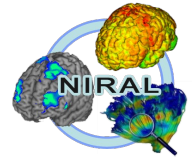
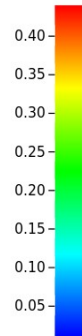
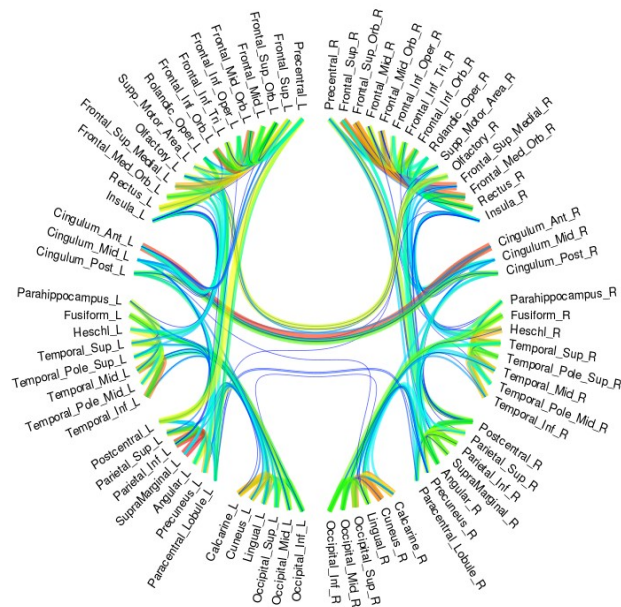


# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome

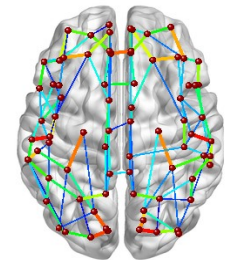
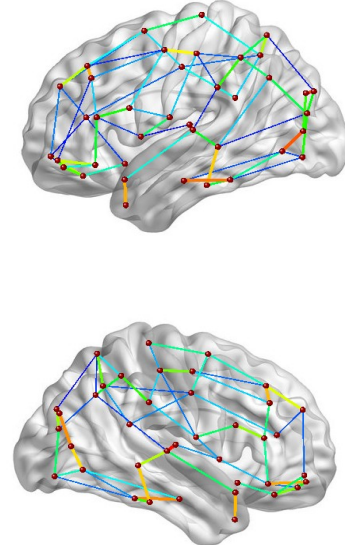


## Circle visualization

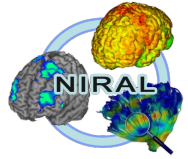


## Tutorial

## Brain template visualization

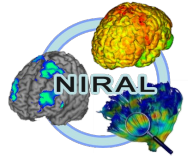


# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



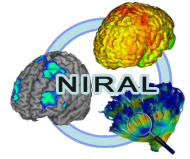
- CIVILITY is an HAPI plugin which launches **tractography** scripts in background (using the HAPI plugin clusterpost-server) and allows the user to visualize the connectivity matrix within an interactive web interface.
- Through this application the user can also to download the tractography output folder in order to save results in user system.

# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



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

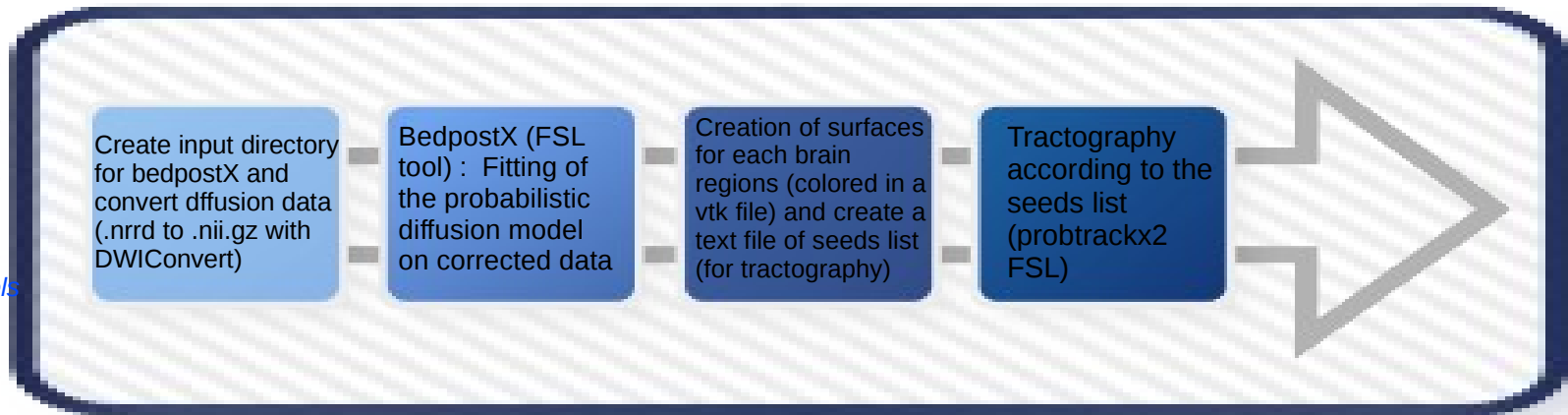
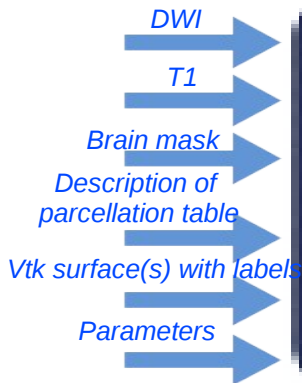
# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



- Tractography pipeline

## Inputs

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



## Outputs

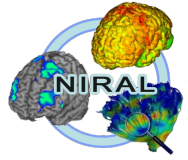
**Connectivity Matrix for visualization**

Output directory contains all necessary files in the tractography pipeline

*BedpostX and probtrackx2 (FSL tools) parameters used are specified in the [Documentation](#).*

*The tractography can take ~1 week of computation*

# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



- Run application

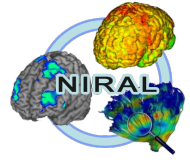
On your terminal create the tunnel to access to the application

***ssh ares.ia.unc.edu -L 8180:localhost:8180***

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

***https://localhost:8180***

# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



- 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

Create an account

User name
Email address
Password
Create and Login

existing user? Login with your account

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

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

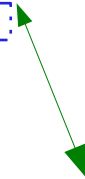
The password **must contains** 6 characters  
including at least one uppercase letter, one  
lowercase letter, one number



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 containing 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

# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome

- Application

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

Otherwise, return to the last slide to be Login.

**Tabs 1 and 2 are accessible only if your administrator authorized you the access. If, you don't have access, send a request of access by email to your administrator.**

This application is composed of 3 tabs.

Tab 1 

*Launch a tractography on a subject*

Tab 2 

*Summarize of all jobs launched. You can visualize results, status, parameters etc.*

Tab 3 

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



## Probabilistic tractography with FSL tools

Job name :

Load data :

DWI Image (.nrrd) :

No file selected.

T1 reference in DWI space (.nrrd) :

No file selected.

Brain mask in DWI space (.nrrd) :

No file selected.

Parcellation table (.json) : [Help](#) 

No file selected.

Inner surface in DWI space (.vtk) :

No file selected.

Inner surface contains color labels ☒

# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome

- 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 : nrrd*
- Upload T1 image (must be on the same space as the DWI image → diffusion space) – *format : nrrd*
- Upload brain mask ( in diffusion space ) – *format : nrrd*



Tractography Jobs Visualization

## Probabilistic tractography with FSL tools

▶ Job name :

▶ [Load data :](#)

▶ DWI Image (.nrrd) :  
 No file selected.

▶ T1 reference in DWI space (.nrrd) :  
 No file selected.

▶ Brain mask in DWI space (.nrrd) :  
 No file selected.

Parcellation table (.json) : [Help](#) ⓘ  
 No file selected.

Inner surface in DWI space (.vtk) :  
 No file selected.

Inner surface contains color labels ☒



# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome

- Run tractography on one subject - Tab1

## 2. Upload description table and surface(s) files

- Upload the parcellation table (json file) – *format : vtk* / see Appendix 1
- Upload the Inner surface (in diffusion space) – *format : vtk*
- 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, same space) containing labels

Inner surface in DWI space :

neo-0416-1-2year\_combined\_InnerSurf.vtk

Inner surface contains color labels ☐

Alternative surface corresponding with color labels in DWI space :

neo-0416-1-2year\_combined\_MiddleSurf\_AALCOLOR.vtk



Tractography

Jobs

Visualization

## Probabilistic tractography with FSL tools

Job name :

Load data :

DWI Image (.nrrd) :

No file selected.

T1 reference in DWI space (.nrrd) :

No file selected.

Brain mask in DWI space (.nrrd) :

No file selected.

Parcellation table (.json) : Help

No file selected.

Inner surface in DWI space (.vtk) :

No file selected.

Inner surface contains color labels ☒

# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome

- Run tractography on one subject - Tab1

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

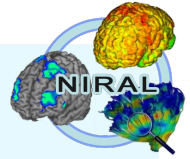
- Fill the text field by the name of the labelset in the vtk file
- If you want to ignore a label in the vtk file, check to box “Ignore label” and enter the value/ID of the label to ignore (example : “0 0 0” )

Inner surface contains color labels ☒

Labelset name in vtk surface file :

Ignore label ☒

- 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)



#### Load data :

DWI Image (.nrrd) :

No file selected.

T1 reference in DWI space (.nrrd) :

No file selected.

Brain mask in DWI space (.nrrd) :

No file selected.

Parcellation table (.json) : [Help](#)

No file selected.

Inner surface in DWI space (.vtk) :

No file selected.

Inner surface contains color labels ☒

Labelset name in vtk surface file :

Ignore label ☐

#### Extract Label Surfaces options :

Overlapping ☒

#### Bedpostx options :

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

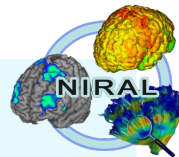
Command line parameters:

Default : **bedpostx DiffusionDirectory** -n 2

Modify ? ☐ (MODIFY ONLY IF YOU KNOW WHAT TO DO)

-n 2  [Help](#)

# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



- 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".

#### Bedpostx options :

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

Command line parameters:

*Default :* **bedpostx DiffusionDirectory** -n 2

Modify ? ☐ (MODIFY ONLY IF YOU KNOW WHAT TO DO)

-n 2 [Help](#)

#### 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)

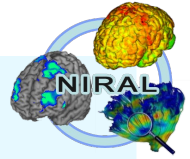
-P 3000 --steplength=0.75 --samp [Help](#)

#### Option for submit job :

Select server to run job :

Start tractography

# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



- 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.*

**Tractography can take +/- 1 week of computation**

### Bedpostx options :

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

Command line parameters:

Default : **bedpostx DiffusionDirectory -n 2**

Modify ? ☐ (MODIFY ONLY IF YOU KNOW WHAT TO DO)

-n 2

Help

### 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

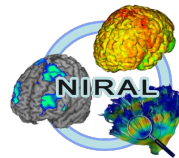
Help

### Option for submit job :

Select server to run job :

Start tractography

# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



- 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 Visualization → see appendix 2

 Download output directory → to save results in your system

 Print job informations → allow user to check files uploaded and parameters submitted

**Job name** : neo-0332-1-1y  
**Job id** : 213fdaf320ce8bc1aa0ef1828c000314  
**Start time** : Thu Jun 09 2016 13:04:35 GMT-0400 (EDT)

 **Status** : RUN

 Kill job

 Print job info

 Delete job in database

**Job name** : 0087-2-1y  
**Job id** : 22521e39a2ded6c2681f896ff400309b  
**Start time** : Thu Jun 02 2016 10:19:16 GMT-0400 (EDT)

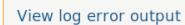
 **Status** : DONE

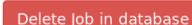
 Connectivity visualisation

 Download output directory

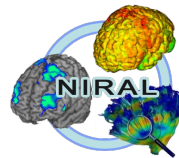
 Print job info  Restart

 View log output

 View log error output

 Delete job in database

# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



- 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 submitted 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 submitted 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

Job name : neo-0332-1-1y

Job id : 213fdaf320ce8bc1aa0ef1828c000314

Start time : Thu Jun 09 2016 13:04:35 GMT-0400 (EDT)



Status : RUN



Kill Job



Print job info



Delete job in database

Job name : 0087-2-1y

Job id : 22521e39a2ded6c2681f896ff400309b

Start time : Thu Jun 02 2016 10:19:16 GMT-0400 (EDT)



Status : DONE



Connectivity visualisation



Download output directory



Print job info



Restart



View log output

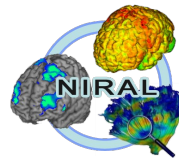


View log error output



Delete job in database

# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



- 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*

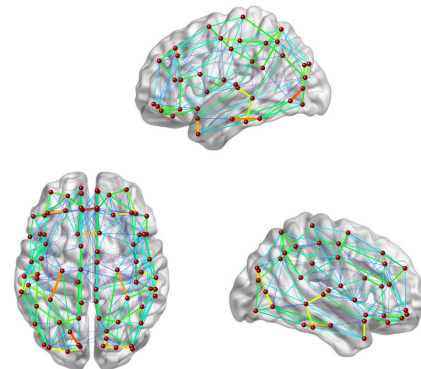
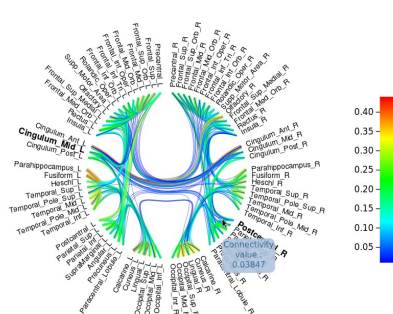
## Visualisation of brain connectivity

Connectivity matrix (probtrackx output : fdt\_network\_matrix )

No file selected.

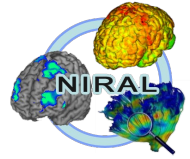
Parcellation table (json file)

No file selected.





# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



- 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

```
[
  {
  },
  {
  },
  ...
  {
  }
]
```

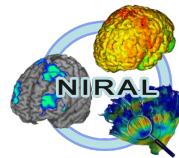
Object 1 / Region 1

Object 2 / Region 2

Object N / Region N



# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



## • 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.*

- 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**

Matrix processing :

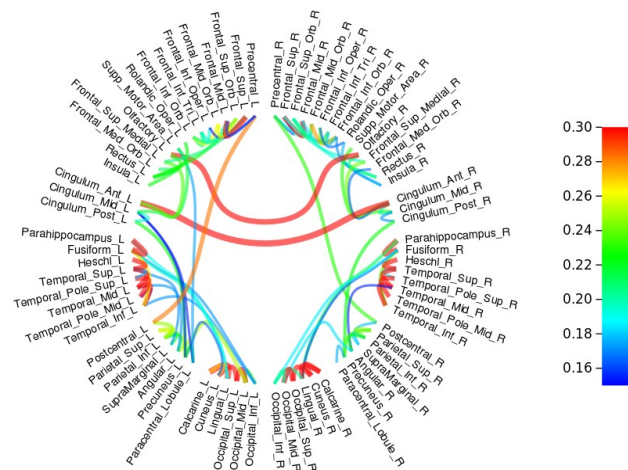
☒ Average ☐ Maximum ☐ Minimum

Maximum upper value :

Threshold value :

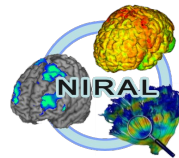
Tension splines value :

Diameter of circle :



Visualisation brain template connectivity : □

# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



## • Appendices

### 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 thickness 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

Matrix processing :

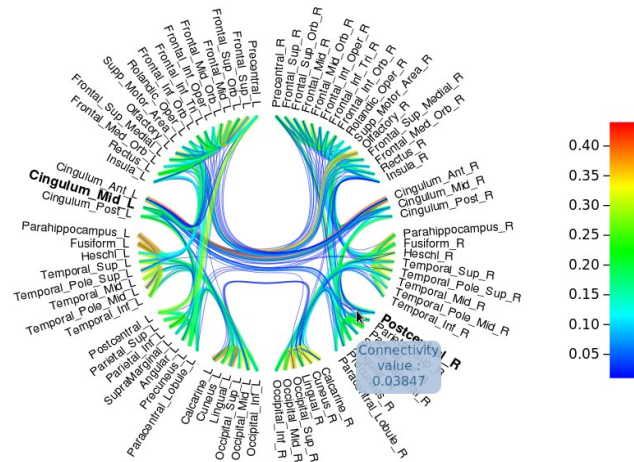
☒ Average ☐ Maximum ☐ Minimum

Maximum upper value :  Threshold value :

Tension splines value :

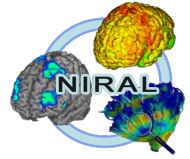


Diameter of circle :



Visualisation brain template connectivity : ☐

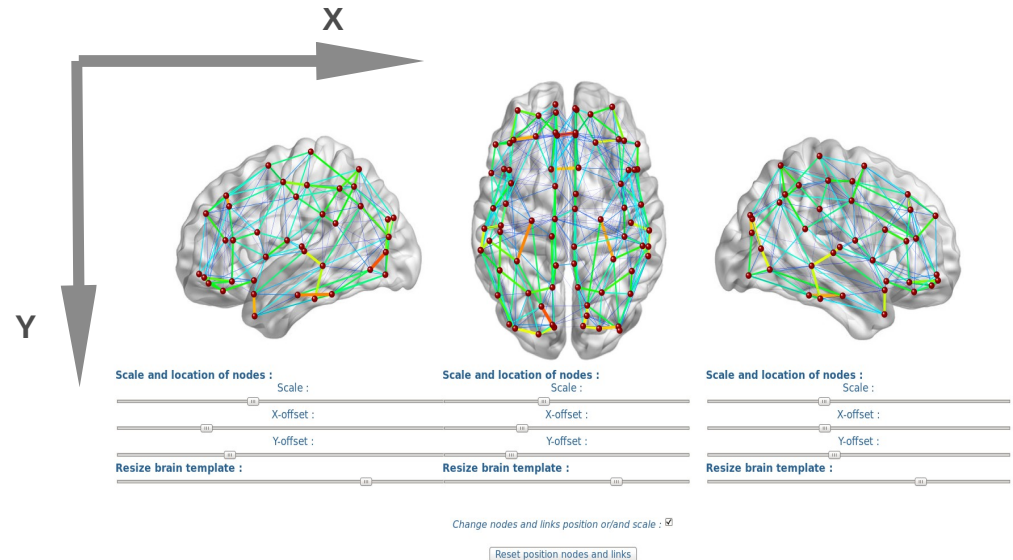
# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



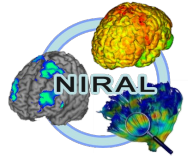
- Appendices

## 2. Visualization of the brain connectome

- Here you can visualize 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



# CIVILITY : cloud based Interactive Visualization of Tractography Brain Connectome



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