`AIC`**(*RSS*, *k*, *n*)

Computes the Akaike Information Criterion.

RSS-residual sum of squares of the fitting errors. k - number of fitted parameters. n - number of observations.

`allensdk.internal.model.AIC.`**`AICc`**(*RSS*, *k*, *n*)

Corrected AIC. formula from Wikipedia.

`allensdk.internal.model.AIC.`**`BIC`**(*RSS*, *k*, *n*)

Bayesian information criterion or Schwartz information criterion. Formula from wikipedia.

allensdk.internal.model.GLM module

`allensdk.internal.model.GLM.`**`create_basis_IPSP`**(*neye*, *ncos*, *kpeaks*, *ks*, *DTsim*, *t0*, *I_stim*, *nkt*, *flag_exp*, *npcut*)

`allensdk.internal.model.GLM.`**`ff`**(*x*, *c*, *dc*)

`allensdk.internal.model.GLM.`**`invnl`**(*x*)

`allensdk.internal.model.GLM.`**`makeBasis_StimKernel`**(*kbasprs*, *nkt*)

`allensdk.internal.model.GLM.`**`makeBasis_StimKernel_exp`**(*kbasprs*, *nkt*)

`allensdk.internal.model.GLM.`**`makeFitStruct_GLM`**(*dtsim*, *kbasprs*, *nkt*, *flag_exp*)

`allensdk.internal.model.GLM.`**`nlin`**(*x*)

`allensdk.internal.model.GLM.`**`normalizecols`**(*A*) allensdk.internal.model.GLM.**sameconv**(*A*, *B*)

allensdk.internal.model.data_access module

allensdk.internal.model.data_access.**load_sweep**(*file_name*, *sweep_number*, *desired_dt=None*, *cut=0*, *bessel=False*)

load a data sweep and do specified data processing. Inputs:

file_name: string name of .nwb data file

sweep_number: number specifying the sweep to be loaded

desired_dt: the size of the time step the data should be subsampled to

cut: indicie of which to start reporting data (i.e. cut off data before this indicie)

bessel: dictionary contains parameters 'N' and 'Wn' to implement standard python bessel filtering

Returns:

dictionary containing voltage: array current: array dt: time step of the returned data start_idx: the index at which the first stimulus starts (excluding the test pulse)

allensdk.internal.model.data_access.**load_sweeps**(*file_name*, *sweep_numbers*, *dt=None*, *cut=0*, *bessel=False*)

load sweeps and do specified data processing. Inputs:

file_name: string name of .nwb data file

sweep_numbers: sweep numbers to be loaded

desired_dt: the size of the time step the data should be subsampled to

cut: indicie of which to start reporting data (i.e. cut off data before this indicie)

bessel: dictionary contains parameters 'N' and 'Wn' to implement standard python bessel filtering

Returns:

dictionary containing voltage: list of voltage trace arrays current: list of current trace arrays dt: list of time step corresponding to each array of the returned data start_idx: list of the indicies at which the first stimulus starts (excluding

the test pulse) in each returned sweep

allensdk.internal.model.data_access.**subsample_data**(*data*, *method*, *present_time_step*, *desired_time_step*)

Module contents

allensdk.internal.morphology package

Submodules

allensdk.internal.morphology.compartment module

class allensdk.internal.morphology.compartment.**Compartment**(*node1*, *node2*)

Bases: `object`

allensdk.internal.morphology.morphology module

class allensdk.internal.morphology.morphology.**Morphology**(*node_list=None*)

Bases: `object`

Keep track of the list of nodes in a morphology and provide a few helper methods (soma, tree information, pruning, etc).

APICAL_DENDRITE = 4

AXON = 2

BASAL_DENDRITE = 3

NODE_TYPES = [1, 2, 3, 4]

SOMA = 1

append(*self*, *nodes*)

Add additional nodes to this Morphology. Those nodes must originate from another morphology object.

Parameters

nodes: list of Morphology nodes

apply_affine(*self*, *aff*, *scale=None*)

Apply an affine transform to all nodes in this morphology. Compartment radius is adjusted as well.

Format of the affine matrix is:

[x0 y0 z0] [tx] [x1 y1 z1] [ty] [x2 y2 z2] [tz]

where the left 3x3 the matrix defines the affine rotation and scaling, and the right column is the translation vector.

The matrix must be collapsed and stored in a list as follows:

[x0 y0, z0, x1, y1, z1, x2, y2, z2, tx, ty, tz]

Parameters

aff: 3x4 array of floats (python 2D list, or numpy 2D array) the transformation matrix

apply_affine_only_rotation(*self*, *aff*)

Apply an affine transform to all nodes in this morphology. Only the rotation element of the transform is performed (i.e., although the entire transformation and translation matrix is supplied, only the rotation element is used). The morphology is translated to the point where the soma root is at 0,0,0.

Format of the affine matrix is:

[x0 y0 z0] [tx] [x1 y1 z1] [ty] [x2 y2 z2] [tz]

where the left 3x3 the matrix defines the affine rotation and scaling, and the right column is the translation vector.

The matrix must be collapsed and stored in a list as follows:

[x0 y0, z0, x1, y1, z1, x2, y2, z2, tx, ty, tz]

Parameters

aff: 3x4 array of floats (python 2D list, or numpy 2D array) the transformation matrix

`change_parent` (*self*, *child*, *parent*)
Change the parent of a node. The child node is adjusted to point to the new parent, the child is taken off of the previous parent's child list, and it is added to the new parent's child list.

Parameters

child: integer or Morphology Object The ID of the child node, or the child node itself

parent: integer or Morphology Object The ID of the parent node, or the parent node itself

Returns

Nothing

`children_of` (*self*, *seg*)
Returns a list of the children of the specified node

Parameters

seg: integer or Morphology Object The ID of the parent node, or the parent node itself

Returns

A list of the child morphology objects. If the ID of the parent

node is invalid, None is returned.

`clone` (*self*)
Create a clone (deep copy) of this morphology

`compartment` (*self*, *n*)
Returns the morphology Compartment having the specified ID.

Parameters

n: integer ID of desired compartment

Returns

A morphology object having the specified ID, or None if such a

node doesn't exist

`compartment_list`

`convert_type` (*self*, *from_type*, *to_type*)
Convert all nodes in morphology from one type to another

Parameters

from_type: enum The node type that will be eliminated and replaced. Use one of the following constants: SOMA, AXON, BASAL_DENDRITE, or APICAL_DENDRITE

to_type: enum The new type that will replace it. Use one of the following constants: SOMA, AXON, BASAL_DENDRITE, or APICAL_DENDRITE

`delete_tree` (*self*, *n*)
Delete tree, and all of its nodes, from the morphology.

Parameters

n: Integer The tree number to delete

`find` (*self*, *x*, *y*, *z*, *dist*, *node_type=None*)
Returns a list of Morphology Objects located within 'dist' of coordinate (x,y,z). If node_type is specified, the search will be constrained to return only nodes of that type.

Parameters

x, y, z: float The x,y,z coordinates from which to search around

dist: float The search radius

node_type: enum (optional) One of the following constants: SOMA, AXON, BASAL_DENDRITE or APICAL_DENDRITE

Returns

A list of all Morphology Objects matching the search criteria

`get_dimensions`(*self*)
Returns tuple of overall width, height and depth of morphology. WARNING: if locations of nodes in morphology are manipulated then this value can become incorrect. It can be reset and recalculated by programmitcally setting self.dims to None.

Returns

3 real arrays: [width, height, depth], [min_x, min_y, min_z],

[max_x, max_y, max_z]

`node`(*self*, *n*)
Returns the morphology node having the specified ID.

Parameters

n: integer ID of desired node

Returns

A morphology node having the specified ID, or None if such a

node doesn't exist

`node_list`
Return the node list. This is a property to ensure that the node list and node index are in sync.

`node_list_by_type`(*self*, *node_type*)
Return an list of all nodes having the specified node type.

Parameters

node_type: int Desired node type

Returns

A list of of Morphology Objects

`num_nodes`
Return the number of nodes in the morphology.

`num_trees`
Return the number of trees in the morphology. A tree is defined as everything following from a single root node.

`parent_of`(*self*, *seg*)
Returns parent of the specified node.

Parameters

seg: integer or Morphology Object The ID of the child node, or the child node itself

Returns

A morphology object, or None if no parent exists or if the

specified node ID doesn't exist

`save` (*self*, *file_name*)
Write this morphology out to an SWC file

Parameters

file_name: string desired name of your SWC file

`soma_root` (*self*)
Returns root node of soma, if present

`sparsify` (*self*, *modulo*)
Return a new Morphology object that has a given number of non-leaf, non-root nodes removed.

Parameters

modulo: int keep 1 out of every modulo nodes.

Returns

Morphology A new morphology instance

`strip_all_other_types` (*self*, *node_type*, *keep_soma=True*)
Strips everything from the morphology except for the specified type. Parent and child relationships are updated accordingly, creating new roots when necessary.

Parameters

node_type: enum The node type to keep in the morphology. Use one of the following constants: SOMA, AXON, BASAL_DENDRITE, or APICAL_DENDRITE

keep_soma: Boolean (optional) True (default) if soma nodes should remain in the morpyhology, and False if the soma should also be stripped

`strip_type` (*self*, *node_type*)
Strips all nodes of the specified type from the morphology. Parent and child relationships are updated accordingly, creating new roots when necessary.

Parameters

node_type: enum The node type to strip from the morphology. Use one of the following constants: SOMA, AXON, BASAL_DENDRITE, or APICAL_DENDRITE

`stumpify_axon` (*self*, *count=10*)
Remove all axon nodes except the first 'count' nodes, as counted from the connected axon root.

Parameters

count: Integer The length of the axon 'stump', in number of nodes

`to_dict` (*self*)
Returns a dictionary of Node objects. These Nodes are a copy of the Morphology. Modifying them will not modify anything in the Morphology itself.

`tree` (*self*, *n*)
Returns a list of all Morphology nodes within the specified tree. A tree is defined as a fully connected graph of nodes. Each tree has exactly one root.

Parameters

n: integer ID of desired tree

Returns

A list of all morphology objects in the specified tree, or None

if the tree doesn't exist

write(*self*, *file_name*)

allensdk.internal.morphology.morphvis module

class allensdk.internal.morphology.morphvis.**MorphologyColors**

Bases: object

set_apical_color(*self*, *r*, *g*, *b*)

set_axon_color(*self*, *r*, *g*, *b*)

set_basal_color(*self*, *r*, *g*, *b*)

set_soma_color(*self*, *r*, *g*, *b*)

allensdk.internal.morphology.morphvis.**calculate_scale**(*morph*, *pix_width*, *pix_height*)

Calculates scaling factor and x,y insets required to auto-scale and center morphology into box with specified numbers of pixels

Parameters

morph: AISDK Morphology object

pix_width: int

Number of image pixels on X axis

pix_height: int

Number of image pixels on Y axis

Returns

real, real, real

First return value is the scaling factor. Second is the

number of pixels needed to adjust x-coordinates so that the

morphology is horizontally centered. Third is the number of

pixels needed to adjust the y-coordinates so that the morphology

is vertically centered.

allensdk.internal.morphology.morphvis.**create_image**(*w*, *h*, *color=None*, *alpha=False*)

allensdk.internal.morphology.morphvis.**draw_density_hist**(*img*, *morph*, *vert_scale*, *inset_left=0*, *inset_right=0*, *inset_top=0*, *inset_bottom=0*, *num_bins=None*, *colors=None*)

Draws density histogram onto image When no scaling is applied, and no insets are provided, the coordinates of the morphology are used directly – i.e., 100 in morphology coordinates is equal to 100 pixels.

The scale factor is multiplied to morphology coordinates before being drawn. If scale_factor=2 then 50 in morphology coordinates is 100 pixels. Left and top insets shift the coordinate axes for drawing. E.g., if left=10 and top=5 then 0,0 in morphology coordinates is 10,5 in pixel space. Bottom and right insets are ignored.

If scale_to_fit is set then scale factor is ignored. The morphology is scaled to be the maximum size that fits in the image, taking into account insets. In a 100x100 image, if all insets=10, then the image is scaled to fit into the center 80x80 pixel area, and nothing is drawn in the inset border areas.

Axons are drawn before soma and dendrite compartments.

Parameters

img: PIL image object

morph: AISDK Morphology object

vert_scale: real

This is the amout required to multiply to a moprhology

y-coordinate to convert it to relative cortical depth (on [0,1]).

This is the inverse of the cortical thickness.

inset_*: real

This is the number of pixels to use as border on top/bottom/

right/left. If scale_to_fit is false then only the top/left

values are used, as the scale_factor will determine how

large the morphology is (it can be drawn beyond insets and even

beyond image boundaries)

num_bins: int

The number of bins in the histogram

colors: MorphologyColors object

This is the color scheme used to draw the morphology. If

colors=None then default coloring is used

Returns

Histogram arrays: [hist, hist2, hist3, hist4]

where hist is the histgram of all neurites, and hist[234] are

the histograms of SWC types 2,3,4

`allensdk.internal.morphology.morphvis.`**`draw_morphology`**(*img*, *morph*, *inset_left=0*, *inset_right=0*, *inset_top=0*, *inset_bottom=0*, *scale_to_fit=False*, *scale_factor=1.0*, *colors=None*)

Draws morphology onto image When no scaling is applied, and no insets are provided, the coordinates of the morphology are used directly – i.e., 100 in morphology coordinates is equal to 100 pixels.

The scale factor is multiplied to morphology coordinates before being drawn. If scale_factor=2 then 50 in morphology coordinates is 100 pixels. Left and top insets shift the coordinate axes for drawing. E.g., if left=10 and top=5 then 0,0 in morphology coordinates is 10,5 in pixel space. Bottom and right insets are ignored.

If scale_to_fit is set then scale factor is ignored. The morphology is scaled to be the maximum size that fits in the image, taking into account insets. In a 100x100 image, if all insets=10, then the image is scaled to fit into the center 80x80 pixel area, and nothing is drawn in the inset border areas.

Axons are drawn before soma and dendrite compartments.

Parameters

img: PIL image object

morph: AISDK Morphology object

inset_*: real

This is the number of pixels to use as border on top/bottom/

right/left. If scale_to_fit is false then only the top/left

values are used, as the scale_factor will determine how

large the morphology is (it can be drawn beyond insets and even

beyond image boundaries)

scale_to_fit: boolean

If true then morphology is scaled to the inset area of the

image and scale_factor is ignored. Morphology is centered

in the image in the sense that the top/bottom and left/right

edges of the morphology are equidistant from image borders.

scale_factor: real

A scalar amount that is multiplied to morphology coordinates

before drawing

colors: MorphologyColors object

This is the color scheme used to draw the morphology. If

colors=None then default coloring is used

Returns

2-dimensional array, the pixel coordinates of the soma root [x,y]

allensdk.internal.morphology.node module

class `allensdk.internal.morphology.node.`**`Node`**(*n*, *t*, *x*, *y*, *z*, *r*, *pn*, ***kwargs*)

Bases: `object`

Represents node in SWC morphology file

classmethod from_dict(*d*)

short_string(*self*)

create string with node information in succinct, single-line form

to_dict(*self*)

Convert the node into a serializable dictionary

`allensdk.internal.morphology.node.`**`euclidean_distance`**(*node1*, *node2*)

`allensdk.internal.morphology.node.`**`midpoint`**(*node1*, *node2*)

allensdk.internal.morphology.validate_swc module

class allensdk.internal.morphology.validate_swc.**TestNode**(*n, t, x, y, z, r, pn*)
Bases: object

allensdk.internal.morphology.validate_swc.**main**()

allensdk.internal.morphology.validate_swc.**resave_swc**(*orig_swc, new_file*)
Reads SWC file into AllenSDK Morphology object and resaves it. This can fix some problems in an SWC file that may disrupt other software tools reading the file (e.g., NEURON)

Parameters

orig_swc: string Name of SWC file to read

new_file: string Name of output SWC file

allensdk.internal.morphology.validate_swc.**validate_swc**(*swc_file*)
Tests SWC files for compatibility with AllenSDK

To be compatible with NEURON, SWC files must have the following properties:

1) a single root node with parent ID '-1'
2) sequentially increasing ID numbers
3) immediate children of the soma cannot branch

To be compatible with feature analysis, SWC files can only have node types in the range 1-4:

1 = soma 2 = axon 3 = [basal] dendrite 4 = apical dendrite

Module contents

allensdk.internal.mouse_connectivity package

Subpackages

allensdk.internal.mouse_connectivity.interval_unionize package

Submodules

allensdk.internal.mouse_connectivity.interval_unionize.cav_unionize module

allensdk.internal.mouse_connectivity.interval_unionize.cav_unionizer module

allensdk.internal.mouse_connectivity.interval_unionize.data_utilities module

allensdk.internal.mouse_connectivity.interval_unionize.data_utilities.**get_cav_density**(*cav_de*

allensdk.internal.mouse_connectivity.interval_unionize.data_utilities.**get_injection_data**(*in*
in
je
tio
in
je
tio

Read nrrd files containing injection signal data

allensdk.internal.mouse_connectivity.interval_unionize.data_utilities.**get_projection_data**(*p*
p
j
t
d

Read nrrd files containing global signal data

allensdk.internal.mouse_connectivity.interval_unionize.data_utilities.**get_sum_pixel_intens**

allensdk.internal.mouse_connectivity.interval_unionize.data_utilities.**get_sum_pixels**(*sum_pix*

allensdk.internal.mouse_connectivity.interval_unionize.data_utilities.**load_annotation**(*annota*
data_n

Read data files segmenting the reference space into regions of valid and invalid data, then further among brain structures

allensdk.internal.mouse_connectivity.interval_unionize.data_utilities.**read**(*path*)

allensdk.internal.mouse_connectivity.interval_unionize.interval_unionizer module

class allensdk.internal.mouse_connectivity.interval_unionize.interval_unionizer.**IntervalUn**

Bases: object

direct_unionize(*self*, *data_arrays*, *pre_sorted=False*, ***kwargs*)

Obtain unionize records from directly annotated regions.

Parameters

data_arrays [dict] Keys identify types of data volume. Values are flattened arrays.

sorted [bool, optional] If False, data arrays will be sorted.

extract_data(*self*, *data_arrays*, *low*, *high*, ***kwargs*)

Given flattened data arrays and a specified interval, generate summary data

Parameters

data_arrays [dict] Keys identify types of data volume. Values are flattened, sorted arrays.

low [int] Index at which interval of interest begins. Inclusive.

high [int] Index at which interval of interest ends. Exclusive.

postprocess_unionizes(*self*, *raw_unionizes*, ***kwargs*)

Carry out additional calculations/formatting derivative of core unionization.

Parameters

raw_unionizes [list of unionizes] Each entry is a unionize record.

classmethod propagate_record(*child_record*, *ancestor_record*, *copy_all=False*)

Updates one unionize corresponding to a rootward structure with information from a unionize corresponding to a leafward structure

Parameters

child_record [unionize] Data will be drawn from this record

ancestor_record [unionize] This record will be updated

classmethod propagate_to_bilateral(*lateral_unionizes*)

classmethod propagate_unionizes(*direct_unionizes*, *ancestor_id_map*)
Structures are arranged in a tree, whose leafward-oriented edges indicate physical containment. This method updates rootward unionize records with information from leafward ones.

Parameters

direct_unionizes [list of unionizes] Each entry is a unionize record produced from a collection of directly labeled voxels in the segmentation volume.

ancestor_id_map [dict] Keys are structure ids. Values are ids of all structures rootward in

the tree, including the key node

Returns

output_unionizes [list of unionizes] Contains completed unionize records at all depths in the structure tree

classmethod record_cb()

setup_interval_map(*self*, *annotation*)
Build a map from structure ids to intervals in the sorted flattened reference space.

Parameters

annotation [np.ndarray] Segmentation label array.

sort_data_arrays(*self*, *data_arrays*)
Apply the precomputed sort to flattened data arrays

Parameters

data_arrays [dict] Keys identify types of data volume. Values are flattened, unsorted arrays.

Returns

dict : As input, but values are sorted

allensdk.internal.mouse_connectivity.interval_unionize.run_tissuecyte_unionize_cav module

allensdk.internal.mouse_connectivity.interval_unionize.run_tissuecyte_unionize_classic module

allensdk.internal.mouse_connectivity.interval_unionize.run_tissuecyte_unionize_classic.**get_**

allensdk.internal.mouse_connectivity.interval_unionize.run_tissuecyte_unionize_classic.**get_**

allensdk.internal.mouse_connectivity.interval_unionize.run_tissuecyte_unionize_classic.**run**

allensdk.internal.mouse_connectivity.interval_unionize.tissuecyte_unionize_record module

class allensdk.internal.mouse_connectivity.interval_unionize.tissuecyte_unionize_record.**Ti**
Bases: *allensdk.internal.mouse_connectivity.interval_unionize.unionize_record.Unionize*

direct_sum_projection_pixels

max_voxel_density

max_voxel_index

output (*self*, *output_spacing_iso*, *volume_scale*, *target_shape*, *sort*)
Generate derived data for this unionize

Parameters

output_spacing_iso [numeric] Isometric spacing of reference space in microns

volume_scale [numeric] Scale factor mapping pixels to microns^3

target_shape [array-like of numeric] Shape of reference space

projection_density

projection_energy

projection_intensity

propagate (*self*, *ancestor*, *copy_all=False*)
Update a rootward unionize with data from this unionize record

Parameters

ancestor [TissuecyteBaseUnionize] will be updated

Returns

ancestor [TissuecyteBaseUnionize]

set_max_voxel (*self*, *density_array*, *low*)
Find the voxel of greatest density in this unionizes spatial domain

Parameters

density_array [ndarray] Float values are densities per voxel

low [int] index in full flattened, sorted array of starting voxel

sum_pixel_intensity

sum_pixels

sum_projection_pixel_intensity

sum_projection_pixels

class allensdk.internal.mouse_connectivity.interval_unionize.tissuecyte_unionize_record.**Tis**
Bases: *allensdk.internal.mouse_connectivity.interval_unionize.tissuecyte_unionize_record.TissuecyteBaseUnionize*

calculate (*self*, *low*, *high*, *data_arrays*)

class allensdk.internal.mouse_connectivity.interval_unionize.tissuecyte_unionize_record.**Tis**
Bases: *allensdk.internal.mouse_connectivity.interval_unionize.tissuecyte_unionize_record.TissuecyteBaseUnionize*

calculate (*self*, *low*, *high*, *data_arrays*, *ij_record*)

allensdk.internal.mouse_connectivity.interval_unionize.tissuecyte_unionizer module

class allensdk.internal.mouse_connectivity.interval_unionize.tissuecyte_unionizer.**Tissuecyt**
Bases: *allensdk.internal.mouse_connectivity.interval_unionize.interval_unionizer.IntervalUnionizer*

A specialization of the IntervalUnionizer set up for unionizing Tissuecyte-derived projection data.

extract_data(*self*, *data_arrays*, *low*, *high*)
As parent

postprocess_unionizes(*self*, *raw_unionizes*, *image_series_id*, *output_spacing_iso*, *volume_scale*, *target_shape*, *sort*)
As parent

classmethod propagate_record(*child_record*, *ancestor_record*, *copy_all=False*)
As parent

classmethod record_cb()

allensdk.internal.mouse_connectivity.interval_unionize.unionize_record module

class allensdk.internal.mouse_connectivity.interval_unionize.unionize_record.**Unionize**(**args*, ***kwa*

Bases: `object`

Abstract base class for unionize records.

calculate(*self*, **args*, ***kwargs*)

output(*self*, **args*, ***kwargs*)

propagate(*self*, *ancestor*, *copy_all*, **args*, ***kwargs*)

slice_arrays(*self*, *low*, *high*, *data_arrays*)
Extract a slice from several aligned arrays

Parameters

low [int] start of slice, inclusive

high [int] end of slice, exclusive

data_arrays [dict] keys are varieties of data. values are sorted, flattened data arrays

Module contents

allensdk.internal.mouse_connectivity.projection_thumbnail package

Submodules

allensdk.internal.mouse_connectivity.projection_thumbnail.generate_projection_strip module

allensdk.internal.mouse_connectivity.projection_thumbnail.generate_projection_strip.**apply_c**

allensdk.internal.mouse_connectivity.projection_thumbnail.generate_projection_strip.**blend_w**

allensdk.internal.mouse_connectivity.projection_thumbnail.generate_projection_strip.**do_blu** allensdk.internal.mouse_connectivity.projection_thumbnail.generate_projection_strip.**handle_**

allensdk.internal.mouse_connectivity.projection_thumbnail.generate_projection_strip.**max_cb**

allensdk.internal.mouse_connectivity.projection_thumbnail.generate_projection_strip.**run**(*volu imin ima ro- ta- tion col- orm*

allensdk.internal.mouse_connectivity.projection_thumbnail.generate_projection_strip.**simple_**

allensdk.internal.mouse_connectivity.projection_thumbnail.image_sheet module

class allensdk.internal.mouse_connectivity.projection_thumbnail.image_sheet.**ImageSheet**

Bases: object

append(*self*, *new_cell*)

apply(*self*, *fn*, **args*, ***kwargs*)

static build_from_image(*image*, *n*, *axis*)

copy(*self*)

get_output(*self*, *axis*)

allensdk.internal.mouse_connectivity.projection_thumbnail.projection_functions module

allensdk.internal.mouse_connectivity.projection_thumbnail.projection_functions.**convert_axis**

allensdk.internal.mouse_connectivity.projection_thumbnail.projection_functions.**max_project** `allensdk.internal.mouse_connectivity.projection_thumbnail.projection_functions.`**`template_pro`**

allensdk.internal.mouse_connectivity.projection_thumbnail.visualization_utilities module

`allensdk.internal.mouse_connectivity.projection_thumbnail.visualization_utilities.`**`blend`**`(`*ima*
wei

Parameters

image_stack :: list of np.ndarray The images to be blended. Shapes cannot differ

weight_stack :: list of np.ndarray The weight of each image at each pixel. Will be normalized.

`allensdk.internal.mouse_connectivity.projection_thumbnail.visualization_utilities.`**`convert_c`**

Generates a matplotlib continuous colormap on [0, 1] from a discrete colormap at N evenly spaced points.

Parameters

data [list of list] Sublists are [r, g, b].

Returns

matplotlib.colors.LinearSegmentedColormap Gamma is 1. Output space is 3 X [0, 1]

`allensdk.internal.mouse_connectivity.projection_thumbnail.visualization_utilities.`**`minmax_no`**

`allensdk.internal.mouse_connectivity.projection_thumbnail.visualization_utilities.`**`normalize`**

`allensdk.internal.mouse_connectivity.projection_thumbnail.visualization_utilities.`**`sitk_safe`**

allensdk.internal.mouse_connectivity.projection_thumbnail.volume_projector module

`class` `allensdk.internal.mouse_connectivity.projection_thumbnail.volume_projector.`**`VolumePro`**

Bases: `object`

`build_rotation_transform``(`*self*, *from_axis*, *to_axis*, *angle*`)`

`extract``(`*self*, *cb*, *volume=None*`)`

`classmethod fixed_factory``(`*volume*, *size*`)`

`rotate``(`*self*, *from_axis*, *to_axis*, *angle*`)`

`rotate_and_extract``(`*self*, *from_axes*, *to_axes*, *angles*, *cb*`)`

`classmethod safe_factory``(`*volume*`)`

allensdk.internal.mouse_connectivity.projection_thumbnail.volume_utilities module

allensdk.internal.mouse_connectivity.projection_thumbnail.volume_utilities.**sitk_get_center**

allensdk.internal.mouse_connectivity.projection_thumbnail.volume_utilities.**sitk_get_diagona**

allensdk.internal.mouse_connectivity.projection_thumbnail.volume_utilities.**sitk_get_image_p**

allensdk.internal.mouse_connectivity.projection_thumbnail.volume_utilities.**sitk_get_size_pa**

allensdk.internal.mouse_connectivity.projection_thumbnail.volume_utilities.**sitk_paste_into_**

Module contents

allensdk.internal.mouse_connectivity.tissuecyte_stitching package

Submodules

allensdk.internal.mouse_connectivity.tissuecyte_stitching.stitcher module

class allensdk.internal.mouse_connectivity.tissuecyte_stitching.stitcher.**Stitcher**(*image_dimen*, *tiles*, *av-er-age_tiles*, *chan-nels*)

Bases: object

run(*self*, *cb=<built-in function array>*)

stitch(*self*, *slice_image*, *stitched_indicator*, *tile*, *cb=<built-in function array>*)

allensdk.internal.mouse_connectivity.tissuecyte_stitching.stitcher.**blend_component_from_poi**

Obtains a normalized component of the blend, which describes depth of overlap along a specified axis in a specified direction

allensdk.internal.mouse_connectivity.tissuecyte_stitching.stitcher.**get_blend**(*indicator_region*, *stup*, *cb=<built-in function array>*)

allensdk.internal.mouse_connectivity.tissuecyte_stitching.stitcher.**get_blend_component**(*indic*, *lg*, *axis*, *mesh*

allensdk.internal.mouse_connectivity.tissuecyte_stitching.stitcher.**get_indicator_bound_poin**

Finds the index of first change in a binary mask along a specified axis in a specified direction `allensdk.internal.mouse_connectivity.tissuecyte_stitching.stitcher.`**`get_overall_blend`**`(`*indicato meshes*`)`

`allensdk.internal.mouse_connectivity.tissuecyte_stitching.stitcher.`**`initialize_image`**`(`*dimension nchannels, dtype, order='C'*`)`

`allensdk.internal.mouse_connectivity.tissuecyte_stitching.stitcher.`**`initialize_images`**`(`*dimensi nchannels*`)`

`allensdk.internal.mouse_connectivity.tissuecyte_stitching.stitcher.`**`make_blended_tile`**`(`*blend, tile, current_reg*

allensdk.internal.mouse_connectivity.tissuecyte_stitching.tile module

`class` `allensdk.internal.mouse_connectivity.tissuecyte_stitching.tile.`**`Tile`**`(`*index, image, is_missing, bounds, channel, size, margins, *args, **kwargs*`)`

Bases: `object`

`apply_average_tile``(`*self, average_tile*`)`

`apply_average_tile_to_self``(`*self, average_tile*`)`

`average_tile_is_untrimmed``(`*self, average_tile*`)`

`get_image_region``(`*self*`)`

`get_missing_path``(`*self*`)`

`initialize_image``(`*self*`)`

`trim``(`*self, image*`)`

`trim_self``(`*self*`)`

Module contents

Module contents

allensdk.internal.pipeline_modules package

Subpackages

allensdk.internal.pipeline_modules.gbm package

Submodules

allensdk.internal.pipeline_modules.gbm.generate_gbm_analysis_run_records module

allensdk.internal.pipeline_modules.gbm.generate_gbm_heatmap module

`allensdk.internal.pipeline_modules.gbm.generate_gbm_heatmap.`**`create_gene_fpkm_table`**`(`*analysis_ru*

Creates a a matrix ("rows x columns = genes x samples") of fpkm gene expression values for each particular (gene, sample) pair. Rows are sorted by entrez_id and columns are by rna_well_id

`allensdk.internal.pipeline_modules.gbm.generate_gbm_heatmap.`**`create_genes_for_transcripts`**`(`*an*

Creates a list that contains the associated gene for each transcript sorted alphabetically

`allensdk.internal.pipeline_modules.gbm.generate_gbm_heatmap.`**`create_sample_metadata`**`(`*sample_me*

Creates a table of sample metadata sorted by rna_well_id

`allensdk.internal.pipeline_modules.gbm.generate_gbm_heatmap.`**`create_transcript_fpkm_table`**`(`*an*

Creates a a matrix ("rows x columns = transcripts x samples") of fpkm gene expression values for each particular (transcript, sample) pair. Rows are sorted by transcript id and columns are by rna_well_id

`allensdk.internal.pipeline_modules.gbm.generate_gbm_heatmap.`**`create_transcripts_for_genes`**`(`*an*

Creates a list that contains the associated transcript for each gene sorted by entrez_id

`allensdk.internal.pipeline_modules.gbm.generate_gbm_heatmap.`**`main`**`()`

allensdk.internal.pipeline_modules.gbm.generate_gbm_sample_metadata module

Module contents

Submodules

allensdk.internal.pipeline_modules.run_annotated_region_metrics module

Run annotated region metrics calculations

`allensdk.internal.pipeline_modules.run_annotated_region_metrics.`**`debug`**`(`*region_id, storage_directory='./', local=True, sdk_path='/data/informatics/C script_path='/data/informatic lims_host='lims2'*`)`

`allensdk.internal.pipeline_modules.run_annotated_region_metrics.`**`load_arrays`**`(`*h5_file*`)`

`allensdk.internal.pipeline_modules.run_annotated_region_metrics.`**`main`**`()`

allensdk.internal.pipeline_modules.run_demixing module

allensdk.internal.pipeline_modules.run_demixing.**assert_exists**(*file_name*)

allensdk.internal.pipeline_modules.run_demixing.**debug**(*experiment_id*, *local=False*)

allensdk.internal.pipeline_modules.run_demixing.**get_path**(*obj*, *key*, *check_exists*)

allensdk.internal.pipeline_modules.run_demixing.**main**()

allensdk.internal.pipeline_modules.run_demixing.**parse_input**(*data*, *exclude_labels*)

allensdk.internal.pipeline_modules.run_dff_computation module

allensdk.internal.pipeline_modules.run_dff_computation.**main**()

allensdk.internal.pipeline_modules.run_dff_computation.**parse_input**(*data*)

allensdk.internal.pipeline_modules.run_eye_tracking module

allensdk.internal.pipeline_modules.run_neuropil_correction module

allensdk.internal.pipeline_modules.run_neuropil_correction.**adjust_r_for_negativity**(*r*, *F_C*, *F_M*, *F_N*)

allensdk.internal.pipeline_modules.run_neuropil_correction.**debug**(*experiment_id*, *local=False*)

allensdk.internal.pipeline_modules.run_neuropil_correction.**debug_plot**(*file_name*, *roi_trace*, *neuropil_trace*, *corrected_trace*, *r*, *r_vals=None*, *err_vals=None*)

allensdk.internal.pipeline_modules.run_neuropil_correction.**main**()

allensdk.internal.pipeline_modules.run_observatory_analysis module

allensdk.internal.pipeline_modules.run_observatory_analysis.**debug**(*experiment_ids*, *local=False*, *OUTPUT_DIR='/data/informatics/CAM/*
SDK_PATH='/data/informatics/CAM
walltime='10:00:00', *python='/shared/utils.x86_64/pytho*
2.7/bin/python', *queue='braintv'*)

allensdk.internal.pipeline_modules.run_observatory_analysis.**get_experiment_nwb_file**(*experimen*

allensdk.internal.pipeline_modules.run_observatory_analysis.**get_experiment_session**(*experiment*

allensdk.internal.pipeline_modules.run_observatory_analysis.**main**()

allensdk.internal.pipeline_modules.run_observatory_container_thumbnails module

allensdk.internal.pipeline_modules.run_observatory_thumbnails module

allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_cell_plots**(*cell_specimen_id* *prefix*, *aspect*, *configs*, *output_dir*, *axes=None*, *transparent=False*)

allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_correlation_plots**(*data_s* *analysis_file* *configs*, *output_di*

allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_drifting_gratings**(*dga*, *configs*, *output_di*

allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_experiment_thumbnails**(*n* *a* *y* *s* *c* *p* *t* *t*

allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_eye_tracking_plots**(*data_* *configs*, *output_c* allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_locally_sparse_noise**(*ls co fig ou pu on*

allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_natural_movie**(*nma, configs, output_dir, name*)

allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_natural_scenes**(*nsa, configs, output_dir*)

allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_plots**(*prefix, aspect, configs, output_dir, axes=None, transparent=False*)

allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_receptive_field**(*lsna, configs, output_dir*)

allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_speed_tuning**(*analysis, configs, output_dir*)

allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_static_gratings**(*sga, configs, output_dir*)

allensdk.internal.pipeline_modules.run_observatory_thumbnails.**build_type**(*nwb_file, data_file, configs, output_dir, type_name*) `allensdk.internal.pipeline_modules.run_observatory_thumbnails.`**`debug`**`(`*experiment_id, plots=None, local=False*`)`

`allensdk.internal.pipeline_modules.run_observatory_thumbnails.`**`get_experiment_analysis_file`**

`allensdk.internal.pipeline_modules.run_observatory_thumbnails.`**`get_experiment_files`**`(`*experiment*

`allensdk.internal.pipeline_modules.run_observatory_thumbnails.`**`get_experiment_nwb_file`**`(`*experi*

`allensdk.internal.pipeline_modules.run_observatory_thumbnails.`**`get_input_data`**`(`*experiment_id*`)`

`allensdk.internal.pipeline_modules.run_observatory_thumbnails.`**`lsna_check_hvas`**`(`*data_set, data_file*`)`

`allensdk.internal.pipeline_modules.run_observatory_thumbnails.`**`main`**`()`

`allensdk.internal.pipeline_modules.run_observatory_thumbnails.`**`parse_input`**`(`*data*`)`

allensdk.internal.pipeline_modules.run_ophys_eye_calibration module

`allensdk.internal.pipeline_modules.run_ophys_eye_calibration.`**`debug`**`(`*experiment_id, local=False*`)`

`allensdk.internal.pipeline_modules.run_ophys_eye_calibration.`**`get_wkf`**`(`*wkf_type, experiment_id*`)`

`allensdk.internal.pipeline_modules.run_ophys_eye_calibration.`**`main`**`()`

`allensdk.internal.pipeline_modules.run_ophys_eye_calibration.`**`parse_input_data`**`(`*data*`)`

`allensdk.internal.pipeline_modules.run_ophys_eye_calibration.`**`write_output`**`(`*filename, position_degrees, position_cm, areas*`)`

allensdk.internal.pipeline_modules.run_ophys_session_decomposition module

`allensdk.internal.pipeline_modules.run_ophys_session_decomposition.`**`convert_frame`**`(`*conversion_de*

`allensdk.internal.pipeline_modules.run_ophys_session_decomposition.`**`create_fake_metadata`**`(`*exp raw cha nels wid heig item size n_p* `allensdk.internal.pipeline_modules.run_ophys_session_decomposition.`**`debug`**`(`*experiment_id, local=False, raw_path=None*`)`

`allensdk.internal.pipeline_modules.run_ophys_session_decomposition.`**`main`**`()`

`allensdk.internal.pipeline_modules.run_ophys_session_decomposition.`**`parse_input`**`(`*data*`)`
Load all input data from the input json.

allensdk.internal.pipeline_modules.run_ophys_time_sync module

`allensdk.internal.pipeline_modules.run_ophys_time_sync.`**`main`**`()`

`allensdk.internal.pipeline_modules.run_ophys_time_sync.`**`write_output`**`(`*output_file, ophys_times, stim_alignment, eye_alignment, behavior_alignment, ophys_delta, stim_delta, eye_delta, behavior_delta*`)`

allensdk.internal.pipeline_modules.run_roi_filter module

`allensdk.internal.pipeline_modules.run_roi_filter.`**`create_input_data`**`(`*experiment_id*`)`

`allensdk.internal.pipeline_modules.run_roi_filter.`**`create_output_data`**`(`*rois, model_id, border, excluded, unexpected_features*`)`

`allensdk.internal.pipeline_modules.run_roi_filter.`**`debug`**`(`*experiment_id, local=False, sdk_path='/data/informatics/CAM/roi_filter/allensd script='/data/informatics/CAM/roi_filter/allensdk/a output_directory='/data/informatics/CAM/roi_filter/'*`)`

`allensdk.internal.pipeline_modules.run_roi_filter.`**`get_genotype_info`**`(`*experiment_id, code*`)`

`allensdk.internal.pipeline_modules.run_roi_filter.`**`get_model_info`**`(`*experiment_id*`)`

`allensdk.internal.pipeline_modules.run_roi_filter.`**`get_motion_filepath`**`(`*experiment_id*`)`

`allensdk.internal.pipeline_modules.run_roi_filter.`**`get_segmentation_filepath`**`(`*experiment_id, file_type*`)`

`allensdk.internal.pipeline_modules.run_roi_filter.`**`is_deprecated_motion_file`**`(`*filename*`)`
Check if a file is an old style motion correction file.

By agreement, new-style files will always have a header and that header will always contain at least 1 alpha character.

`allensdk.internal.pipeline_modules.run_roi_filter.`**`load_all_input`**(*data*)
Load all input data from the input json.

`allensdk.internal.pipeline_modules.run_roi_filter.`**`load_object_list`**(*filename*)
Load the object list file.

`allensdk.internal.pipeline_modules.run_roi_filter.`**`load_rigid_motion_transform`**(*filename*)
Load the rigid motion transform file.

`allensdk.internal.pipeline_modules.run_roi_filter.`**`main`**()

allensdk.internal.pipeline_modules.run_tissuecyte_projection_thumbnail_from_json module

allensdk.internal.pipeline_modules.run_tissuecyte_stitching_classic module

allensdk.internal.pipeline_modules.run_tissuecyte_unionize_cav_from_json module

allensdk.internal.pipeline_modules.run_tissuecyte_unionize_classic_counts_from_json module

allensdk.internal.pipeline_modules.run_tissuecyte_unionize_classic_from_json module

`allensdk.internal.pipeline_modules.run_tissuecyte_unionize_classic_from_json.`**`main`**()

Module contents

Module contents

6.1.7 allensdk.model package

Subpackages

allensdk.model.biophys_sim package

Subpackages

allensdk.model.biophys_sim.neuron package

Submodules

allensdk.model.biophys_sim.neuron.hoc_utils module

class `allensdk.model.biophys_sim.neuron.hoc_utils.`**`HocUtils`**(*description*)
Bases: `object`

A helper class for containing references to NEUORN.

Attributes

h [object] The NEURON hoc object.

nrn [object] The NEURON python object.

neuron [module] The NEURON module.

h = None

initialize_hoc(*self*)
Basic setup for NEURON.

neuron = None

nrn = None

Module contents

allensdk.model.biophys_sim.scripts package

Module contents

Submodules

allensdk.model.biophys_sim.bps_command module

allensdk.model.biophys_sim.bps_command.**choose_bps_command**(*command='bps_simple'*, *conf_file=None*)

allensdk.model.biophys_sim.bps_command.**run_module**(*description*, *module_name*, *function_name*)

allensdk.model.biophys_sim.config module

class allensdk.model.biophys_sim.config.**Config**
Bases: *allensdk.config.app.application_config.ApplicationConfig*

load(*self*, *config_path*, *disable_existing_logs=False*)
Parse the application configuration then immediately load the model configuration files.

Parameters

disable_existing_logs [boolean, optional] If false (default) leave existing logs after configuration.

read_model_description(*self*)
parse the model_file field of the application configuration and read the files.

The model_file field of the application configuration is first split at commas, since it may list more than one file.

The files may be uris of the form `file:filename?section=name`, in which case a bare configuration object is read from filename into the configuration section with key 'name'.

A simple filename without a section option is treated as a standard multi-section configuration file.

Returns

description [Description] Configuration object.

Module contents

allensdk.model.biophysical package

Submodules

allensdk.model.biophysical.run_simulate module

class allensdk.model.biophysical.run_simulate.**RunSimulate**(*input_json*, *output_json*)

Bases: object

load_manifest(*self*)

nrnivmodl(*self*)

simulate(*self*)

allensdk.model.biophysical.run_simulate.**main**(*command*, *lims_strategy_json*, *lims_response_json*)

Entry point for module. :param command: select behavior, nrnivmodl or simulate :type command: string :param lims_strategy_json: path to json file output from lims. :type lims_strategy_json: string :param lims_response_json: path to json file returned to lims. :type lims_response_json: string

allensdk.model.biophysical.runner module

allensdk.model.biophysical.runner.**load_description**(*manifest_json_path*)

Read configuration file.

Parameters

manifest_json_path [string] File containing the experiment configuration.

Returns

Config Object with all information needed to run the experiment.

allensdk.model.biophysical.runner.**prepare_nwb_output**(*nwb_stimulus_path*, *nwb_result_path*)

Copy the stimulus file, zero out the recorded voltages and spike times.

Parameters

nwb_stimulus_path [string] NWB file name

nwb_result_path [string] NWB file name

allensdk.model.biophysical.runner.**run**(*description*, *sweeps=None*, *procs=6*)

Main function for simulating sweeps in a biophysical experiment.

Parameters

description [Config] All information needed to run the experiment.

procs [int] number of sweeps to simulate simultaneously.

sweeps [list] list of experiment sweep numbers to simulate. If None, simulate all sweeps.

allensdk.model.biophysical.runner.**run_sync**(*description*, *sweeps=None*)

Single-process main function for simulating sweeps in a biophysical experiment.

Parameters

description [Config] All information needed to run the experiment.

sweeps [list] list of experiment sweep numbers to simulate. If None, simulate all sweeps.

`allensdk.model.biophysical.runner.`**`save_nwb`**(*output_path*, *v*, *sweep*, *sweeps_by_type*)

Save a single voltage output result into an existing sweep in a NWB file. This is intended to overwrite a recorded trace with a simulated voltage.

Parameters

output_path [string] file name of a pre-existing NWB file.

v [numpy array] voltage

sweep [integer] which entry to overwrite in the file.

allensdk.model.biophysical.utils module

`class` `allensdk.model.biophysical.utils.`**`AllActiveUtils`**(*description*)

Bases: *`allensdk.model.biophysical.utils.Utils`*

`generate_morphology`(*self*, *morph_filename*)

Load a neurolucida or swc-format cell morphology file.

Parameters

morph_filename [string] Path to morphology.

`load_cell_parameters`(*self*)

Configure a neuron after the cell morphology has been loaded.

`class` `allensdk.model.biophysical.utils.`**`Utils`**(*description*)

Bases: *`allensdk.model.biophys_sim.neuron.hoc_utils.HocUtils`*

A helper class for NEURON functionality needed for biophysical simulations.

Attributes

h [object] The NEURON hoc object.

nrn [object] The NEURON python object.

neuron [module] The NEURON module.

`generate_morphology`(*self*, *morph_filename*)

Load a swc-format cell morphology file.

Parameters

morph_filename [string] Path to swc.

`get_recorded_data`(*self*, *vec*)

Extract recorded voltages and timestamps given the recorded Vector instance. If self.stimulus_sampling_rate is smaller than self.simulation_sampling_rate, resample to self.stimulus_sampling_rate.

Parameters

vec [neuron.Vector] constructed by self.record_values

Returns

dict with two keys: ‘v’ = numpy.ndarray with voltages, ‘t’ = numpy.ndarray with timestamps

load_cell_parameters(*self*)
Configure a neuron after the cell morphology has been loaded.

static nearest_neuron_sampling_rate(*hz*, *target_hz=40000*)

read_stimulus(*self*, *stimulus_path*, *sweep=0*)
Load current values for a specific experiment sweep and setup simulation and stimulus sampling rates.

NOTE: NEURON only allows simulation timestamps of multiples of 40KHz. To avoid aliasing, we set the simulation sampling rate to the least common multiple of the stimulus sampling rate and 40KHz.

Parameters

stimulus path [string] NWB file name

sweep [integer, optional] sweep index

record_values(*self*)
Set up output voltage recording.

setup_iclamp(*self*, *stimulus_path*, *sweep=0*)
Assign a current waveform as input stimulus.

Parameters

stimulus_path [string] NWB file name

update_default_cell_hoc(*self*, *description*, *default_cell_hoc='cell.hoc'*)
replace the default 'cell.hoc' path in the manifest with 'cell.hoc' packaged within AllenSDK if it does not exist

allensdk.model.biophysical.utils.**create_utils**(*description*, *model_type=None*)
Factory method to create a Utils subclass.

Parameters

description [Config instance] used to initialize Utils subclass

model_type [string] Must be one of [PERISOMATIC_TYPE, ALL_ACTIVE_TYPE]. If none, defaults to PERISOMATIC_TYPE

Returns

Utils instance

Module contents

allensdk.model.glif package

Submodules

allensdk.model.glif.glif_neuron module

exception allensdk.model.glif.glif_neuron.**GlifBadResetException**(*message*, *dv*)
Bases: `Exception`

Exception raised when voltage is still above threshold after a reset rule is applied.

class `allensdk.model.glif.glif_neuron.`**`GlifNeuron`**(*El*, *dt*, *asc_tau_array*, *R_input*, *C*, *asc_amp_array*, *spike_cut_length*, *th_inf*, *th_adapt*, *coeffs*, *AScurrent_dynamics_method*, *voltage_dynamics_method*, *threshold_dynamics_method*, *AScurrent_reset_method*, *voltage_reset_method*, *threshold_reset_method*, *init_voltage*, *init_threshold*, *init_AScurrents*, ***kwargs*)

Bases: `object`

Implements the current-based Mihalas Neiber GLIF neuron. Simulations model the voltage, threshold, and afterspike currents of a neuron given an input stimulus. A set of modular dynamics rules are applied until voltage crosses threshold, at which point a set of modular reset rules are applied. See glif_neuron_methods.py for a list of what options there are for voltage, threshold, and afterspike current dynamics and reset rules.

Parameters

El [float]

resting potential

dt [float] duration between time steps

asc_tau_array: np.ndarray TODO

R_input [float] input resistance

C [float] capacitance

asc_amp_arrap [np.ndarray] afterspike current vector. one element per element of asc_tau_array.

spike_cut_length [int] how many time steps to replace with NaNs when a spike occurs.

th_inf [float] instantaneous threshold

coeffs [dict] dictionary coefficients premultiplied to neuron properties during simulation. used for optimization.

AScurrent_dynamics_method [dict] dictionary containing the 'name' of the afterspike current dynamics method to use and a 'params' dictionary parameters to pass to that function.

voltage_dynamics_method [dict] dictionary containing the 'name' of the voltage dynamics method to use and a 'params' dictionary parameters to pass to that function.

threshold_dynamics_method [dict] dictionary containing the 'name' of the threshold dynamics method to use and a 'params' dictionary parameters to pass to that function.

AScurrent_reset_method [dict] dictionary containing the 'name' of the afterspike current dynamics method to use and a 'params' dictionary parameters to pass to that function.

voltage_reset_method [dict] dictionary containing the 'name' of the voltage dynamics method to use and a 'params' dictionary parameters to pass to that function.

threshold_reset_method [dict] dictionary containing the 'name' of the threshold dynamics method to use and a 'params' dictionary parameters to pass to that function.

init_voltage [float] initial voltage value

init_threshold [float] initial spike threshold value

init_AScurrents [np.ndarray] initial afterspike current vector. one element per element of asc_tau_array.

TYPE = 'GLIF'

append_threshold_components(*self*, *spike*, *voltage*)

static configure_library_method(*method_type*, *params*)

Create a GlifNeuronMethod instance out of a library of functions organized by type name. This refers to the METHOD_LIBRARY in glif_neuron_methods.py, which lays out the available functions that can be used for dynamics and reset rules.

Parameters

method_type [string] the name of a function category (e.g. 'AScurrent_dynamics_method' for the afterspike current dynamics methods)

params [dict] a dictionary with two members. 'name': the string name of function you want, and 'params': parameters you want to pass to that function

Returns

GlifNeuronMethod a GlifNeuronMethod instance

static configure_method(*method_name*, *method*, *method_params*)

Create a GlifNeuronMethod instance given a name, a function, and function parameters. This is just a shortcut to the GlifNeuronMethod constructor.

Parameters

method_name [string] name for refering to this method later

method [function] a python function

method_parameters [dict] function arguments whose values should be fixed

Returns

GlifNeuronMethod a GlifNeuronMethod instance

dynamics(*self*, *voltage_t0*, *threshold_t0*, *AScurrents_t0*, *inj*, *time_step*, *spike_time_steps*)

Update the voltage, threshold, and afterspike currents of the neuron for a single time step.

Parameters

voltage_t0 [float] the current voltage of the neuron

threshold_t0 [float] the current spike threshold level of the neuron

AScurrents_t0 [np.ndarray] the current state of the afterspike currents in the neuron

inj [float] the current value of the current injection into the neuron

time_step [int] the current time step of the neuron simulation

spike_time_steps [list] a list of all of the time steps of spikes in the neuron

Returns

tuple voltage_t1 (voltage at next time step), threshold_t1 (threshold at next time step), AScurrents_t1 (afterspike currents at next time step)

classmethod from_dict(*d*)

reset (*self*, *voltage_t0*, *threshold_t0*, *AScurrents_t0*)
Apply reset rules to the neuron's voltage, threshold, and afterspike currents assuming a spike has occurred (voltage is above threshold).

Parameters

voltage_t0 [float] the current voltage of the neuron

threshold_t0 [float] the current spike threshold level of the neuron

AScurrents_t0 [np.ndarray] the current state of the afterspike currents in the neuron

Returns

tuple voltage_t1 (voltage at next time step), threshold_t1 (threshold at next time step), AScurrents_t1 (afterspike currents at next time step)

run (*self*, *stim*)
Run neuron simulation over a given stimulus. This steps through the stimulus applying dynamics equations. After each step it checks if voltage is above threshold. If so, self.spike_cut_length NaNs are inserted into the output voltages, reset rules are applied to the voltage, threshold, and afterspike currents, and the simulation resumes.

Parameters

stim [np.ndarray] vector of scalar current values

Returns

dict

a dictionary containing: 'voltage': simulated voltage values, 'threshold': threshold values during the simulation, 'AScurrents': afterspike current values during the simulation, 'grid_spike_times': spike times (in uits of self.dt) aligned to simulation time steps, 'interpolated_spike_times': spike times (in units of self.dt) linearly interpolated between time steps, 'spike_time_steps': the indices of grid spike times, 'interpolated_spike_voltage': voltage of the simulation at interpolated spike times, 'interpolated_spike_threshold': threshold of the simulation at interpolated spike times

tau_m

to_dict (*self*)
Convert the neuron to a serializable dictionary.

allensdk.model.glif.glif_neuron.**interpolate_spike_time** (*dt*, *time_step*, *threshold_t0*, *threshold_t1*, *voltage_t0*, *voltage_t1*)
Given two voltage and threshold values, the dt between them and the initial time step, interpolate a spike time within the dt interval by intersecting the two lines.

allensdk.model.glif.glif_neuron.**interpolate_spike_value** (*dt*, *interpolated_spike_time_offset*, *v0*, *v1*)
Take a value at two adjacent time steps and linearly interpolate what the value would be at an offset between the two time steps.

allensdk.model.glif.glif_neuron.**line_crossing_x** (*dx*, *a0*, *a1*, *b0*, *b1*)
Find the x value of the intersection of two lines.

allensdk.model.glif.glif_neuron.**line_crossing_y** (*dx*, *a0*, *a1*, *b0*, *b1*)
Find the y value of the intersection of two lines.

allensdk.model.glif.glif_neuron_methods module

The methods in this module are used for configuring dynamics and reset rules for the GlifNeuron. For more details on how to use these methods, see *Generalized LIF Models*.

class allensdk.model.glif.glif_neuron_methods.**GlifNeuronMethod**(*method_name*, *method*, *method_params*)

Bases: object

A simple class to keep track of the name and parameters associated with a neuron method. This class is initialized with a name, function, and parameters to pass to the function. The function then has those passed parameters fixed to a partial function using functools.partial. This class then mimics a function itself using the __call__ convention. Parameters that are not fixed in this way are assumed to be passed into the method when it is called. If the passed parameters contain an argument that is not part of the function signature, an exception will be raised.

Parameters

method_name [string] A shorthand name that will be used to reference this method in the *GlifNeuron*.

method [function] A python function to be called when this instance is called.

method_params [dict] A dictionary mapping function arguments to values for values that should be fixed.

modify_parameter(*self*, *param*, *operator*)

Modify a function parameter needs to be modified after initialization.

Parameters

param [string] the name of the parameter to modify

operator [callable] a function or lambda that returns the desired modified value

Returns

type the new value of the variable that was just modified.

to_dict(*self*)

allensdk.model.glif.glif_neuron_methods.**dynamics_AScurrent_exp**(*neuron*, *AScurrents_t0*, *time_step*, *spike_time_steps*)

Exponential afterspike current dynamics method takes a current at t0 and returns the current at a time step later.

allensdk.model.glif.glif_neuron_methods.**dynamics_AScurrent_none**(*neuron*, *AScurrents_t0*, *time_step*, *spike_time_steps*)

This method always returns zeros for the afterspike currents, regardless of input.

allensdk.model.glif.glif_neuron_methods.**dynamics_threshold_inf**(*neuron*, *threshold_t0*, *voltage_t0*, *AScurrents_t0*, *inj*)

Set threshold to the neuron's instantaneous threshold.

Parameters

neuron [class]

threshold_t0 [not used here]

voltage_t0 [not used here]

AScurrents_t0 [not used here]

inj [not used here]

AScurrents_t0 [not used here]

inj [not used here]

`allensdk.model.glif.glif_neuron_methods.`**`dynamics_threshold_spike_component`**(*neuron*, *threshold_t0*, *voltage_t0*, *AScurrents_t0*, *inj*, *a_spike*, *b_spike*, *a_voltage*, *b_voltage*)

Analytical solution for spike component of threshold. The threshold will adapt via a component initiated by a spike which decays as an exponential. The component is in reference to threshold infinity and are recorded in the neuron's threshold components. The voltage component of the threshold is set to zero in the threshold components because it is zero here The third component refers to th_inf which is added separately as opposed to being included in the voltage component of the threshold as is done in equation 2.1 of Mihalas and Nieber 2009. Threshold infinity is removed for simple optimization.

Parameters

neuron [class]

threshold_t0 [float] threshold input to function

voltage_t0 [float] voltage input to function

AScurrents_t0 [vector] values of after spike currents

inj [float] current injected into the neuron

`allensdk.model.glif.glif_neuron_methods.`**`dynamics_threshold_three_components_exact`**(*neuron*, *threshold_t0*, *voltage_t0*, *AScurrents_t0*, *inj*, *a_spike*, *b_spike*, *a_voltage*, *b_voltage*)

Analytical solution for threshold dynamics. The threshold will adapt via two mechanisms: 1. a voltage dependent adaptation. 2. a component initiated by a spike which decays as an exponential. These two component are in reference to threshold infinity and are recorded in the neuron's threshold components. The third component refers to th_inf which is added separately as opposed to being included in the voltage component of the threshold as is done in equation 2.1 of Mihalas and Nieber 2009. Threshold infinity is removed for simple optimization.

Parameters

neuron [class]

threshold_t0 [float] threshold input to function

voltage_t0 [float] voltage input to function

AScurrents_t0 [vector] values of after spike currents

inj [float] current injected into the neuron

`allensdk.model.glif.glif_neuron_methods.`**`dynamics_voltage_linear_exact`**(*neuron*, *voltage_t0*, *AScurrents_t0*, *inj*)

(TODO) Linear voltage dynamics.

`allensdk.model.glif.glif_neuron_methods.`**`dynamics_voltage_linear_forward_euler`**(*neuron*, *voltage_t0*, *AScurrents_t0*, *inj*)

(TODO) Linear voltage dynamics.

`allensdk.model.glif.glif_neuron_methods.`**`max_of_line_and_const`**(*x*, *b*, *c*, *d*)

Find the maximum of a value and a position on a line

Parameters

x: float x position on line 1

c: float slope of line 1

d: float y-intercept of line 1

b: float y-intercept of line 2

Returns

float the max of a line value and a constant

`allensdk.model.glif.glif_neuron_methods.`**`min_of_line_and_zero`**(*x*, *c*, *d*)

Find the minimum of a value and a position on a line

Parameters

x: float x position on line 1

c: float slope of line 1

d: float y-intercept of line 1

b: float y-intercept of line 2

Returns

float the max of a line value and a constant

`allensdk.model.glif.glif_neuron_methods.`**`reset_AScurrent_none`**(*neuron*, *AScurrents_t0*)

Reset afterspike currents to zero.

`allensdk.model.glif.glif_neuron_methods.`**`reset_AScurrent_sum`**(*neuron*, *AScurrents_t0*, *r*)

Reset afterspike currents by adding summed exponentials. Left over currents from last spikes as well as newly initiated currents from current spike. Currents amplitudes in neuron.asc_amp_array need to be the amplitudes advanced though the spike cutting. I.e. In the preprocessor if the after spike currents are calculated via the GLM from spike initiation the amplitude at the time after the spike cutting needs to be calculated and neuron.asc_amp_array needs to be set to this value.

Parameters

r [np.ndarray] a coefficient vector applied to the afterspike currents

`allensdk.model.glif.glif_neuron_methods.`**`reset_threshold_inf`**(*neuron*, *threshold_t0*, *voltage_v1*)

Reset the threshold to instantaneous threshold.

`allensdk.model.glif.glif_neuron_methods.`**`reset_threshold_three_components`**(*neuron*, *threshold_t0*, *voltage_v1*, *a_spike*, *b_spike*)

This method calculates the two components of the threshold: a spike (fast) component and a voltage (slow) component. The threshold_components vectors are then updated so that the traces match the voltage, current, and total threshold traces. The spike component of the threshold decays via an exponential fit specified by the amplitude a_spike and the time constant b_spike fit via the multiblip data. The voltage component does not change during the duration of the spike. The spike component are threshold component are summed along with threshold infinity to return the total threshold. Note that in the current implementation a_spike is added to the last value of the threshold_components which means that a_spike is the amplitude after spike cutting (if there is any).

Inputs:

neuron: class contains attributes of the neuron

threshold_t0, voltage_t0: float are not used but are here for consistency with other methods

a_spike: float amplitude of the exponential decay of spike component of threshold after spike cutting has been implemented.

b_spike: float amplitude of the exponential decay of spike component of threshold

Outputs:

Returns: float the total threshold which is the sum of the spike component of threshold, the voltage component of threshold and threshold infinity (with it's corresponding coefficient)

neuron.threshold_components: dictionary containing

a spike: list vector of spiking component of threshold that corresponds to the voltage, current, and total threshold traces

b_spike: list

vector of voltage component of threshold that corresponds to the voltage, current, and total threshold traces.

Note that this function can be changed to use a_spike at the time of the spike and then have the the spike component plus the residual decay thought the spike. There are benefits and drawbacks to this. This potential change would be beneficial as it perhaps makes more biological sense for the threshold to go up at the time of spike if the traces are ever used. Also this would mean that a_spike would not have to be adjusted thought the spike cutting after the multiblip fit. However the current implementation makes sense in that it is similar to how afterspike currents are implemented.

`allensdk.model.glif.glif_neuron_methods.`**`reset_voltage_v_before`**(*neuron*, *voltage_t0*, *a*, *b*)

Reset voltage to the previous value with a scale and offset applied.

Parameters

a [float] voltage scale constant

b [float] voltage offset constant

`allensdk.model.glif.glif_neuron_methods.`**`reset_voltage_zero`**(*neuron*, *voltage_t0*)

Reset voltage to zero.

`allensdk.model.glif.glif_neuron_methods.`**`spike_component_of_threshold_exact`**(*th0*, *b_spike*, *t*)

Spike component of threshold modeled as an exponential decay. Implemented here as exact analytical solution.

Parameters

th0 [float] threshold input to function

b_spike [float] decay constant of exponential

t [float or array] time step if used in an Euler setup time if used analytically

`allensdk.model.glif.glif_neuron_methods.`**`spike_component_of_threshold_forward_euler`**(*th_t0*, *b_spike*, *dt*)

Spike component of threshold modeled as an exponential decay. Implemented here for forward Euler

Parameters

th_t0 [float] threshold input to function

b_spike [float] decay constant of exponential

dt [float] time step

`allensdk.model.glif.glif_neuron_methods.`**`voltage_component_of_threshold_exact`**(*th0*, *v0*, *I*, *t*, *a_voltage*, *b_voltage*, *C*, *g*, *El*)

Note this function is the exact formulation; however, dt is used because t0 is the initial time and dt is the time the function is exactly evaluated at. Note: that here, this equation is in reference to th_inf. Therefore th0 is the total threshold-thr_inf (threshold_inf replaced with 0 in the equation to be verbose). This is done so that th_inf can be optimized without affecting this function.

Parameters

th0 [float] threshold input to function

v0 [float] voltage input to function

I [float] total current entering neuron (note if there are after spike currents these must be included in this value)

t [float or array] time step if used in an Euler setup time if used analytically

a_voltage [float] constant a

b_voltage [float] constant b

C [float] capacitance

g [float] conductance (1/resistance)

El [float] reversal potential

`allensdk.model.glif.glif_neuron_methods.`**`voltage_component_of_threshold_forward_euler`**(*th_t0*, *v_t0*, *dt*, *a_volta*, *b_volta*, *El*)

Equation 2.1 of Mihalas and Nieber, 2009 implemented for use in forward Euler. Note here all variables are in reference to threshold infinity. Therefore thr_inf is zero here (replaced threshold_inf with 0 in the equation to be verbose). This is done so that th_inf can be optimized without affecting this function.

Parameters

th_t0 [float] threshold input to function

v_t0 [float] voltage input to function

dt [float] time step

a_voltage [float] constant a

b_voltage [float] constant b

El [float] reversal potential

allensdk.model.glif.simulate_neuron module

`allensdk.model.glif.simulate_neuron.`**`load_sweep`**(*file_name*, *sweep_number*)

Load the stimulus for a sweep from file.

`allensdk.model.glif.simulate_neuron.`**`main`**()

`allensdk.model.glif.simulate_neuron.`**`parse_arguments`**()

Use argparse to get required arguments from the command line

`allensdk.model.glif.simulate_neuron.`**`simulate_neuron`**(*neuron*, *sweep_numbers*, *input_file_name*, *output_file_name*, *spike_cut_value*)

`allensdk.model.glif.simulate_neuron.`**`simulate_sweep`**(*neuron*, *stimulus*, *spike_cut_value*)

Simulate a neuron given a stimulus and initial conditions.

`allensdk.model.glif.simulate_neuron.`**`simulate_sweep_from_file`**`(`*neuron*, *sweep_number*, *input_file_name*, *output_file_name*, *spike_cut_value*`)`

Load a sweep stimulus, simulate the response, and write it out.

`allensdk.model.glif.simulate_neuron.`**`write_sweep_response`**`(`*file_name*, *sweep_number*, *response*, *spike_times*`)`

Overwrite the response in a file.

Module contents

A Generalized Linear Integrate and Fire (GLIF) neuron modeling package. Use this code to run the GLIF models available in the Allen Cell Types Atlas. See *Generalized LIF Models* for more details.

Module contents

6.1.8 allensdk.morphology package

Submodules

allensdk.morphology.validate_swc module

`allensdk.morphology.validate_swc.`**`main`**`()`

`allensdk.morphology.validate_swc.`**`validate_swc`**`(`*swc_file*`)`

To be compatible with NEURON, SWC files must have the following properties:

1) a single root node with parent ID '-1'
2) sequentially increasing ID numbers
3) immediate children of the soma cannot branch

Module contents

6.1.9 allensdk.mouse_connectivity package

Subpackages

allensdk.mouse_connectivity.grid package

Subpackages

allensdk.mouse_connectivity.grid.subimage package

Submodules

allensdk.mouse_connectivity.grid.subimage.base_subimage module

allensdk.mouse_connectivity.grid.subimage.cav_subimage module

allensdk.mouse_connectivity.grid.subimage.classic_subimage module

allensdk.mouse_connectivity.grid.subimage.count_subimage module

Module contents

allensdk.mouse_connectivity.grid.utilities package

Submodules

allensdk.mouse_connectivity.grid.utilities.downsampling_utilities module

`allensdk.mouse_connectivity.grid.utilities.downsampling_utilities.`**`apply_divisions`**(*image*, *window_size*)

`allensdk.mouse_connectivity.grid.utilities.downsampling_utilities.`**`block_average`**(*volume*, *factor*)

`allensdk.mouse_connectivity.grid.utilities.downsampling_utilities.`**`conv`**(*image*, *factor*, *window_size*)

`allensdk.mouse_connectivity.grid.utilities.downsampling_utilities.`**`downsample_average`**(*volume*, *current_spa* *target_spa*

`allensdk.mouse_connectivity.grid.utilities.downsampling_utilities.`**`extract`**(*image*, *factor*, *window_size*, *window_step*, *output_shape*)

`allensdk.mouse_connectivity.grid.utilities.downsampling_utilities.`**`window_average`**(*volume*, *factor*)

allensdk.mouse_connectivity.grid.utilities.image_utilities module

Module contents

allensdk.mouse_connectivity.grid.writers package

Module contents

Submodules

allensdk.mouse_connectivity.grid.image_series_gridder module

Module contents

Module contents

6.1.10 allensdk.test_utilities package

Submodules

allensdk.test_utilities.custom_comparators module

class allensdk.test_utilities.custom_comparators.**WhitespaceStrippedString**(*string: str, whitespace_chars: str = '\s', ASCII: bool = False*)

Bases: object

Comparator class to compare strings that have been stripped of whitespace. By default removes any unicode whitespace character that matches the regex s, (which includes [

], and other unicode whitespace characters).

allensdk.test_utilities.regression_fixture module

allensdk.test_utilities.regression_fixture.**get_list_of_path_dict**()

allensdk.test_utilities.temp_dir module

allensdk.test_utilities.temp_dir.**temp_dir**(*request*)

Module contents

6.2 Submodules

6.2.1 allensdk.deprecated module

`allensdk.deprecated.`**`class_deprecated`**`(`*message=None*`)`

`allensdk.deprecated.`**`deprecated`**`(`*message=None*`)`

`allensdk.deprecated.`**`legacy`**`(`*message=None*`)`

6.2.2 allensdk.tmp module

6.3 Module contents

`exception` `allensdk.`**`OneResultExpectedError`**

Bases: `RuntimeError`

`allensdk.`**`one`**`(`*x*`)`

The Allen Software Development Kit houses source code for reading and processing Allen Brain Atlas data. The Allen SDK focuses on the Allen Brain Observatory, Cell Types Database, and Mouse Brain Connectivity Atlas.

Attention: As of October 2019, we have dropped Python 2 support and any files with a py2 dependency (for example analysis files) have been updated.

_static/sdk_cam.png

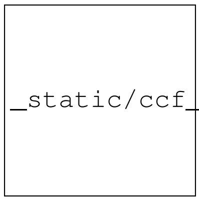
CHAPTER 7

Allen Brain Observatory

The Allen Brain Observatory is a data resource for understanding sensory processing in the mouse visual cortex. This study systematically measures visual responses in multiple cortical areas and layers using two-photon calcium imaging of GCaMP6-labeled neurons targeted using Cre driver lines. Response characterizations include orientation tuning, spatial and temporal frequency tuning, temporal dynamics, and spatial receptive field structure.

The mean fluorescence traces for all segmented cells are available in the Neurodata Without Borders file format (NWB files). These files contain standardized descriptions of visual stimuli to support stimulus-specific tuning analysis. The Allen SDK provides code to:

- download and organize experiment data according to cortical area, imaging depth, and Cre line
- remove the contribution of neuropil signal from fluorescence traces
- access (or compute) dF/F traces based on the neuropil-corrected traces
- perform stimulus-specific tuning analysis (e.g. drifting grating direction tuning)



CHAPTER 8

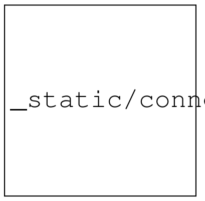
Allen Cell Types Database

The Allen Cell Types Database contains electrophysiological and morphological characterizations of individual neurons in the mouse primary visual cortex. The Allen SDK provides Python code for accessing electrophysiology measurements (NWB files) for all neurons and morphological reconstructions (SWC files) for a subset of neurons.

The Database also contains two classes of models fit to this data set: biophysical models produced using the NEURON simulator and generalized leaky integrate and fire models (GLIFs) produced using custom Python code provided with this toolkit.

The Allen SDK provides sample code demonstrating how to download neuronal model parameters from the Allen Brain Atlas API and run your own simulations using stimuli from the Allen Cell Types Database or custom current injections:

- *Biophysical Models*
- *Generalized LIF Models*



CHAPTER 9

Allen Mouse Brain Connectivity Atlas

The Allen Mouse Brain Connectivity Atlas is a high-resolution map of neural connections in the mouse brain. Built on an array of transgenic mice genetically engineered to target specific cell types, the Atlas comprises a unique compendium of projections from selected neuronal populations throughout the brain. The primary data of the Atlas consists of high-resolution images of axonal projections targeting different anatomic regions or various cell types using Cre-dependent specimens. Each data set is processed through an informatics data analysis pipeline to obtain spatially mapped quantified projection information.

The Allen SDK provides Python code for accessing experimental metadata along with projection signal volumes registered to a common coordinate framework. This framework has structural annotations, which allows users to compute structure-level signal statistics.

See the mouse connectivity section for more details.

CHAPTER 10

What's New - 1.3.0 (December 12, 2019)

The 1.3.0 release adds

- Improved Neuropixels data download performance by enabling asynchronous transfers. Users can now also specify a timeout and number of retries when downloading data.

and fixes

- Hanging downloads for Neuropixels NWB files
- Updated AllenSDK readme and contributing documentation

CHAPTER 11

What's New - 1.2.0 (November 21, 2019)

The 1.2.0 release adds

- (internal feature) A project cache for the Behavior Ophys project, with example notebook
- (internal feature) A major overhaul of the *BehaviorOphysLimsApi*
- (internal feature) Updates to the *EcephysProjectLimsApi* such that it returns data in the same format as the *EcephyProjectWarehouseApi*
- improved eye-tracking area calculation

and fixes

- several flaky tests
- regress tests which depend on scipy's *ks_2samp*
- (internal feature) duplicate caching on the Bevavior Ophys Lims Api

CHAPTER 12

Previous Release Notes

- '1.1.1 <https://github.com/AllenInstitute/AllenSDK/releases/tag/v1.1.1>
- 1.1.0
- 1.0.2
- 0.16.3
- 0.16.2
- 0.16.1
- 0.16.0
- 0.14.5
- 0.14.4
- 0.14.3
- 0.14.2
- 0.13.2
- 0.13.1
- 0.13.0
- 0.12.4

Bibliography

[1] Allen Brain Atlas Data Portal: Downloading a WellKnownFile.

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