

Abstract

This thesis contains original contributions to many different aspects of diffusion weighted MR imaging (dMRI), from the signal reconstruction, via propagation of tracks, clustering of tracks, detection of bundles of tracks, and creation of atlases of white matter, to visualization tools with high interactivity with data, and for several brains simultaneously.

Our most important new achievements are a powerful way of reconstructing the diffusion signal and a method for simplifying tractographies using a new super-efficient clustering algorithm.

In more detail we give novel and robust solutions for all the following problems

- **How to reconstruct and interpret the directional information in the diffusion signal:**

We compare and evaluate different Cartesian-grid q-space dMRI acquisition schemes, using methods based on the inverse Fourier transform of the diffusion signal, with reconstructions by diffusion spectrum imaging or generalised q-ball imaging methods. These are applied to both software phantom and human data. We propose a new reconstruction method diffusion nbla imaging (DNI) which works with the same grid type of acquisition schemes, using an algorithm that directly approximates the orientation distribution function using the Laplacian of the signal in q-space.

- **How to integrate tracks from voxel to voxel:**

Most previously published reconstruction methods are closely linked to their own specific track integration method. We have formulated a general, free-standing, data-representative, non-inferential, fast, deterministic tractography algorithm (EuDX) which is based on Euler integration and trilinear interpolation, which works with voxel level information about fibre orientations including multiple crossings, and employs a range of stopping criteria. The purpose of this algorithm is to be faithful to the reconstruction results rather than try to correct or enhance them by introducing regional or global considerations.

- **How to cluster tracks together into meaningful bundles:**

We have developed an entirely new, fully automatic, linear time, clustering method (QuickBundles) which reduces massive tractographies into just a few bundles. These bundles are characterised by representative tracks which are multi-purpose and can be used for interaction with the data or as the basis for applying higher-complexity clustering methods which would have been impossible or too slow with the full data set. QuickBundles is currently the fastest known tractography clustering algorithm.

- **How to directly register tractographies:**

After applying QuickBundles to tractographies from different subjects, we show how to use the representative tracks to identify robust landmarks within each subject which, with similarity metrics which we have introduced, we use to directly register the different tractographies together in a highly efficient way. We believe the resulting correspondences provide important evidence for the anatomical plausibility of the derived bundles. We demonstrate how these methods can be used for group analysis, and for atlas creation.

This thesis contributes to the understanding of the diffusion signal in the context of dMRI acquisitions and builds on this foundation towards a more robust brain tractography which hopefully approximates more closely the underlying fibre architecture.