

# NLMorphologyConverter (Version 0.8.0)

## User Manual (Version 0.2)

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[www.neuronland.org](http://www.neuronland.org)

### Overview

“NLMorphologyConverter” is a simple command-line program for converting between the various neuron morphology data formats which are used to describe the three-dimensional physical branching structure of biological neurons. The aim is to provide coverage of all formats, old and new, in which data is available online, and/or which are supported by free and commercial software packages (e.g. software for neuron reconstruction, generation, simulation, visualisation, and analysis of neuron morphology).

Currently 21 formats are supported. Some are associated with morphology reconstruction systems (e.g. Neurolucida, NeuroZoom, Eutectics); others are the native formats of specific software packages used by the neuron reconstruction and neuron modeling community (e.g. NeuronJ, Genesis, Neuron, ArborVitae, SWC); some older formats have been superseded, and others see no use nowadays (Nevin, Douglas, Oxford); others are relatively new, and have a lot of potential (MorphML). (A full history of the various formats would be interesting to recount, but will have to wait for another time, and more research).

There is movement within the neuroscience community towards a smaller number of formats, with the most commonly used being Neurolucida ([www.mbfbioscience.com/neurolucida](http://www.mbfbioscience.com/neurolucida)), due to its dominance in the market for reconstruction tools, and SWC, a clear, flexible, and memory-efficient format which has now been adopted by the NeuroMorpho database ([www.neuromorpho.org](http://www.neuromorpho.org)). MorphML (part of the NeuroML standard – see [www.neuroml.org](http://www.neuroml.org)) should also be noted as a format whose level of adoption should grow in the future, as direct support is added to more software.

The need to convert between different neuron morphology file formats is of course not new. Various converters are available, either as part of other software packages, standalone executable, or scripts. These converters have been fairly limited in the number of file formats supported, and the conversion is usually unidirectional. NLMorphologyConverter tries to provide a bi-directional bridge between all 3D morphology formats, helping efforts to avoid the loss of data, and facilitating compatibility between all software programs which employ one or more of the supported formats. If any new formats are adopted in the future by the neuroscience community, they will be supported too.

The NLMorphologyConverter software is currently only available as a binary download for Microsoft Windows, Apple Mac OSX and Linux operating systems. There is a plan to release source code eventually, but no timescale can be given for this yet.

A new software package, NLMorphologyViewer is also now available from the website. It is built on top of the conversion technology developed for the NLMorphologyConverter, and provides an interactive graphical view of the neuron data, as well as access to the main functionality provided by the converter.

The testing regime which is applied to the software is detailed on the website ([www.neuronland.org](http://www.neuronland.org)). The purpose is to demonstrate the lengths being taken to ensure the correctness of the import/export algorithms, and thereby make the user more confident in the validity of the generated data files.

## Main Features

- Currently 21 different morphology file formats fully or partially supported.
- Automatic detection of input file format.
- Faithful reproduction of output file formatting.
- Many command line options for manipulating the imported data
- Intensively tested using over 10000 publicly available morphology data files.

All users are advised to check the generated output data before making further use of it. Although import and export algorithms are well tested and generally reliable, there may be special cases which are not imported correctly - for certain file formats, original data often contains errors which the importer may not be able to deal with correctly; other formats are not sufficiently strictly specified that correct import can be guaranteed under all circumstances.

## The Future

NLMorphologyConverter is likely to see various improvements in the coming year (2009), including the release of an SDK. Bug-fixes will have priority, along with requests for useful command-line options, and improved support for existing file formats. However, the fundamental functionality now exists in a reasonably advanced form, and will hopefully not require the investment of too much more development time.

The technology created during the development of the converter will be incorporated into two new applications. One is a fairly simple neuron viewer (NLMorphologyViewer, already released). The second is a more ambitious simulation project which may not see the light of day for several years.

When the SDK is released, anyone will be free to incorporate the conversion functionality into their own software.

## Installation

### Windows

The Win32 version comes in a standard Microsoft installer package (msi). Simply double-click on the installation package to install.

### Mac OSX

The Mac OSX version is currently a simple zipped universal binary. Installation is simply a matter of decompressing and placing the executable in a suitable location. The program will work on both PPC and Intel based Macs. (Current version is compiled on OSX 10.4. PPC.)

### Linux

Linux is the least well supported operating system, at the moment. Efforts will be made to improve this. As with the Mac version, the installation file is a compressed binary. Installation is simply a matter of decompressing and placing the executable in a suitable location. (Current version is compiled on Open Suse Linux 10.2, kernel 2.6.18, with gcc 4.1. If this version does not work on your Linux system, please contact [feedback@neuronland.org](mailto:feedback@neuronland.org), to request a version specific to your Linux configuration.)

# Tutorial

For a full list of command line parameters, see the Command Line Options Reference section of this user manual.

## 1. *Basic Conversion*

To convert a file containing morphology data directly from one format to another, the simplest way to do so is

```
NLMorphologyConverter <input file> <output file> <output format>
```

For example,

```
NLMorphologyConverter neuron.asc neuron.swc SWC
```

In this case, a NeuroLucidaASC file is converted into an SWC file. Note that the input file format is not specified. It is automatically determined by the converter. If the input format cannot be determined, the conversion will fail. Note that the order of the parameters is important. A list of output format names can be found in the command reference. Note that any command line parameters which do not start with a “--” are assumed to be, in order, the input file, output file, and output format.

## 2. *Query*

Sometimes, one only wishes to query an input file, and not generate an output file. For example

```
NLMorphologyConverter neuron.asc --stats --warnings --report neuron.log
```

This will

- Output statistics for the neuron as a whole, and for the individual axonal and dendritic trees.
- Output a list of warnings (if any) indicating unusual/unrealistic/problematic data.
- Generate a detailed report file (neuron.log) containing a description of the import process, and also the statistics and warning data already displayed.

## 3. *Modification*

There are several command-line options which allow the neuron to be manipulated.

- The spatial co-ordinate of the tree can be globally manipulated, by rotating, scaling and translating.
- Various parts of the neuron structure can be omitted, using the “--omit\*” options.
- The nature of axonal and dendritic can be swapped (i.e. axonal trees can be converted into dendritic trees, and vice versa).

These options are all useful for fixing reconstructed data, or removing structure which is not of interest. For example, the command

```
NLMorphologyConverter neuron.asc neuron.xml MorphML --omitSoma
--translate 10.0 0 0
```

will import the NeuroLucidaASC file, omit any soma data, and add 10.0 to all x coordinates, then export in MorphML format.

Sometimes, it is necessary to query the tree first (using the “--stats” option), to obtain the IDs of the axonal or dendritic trees which we want to manipulate using the modify options.

```
NLMorphologyConverter neuron.asc neuron.xml MorphML
--omitTrees 1,5,9 --flipTreeType 3,4
```

In this case, the trees with ids 1, 5, and 9 are omitted before exporting the MorphML file. Trees 3 and 4 are converted from dendritic to axonal trees (or vice versa).

#### *4. Merging*

Sometimes, reconstructed neuron data is distributed across multiple files. They can be merged using the “--merge” option. For example,

```
NLMorphologyConverter --omitAxons --merge neuron1.asc --rotate 0 1 0 25
--translate 10 5 0 --omitMarkers
--merge neuron2.txt --rotate 0 1 0 75
--scale 0.9 0.9 1.0 1.0
--merge neuron3.swc
--export mergedNeuron.asc NeuroLucidaASC
```

Note that modify options can be specified for each neuron merged. Modify options specified before the first “--merge” are applied globally. Modify options specified after a specific “--merge” option, are applied to the particular file being merged. The export file name and format must be specified with the “--export” option.

#### *5. Splitting*

The morphology data of a neuron's individual trees can be exported using the “--split” option. For example, if the neuron data file neuron.asc only has dendritic tree data,

```
NLMorphologyConverter neuron.asc --split tree .xml MorphML
```

will export the files, tree\_dend\_01.xml, tree\_dend\_02.xml, tree\_dend\_03.xml.....one file for each tree.

# Command Line Options Reference

| Option | Additional Parameters | Since | Description |
|--------|-----------------------|-------|-------------|
|--------|-----------------------|-------|-------------|

## Help Options

|           |      |       |   |
|-----------|------|-------|---|
| --version | none | 0.6.0 | Displays the current version number (ignored if not the unique option)  |
| --help    | none | 0.6.0 | Displays a list of command-line parameters which can be passed to the program, with descriptions (ignored if not the unique option) |

## Query Options

|            |             |       |   |
|------------|-------------|-------|---|
| --stats    | none        | 0.6.0 | Displays the following statistics, for the entire neuron, and also per dendritic and axonal tree.<br><br>Number of sample points<br>Number of branch points<br>Branching order<br>Number of terminals<br>Total tree branch length (microns)<br>Tree surface area (microns^2)<br>Tree volume (microns^3)<br>Maximum terminal path distance (microns)<br>Maximum terminal physical distance (microns) |
| --warnings | none        | 0.6.0 | Displays the following warnings:<br>Tree root too distant from soma<br>Unary branch point<br>Non-binary branch point<br>Disjoint branch connection<br>Branch has zero samples<br>Branch formed from only one sample<br>Sample diameter is excessively large<br>Sample diameter is unusually small<br>Sample diameter is zero  |
|            |             | 0.7.0 | Unusually large change in diameter<br>Large terminal diameter<br>Unusually long section<br>Unusually short section<br>Intersecting sections<br>Encapsulated branch (a child branch lies completely within the extent of its parent).  |
| --report   | 1. filename | 0.7.0 | Generate a report file, detailing import, modification, statistics, warnings, and export.   |
| --verbose  | none        | 0.7.0 | Normally, only minimal information is printed to the terminal. This option provides more detailed information about the import, modification, and export processes.   |

## Import Options

|                    |             |       |  |
|--------------------|-------------|-------|--|
| --merge <filename> | 1. filename | 0.7.0 | Specifies a neuron data file to be merged. All subsequent modify options are applied to the this neuron. |
|--------------------|-------------|-------|--|

## Modify Options

|                      |  |       |  |
|----------------------|--|-------|--|
| --omitSoma           | none   | 0.6.0 | Soma data is not passed through to the exported data file.   |
| --omitAllAxons       | none   | 0.6.0 | Axon data is not passed through to the exported data file.   |
| --omitMarkers        | none   | 0.7.0 | Marker data is not passed through to the exported data file.   |
| --omitAllDends       | none   | 0.6.0 | Dendritic tree data is not passed through to the exported data file.   |
| --omitTrees n,m,a    | List of tree IDs   | 0.6.0 | Specific trees (axonal or dendritic) are not passed through to the exported data file. Note, the "--stats" option needs to be used to obtain the IDs of trees to be omitted. |
| --allDendsAsAxons    | none   | 0.6.0 | All dendritic trees in the imported file are passed to export as axon trees.   |
| --allAxonsAsDends    | none   | 0.6.0 | All axons in the imported file are passed to export as dendritic trees.  |
| --flipTreeType n,m,a | List of tree IDs   | 0.6.0 | The specified axonal (dendritic) trees are passed through to export as dendritic (axonal) trees.   |
| --scale x y z d      | 1. x-axis scale<br>2. y-axis scale<br>3. z-axis scale<br>4. diameter scale | 0.6.0 | All 3D co-ordinate data points (sample, and marker positions) are scaled by the given values   |
| --translate x y z    | 1. x-axis shift<br>2. y-axis shift<br>3. z-axis shift                      | 0.6.0 | All 3D co-ordinate data points (sample, and marker positions) are offset by the given 3D vector (x, y, z)  |
| --rotate x y z A     | 1. x<br>2. y<br>3. z<br>4. A   | 0.7.0 | All 3D co-ordinate data points (sample, and marker positions) are rotated 'A' degrees around the given direction vector (x, y, z).   |

## Export Options

|                                 |                          |       |  |
|---------------------------------|--------------------------|-------|--|
| --split <prefix><br><postfix>   | 1. prefix<br>2. postfix  | 0.7.0 | The imported data is exported one file per tree, with filenames of the form prefix_dend_XX.postfix, or prefix_axon_XX.postfix.   |
| --export <filename><br><format> | 1. filename<br>2. format | 0.6.0 | <p>Specify output filename and morphology format. This option is only essential when using the "--merge" option, otherwise it can be omitted.</p> <p>Format can be one of the following</p> <p>ArborVitae, Douglas3D, Eutectics, Genesis, Glasgow, GulyasTree, LNeuronAmiraMesh, MaxSim, MorphML, NeurolucidaASC, NeurolucidaClassic, NeurolucidaDAT, NeuronGeneric, NeuronNTSCable, NeuronSWC2HOC, NeuroZoom, Nevin, NINDS3D, Oxford, SWC</p> |

## **References**

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## **Links**

NLMorphologyConverter website - [www.neuronland.org/NLMorphologyConverter](http://www.neuronland.org/NLMorphologyConverter)

NeuroMorpho morphology data archive – [www.neuromorpho.org](http://www.neuromorpho.org)