Automatic Segmentation of Anatomical Structures using Deformable Models and Bio-Inspired/Soft Computing

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Date and location of PhD thesis defense: 10 March 2014, University of Parma

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1 Abstract

This PhD dissertation, carried out within the Marie Curie project MIBISOC ("Medical Imaging using Bio-Inspired and SOft Computing", EU FP7 G.A. n. 238819), describes the accomplishments of our research on the development of algorithms for the automatic and accurate segmentation of anatomical structures in biomedical images. Firstly, hybridizations between soft computing (SC) and computer vision (CV) techniques have been investigated to help in biomedical imaging-related tasks. Secondly, in collaboration with the Molecular Biotecnology Center of Torino, we have developed a specific tool aimed at extending the current understanding of the complex signaling events occurring in dendritic spines (DS), by integrating state of the art computational and experimental approaches. DS are neuronal protrusions, which receive input typically from one excitatory synapse, containing neurotransmitter receptors, organelles, and signaling systems essential for synaptic function and plasticity.

We initially aimed at developing new recognition algorithms for brain anatomical structures, capable of automatically extracting two types of information: 1) the relative abundance of the mRNA of every gene in the main brain areas; and 2) the identity of mRNAs that are particularly enriched in dendrites, which are very likely to be involved in DS biogenesis/functions. The main motivation can be found in the great interest that neurobiologist have for RNA molecules specifically enriched in the neuropil of neuronal cells (and, in particular, in DS), in virtue of their involvement in synaptic structure, plasticity and neuropsychiatric disorders (like fragile-X syndrome, autism spectrum disorders, or schizophrenia). The systematic identification of these molecules is, therefore, a very important task and can be based on visual features, such as image texture, which recur in the regions where they are more densely present. In that regard, the high-resolution images of RNA In Situ Hybridization (ISH)* experiments contained in the Allen Brain Atlas (ABA) represent a very rich resource to identify them and, for this task, they have been so far exploited based on human-expert analysis. However, software tools that automatically address the same objective are not easily available or effective. Since the regions of interest, where the molecules under study are more densely present, occupy only a small part of the whole images, a tool for automatically focusing on such regions is essential if a huge number of images is available for processing. To accomplish such a goal, three different segmentation methods that allow for the accurate delineation of a specific anatomical region have been developed.

The first method [1, 2, 3] preliminarily processes a training set of images, from which the deformation range and the main modes of variation of a parametric deformable model (DM) are empirically assessed. Based on these data one can define very simple templates, managed by a fast method which allows genome-wide experiments on thousands of images. This approach is divided into four different stages (initialization, localization

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*ISH is a technique that allows for precise localization of a specific segment of nucleic acid within a histologic section.

using DMs and metaheuristics (MHs), segmentation, and expansion of the segmentation using ensemble classifiers), and can be seen as a smart way of selecting promising regions to be subsequently processed by a fast and well-established image segmentation/analysis technique. The main advantages of this approach are its execution time and accuracy, and the simplicity in the definition of the models, while its main disadvantages are its ad-hoc nature (it needs a training set of shapes/textures, and suitable parametric models of the object to locate), and the impossibility of managing topological changes.

The second method [4] uses the Level Set (LS) method to allow topological changes. The templates are created automatically using principal components analysis to derive texture, mean shape and shape variability from the training set. After that, a MH is used to evolve the segmenting contour by optimizing the weights of a linear combination of the different eigenshapes and the mean shape, based on an intensity- and texture-based fitness function. This method has obtained reasonably good results, even if it is less precise than the previous approach and requires a longer execution time. Thus, it can be looked upon as an intermediate stage that led us to develop the third segmentation method.

The third method [5] tries to solve all the previous problems found. Firstly, the LS method is again used to manage possible topological changes. Secondly, three different sources of information are taken into account (intensity, boundaries, and shape). Thirdly, the automatic MH-based tuning procedure allows one to apply the same method to different image modalities and anatomical structures, and makes this a general approach (tested on CT, MRI and microscopy histological images). Finally, only a single previously segmented reference image is necessary to perform the segmentation instead of a complete training set, as in the previous methods. This is possible thanks to a deformable registration process in which the target image is aligned with the corresponding image of an Atlas. In terms of generalization and accuracy, this method obtained the best results compared with seven state of the art segmentation approaches.

References

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