

Poster presentation

## Improved automatic midline tracing of neurites with Neuromantic

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### Background

The accurate reconstruction of neuronal morphology from image stacks obtained via microscopy is of significant importance to computational neuroscience. Firstly, it facilitates the validation of models of neuronal behaviour by allowing for comparisons between electrophysiological testing and simulation (through NEURON [1], for example). Secondly, through the use of appropriate morphometrics [2], significant differences between the shape of neurons in control and experimental conditions may be identified, thus lending insight into low-level components of neurological diseases. Also, there is a high level of interest in the reconstruction of larger scale networks within the nervous system and the identification of patterns of connectivity.

Neuromantic is a freeware application in development at the University of Reading for reconstructing and analyzing neuronal morphology. It has been designed to be intuitive to use for reconstruction, and to provide useful tools for both manual and more automatic reconstruction. The motivation behind its development is that, by providing good quality freeware that may be installed on as many machines as necessary, laboratory throughput can be significantly increased by easing the reliance on what is often a single license of a commercial product. Similarly, the availability of such software can encourage the reconstruction of neurons in experiments where it otherwise may have been ignored.

### Methods

The semi-automatic reconstruction employs an extension of the interactive method introduced in [3]. The primary factor determining the quality of the tracing is the pixel-

to-pixel cost function minimised by the algorithm. The cost function has two terms: the neurite cost, which penalises pixels less likely to belong to neurites, and the directionality term, vanishing as the estimate of directional flow becomes parallel to the pixel-to-pixel direction change.

Several variants of the original cost function that used different exponents for the main terms were compared against each other for the automatic tracing of ten neurites taken from two test image stacks.

### Results and discussion

It was found that by increasing the exponent of the neurite cost term, the midline tracking and length estimation of the neurites was improved in a statistically significant way. No such effect was observed for the directionality term. Therefore, this experiment has demonstrated that better semi-automatic neuronal tracing can be achieved with no real increase in the computational expense of the tracing algorithm. In particular, the observed improvement of length estimation will have a direct and positive impact on the accuracy of simulated neuronal behaviour.

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### References

1. Carnevale NT, Hines ML: *The NEURON Book* Cambridge University Press; 2006.
2. Scorcioni R, Ascoli GA: **Algorithmic extraction of morphological statistics from electronic archives of neuroanatomy.** *Lect Notes Comput Sci* 2001, **2084**:30-37.

3. Meijering E, Jacob M, Sarria JCF, Steiner P, Hirling H, Unser M: **Design and Validation of a Tool for Neurite Tracing and Analysis in Fluorescence Microscopy Images.** *Cytometry* 2004, **58A**:167-176.

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