

**SEMIPARAMETRIC GEOMETRIC METHODS FOR EXTRACTING
AND MODELING WHITE MATTER VOLUMETRIC STRUCTURES
OF THE BRAIN**

by

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Abstract

There are important questions that require an understanding of white matter connectivity in the brain, such as how the brain integrates sensory inputs, how white matter tissue and connections are altered by disease, or how cancer tumors should be excised without destroying healthy tissues. These questions require a global understanding of the geometric nature of white matter tissue as well as the organization of white matter structure in local regions of the brain. This thesis presents novel approaches and methods that simultaneously combine local and global geometry of white matter into a single model.

The methods presented in this thesis are called Semiparametric Geometric Modeling (SGM). The SGM fits a nonlinear manifold to Diffusion Weighted Magnetic Resonance Imaging data and produces a nonlinear coordinate system. Specifically, an SGM simultaneously extracts white matter structures and produces a set of functions that together define a model of the white matter. An SGM produces manifold models of the physical white matter structures. This allows the physical structures to be mapped by a multi-dimensional, nonlinear coordinate system that allows points, curves, surfaces, and volumes to be defined by the manifold model. Associated SGM functions can interpolate to the level of a single neural fiber, reveal the path of nerve fiber bundles, and be used to study the interaction e.g. crossing, touching, bifurcating, of fiber bundles throughout the brain. SGM functions can be used to query the manifold structure, allowing data to be organized so as to enable methods such as Functional Data Analysis to be used for statistical analysis of the data.

Software to build SGMs was implemented and a series of experiments were carried out on Diffusion Weighted Magnetic Resonance Imaging data. The data consisted of control subjects and subjects with autism. An SGM was used to simultaneously extract and model two structures for each subject: a portion of the genu of the corpus callosum and the right corticospinal tract. The SGMs were used to map data from imaging space to curves on the manifold. These data curves were the input for group differential analysis using Functional Data Analysis. Group differences were found, based on these structures that are consistent with results from other sources. However, the results also indicate that the group differences were the result of differences in rates in change in data distributions along the structure rather than simply point-wise differences in data at specific locations.