

MICCAI DiSCo Challenge Team Report

*Thank you for participating. Please fill one report per team then rename it **TeamName_Report.doc** and email this report alongside a zip file containing your connectivity matrices to challenge.disco2021@gmail.com. The zip file should be named **TeamName_Submissions.zip**. Each submission (a 16x16 matrix in a text file format) should be named **TeamName_Submission_XY.txt**, where **XY** is a unique index (e.g. 01 for the first submission, 02 for the second, etc.).*

Participants

Team Name

Please indicate the name of your team. Team names will be public. Please don't use words that could identify the team members. Your team name may be changed from the name used on the registration form.

UWMadison

Team Leader

Team member leading the submission. Primary contact for the challenge organizers.

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Team members, affiliations, and contributions

Please list all team members including their full affiliations and email addresses. Please also briefly describe their role and/or the tasks they performed.

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Submissions

Please detail your connectivity matrix estimation pipelines in the following sections. Please detail the processing steps for the different matrices whenever they differ from a main strategy. This section should be detailed enough to allow reproducibility of the processing steps leading to the submitted matrices. Please list the software used, add relevant references, and detailed the selected method parameters.

Script to help reproduce our experiments is available at <http://github.com/nadluru/disco-cdmri2021>.

Submitted Filename and number of submissions

Please indicate the number of connectivity matrices submitted. The best performing submission among the first 10 connectivity matrices will be used for the challenge leaderboard. Participants are welcome to submit more connectivity matrices, which will be used for further analysis.

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DW-MRI data Preprocessing

Signal processing steps (e.g. denoising).

Noise, Gibbs ringing and Rician bias were reduced using tools implemented in MRtrix3. This step is common for the full set of submissions.

Code snippet:

```
# mrtrix3
mrconvert dwi.nii.gz -fslgrad bvecs bvals | dwidenoise - dwi_denoised.mif -
noise noise.mif
mrdegibbs dwi_denoised.mif - | mrcalc - 2 -pow $(mrcalc noise.mif -
finite noise.mif 0 -if -) 2 -pow -sub -abs -sqrt - | mrcalc - -finite - 0 -
if rc.mif
```

Local Modeling

Voxel orientation estimations (e.g. Diffusion tensors, Constrained Spherical Deconvolution).

Fiber orientation distributions were estimated using constrained spherical deconvolution with multi-shell multi-tissue response function (dhollander algorithm with non-default options shown below) using tools implemented in MRtrix3. This step is common for the full set of submissions.

Code snippet:

```
# mrtrix3
dwi2response dhollander -lmax 0,10,10,10,10 -sfwm 1 -gm 0.5 -
csf 5 rc.mif sfwm.txt gm.txt csf.txt
dwi2fod -lmax 10,0 msmt_csd rc.mif sfwm.txt wmfod.nii.gz csf.txt csffod.nii.gz
```

Tractography Method

Trajectory estimation method (e.g. deterministic tractography).

Seed mask for the streamlines was computed by thresholding (≥ 0.02) the constant term of the spherical harmonic representation of the FODs, and keeping the largest connected component, and subtracting the node regions. This step is common for the full set of submissions.

Code snippet:

```
# mrtrix3
mrconvert wmfod.nii.gz -coord 3 0 -axes 0:2 - | mrcalc - 0.02 -ge 1 0 -if
node_rois.nii.gz -subtract 0 -ge 1 0 -if wmfod_dc_mask_sub_roi.nii.gz
```

```
# fsl
connectedcomp wmfd_dc_mask_sub_roi wmfd_dc_mask_sub_roi_conncomp
# mrtrix3
mrcalc wmfd_dc_mask_sub_roi_conncomp.nii.gz $(LabelGeometryMeasures 3 wmfd_dc_mask_sub_roi_conncomp.nii.gz | awk -F " " '{print $1,$2}' | sed 1d | sort -k2 -g -r | head -n1 | awk '{print $1}') -eq 1 0 -
if wmfd_dc_mask_sub_roi_conncomp_filtered.nii.gz
# LabelGeometryMeasures is part of ANTS
```

Streamlines were generated using TREKKER with bi-directional pathway entry constraints from the node regions. Two sets of streamlines were generated: (1) 1 million tracts (submission 01), (2) 10 million tracts (submission 02). We would like to note that TCKGEN tool from MRtrix3 gave slightly lower Pearson correlation coefficient scores on training and validation datasets compared to those from TREKKER, so we did not include those results from those attempts. We can provide those attempts if there is interest.

Code snippet: (1 million tracts)

```
# trekker
trekker -fod wmfd.nii.gz -
seed_image wmfd_dc_mask_sub_roi_conncomp_filtered.nii.gz -seed_count 1000000 -
pathway_A=require_entry node_rois.nii.gz -
pathway_B=require_entry node_rois.nii.gz -output tracts
# mrtrix3
tckconvert tracts.vtk tracts.tck
```

Code snippet: (10 million tracts)

```
parallel '
# trekker
trekker -fod wmfd.nii.gz -
seed_image wmfd_dc_mask_sub_roi_conncomp_filtered.nii.gz -seed_count 1000000 -
pathway_A=require_entry node_regions.nii.gz -
pathway_B=require_entry node_regions.nii.gz -enableOutputOverwrite -
output tracts_run_{ }
# mrtrix3
tckconvert tracts_run_{ }.vtk tracts_run_{6}.tck' ::: {01..10}
# mrtrix3
tckedit tracts_run_*.tck tracts_10M.tck
```

Tractography Post Processing

Streamlines filtering method (e.g. outlier removal).

Since the ground truth was referred to as the cross-sectional area, streamlines were assigned weights using SIFT2 in MRtrix3. Default parameters were used for the submissions 01 and 02. Additional

parameter combinations were attempted for additional submissions. We would like to note that the additional parameters combinations were not significantly different from the default combination for the training and validation datasets.

Code snippet: (submissions 01 and 02)

```
# mrtrix3
tcksift2 tracts.tck wmfd.nii.gz weights.txt
```

Code snippet: (additional submissions)

```
parallel '
tcksift2 tracts_10M.tck wmfd.nii.gz weights_{1}_{2}{3/default/}.txt -
min_td_frac {1} -
min_iters {2} $(echo {3/default/})' ::: 0.05 0.1 0.2 ::: 10 20 30 ::: default -
no_dilate_lut "-no_dilate_lut -make_null_lobes"
```

Connectivity Matrix Construction

Matrix weight estimation method (e.g. streamline count). Please indicate any further processing of the matrix (e.g. thresholding).

SIFT2 weights of the streamlines connecting each pair of the regions were summed using TCK2CONNECTOME tool in MRtrix3. Default parameters were used for submissions 01 and 02. Additional parameter combinations were attempted for additional submissions. We would like to note that the additional parameters combinations were not significantly different from the default combination for the training and validation datasets.

Code snippet: (submissions 01 and 02)

```
# mrtrix3
tck2connectome tracts.tck node_rois.nii.gz connectome.csv -
tck_weights_in weights.txt -symmetric
sed -i 's,:, :g' connectome.csv
```

Code snippet: (additional submissions)

```
parallel '
tck2connectome tracts_10M.tck node_rois.nii.gz connectome_{1}_{2}{3/default/}{4/default/}.csv -tck_weights_in weights_{1}_{2}{3/default/}.txt -
symmetric $(echo {4/default/})
sed -
i "s,:, :g" connectome_{1}_{2}{3/default/}{3/default/}.csv' ::: 0.05 0.1 0.2 :::
10 20 30 ::: default -no_dilate_lut "-no_dilate_lut -
make_null_lobes" ::: default -assignment_end_voxels "-assignment_radial_search 2"
```

References

Key references.

1. Tournier, J.D., Smith, R., Raffelt, D., Tabbara, R., Dhollander, T., Pietsch, M., Christiaens, D., Jeurissen, B., Yeh, C.H. and Connelly, A., 2019. MRtrix3: A fast, flexible and open software framework for medical image processing and visualisation. *Neuroimage*, 202, p.116137.
2. Smith, R.E., Tournier, J.D., Calamante, F. and Connelly, A., 2015. SIFT2: Enabling dense quantitative assessment of brain white matter connectivity using streamlines tractography. *Neuroimage*, 119, pp.338-351.
3. Aydogan, D.B. and Shi, Y., 2020. Parallel Transport Tractography. *IEEE Transactions on Medical Imaging*, 40(2), pp.635-647.
4. Tange, O., 2021. GNU Parallel. *Zenodo*, doi:10.5281/zenodo.5123056.
5. Jeurissen, B., Tournier, J.D., Dhollander, T., Connelly, A. and Sijbers, J., 2014. Multi-tissue constrained spherical deconvolution for improved analysis of multi-shell diffusion MRI data. *NeuroImage*, 103, pp.411-426.
6. Tournier, J.D., Calamante, F., Gadian, D.G. and Connelly, A., 2004. Direct estimation of the fiber orientation density function from diffusion-weighted MRI data using spherical deconvolution. *Neuroimage*, 23(3), pp.1176-1185.
7. Dhollander, T., Mito, R., Raffelt, D. and Connelly, A., 2019. Improved white matter response function estimation for 3-tissue constrained spherical deconvolution. In *Proc. Intl. Soc. Mag. Reson. Med* (Vol. 555).
8. Veraart, J., Novikov, D.S., Christiaens, D., Ades-Aron, B., Sijbers, J. and Fieremans, E., 2016. Denoising of diffusion MRI using random matrix theory. *Neuroimage*, 142, pp.394-406.
9. Cordero-Grande, L., Christiaens, D., Hutter, J., Price, A.N. and Hajnal, J.V., 2019. Complex diffusion-weighted image estimation via matrix recovery under general noise models. *Neuroimage*, 200, pp.391-404.
10. Kellner, E., Dhital, B., Kiselev, V.G. and Reisert, M., 2016. Gibbs-ringing artifact removal based on local subvoxel-shifts. *Magnetic resonance in medicine*, 76(5), pp.1574-1581.