
TractoFlow-documentation Documentation

SCIL

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Note: New release available: 2.2.1. TractoFlow now support BIDS as input data.

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, we highly recommends to use our devrived version of TractoFlow: TractoFlow Atlas based Segmentation (ABS) <https://github.com/scilus/TractoFlow-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

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:

```
$> wget https://github.com/nextflow-io/nextflow/releases/download/v19.04.0/nextflow && \
↪ chmod +x nextflow && \
echo 'export PATH=$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`.

```
$> wget https://github.com/nextflow-io/nextflow/releases/download/v19.04.0/nextflow-
↪ 19.04.0-all && \
mv nextflow-19.04.0-all nextflow && \
chmod +x nextflow && echo 'export PATH=$PATH:$(pwd) >> ~/.bash_profile && source ~/.
↪ bash_profile
```

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
```

1.2.2 High Performance computer (HPC)

Please try `module load singularity/3.5` 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>

2.1 Easy install method

Enter this command in your terminal (it downloads the container and TractoFlow code in the current directory):

```
curl -s https://tractoflow-documentation.readthedocs.io/en/2.2.1/install.sh | bash
```

2.2 TractoFlow pipeline

2.2.1 Release

Download the last release of TractoFlow pipeline:

```
$> wget https://github.com/scilus/tractoflow/releases/download/2.2.1/tractoflow-2.2.1.  
↪zip && unzip tractoflow-2.2.1.zip
```

2.2.2 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
```

2.3 Singularity for TractoFlow

2.3.1 Release

Download the last release of the Singularity container for TractoFlow:

```
$> wget http://scil.dinf.usherbrooke.ca/containers_list/tractoflow_2.2.1_b9a527_2021-  
→04-13.sif
```

2.3.2 For developers

Clone the singularity repository for TractoFlow pipeline:

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

Then, you can build the singularity image:

```
$> singularity build singularity_name.img singularity_tractoflow.def
```

2.4 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:

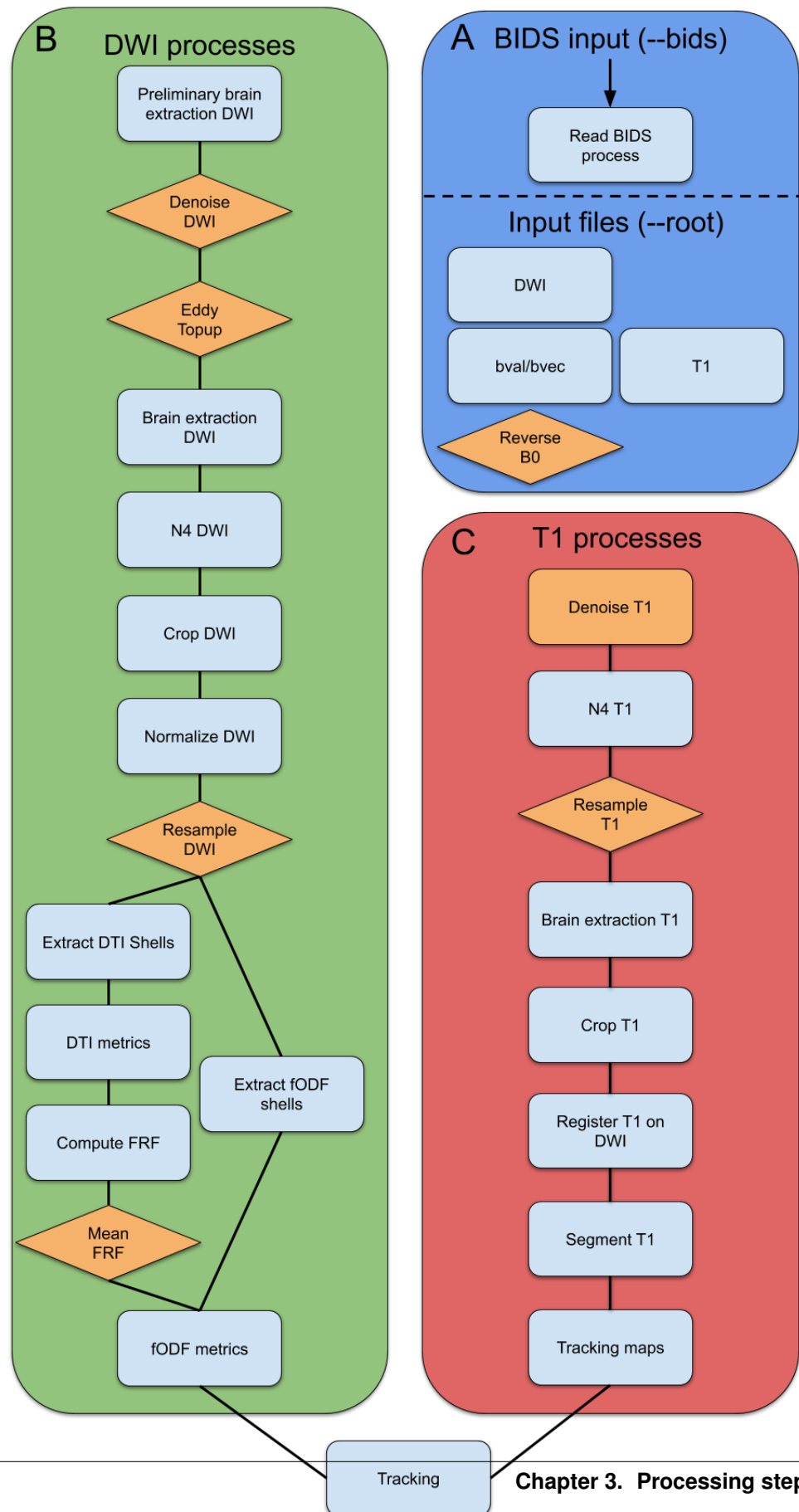
```
$> docker pull scilus/tractoflow:2.2.1
```

Please see [Profiles](#) section to use *macos* profile.

CHAPTER 3

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.



3.1 Input

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

3.2 DWI processes

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

3.3 T1 processes

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

3.4 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.

Input structure

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

4.1 BIDS parameter

We recommend to use `dcm2bids` (<https://github.com/unfmontreal/Dcm2Bids>) to create BIDS datasets.

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

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 any problems, contact us on NeuroStar (<https://neurostars.org/tag/tractoflow>).

4.2 Root parameter

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

```
[root]
├── S1
│   ├── dwi.nii.gz
│   ├── bval
│   ├── bvec
│   ├── rev_b0.nii.gz (optional)
│   └── t1.nii.gz
└── S2
    ├── dwi.nii.gz
    ├── bval
    └── bvec
```

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<pre>└─ rev_b0.nii.gz (optional) └─ t1.nii.gz</pre>
--

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.
- `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](#)).
- `t1.nii.gz` is the T1 weighted image.

To display the options of Tractoflow, please use `nextflow run tractoflow/main.nf --help`.

5.1 Optional BIDS arguments

- participants_label "SUBID1 SUBID2" (default: none)** The label(s) of the specific participant(s) you want to analyzed. It does not include "sub-". Please write one or more subjects between quotes e.g. (`--participants_label "01 02 04"`) If this parameter is not provided all subjects should be analyzed
- clean_bids BOOL (default: false)** If set, it will remove all the participants that are missing any information.

5.2 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 (dwdenoise from Mrtrix3). See Mrtrix3 dwdenoise documentation for more info.
- extent SIZE (default: 7)** Denoising block size. Recommended block size should follow the following rule of thumb: $\text{extent}^3 \geq \# \text{ directions}$. See Mrtrix3 dwdenoise 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 (-re-pol) 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].

--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.

--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) $\times 10^{-4} \text{ mm}^2/\text{s}$ 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 ventricle voxel. Used to compute the ventricles mask and find the maximum fODF amplitude in the ventricles.

--min_md_in_ventricle THRESHOLD (default: 0.003) Minimal threshold of MD in mm²/s to be considered as ventricle voxel. Used to compute the ventricles mask and find the maximum fODF amplitude in the ventricles.

5.3 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 comma WITHOUT SPACE e.g. (`--pft_random_seed 0,1,2`)

5.4 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 ants-BrainExtraction. 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.

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

```
$> nextflow run tractoflow/main.nf --root input_folder --dti_shells "DTI_SHELLS" --  
↪fodf_shells "FODF_SHELLS" -profile macos,fully_reproducible -with-singularity_  
↪singularity_name.img -resume
```

6.1 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.

How to launch TractoFlow

7.1 Local computer

To run the pipeline, use the following command:

```
# With Singularity
$> nextflow run tractoflow/main.nf --bids input_bids --dti_shells "DTI_SHELLS" --fodf_
↪shells "FODF_SHELLS" -with-singularity singularity_name.img -resume
# Or
$> nextflow run tractoflow/main.nf --root input_folder --dti_shells "DTI_SHELLS" --
↪fodf_shells "FODF_SHELLS" -with-singularity singularity_name.img -resume

# With Docker
$> nextflow run tractoflow/main.nf --bids input_bids --dti_shells "DTI_SHELLS" --fodf_
↪shells "FODF_SHELLS" -with-docker scilus/docker-tractoflow:2.1.1 -resume
# Or
$> nextflow run tractoflow/main.nf --root input_folder --dti_shells "DTI_SHELLS" --
↪fodf_shells "FODF_SHELLS" -with-docker scilus/docker-tractoflow:2.1.1 -resume
```

Where DTI_SHELLS are the shells used to compute the DTI metrics (typically b-value < 1200 e.g. “0 1000”) and FODF_SHELLS are the shells used to compute the fODF metrics (typically b > 700 e.g. “0 1000 2000”).

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

7.2 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 following 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
#SBATCH --mem=0
#SBATCH --time=48:00:00

nextflow -c singularity.conf run tractoflow/main.nf --root input_folder --dti_shells
↪ "DTI_SHELLS" --fodf_shells "FODF_SHELLS" -with-singularity singularity_name.img -
↪ resume
```

To launch on multiple nodes, you must use the MPI option that use Ignite executor. The following example use 2 nodes with 32 threads on each nodes. The following 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/main.nf --root input_folder --dti_
↪ shells "DTI_SHELLS" --fodf_shells "FODF_SHELLS" -with-singularity singularity_name.
↪ img -with-mpi -resume
```

To launch the pipeline on the HPC:

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


CHAPTER 8

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
```

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 10

Contact

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

11.1 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)

11.2 2.1.1

Date: 08 Jul 2020

New features:

- Support 4D reverse B0 images.

11.3 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

11.4 2.0.1

Date: 8 May 2019

Modify normalization mask and change some default option values

11.5 2.0.0

Date: 27 Mar 2019

First release for public access

CHAPTER 12

Github repositories

TractoFlow pipeline repository: [TractoFlow](#)

TractoFlow Containers repository: [Containers-TractoFlow](#)

CHAPTER 13

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
"Licensor" means Sherbrooke Connectivity Imaging Laboratory (SCIL).


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