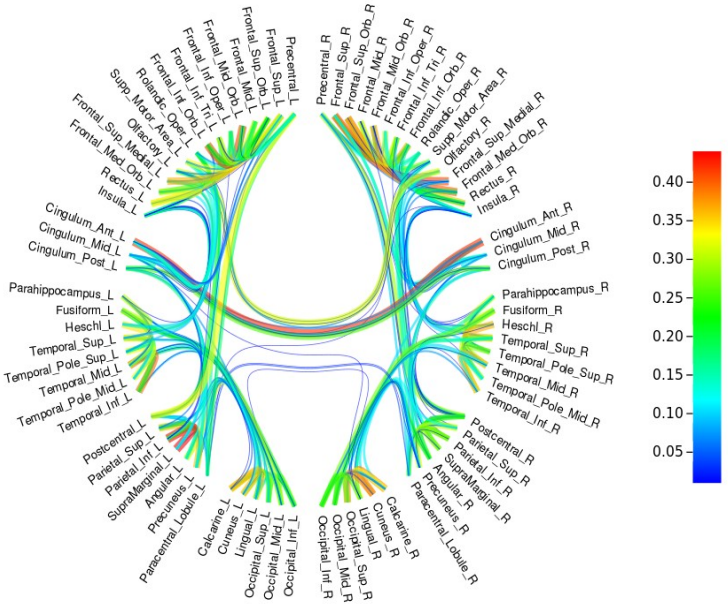
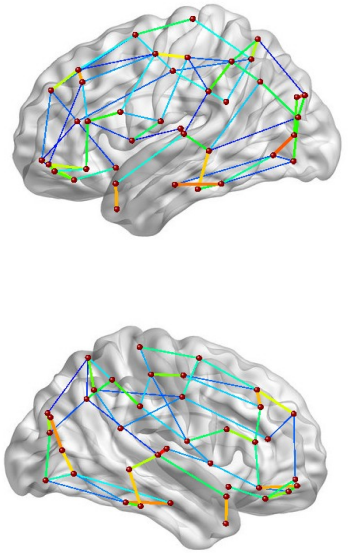
CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome

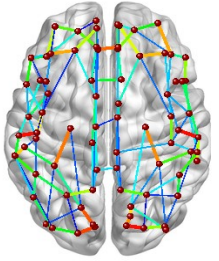
Tutorial

Circle visualization



Brain template visualization





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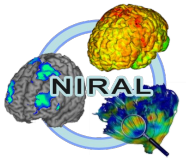

- CIVILITY is a web application with run **tractography** scripts in background and allow the user to visualize the connectivity matrix within an interactive web interface.

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

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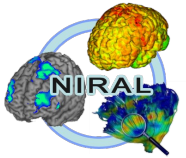

- Tractography pipeline
- Run application
- Login, create account, reset password
- Run tractography on one subject
- View jobs launched
- Visualization of the connectivity
- Download outputs

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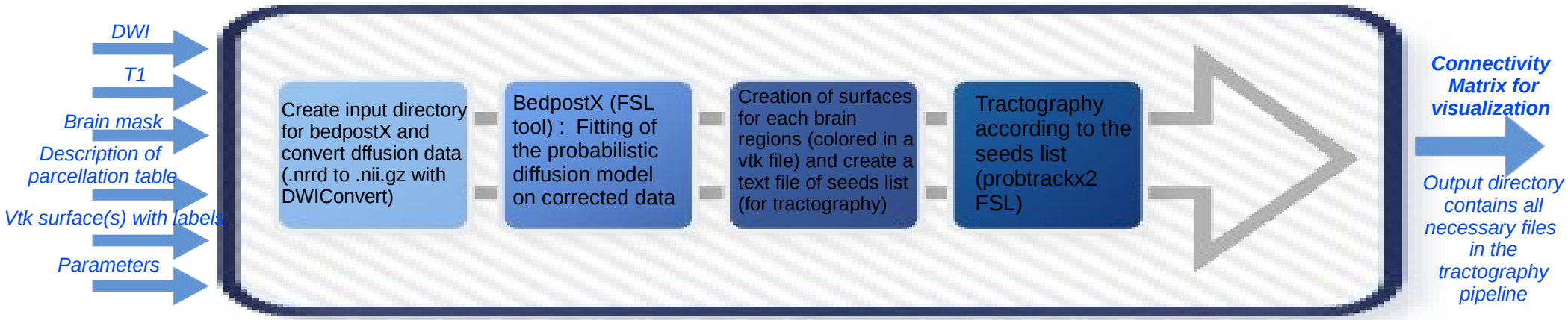
- Tractography pipeline

Inputs

All images and surface(s) must be in **diffusion space** (DWI space)

Outputs



BedpostX and probtrackx2 (FSL tools) parameters used are specified in the Documentation

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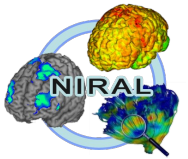

- Run application

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

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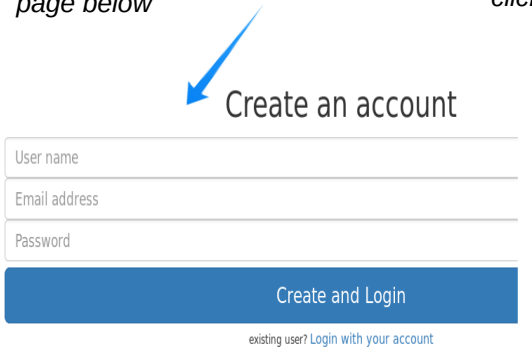
- Home page : Login, create an account, reset password

Do you have an account ?

No

Click on create new account
You will be redirected to the page below



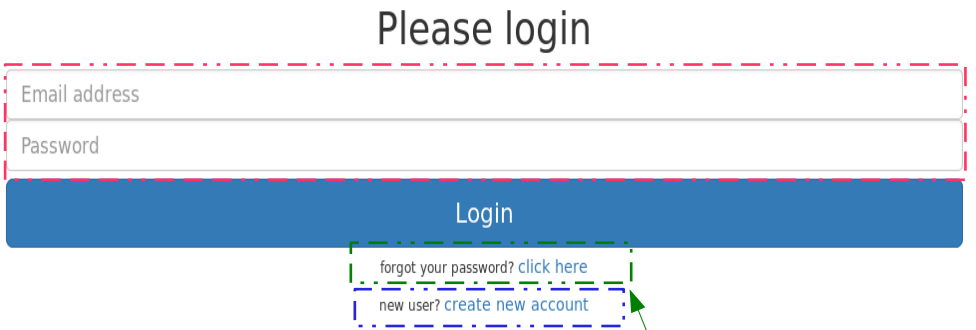
Fill this form with : an username, a valid email address and a password and then click on **Create and Login** button

The password **must contains** 6 characters including at least one uppercase letter, one lowercase letter, one number

You still can return to the login page by clicking to Login with your account

Yes

*Enter your Email address and password and then click to **Login** button*



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*

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- Application

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

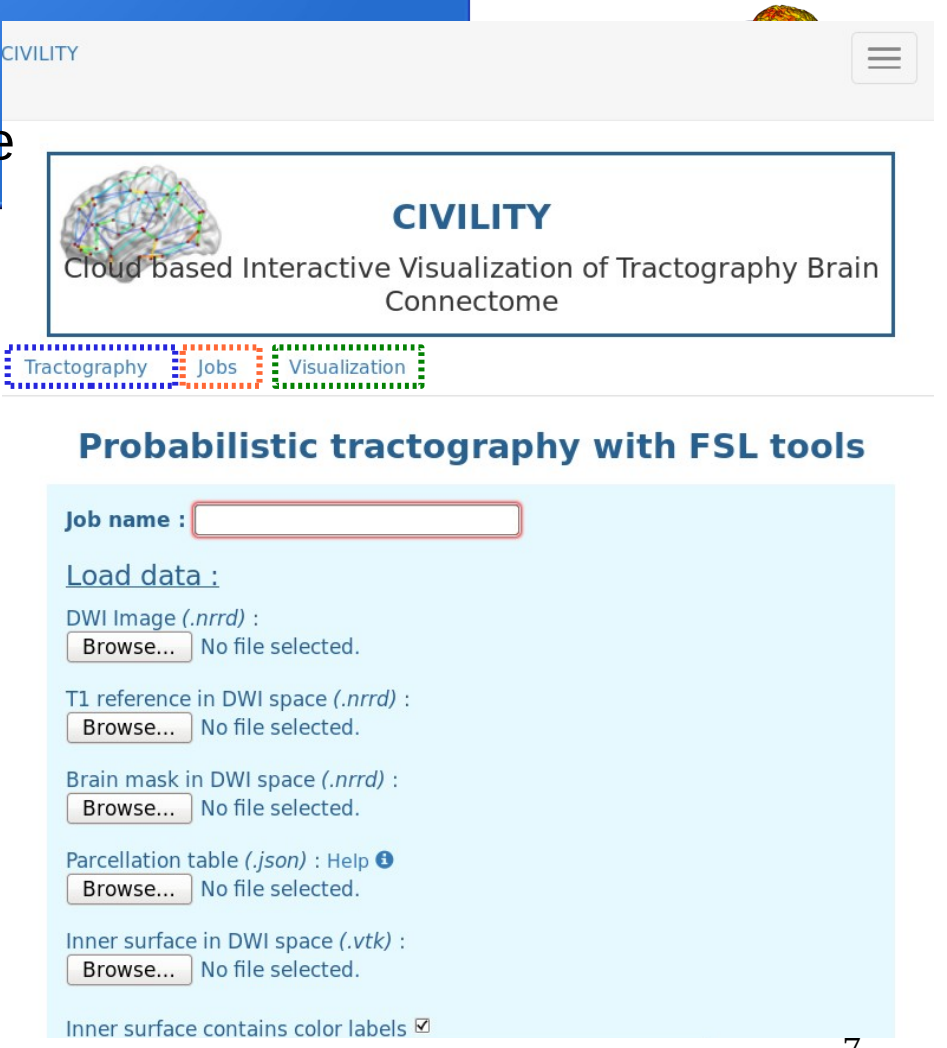
Otherwise, return to the last slide to be Login.

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.

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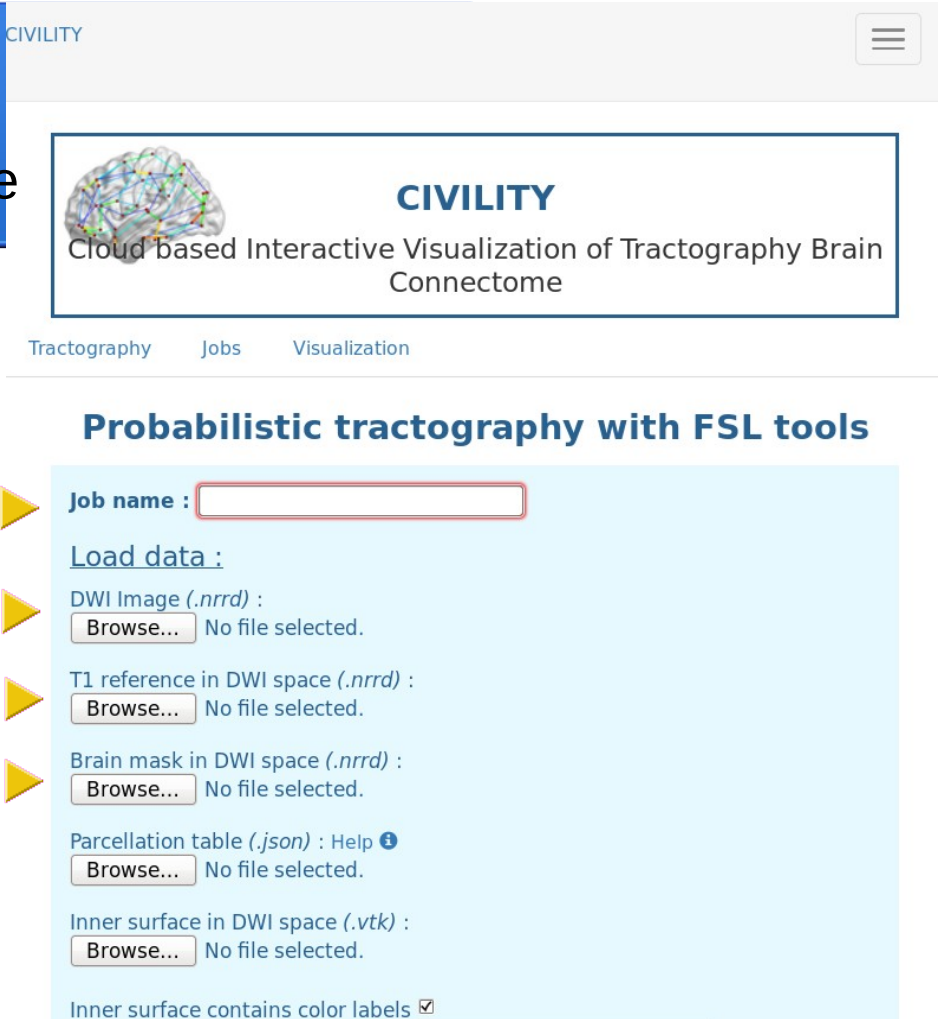
- Run tractography on one subject – Tab 1

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 same space as the DWI image → diffusion space) – *format : nnrd*
- Upload brain mask (in diffusion space) – *format : nnrd*



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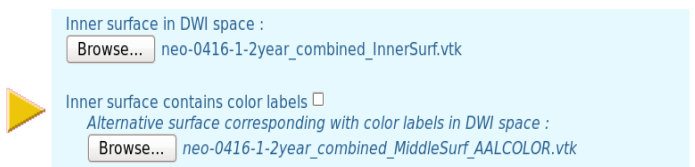
- Run tractography on one subject - Tab1

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



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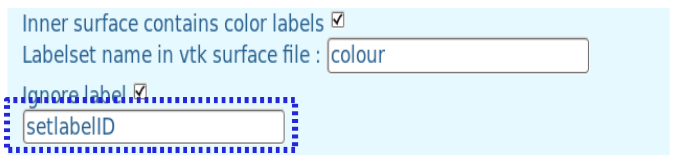
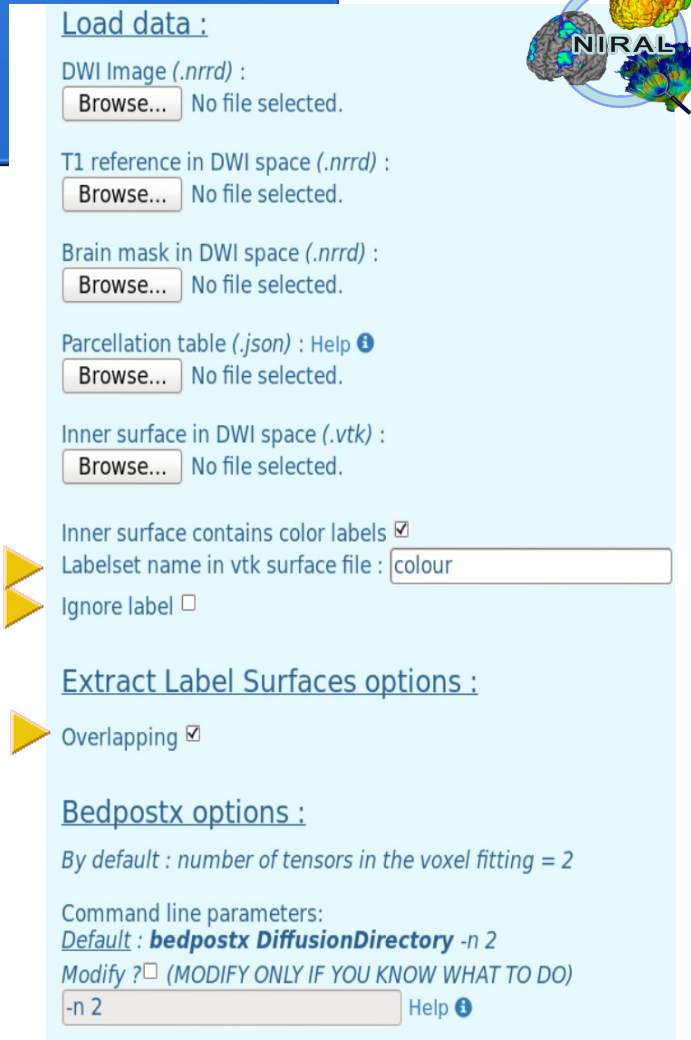
- Run tractography on one subject - Tab1

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 to 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”)



- 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)



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- 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

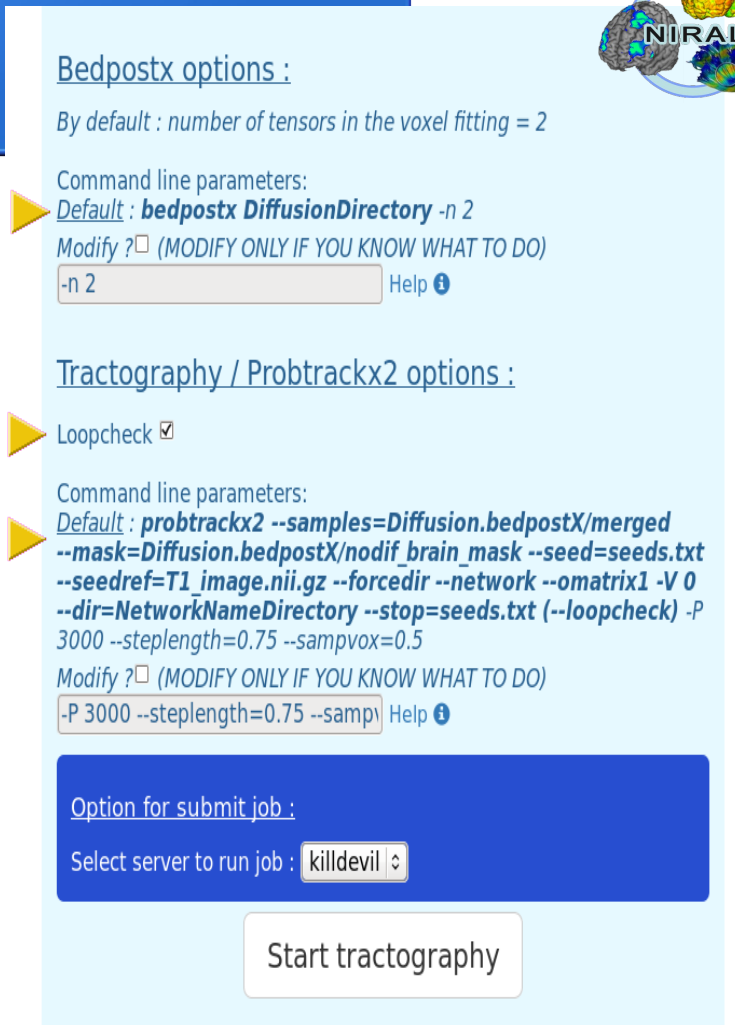
- By default the number of tensors in the voxel fitting is equal to 2. You can modify bedpostx parameters if you are familiar with this tool by clicking on the checkbox “Modify“.

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“.



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- 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 created and submit.

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- View jobs – Tab 2

This tab allows 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 :

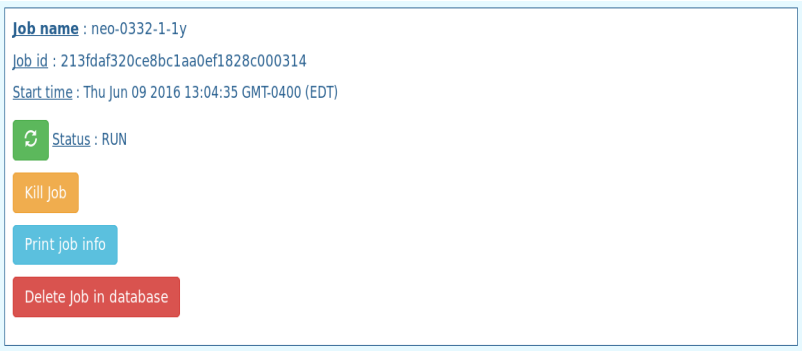
According to the status of the job, options are available or not.

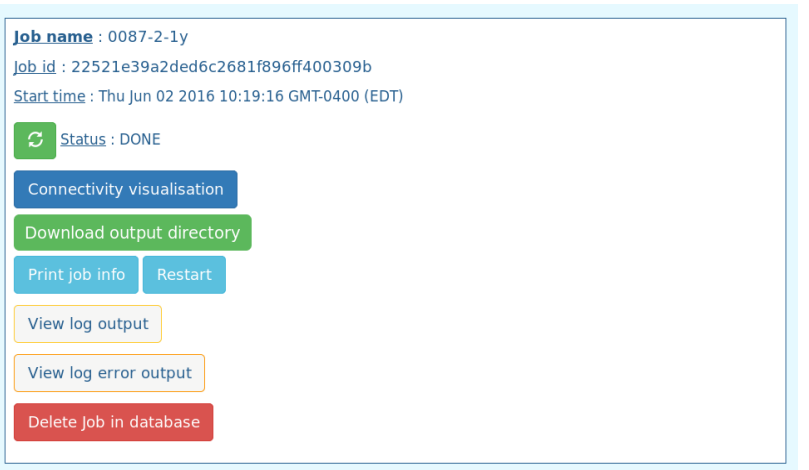
Update status → you can update the status of the job by clicking on this button

Connectivity visualisation → Connectivity Visualization → see appendix 2

Download output directory → Download output directory → to save results in your system

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





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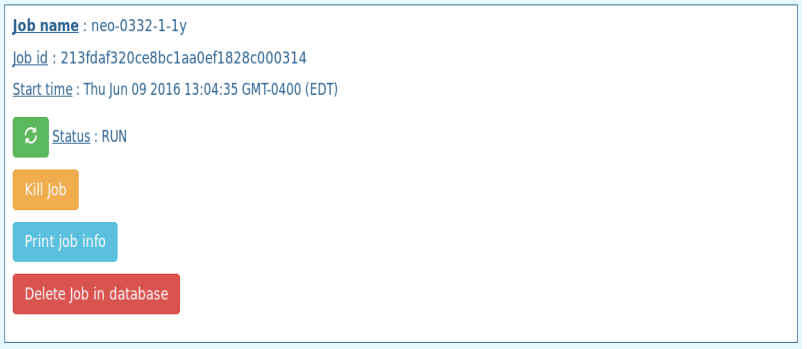
- View jobs – Tab 2

Restart

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

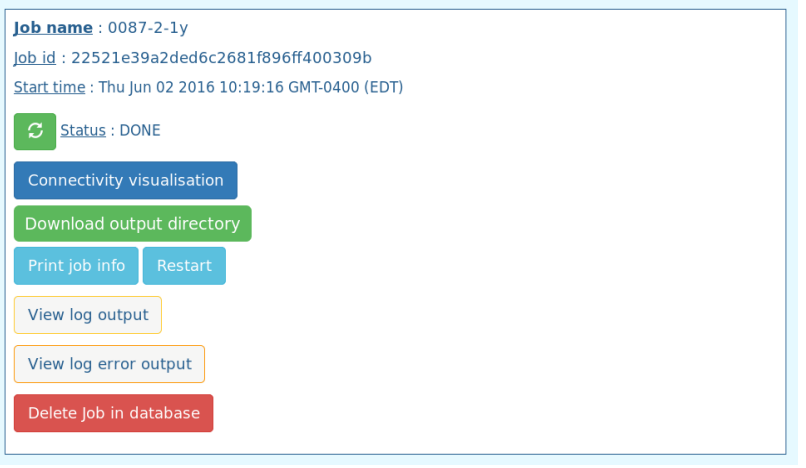
If the status is CREATE you can restart the job easily. For all other status you had to force the job submission. Before force the job submission, check the output log files and check inputs files you've uploaded to be sure you've submited nothing wrong.



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 Job → kill the job which is currently running

Delete Job in database

Delete Job → delete the job from the database

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- Visualize the connectivity matrix – Tab 3

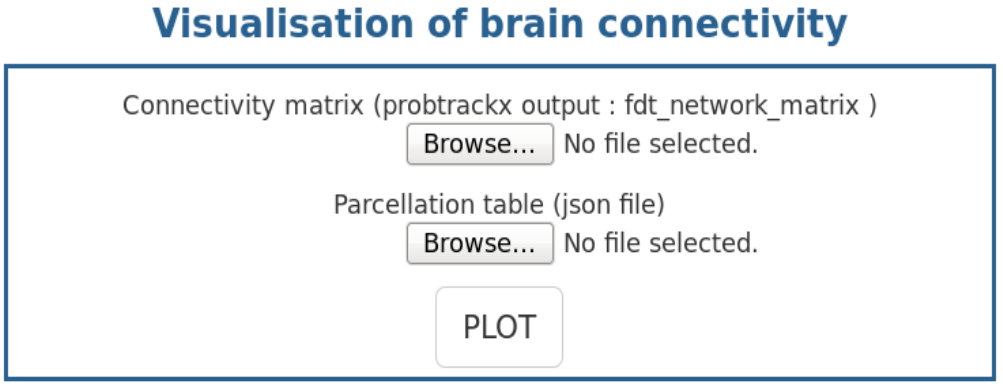
- This tab allow users to plot connectivity matrix from the user system files by uploading 2 files :

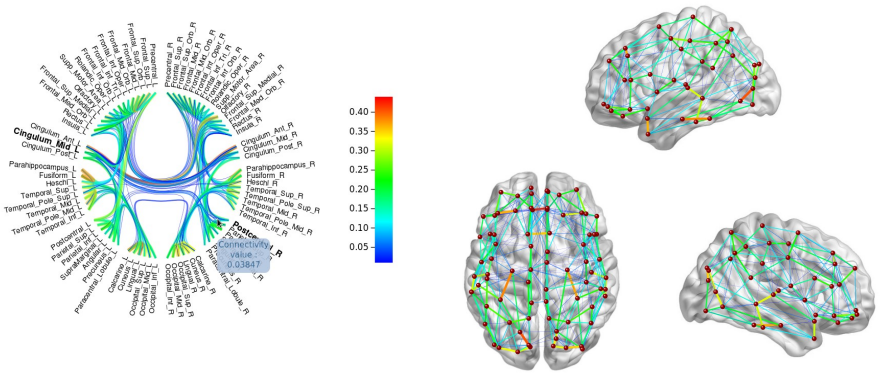
  -connectivity matrix : output of probtrackx2

  -parcellation table : json file → *see appendix 1*

- To visualize the brain connectome click on PLOT,

  and the circle plot appear. → *see appendix 2*





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- 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
    }
]
```

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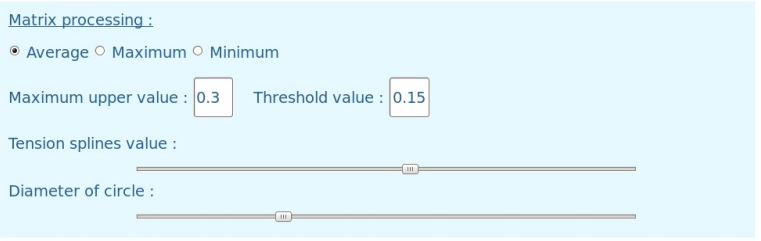
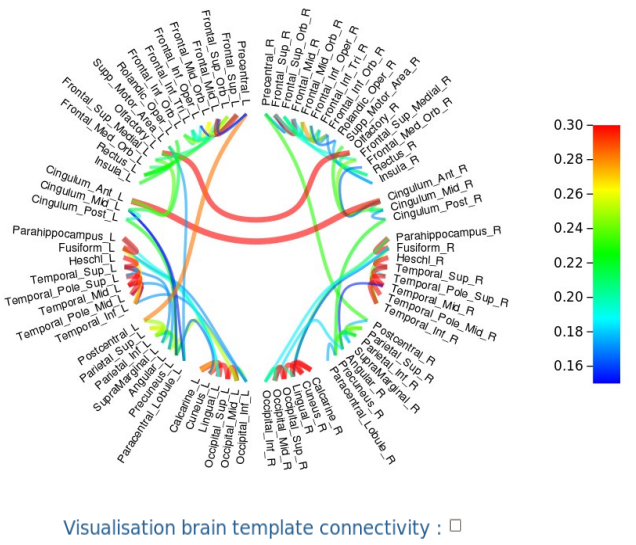
2. Visualization of the brain connectome – Parameters

- The brain connectome plot is the result of connectivity matrix (outptut 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.
- Threshold : 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





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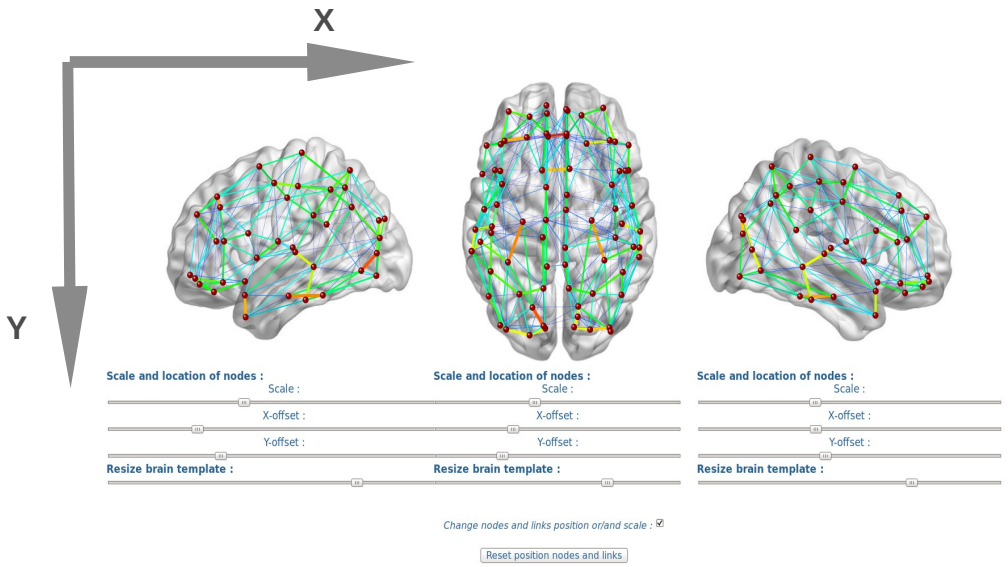
- Appendices

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



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2. Visualization of the brain connectome

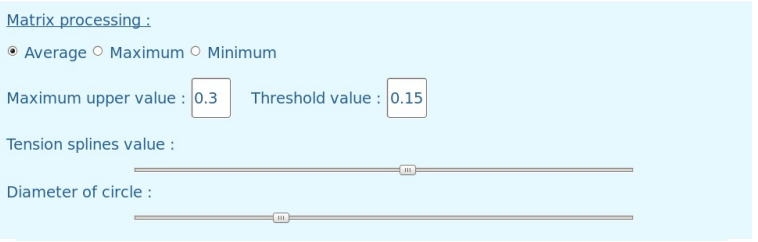
- The slide bar above “Tension splines value“ modifies the shape of links by changing their tension value.
- The diameter circle can also be set.
- Links : - Links colors indicate the connectivity value according the color bar

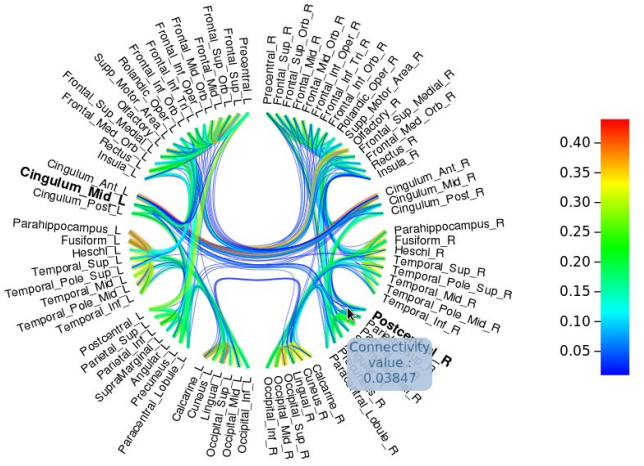
  - The thinkness of links is proportional to the connectivity value

  - Mouse over links :

    - A tooltip indicates 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





Visualisation brain template connectivity : ☐

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2. Visualization of the brain connectome

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- You can also re-size brains template