

Morphology Processing Workflow

version 0.0.4.dev0

Neuromathematics team

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Validation report

CurateDataset

Run Curation step.

Validated features

AA0319, C270106A, astrocyte, circle_contour, complexe, disconnected_neurite, iterators, mono-type, multiple_point_section, nested_single_children, neurite_wrong_root_point, nrn-order-already-sorted, nrn_ordering, pia, reversed_NRN_neurite_order, rp100427-123_idC, sections-block, simple, simple-with-font, simple-with-image-coord, simple2, soma_cylinders, soma_multiple_frustums, soma_three_points_cylinder, spine, three_point_soma

Failed features

multiple_soma, soma_single_frustum

Sub tasks

Collect

Collect external dataset from .csv file.

Original dataset has to have a 'morph_name' and 'morph_path' column, with the name and path to the corresponding morphologies. Any other valid columns will be gathered as well. In addition, it will only collect morphologies with allowed extension: .asc, .h5, .swc.

Validated features

AA0319, C270106A, astrocyte, circle_contour, complexe, disconnected_neurite, iterators, mono-type, multiple_point_section, multiple_soma, nested_single_children, neurite_wrong_root_point, nrn-order-already-sorted, nrn_ordering, pia, reversed_NRN_neurite_order, rp100427-123_idC, sections-block, simple, simple-with-font, simple-with-image-coord, simple2, soma_cylinders, soma_multiple_frustums, soma_single_frustum, soma_three_points_cylinder, spine, three_point_soma

ExtractMarkers

Extract marker informations from the original morphology files, if any.

Markers are additional spatial information contained in some reconstructed morphologies. Some can be read by MorphIO (<https://github.com/BlueBrain/MorphIO/pull/186>). The markers are stored in a custom API (morphology-processing-workflow/marker_helper.py).

Validated features

AA0319, C270106A, astrocyte, circle_contour, complexe, disconnected_neurite, iterators, mono-type, multiple_point_section, nested_single_children, neurite_wrong_root_point, nrn-order-already-sorted, nrn_ordering, pia, reversed_NRN_neurite_order, rp100427-123_idC, sections-block, simple, simple-with-font, simple-with-image-coord, simple2, soma_cylinders, soma_multiple_frustums, soma_single_frustum, soma_three_points_cylinder, spine, three_point_soma

Failed features

- **multiple_soma**
 - return code: 1
 - comment: None

- exception:

```
Traceback (most recent call last):
  File "/mnt/Stockage/Adrien/Work/BBP/codes/morphology-processing-workflow/src/morphology_processing_workflow/utils.py", line 42, in try_operation
    res = func(row, *args, **kwargs)
  File "/mnt/Stockage/Adrien/Work/BBP/codes/morphology-processing-workflow/src/morphology_processing_workflow/curation.py", line 73, in extract_marker
    markers = _get_markers(row, Morphology(row.morph_path))
morphio._morphio.SomaError: Multiple somata found:

/mnt/Stockage/Adrien/Work/BBP/codes/morphology-processing-workflow/examples/Collect/data/multiple_soma.swc:2:error

/mnt/Stockage/Adrien/Work/BBP/codes/morphology-processing-workflow/examples/Collect/data/multiple_soma.swc:11:error
```

Sanitize

Sanitize the morphologies.

Sanitization is done with `neuror.sanitize.sanitize` and does:

- fixes non zero segments
- raises if the morphology has no soma
- raises if the morphology has negative diameters
- raises if the morphology has a neurite whose type changes along the way

Note that the `tasks.curation.CheckNeurite` task adds a soma if missing, so a failure here means that the soma does not have a valid type.

Validated features

AA0319, C270106A, astrocyte, circle_contour, complexe, disconnected_neurite, iterators, mono-type, multiple_point_section, nested_single_children, neurite_wrong_root_point, nrn-order-already-sorted, nrn_ordering, pia, reversed_NRN_neurite_order, rp100427-123_idC, sections-block, simple, simple-with-font, simple-with-image-coord, simple2, soma_cylinders, soma_multiple_frustums, soma_three_points_cylinder, spine, three_point_soma

Failed features

- **multiple_soma**

- return code: 1
- comment: None
- exception:

- **soma_single_frustum**

- return code: 1
- comment: /mnt/Stockage/Adrien/Work/BBP/codes/morphology-processing-workflow/examples/CheckNeurites/data/soma_single_frustum.swc has an invalid or no soma
- exception:

CheckNeurites

Detect which neurite are present in the morphology, and add soma if missing.

This task adds three important boolean flags:

- has_axon
- has_basal
- has_apical

set to false if any are absent.

If soma is absent, a soma is added as a circle, with center the mean of the first points of root sections, and radius as standard deviation of these points around the center.

TODO: set various levels, a one section neurite can be set to has_basal=False for example.

Validated features

AA0319, C270106A, astrocyte, circle_contour, complexe, disconnected_neurite, iterators, mono-type, multiple_point_section, nested_single_children, neurite_wrong_root_point, nrn-order-already-sorted, nrn_ordering, pia, reversed_NRN_neurite_order, rp100427-123_idC, sections-block, simple, simple-with-font, simple-with-image-coord, simple2, soma_cylinders, soma_multiple_frustums, soma_single_frustum, soma_three_points_cylinder, spine, three_point_soma

Failed features

• multiple_soma

- return code: 1
- comment: None
- exception:

```
Traceback (most recent call last):
  File "/mnt/Stockage/Adrien/Work/BBP/codes/morphology-processing-workflow/src/morphology_processing_workflow/utils.py", line 42, in try_operation
    res = func(row, *args, **kwargs)
  File "/mnt/Stockage/Adrien/Work/BBP/codes/morphology-processing-workflow/src/morphology_processing_workflow/curation.py", line 171, in check_neurites
    morph = Morphology(row.morph_path)
morphio._morphio.SomaError: Multiple somata found:

/mnt/Stockage/Adrien/Work/BBP/codes/morphology-processing-workflow/examples/Collect/data/multiple_soma.swc:2:error

/mnt/Stockage/Adrien/Work/BBP/codes/morphology-processing-workflow/examples/Collect/data/multiple_soma.swc:11:error
```

Recenter

Recenter morphologies.

Often, morphologies do not have a soma centered at [0, 0, 0], so we recenter and save the original location, in case it is important to know where the morphology is located in atlas.

Validated features

AA0319, C270106A, astrocyte, circle_contour, complexe, disconnected_neurite, iterators, mono-type, multiple_point_section, nested_single_children, neurite_wrong_root_point, nrn-order-already-sorted, nrn_ordering, pia, reversed_NRN_neurite_order, rp100427-123_idC, sections-block, simple, simple-with-font, simple-with-image-coord, simple2, soma_cylinders, soma_multiple_frustums, soma_three_points_cylinder, spine, three_point_soma

Failed features

- **multiple_soma**
 - return code: 1
 - comment: None
 - exception:
- **soma_single_frustum**
 - return code: 1
 - comment: None
 - exception:

DetectErrors

Detect errors in reconstructions.

Reconstructions may contain errors, which are detected here. They are of the following type:

- fat ends
- z-jumps
- narrow start
- dangling branch
- multifurcation

This task uses NeuroR/neuror/error_annotation.py (<https://github.com/BlueBrain/NeuroR>), and reproduces part of what is in MorphService. This task creates new .asc file with error annotated so it can be read by NeuroLiscida, and a MarkerSet container of the errors, for later plotting.

Validated features

AA0319, C270106A, astrocyte, circle_contour, complexe, disconnected_neurite, iterators, mono-type, multiple_point_section, nested_single_children, neurite_wrong_root_point, nrn-order-already-sorted, nrn_ordering, pia, reversed_NRN_neurite_order, rp100427-123_idC, sections-block, simple, simple-with-font, simple-with-image-coord, simple2, soma_cylinders, soma_multiple_frustums, soma_three_points_cylinder, spine, three_point_soma

Failed features

- **multiple_soma**
 - return code: 1
 - comment: None
 - exception:
- **soma_single_frustum**
 - return code: 1
 - comment: None

- exception: