Comparison of novel ICA-based approach to existing diffusion MRI multi-fiber reconstruction methods

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Introduction:
Fiber tractography derived from diffusion-weighted MRI (DW-MRI) uniquely reveals the complex white-matter pathways of the human-brain, *in vivo*. The most common approach to DW-MRI analysis, Diffusion Tensor Imaging (DTI), is limited to representing a single-fiber direction per voxel, which has lead to several "multiple-fibers per voxel" alternatives to resolve complex intra-voxel geometry such as crossing- and kissing-fibers. This work compares a novel Independent Component Analysis (ICA) based approach [1] to four alternative methods, and specifically examines results when data acquisition is limited. The performance of methods when processing limited sample data is unclear and remains an important consideration as it is often the case in clinical environments, where acquisition time is constrained. We present quantitative tractography results obtained from five different multi-fiber analysis methods applied to two physical phantoms and human data. Also, results from a "full-sample" data set are compared to those from a "limited-sample" data set, which has approximately half the number of samples.

Methods:
The five multi-fiber analysis methods chosen include ICA [1], Generalized q-Sampling Imaging (GQI) [2], Constrained Spherical Deconvolution (CSD) [3], analytical Q-Ball Imaging (QBI) [4] and Higher-Order Tensor (HOT) [5]. In-house codes were used for ICA and analytical QBI, mrTrix [6] was used for CSD, DSI Studio [7] for GQI, and code by Barmpoutis [8] for HOT. The phantom data analyzed included FiberCup [9] (3x3x3mm^3 voxels, b=1500 s/mm^2, 64 gradient directions) and BrainVoyager [10] (2x2x2mm^3 voxels, b = 1000 s/mm^2, 49 gradient directions). The human data was acquired from a normal elderly subject on a 3T MRI with 2.03x2.03x4mm^3 voxels, b=1000 s/mm^2, and 25 gradient directions, in approximately 7 minutes as part of a clinical study.

Quantitative metrics were used to objectively compare the resulting tractography. For the FiberCup phantom, the L2 norm error between the known ground truth and estimated fiber pathway was evaluated using code provided by the FiberCup authors [9]. For the BrainVoyager phantom and human data, the evaluation metric was the fraction of tracts propagating successfully from a seed region to target region through one or more crossing regions.

From both phantom data sets, a "limited-sample" data set was created by selecting the data corresponding to 25 uniformly distributed gradient directions. The limited sample data set was idealized as representative of what could be acquired under time constrained clinical scanning situations, as in our elderly subject data. The limited sample data was processed using the exact same methods as the full-sample data set.

Results:
Figures 1, 2 and 3 illustrate filtered tractography results of the FiberCup phantom, BrainVoyager phantom, and human data, respectively. The individual figures include the metric scores for quantitative comparison.

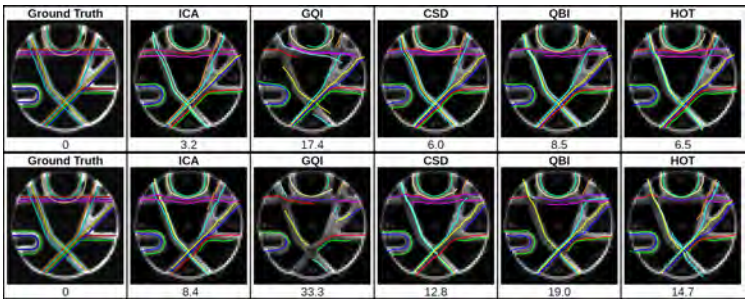

Figure 1 - FiberCup tractography. Only tracts through specific ROI voxels shown along with corresponding average L2 norm error metric listed under each approach. (top-row) 64-gradient direction data, (bottom-row) 25-gradient data.

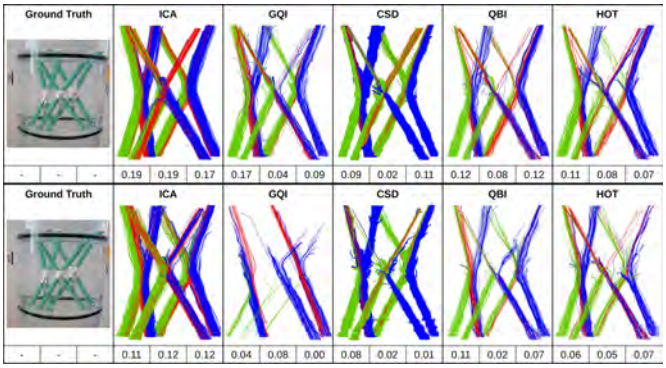

Figure 2 - BrainVoyager tractography. (red) Tracts propagating successfully through the crossing regions, (blue or green) tracts that steer in the wrong direction. The fraction of tracts propagating correctly through the 30°, 50° and 65° crossing are listed under each approach. (top-row) 49-gradient direction data, (bottom-row) 25-gradient data.

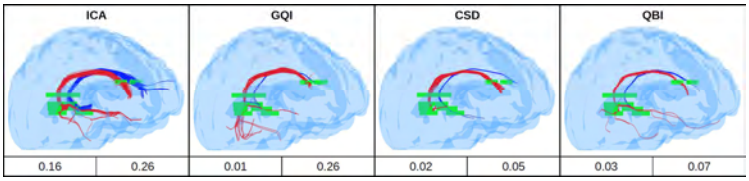

Figure 3 - Human cingulum tracts starting from a hippocampal ROI and successfully reaching the anterior cingulate. (blue) Left and (red) Right cingulum. The fraction of left and right cingulum tracts successfully reaching the anterior ROI are listed under each approach.

Discussion:
Figure 1 indicates lower L2 norm (error) for the ICA method compared to all alternatives, and this is emphasized in the limited sampling (25 gradient direction) results. Also, ICA was the only method that lead to "full-length" tracts covering the extent of the phantoms fiber pathways. In Figure 2, ICA generates a greater fraction of tracts that successfully propagate through the crossing region, for each of the different crossing angles, and again performed better under limited sampling. Lastly, in Figure 3, the ICA approach leads to a greater number of cingulum tracts, and also more complete cingulum than the other methods. Results are not included for HOT in Figure 3 due to the prohibitive computation time that was estimated for processing data using that method (~23 hours).

All the results show the versatility of this novel ICA-based approach to estimating multiple fiber orientations, particularly when applied to data sets of limited gradient sampling likely to be acquired in clinical studies. ICA could also be used to process data already acquired in many clinical studies.

References:
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