A HYBRID DIFFUSION IMAGING ATLAS IN Q-SPACE

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Introduction

A recent acquisition and diffusion encoding strategy, called hybrid diffusion imaging (HYDI) [1], consists of acquiring multiple shells of constant diffusion weighting. In the context of diffusion weighted imaging (DWI) in general (and HYDI in particular), the number of methods for atlas construction (and registration) is at least equal to the number of possible models which can be reconstructed from the original data in q-space. Therefore, we aim at constructing an atlas ***before*** the reconstruction of any of these models: a HYDI atlas containing signal functions for multiple shells of q-space. From this generalized atlas, any model can still be reconstructed to the fullest possible extent.

Materials & Methods

All methods involved in the construction of the atlas are free of the reconstruction of any particular DWI models, and as such are independent of and unbiased by them.

Acquisition

Data were acquired from 10 healthy subjects on a Siemens 3T scanner, with a 2.5*mm* isotropic voxel size and using a HYDI approach: 10 repetitions of b = 0*s/mm²* (averaged), 25 gradient directions at b = 700*s/mm²*, 40 gradient directions at b = 1000*s/mm²* and 75 gradient directions at b = 2800*s/mm²*.

Matching

We constructed a multi-subject multi-channel diffeomorphic matching algorithm which brings all subjects simultaneously into correspondence in the average subject space. We used 7 "channels" to guide the matching process. The first is the average B0. For the other ones, we calculated the apparent diffusion coefficient (ADC) for all measurements on the b700, b1000 and b2800 shells. The next 3 channels are calculated as the average ADC for each of these shells. The final 3 channels consist of a generalized fractional anisotropy (GFA) measure, calculated by *std(ADC)/rms(ADC)* for all 3 shells. At each iteration, the algorithm calculates in every voxel an unconstrained symmetric demons force [2] between each pair of subjects, for all channels. For each subject, the 9x7=63 force fields acting on that particular subject are averaged, resulting in its unconstrained update field. A fluid regularization (Gaussian filter) is applied to each update field. The diffeomorphic update step [2] (composition of the partial solution with the exponential of the update field) is then applied for each subject. An elastic regularization (Gaussian filter) is applied to each partial solution. Finally, for each subject, all channel images are deformed by the partial solution. The algorithm iterates until convergence. We ran this algorithm 3 times: the second and third time use the output from the previous run for initialization. During the first run, the maximum step size as well as sigma for both the fluid and the elastic regularization are set to 2. The second run uses a value of 1 for all parameters. The third and final run has them set at 0.5. The final output consists of 10 "pull-back" deformation fields: one for each subject.

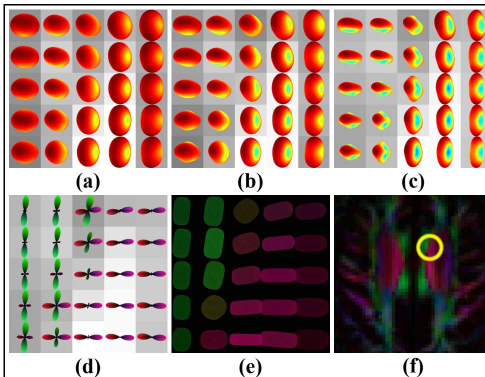

Fig. 1. 5x5 voxel detail of: **(a-b-c)** the actual atlas, i.e. 3 shells (b700, b1000, b2800) of q-space, **(d)** fODF's reconstructed from b2800, **(e)** tensors reconstructed from b1000. **(f)** shows the location of this 5x5 region.

Deformation and averaging

Deforming DWI data is a challenge of its own because of the angular dependence between the data and the underlying microstructure of the tissue: a retransformation step is needed for every sampled voxel. We used a recently proposed method [3] to retransform our sampled shells in q-space. To this end, we represented each shell of signal measurements (divided by the average B0) in a symmetric real spherical harmonics (SH) basis of order 6. This was achieved using a linear least-squares method while incorporating a local Laplace-Beltrami regularization with lambda = 0.006. Based on the Jacobian matrix of the deformation field at each voxel, the 3 shells where independently retransformed while preserving isotropic and anisotropic volume fractions [3], using 300 uniformly distributed directions (obtained by electrostatic repulsion) and a single fiber response function shaped by eigenvalues 0.0018*s/mm²* and 0.0003*s/mm²*. The SH coefficients of the retransformed shells were then averaged over all 10 subjects. This finally yielded the atlas. Each voxel of this atlas contains 3x28 SH coefficients that analytically represent 3 shells of q-space: b700, b1000 and b2800.

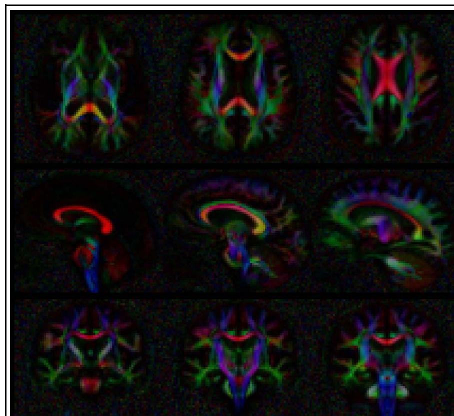

Fig. 2. Preview of some CFA maps of the tensors reconstructed from the b1000 shell

Results

The result is a full brain atlas with analytical representations of 3 shells of q-space data. For all purposes of reconstruction, these shells can be sampled by any set of directions (or the SH representations themselves can be used). A 5x5 voxel detail of the atlas is presented in Fig. 1a-b-c. The area shown is in a region where the cingulum passes closely over the corpus callosum: it contains single fiber as well as 2-fiber voxels. The region is also indicated on a larger axial slice in Fig. 1f. As an example of the possibilities, we made 2 reconstructions: tensors (i.e. diffusion tensor imaging (DTI)) from the b1000 shell and fiber orientation distribution functions (fODF's) using spherical deconvolution on the b2800 shell. The results are shown in Fig. 1d-e. From the reconstructed tensors, we also calculated color-encoded fractional anisotropy (CFA) maps, some of which are shown in Fig. 2. In the atlas and these reconstructions, we could clearly identify all known structures, even voxel sized ones. This indicates that the combination of the matching and deformation algorithms must have brought the subjects in very good correspondence, as well spatially as on the level of the angular structure and orientation of the shells in each voxel. This was further confirmed by inspecting the transformed images before they were averaged. The averaging itself has also successfully suppressed most of the noise on the angular structure of the shells, resulting in smooth but clearly structured shells in the atlas.
Future work might include the reconstruction of other diffusion models and measures from the atlas (so as to fully exploit all information contained within), such as: a full brain fiber tractography on fODF's from constrained spherical deconvolution (CSD), the kurtosis tensor from diffusion kurtosis imaging (DKI), the ensemble average diffusion propagator (EAP) from diffusion propagator imaging (DPI), ... amongst others.

References

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