Robust Segmentation in Low SNR Fluorescence Microscopy by Homological Persistence: An Application to Shape Analysis of Neuroblasts in Development *(Work In Progress)*

Oberson Ausoni C.,* Hillje A.L.,† Schwamborn J.C.,‡ Müller J.,§
Brune C.,¶ Burger M.‖

September 23, 2011

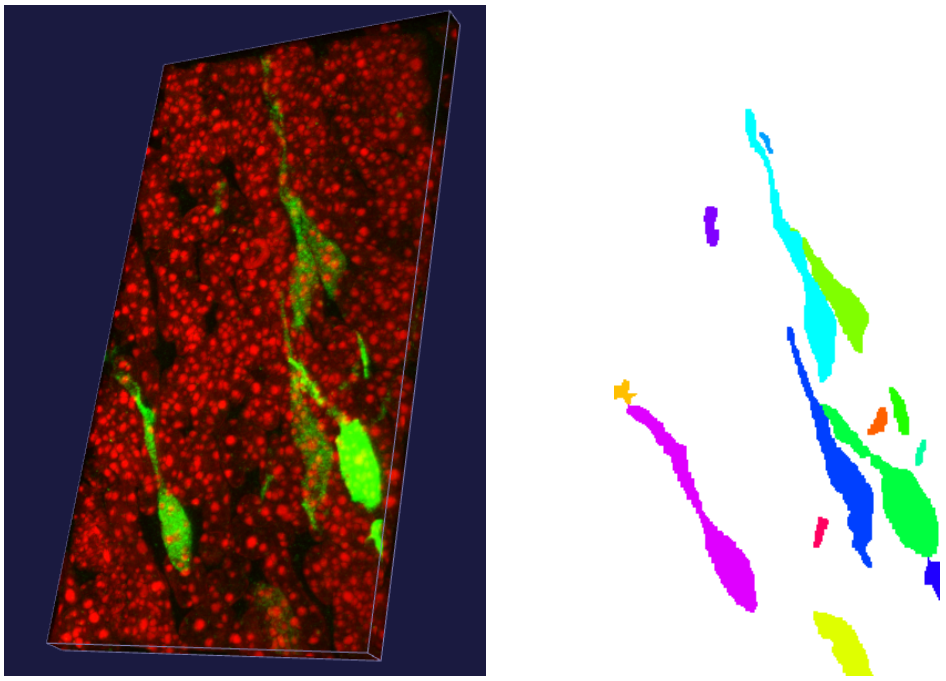

Figure 1: *Left:* Neuroblast overexpressing ProteinX in the middle part of the rostral migratory stream of the mouse, sagittal section, 12 μm. *Right:* Connected component identification for the same sample, 2D projection.

*Dr. Chantal Oberson Ausoni, Workgroup Imaging, Institute for Computational and Applied Mathematics, University of Münster, *would present the poster*

†Anna-Lena Hillje, doctoral student, Center for Molecular Biology of Inflammation - ZMBE, Cell Biology, University of Münster

‡Dr. Jens Schwamborn, Center for Molecular Biology of Inflammation - ZMBE, Cell Biology, University of Münster

§Jahn Müller, doctoral student, Workgroup Imaging, Institute for Computational and Applied Mathematics, University of Münster

¶Dr. Christoph Brune, Department of Applied Mathematics, University of California, Los Angeles

‖Prof. Dr. Martin Burger, Workgroup Imaging, Institute for Computational and Applied Mathematics, University of Münster

Abstract

In the adult mammalian brain, neuronal precursor cells are continuously produced in the subventricular zone and evolve during their migration along the rostral migratory stream to integrate the olfactory bulb, where they further differentiate. During the last years, several factors involved in migration and differentiation of neuroblasts have been identified, but a lot of them remain unknown, for example the role of ProteinX investigated here. Retroviruses carrying a transgene for ProteinX are injected into the subventricular zone of the mouse. At different stages along the rostral migratory stream, the changes are monitored by fluorescence microscopy : the transfected neuroblasts are identified by green fluorescent protein expression, whereas cell nuclei are stained in red.

In order to obtain further insight into the alterations, a comparative shape analysis is needed, which relies on robust segmentation of neuroblasts as a first step. The latter is a particular challenge due to very low SNR and the complicated elongated shapes of neuroblasts. Standard shape priors based on small surface areas or curvatures are not suitable for this application and higher-level priors cannot be built due to a missing database of typical shapes. Consequently, state-of-the art variational or probabilistic methods lead to severe segmentation errors with respect to shape and topology and it becomes attractive to investigate alternative approaches based on persistent homology. Even more challenging is the segmentation of the red channel picture; since each neuroblast should contain exactly one nucleus, a correct identification of the nuclei would enable a further test on the correctness of the neuroblast segmentation.

After edge preserving preprocessing with a Bregman-Total-Variation method, we apply an union-find algorithm, constructing a forest where each tree is a connected component of the 3D green channel picture. At the beginning, all voxels having maximal green intensity are selected and the connected components they define are listed (these voxels are the black ones of a black and white image). The lower intensity voxels are added gradually and the list of the connected components is actualized with the possible birth of a new component or the fusion of two objects. The green intensity value can therefore be interpreted as the time component of our filtration. After a first run until the minimal intensity, we are able, considering the persistence barcode, to identify an optimal stop time, which will be used for the second run. For each of the components obtained at the end of the second run, we examine its own "history" by constructing a local forest. In particular, a "late" fusion, where two objects are separated from each other by low intensity voxels, can be detected and we can "rewind" locally to a time before the fusion. In the same way, we can get locally to the point before the fusion if the final object exhibits several nuclei.

In a further step, the size of every neuroblast will be measured, a shape factor and an orientation tensor will be computed, which enables a differential analysis at the different places of the migratory stream.

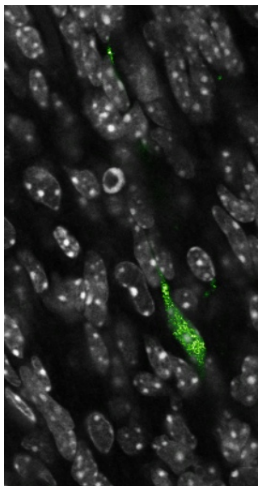

Figure 2: Grayscale nuclei and green neuroblasts (slice of the same sample as in Fig. 1).