

Brain Connectome Visualization

Tutorial

Slicer3D Module

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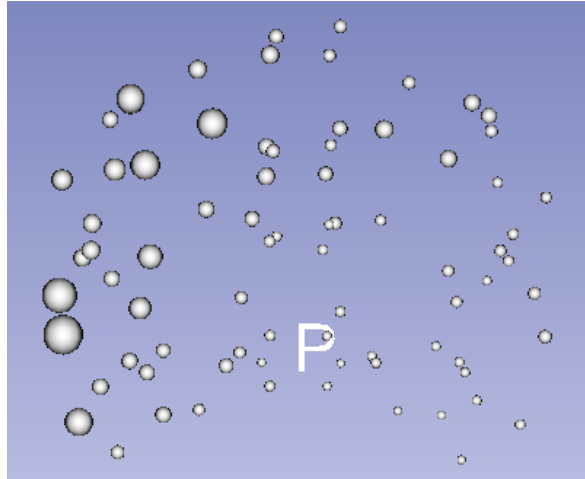
1. Introduction :

The Brain Connectome Visualization Module is a Slicer3D extension. It is programmed in Python and uses VTK (Visualization Tool Kit), CTK (Common TK) and Qt libraries.

What do we want to visualize?

Visualizations are based on symmetric and normalized matrices (AAL: 78 ROIs (Regions of Interest) or Destrieux: 75 ROIs) with connectivity values that may be obtained from diffusion connectivity or resting state connectivity studies (region-to-region values).

The matrices represent a graph, where the edges are the connectivity values and the nodes are brain regions.



1. Node representation with AAL matrix : 78 ROIs

What do we mean by connectome?

The mapping of all neural connections within the brain is what we call a connectome.

Each connection is defined by its strength (visually it represents the thickness of the connection between two nodes) and this value is found in the matrices (edge files).

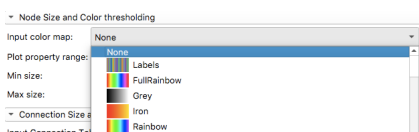
2. Rendering process:

In order to create a 3D visualisation, there are a few steps to follow:

- First we create the object to render (for example a node/sphere)



- Then we set the properties (node size and colour, and we set a default colour and node size)
- Allow the user to change the properties



- Create the renderer and add the objects to it

3. Input JSON File, first step to use the module

The first section of the module is : “Import Node Graph Json File”.

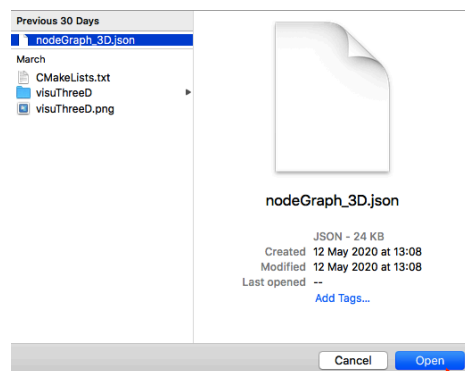
▼ Import Node Graph Json File

Input Json File: /Users/wieke/Documents/visuThreeD/visuThreeD/nodeGraph_3D.json

...

Load Files

To load your Node Graph Json file you need to click on the “...” . A file dialog will pop up and give you access to the files and servers on your computer.



Select your file and click on Open.

The path to your file will appear in the box after “Input Node File”.

Then click on Load File to access the data in the Json File.

Load Files

4. Formatting of JSON File

It is important that the input Json File follows the same structure as the JsonFile given with the module. Below we put a screenshot of the two first nodes/Brain regions. This Json File is a dictionary where each key is associated to a value. The keys are for example “VisuOrder”, “MatrixRow” or “coord”. You should keep the same keys and values. (The values associated to “coord” and “name” are not fixed)

1st Node (Brain Region)

Value: 2

Key: “MatrixRow”

2nd Node

```

[
  {
    "VisuOrder": 78,
    "MatrixRow": 1,
    "name": "Precentral_L",
    "VisuHierarchy": "seed.left.frontal.",
    "coord": [
      -38.64999999999999,
      -5.679999999999997,
      50.939999999999998
    ],
    "labelValue": "1",
    "AAL_ID": 1
  },
  {
    "VisuOrder": 1,
    "MatrixRow": 2,
    "name": "Precentral_R",
    "VisuHierarchy": "seed.right.frontal.",
    "coord": [
      41.369999999999997,
      -8.210000000000009,
      52.090000000000003
    ],
    "labelValue": "2",
    "AAL_ID": 2
  }
]

```

3. Input Node Table, 2nd step to use the module

The second section of the module is : “Node Table”.

Node Table

Header in Node Table

☐

Input Table:

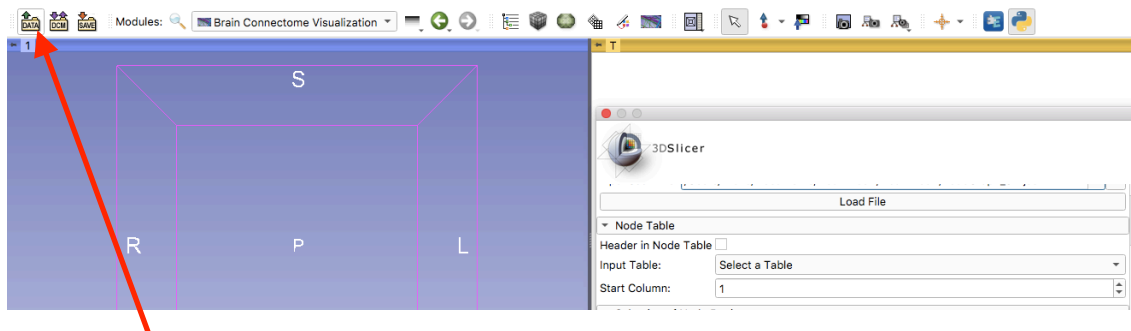
Select a Table

Start Column:

1

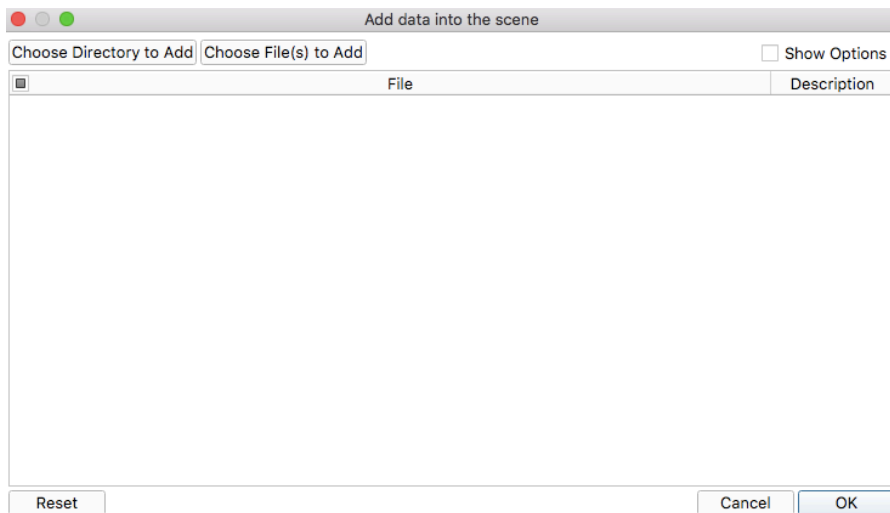
Your Node Table is a normalised matrix(.csv file) with only one row of data. This matrix can be anything you want to visualise such as Node degree, Eigen Vector Centrality...

Load the Node Table through the DATA module:



Click on DATA.

The following window will pop up :



Choose the Node table you want to import and make sure that the description is a table. Then click on OK.

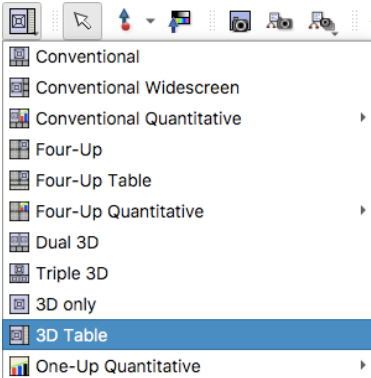


Your Node Table is now loaded and can be seen in the Table Module.

In the ToolBar click on 3D Table.



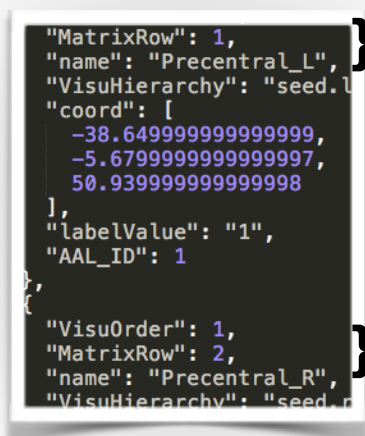
Select 3D Table in the drop down menu, this will show your table and the 3D Visualization window.



Your Table should look like this:

	A	B	C	D	E	F	G
1	subject	PreCG.L	PreCG.R	SFGdor.L	SFGdor.R	ORBsup.L	ORBsup.R
2	neo-0042-2-4year	0.106492309462	0.2436981264	0.125246236184	0.265214111929	0.0294209276038	0.081984592909

The table above has a header (first row with the name of all the brain Regions). These brain regions are ordered by MatrixRow like in the Json File.



MatrixRow: 1 corresponds to the first column and "name": Precentral_L corresponds to PreCG.L

1	subject	PreCG.L	PreCG.R	SFGdor.L	SFGdor.R
2	neo-0042-2-4year	0.106492309462	0.2436981264	0.125246236184	0.265214111929

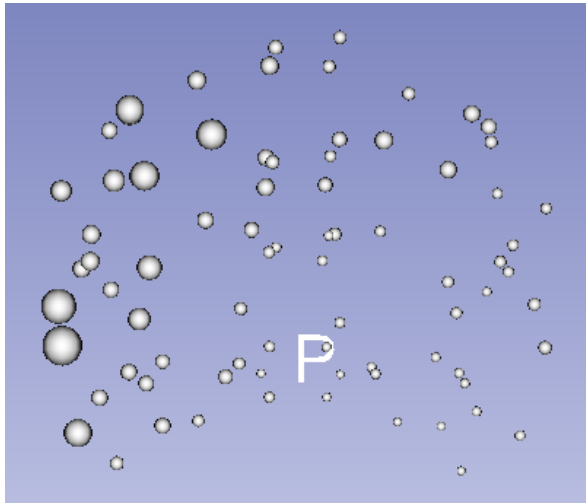
MatrixRow: 2 corresponds to the second column and "name": Precentral_R corresponds to PreCG.R

Check the header box if your table has a table, otherwise leave it unchecked.



Then, the table loaded through the Table Module will appear automatically in this area. But in order to take the table into account you need to click on the drop down arrow and select the table.

Once you have selected the Node Table, the nodes will appear in the renderer like this:



*The values given in the
Node Table influence the
Node Size*

Node representation with AAL matrix : 78 ROIs

NB : If the Nodes don't show up in the renderer, click on the renderer to update the view.

Below the "Input Table" section there is the "Start Column" section.

Input Table:

Start Column:

By default "Start Column" is at one, because in the Node Table example the first column (number 0) contains a subject name. The data only starts at column number 1. (Keep in mind that the numbering of the columns goes from 0 to max number of Brain Regions).

Subject name

1	subject	PreCG.L	PreCG.R	SFGdor.L	SFGdor.R
2	neo-0042-2-4year	0.106492309462	0.2436981264	0.125246236184	0.2651

Column 0

Column 1

Column 2

Column 3

3. Selection of Node Region Through Search Box

Selection of Node Region

Search:

Regions: All

Select:

Deselect:

Regions: All

Select: ☒ seed.left.frontal.
☒ seed.right.frontal.

Deselect: ☒ seed.left.cingulate.
☒ seed.right.cingulate.
☒ seed.left.
☒ seed.right.

Input Color: ☒ seed.right.

Plot Properties: ☒ seed.left.temporal.
☒ seed.right.temporal.
☒ seed.left.occipital.
☒ seed.right.occipital.

Min Size:

Initially all the regions in the drop down menu are selected. You can choose to filter this drop down combobox by writing a key word present in the name region. For example if we write "right" in the search box we will only see the checkboxes linked to the right hemisphere:

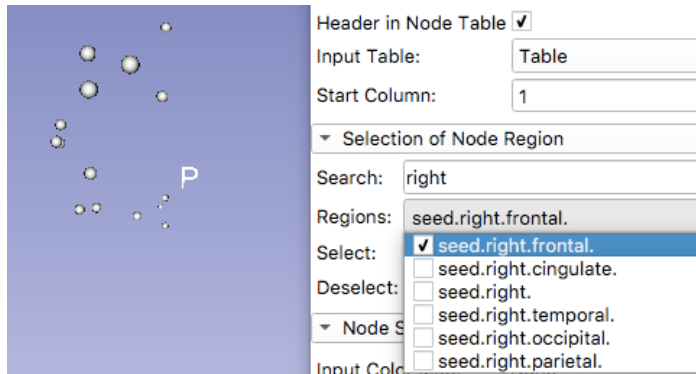
Search:

Regions: None

Select: ☒ seed.right.frontal.
☐ seed.right.cingulate.

Deselect: ☐ seed.right.
☐ seed.right.temporal.
☐ seed.right.occipital.
☐ seed.right.parietal.

We can then choose to represent just one region of the right hemisphere:



Only seed.right.frontal
is plotted in the renderer

The buttons:

Select All	Select Filtered
Deselect All	Deselect Filtered

- Select All: selects all the possible brain regions
- Select Filtered: selects only the regions in the filtered list
- Deselect All: deselects all the possible brain regions
- Deselect Filtered: deselects only the regions in the filtered list

4. Node Properties: “Node Size and Color Thresholding”

Node Size and Color Thresholding

Input Color Map:

None

Plot Property Range:

0.00

1.00

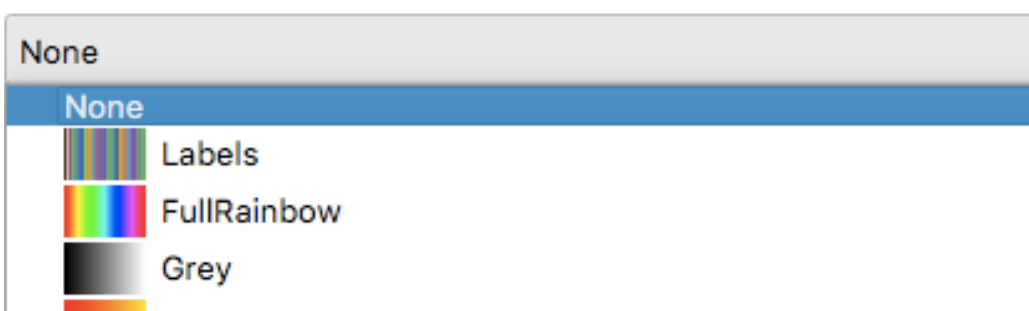
Min Size:

0.00

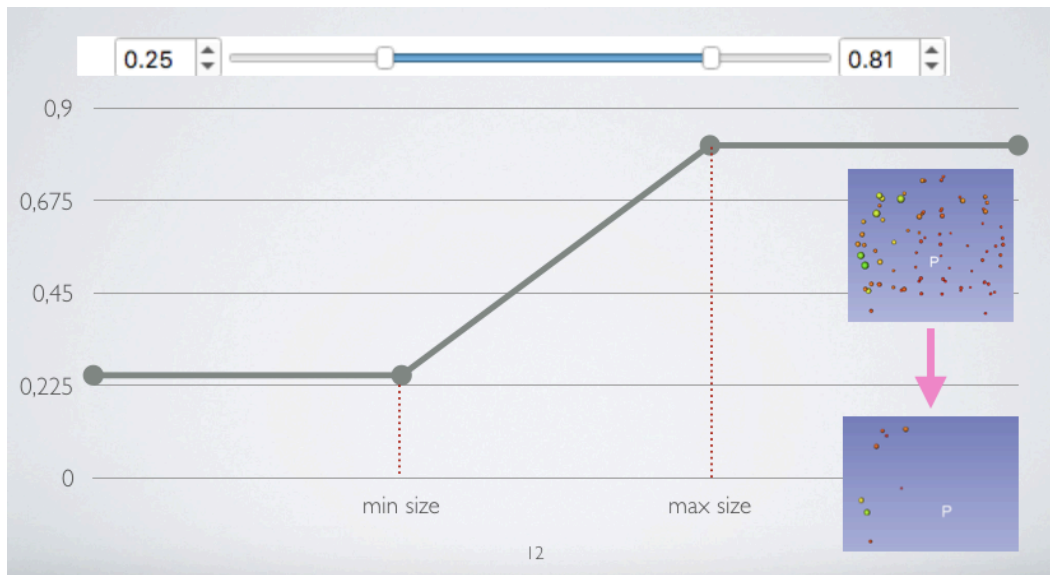
Max Size:

0.00

Next to “Input Color Map” , in a drop down menu you choose which colour map you attribute to your nodes. Keep in mind that the colour depends on the size of each node.

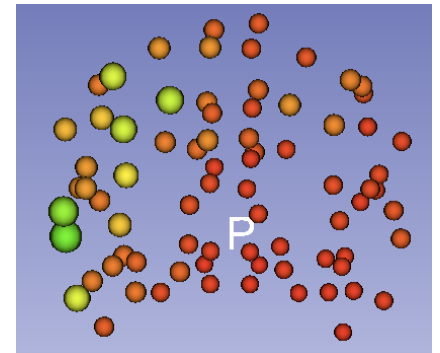
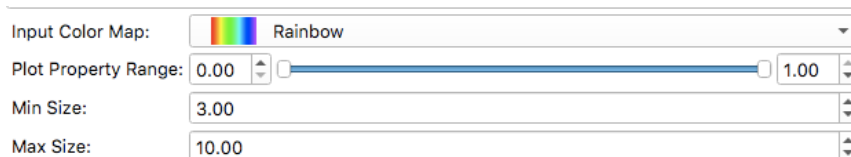


Then there is the “Plot Property Range”, the illustration below gives an example of the influence of this slider bar on the node plot.



This illustration shows that every node that has its value below the slider bar’s min (here 0.25), has its visibility set to OFF (image on the bottom right). Every node value that is located above the max value of the slider bar gets the max value (here: 0.81).

Then there is a possibility to change the “Min Size” and “Max Size” to enhance the visualisation. For example with a node min of 3 and a node max of 10, we obtain the following output visualisation:



5. Input Connection Table

Before loading your table, make sure that your connection matrix contains a header for it to be readable.

Add a header of strings to your csv file. You can use these string characters:

[PreCG.L, PreCG.R, SFGdor.L, SFGdor.R, ORBsup.L, ORBsup.R, MFG.L, MFG.R, ORBmid.L, ORBmid.R, IFGoperc.L, IFGoperc.R, IFGtriang.L, IFGtriang.R, ORBinf.L, ORBinf.R, ROL.L, ROL.R, SMA.L, SMA.R, OLF.L, OLF.R, SFGmed.L, SFGmed.R, ORBsupmed.L, ORBsupmed.R, REC.L, REC.R, INS.L, INS.R, ACG.L, ACG.R, DCG.L, DCG.R, PCG.L, PCG.R, PHG.L, PHG.R, CAL.L, CAL.R, CUN.L, CUN.R, LING.L, LING.R, SOG.L, SOG.R, MOG.L, MOG.R, IOG.L, IOG.R, FFG.L, FFG.R, PoCG.L, PoCG.R, SPG.L, SPG.R, IPL.L, IPL.R, SMG.L, SMG.R, ANG.L, ANG.R, PCUN.L, PCUN.R, PCL.L, PCL.R, HES.L, HES.R, STG.L, STG.R, TPOsup.L, TPOsup.R, MTG.L, MTG.R, TPOmid.L, TPOmid.R, ITG.L, ITG.R]

Now that you added a header to your connection matrix, load your .csv file through the DATA Module (same as previously with the Node Table).

Once your connection matrix is loaded you can see it in the table Module:

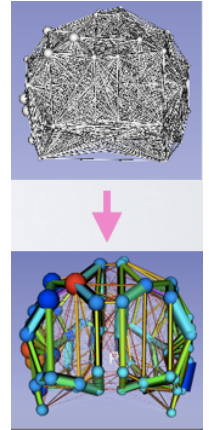
Wherever there is a zero in the matrix there is no connection.

T	A	B	C	D
1	PreCG.L	PreCG.R	SFGdor.L	SFGdor.R
2	0	2.30481138373834E-05	0.002370561773804	5.80856714174019E-06
3	2.30481138373834E-05	0	1.1479541657271E-05	0.002790105972168
4	0.002370561773804	1.1479541657271E-05	0	0.000704622630397
5	5.80856714174019E-06	0.002790105972168	0.000704622630397	0
6	1.71046519640654E-06	8.09368389466817E-08	0.001183631124335	7.69439548919788E-06
7	2.45508411471601E-07	1.6457157252492E-06	0.000203434744692	0.001114783551232
8	0.003707346980583	4.69433665890754E-07	0.007878157186237	6.82918068085785E-05
9	4.02256089565008E-06	0.003432234571319	2.33340906683283E-05	0.008104262339519
10	2.69789463155606E-08	0	0.000173372104813	1.6457157252492E-07
11	2.69789463155606E-09	8.36347335782378E-08	9.22679963992172E-07	0.000221348765046
12	0.001692076346598	1.0683662740962E-06	0.000228487394241	1.61064309503897E-06

Header

Portion of connection matrix with header.

The values in the matrix represent the strength (thickness) of the connections.



Select the connection matrix by clicking on the drop down arrow, click on the connection matrix.

Connection Size and Color Thresholding

Input Connection Table: Select a Table

Log Distribution: ☐

Input Color Map: None

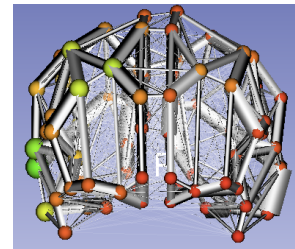
Plot Strength Range: 0.00 to 1.00

Min Strength: 0.00

Max Strength: 0.00

Table

Table
neo-0042-4year_AvgSym_normFull



The connections will appear in the visualisation window.

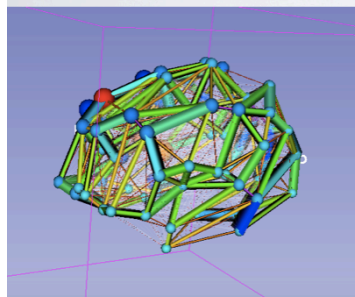
6. Distribution : computed by the number of connections or log scale

By default, when the “Log Distribution” checkbox is not checked, each value in the connection matrix is computed by the total number of connections. There are over 3000 connections, therefore we multiply once more the value in the matrix by a factor : “f” so that the range stays between 0 and 1. (illustration bellow on the left).

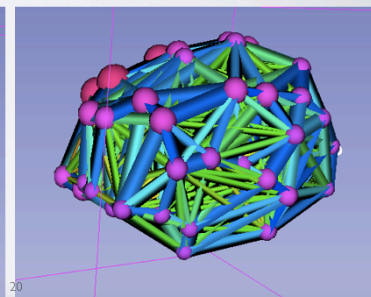
Then, if the “Log Distribution” checkbox is checked. It takes the log function of each value in the matrix and adds a C factor so that the values are positive. (illustration bellow on the right).

Default
distribution

- Distribution computes by number of connections
- $$s = n*(n-1)/2 * f$$
- $$y' = \text{value in matrix}$$
- $$y = y' * s$$



- Log distribution
- $$C = 10$$
- $$y = (\log(10)y' + C)/C$$



Log
Distribution

7. Connection Properties (Connection Color and Connection Size)

Connection Size and Color Thresholding

Input Connection Table: Select a Table

Log Distribution

Input Color Map: None

Plot Strength Range: 0.00 1.00

Min Strength: 0.00

Max Strength: 0.00

Next to “Input Color Map”, in a drop down menu you choose which colour map you attribute to your connections. Keep in mind that the colour depends on the thickness of each connection.

Then, just like the Nodes we have a slider bar to “Plot Strength Range”.



This illustration shows that every connection that has its strength below the slider bar’s min (here 0.25), has its visibility set to OFF (image on the bottom right). Every node value that is located above the max value of the slider bar gets the max value (here: 0.81).

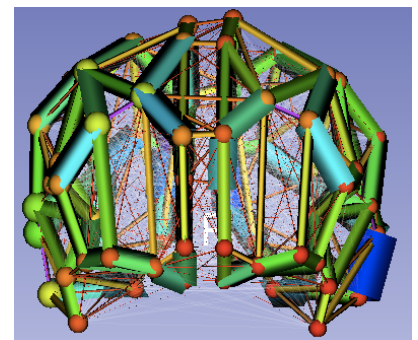
Then there is a possibility to change the “Min Strength” and “Max Strength” to enhance the visualisation. For example with a min strength of 8 and a max strength of 9, we obtain the following output visualisation:

Rainbow

0.00 1.00

8.00

9.00



8. Advanced Connection Scale Factors

This section is optional. The f factor for the default distribution and the C factor for the Log distribution can be changed in this section.

▼ Advanced Connection Scale Factors	
f Scale:	<input type="text" value="0.000033"/>
C Log Scale:	<input type="text" value="10"/>

If the Log distribution checkbox is not checked, this means that you're in the default distribution scenario and only the f scale factor can then be changed.

If the checkbox is checked, then you're in the Log Distribution scenario and only the C scale can be changed.