
neuron morphology

Release 1.0.0.beta0

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Contents

1.1 Introduction

Morphological features are useful for investigating and clustering neuron morphologies. The Feature Extractor package is designed to allow flexible morphological feature extraction from swc neuron reconstruction files and supplementary data. The default_feature set is a combination of [L-measure](#) and other features used by the Allen Institute.

1.2 Running Feature Extraction from the Command Line

The feature extractor module is an [argschema module](#), which can be run from the command line:

```
feature_extractor --input_json path_to_inputs.json --output_json write_outputs_here.  
↪ json
```

Please see the [schema file](#) for usage details and options.

1.3 Running in Python/Notebooks

You can take advantage of all of the capabilities of Feature Extractor by running it in python and jupyter notebooks. By running in python and notebooks, you can easily add your own features, create different feature sets, and customize your feature extractor to meet your needs.

Here are two basic examples for running IVSCC and fMOST data:

- [IVSCC example notebook](#)
- [fMOST example notebook](#)

For a more detailed look at the feature extractor capabilities, checkout [feature_extractor_example](#)

IVSCC Spatial Transformation

For [feature extraction](#) or visualization, we often need to apply a transformation to the space in which our reconstruction dwells. Some examples:

- **unshrink** : If a neuron is reconstructed from slice, the depth dimension may not scaled equivalently to the width and height dimensions, due to tissue shrinkage. In this case, the neuron must be rescaled along the depth dimension in order for features like compartment volume to be meaningful.
- **upright** : Images of single cortical neurons reconstructed in slice may be rotated arbitrarily. In order to visualize or calculate the symmetry of a neuron’s apical dendrites, we must rotate the neuron so that the pia-ward direction is “up”.

The `neuron_morphology` repository contains a set of utilities for calculating and applying such transformations. These utilities are ones that we, the Allen Institute, use for processing our in-vitro single cell characterization data (IVSCC, [whitepaper here](#)), but you may also find them handy if your data are similar.

2.1 Components

Here are the spatial transform components that we use for our IVSCC data. For each one, we’ve also included a link to the detailed input and output specification for that executable.

- `pia_wm_streamlines` ([schema](#)) : Given 2D linestrings describing the pia and white matter surfaces local to a neuron, calculate a cortical depth field, whose values are the depth between pia and white matter.
- `upright_angle` ([schema](#)) : Given an swc-formatted reconstruction and the outputs of `pia_wm_streamlines`, find the angle of rotation about the soma which will align the “y” axis of the reconstruction with the pia-ward direction.
- `apply_affine_transform` ([schema](#)) : Given a 3D affine transform and an swc-formatted reconstruction, produce a transformed reconstruction also in swc format.

2.2 Command-line invocation

Once you have installed `neuron_morphology`, you can run these utilities from the command line as you would any `argschema` module. Here is an example:

```
pia_wm_streamlines --input_json path_to_inputs.json --output_json write_outputs_here.  
↪ json
```

In this case, the contents of `path_to_inputs.json` might look like:

```
{  
  "pia_path_str": "10.0,1.0,10.0,3.0,9.0,5.0",  
  "wm_path_str": ".0,1.0,1.0,3.0,1.0,4.0"  
}
```

Please see the `schema` file for more details and options.

2.3 Putting it all together

Most likely, you would like to run several of these components in sequence. Here is a `jupyter notebook` which demonstrates in depth how to go from a “raw” morphology and cortical boundaries to an upright-transformed morphology.

3.1 requirements

We support Python 3.7 on Linux, OSX, and Windows. Similar Python versions (e.g. 3.6, 3.8) will probably work, but we don't regularly test using those versions.

3.2 managing your Python environment

We recommend installing *neuron_morphology* into a managed Python environment. Having multiple isolated environments lets you install incompatible packages (or different versions of the same package!) simultaneously and prevents unexpected behavior by utilities that rely on the system Python installation.

Two popular tools for managing Python environments are [anaconda](#) and [venv](#). The rest of this document assumes that you have created and activated an environment using one of these tools. Using *anaconda*, this looks like:

```
conda create -y --name environment-name python=3.6
conda activate environment-name
```

and using *venv*:

```
python -m venv path/to/environment
source path/to/environment/bin/activate
```

3.3 installing from github

If you want to install a specific branch, tag, or commit of *neuron_morphology*, you can do so using *pip*:

```
pip install git+https://github.com/alleninstitute/neuron_morphology@dev
```

The *dev* branch contains cutting-edge features that might not have been formally released yet. By installing this way, you can access those features.

3.4 installing for development

If you want to work on *neuron_morphology*, you should first clone the repository, then install it in editable mode so that you can easily test your changes:

```
git clone https://github.com/alleninstitute/neuron_morphology
cd neuron_morphology

conda install -c conda-forge fenics mshr # optional, these dependencies' pypi
↪ packages don't work out of the box on all platforms
pip install -r requirements.txt -U
pip install -r test_requirements.txt -U

pip install -e .
```

3.5 installing from conda-forge [coming soon!]

To install using conda (, run

```
conda install -c conda-forge -y neuron_morphology
```

This method is preferred vs. `pip`, since some subpackages of *neuron_morphology* depend on 3rd party packages which don't `pip` install well on all major platforms. Note that this use of conda as a *package* manager does not require or depend on using conda as your *environment* manager

3.6 installing from pypy [coming soon!]

You can install the latest release from pypy by running:

```
pip install neuron_morphology
```

4.1 neuron_morphology package

4.1.1 Subpackages

neuron_morphology.feature_extractor package

Submodules

neuron_morphology.feature_extractor.data module

```
class neuron_morphology.feature_extractor.data.Data (morphology:          neu-
                                                    ron_morphology.morphology.Morphology,
                                                    **other_things)
    Bases: object
neuron_morphology.feature_extractor.data.get_morphology (data:
                                                    Union[neuron_morphology.feature_extractor.data.L
                                                    neu-
                                                    ron_morphology.morphology.Morphology])
    Decay a Data to a Morphology, leaving Morphologies untouched
```

neuron_morphology.feature_extractor.feature_extraction_run module

```
class neuron_morphology.feature_extractor.feature_extraction_run.FeatureExtractionRun (data)
    Bases: object
```

Methods

<code>extract(self)</code>	For each selected feature, carry out calculation on this run's dataset.
<code>select_features(self, features, only_marks, ...)</code>	Choose features to calculated for this run on the basis of selected marks.
<code>select_marks(self, marks, required_marks)</code>	Choose marks for this run by validating a set of candidates against the data.
<code>serialize(self)</code>	Return a dictionary describing this run

extract (*self*)

For each selected feature, carry out calculation on this run's dataset.

Returns

self [This FeatureExtractionRun, with results updated]

select_features (*self*, *features*: *Collection*[*neuron_morphology.feature_extractor.marked_feature.MarkedFeature*], *only_marks*: *Union*[*AbstractSet*[*Type*[*neuron_morphology.feature_extractor.mark.Mark*]], *NoneType*] = *None*)

Choose features to calculated for this run on the basis of selected marks.

Parameters

features [Candidates features for selection]

only_marks [if provided, reject features not marked with marks in] this set

Returns

self [This FeatureExtractionRun, with selected_features updated]

select_marks (*self*, *marks*: *Collection*[*Type*[*neuron_morphology.feature_extractor.mark.Mark*]], *required_marks*: *AbstractSet*[*Type*[*neuron_morphology.feature_extractor.mark.Mark*]] = *frozenset*())

Choose marks for this run by validating a set of candidates against the data.

Parameters

marks [candidate marks to be validated]

required_marks [if provided, raise an exception if any of these marks] do not validate successfully

Returns

self [This FeatureExtractionRun, with selected_marks updated]

serialize (*self*)

Return a dictionary describing this run

neuron_morphology.feature_extractor.feature_extractor module

```
class neuron_morphology.feature_extractor.feature_extractor.FeatureExtractor (features:
    Sequence[Union[Callable, Any],
    neuron_morphology.feature_extractor.mark.Mark],
    required_marks: AbstractSet[neuron_morphology.feature_extractor.mark.Mark] =
    frozenset())
```

Bases: object

Methods

<code>extract(self, data, only_marks, ...)</code>	Run the feature extractor for a single dataset
<code>register_features(self, features, Any], ...)</code>	Add a new feature to the list of options

extract (*self*, *data*: *neuron_morphology.feature_extractor.data.Data*, *only_marks*: *Union[AbstractSet[Type[neuron_morphology.feature_extractor.mark.Mark]], NoneType]* = *None*, *required_marks*: *AbstractSet[Type[neuron_morphology.feature_extractor.mark.Mark]]* = *frozenset()*) → *neuron_morphology.feature_extractor.feature_extraction_run.FeatureExtractionRun*
Run the feature extractor for a single dataset

Parameters

data [the dataset from which features will be calculated]

only_marks [if provided, reject marks not in this set]

required_marks [if provided, raise an exception if any of these marks] do not validate successfully

Returns

The calculated features, along with a record of the marks and features selected.

register_features (*self*, *features*: *Sequence[Union[Callable[[neuron_morphology.feature_extractor.data.Data], Any], neuron_morphology.feature_extractor.marked_feature.MarkedFeature, Mapping[Any, Union[Callable[[neuron_morphology.feature_extractor.data.Data], Any], neuron_morphology.feature_extractor.marked_feature.MarkedFeature]], Iterable[Union[Callable[[neuron_morphology.feature_extractor.data.Data], Any], neuron_morphology.feature_extractor.marked_feature.MarkedFeature]]])*)
Add a new feature to the list of options

Parameters

features [the features to be registered. If it is not already marked,] it will be registered with no marks

neuron_morphology.feature_extractor.feature_specialization module

class *neuron_morphology.feature_extractor.feature_specialization.AllNeuriteCompareSpec*
Bases: *neuron_morphology.feature_extractor.feature_specialization.FeatureSpecialization*

Methods

<code>factory(name, marks, kwargs, Any], ...)</code>	A utility for quickly generating feature specializations
--	--

```
kwargs = {'node_types_to_compare': None}
```

```
marks = {<class 'neuron_morphology.feature_extractor.mark.AllNeuriteTypes'>}
```

```
name = 'all_neurites'
```

class *neuron_morphology.feature_extractor.feature_specialization.AllNeuriteSpec*
Bases: *neuron_morphology.feature_extractor.feature_specialization.*

FeatureSpecialization

Methods

<code>factory(name, marks, kwargs, Any], ...)</code>	A utility for quickly generating feature specializations
--	--

```
kwargs = {'node_types': None}
```

```
marks = {<class 'neuron_morphology.feature_extractor.mark.AllNeuriteTypes'>}
```

```
name = 'all_neurites'
```

```
class neuron_morphology.feature_extractor.feature_specialization.ApicalDendriteCompareSpec
    Bases: neuron_morphology.feature_extractor.feature_specialization.FeatureSpecialization
```

Methods

<code>factory(name, marks, kwargs, Any], ...)</code>	A utility for quickly generating feature specializations
--	--

```
kwargs = {'node_types_to_compare': [4]}
```

```
marks = {<class 'neuron_morphology.feature_extractor.mark.RequiresApical'>}
```

```
name = 'apical_dendrite'
```

```
class neuron_morphology.feature_extractor.feature_specialization.ApicalDendriteSpec
    Bases: neuron_morphology.feature_extractor.feature_specialization.FeatureSpecialization
```

Methods

<code>factory(name, marks, kwargs, Any], ...)</code>	A utility for quickly generating feature specializations
--	--

```
kwargs = {'node_types': [4]}
```

```
marks = {<class 'neuron_morphology.feature_extractor.mark.RequiresApical'>}
```

```
name = 'apical_dendrite'
```

```
class neuron_morphology.feature_extractor.feature_specialization.AxonCompareSpec
    Bases: neuron_morphology.feature_extractor.feature_specialization.FeatureSpecialization
```

Methods

factory(name, marks, kwargs, Any], ...)	A utility for quickly generating feature specializations
---	--

```
kwargs = {'node_types_to_compare': [2]}
marks = {<class 'neuron_morphology.feature_extractor.mark.RequiresAxon'>}
name = 'axon'
```

```
class neuron_morphology.feature_extractor.feature_specialization.AxonSpec
    Bases: neuron_morphology.feature_extractor.feature_specialization.
           FeatureSpecialization
```

Methods

factory(name, marks, kwargs, Any], ...)	A utility for quickly generating feature specializations
---	--

```
kwargs = {'node_types': [2]}
marks = {<class 'neuron_morphology.feature_extractor.mark.RequiresAxon'>}
name = 'axon'
```

```
class neuron_morphology.feature_extractor.feature_specialization.BasalDendriteCompareSpec
    Bases: neuron_morphology.feature_extractor.feature_specialization.
           FeatureSpecialization
```

Methods

factory(name, marks, kwargs, Any], ...)	A utility for quickly generating feature specializations
---	--

```
kwargs = {'node_types_to_compare': [3]}
marks = {<class 'neuron_morphology.feature_extractor.mark.RequiresBasal'>}
name = 'basal_dendrite'
```

```
class neuron_morphology.feature_extractor.feature_specialization.BasalDendriteSpec
    Bases: neuron_morphology.feature_extractor.feature_specialization.
           FeatureSpecialization
```

Methods

factory(name, marks, kwargs, Any], ...)	A utility for quickly generating feature specializations
---	--

```
kwargs = {'node_types': [3]}
marks = {<class 'neuron_morphology.feature_extractor.mark.RequiresBasal'>}
name = 'basal_dendrite'
```

```
class neuron_morphology.feature_extractor.feature_specialization.DendriteCompareSpec
    Bases:          neuron_morphology.feature_extractor.feature_specialization.
                   FeatureSpecialization
```

Methods

factory(name, marks, kwargs, Any], ...)	A utility for quickly generating feature specializa- tions
---	---

```
    kwargs = {'node_types_to_compare':  [4, 3]}
    marks = {<class 'neuron_morphology.feature_extractor.mark.RequiresDendrite'>}
    name = 'dendrite'
```

```
class neuron_morphology.feature_extractor.feature_specialization.DendriteSpec
    Bases:          neuron_morphology.feature_extractor.feature_specialization.
                   FeatureSpecialization
```

Methods

factory(name, marks, kwargs, Any], ...)	A utility for quickly generating feature specializa- tions
---	---

```
    kwargs = {'node_types':  [4, 3]}
    marks = {<class 'neuron_morphology.feature_extractor.mark.RequiresDendrite'>}
    name = 'dendrite'
```

```
class neuron_morphology.feature_extractor.feature_specialization.FeatureSpecialization
    Bases: object
```

Attributes

```
    kwargs
    marks
    name
```

Methods

factory(name, marks, kwargs, Any], ...)	A utility for quickly generating feature specializa- tions
---	---

```
classmethod factory (name: str, marks: Set[Type[neuron_morphology.feature_extractor.mark.Mark]],
                    kwargs: Dict[str, Any], display_name: Union[str, NoneType] = None) →
                    Type[~Fs]
```

A utility for quickly generating feature specializations

Parameters

name [The name of the generated class. If display_name is not] provided, this will also be used as the name attribute of the generated class

marks [the marks which this specialization implies.]
kwargs [the keyword argument values defining this specialization]
display_name [if provided, the name attribute of the generated] specialization.

Returns

A generated `FeatureSpecialization` subclass

kwargs
marks
name

neuron_morphology.feature_extractor.feature_writer module**neuron_morphology.feature_extractor.mark module**

class `neuron_morphology.feature_extractor.mark.AllNeuriteTypes`

Bases: `neuron_morphology.feature_extractor.mark.Mark`

Indicates features that are calculated for all neurite types.

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
---------	--

class `neuron_morphology.feature_extractor.mark.BifurcationFeatures`

Bases: `neuron_morphology.feature_extractor.mark.Mark`

Indicates a feature calculated on bifurcations.

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
---------	--

class `neuron_morphology.feature_extractor.mark.CompartmentFeatures`

Bases: `neuron_morphology.feature_extractor.mark.Mark`

Indicates a feature calculated on compartments.

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
----------------	--

class `neuron_morphology.feature_extractor.mark.Geometric`
 Bases: `neuron_morphology.feature_extractor.mark.Mark`
 Indicates features that change depending on coordinate frame.

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
----------------	--

class `neuron_morphology.feature_extractor.mark.Intrinsic`
 Bases: `neuron_morphology.feature_extractor.mark.Mark`
 Indicates intrinsic features that don't rely on a ccf or scale.

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
----------------	--

class `neuron_morphology.feature_extractor.mark.Mark`
 Bases: `object`
 A tag, intended for use in feature selection.

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
----------------	--

classmethod `factory` (*name: str*) → `Type[~Mr]`

classmethod `validate` (*data: neuron_morphology.feature_extractor.data.Data*) → `bool`
 Determine if this feature is calculable from the provided data.

Parameters**data** [Data from a single morphological reconstruction]**Returns****whether marked features can be calculated from these data****class** `neuron_morphology.feature_extractor.mark.NeuriteTypeComparison`Bases: `neuron_morphology.feature_extractor.mark.Mark`

Indicates a feature that is a comparison between neurite types.

Function should be decorated with the appropriate RequiresType marks

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
----------------	--

class `neuron_morphology.feature_extractor.mark.RequiresApical`Bases: `neuron_morphology.feature_extractor.mark.Mark`

Indicates that these features require an apical dendrite.

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
----------------	--

classmethod validate (*data: neuron_morphology.feature_extractor.data.Data*) → bool

Determine if this feature is calculable from the provided data.

Parameters**data** [Data from a single morphological reconstruction]**Returns****whether marked features can be calculated from these data****class** `neuron_morphology.feature_extractor.mark.RequiresAxon`Bases: `neuron_morphology.feature_extractor.mark.Mark`

Indicates that these features require an axon.

Methods

validate(data)

Determine if this feature is calculable from the provided data.

factory	
---------	--

classmethod validate (*data: neuron_morphology.feature_extractor.data.Data*) → bool

Determine if this feature is calculable from the provided data.

Parameters

data [Data from a single morphological reconstruction]

Returns

whether marked features can be calculated from these data

class *neuron_morphology.feature_extractor.mark.RequiresBasal*

Bases: *neuron_morphology.feature_extractor.mark.Mark*

Indicates that these features require a basal dendrite.

Methods

validate(data)

Determine if this feature is calculable from the provided data.

factory	
---------	--

classmethod validate (*data: neuron_morphology.feature_extractor.data.Data*) → bool

Determine if this feature is calculable from the provided data.

Parameters

data [Data from a single morphological reconstruction]

Returns

whether marked features can be calculated from these data

class *neuron_morphology.feature_extractor.mark.RequiresDendrite*

Bases: *neuron_morphology.feature_extractor.mark.Mark*

This feature can only be calculated for neurons with at least one dendrite node

Methods

validate(data)

Determine if this feature is calculable from the provided data.

factory	
---------	--

classmethod validate (*data: neuron_morphology.feature_extractor.data.Data*) → bool

Determine if this feature is calculable from the provided data.

Parameters

data [Data from a single morphological reconstruction]

Returns

whether marked features can be calculated from these data

class `neuron_morphology.feature_extractor.mark.RequiresLayerAnnotations`

Bases: `neuron_morphology.feature_extractor.mark.Mark`

Methods

<code>validate(data)</code>	Checks whether each node in the data's morphology is annotated with a cortical layer.
-----------------------------	---

factory	
---------	--

classmethod `validate` (*data: neuron_morphology.feature_extractor.data.Data*) → bool

Checks whether each node in the data's morphology is annotated with a cortical layer. Returns False if any are missing.

class `neuron_morphology.feature_extractor.mark.RequiresLayeredPointDepths`

Bases: `neuron_morphology.feature_extractor.mark.Mark`

This feature can only be calculated if (cortical) points are annotated with a collection of within-layer depths. See `features.layer.layered_point_depths` for more information.

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
---------	--

classmethod `validate` (*data: neuron_morphology.feature_extractor.data.Data*) → bool

Determine if this feature is calculable from the provided data.

Parameters

data [Data from a single morphological reconstruction]

Returns

whether marked features can be calculated from these data

class `neuron_morphology.feature_extractor.mark.RequiresRadii`

Bases: `neuron_morphology.feature_extractor.mark.Mark`

This feature can only be calculated if the radii of nodes are annotated.

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
---------	--

classmethod `validate` (*data: neuron_morphology.feature_extractor.data.Data*) → bool

Determine if this feature is calculable from the provided data.

Parameters

data [Data from a single morphological reconstruction]

Returns

whether marked features can be calculated from these data

class `neuron_morphology.feature_extractor.mark.RequiresReferenceLayerDepths`

Bases: `neuron_morphology.feature_extractor.mark.Mark`

This feature can only be calculated if a referenceset of average depths for cortical layers is provided. See `features.layer.reference_layer_depths` for more information.

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
---------	--

classmethod `validate` (*data: neuron_morphology.feature_extractor.data.Data*) → bool

Determine if this feature is calculable from the provided data.

Parameters

data [Data from a single morphological reconstruction]

Returns

whether marked features can be calculated from these data

class `neuron_morphology.feature_extractor.mark.RequiresRegularPointSpacing`

Bases: `neuron_morphology.feature_extractor.mark.Mark`

This features can only be (meaningfully) calculated if the points (e.g. node positions) on which it is based are resampled to have regular spacing.

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
---------	--

class neuron_morphology.feature_extractor.mark.RequiresRelativeSomaDepth

Bases: neuron_morphology.feature_extractor.mark.Mark

This feature can only be calculated for relative soma depth

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
---------	--

classmethod validate (data: neuron_morphology.feature_extractor.data.Data) → bool

Determine if this feature is calculable from the provided data.

Parameters

data [Data from a single morphological reconstruction]

Returns

whether marked features can be calculated from these data

class neuron_morphology.feature_extractor.mark.RequiresRoot

Bases: neuron_morphology.feature_extractor.mark.Mark

Indicates that this features require a root. Warns if the root is not unique

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
---------	--

classmethod validate (data: neuron_morphology.feature_extractor.data.Data) → bool

Determine if this feature is calculable from the provided data.

Parameters

data [Data from a single morphological reconstruction]

Returns

whether marked features can be calculated from these data

class neuron_morphology.feature_extractor.mark.RequiresSoma

Bases: neuron_morphology.feature_extractor.mark.Mark

Indicates that these features require a soma.

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
---------	--

classmethod validate (*data: neuron_morphology.feature_extractor.data.Data*) → bool
 Determine if this feature is calculable from the provided data.

Parameters

data [Data from a single morphological reconstruction]

Returns

whether marked features can be calculated from these data

class `neuron_morphology.feature_extractor.mark.TipFeatures`

Bases: `neuron_morphology.feature_extractor.mark.Mark`

Indicates a feature calculated on tips (leaf nodes).

Methods

<code>validate(data)</code>	Determine if this feature is calculable from the provided data.
-----------------------------	---

factory	
---------	--

<p><code>neuron_morphology.feature_extractor.mark.check_nodes_have_key</code> (<i>data:</i></p> <p>Checks whether each node in a morphology is annotated with some key.</p>	<p><i>neuron_morphology.feature_extractor.data.Data</i> <i>key: str</i>) → bool</p>
---	--

neuron_morphology.feature_extractor.marked_feature module

```
class neuron_morphology.feature_extractor.marked_feature.MarkedFeature (marks:
    Set[Type[neuron_morphology.feature_extractor.marked_feature.Mark],
    Union[Callable[[neuron_morphology.feature_extractor.marked_feature.Mark],
    Any],
    neuron_morphology.feature_extractor.marked_feature.Mark],
    name:
    Optional[str]
    =
    None,
    pre_serve_marks:
    bool
    =
    True)
```

Bases: object

Attributes

feature

marks

name

Methods

<code>__call__(self, *args, **kwargs)</code>	Execute the underlying feature, passing along all arguments
<code>add_mark(self, mark)</code>	Assign an additional mark to this feature
<code>deepcopy(self, **kwargs)</code>	Make a deep copy of this marked feature
<code>ensure(feature)</code>	If a function is not a MarkedFeature, convert it.
<code>partial(self, *args, **kwargs)</code>	Fix one or more parameters on this feature's callable
<code>specialize(self, option)</code>	Apply a specialization option to this feature.

add_mark (self, mark: Type[neuron_morphology.feature_extractor.mark.Mark])

Assign an additional mark to this feature

deepcopy (self, **kwargs)

Make a deep copy of this marked feature

classmethod ensure (feature: 'Feature') → ~M

If a function is not a MarkedFeature, convert it.

Parameters

feature [the feature to be converted]

Returns

Either a marked feature generated from the input, or the input marked feature.

feature

marks

name

partial (*self*, **args*, ***kwargs*)

Fix one or more parameters on this feature's callable

specialize (*self*, *option*: *Type*[*neuron_morphology.feature_extractor.feature_specialization.FeatureSpecialization*])

Apply a specialization option to this feature. This binds parameters on the feature's `__call__` method, sets 0 or more additional marks, and namespaces the feature's name.

Parameters

option [The specialization option with which to specialize this] feature.

Returns

a deep copy of this feature with updated callable, marks and name

`neuron_morphology.feature_extractor.marked_feature.marked` (*mark*:

Type[*neuron_morphology.feature_extractor.marked*])

Decorator for adding a mark to a function.

Parameters

mark [the mark to be applied]

Examples

```
@marked(RequiresA) @marked(RequiresB) def some_feature_requiring_a_and_b(...):
```

```
...
```

```
neuron_morphology.feature_extractor.marked_feature.nested_specialize (feature:
```

Union[*Callable*[[*neuron_morphology.feature_extractor.feature_extractor*],

Any],

neuron_morphology.feature_extractor.feature_extractor

specialization_sets:

List[*Set*[*Type*[*neuron_morphology.feature_extractor.feature_extractor*],

→

Dict[*str*,

neuron_morphology.feature_extractor.feature_extractor

→

Dict[*str*,

neuron_morphology.feature_extractor.feature_extractor

→

Apply specializations hierarchically to a base feature. Generating a new collection of specialized features.

Parameters

feature [will be used as a basis for specialization]

specialization_sets [each element describes a set of specialization] options. The output will have one specialization for each element of the cartesian product of these sets.

Returns

A dictionary mapping namespaced feature names to specialized features.

Notes

Specializations are applied from the start of the specialization_sets to the end. This means that the generated names are structures like:

“last_spec.middle_spec.first_spec.base_feature_name”

```
neuron_morphology.feature_extractor.marked_feature.specialize (feature:
                                                                Union[Callable[[neuron_morphology.feature_extractor.marked_feature.Any],
                                                                neuron_morphology.feature_extractor.marked_feature.SpecializationSet],
                                                                Set[Type[neuron_morphology.feature_extractor.marked_feature.SpecializationSet]]
                                                                → Dict[str, neuron_morphology.feature_extractor.marked_feature.SpecializationSet])
```

Bind some of a feature’s keyword arguments, using provided specialization options.

Parameters

feature [will be used as a basis for specialization]

specialization_set [each element defines a particular specialization (i.e) a set of keyword argument values and marks) to be applied to the feature

Returns

A dictionary mapping (namespaced) feature names to specialized features.

Note that names are formatted as “specialization_name.base_feature_name”

neuron_morphology.feature_extractor.run_feature_extraction module

```
neuron_morphology.feature_extractor.run_feature_extraction.hydrate_parameters (parameters:
                                                                                      Dict[str,
                                                                                      Any])
                                                                                      →
                                                                                      Dict[str,
                                                                                      Any]
```

Resolve argued feature parameters to a format comprehensible by the features. e.g. loading data from a path.

Parameters

parameters [to be hydrated]

Returns

The hydrated parameters

```
neuron_morphology.feature_extractor.run_feature_extraction.resolve_reference_layer_depths (names: List[str],
                                                                                          boundaries: List[Boundary])
                                                                                          →
                                                                                          ReferenceLayerDepths
```

Given either the name of a well known depths set or a set of names and corresponding boundaries, produce a ReferenceLayerDepths

Parameters

key [of a well known reference layer]

names [the names of each layer in a custom sequence]

boundaries [the upper and lower depths of each layer in a custom sequence]

Returns

the requested reference layer depths

`neuron_morphology.feature_extractor.run_feature_extraction.run_feature_extraction` (*reconstruction: Dict[str, Any], feature_set: str, only_marks: List[str], required_marks: List[str], global_parameter_spec: Dict[str, Any]*)
 → Tuple[str, Dict]

Run feature extraction for a single reconstruction.

Parameters

reconstruction_spec [a dictionary specifying a reconstruction. Must] have an `swc_path`.
feature_set [names the set of features for which calculation will be] attempted
only_marks [names marks to which calculation will be restricted]
required_marks [raise an exception if these named marks fail validation]
global_parameter_spec [a dictionary specifying cross-reconstruction] parameters

Returns

identifier [a label for this reconstruction]
A dict with keys: `results` - a dict, mapping features to calculated values `selected_marks` - the set of marks that passed validation `selected_features` - the set of features for which calculation was attempted

`neuron_morphology.feature_extractor.run_feature_extraction.setup_data` (*reconstruction: Dict[str, Any], global_parameters: Dict[str, Any]*)
 → Tuple[str, neuron_morphology.feature_extractor]

Construct a Data for extracting features from a single reconstruction.

Parameters

reconstruction [The reconstruction to be setup. Must specify an swc_path]

global_parameters [any cross-reconstruction feature parameters]

Returns

identifier [a label for this reconstruction]

data suitable for feature extraction

neuron_morphology.feature_extractor.utilities module

A collection of miscellaneous tools used by the feature extractor

`neuron_morphology.feature_extractor.utilities.unnest` (*inputs: Dict[str, Any], _prefix: str, _fix: str*) → Dict[str, Any]

Convert nested dictionaries (with string keys) to a dot-notation flat dictionary.

inputs: The dictionary to unnest. Must have all string keys *_prefix* : Used during recursion to build up a dot-notation prefix. Don't

argue this yourself!

Returns

a flattened dictionary

Module contents

neuron_morphology.features package

Subpackages

neuron_morphology.features.branching package

Submodules

neuron_morphology.features.branching.bifurcations module

`neuron_morphology.features.branching.bifurcations.calculate_outer_bifs` (*morphology: neuron_morphology.morphology.soma: Dict, node_types: Union[List[int], NoneType]*) → int

Counts the number of bifurcation points beyond the a sphere with 1/2 the radius from the soma to the most distant point in the morphology, with that sphere centered at the soma.

Parameters

morphology: Describes the structure of a neuron

soma: Must have keys “x”, “y”, and “z”, describing the position of this morphology’s soma in

node_types: Restrict included nodes to these types. See `neuron_morphology.constants` for available node types.

Returns

the number of bifurcations

Module contents

neuron_morphology.features.layer package

Submodules

neuron_morphology.features.layer.layer_histogram module

class `neuron_morphology.features.layer.layer_histogram.EarthMoversDistanceInterpretation`

Bases: `enum.Enum`

Describes how to understand an earth mover’s distance result. This is useful in the case that one or both histograms are all 0.

BothEmpty = 2

BothPresent = 0

OneEmpty = 1

class `neuron_morphology.features.layer.layer_histogram.EarthMoversDistanceResult`

Bases: `tuple`

The result of comparing two histograms using earth mover’s distance

Attributes

interpretation Alias for field number 1

result Alias for field number 0

Methods

<code>count(self, value, /)</code>	Return number of occurrences of value.
------------------------------------	--

<code>index(self, value[, start, stop])</code>	Return first index of value.
--	------------------------------

<code>to_dict_human_readable</code>	
-------------------------------------	--

interpretation

Alias for field number 1

result

Alias for field number 0

to_dict_human_readable (*self*)

class neuron_morphology.features.layer.layer_histogram.**LayerHistogram**

Bases: tuple

The results of calculating a within-layer depth histogram of points within some cortical layer.

Attributes

bin_edges Alias for field number 1

counts Alias for field number 0

Methods

<code>count(self, value, /)</code>	Return number of occurrences of value.
------------------------------------	--

<code>index(self, value[, start, stop])</code>	Return first index of value.
--	------------------------------

bin_edges

Alias for field number 1

counts

Alias for field number 0

neuron_morphology.features.layer.layer_histogram.**ensure_layers** (*layers*)

Make sure the argued layer array is a tuple

neuron_morphology.features.layer.layer_histogram.**ensure_node_types** (*node_types*)

Make sure the argued node types are a tuple

neuron_morphology.features.layer.layer_histogram.**ensure_tuple** (*inputs:* Any,
item_type: Type, *if_none:* Union[str, Tuple]
= 'raise') → Tuple

Try to smartly coerce inputs to a tuple.

Parameters

inputs [the data to be coerced]

item_type [which type do/should the elements of the tuple have?]

if_none [if the inputs are none, return this value. If the value is] “raise”, instead raise an exception

Returns

the coerced inputs

neuron_morphology.features.layer.layer_histogram.**histogram_earth_movers_distance** (*from_hist:* numpy.ndarray,
to_hist: numpy.ndarray
→ neu-
morphology

Calculate the earth mover’s distance between to histograms, normalizing each. If one histogram is empty, return the sum of the other and a flag. If both are empty, return 0 a and a flag.

Parameters

from_hist [distance is calculated between (the normalized form of) this] histogram and to_hist. The result is symmetric.

to_hist [distance is calculated between (the normalized form of) this] histogram and from_hist

Returns

The distance between input histograms, along with an enum indicating whether one or both of the histograms was all 0.

`neuron_morphology.features.layer.layer_histogram.normalized_depth_histogram_within_layer` (pa

Calculates a histogram of node depths within a single (cortical) layer. Uses reference information about layer boundaries to normalize these depths for cross-reconstruction comparison.

Parameters

depths [Each item corresponds to a point of interest (such as a node) in a morphological reconstruction). Values are the depths of these points of interest from the pia surface.

local_layer_pia_side_depths [Each item corresponds to a point of interest.] Values are the depth of the intersection point between a path of steepest descent from the pia surface to the point of interest and the upper surface of the layer.

local_layer_wm_side_depths [Each item corresponds to a point of interest.] Values are the depth of the intersection point between the layer's lower boundary and the path described above.

reference_layer_depths [Used to provide normalized depths suitable] for comparison across reconstructions. Should provide a generic equivalent of local layer depths for a population or reference space.

bin_size [The width of each bin, in terms of depths from pia in the] reference space. Provide only one of bin_edges or bin_size.

Returns

A numpy array listing for each depth bin the number of nodes falling within that bin.

Notes

This function relies on the notion of a steepest descent path through cortex, but is agnostic to the method used to obtain such a path and to features of the path (e.g. whether it is allowed to curve). Rather the caller must ensure that all depths have been calculated according to a consistent scheme.

```
neuron_morphology.features.layer.layer_histogram.normalized_depth_histograms_across_layers
```

A helper function for running cortical depth histograms across multiple layers.

Parameters

data [must have reference_layer_depths and layered_point_depths]

point_types [calculate histograms for points labeled with these types]

only_layers [exclude other layers from this calculation]

bin_size [the size of each depth bin. Default is appropriate if the units] are microns.

neuron_morphology.features.layer.layered_point_depths module

```
class neuron_morphology.features.layer.layered_point_depths.LayeredPointDepths (ids:
    Sequence[T_co],
    layer_name:
    Sequence[str],
    depth:
    Sequence[T_co],
    lo-
    cal_layer_pia_si-
    Sequence[T_co],
    lo-
    cal_layer_wm_si-
    Sequence[T_co],
    point_type:
    Sequence[T_co])
```

Bases: object

Methods

from_csv	
from_dataframe	
from_hdf5	
read	
to_csv	

```
DF_COLS = {'depth', 'ids', 'layer_name', 'local_layer_pia_side_depth', 'local_layer_wm'
```

```
classmethod from_csv(path: str)
```

```
classmethod from_dataframe(df: pandas.core.frame.DataFrame)
```

```
classmethod from_hdf5(path: str)
```

```
classmethod read(path: str)
```

```
to_csv(self, path: str)
```

neuron_morphology.features.layer.reference_layer_depths module

```
class neuron_morphology.features.layer.reference_layer_depths.ReferenceLayerDepths
```

Bases: tuple

Reference (e.g. average across specimens and regions) depths of cortical layer boundaries. Depths are given from pia. Units are not specified, but the user should ensure they are consistent with other positional and size units (e.g. node positions and radii, point depths). Several features in this package specify defaults in microns; if you provide reference layer depths in other units, you should review features which use these depths and ensure that any default values agree with your units.

Attributes

pia_side [the (average) depth of the upper surface of the layer]

wm_side [the (average) depth of the lower (closer to white matter) surface] of the layer

scale [if True, these depths are taken as describing the upper and lower] surfaces of a real feature of the data. If False, one or both of them is taken to represent a user-selected boundary. In the latter case, features such as the layer histograms will not attempt to rescale point depths based on observed local layer thicknesses.

Methods

<code>count(self, value, /)</code>	Return number of occurrences of value.
<code>index(self, value[, start, stop])</code>	Return first index of value.
<code>sequential(names, boundaries[, last_is_scale])</code>	A utility for constructing multiple ordered reference layer depths without intervening space.

pia_side

Alias for field number 0

scale

Alias for field number 2

classmethod sequential (*names:* *Sequence[str]*, *boundaries:* *Sequence[float]*,
last_is_scale=False)

A utility for constructing multiple ordered reference layer depths without intervening space.

Parameters

names [The name of each layer]

boundaries [The pia and wm side depth of each layer. Should be a flat] sequence that has 1 more element than names.

last_is_scale [If True, the last boundary will be interpreted as a] true anatomical boundary. If false, as an arbitrary cutoff.

thickness

wm_side

Alias for field number 1

Module contents

neuron_morphology.features.statistics package

Submodules

neuron_morphology.features.statistics.coordinates module

class neuron_morphology.features.statistics.coordinates.**BifurcationSpec**
 Bases: *neuron_morphology.feature_extractor.feature_specialization.FeatureSpecialization*

Methods

<code>factory(name, marks, kwargs, Any], ...)</code>	A utility for quickly generating feature specializations
--	--

```
kwargs = {'coord_type': <COORD_TYPE.BIFURCATION: 2>}
```

```
marks = {<class 'neuron_morphology.feature_extractor.mark.BifurcationFeatures'>}
```

```
name = 'bifurcation'
```

class neuron_morphology.features.statistics.coordinates.**COORD_TYPE**

Bases: *enum.Enum*

An enumeration.

```
BIFURCATION = 2
```

```
COMPARTMENT = 1
```

```
NODE = 0
```

```
TIP = 3
```

```
get_coordinates(self, morphology, node_types: Union[List[int], NoneType] = None)
```

```
class neuron_morphology.features.statistics.coordinates.CompartmentSpec
    Bases:          neuron_morphology.feature_extractor.feature_specialization.
                    FeatureSpecialization
```

Methods

factory(name, marks, kwargs, Any], ...)	A utility for quickly generating feature specializa- tions
---	---

```
kwargs = {'coord_type':  <COORD_TYPE.COMPARTMENT: 1>}
marks = {<class 'neuron_morphology.feature_extractor.mark.CompartmentFeatures'>}
name = 'compartment'
```

```
class neuron_morphology.features.statistics.coordinates.NodeSpec
    Bases:          neuron_morphology.feature_extractor.feature_specialization.
                    FeatureSpecialization
```

Methods

factory(name, marks, kwargs, Any], ...)	A utility for quickly generating feature specializa- tions
---	---

```
kwargs = {'coord_type':  <COORD_TYPE.NODE: 0>}
marks = {}
name = 'node'
```

```
class neuron_morphology.features.statistics.coordinates.TipSpec
    Bases:          neuron_morphology.feature_extractor.feature_specialization.
                    FeatureSpecialization
```

Methods

factory(name, marks, kwargs, Any], ...)	A utility for quickly generating feature specializa- tions
---	---

```
kwargs = {'coord_type':  <COORD_TYPE.TIP: 3>}
marks = {<class 'neuron_morphology.feature_extractor.mark.TipFeatures'>}
name = 'tip'
```

neuron_morphology.features.statistics.moments module

neuron_morphology.features.statistics.overlap module

```
neuron_morphology.features.statistics.overlap.calculate_coordinate_overlap(coordinates_a,
                                                                           co-
                                                                           or-
                                                                           di-
                                                                           nates_b,
                                                                           di-
                                                                           men-
                                                                           sion:
                                                                           int
                                                                           =
                                                                           1)
```

Return the % of coordinates_a that are above, overlapping, and below coordinates_b, and the same for b over a

Parameters

coordinates_a: 2d array-like with x, y, z cols

coordinates_b: 2d array-like with x, y, z cols

dimension: dimension to compare (0, 1, 2 for x, y, z), default 1 (y)

Returns

dict: a_above_b, a_overlap_b, a_below_b, or -1's if coordinates_b is empty

```
neuron_morphology.features.statistics.overlap.calculate_coordinate_overlap_from_min_max(coordinates_a,
                                                                                       minv,
                                                                                       maxv,
                                                                                       dimension)
num
min
float
max
float
di-
men
sion
int
=
1)
```

Return the % of coordinates that are above the max, between, or below the min

Parameters

coordinates: np.ndarray with x, y, z columns

minv: min to check against

maxv: max to check against

dimension: dimension to compare (0, 1, 2 for x, y, z), default 1 (y)

Module contents**Submodules**

neuron_morphology.features.default_features module

neuron_morphology.features.dimension module

neuron_morphology.features.intrinsic module

```
neuron_morphology.features.intrinsic.calculate_branches_from_root (morphology,  
                                                                    root,  
                                                                    node_types=None)
```

Calculate the number of branches of a specific neuron type in a morphology. A branch is defined as being between two bifurcations or between a bifurcation and a tip if a node has three or more children, it is treated as successive bifurcations, e.g a trifurcation: `/_/_` creates 4 branches since the branch between the two bifurcations counts

Parameters

morphology: a morphology object

root: the root node to traverse from

node_types: a list of node types (see neuron_morphology constants)

```
neuron_morphology.features.intrinsic.calculate_max_branch_order_from_root (morphology,  
                                                                              root,  
                                                                              node_types=None)
```

Calculate the maximum number of branches from a root to a tip in a morphology. A branch is defined as being between two bifurcations or between a bifurcation and a tip Unlike mean_fragmentation and num_branches, if a node has multiple children it is counted as a single bifurcation point

Parameters

morphology: a morphology object

root: the root node to traverse from

node_types: a list of node types (see neuron_morphology constants)

```
neuron_morphology.features.intrinsic.calculate_mean_fragmentation_from_root (morphology,  
                                                                               root,  
                                                                               node_types=None)
```

Calculate the mean fragmentation from a root in a morphology. Mean fragmentation is the number of compartments over the number of branches. A branch is defined as being between two bifurcations or between a bifurcation and a tip if a node has three or more children, it is treated as successive bifurcations, e.g a trifurcation: `/_/_` creates 4 branches since the branch between the two bifurcations counts

Parameters

morphology: a morphology object

root: the root node to traverse from

node_types: a list of node types (see neuron_morphology constants)

```
neuron_morphology.features.intrinsic.child_ids_by_type (node_id,      morphology,  
                                                         node_types=None)
```

Helper function for the traversal functions

neuron_morphology.features.path module

```
neuron_morphology.features.path.calculate_max_path_distance (morphology,  
                                                             root=None,  
                                                             node_types=None)
```

Helper for max_path_distance. See below for more information.

```
neuron_morphology.features.path.calculate_mean_contraction(morphology,  
                                                         root=None,  
                                                         node_types=None)
```

See `mean_contraction`

neuron_morphology.features.size module

```
neuron_morphology.features.size.parent_daughter_ratio_visitor(node:    Dict[str,  
                                                                Any],        mor-  
                                                                phology:    neu-  
                                                                ron_morphology.morphology.Morphology,  
                                                                counters:  
                                                                Dict[str,  
                                                                Union[int, float]],  
                                                                node_types:  
                                                                Union[List[int],  
                                                                NoneType]      =  
                                                                None)
```

Calculates for a single node the ratio of the node's parent's radius to the node's radius. Stores these values in a provided dictionary.

Parameters

node [The node under consideration]

morphology [The reconstruction to which this node belongs]

counters [a dictionary used for storing running ratio totals and counts.]

node_types [skip nodes not of one of these types]

Notes

see `mean_parent_daughter_ratio` for usage

neuron_morphology.features.soma module

Module contents

neuron_morphology.layered_point_depths package

Module contents

neuron_morphology.pipeline package

Submodules

neuron_morphology.pipeline.post_data_to_s3 module

Module contents

neuron_morphology.snap_polygons package

Submodules

neuron_morphology.snap_polygons.bounding_box module

class neuron_morphology.snap_polygons.bounding_box.**BoundingBox** (*horigin: float,*
vorigin: float,
hextent: float,
vextent: float)

Bases: object

Attributes

aspect_ratio
coordinates
extent
height
hextent
horigin
origin
vextent
vorigin
width

Methods

<i>copy</i> (self)	Duplicates this bounding box
<i>round</i> (self, inplace, origin_via, ...)	Round the coordinates of this box
<i>transform</i> (self, transform, float[, ...])	Apply a transform to this box
<i>update</i> (self, horigin, vorigin, hextent, vextent)	Potentially enlarges this box.

aspect_ratio

coordinates

copy (*self*) → 'BoundingBox'
Duplicates this bounding box

Returns

A copy of this object.

extent

height

hextent

horigin

origin

round (*self*, *inplace: bool = False*, *origin_via: Callable[[float], float] = <function around at 0x7f5b72f38c10>*, *extent_via: Callable[[float], float] = <function around at 0x7f5b72f38c10>*)

Round the coordinates of this box

Parameters

inplace [If True, round the coordinates of this object]

origin_via [method to use when rounding the origin]

extent_via [method to use when rounding the extent]

Returns

The rounded box (potentially self).

transform (*self*, *transform*: Callable[[float, float], Tuple[float, float]], *inplace*: bool = False) → 'BoundingBox'

Apply a transform to this box

Parameters

transform [A callable which maps (vertical, horizontal) coordinates to] new (vertical, horizontal) coordinates.

inplace [if True, apply the transform to this object]

Returns

The transformed box (potentially self)

update (*self*, *horigin*: float, *vorigin*: float, *hextent*: float, *vextent*: float)

Potentially enlarges this box.

Parameters

As to the constructor of BoundingBox. The new shape of this box is the smallest box enclosing both this and the inputs.

vextent

vorigin

width

neuron_morphology.snap_polygons.geometries module

class neuron_morphology.snap_polygons.geometries.Geometries

Bases: object

Attributes

close_bounds

Methods

<i>rasterize</i> (<i>self</i> , <i>box</i> , NoneType] = None, ...)	Rasterize one or more owned geometries.
--	---

<i>register_polygon</i> (<i>self</i> , <i>name</i> , <i>path</i> , ...)	Adds a named polygon path to this object.
--	---

<i>register_polygons</i> (<i>self</i> , <i>polygons</i> , Union[str, ...])	utility for registering multiple polygons.
---	--

<i>register_surface</i> (<i>self</i> , <i>name</i> , <i>path</i> , ...)	Adds a line (e.g.
--	-------------------

Continued on next page

Table 43 – continued from previous page

<code>register_surfaces(self, surfaces, Union[str, ...])</code>	utility for registering multiple surfaces.
<code>to_json(self)</code>	Write contained polygons to a json-serializable format
<code>transform(self, transform, float[, ...])</code>	Apply a transform to each owned geometry.

close_bounds

rasterize (*self*, *box*: *Union[neuron_morphology.snap_polygons.bounding_box.BoundingBox, NoneType]* = *None*, *polygons*: *Union[Sequence[str], bool]* = *True*, *surfaces*: *Union[Sequence[str], bool]* = *False*) → *Dict[str, numpy.ndarray]*
 Rasterize one or more owned geometries. Produce a mapping from object names to masks.

Parameters

shape [if provided, the output image shape. Otherwise, use the rounded close bounding box shape]

polygons [a list of names. Alternatively all (True) or none (False)]

lines [a list of names. Alternatively all (True) or none (False)]

Notes

uses rasterio.features.rasterize

register_polygon (*self*, *name*: *str*, *path*: *Union[str, Sequence[Sequence[float]], shapely.geometry.polygon.Polygon, shapely.geometry.polygon.LinearRing]*)
 Adds a named polygon path to this object. Updates the close bounding box.

Parameters

name [identifier for this polygon]

path [defines the exterior of this (simple) polygon]

register_polygons (*self*, *polygons*: *Union[Dict[str, Union[str, Sequence[Sequence[float]], shapely.geometry.polygon.Polygon, shapely.geometry.polygon.LinearRing]], Sequence[Dict[str, Union[str, Sequence[Sequence[float]], shapely.geometry.polygon.Polygon, shapely.geometry.polygon.LinearRing]]]]*)
 utility for registering multiple polygons. See register_polygon

register_surface (*self*, *name*: *str*, *path*: *Union[str, Sequence[Sequence[float]], shapely.geometry.linestring.LineString]*)
 Adds a line (e.g. the pia/wm surfaces) to this object. Updates the bounding box.

Parameters

name [identifier for this surface]

path [defines the surface]

register_surfaces (*self*, *surfaces*: *Dict[str, Union[str, Sequence[Sequence[float]], shapely.geometry.linestring.LineString]]*)
 utility for registering multiple surfaces. See register_surface

to_json (*self*) → *Dict*
 Write contained polygons to a json-serializable format

transform (*self*, *transform*: Callable[[float, float], Tuple[float, float]]) → 'Geometries'

Apply a transform to each owned geometry. Return a new collection.

Parameters

transform [A callable which maps (vertical, horizontal) coordinates to] new (vertical, horizontal) coordinates.

`neuron_morphology.snap_polygons.geometries.clear_overlaps` (*stack*: Dict[str, numpy.ndarray])

Given a stack of masks, remove all inter-mask overlaps inplace

Parameters

stack [Keys are names, values are masks (of the same shape). 0 indicates] absence

`neuron_morphology.snap_polygons.geometries.closest_from_stack` (*stack*: Dict[str, numpy.ndarray])

Given a stack of images describing distance from several objects, find the closest object to each pixel.

Parameters

stack [Keys are names, values are ndarrays (of the same shape). Each pixel] in the values describes the distance from that pixel to the named object

Returns

closest [An integer array whose values are the closest object to each] pixel

names [A mapping from the integer codes in the “closest” array to names]

`neuron_morphology.snap_polygons.geometries.find_vertical_surfaces` (*polygons*: Dict[str, shapely.geometry.polygon.Polygon], *order*: Sequence[str], *pia*: Union[shapely.geometry.linestring.LineString, NoneType], *wm*: Union[shapely.geometry.linestring.LineString, NoneType]) = None

Given a set of polygons describing cortical layer boundaries, find the boundaries between each layer.

Parameters

polygons [named layer polygons]

order [A sequence of names defining the order of the layer polygons from] pia to white matter

pia [The upper pia surface.]

wm [The lower white matter surface.]

Returns

dictionary whose keys are as “{name}_{side}” and whose values are linestrings describing these boundaries.

```
neuron_morphology.snap_polygons.geometries.get_snapped_polys(closest:  
                                                             numpy.ndarray,  
                                                             name_lut: Dict[int,  
                                                             str]) → Dict[str,  
                                                             shapely.geometry.polygon.Polygon]
```

Obtains named shapes from a label image.

Parameters

closest [label integer with integer codes]

name_lut [look up table from integer codes to string names]

Returns

mapping from names to polygons describing each labelled region

```
neuron_morphology.snap_polygons.geometries.make_scale(scale: float = 1.0) →  
                                                         Callable[[float, float], Tu-  
                                                         ple[float, float]]
```

A utility for making a 2D scale transform, suitable for transforming bounding boxes and Geometries

Parameters

scale [isometric scale factor]

Returns

A transform function

```
neuron_morphology.snap_polygons.geometries.rasterize(geometry:  
                                                         shapely.geometry.base.BaseGeometry,  
                                                         box: neuron_morphology.snap_polygons.bounding_box.Boundin  
                                                         → <built-in function array>
```

Rasterize a shapely object to a grid defined by a provided bounding box.

Parameters

geometry [to be rasterized]

box [defines the window (in the same coordinate space as the geometry)] into which the geometry will be rasterized

Returns

A mask, where 1 indicates presence and 0 absence

neuron_morphology.snap_polygons.image_outputter module

```

class neuron_morphology.snap_polygons.image_outputter.ImageOutputter (native_geo:
    neu-
    ron_morphology.snap_polygons
    re-
    sult_geo:
    neu-
    ron_morphology.snap_polygons
    im-
    age_specs:
    Op-
    tional[Sequence[Dict[KT,
    VT]]],
    alpha:
    float
    = 0.4,
    color_cycle:
    Op-
    tional[Sequence[T_co]]
    =
    None,
    save-
    fig_kwargs:
    Op-
    tional[Dict[KT,
    VT]] =
    None)

```

Bases: object

Methods

<code>draw_after(self, image, scale)</code>	Display the post-fill polygons and surfaces overlaid on an image.
<code>draw_before(self, image, scale)</code>	Display the pre-fill polygons and surfaces overlaid on an image.
<code>write_images(self)</code>	For each image specified in this outputter and each overlay type requested for that image, produce and save an overlay.

```
DEFAULT_COLOR_CYCLE = ('c', 'm', 'y', 'k', 'r', 'g', 'b')
```

```
OVERLAY_TYPES = {'after': 'draw_after', 'before': 'draw_before'}
```

```
draw_after (self, image: numpy.ndarray, scale: float = 1.0)
```

Display the post-fill polygons and surfaces overlaid on an image.

Parameters

image [onto which objects will be drawn]

scale [required to transform from object space to image space]

Returns

A matplotlib figure containing the overlay

draw_before (*self*, *image*: *numpy.ndarray*, *scale*: *float = 1.0*)

Display the pre-fill polygons and surfaces overlaid on an image.

Parameters

image [onto which objects will be drawn]

scale [required to transform from object space to image space]

Returns

A matplotlib figure containing the overlay

write_images (*self*)

For each image specified in this outputter and each overlay type requested for that image, produce and save an overlay.

`neuron_morphology.snap_polygons.image_outputter.fname_suffix` (*path*: *str*, *suffix*: *str*)

Utility for adding a suffix to a path string. The suffix will be inserted before the extension.

`neuron_morphology.snap_polygons.image_outputter.make_pathpatch` (*vertices*: *Sequence[Tuple[float, float]]*, ***patch_kwargs*)
 → *matplotlib.patches.PathPatch*

Utility for building a matplotlib pathpatch from an array of vertices

Parameters

vertices [Defines the path. May be closed or open]

****patch_kwargs** [passed directly to pathpatch constructor]

`neuron_morphology.snap_polygons.image_outputter.read_image` (*path*: *str*, *decimate*: *int = 1*)

Read an image. Dispatch to an appropriate library based on that image's extension.

Parameters

path [to the image]

decimate [apply a decimation of this factor along each axis of the image]

`neuron_morphology.snap_polygons.image_outputter.read_jp2` (*path*: *str*, *decimate*: *int*)

`neuron_morphology.snap_polygons.image_outputter.read_with_ndimage` (*path*: *str*, *decimate*: *int*)

`neuron_morphology.snap_polygons.image_outputter.write_figure` (*fig*: *matplotlib.figure.Figure*, **args*, ***kwargs*)

Write a matplotlib figure without respect to the current figure.

Parameters

fig [the figure to be written]

***args, **kwargs** [passed to plt.savefig]

neuron_morphology.snap_polygons.postgres_source module

class neuron_morphology.snap_polygons.postgres_source.**PostgresInputConfigSchema** (*only=None, exclude=(), many=False, context=None, load_only=(), dump_only=(), partial=False, unknown=None*)

Bases: `marshmallow.schema.Schema`

Attributes

dict_class

set_class

Methods

Meta	Options object for a Schema.
OPTIONS_CLASS	alias of <code>marshmallow.schema.SchemaOpts</code>
<code>dump(self, obj[, many])</code>	Serialize an object to native Python data types according to this Schema's fields.
<code>dumps(self, obj[, many])</code>	Same as <code>dump()</code> , except return a JSON-encoded string.
<code>get_attribute(self, obj, attr, default)</code>	Defines how to pull values from an object to serialize.
<code>handle_error(self, error, data)</code>	Custom error handler function for the schema.
<code>load(self, data[, many, partial, unknown])</code>	Deserialize a data structure to an object defined by this Schema's fields.
<code>loads(self, json_data[, many, partial, unknown])</code>	Same as <code>load()</code> , except it takes a JSON string as input.
<code>on_bind_field(self, field_name, field_obj)</code>	Hook to modify a field when it is bound to the <i>Schema</i> .
<code>validate(self, data[, many, partial])</code>	Validate <i>data</i> against the schema, returning a dictionary of validation errors.

opts = `<marshmallow.schema.SchemaOpts object>`

neuron_morphology.snap_polygons.types module

neuron_morphology.snap_polygons.types.**ensure_linestring** (*candidate: Union[str, Sequence[Sequence[float]], shapely.geometry.linestring.LineString]*)
 →
 shapely.geometry.linestring.LineString

Convert from one of many line representations to LineString

```
neuron_morphology.snap_polygons.types.ensure_path(candidate: Union[str, Sequence[Sequence[float]]],
                                                    num_dims: int = 2) → Sequence[Sequence[float]]
```

Ensure that an input path, which might be a “x,y,x,y” string, is represented as a list of lists instead.

Parameters

candidate [input coordinate sequence]

num_dims [how manu elements define a coordinate]

Returns

Contents of inputs, with each coordinate a list of float

```
neuron_morphology.snap_polygons.types.ensure_polygon(candidate: Union[str, Sequence[Sequence[float]],
                                                         shapely.geometry.polygon.Polygon,
                                                         shapely.geometry.polygon.LinearRing])
                                                    →
                                                    shapely.geometry.polygon.Polygon
```

Convert from one of many polygon representations to Polygon

```
neuron_morphology.snap_polygons.types.split_pathstring(pathstring: str, num_dims:
                                                         int = 2, sep: str = ', ') →
                                                         Sequence[Sequence[float]]
```

Converts a pathstring (“x,y,x,y...”) to a num_points X num_dims list of lists of float

Parameters

pathstring [input coordinate sequence]

num_dims [how manu elements define a coordinate]

sep [character separating elements]

Returns

Contents of pathstring, with each coordinate a list of float

Module contents

[neuron_morphology.transforms package](#)

[Subpackages](#)

[neuron_morphology.transforms.affine_transformer package](#)

[Submodules](#)

[neuron_morphology.transforms.affine_transformer.apply_affine_transform module](#)

```
neuron_morphology.transforms.affine_transformer.apply_affine_transform.main()
```


Module contents

neuron_morphology.transforms.pia_wm_streamlines package

Submodules

neuron_morphology.transforms.pia_wm_streamlines.calculate_pia_wm_streamlines module

Module contents

neuron_morphology.transforms.upright_angle package

Submodules

neuron_morphology.transforms.upright_angle.compute_angle module

Module contents

Submodules

neuron_morphology.transforms.affine_transform module

```
class neuron_morphology.transforms.affine_transform.AffineTransform(affine:
                                                                    Op-
                                                                    tional[Any]
                                                                    = None)
```

Bases: *neuron_morphology.transforms.transform_base.TransformBase*

Handles transformations to a pia/wm aligned coordinate frame.

Methods

<i>from_dict</i> (affine_dict, float))	Create an AffineTransform from a dict with keys and values.
<i>from_list</i> (affine_list)	Create an Affine Transform from a list
<i>to_dict</i> (self)	Create dictionary defining the transformation.
<i>to_list</i> (self)	Create a list defining the transformation.
<i>transform</i> (self, vector)	Apply this transform to (3,) point or (n,3) array-like of points.
<i>transform_morphology</i> (self, morphology, clone)	Apply this transform to all nodes in a morphology.

classmethod **from_dict** (*affine_dict: Dict[str, float]*)

Create an AffineTransform from a dict with keys and values.

Parameters

affine_dict: keys and values corresponding to the following

```
[[tvr_00 tvr_01 tvr_02 tvr_09] [tvr_03 tvr_04 tvr_05 tvr_10] [tvr_06 tvr_07 tvr_08
tvr_11] [0 0 0 1]]
```

Returns**AffineTransform object****classmethod** **from_list** (*affine_list: List[float]*)

Create an Affine Transform from a list

Parameters**affine_list:** list of tvr values corresponding to:

```
[[tvr_00 tvr_01 tvr_02 tvr_09] [tvr_03 tvr_04 tvr_05 tvr_10] [tvr_06 tvr_07 tvr_08
tvr_11] [0 0 0 1]]
```

Returns**AffineTransform object****to_dict** (*self*) → Dict

Create dictionary defining the transformation.

Returns**Dict with keys and values corresponding to the following:**

```
[[tvr_00 tvr_01 tvr_02 tvr_09] [tvr_03 tvr_04 tvr_05 tvr_10] [tvr_06 tvr_07 tvr_08
tvr_11] [0 0 0 1]]
```

to_list (*self*) → List

Create a list defining the transformation.

Returns**List with values corresponding to the following:**

```
[[tvr_00 tvr_01 tvr_02 tvr_09] [tvr_03 tvr_04 tvr_05 tvr_10] [tvr_06 tvr_07 tvr_08
tvr_11] [0 0 0 1]]
```

transform (*self, vector: Any*) → numpy.ndarray

Apply this transform to (3,) point or (n,3) array-like of points.

Parameters**vector:** a (3,) array-like point or a (n,3) array-like array of points to be transformed**Returns****numpy.ndarray with same shape as input****transform_morphology** (*self, morphology: neuron_morphology.morphology.Morphology, clone: bool = False*) → neuron_morphology.morphology.Morphology

Apply this transform to all nodes in a morphology.

Parameters**morphology:** a Morphology loaded from an swc file**Returns****A Morphology****neuron_morphology.transforms.affine_transform.affine_from_transform** (*transform: Any*)

Create affine transformation.

Parameters**transformation:** (3, 3) row major array-like transformation

Returns**(4, 4) numpy.ndarray affine matrix**

neuron_morphology.transforms.affine_transform.**affine_from_transform_translation**(*transform:*
*Union[Any, None-
Type]*
 =
*None, trans-
la-
tion:*
*Union[Any, None-
Type]*
 =
*None, trans-
late_first:*
bool
 =
False)

Create affine from linear transformation and translation.

Affine transformation of vector $x \rightarrow Ax + b$ in 3D: [A, b
 0, 0, 0, 1]

A is a 3x3 linear transformation b is a 3x1 translation

Parameters**transform:** linear transformation (3, 3) array-like**translation:** linear translation (3,) array-like**translate_first:** apply the translation before the transform**Returns****(4, 4) numpy.ndarray affine matrix**

neuron_morphology.transforms.affine_transform.**affine_from_translation**(*translation:*
Any)

Create an affine translation.

Parameters**translation:** array-like vector of x, y, and z translations**Returns****(4, 4) numpy.ndarray affine matrix**

neuron_morphology.transforms.affine_transform.**rotation_from_angle**(*angle: float,*
axis: int =
2)

Create an affine matrix from a rotation about a specific axis.

Parameters**angle:** rotation angle in radians**axis:** axis to rotate about, 0=x, 1=y, 2=z (default z axis)

Returns

(3, 3) numpy.ndarray rotation matrix

neuron_morphology.transforms.geometry module

Some handy utilities for working with vector geometries

`neuron_morphology.transforms.geometry.get_ccw_vertices(vertices: List[Tuple])`

Generates counter clockwise vertices from vertices describing a simple polygon

Method: Simplification of the shoelace formula, which calculates area of a simple polygon by integrating the area under each line segment of the polygon. If the total area is positive, the vertices were traversed in clockwise order, and if it is negative, they were traversed in counterclockwise order.

Parameters

vertices: vertices describing a convex polygon (vertices[0] = vertices[-1])

Returns

vertices in counter clockwise order

`neuron_morphology.transforms.geometry.get_ccw_vertices_from_two_lines(line1: List[Tuple], line2: List[Tuple])`

Convenience method two do both `get_vertices_from_two_lines()` and `get_ccw_vertices()`

`neuron_morphology.transforms.geometry.get_vertices_from_two_lines(line1: List[Tuple], line2: List[Tuple])`

Generates circular vertices from two lines

Parameters

line1, line2: List of coordinates describing two lines

Returns

vertices of the simple polygon created from line 1 and 2

(first vertex = last vertex)

1-2-3-4

5-6-7-8 -> [1-2-3-4-8-7-6-5-1]

neuron_morphology.transforms.streamline module**neuron_morphology.transforms.transform_base module**

class `neuron_morphology.transforms.transform_base.TransformBase`

Bases: `abc.ABC`

Abstract base class for implementing swc transforms. Each child class should implement these methods.

Methods

<code>transform(self)</code>	Apply this transform to (3,) point or (3,n) array-like of points.
<code>transform_morphology(self)</code>	Apply this transform to all nodes in a morphology.

transform(*self*)

Apply this transform to (3,) point or (3,n) array-like of points.

Returns

numpy.ndarray with same shape as input

transform_morphology(*self*) → neuron_morphology.morphology.Morphology

Apply this transform to all nodes in a morphology.

Returns

A Morphology

Module contents

neuron_morphology.validation package

Submodules

neuron_morphology.validation.bits_validation module

neuron_morphology.validation.bits_validation.**validate**(*morphology*)

neuron_morphology.validation.bits_validation.**validate_independent_axon_has_more_than_four_r**

This function checks if an independent (parent is -1) axon has more than three nodes

neuron_morphology.validation.bits_validation.**validate_types_three_four_traceable_back_to_s**

This function checks if types 3,4 are traceable back to soma

neuron_morphology.validation.marker_validation module

neuron_morphology.validation.marker_validation.**validate**(*marker_file*, *morphology*)

neuron_morphology.validation.marker_validation.**validate_coordinates_corresponding_to_axon_t**

This function checks whether the coordinates for each axon marker corresponds to a tip of a axon type in the related morphology

neuron_morphology.validation.marker_validation.**validate_coordinates_corresponding_to_dendr**

This function checks whether the coordinates for each dendrite marker corresponds to a tip of a dendrite type in the related morphology

`neuron_morphology.validation.marker_validation.validate_expected_name(marker_file)`

This function checks whether the markers have the expected types

`neuron_morphology.validation.marker_validation.validate_no_reconstruction_count(marker_file)`

This function checks whether there is exactly one type 20 in the file

`neuron_morphology.validation.marker_validation.validate_type_thirty_count(marker_file)`

This function checks whether there is exactly one type 30 in the file

neuron_morphology.validation.morphology_statistics module

`neuron_morphology.validation.morphology_statistics.count_number_of_independent_axons(morphology)`

This functions counts the number of independent axons (parent is -1)

`neuron_morphology.validation.morphology_statistics.morphology_statistics(morphology)`

neuron_morphology.validation.radius_validation module

`neuron_morphology.validation.radius_validation.slope_linear_regression_branch_order_avg_radius(morphology)`

Use linear regression to find the slope of the best fit line

`neuron_morphology.validation.radius_validation.validate(morphology)`

`neuron_morphology.validation.radius_validation.validate_constrictions(morphology)`

This function checks if the radius of basal dendrite and apical dendrite nodes is smaller 2.0px

`neuron_morphology.validation.radius_validation.validate_extreme_taper(morphology)`

This function checks whether there is an extreme taper. Extreme taper occurs when for each segment, the average radius of the first two nodes is more than two times the average radius of the last two nodes.

Note: This tests is limited to segments of at lease 8 nodes.

`neuron_morphology.validation.radius_validation.validate_radius_has_negative_slope_dendrite(morphology)`

This function checks whether the radius for dendrite nodes decreases when you are going away from the soma.

`neuron_morphology.validation.radius_validation.validate_radius_threshold(morphology)`

This function validates the radius for types 1, 3, and 4

neuron_morphology.validation.report module

class `neuron_morphology.validation.report.Report`

Bases: `object`

Methods

<code>add_swc_stats(self, swc_file, stats)</code>	This function creates a report for swc statistics
---	---

add_marker_results	
add_swc_results	
has_results	
to_json	

add_marker_results (*self*, *marker_file*, *results*)

add_swc_results (*self*, *swc_file*, *results*)

add_swc_stats (*self*, *swc_file*, *stats*)

This function creates a report for swc statistics

has_results (*self*)

to_json (*self*)

neuron_morphology.validation.resample_validation module

neuron_morphology.validation.resample_validation.**validate** (*morphology*)

neuron_morphology.validation.resample_validation.**validate_distance_between_connected_nodes**

neuron_morphology.validation.result module

exception neuron_morphology.validation.result.**InvalidMarkerFile** (*validation_errors*)

Bases: ValueError

validation_errors

exception neuron_morphology.validation.result.**InvalidMorphology** (*validation_errors*)

Bases: ValueError

validation_errors

class neuron_morphology.validation.result.**MarkerValidationError** (*message*,
marker, *level*)

Bases: object

Attributes

level

marker

message

level

marker

message

class neuron_morphology.validation.result.**NodeValidationError** (*message*,
node_ids, *level*)

Bases: object

Attributes

level

message

```

        node_ids
    level
    message
    node_ids

```

neuron_morphology.validation.structure_validation module

```

neuron_morphology.validation.structure_validation.validate(morphology)
neuron_morphology.validation.structure_validation.validate_children_nodes_appear_before_pa

```

neuron_morphology.validation.type_validation module

```

neuron_morphology.validation.type_validation.valid_dendrite_parent(morphology,
                                                                    node,
                                                                    valid_parent_type)

neuron_morphology.validation.type_validation.validate(morphology)
neuron_morphology.validation.type_validation.validate_count_node_parent(morphology,
                                                                    node_type,
                                                                    par-
                                                                    ent_type,
                                                                    ex-
                                                                    pected_count)

```

This function validates the number of nodes that have a specific type of parent

```

neuron_morphology.validation.type_validation.validate_expected_types(morphology)
    This function validates the expected types of the nodes

```

```

neuron_morphology.validation.type_validation.validate_immediate_children_of_soma_cannot_br
    This function validates that immediate children of soma cannot branch

```

```

neuron_morphology.validation.type_validation.validate_multiple_axon_initiation_points(morph
    This function validates that the parent of axon (either type 1 or 3) only happens once

```

```

neuron_morphology.validation.type_validation.validate_node_parent(morphology)
    This function validates the type of parent node for a specific type of child node

```

```

neuron_morphology.validation.type_validation.validate_number_of_soma_nodes(morphology)
    This function validates the number of type 1 nodes

```

neuron_morphology.validation.validate_reconstruction module

```

neuron_morphology.validation.validate_reconstruction.main()
neuron_morphology.validation.validate_reconstruction.parse_arguments(args)
    This function parses command line arguments

```

Module contents

```

neuron_morphology.validation.validate_marker(marker, morphology)
neuron_morphology.validation.validate_morphology(morphology)

```


neuron_morphology.vis package

Submodules

neuron_morphology.vis.morphovis module

```

neuron_morphology.vis.morphovis.plot_cortical_boundary(pia_coords,      wm_coords,
                                                         ax)
neuron_morphology.vis.morphovis.plot_depth_field(depth_field, ax)
neuron_morphology.vis.morphovis.plot_gradient_field(gradient_field, ax)
neuron_morphology.vis.morphovis.plot_morphology_xy(morphology, ax)
neuron_morphology.vis.morphovis.plot_morphology_zy(morphology, ax)
neuron_morphology.vis.morphovis.plot_soma(soma_center, ax)

```

Module contents

4.1.2 Submodules

neuron_morphology.constants module

neuron_morphology.lims_apical_queries module

neuron_morphology.marker module

```
class neuron_morphology.marker.Marker(*args, **kwargs)
```

Bases: dict

Simple dictionary class for handling reconstruction marker objects.

Methods

<code>clear()</code>	
<code>copy()</code>	
<code>fromkeys(iterable[, value])</code>	Create a new dictionary with keys from iterable and values set to value.
<code>get(self, key[, default])</code>	Return the value for key if key is in the dictionary, else default.
<code>items()</code>	
<code>keys()</code>	
<code>pop()</code>	If key is not found, d is returned if given, otherwise KeyError is raised
<code>popitem(self, /)</code>	Remove and return a (key, value) pair as a 2-tuple.
<code>setdefault(self, key[, default])</code>	Insert key with a value of default if key is not in the dictionary.

Continued on next page

Table 49 – continued from previous page

<code>update()</code>	If E is present and has a <code>.keys()</code> method, then does: for k in E: D[k] = E[k] If E is present and lacks a <code>.keys()</code> method, then does: for k, v in E: D[k] = v In either case, this is followed by: for k in F: D[k] = F[k]
<code>values()</code>	

`neuron_morphology.marker.read_marker_file(file_name)`
read in a marker file and return a list of dictionaries

neuron_morphology.morphology module

class `neuron_morphology.morphology.Morphology(nodes, node_id_cb, parent_id_cb)`
Bases: `sphinx.ext.autodoc.importer._MockObject`

Methods

<code>__call__(self, *args, **kw)</code>	Call self as a function.
<code>breadth_first_traversal(self, visit[, ...])</code>	Apply a function to each node of a connected graph in breadth-first order
<code>depth_first_traversal(self, visit[, ...])</code>	Apply a function to each node of a connected graph in depth-first order
<code>get_compartment_surface_area(self, compartment)</code>	Calculate the surface area of a single compartment.
<code>get_compartment_volume(self, compartment)</code>	Calculate the volume of a single compartment.
<code>get_root(self)</code>	Return the first found root node If the input SWC file does not have any root node, it will return None
<code>get_roots_for_analysis(self[, root, node_types])</code>	Returns a list of all trees to be analyzed, based on the supplied root.
<code>get_soma(self)</code>	Return one soma node labeled with SOMA If the input SWC file does not have any node labeled with SOMA, it will return None
<code>swap_nodes_edges(self[, merge_cb, ...])</code>	Build a new tree whose nodes are the edges of this tree and vice-versa
<code>validate(self[, strict])</code>	Validate the neuron morphology in

build_intermediate_nodes	
children_of	
clone	
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get_branch_order_for_node	
get_branch_order_for_segment	
get_branching_nodes	
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is_node_at_end_of_segment	
is_soma_child	
midpoint	
node_by_id	
parent_of	

breadth_first_traversal (*self, visit, neighbor_cb=None, start_id=None*)

Apply a function to each node of a connected graph in breadth-first order

Parameters

visit [callable] Will be applied to each node. Signature must be visit(node). Return is ignored.

neighbor_cb [callable, optional] Will be used during traversal to find the next nodes to be visited. Signature must be neighbor_cb(node id) -> list of node_ids. Defaults to self.child_ids.

start_id [hashable, optional] Begin the traversal from this node. Defaults to self.get_root_id().

Notes

assumes rooted, acyclic

build_intermediate_nodes (*self, make_intermediates_cb, set_parent_id_cb*)

children_of (*self, node*)

clone (*self*)

depth_first_traversal (*self, visit, neighbor_cb=None, start_id=None*)

Apply a function to each node of a connected graph in depth-first order

Parameters

visit [callable] Will be applied to each node. Signature must be visit(node). Return is ignored.

neighbor_cb [callable, optional] Will be used during traversal to find the next nodes to be visited. Signature must be `neighbor_cb(node_id) -> list of node_ids`. Defaults to `self.child_ids`.

start_id [hashable, optional] Begin the traversal from this node. Defaults to `self.get_root_id()`.

Notes

assumes rooted, acyclic

static euclidean_distance (*node1*, *node2*)

get_branch_order_for_node (*self*, *node*)

get_branch_order_for_segment (*self*, *segment*)

get_branching_nodes (*self*, *node_types=None*)

get_children (*self*, *node*, *node_types=None*)

get_children_of_node_by_types (*self*, *node*, *node_types*)

get_compartment_for_node (*self*, *node*, *node_types=None*)

get_compartment_length (*self*, *compartment*)

get_compartment_midpoint (*self*, *compartment*)

get_compartment_surface_area (*self*, *compartment: Sequence[Dict]*) \rightarrow float

Calculate the surface area of a single compartment. Treats the compartment as a circular conic frustum and calculates its lateral surface area. This is:

$$\pi * (r_1 + r_2) * \text{sqrt}((r_2 - r_1)^2 + L^2)$$

Parameters

compartment [two-long sequence. Each element is a node and must have] 3d position data (“x”, “y”, “z”) and a “radius”

Returns

The surface area of the sides of the compartment

get_compartment_volume (*self*, *compartment: Sequence[Dict]*) \rightarrow float

Calculate the volume of a single compartment. Treats the compartment as a circular conic frustum and calculates its volume as:

$$\pi * L * (r_1^2 + r_1 * r_2 + r_2^2) / 3$$

Parameters

compartment [two-long sequence. Each element is a node and must have] 3d position data (“x”, “y”, “z”) and a “radius”

Returns

The volume of the compartment

get_compartments (*self*, *nodes=None*, *node_types=None*)

get_dimensions (*self*, *node_types=None*)

get_leaf_nodes (*self*, *node_types=None*)

`get_max_id (self)`

`get_node_by_types (self, node_types=None)`

`get_non_soma_nodes (self)`

`get_number_of_trees (self, nodes=None)`

`get_root (self)`

Return the first found root node If the input SWC file does not have any root node, it will return None

Parameters

morphology: Morphology object

Returns

Root node object

`get_root_for_tree (self, tree_number)`

`get_root_id (self)`

`get_roots (self)`

`get_roots_for_analysis (self, root=None, node_types=None)`

Returns a list of all trees to be analyzed, based on the supplied root. These trees are the list of all children of the root, if root is not None, and the root node of all trees in the morphology if root is None.

Parameters

morphology: Morphology object

root: dict

This is the node from which to count branches under. When root=None, all separate trees in the morphology are returned.

node_types: list (AXON, BASAL_DENDRITE, APICAL_DENDRITE)

Type to restrict search to

Returns

Array of Node objects

`get_roots_for_nodes (self, nodes)`

`get_segment_length (self, segment)`

`get_segment_list (self, node_types=None)`

`get_soma (self)`

Return one soma node labeled with SOMA If the input SWC file does not have any node labeled with SOMA, it will return None

Parameters

morphology: Morphology object

Returns

Soma node object

`get_tree_list (self)`

`has_type (self, node_type)`

`is_node_at_beginning_of_segment (self, node)`

```
is_node_at_end_of_segment (self, node)  
is_soma_child (self, node)  
static midpoint (node1, node2)  
node_by_id (self, node_id)  
parent_of (self, node)  
swap_nodes_edges (self, merge_cb=None, parent_id_cb=None, make_root_cb=None,  
                    start_id=None)  
    Build a new tree whose nodes are the edges of this tree and vice-versa
```

Parameters

merge_cb [callable, optional]
parent_id_cb [callable, optional]
make_root_cb [callable, optional]
start_id [hashable, optional]

Notes

assumes rooted, acyclic

```
validate (self, strict=False)
```

Validate the neuron morphology in [bits, radius, resample, type, structure]

neuron_morphology.morphology_builder module

```
class neuron_morphology.morphology_builder.MorphologyBuilder
```

Bases: object

Attributes

active_node_id
next_id
parent_id

Methods

<i>apical_dendrite</i> (<i>self</i> [, <i>x</i> , <i>y</i> , <i>z</i> , <i>radius</i>])	Convenience for creating an apical dendrite node.
<i>axon</i> (<i>self</i> [, <i>x</i> , <i>y</i> , <i>z</i> , <i>radius</i>])	Convenience for creating an axon node.
<i>basal_dendrite</i> (<i>self</i> [, <i>x</i> , <i>y</i> , <i>z</i> , <i>radius</i>])	Convenience for creating a basal dendrite node.
<i>build</i> (<i>self</i>)	Construct a Morphology object using this builder.
<i>child</i> (<i>self</i> , <i>x</i> , <i>y</i> , <i>z</i> , <i>node_type</i> [, <i>radius</i>])	Add a child node to the current active node.
<i>root</i> (<i>self</i> [, <i>x</i> , <i>y</i> , <i>z</i> , <i>node_type</i> , <i>radius</i>])	Add a new root node (parent -1) to this reconstruction.
<i>up</i> (<i>self</i> [, <i>by</i>])	Terminate a branch.

active_node_id
apical_dendrite (*self*, *x*=None, *y*=None, *z*=None, *radius*=1)

Convenience for creating an apical dendrite node. Will not create a root.

axon (*self*, *x=None*, *y=None*, *z=None*, *radius=1*)

Convenience for creating an axon node. Will not create a root.

basal_dendrite (*self*, *x=None*, *y=None*, *z=None*, *radius=1*)

Convenience for creating a basal dendrite node. Will not create a root.

build (*self*)

Construct a Morphology object using this builder. This is a non- destructive operation. The Morphology will be validated at this stage.

child (*self*, *x*, *y*, *z*, *node_type*, *radius=1*)

Add a child node to the current active node. This will become the new active node.

next_id

parent_id

root (*self*, *x=0*, *y=0*, *z=0*, *node_type=1*, *radius=1*)

Add a new root node (parent -1) to this reconstruction. This will be the new active node.

up (*self*, *by=1*)

Terminate a branch. Set the active node to the previous active node's ancestor.

Parameters

by [how far (up the tree) to set the new active node. Default is the] parent of the current node (1). 2 would correspond to the

neuron_morphology.swc_io module

`neuron_morphology.swc_io.apply_casts` (*df*, *casts*)

`neuron_morphology.swc_io.morphology_from_swc` (*swc_path*)

`neuron_morphology.swc_io.morphology_to_swc` (*morphology*, *swc_path*, *comments=None*)

Write an swc file from a morphology object

`neuron_morphology.swc_io.read_swc` (*path*, *columns=('id', 'type', 'x', 'y', 'z', 'radius', 'parent')*,
sep=' ', *casts={'id': <class 'int'>, 'parent': <class 'int'>, 'type': <class 'int'>}*)

Read an swc file into a pandas dataframe

`neuron_morphology.swc_io.write_swc` (*data*, *path*, *comments=None*, *sep=' '*, *columns=('id', 'type', 'x', 'y', 'z', 'radius', 'parent')*, *casts={'id': <class 'int'>, 'parent': <class 'int'>, 'type': <class 'int'>}*)

Write an swc file from a pandas dataframe

4.1.3 Module contents

Top-level package for neuron_morphology.

neuron morphology is an open-source Python package for working with single-neuron morphological reconstruction data, such as those in the [Allen Cell Types Database](#). It provides tools for transforming, analyzing, and visualizing these data. To get started, take a look at the [installation instructions](#) and the [usage guides](#).

To report a bug or request a feature, see [the issues page](#).

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