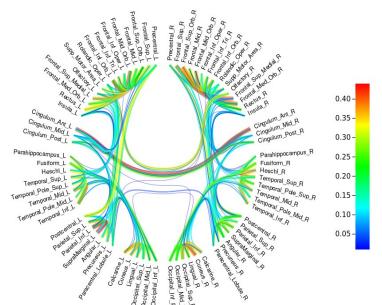
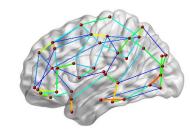
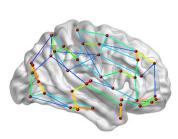


Circle visualization



Tutorial





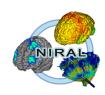
Brain template visualization



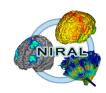


• This is a <u>web application</u> with launch **tractography** scripts in background and allow the user to <u>visualize the connectivity matrix</u> within an interactive web interface.

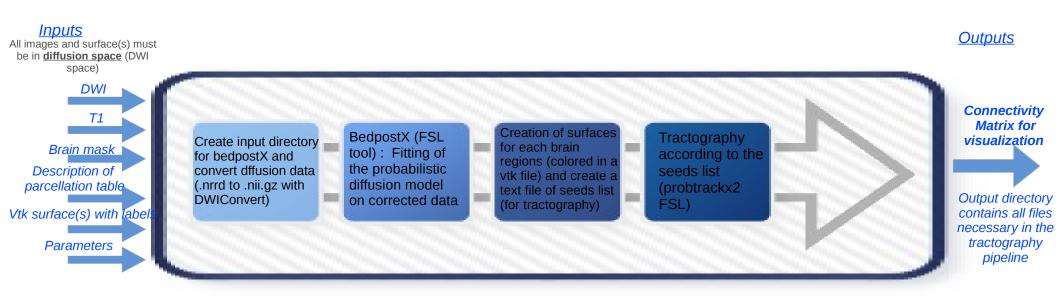
 Through this application the user can also to download the tractography output folder in order to save results on user system.

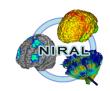


- Tractography pipeline
- Run application
- Login, create account, reset password
- Run tractography on one subject
- View jobs launched
- Visualization of the connectivity
- Download outputs



Tractography pipeline





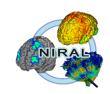
Run application

On your terminal create the tunnel to access to the application

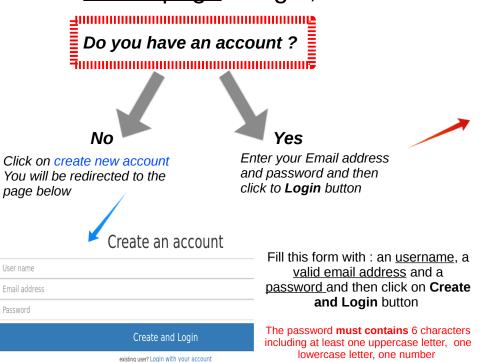
ssh ares -L 8180:localhost:8180

Then, open an internet browser and go to this web page:

https://localhost:8180



• Home page: Login, create an account, reset password



Please login

Email address

Password

Login

forgot your password? click here
new user? create new account

Forget password?

If you don't remember your password, fill the field Email Address in the Login page and then click on the link: click here.

An email will be sent to your email address containint a link. This link will redirect you to a reset page. In the page you need to type 2 times your password and then click on **Reset and Login** button

Application

At this point, you must be **connected**.

Otherwise, return to the last slide to be Login.

This application is composed of 3 tabs.

Tab 1 Tractography
Launch a tractography on a subject

Tab 2 Jobs
Summarize of all jobs launched. You can visualize results, status, parameters etc.

Tab 3 Visualization
Here, you can visualize brain connectivity by uploading a matrix file (probtrackx2 output) and a description table (json file).

Preview of the application when you are Login.



Probabilistic tractography with FSL tool

Job name :
Load data:
DWI Image (.nrrd) : Browse No file selected.
T1 reference in DWI space (.nrrd) : Browse No file selected.
Brain mask in DWI space (.nrrd) : Browse No file selected.
Parcellation table (.json): Help 3 Browse No file selected.
Inner surface in DWI space (.vtk) : Browse No file selected.
Inner surface contains color labels Labelset name in vtk surface file: colour Ignore label

Run tractography on one subject – Tab 1

Now, let's try to run the tractography on one subject.

1. Specify an id for the subject and upload images

- Specify the id/name of the subject (This id/name gonna be the name of the directory containing all outputs of the pipeline)
- Upload the DWI (diffusion) image format : nnrd
- Upload T1 image (must be on the space space as the DWI image → diffusion space) format : nnrd
- Upload brain mask (in diffusion space) format : nnrd



Traceography jobb Tradition

Probabilistic tractography with FSL tool

Job name :
Load data:
DWI Image (.nrrd) : Browse No file selected.
T1 reference in DWI space (.nrrd) : Browse No file selected.
Brain mask in DWI space (.nrrd) : Browse No file selected.
Parcellation table (.json): Help 1 Browse No file selected.
Inner surface in DWI space (.vtk) : Browse No file selected.
Inner surface contains color labels ☑ Labelset name in vtk surface file : colour Ignore label □

Run tractography on one subject - Tab1

2. Upload description table and surface(s) files

- Upload the parcellation table (json file) see Appendix 1
- Upload the Inner surface (vtk file)
- This surface contains labels for each regions? Check the box if yes, unchecked if no (default: check)
- If the surface doesn't contain labels, you must upload an other surface (same mesh) containing labels







Probabilistic tractography with FSL tool

Visualization

lobs

Tractography

	Job name :
	Load data :
	DWI Image (.nrrd) : Browse No file selected.
f	T1 reference in DWI space (.nrrd) : Browse No file selected.
	Brain mask in DWI space (.nrrd) : Browse No file selected.
<u> </u>	Parcellation table (.json): Help Browse No file selected.
<u> </u>	Inner surface in DWI space (.vtk) : Browse No file selected.
	Inner surface contains color labels Labelset name in vtk surface file : colour Ignore label

Run tractography on one subject - Tab1

3. Parameters specific to the extraction of label surfaces in the whole brain surface

- Fill the text field by the name of the labelset in the vtk file
- If you want ignore a label in the vtk file, check to box "Ignore label" and enter the value/ID of the label to ignore (example: "0 0 0")

	Inner surface contains color labels ✓	
	Labelset name in vtk surface file : colour	
	- Ignora label - M	
	setlabelID	
1	hiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	

 There is an additional option in the surfaces extraction: overlapping. If the checkbox corresponding to "Overlapping" is selected that mean each region overlaps the neighbors regions. (by default: selected)



Run tractography on one subject - Tab1

For FSL tools, it's possible to modify their parameters. Parameters write in **bold** can't be modify.

4. Bedpostx parameters

By default the number of tensors in the voxel fitting = 2. You can modify bedpostx parameters if you are familiar with this tool by clicking on the checkbox "Modify".

5. Probtrackx2 parameters

Select loopcheck or not for the tractography computation

Probtrackx2 help → Loopcheck: By default, we terminate pathways that loop back on themselves -i.e paths that travel to a point where they have already been.

You can modify probtrackx2 parameters if you are familiar with this tool by clicking on the checkbox "Modify".



Bedpostx options:

By default: number of tensors in the voxel fitting = 2

Command line parameters:

<u>Default</u>: **bedpostx DiffusionDirectory** -n 2 Modify ?□ (MODIFY ONLY IF YOU KNOW WHAT TO DO) -n 2

Help 6

Tractography / Probtrackx2 options:

Loopcheck ✓

Command line parameters:

Default: probtrackx2 --samples=Diffusion.bedpostX/merged --mask=Diffusion.bedpostX/nodif brain mask --seed=seeds.txt --seedref=T1 image.nii.gz --forcedir --network --omatrix1 -V 0 --dir=NetworkNameDirectory --stop=seeds.txt (--loopcheck) -P 3000 --steplength=0.75 --sampvox=0.5

Modify ?□ (MODIFY ONLY IF YOU KNOW WHAT TO DO) -P 3000 --steplength=0.75 --samp\ Help 6

Option for submit job:

Select server to run job : killdevil :

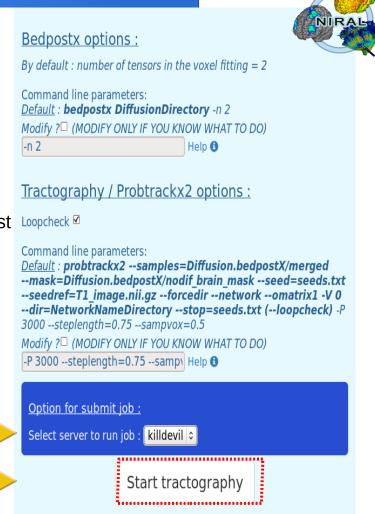
Start tractography

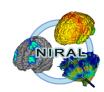
Run tractography on one subject - Tab1

6. Select server and run tractography

- Select server where the tractography is computed by default the first server found is selected
- Finally click on "Start tractography" button to submit the job to server selected before.

During the job submission the button "Start tractography" is disabled and it will be usable again when the job is submit.





View jobs – Tab 2

This tab allow the user to have a summary of all jobs (tractography on one subject) launched.

First, select which jobs to print by selecting a status. (Default : DONE)



Options :

According to the status of the job, options are available or not.

Update status → you can update the status of the job by clicking on this button

Connectivity visualisation

Connectivity Visualization → see appendix 2

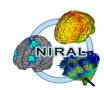
Download output directory → to save results in your system

Print job info

Print job informations → allow user to check files ulpoaded and parameters submited







<u>View jobs – Tab 2</u>

Restart

Restart job → you can restart the job at any time.

If the status is CREATE you can restart the job easily. For all other status you had to force the job submission. Before force the job submission, check the output log files and check inputs files you've uploaded to be sure you've submited nothing wrong.



View log output

View log output → Print the content of log output file

If the line: ERROR PIPELINE PROBTRACKBRAINCONNECTIVITY appears in the log file, that means there is an error during the pipeline so inputs files or parameters submited are false.

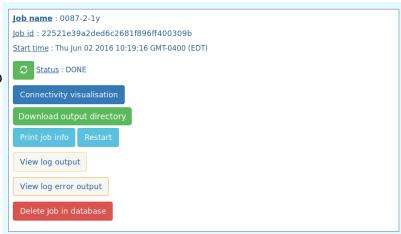
View log error output

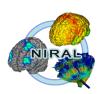
View log error output → Print the content of log error output file



Kill Job → kill the job which is currently running

Delete Job in database Delete Job - delete the job from the database





Visualize the connectivity matrix – Tab 3

This tab allow users to plot connectivity matrix from the user system files by uploading 2 files:

- -connectivity matrix : output of probtrackx2
- -parcellation table : json file → see appendix 1
- To visualize the brain connectome click on PLOT,
 and the circle plot appear. → see appendix 2

Visualisation of brain connectivity

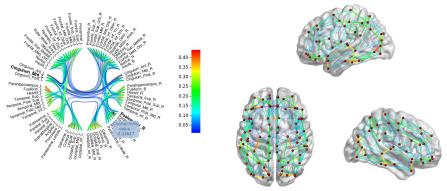
Connectivity matrix (probtrackx output : fdt_network_matrix)

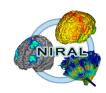
Browse... No file selected.

Parcellation table (json file)

Browse... No file selected.

PLOT





Appendices

1. Description table template - json file

This file is a description of the parcellation table. This json object is an array of objects defined like bellow:

```
{ //Object corresponding to one region - this example is based on the AAL90 parcellation table
  "VisuOrder": 78.
                        //This is the rank in the circle plotting
  "MatrixRow": 1, // Rank in the connectivity matrix - first row = 1 = first column (if = -1 not in the matrix)
  "name": "Precentral L",
                                  //Name of the region/seed
  "VisuHierarchy": "seed.left.frontal.", //Hierachy of the seed (for circle plotting)
  "coord": [
                //Coordinates of the seed
     -38.65, // X
     -5.68, // Y
      50.94 // Z
  "labelValue": "131 44 78", //Value of the label in the vtk file
  "AAL ID": 1
                           // label/seed ID in the AAL90 table
```

```
Json file / Description table
          Object 1 / Region 1
          Object 2 / Region 2
          Object N / Region N
```

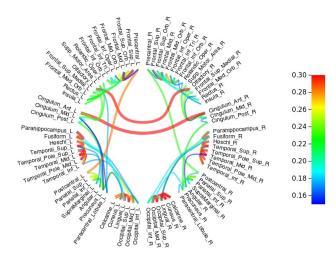


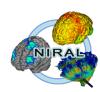
Appendices

2. Visualization of the brain connectome - Parameters

- The brain connectome plot is the result of connectivity matrix (output of probtrackx2) normalized by the number of streamlines per seeds (rows) and then triangulate. The triangular matrix can be compute by 3 differents way.
 - Average between the lower and upper triangular matrix
 - Maximun value between the lower and upper triangular matrix
 - Minimum value between the lower and upper triangular matrix
 Select the method you prefer.
- <u>Threshold</u>: The connectivity visualized can be threshold between 2 value.
 - All links with a connectivity value inferior to the threshold value are not print
 - All links with a connectivity value superior to the maximum threshold value are red







Appendices

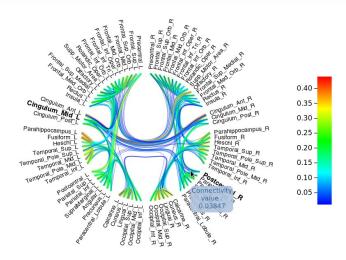
2. Visualization of the brain connectome

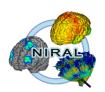
- The slide bar above "Tension splines value" modify the shape of links by changing their tension value.
- The diameter circle can also be set.
- <u>Links</u>: Links colors indicate the connectivity value according the color bar
 - The thinkness of links is proportional to the connectivity value
 - Mouse over links :
 - > A tooltip indicate the connectivity value
 - > Seeds name are bigger and bold for a better visualization
- Brain connectome on brain templates :

An other visualization is available : brain connectome above brain templates

Click on the checkbox to visualize them







Appendices

2. Visualization of the brain connectome

- Here you can vizualize the connectivity on brains templates.
- If your mouse is over the node, a tooltip indicate the seed name
- The links are print according to the threshold values specified.
- You can re-scale and translate nodes and links
- You can also re-size brains template

