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New insights from the IronTract challenge: Simple post-processing enhances the accuracy of diffusion tractography

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Synopsis

We present results from round 2 of IronTract, the first challenge to evaluate the accuracy of tractography using i) tracer injections and diffusion MRI from the same macaque brains, and ii) DSI and HCP two-shell diffusion acquisition schemes. In round 1, only two teams achieved similarly high performance between the two different injection sites that we used for training and validation. Here we investigate the extent to which this was due to the pre- and post-processing used by those teams. We show that, when other teams use the same pre- and post-processing, their accuracy and robustness can improve as well.

Introduction

The IronTract challenge evaluates the accuracy of diffusion MRI (dMRI) tractography methods by comparing them to anatomical tracing, using dMRI and tracer data from the same macaque brains. We investigate which dMRI analysis methods lead to optimal accuracy for the two-shell acquisition scheme of the lifespan and disease HCP. Results from round 1 (R1) showed that, when analysis methods were optimized, the HCP acquisition could achieve similar accuracy as a more demanding DSI acquisition¹. However, only two out of twelve teams could achieve as high performance on the injection/seed area used for validation (vIPFC) as on the one used for training (frontal pole). Here we seek to disentangle the contributions of the dMRI pre- and post-processing methods from those of the orientation reconstruction and tractography methods, by asking all participants in round 2 (R2) to use the same pre- and post-processing as the two teams that achieved robustness across the two injection sites in R1.

Methods

Details on data collection, including in-vivo tracing and ex-vivo dMRI, have been described previously¹⁻³. In R2, all teams used data that had undergone pre-processing by Team1 (denoising⁴ and Gibbs ringing correction with MRtrix3^{5,6}, and motion/eddy-current correction with FSL^{7,8}). All teams were also provided with scripts that implemented the R1 post-processing strategies of Team1 (Gaussian filtering with sigma=0.5 to increase coverage, followed by iterative thresholding of 200 steps on the log of the streamline count) and Team2 (inclusion ROIs from the PennCHOP macaque atlas⁹, based on general knowledge of projections of the prefrontal cortex). The challenge was administered on the QMENTA platform (qmenta.com/irontract-challenge/). As in R1, participants were blind to the tracer data. Each team submitted tractography volumes thresholded at multiple levels. For each level, the true positive rate (TPR) and false positive rate (FPR) of tractography was computed by voxel-wise comparison to the tracer data. The score was the area under the ROC curve (AUC), for FPRs in [0,0.3]. Thus the maximum AUC was 0.3. For the training case, participants were shown their AUC after uploading their tractography results. They could repeat this up to ten times and fine-tune the free parameters of their methods to optimize their AUC. They then applied the fine-tuned methods to the data of the validation case. Each of the teams that had participated in R1 had to submit results with the orientation reconstruction and tractography methods that they had used in R1, but could also submit results with new methods. We ranked submissions based on overall best AUC score in the validation case.

Results

Of the twelve teams that completed R2, nine had also completed R1, while three were new. There was a total of 247 submissions (training: 99, validation: 148) and 50 final submissions that were ranked. Orientation reconstruction and tractography algorithms used by each team are reported in Fig. 1. The performance of most returning teams improved when compared to R1, as a result of applying the pre- and post-processing of Team1 and Team2. This improvement was greater for the validation case (2%-85%) than the training case (2%-30%) (Fig. 2a-b,d-e). For teams that had achieved much lower accuracy on the validation case than the training case in R1, this difference decreased substantially in R2 (Fig. 2c,f). Thus many more teams achieved similar performance between the training and validation case in R2 (Fig. 3a). Of the two post-processing strategies, the use of a priori inclusion ROIs led to consistently higher TPR at the same FPR for all submissions, as expected. Remarkably, the use of Gaussian filtering, which does not assume any prior anatomical knowledge, also improved results for most submissions (Fig. 3b). Only two teams (6 and 8) did not show improvement with Gaussian filtering and one of them (8) did not show improvement (9). Fig. 4 shows histograms of true positives of tractography compared to the tracing, across all teams. Despite the improved coverage resulting from optimized pre- and post-processing, certain brain regions continue to pose challenges for most teams. Examples of such brain areas where errors occur are shown in Fig. 5.

Discussion and Conclusion

The injection sites of the training and validation case, while projecting through similar white-matter pathways (Fig. 5), follow very different routes to reach these pathways⁹ and pose different challenges to tractography. Most submissions made errors in anatomical locations where fibers from the injection site cross bigger bundles, branch into smaller bundles, travel through bottle-neck regions, or take sharp turns (Fig. 4b-c for some examples). The post-processing used here improved accuracy in these regions and decreased accuracy differences between the two injection sites. However, even after harmonizing pre- and post-processing across teams, Team1 continued to achieve the highest accuracy. When using DSI data, Team1 could reach a

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TPR as high as 0.96 at FPR=0.1. This suggests that the orientation reconstruction method employed by this team (RUMBA-SD10), in combination with probabilistic tractography, contributed to its high performance.

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Figures



Figure 1. The figure displays the orientation reconstruction and tractography methods, as well as the number of submissions, for each team. RUMBA-SD: robust and unbiased model-based spherical deconvolution¹⁰; CSD: constrained spherical deconvolution¹¹; MSMT-CSD: multi-shell multi-tissue CSD^{12,13}; 3-Comp: three-compartment model¹⁴; ASI: asymmetry spectrum imaging¹⁵; GQI: generalized q-ball imaging¹⁶; RL-CSD: Richardson-Lucy CSD¹⁷.



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Figure 2. Top row: HCP acquisition. **Bottom row**: DSI acquisition. (a,d) Percent change in AUC scores between R1 and R2 submissions for training and validation cases, where R2 submissions were post-processed with Gaussian filtering. (b,e) As above, for R2 submissions post-processed with anatomical ROIs. (c,f) Difference in AUC scores between the training and validation cases, for R1 and for each of the two post-processing strategies in R2.



Figure 3. Top row: AUC scores for the training and validation cases, with standard error bars showing the variability across each team's submissions (left: HCP; right: DSI). Bottom row: TPR at FPR=0.1 for the validation case, in R1 and with each of the two post-processing strategies in R2 (left: HCP; right: DSI).



Figure 4. Maximum intensity projections of the number of teams that achieved a true positive at FPR = 0.1, for the HCP acquisition scheme. The tracer, shown in blue, is overlaid with the true positive histograms, shown as heat maps. Results are shown for the training and validation case, and for R1 and the two post-processing strategies (Gaussian filtering, anatomical ROIs) in R2. Cyan arrows point to regions where post-processing led to improvement.



Figure 5. Challenging areas for tractography. (a) Training and validation injections. (b) Training: Streamlines follow the ILF, instead of crossing it to continue into the UF (left). Streamlines do not reach the superior orbitofrontal WM (right). (c) Validation: Streamlines follow EC instead of entering IC (left). Streamlines jump onto EC instead of projecting medially (right). EC: external capsule. IC: internal capsule. ILF: inferior longitudinal fasciculus. UF: uncinate fasciculus.

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