A Novel White Matter Fibre Tracking Algorithm Using Probabilistic Tractography and Average Curves

Nagulan Ratnarajah¹, Andrew Simmons^{2,3}, Oleg Davydov⁴, and Ali Hojjatoleslami¹

¹ Medical Image Computing, School of BioSciences, University of Kent, U.K.

² Neuroimaging Department, Institute of Psychiatry, Kings College London, U.K.

³ NIHR Biomedical Research Centre for Mental Health at the South London and Maudsley

NHS Foundation Trust and Institute of Psychiatry, King's College London, U.K.

⁴ Department of Mathematics and Statistics, University of Strathclyde, Glasgow, U.K.

Abstract. This paper presents a novel white matter fibre tractography approach using average curves of probabilistic fibre tracking measures. We compute "representative" curves from the original probabilistic curve-set using two different averaging methods. These typical curves overcome a number of the limitations of deterministic and probabilistic approaches. They produce strong connections to every anatomically distinct fibre tract from a seed point and also convey important information about the underlying probability distribution. A new clustering algorithm is employed to separate fibres into branches before applying averaging methods. The performance of the technique is verified on a wide range of seed points using a phantom dataset and an *in vivo* dataset.

1 Introduction

Fibre tractography using diffusion tensor magnetic resonance imaging (DT-MRI) is a promising method for reconstructing the pathways of white matter fasciculi in the human brain noninvasively. A variety of algorithms have been proposed aiming to generate fibre-tract trajectories [1-5]. Generally these algorithms can be categorised into two main types, deterministic and probabilistic. Deterministic approaches are capable of creating anatomically reliable reconstructions of major white matter tracts. However, they do not correctly deal with branching of white matter tracts as such techniques produce only one path per seed point and there is no measure describing the confidence or uncertainty of the reconstructed trajectories. Probabilistic tractography algorithms have been developed to overcome these shortcomings.

The aim of probabilistic tracking methods is to provide a natural approach for modelling uncertainty and generate multiple curves originating from a seed point. Probabilistic methods have also been developed to resolve fibre crossings at the intravoxel level [6] and these methods allow branching of white matter tracts. However, the deterministic tractography approaches have several advantages over probabilistic tractography for some applications such as neurosurgery. Firstly, visualization of the deterministic streamline trajectories is similar to the expected *in vivo* white matter fibre tracts, whereas the output of probabilistic methods is a connectivity map, which is not a single well-defined trajectory, but rather a spatial distribution. These connectivity maps contain dense 3D volumes of potential connectivities, which cannot be easily inspected. The determination of a connectivity map is also a time-consuming process and requires