Tractography Gone Wild: Probabilistic Tracking Using the Wild Bootstrap

D. K. Jones[1]

[1]Centre for Neuroimaging Sciences, Institute of Psychiatry, London, United Kingdom

INTRODUCTION: DT-MRI is inherently a noisy technique, leading to uncertainty in estimates of the eigensystem of the diffusion tensor[1,2]. Many tractography algorithms (particularly streamline approaches, e.g. 3,4) do not account for this uncertainty and thus provide no indication of the confidence one can assign to reconstructed pathways. Probabilistic approaches attempt to assign such a confidence, but typically do so by making *a priori* assumptions about the data. In contrast, bootstrap DT-MRI[2] derives the uncertainty from the data itself without making any assumptions and has been used previously to derive uncertainty in the tensor eigensystem[2,5]. Bootstrapping has been combined with tractography to create confidence maps for fiber trajectories[6,7] and to examine *distributions* of parameters (principal eigenvector, eigenvalues, FA) at each vertex of a streamline as a way of identifying a range of artefacts[8]. While the limited assumptions of the bootstrap make it an attractive option, the time required to collect sufficient data for accurate and precise bootstrapping can be prohibitive[9], leading to reduced subject compliance and increased movement artefact. Whitcher *et al*.[9] recently proposed an alternative approach to deriving distributions of tensor-derived parameters using the Wild Bootstrap[10]. In brief, this approach obtains probability distributions for model-parameters by permuting the residuals to the fitted model and refitting the model (see ref. 11 for full details). The huge advantage over previously implemented bootstrap methods is that it does not require the collection of extra data, and therefore brings the technique into the clinical realm. Whitcher *et al.* have shown that results obtained with the wild bootstrap are comparable with the 'conventional' bootstrap[10] when considering data on a voxel-by-voxel basis. Here we combine the Wild Bootstrap with tractography and show 'probabilistic' tracking results that are comparable with those from the (much more time-consuming) conventional bootstrap.

METHODS: Acquisition: Data were collected on a GE 1.5T system with 40 mT/m gradients using an optimized and peripherally-gated multislice single-shot EPI sequence. The data set consisted of 9 replicates of 34 images acquired at each slice location: 4 B = 0 images and 30 diffusion-weighted images in which gradient directions were isotropically distributed. Subject motion and eddy current distortions were corrected using the approach described elsewhere[12]. Full details of the acquisition are provided in ref. 6. **Bootstrap Analysis:** For 'conventional' bootstrapping, all nine replicates were used and 1000 bootstrapped estimates of the tensor volume were generated, using the approach described in ref .6. For the Wild Bootstrap, only the first replicate of 34 images per slice location was used and 1000 tensor volumes generated by permuting residuals to the fitted tensor[10,11]**.** In each of the 1000 volumes, tracking was initiated from a series of seedpoints using the algorithm described elsewhere[12]. At each vertex of the streamline, the 95% cone of uncertainty[5] in fiber orientation was derived and visualized along with the trajectory using hyperstreamlines [8,14]. 'Visitation' maps were generated by coloring each voxel in the data set according to how many of the bootstrapped trajectories passed through it[6,7].

RESULTS: Fig. 1 shows Wild and Conventional bootstrapping results obtained from a seedpoint placed in the internal capsule. The topologies of the bootstrapped volumes are similar. Both methods indicate that a number of 'deterministic' streamlines erroneously cross the pons and project into the contralateral hemisphere. The pseudo-probabilistic maps (B and C) allow a more qualitative comparison. Anatomically implausible pathways are mostly represented by low visitation counts. When thresholded at > 50% visitation count, the results from the two methods are almost identical – suggesting a very plausible route from the cerebral peduncle to the motor-strip. Figure 2 shows results from a seed placed in the superior longitudinal fasciculus – where both methods depict large uncertainty 'bumps' in the hyperstreamlines in almost identical positions (i.e., at places of branching) Although the bootstrapped trajectories are complex in nature, the reconstructions obtained with the two techniques are surprisingly similar.

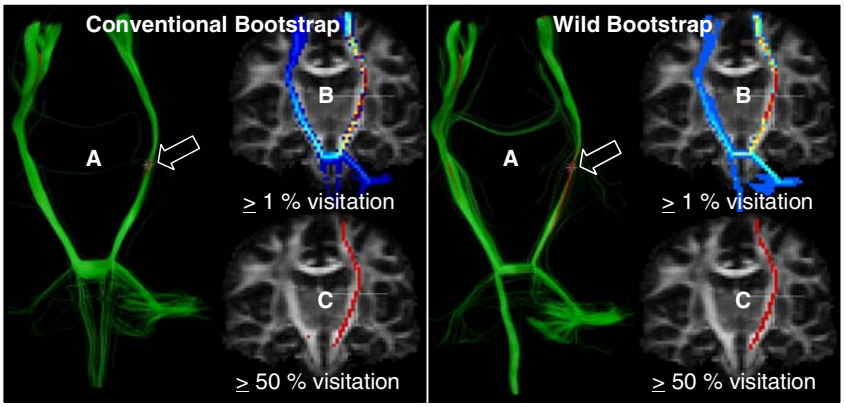

Figure 1. Conventional and wild bootstrap results from seedpoint placed in the cortico-spinal tract (location of seedpoint is indicated by the arrow). A. shows bootstrapped trajectories with translucent tubes, such that more overlap of tracts = more opacity. The trajectory computed from the superset of 9×34 images is represented by the red tube. **B** and **C** show the visitation maps thresholded at ≥1% and ≥50% respectively.

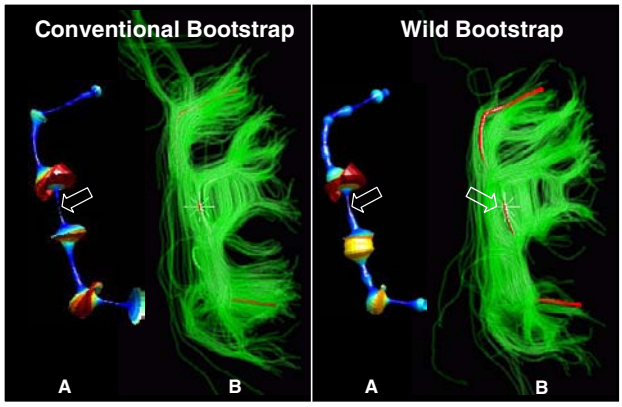

Figure 2. Results obtained in the superior longitudinal fasciculus, viewed from directly above. **A** shows the superset streamline trajectory encoded using a *hyperstreamline* for the 95% confidence interval in the principal eigenvector orientation. **B**. shows the individual bootstrapped (green) and superset (red) trajectories.

DISCUSSION/ CONCLUSION: The results suggest that Wild Bootstrap Tractography performed on a data set containing only 34 images per slice location gives results that are surprisingly similar to those obtained using 'conventional' bootstrapping on a data set containing (9 ×34 = 306) images per slice location, allowing assessment of the confidence that can be assigned to a given pathway with data collected in a clinically appropriate time. Importantly, this approach can be used by any researcher to retrospectively assign confidence levels to tracking results they have previously obtained using deterministic tracking algorithms. As the technique does not require acquisition of additional data, previously reported bootstrap methods (e.g. bootstrap tractography[6,7] and PASTA[8]) can now be applied to 'regular' DT-MRI data sets acquired within a clinically feasible time.

REFERENCES: 1. Basser et al. *Proc ISMRM* 1997, 1740 ; **2.** Pajevic et al. *J Mag Res*. 2003;161:1- ; **3**. Mori et al. *Ann Neurol* 1999; 45:265- ; **4.** Conturo *et al*. PNAS 1999; 96:10422- ; **5.** Jones MRM 2003; 49: 7- ; **6.** Jones et al. MRM 2005:53:1143-; **7.** Lazar and Alexander *NeuroImage* 2005;15:524- ; **8.** Jones et al. 53: 1462- ; **9.** O'Gorman et al. *Proc ISMRM* 2005, 225; **10.** Whitcher et al. *Proc ISMRM* 2005, 1333 ; **11.** Liu *Ann Stat*. 1998;16:1696. **12.** Rohde et al. *MRM* 2004; 51:103.**13.** Basser et al. *MRM* 2000; 44: 625-.**14.** Delmarcelle *et al*. *IEEE Comput Graph Appl* 199313:25-.