

## GENERAL PROGRAM DESCRIPTION:

Dices user-defined ROIs into component voxels. Runs network tractography analyses on all possible combinations of diced ROIs and merges the resulting files into a single, “panoramic” track file.

Additional functionality for calculating edge weight needs debugging and is not included in the current version of this program, and will not be addressed further by this document. Functionality for multiple ROIs and alternative pipeline options are possible/desired for future versions, pending validation of current methodology.

Supporting scripts for calculating percentage of intra-ROI overlap, creating lists of track counts, upsampling tractography data, and performing other post-processing operations are in development.

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## FINAL OUTPUT:

1. Single network track file (.trk format), *or*
  2. Simple text file indicating if 0 network tracks were detected
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## INPUT ARGUMENTS:

|    |                                            |                                                                       |
|----|--------------------------------------------|-----------------------------------------------------------------------|
| -s | <i>Subject ID</i>                          | <user preference>                                                     |
| -t | <i>Whole-brain .trk file</i>               | Can be substituted with any .trk file of choice for the given subject |
| -R | <i>Single ROI mask file</i>                | Any nifti file                                                        |
| -N | <i>Name of ROI</i>                         | <user preference>                                                     |
| -r | <i>2<sup>nd</sup> single ROI mask file</i> | Any nifti file                                                        |
| -n | <i>Name of 2<sup>nd</sup> ROI</i>          | <user preference>                                                     |

|    |                        |                                               |
|----|------------------------|-----------------------------------------------|
| -D | <i>Dice mode</i>       | Indicates that ROIs need to be diced          |
| -e | <i>Early exit mode</i> | Will exit pantrack 'early', before networking |
| -v | <i>Verbose mode</i>    | Debugging only; not “user friendly”           |
| -h | <i>Help</i>            | Prints usage to terminal                      |

The first two arguments are not required if *pantrack\_prepare* is first executed. This is a simple script that stores the subject ID and reference whole-brain track file for user convenience.

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## ROI PROCESSING STEPS:

1. ROIs tested for program compatibility; *exits if non-integer format or multiple intensity values detected*
2. ROIs diced into single voxels; # of resulting files per ROI = number of non-zero voxels per mask
3. Single voxels from each ROI combined to form all possible pairs; # of total resulting files = # of single-voxel masks per ROI multiplied by each other

### **TRACTOGRAPHY PROCESSING STEP #1:**

For a single ROI (*files corresponding to “-R” input file used; distinction is otherwise arbitrary*):

Generate track file representing all streamlines passing through a single voxel. This is done separately for every single-voxel mask, and thus results in a total # of track files equal to the # of single-voxel masks.

*Program used: “track\_intersect” from TrackTools package; <command> -r [track.trk] [roi.nii.gz] [step1output.trk]*

*Note: does not represent a tractography processing step used in the Mareci Lab pipeline*

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### **TRACTOGRAPHY PROCESSING STEP #2:**

For every track file resulting from the previous processing step, generate track file representing all streamlines passing through each voxel of the *second ROI*. This is done separately for every single-voxel mask (*corresponding to the “-r” input file*) with each of the Step #1 track files.

*Program used: “track\_intersect” from TrackTools package; <command> -r [step1output.trk] [roi.nii.gz] [step2output.trk]*

*Note: does not represent a tractography processing step used in the Mareci Lab pipeline*

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### **TRACTOGRAPHY PROCESSING STEP #3:**

For every track file resulting from the previous processing step, eliminate streamlines that do not lie within the edge directly connecting the nodes of the single-voxel ROI pair. ROIs generated during “ROI PROCESSING STEP #3” used as input, in addition to the respective track file.

This step generates 3 files per voxel-to-voxel network: a track file, a “seeds” file, and a text file with variables necessary for calculating edge weight. Variables from these text files, in combination with variables provided as input arguments (-A; -L; -p), are used to generate final output file #2.

*Program used: “track\_network” from TrackTools package; <command> -r -m [pass/term] -save-matching [step2output.trk] [roi+roi.nii.gz] [step3network]*

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### **TRACTOGRAPHY PROCESSING STEP #4:**

Merge every network track file generated in Step #3 into a single file to generate the final output track.

Program used: “track\_merge” from TrackVis’ dtk

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### **SYSTEM REQUIREMENTS:**

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|----------------------|--------------------------------------|--------|
| 1. MAC OS X or LINUX | 4. TrackVis’ Diffusion Toolkit (dtk) | 7. sed |
| 2. FSL               | 5. Mareci Lab TrackTools             | 8. cut |
| 3. AFNI              | 6. shflags + getopt                  | 9. bc  |