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3D-SSF: A Bio-inspired Approach for Dynamic Multi-Subject Clustering of White Matter Tracts

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Abstract

There is growing interest in the study of white matter (WM) variation across subjects, and in particular the analysis of specific WM bundles, to better understand brain development and aging, as well as to improve early detection of some diseases. Several WM multi-subject clustering methods have been proposed to study WM bundles. These methods aim to overcome the complexity of the problem, which includes the huge size of the WM tractography datasets generated from multiple subjects, the existence of various streamlines with different positions, lengths and geometric forms, as well as the presence of outliers. However, the current methods are not sufficiently flexible to address all of these constraints. Here we introduce a novel dynamic multi-subject clustering framework based on a distributed multiagent implementation of the Multiple Species Flocking model, that we name 3D-Streamlines Stream Flocking (3D-SSF). Specifically, we consider streamlines from different subjects as data streams, and each streamline is assigned to a mobile agent. Agents work together following flocking rules in order to form a flock. Thanks to a similarity function, the agents that are associated with similar streamlines form a flock, whereas the agents that are associated with dissimilar streamlines are considered outliers. We use various experiments performed on noisy synthetic and real human brain data to validate 3D-SSF and demonstrate that it is more efficient and robust to outliers compared to other classical approaches. 3D-SSF is able to extract WM bundles at a population level, while considering WM variation across subjects and eliminating outlier streamlines.

Keywords: Data stream, multi-agent system, Multiple Species Flocking model, multi-subject clustering, outliers, White Matter tractography.

1 INTRODUCTION

Diffusion Magnetic Resonance Imaging (dMRI) [1, 2] is a powerful, non-invasive imaging tool for the study of WM in vivo based on the measurement of water molecule diffusion in human brain tissue.

The diffusion is represented by a model [3] that estimates the underlying fiber orientations based on the average displacement of water molecules for every voxel along several directions. The fiber orientations are exploited to trace 3D trajectories representing the potential pathway of WM via a process called tractography [4]. In this paper, we use the term ”streamline” to describe a set of 3D points representing a virtual anatomical fiber [5].

The clustering of the streamlines into anatomically meaningful bundles is a very important task. Streamline clustering is used to study brain connectivity and contribute to a better understanding of the human brain. A whole-brain tractography dataset is highly complex, ranging from 100,000 to 1,000,000 streamlines per subject. Streamline clustering is challenging due to the following reasons:

- The complexity of WM architecture and frequently unclear definitions of the structure and the organization of WM bundles [6].
- The huge size of the WM tractography dataset composed of various streamlines with complex geometries.
- The variability of human brain WM architecture across subjects in terms of geometric properties, connectivity strengths, and patterns, which complicates the development of a generalized solution for streamline clustering.
- The presence of outliers due to tractography errors and patient movements, which may distort the clustering results via erroneous streamlines.

Given these constraints, several streamlines clustering techniques have been proposed in the literature and can be divided into two main categories. The first uses regions of interest (ROIs) to select and/or exclude streamlines passing through these ROIs [7]. This strategy has been used to create WM bundle atlases [8, 9] but requires extensive knowledge of brain anatomy and inten-

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