# TractoFlow-documentation Documentation

SCIL

Jan 24, 2023

# Install

**Note:** New release available: 2.4.1.

TractoFlow pipeline is developed by the Sherbrooke Connectivity Imaging Lab (SCIL) in order to process diffusion MRI dataset from the raw data to the tractography. The pipeline is based on Nextflow and Singularity. The goal with this pipeline is to be fast and reproducible.

Use TractoFlow in published works should be accompanied by the following citation:

> Theaud, G., Houde, J.-C., Boré, A., Rheault, F., Morency, F., Descoteaux, M.,TractoFlow: A robust, efficient and reproducible diffusion MRI pipeline leveraging Nextflow & Singularity, NeuroImage, https://doi.org/10.1016/j.neuroimage.2020.116889.

Other citations can be added if TractoFlow is used in a publication. Please see *How to cite TractoFlow*

For Linux users, please see this section *Singularity for TractoFlow* for setup.

For MacOS users, please see this section *Docker for TractoFlow* for setup.

For any issues or difficulties with TractoFlow, please use our Neurostar tag: https://neurostars.org/tag/tractoflow

**Tip:** If you want to analyse datasets with white-matter lesions use profile ABS.

CHAPTER 1

# Requirements

To run the pipeline you must install Nextflow. To use our Singularity container, you must install the Singularity package.

## 1.1 Nextflow

Note that the below sections use `nextflow` version `v19.04.0` for illustrative purposes: newer versions might work or be required depending on the pipeline at issue.

### 1.1.1 Local Computer

1. Before installing check your current version `java -version`. If return something as `java version "1.X"` and X is 8 up to 11, you can skip this step else install java.
2. Install Nextflow:

```
$> wget https://github.com/nextflow-io/nextflow/releases/download/v21.10.6/nextflow &&
↪ chmod +x nextflow && \
echo 'export PATH=$PATH:'$(pwd) >> ~/.bash_profile && source ~/.bash_profile
```

### 1.1.2 High Performance computer (HPC)

1. Try `module load nixpkgs/16.09 module load java/1.8.0_192` or check with your administrator or on the HPC website.
2. Use `wget` to install Nextflow, change the name, add execution rights and add the Nextflow path in the bash_profile.

```
$> wget https://github.com/nextflow-io/nextflow/releases/download/v21.10.6/nextflow-
↪21.10.6-all && \
mv nextflow-21.10.6-all nextflow && \
chmod +x nextflow && echo 'export PATH=$PATH:'$(pwd) >> ~/.bash_profile && source ~/.
↪bash_profile
```

Note that a given HPC system might offer (a) readily available `nextflow` version(s). If any of provided versions suffice for the pipeline at issue, the above step can be omitted, and reading the documentation of the HPC system is encouraged in order to load the suitable version. In the case of the Allianca Canada clusters, the above step might be substituted by adding the line `module load nextflow/19.04.0` (depending on the desired and available versions) to the `.bash_profile` file and sourcing it.

## 1.2 Singularity

Our Singularity container currently works on Linux. We highly recommend to use Singularity on a Linux local computer or on a HPC.

If you want to use Docker on Windows or MacOS, please see the *Docker for TractoFlow* section.

### 1.2.1 Local Computer

Install `singularity-container`. Our current singularity container works only on Linux. A macOS version will be released soon.

If you are Debian/Ubuntu, you can get neurodebian:

```
$> sudo wget -O- http://neuro.debian.net/lists/xenial.us-ca.full | sudo tee /etc/apt/
↪sources.list.d/neurodebian.sources.list && \
sudo apt-key adv --recv-keys --keyserver hkp://pool.sks-keyservers.net:80␣
↪0xA5D32F012649A5A9 && \
sudo apt-get update && sudo apt-get install -y singularity-container
```

Note that the first command contains the OS codename *xenial* (corresponding to Ubuntu 16.04) as an example; if your OS is different, you will need to retrieve the corresponding type/version from the menus in https://neuro.debian.net/index.html#get-neurodebian so that you can use the appropriate URL for the *wget* command.

### 1.2.2 High Performance computer (HPC)

Please try `module load singularity/3.7` or check with an administrator or on the HPC website.

## 1.3 Docker

### 1.3.1 MacOS

To install Docker on your MacOS computer, please check the following link:

https://hub.docker.com/editions/community/docker-ce-desktop-mac

### 1.3.2 Windows

To install Docker on your Windows computer, please check the following link:

https://hub.docker.com/editions/community/docker-ce-desktop-windows

CHAPTER 2

# Fast Installation

## 2.1 Easy install method

Enter this command in your terminal (it downloads the container and TractoFlow code in the current directory - Make sure nextflow is already installed before running this command):

```
curl -s https://tractoflow-documentation.readthedocs.io/en/2.4.1/install.sh | bash
```

CHAPTER 3

# Detailed Installation

## 3.1 TractoFlow pipeline

### 3.1.1 Release

Download TractoFlow pipeline:

```
$> nextflow pull scilus/tractoflow
```

### 3.1.2 For developers

Clone TractoFlow pipeline repository:

```
# Clone with HTTPS
$> git clone https://github.com/scilus/tractoflow.git

# Clone with SSH
$> git clone git@github.com:scilus/tractoflow.git
```

As a developer you will have to run tractoflow using this command:

```
nextflow run tractoflow/main.nf --help
```

## 3.2 Singularity for TractoFlow

### 3.2.1 Release

Download the last release of the Singularity container for TractoFlow:

```
$> wget http://scil.usherbrooke.ca/containers_list/scilus_1.4.2.sif
```

Or if you have sudo privileges

```
$> sudo singularity build scilus_1.4.2.sif docker://scilus/scilus:1.4.2
```

### 3.2.2 For developers

Clone the singularity repository for TractoFlow pipeline:

```
# Clone with HTTPS
$> git clone https://github.com/scilus/containers-scilus.git

# Clone with SSH
$> git clone git@github.com:scilus/containers-scilus.git
```

Then, you can build the singularity image:

```
$> singularity build scilus_1.4.2.sif singularity_scilus.def
```

## 3.3 Docker for TractoFlow

First, change the number of CPUs and RAM (recommended: 8 CPUs and 16Gb of RAM) in Docker (Preferences -> Advanced) and click on Apply & Restart.

Download the last release of the Docker container for TractoFlow:

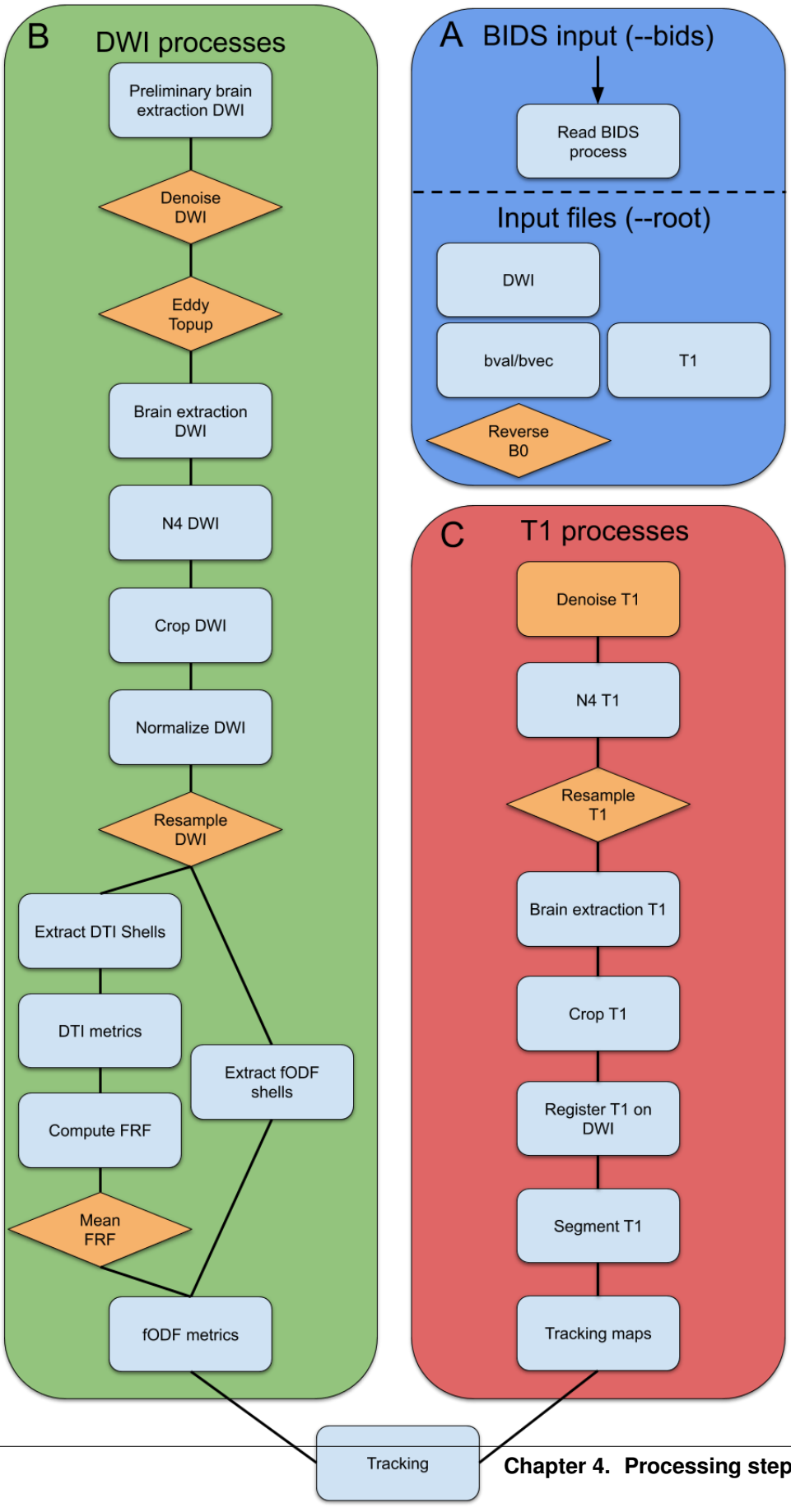
```
$> docker pull scilus/scilus:1.4.2
```

Please see *Profiles* section to use *macos* profile.

CHAPTER 4

# Processing steps

TractoFlow pipeline consist of 23 different steps : 14 steps for the diffusion weighted image (DWI) processing and 8 steps for the T1 weighted image processing.


B
DWI processes
Preliminary brain extraction DWI
Denoise DWI
Eddy Topup
Brain extraction DWI
N4 DWI
Crop DWI
Normalize DWI
Resample DWI
Extract DTI Shells
DTI metrics
Compute FRF
Mean FRF
Extract fODF shells
fODF metrics
A
BIDS input (--bids)
Read BIDS process
Input files (--root)
DWI
bval/bvec
T1
Reverse B0
C
T1 processes
Denoise T1
N4 T1
Resample T1
Brain extraction T1
Crop T1
Register T1 on DWI
Segment T1
Tracking maps
Tracking

## 4.1 Input

- Diffusion weighted image (DWI)
- b-values
- b-vectors
- T1 weighted image
- Reverse phase encoding B0 (Optional)

## 4.2 DWI processes

- Brain extraction (FSL)
- Denoising (Mrtrix3)
- Topup (FSL)
- Eddy (FSL)
- N4 bias correction (ANTs)
- Resample (Dipy)
- DTI metrics (Dipy)
- fODF metrics (Dipy)

## 4.3 T1 processes

- Brain extraction (ANTs)
- Denoising (Dipy)
- N4 bias correction (ANTs)
- Resample (Dipy)
- Registration (ANTs)
- Tissue segmentation (FSL)

## 4.4 Tractography

- Particule Filter Tractography
- Local tracking (Optional)

The particle filter tractography is performed by default. Three types of seeding are available: WM-GM interface, WM mask or FA.

CHAPTER 5

# Input structure

Two types of input are available in TractoFlow: BIDS and an in-house structure.

## 5.1 BIDS parameter

We recommend to use `dcm2bids` (https://github.com/unfmontreal/Dcm2Bids) or `heuviconv` (https://github.com/nipy/heudiconv) to create BIDS datasets.

TractoFlow supports BIDS as input data using `--bids YOUR_BIDS_DATASET`. TractoFlow does some verifications before launching the processing to valide the BIDS format.

If you need to filter some subjects/sessions/runs or some files you can create a bidsignore file using `--bidsignore bids_ignore_path`. (Check: https://github.com/bids-standard/bids-validator#bidsignore)

In the case that some tags or informations are missing, TractoFlow will create a json file in `results/Read_BIDS`. Please complete missing informations and relaunch the pipeline replacing `--bids YOUR_BIDS_DATASET` with `--bids_config results/Read_BIDS/tractoflow_bids_struct.json`.

If you have a BIDS structure and want to use *-profile ABS* you need to use the *–fs* option to point to your freesurfer folder output.

If you have any problems, contact us on NeuroStar (https://neurostars.org/tag/tractoflow).

## 5.2 Root parameter

It is possible not to follow the BIDS format. In that case, the input root parameter is called using `--input` and requires the following file structure:

```
[root]
├── S1
│   ├── dwi.nii.gz
│   ├── bval
```

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```
│   ├── bvec
│   ├── t1.nii.gz
│   ├── rev_b0.nii.gz  (optional)
│   ├── aparc+aseg.nii.gz (optional)
│   └── wmparc.nii.gz  (optional)
└── S2
    ├── dwi.nii.gz
    ├── bval
    ├── bvec
    ├── t1.nii.gz
    ├── rev_b0.nii.gz  (optional)
    ├── aparc+aseg.nii.gz (optional)
    └── wmparc.nii.gz  (optional)
```

The *root* folder must contains subjects folders (e.g. *S1*, *S2*,. . . ). Each subject folder contains the required images:

- `dwi.nii.gz` are the diffusion weighted images.
- `bval` is the b-value file in the FSL format.
- `bvec` is the b-vector file in the FSL format.
- `t1.nii.gz` is the T1 weighted image.
- `rev_b0.nii.gz` (optional) is the reversed phase encoded b0 image also called blip-up/blip-down. Used to correct distortion due to diffusion acquisition (Documentation).
- `aparc+aseg.nii.gz` (optional) is the freesurfer gm segmented image.
- `wmparc.nii.gz` (optional) is the freesurfer wm segmented image.

CHAPTER 6

# Options

To display the options of Tractoflow, please use `nextflow run tractoflow -r 2.4.1 --help`.

## 6.1 Optional BIDS arguments

**`--bidsignore "bids_ignore_path"` (default: none)** If you want to ignore some subjects/sessions/runs or some files, you can provide an extra bidsignore file. Check: https://github.com/bids-standard/bids-validator#bidsignore

**`-clean_bids BOOL` (default: false)** If set, it will remove all the participants that are missing any information.

**`--fs "freesurfer_output_folder"` (default: none)** If you want to run Tractoflow-ABS (Atlas Based Segmentation) combined with a BIDS structure input you need to have this argument.

## 6.2 Options list

**`--b0_thr_extract_b0 MAX_VALUE` (default: 10)** All b-values below a maximum value are considered b=0 images.

**`--dwi_shell_tolerance TOLERANCE` (default: 20)** All b-values to +-tolerance are considered as the same b-value.

**`--bet_prelim_f THRESHOLD` (default: 0.16)** Fractional Intensity threshold (-f for the bet FSL command) for preliminary DWI brain extraction. See FSL bet documentation for more info.

**`--dilate_b0_mask_prelim_brain_extraction FACTOR` (default: 5)** Dilation factor to keep the whole brain and be more robust to the geometric distortions. This is only applied to the preliminary BET. Not the final extraction.

**`--run_dwi_denoising BOOL` (default: true)** Run dwi denoising (dwidenoise from Mrtrix3). See Mrtrix3 dwidenoise documentation for more info.

**--extent SIZE (default: 7)** Denoising block size. Recommended block size should follow the following rule of thumb: extent^3 >= # directions. See Mrtrix3 dwidenoise documentation for more info.

**--run_topup BOOL (default: true)** Run Topup. If TractoFlow find any reversed phase encoded b=0 images. Topup will be automatically ignored. See FSL Topup documentation for more info.

**--encoding_direction DIRECTION (default: y)** Encoding direction of the DWI [x, y, z]. See FSL Topup documentation for more info.

**--readout VALUE (default: 0.062)** Readout time value.

**--run_eddy BOOL (default: true)** Run Eddy.

**--eddy_cmd COMMAND (default: eddy_openmp)** Eddy command to use [eddy_openmp, eddy_cuda].

**--bet_topup_before_eddy_f THRESHOLD (default: 0.16)** Fractional Intensity threshold (-f for the bet FSL command) for intermediate BET operation on topup corrected images.

**--use_slice_drop_correction BOOL (default: true)** If set, will use the slice drop correction option (–repol) from Eddy.

**--bet_dwi_final_f THRESHOLD (default: 0.16)** Fractional Intensity threshold (-f for the bet FSL command) for the final DWI BET.

**--fa_mask_threshold THRESHOLD (default: 0.4)** FA maximum value to be considered as WM for Normalize DWI.

**--run_resample_dwi BOOL (default: true)** Run resample DWI. Resampling is done at the resolution given by –dwi_resolution option.

**--dwi_resolution RESOLUTION (default: 1)** DWI resolution (in mm).

**--dwi_interpolation METHOD (default: lin)** Interpolation method [nn, lin, quad, cubic].

**--max_dti_shell_value (default: 1200)** Maximum shell threshold to be consider as a DTI shell (b <= 1200). This is the default behaviour to select DTI shells.

**--dti_shells** Shells selected to compute the DTI metrics (generally b <= 1200). Please write them between quotes e.g. (–dti_shells “0 300 1000”). If selected, it will overwrite max_dti_shell_value.

**--min_fodf_shell_value (default: 700)** Minimum shell threshold to be consider as a fODF shell (b >= 700). This is the default behaviour to select fODF shells.

**--fodf_shells** Shells selected to compute the fODF metrics (generally b >= 700). Please write them between quotes e.g. (–fodf_shells “0 1000 2000”). If selected, it will overwrite min_fodf_shell_value.

**--run_t1_denoising BOOL (default: true)** Run T1 denoising using NLmean algorithm.

**--run_resample_t1 BOOL (default: true)** Run resample T1. Resampling is done at the resolution given by –t1_resolution option.

**--t1_resolution RESOLUTION (default: 1)** T1 resolution (in mm).

**--t1_interpolation METHOD (default: lin)** Interpolation method [nn, lin, quad, cubic].

**--number_of_tissues NUMBER (default: 3)** Number of tissue classes (-n for the fast FSL command).

**--fa THRESHOLD (default: 0.7)** Initial FA threshold to compute the fiber response function (FRF).

**--min_fa MIN_THRESHOLD (default: 0.5)** Minimum FA threshold to compute the FRF.

**--min_nvox MIN_NVOX_THRESHOLD (default: 300)** Minimum number of voxels to compute the FRF.

**--roi_radius RADIUS (default: 20)** Region of interest radius to compute the FRF. This ROI starts from the center of the 3D volume (sizeX/2, sizeY/2, sizeZ/2).

**--set_frf BOOL (default: false)** Set manually the FRF.

**--manual_frf FRF (default: "15,4,4")** FRF set manually. The FRF must be at 10^-4 scaling in mm^2/s. This corresponds to an elongated symmetric diffusion tensor with eigenvalues (15, 4, 4) x 10^-4 mm^2/s along the principal axis and radial axes respectively.

**--mean_frf BOOL (default: true)** Mean the frf of all subjects. USE ONLY IF ALL OF SUBJECTS COME FROM THE SAME SCANNER AND HAVE THE SAME ACQUISITION.

**--sh_order ORDER (default: 8)** Spherical harmonics order.

Suggested rule of thumb :
–sh_order=8 for 45+ directions
–sh_order=6 for 20+ directions
–sh_order=4 otherwise

**--basis BASIS (default: descoteaux07)** fODF spherical harmonics (SH) basis type [descoteaux07, tournier07].

**--fodf_metrics_a_factor FACTOR (default: 2.0)** Multiplicative factor for AFD max in ventricles. As recommended in [Dell'Acqua et al HBM 2013].

**--relative_threshold THRESHOLD (default: 0.1)** Relative threshold on fODF amplitude in ]0,1].

**--max_fa_in_ventricle THRESHOLD (default: 0.1)** Maximal threshold of FA to be considered as ventricule voxel. Used to compute the ventricules mask and find the maximum fODF amplitude in the ventricules.

**--min_md_in_ventricle THRESHOLD (default: 0.003)** Minimal threshold of MD in mm^2/s to be considered as ventricule voxel. Used to compute the ventricules mask and find the maximum fODF amplitude in the ventricules.

## 6.3 Optional PFT Tracking arguments

**--run_pft_tracking BOOL (default: true).** [PFT] Run Particle Filter Tracking (PFT)

**--pft_seeding_mask_type TYPE (default: wm)** [PFT] Seeding mask type [wm, interface, fa].

**--pft_fa_seeding_mask_threshold THRESHOLD (default: 0.1)** [PFT] FA threshold for FA seeding mask.

**--pft_algo ALGO (default: prob)** [PFT] Tracking algorithm [prob, det].

**--pft_seeding SEEDING (default: npv)** [PFT] Seeding type [npv, nt].

**--pft_nbr_seeds NBRSEEDS (default: 10)** [PFT] Number of seeds related to the seeding type param.

**--pft_step SIZE (default: 0.5)** [PFT] Step size.

**--pft_theta ANGLE (default: 20)** [PFT] Maximum angle between 2 steps.

**--pft_min_len LENGTH (default: 20)** [PFT] Minimum length.

**--pft_max_len LENGTH (default: 200)** [PFT] Maximum length.

**--pft_compress_streamlines BOOL (default: true)** [PFT] Compress streamlines.

**--pft_compress_value THRESHOLD (default: 0.2)** [PFT] Compression error threshold. See [Presseau et al Neuroimage 2015] and [Rheault et al Front Neuroinform 2017].

**--pft_random_seed RANDOMSEED (default: 0)** [PFT] List of random seed numbers for the random number generator. Please write them as list separated using commat WITHOUT SPACE e.g. (–pft_random_seed 0,1,2)

## 6.4 Optional Local Tracking arguments

**--run_local_tracking BOOL (default: false).** [LOCAL] Run Local Tracking

**--local_seeding_mask_type TYPE (default: wm)** [LOCAL] Seeding mask type [wm, interface, fa].

**--local_fa_seeding_mask_threshold THRESHOLD (default: 0.1)** [LOCAL] FA threshold for FA seeding mask.

**--local_algo ALGO (default: prob)** [LOCAL] Tracking algorithm [prob, det].

**--local_seeding SEEDING (default: npv)** [LOCAL] Seeding type [npv, nt].

**--local_nbr_seeds NBRSEEDS (default: 10)** [LOCAL] Number of seeds related to the seeding type param.

**--local_step SIZE (default: 0.5)** [LOCAL] Step size.

**--local_theta ANGLE (default: 20)** [LOCAL] Maximum angle between 2 steps.

**--local_min_len LENGTH (default: 20)** [LOCAL] Minimum length.

**--local_max_len LENGTH (default: 200)** [LOCAL] Maximum length.

**--local_compress_streamlines BOOL (default: true)** [LOCAL] Compress streamlines.

**--local_compress_value THRESHOLD (default: 0.2)** [LOCAL] Compression error threshold. See [Presseau et al Neuroimage 2015] and [Rheault et al Front Neuroinform 2017].

**--local_random_seed RANDOMSEED (default: 0)** [LOCAL] List of random seed numbers for the random number generator. Please write them as list separated using commat WITHOUT SPACE e.g. (–local_random_seed 0,1,2)

**--template_t1 PATH (default: /human-data/mni_152_sym_09c/t1)** Path to the template T1 directory for antsBrainExtraction. The folder must contain t1_template.nii.gz and t1_brain_probability_map.nii.gz. The default path is the human_data folder in the Singularity/Docker container.

**--processes_brain_extraction_t1 NUMBER (default: 4)** Number of processes for T1 brain extraction task.

**--processes_denoise_dwi NUMBER (default: 4)** Number of processes for DWI denoising task.

**--processes_denoise_t1 NUMBER (default: 4)** Number of processes for T1 denoising task.

**--processes_eddy NUMBER (default: 1)** Number of processes for eddy task.

**--processes_fodf NUMBER (default: 4)** Number of processes for fODF task.

**--processes_registration NUMBER (default: 4)** Number of processes for registration task.

**--output_dir PATH (default: ./results)** Directory where to write the final results.

**--processes NUMBER (default: Maximum number of threads)** The number of parallel processes to launch. Only affects the local scheduler.

CHAPTER 7

# Profiles

To select one or multiple profiles, please use the `-profile` option. For example:

```
$> nextflow run tractoflow -r 2.4.1 --input input_folder -profile macos,fully_
↪reproducible -with-singularity singularity_name.sif -resume
```

## 7.1 Profiles available

**`macos`** When this profile is used, TractoFlow will modify a parameter (scratch) for MacOS users.

**`use_cuda`** When this profile is used, TractoFlow will use eddy_cuda for Eddy process. This feature is available with NVidia GPUs only. Without this profile, TractoFlow will run eddy_openmp.

**`fully_reproducible`** When this profile is used, all the parameters will be set to have 100% reproducible results. This profile consist to set multi-thread parameters to be fully reproducible [Theaud20].

**`cbrain`** When this profile is used, Nextflow will copy all the output files in publishDir and not use symlinks.

**`ABS`** When this profile is used, TractoFlow-ABS (Atlas Based Segmentation) is used. This profile must be used for pathological data. The aparc+aseg.nii.gz and wmparc.nii.gz must be in the same space than t1.nii.gz

**`bundling`** When this profile is used, it will activate custom tracking parameters to improve recobundle results.

**`connectomics`** When this profile is used, it will activate custom tracking parameters to improve connectomics analysis.

# CHAPTER 8

# How to launch TractoFlow

## 8.1 Local computer

To run the pipeline, use the following command:

```
# With Singularity
$> nextflow run tractoflow -r 2.4.1 --bids input_bids -with-singularity scilus_1.4.2.
↪sif -resume
# Or
$> nextflow run tractoflow -r 2.4.1 --input input_folder -with-singularity scilus_1.4.
↪2.sif -resume

# With Docker
$> nextflow run tractoflow -r 2.4.1 --bids input_bids -with-docker scilus/scilus:1.4.
↪2 -resume
# Or
$> nextflow run tractoflow -r 2.4.1 --input input_folder -with-docker scilus/scilus:1.
↪4.2 -resume
```

If you want to skip steps already processed by an anterior run, you can add *-resume* option in the command line.

## 8.2 High Performance Computer (HPC)

The following example is based on the SLURM executor:

If you want to use only one node, please use the same commands presented for the local computer. The follwing lines must be saved in `.sh` file (e.g. `cmd.sh`) to be executed with `sbatch`.

```
#!/bin/sh

#SBATCH --nodes=1
#SBATCH --cpus-per-task=32
```

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```
#SBATCH --mem=0
#SBATCH --time=48:00:00

nextflow -c singularity.conf run tractoflow -r 2.4.1 --input input_folder --dti_
↪shells "DTI_SHELLS" --fodf_shells "FODF_SHELLS" -with-singularity singularity_name.
↪sif -resume
```

To launch on multiple nodes, you must to use the MPI option that use Ignite executor. The following example use 2 nodes with 32 threads on each nodes. The follwing lines must be saved in `.sh` file (e.g. `cmd.sh`) to be executed with `sbatch`.

```
#!/bin/sh

#SBATCH --nodes=2
#SBATCH --cpus-per-task=32
#SBATCH --mem=0
#SBATCH --time=48:00:00

export NXF_CLUSTER_SEED=$(shuf -i 0-16777216 -n 1)

srun nextflow -c singularity.conf run tractoflow -r 2.4.1 --input input_folder --dti_
↪shells "DTI_SHELLS" --fodf_shells "FODF_SHELLS" -with-singularity singularity_name.
↪sif -with-mpi -resume
```

To launch the pipeline on the HPC:

```
$> sbatch cmd.sh
```

CHAPTER 9

# Results

The pipeline creates 2 folders: `results` and `work`. The files in results are symlinks in works. We highly recommend to not remove work folder.

To transfert or copy-paste the `results` folder, please use one of the following commands:

```
# On local computer
$> cp -rL results NEW_PATH/results

# On HPC
$> rsync -rL login@adress:/HPC_PATH/results NEW_PATH/results
# Or compress before and rsync after
$> tar cvzfh /HPC_PATH/results.tar.gz /HPC_PATH/results
$> rsync login@adress:/HPC_PATH/results.tar.gz NEW_PATH/results.tar.gz
```

# CHAPTER 10

## How to cite TractoFlow

**Tip:** If you want to analyse datasets with white-matter lesions, we highly recommends to use our devrived version of TractoFlow: TractoFlow Atlas based Segmentation (ABS) https://github.com/scilus/TractoFlow-ABS

If TractoFlow is used in a publication, please cite the following references:

If TractoFlow-ABS is used in a publication, please cite the following references:

Download:

`References Bibtex`

CHAPTER 11

# Contact

For any issues, difficulties or questions about TractoFlow please use our Neurostar tag: https://neurostars.org/tag/tractoflow

# CHAPTER 12

# Changelog

## 12.1 2.4.1

Date: November 2022

**New features**

- Automatic extraction of shells when computing DTI and fODF
- Skip step bet_prelim_dwi when not needed
- Add remove_invalid step in Tracking processes
- Add possibility for complex BIDS structure with multiband acquisition and full reverse encoding acquisitions. (only available with cuda profile)
- New profile “bundling”. It will activate custom tracking parameters to improve recobundle results. Local tracking will be enable with fa seeding mask and tracking mask.
- New profile “connectomics”. It will activate custom tracking parameters to improve connectomics analysis.

## 12.2 2.3.0

Date: 05 April 2022

**New features**

- New profile Atlas Based Segmentation (-profile ABS)
- New profile “skip preprocessing” for HCP dataset (-profile skip_preprocessing)
- Add option to compute dwi sh (-sh_fitting true)
- Gibbs correction (-run_gibbs_correction true)

## 12.3 2.2.1

Date: 09 April 2021

**Bug Fixed:**

- fully reproducible (ANTS_RANDOM_SEED fixed)
- Tracking with FA (typo)

**New options:**

- participants_label: select specific subjects (BIDS input)
- clean_bids: remove subject that are not complete (BIDS input)

## 12.4 2.1.1

Date: 08 Jul 2020

New features:

- Support 4D reverse B0 images.

## 12.5 2.1.0

Date: 29 Jun 2020

New features:

- BIDS support
- Partitions (External drive, etc) automatically mounted. No supplementary config file needed
- New processing profiles: use_cuda (for eddy_cuda use), fully_reproducible, macos

New options:

- run_t1_denoising: Activate or deactivate T1 denoising

## 12.6 2.0.1

Date: 8 May 2019

Modify normalization mask and change some default option values

## 12.7 2.0.0

Date: 27 Mar 2019

First release for public access

CHAPTER 13

# Github repositories

TractoFlow pipeline repository: TractoFlow

TractoFlow Containers repository: Containers-Scilus

# CHAPTER 14

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