

### Blue Brain NeuroM is an open-source Python library dedicated to the study and extraction of neuron morphological features. Neuron morphologies are tightly coupled to neuron electrical properties and therefore, are a crucial part of understanding the neuron as a functional unit.

The NeuroM software has been designed to enable researchers to quickly pinpoint the characteristics and specificities of every neuron. It is composed of a low-level API for reading morphology files on top of which are built several applications: a morphology file validator, a feature extractor and a morphology viewer.

## Blue Brain NeuroM provides multiple ways to study morphologies at different levels:

#### As a helper for data curation

NeuroM provides a tool to detect errors present in reconstructed neurons. The tool makes the distinction between structural and biological anomalies. Structural anomalies arise when a file does not respect its file format specifications because it is missing mandatory information of the neuron topology. Structural checks detect the most common sources of file corruption. Biological anomalies relate to the quality of the reconstructed cell as well as its biological properties. NeuroM can detect those issues automatically and signal the reconstructor who can then correct these errors.

#### As a feature extractor program

NeuroM comes with a list of more than 40 out-of-the-box morphological properties whose values can be computed for any neuron. Morphometrics can exist at the neurite level, such as their length or their number of bifurcations, or at the neuron level, such as the number of neurites or the angles between each neurite initial segments. For more extensive analyses, features can be extracted for groups of neurons and common statistical variables (mean, variance, min, max...) can be obtained for each of them.

#### As a morphology viewer to quickly visualize neuron shapes

The viewer provides 2D and 3D representations of neurons, neurites and somas as well as a dendrogram viewer.

#### As a simple API to navigate through the different parts of a neuron and access low level data

The API can be used to perform more in-depth morphological analyses and derive new features. Since the API handles most common file formats. it can also be used as an I/O interface library for building new applications.

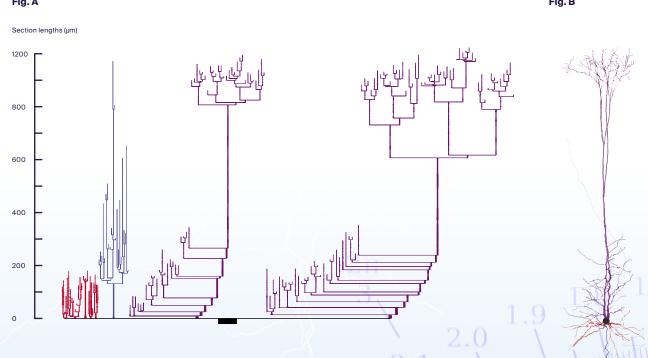


Fig. A and B: Representation of a neuron morphology plotted with NeuroM, as a dendrogram (left) and in the XY plane (right)

#### Fig. A

Fig. B

## NeuroM for Neuroscientists

**NeuroM comes with an extensive collection of validity checks.** Checks are divided into structural and biological. As neuron reconstruction is still a semi-automated process, NeuroM can be used to improve the quality and fidelity of reconstructions. While structural checks ensure that the file meets requirements of the file format specification, biological checks can be used to detect reconstruction induced artefacts.

**NeuroM comes with a comprehensive set of features.** It can be used to quickly get information about a particular morphology. By providing an easy to use tool that handles major morphology file formats, NeuroM allows neuroscientists to focus on the analysis of morphological features and not on their implementation.

**NeuroM offers a unified morphology representation abstracted away from its original file format.** ASC, SWC and H5 have very different ways of representing a neuron and its various components. By converting all files to its own representation, NeuroM alleviates the burden of having to deal with multiple file formats.

**NeuroM is plain Python**. During the last decade, Python has become the de-facto language of many scientific communities.

**NeuroM can be easily extended.** New features can be implemented using NeuroM internal API and because NeuroM is open-source, many current features are actual contributions from external users.

## **Early Adopters**

#### **EPFL's Blue Brain Project**

Blue Brain uses NeuroM throughout its entire pipeline of digital reconstruction and simulation of the rodent brain. At the beginning of the process it is used to help experimentalists reconstructing cells to identify artefacts and to correct them. It is then used to analyze and compare the reconstructed cells by extracting basic morphological features. Finally NeuroM's API is used to query spatial information (coordinates and neurite diameters) about any neuron constituting the reconstructed brain.

#### **BigNeuron**

The software has been used in collaboration with BigNeuron to evaluate the quality of automatically reconstructed neurons, during a series of Hackathons (Cambridge 2015 and London 2016). During this collaboration, NeuroM was used for the ranking of automatically reconstructed neurons and the detection of errors in the resulting morphologies. The software was useful for extracting standard features, performing statistical analysis on them and displaying the results.

#### **Human Brain Project summit**

NeuroM was presented during livecoding sessions in multiple HBP summits (2014-2016). Scientists analyzed morphologies by using basic functionalities of NeuroM. They loaded files of various formats, checked their data, visualized neurons and corrected errors in their reconstructions based on the NeuroM reports. Through this opportunity, NeuroM was introduced to the general public. In the years following this introduction, the input received from these users has guided the development of the software.

Fig. C

Fig C: Interactive 3D representation generated by NeuroM

## About EPFL's Blue Brain Project

The aim of the EPFL Blue Brain Project, a Swiss brain research initiative founded and directed by Professor Henry Markram, is to establish simulation neuroscience as a complementary approach alongside experimental, theoretical and clinical neuroscience to understanding the brain, by building the world's first biologically detailed digital reconstructions and simulations of the mouse brain.

# **Blue Brain NeuroM** is available under BSD 3-Clause Licence at: github.com/BlueBrain/NeuroM

NeuroM is available as a Python package. Sources and installation instructions are available at: github.com/BlueBrain/NeuroM

Further help or contact can be requested at: github.com/BlueBrain/NeuroM/issues

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