Summary

Advances in diffusion MRI acquisition and processing in the Human Connectome Project

By Sotiropoulos, 2013

Background:

Structural connectivity analysis of human brains benefit from 2 main techniques, diffusion MRI and tractography algorithms. The tractography algorithms help to localize fibre bundles within white matters so that we can study specific brain pathways. Problems remain when people want to analyse the whole brain connectivity since it cannot show the quantitative connections of those pathways. To solve this problem, higher-quality data and better approaches to analyse data are needed. That's exactly what HCP (Human Connectome Project) is doing.

HCP:

This project aims at mapping the macroscopic connections of human brains and their variability in health adults. It provides data and analysis pipelines of 1200 healthy adults. HCP is unique for its diversity of imaging modalities and richness of the behavioral and genetic information. Also it has undertaken major improvements in methodology and instrumentation in order to significantly advance the quality of data acquisition techniques for brain connectivity studies.

Multi-shell applications in dMRI acquisition protocol:

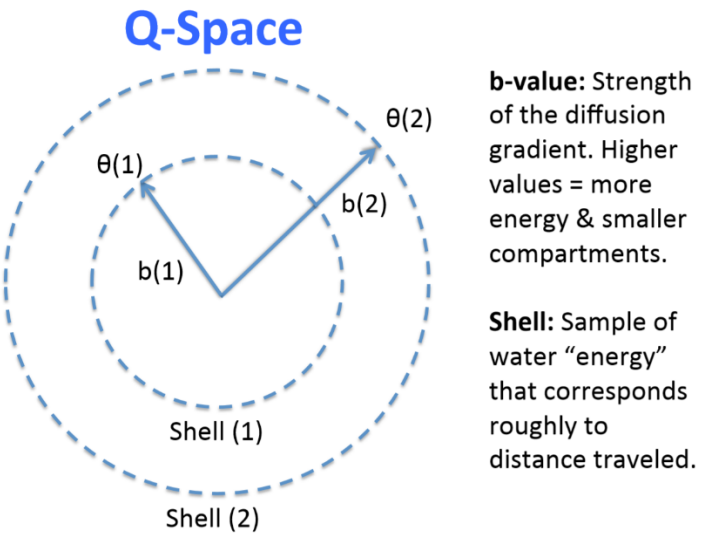
The advances people made by using multi-shell happened in several aspects: accelerated imaging, Q-space sampling, spatial resolution, while other aspects (gradient nonlinearities,) do not include multi-shell.

Accelerated imaging: (×)

Data acquisitions accelerate using simultaneous multi-slice echo planar imaging with multiband excitation and multiple receivers. However, MB3 scans were found to be superior when estimating fibre complexity, especially crossing fibre sensitivity, compared to MB1 scan using multi-shell.

Q-space sampling: (√)

Q-space sampling options include: HARDI (high angular resolution), multi-shells, Cartesian grids (similar to multi-shells). Multi-shell scheme shows a better sensitivity for detecting fibre crossings.



In all, multi-shell schemes apply mainly to q-space sampling in the applications in dMRI acquisition protocol.

Multi-shell data processed in diffusion MRI pipelines:

The pipelines include processes of image reconstruction, distortion correction, fibre orientation estimation, tractography, computing using GPUs

Distortion correction:

Researchers have already developed an approach that considers and corrects all types of distortions, susceptibility and eddy-current induced, as well as head motion. The distortion correction is based on the idea of manipulating the acquisitions so that a given field inhomogeneity manifests itself differently in different images. One can then use a generative model to make predictions about what the 3D dMRI volumes should look like. Inversion of this model enables accurate estimation of the corrected data. They apply Gaussian Process predictor to the raw signals collected and then compute the signal variance and the noise variance. In the case of multi-shell data, there is one signal variance per shell and a common noise variance.

Fibre orientation estimation:

Figs. 8 highlight the difference in crossing-fibre sensitivity between single shell and multi-shells. Fig. 8 shows the better sensitivity of the multi-shell approach in detecting crossings at the centrum semiovale. Note for instance the more continuous anterior–posterior orientations (green vectors, close to yellow arrows) that are resolved using the multi-shell approach. These orientations are representative of longitudinal fibres.

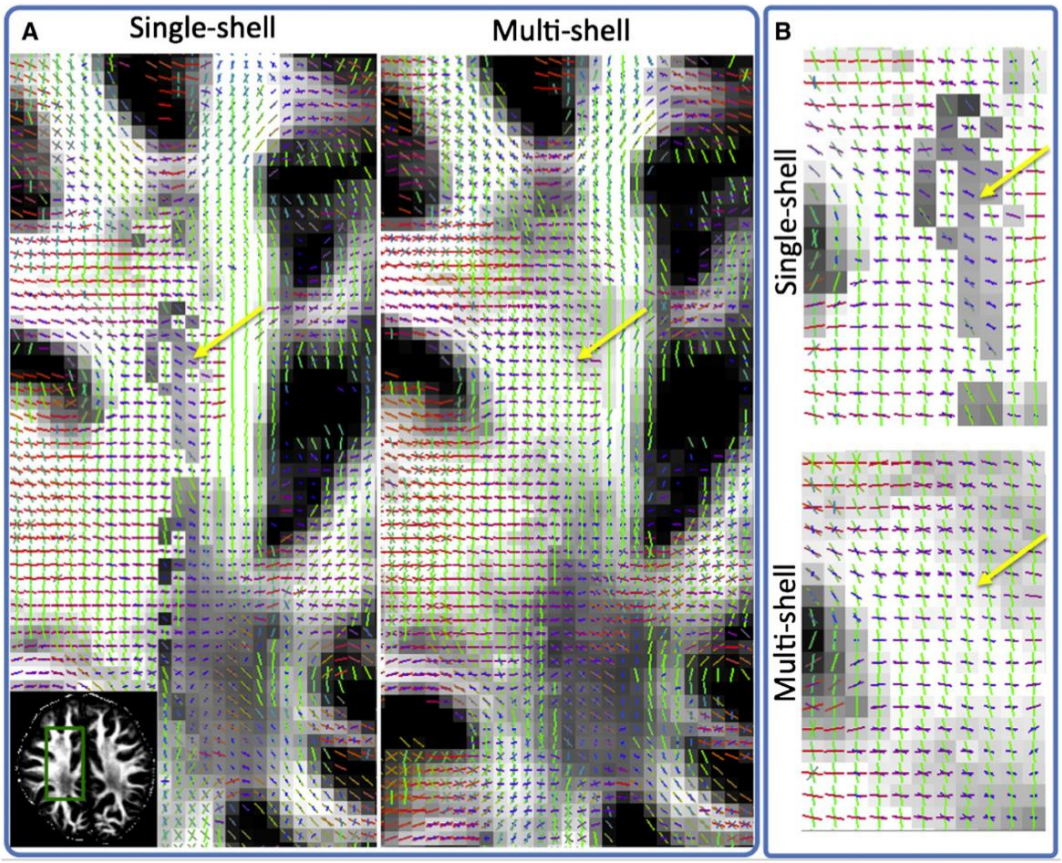


Fig. 8. Fibre orientations (RGB-color coded red: left–right, green: anterior–posterior, blue: inferior–superior) using single and multi-shell datasets, matched for acquisition time (spatial resolution 1.25 mm isotropic) (axial views). The single-shell ball & stick (Behrens et al., 2007) and its multi-shell extension (Jbabdi et al., 2012) have been employed for the respective datasets (each with up to three fibre compartments per voxel). Yellow arrows show example areas of improvement using multi-shell as discussed in main text. Zoomed-in versions of these areas are shown in panel B. Orientation vectors are superimposed on gray-scale maps representing the total anisotropic volume fraction in each voxel (i.e. the sum of volume fractions of compartments that model anisotropic diffusion in the multi-compartment ball & stick model). Orientations are shown only when the respective volume fraction is larger than 5%.

Due to the benefits, multi-shell approach was used for the HCP datasets. People estimated fibre orientations and their uncertainty using Bayesian inference on the multi-shell spherical deconvolution framework and a Rician noise model.

Conclusion about multi-shells:

Multi-shells data mostly happen in Q-space sampling, different in b-vectors with single-shell data. Multi-shell schemes (and multi-shell spherical deconvolution) offer greater sensitivity for resolving complex fibre geometries than single-shell schemes (and single-shell deconvolution), which are widely used and can be found in the HCP datasets.