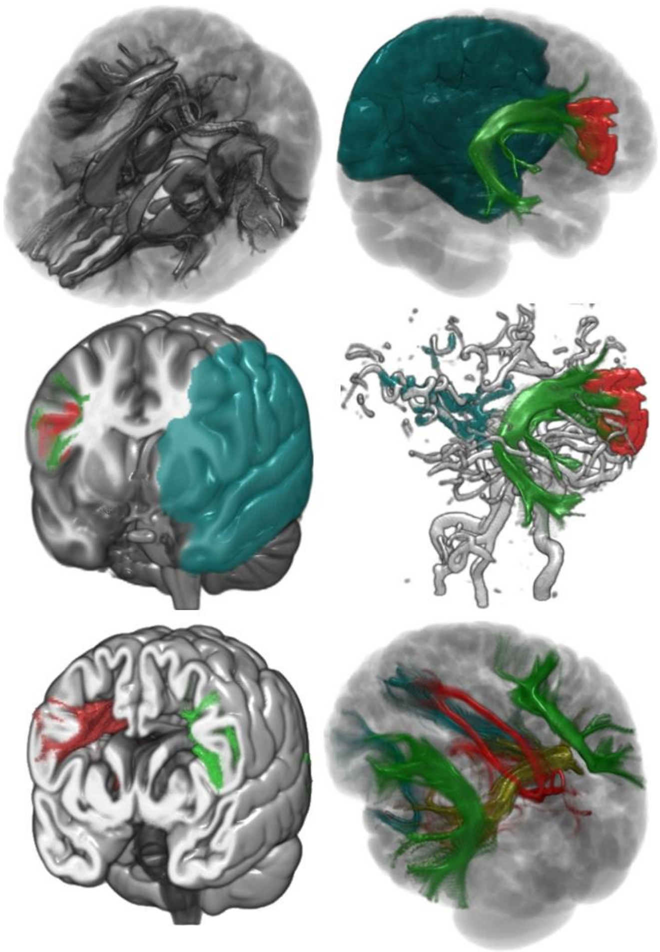
Connectopedia

Version 2.6



Interactive Atlas of Humain Brain

Functions, Connectomics and Vasculature

Promotion, Conception, Coding: *Pr D. Ducreux*, DataBase Collection : *Pr D. Ducreux, Dr S. Espinoza*

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Acknowledgment : Pr Chris Rorden, McCausland Center, University of South Carolina, USA

Summary

I. General Overview

Connectopedia is an interactive atlas of human brain structures, functions and vasculature, using brain connectomics to assess functional pathways of the tasks performed by the brain.

Connectopedia is linked with the DPTOOLS package from version 6 and above, and is distributed standalone, free of charge, for academic purposes only, with BSD licensing.

Connectopedia was coded using C++ and Delphi, with OpenGL 2D and 3D reconstructions for volume rendering purposes (thanks to the Chris Rorden MRIcroGL sources), and is compatible with NIFTI files. Connectopedia requieres Microsoft Windows Vista or Mac OSX 10.8 and above, a minimum of 4 GB of RAM (8 recommended), and an OpenGl capable graphic card. A display capable of 1080p or two displays are recommended.

Connectopedia uses the 152 MNI T1 and Cortical Areas (116 areas) Atlas templates for 3D rendering of the structural grey matter of the brain. The 58 Fiber bundles were reconstructed from my own brain, using HARDI 60 directions, b value of 1500, and automatically generated and coregistered to the T1 MNI template using DPTOOLS 6.1 and the MedInria 1.9 software suite. The 90 arterial and 54 venous referenced structures were set by manual segmentation on the T1 MNI 152 isotropic 1 mm^3 template. Arterial and Venous 3D VR reconstructions were set on TOF and 3D Phase Contrast MR sequences and isotropically 1 mm^3 coregistered to the T1 MNI template.

Connectopedia was created to provide to neuroscientists as well as students an easy way of learning, teaching or checking functional neuroanatomy, and is linked to DPTools v6 and above, which was used to study structural and functional connectomics with real time reconstructions and assessment of the brain structural and functional connectoms using RTConTrack.

RTConTrack, acronym for Real Time Connectom Tracking, is a special algorithm dedicated to identifying the Brain Grey and White Matter Structures involved in the Brain Functions occurring during a fMRI performed task, and to creating dynamic maps of their information exchanges patterns.

RTConTrack can be compared to a « GPS » system, where the « Cities » are the Grey Matter Structures, the « Highways » the White Matter Bundles, and the « Cars » the neuronal informations going through specific maps, each map characterizing a specific brain function.

To be able to identify those structures and informations, RTConTrack uses functional fMRI Bold activation maps, analyzed in « Pseudo Real-Time » using a dedicated interpolation algorithm (Static fMRI maps are not accurate enough for this purpose) in order to see the informations going from one « city » to another, and Diffusion MRI sequences to individualize the «Highways» using Tractography (HARDI sequences).

To identify the Grey and White Matter Structures involved in a specific function, RTConTrack uses dedicated Brain Functional and Structural Anatomy Atlases.

When those structures are identified, RTConTrack computes the Structural and Functional Dynamic Connectoms maps involved in all functions performed by the Brain during the fMRI acquisition.

When the Structural and Functional Connectoms are computed for each fMRI activation Timeline, RTConTrack reconstructs in 4D the Connectoms evolutions patterns.

Then RTConTrack back reconstructs the identified Grey and White Matter structures to match the Anatomy Templates in a Dynamic Anatomy Activation Mapping and in a Dynamic 4D (Time and Space) Functional Anatomic Reconstruction.

These Dynamic Functional Anatomic and Connectomic Reconstructions are then coded into «GPS» maps, and these maps and compared using an artificial intelligence algorithm with other similar maps included in a dedicated database, to assess similarity scores among the known brain functions, the tasks and the subjects.

Brain Functions occurring during the fMRI acquisition are then identified, compared and scored, and a report is generated with percentage of Occurrences for the Major and Minor identified brain functions.

These scores can then be used to assess the therapy efficacy (brain functions occurrences variations before and after treatment) in psychiatric patients (depressed, schizoid, autistic …), in coma patients (existence of emotional and cognitive processes during e.g. an auditory stimulation), in lie detection, in consumer satisfaction scores, aso...

From the 2.2 version and above of Connectopedia, multithread processing is enabled (speeds up to 250% the rendering and analysis functions), and 408 identified brain functions (from behavior to cognitive or emotional patterns, aso…) are included and referenced in the Connectopedia Explorer database and within the RTConTrack algorithm, as well as on the web site.

Version 2.3 enables the vascular and structural anatomy labeling, as well as importing and co-registering Raw Gis map files from DPTools (diffusion/perfusion/activation maps) using the 'Drag and Drop' feature of the 3D Renderer window (MS Windows version only).

Version 2.4 has improved Connectoms rendering of the Grey and White Matter Structures connections with simplified views of the connected items and skeleton view of the global structures connections, as well as interactive selecting process of the connectomic mapping of Grey and White Matters.

Version 2.5 has a simplified 'Sequencer Window' interface and new filtering features to explore the Brain Functions.

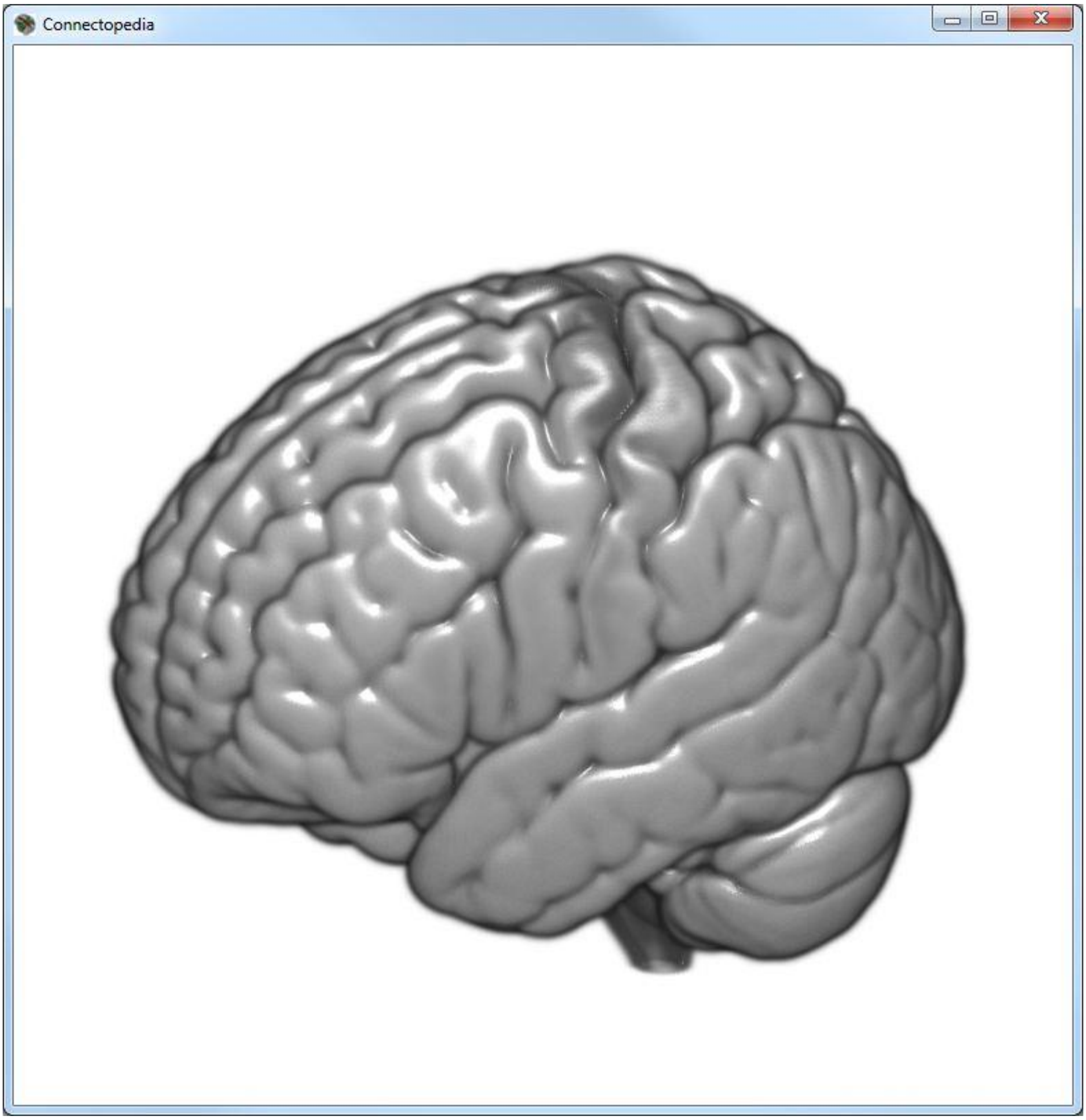
Version 2.6 has Statistics Functions for Single Subject or Group Analysis and assessment of the Effective Connectomics and Brain Functions Usage comparison through Time.

Neuro-functional and vascular knowledge database were set using Wikipedia, and some other references:

1. Bases of Functional Neuroanatomy, Monica Baciu, de Boeck Editions, 2011
2. Fiber Pathways of the Brain, Jeremy Schmahmann, Deepak Pandya, Oxford Editions, 2006
3. Networks of the Brain, Olaf Sporns, MIT Press, 2011
4. Atlas of Human Brain Connections, Marco Catani, Michel Thiebaut de Schotten, Oxford Editions, 2012
5. Diagnostic Imaging Brain, Ann Osborn, Elsevier 2005
6. Brain Vasculature, G. Lazorthes, Masson 1961.

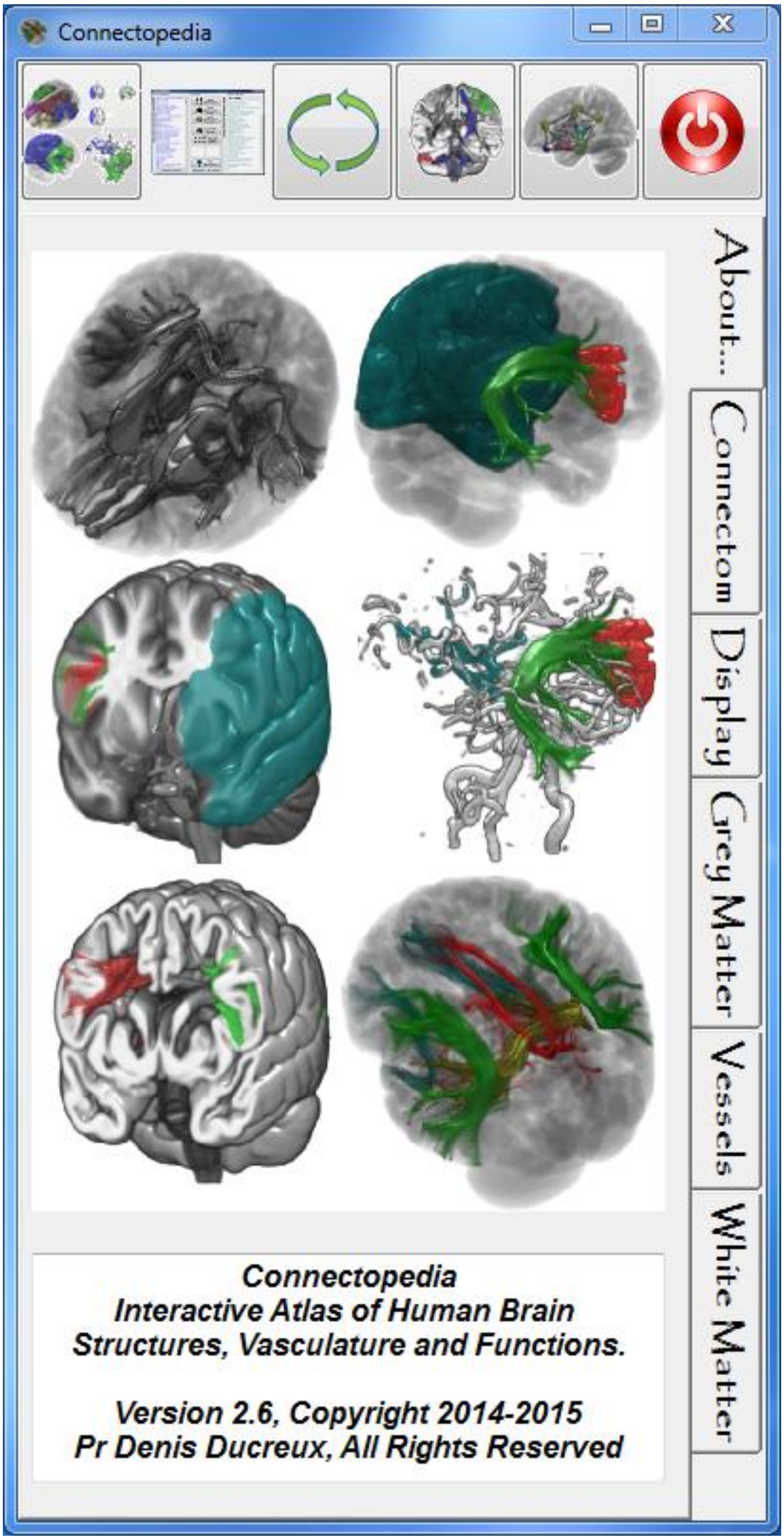
Connectopedia includes :

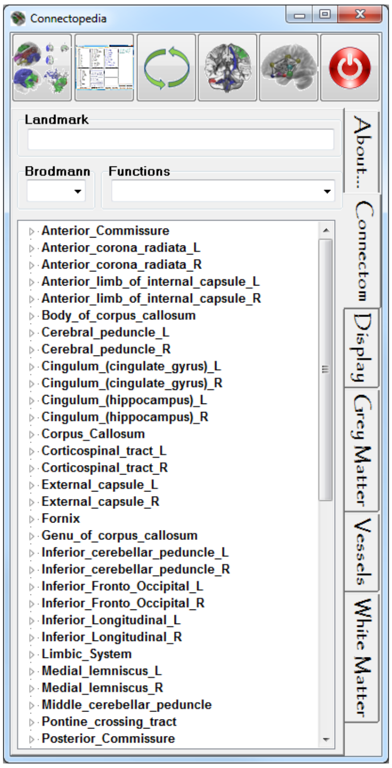
- The **3D Rendering** viewer window of brain cortex (only grey matter), brain (grey and white matter), fiber bundles and vasculature (arteries and veins):



Analyze '.img/hdr' or NIFTI '.nii' files may be imported using the 'Drag and Drop' feature of this 3D Renderer window, as well as DPTools Raw Gis map files (with or without prior co-registering).

- The **Selector** window with specific buttons and tabs:



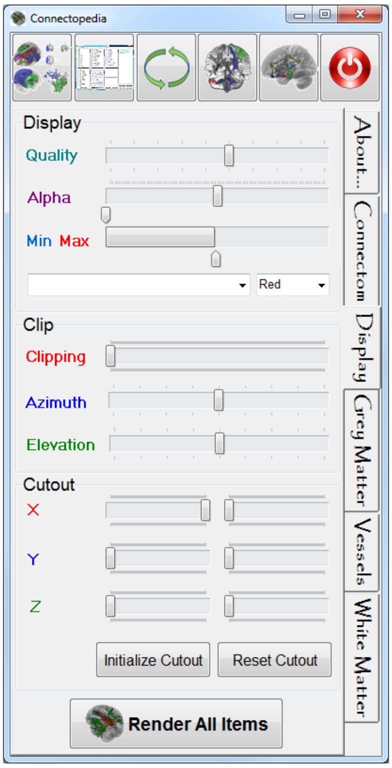


* The *Connectom Tab*:

- a brodmann area (BA) selector, with all BA linked to cortical areas and to brain functions

- a brain function (BF) selector linked to the BA selector

- a connectom path selector to select either bundle by bundle, area by area, areas by bundles, or bundles by areas, showing how cortical areas are structurally linked to each other by the fiber bundles, as well as vasculature branches treeview



*The *Display* Tab:

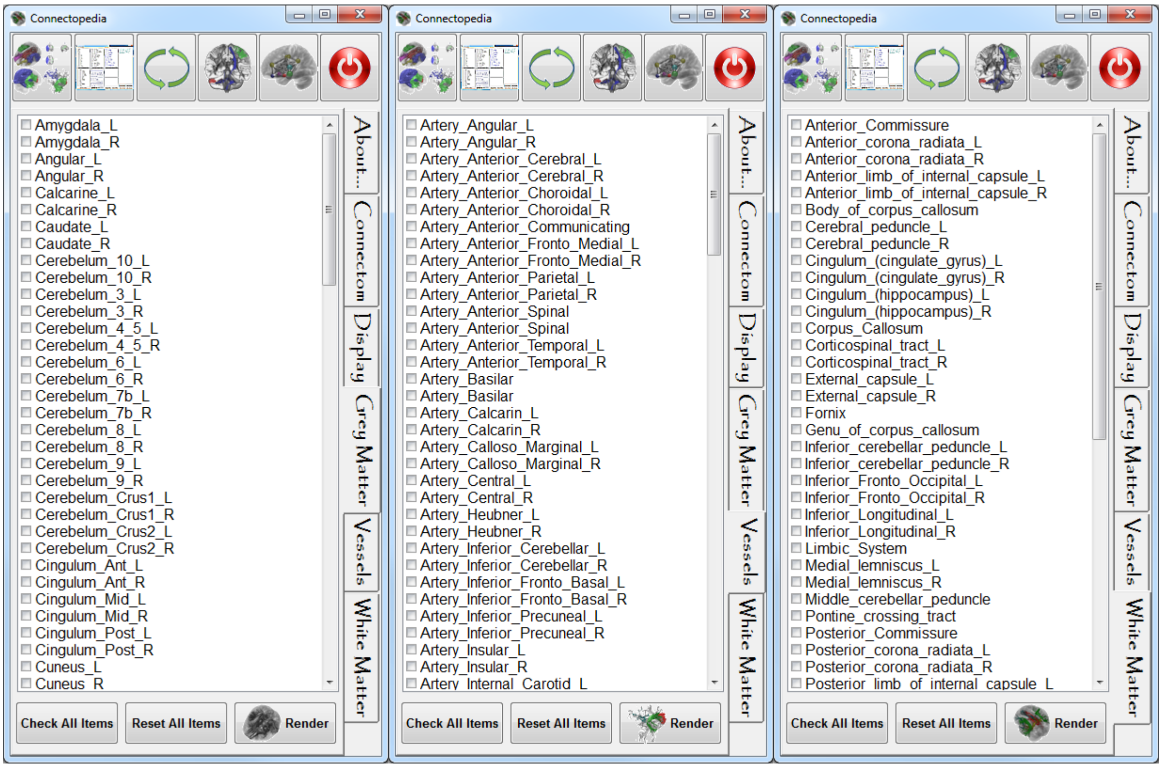
Display settings :

- Quality
- Alpha Blending
- Minimum and Maximum Thresholding
- Items color setting

Clipping and Cutout Tools

“Render All Items” button

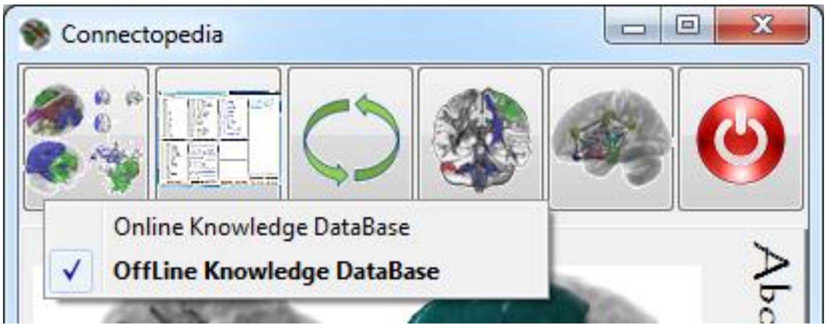
*The *Grey Matter*, *Vessels*, *White Matter* Tabs:



to study or show either cortical areas and/or fiber bundles and/or vessels one by one or by group, sorted by Name or Topology (RC to select sorting type).

Buttons to check, uncheck all items, and to render the selected items in the 3D Render Window.

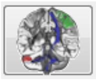
*Functions buttons:



. the “KdB Enabler” Button  to enable or disable Preview of the KdB Files, and selecting between Offline and Online KDB (RC on it to select DataBase source):

. the “Sequencer” Button  to enable or disable the Connectopedia Sequencer Window

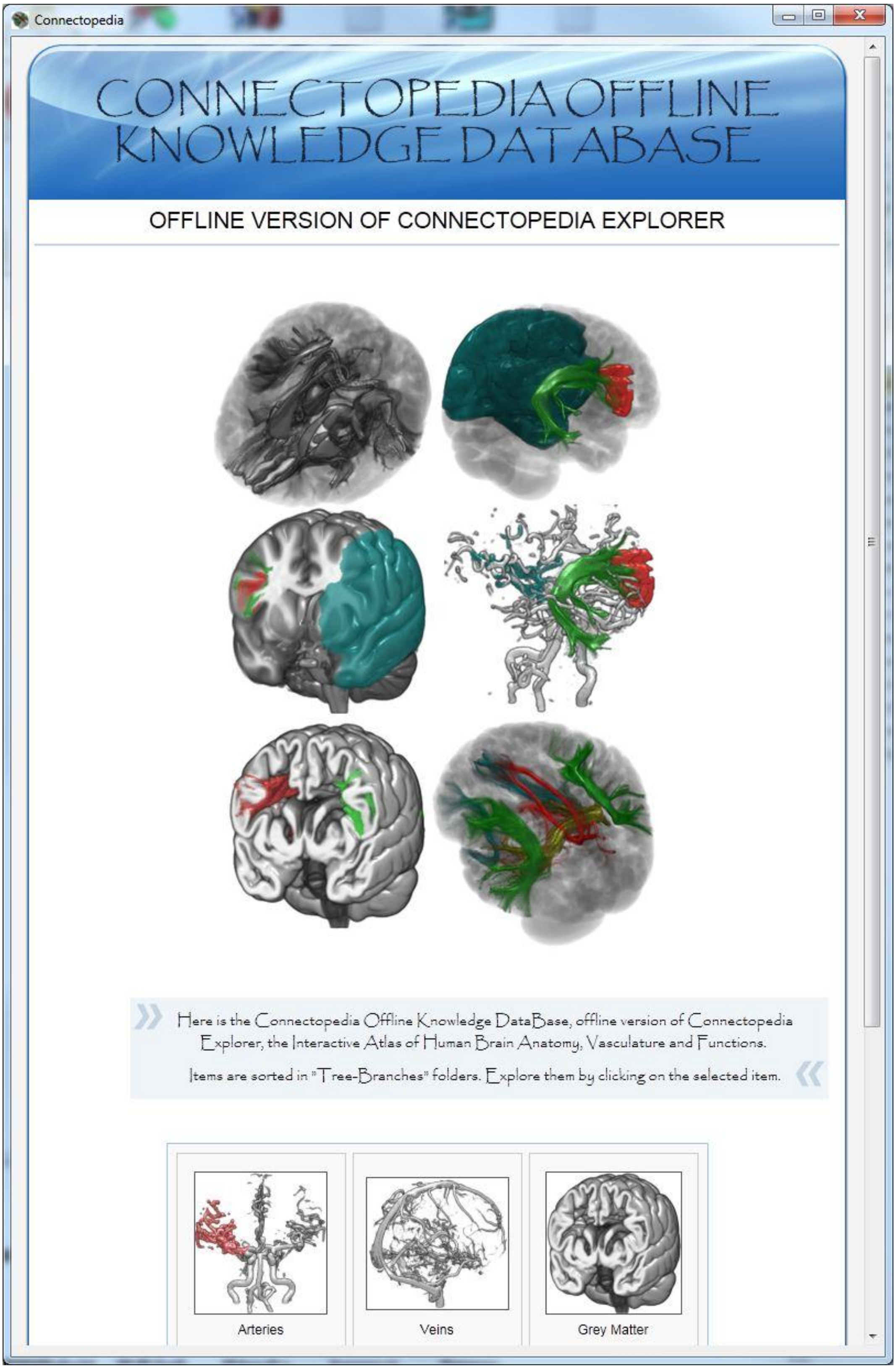
. the “Synchronize” Button  to sync Connectopedia and DPTools

. The “Tracking Pathways” Button 

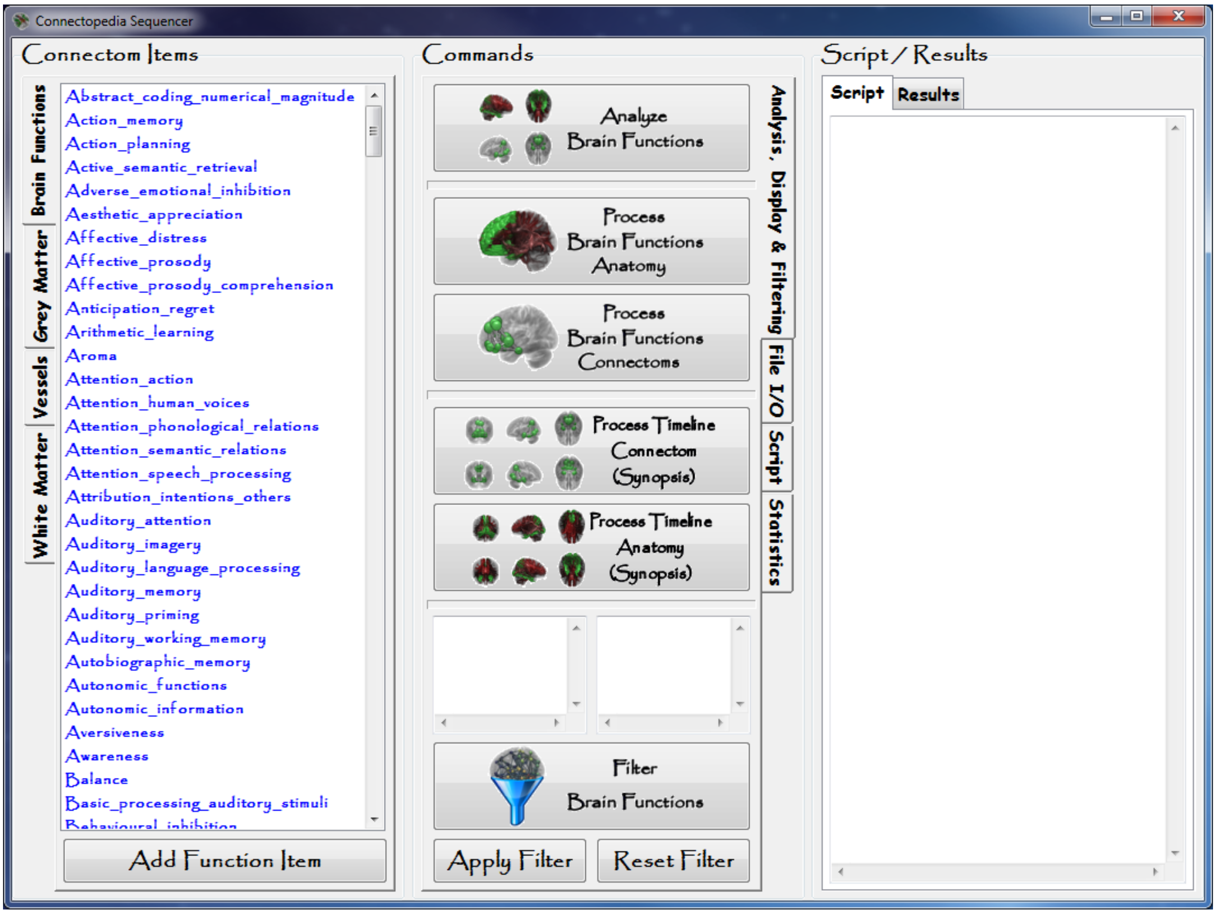
. The “Movie” Button 

. the “Exit” Button 

- The **Knowledge Database Browser** (KDB) with anatomical and functional descriptions of the grey matter areas, the white matter bundles, and the vasculature, either online if you have a high speed internet connection, or offline.



- The **Connectopedia Sequencer Window** to batch/script 2D/3D reconstructions, analyze the connectomic, analyze brain functions, …

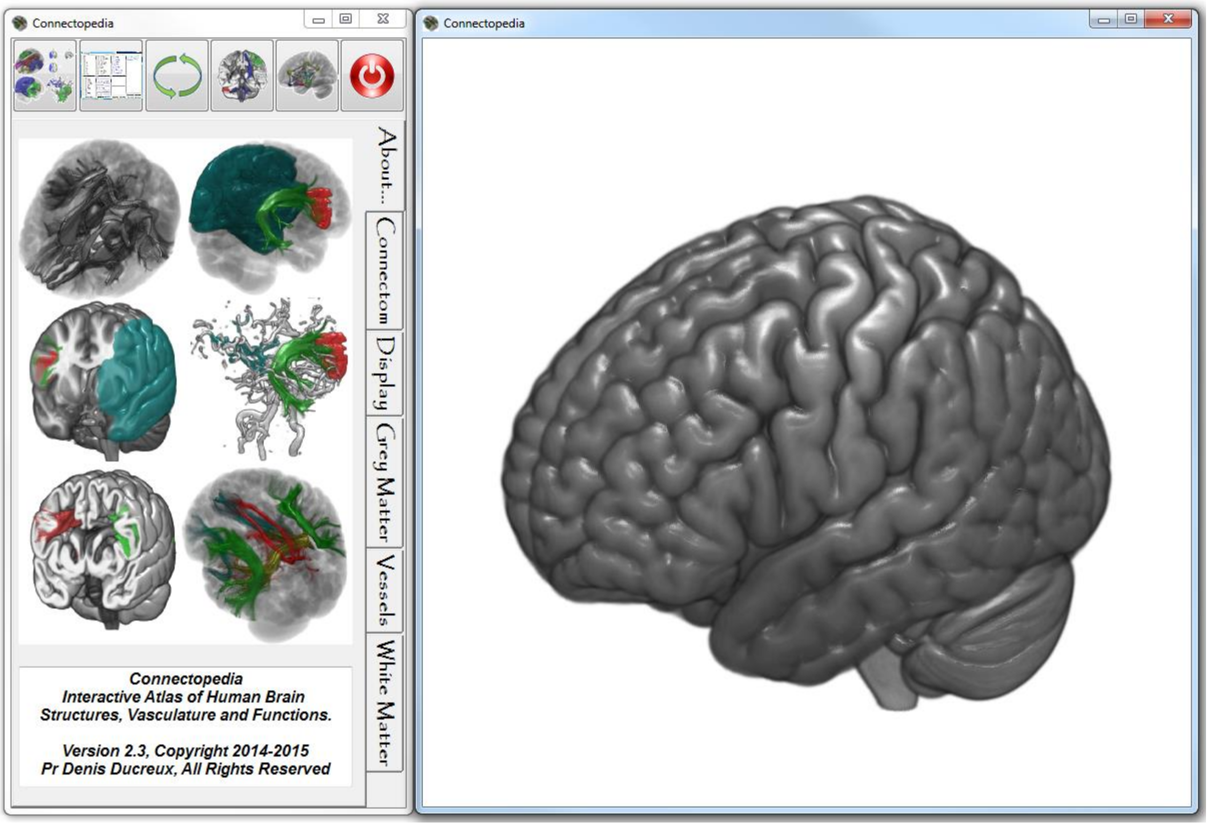


With Connectopedia user can select a fiberbundle, see the cortical areas linked by this bundle to each other, add vasculature to see the vascular territories, and view how the brain is working within this network using the Real Time fMRI Movie Selector.

User can also select two cortical areas and track the pathways linking the two.

When used combined to DPTools, user can automatically identify arterial or venous territory (stroke) and identify damaged brain structures.

All the movies of the brain included in the KdB are showing real time activations, and structural and functional connectomics involved in the selected functional task.



II. Installation

Standalone Connectopedia comes with two distributions, for Microsoft Windows Vista and above, and for Apple OSX 10.8 and above, each either online (lightweight client around 50 MB) or offline (<500 MB).

Requierements are: minimum of 4GB RAM (8 recommended), 500 Mo (for Windows and OSX Standalone distributions) or 2 GB of free hard disk space (for DPTools distribution), and an OpenGL compatible video card (embedded in chipset e.d. Intel, ATI, nVidia or separate card).

II.I Windows installation:

Download the software "Connectopedia-Install.exe" on the web site and double-click on it to install.

By default, installation directory ($INSTDIR) will be DPTools related (e.g. C:\DPTools\bin\Connectopedia). One link will be created in the "Start Program" menu as "Connectopedia". To run the program, just click on this link.

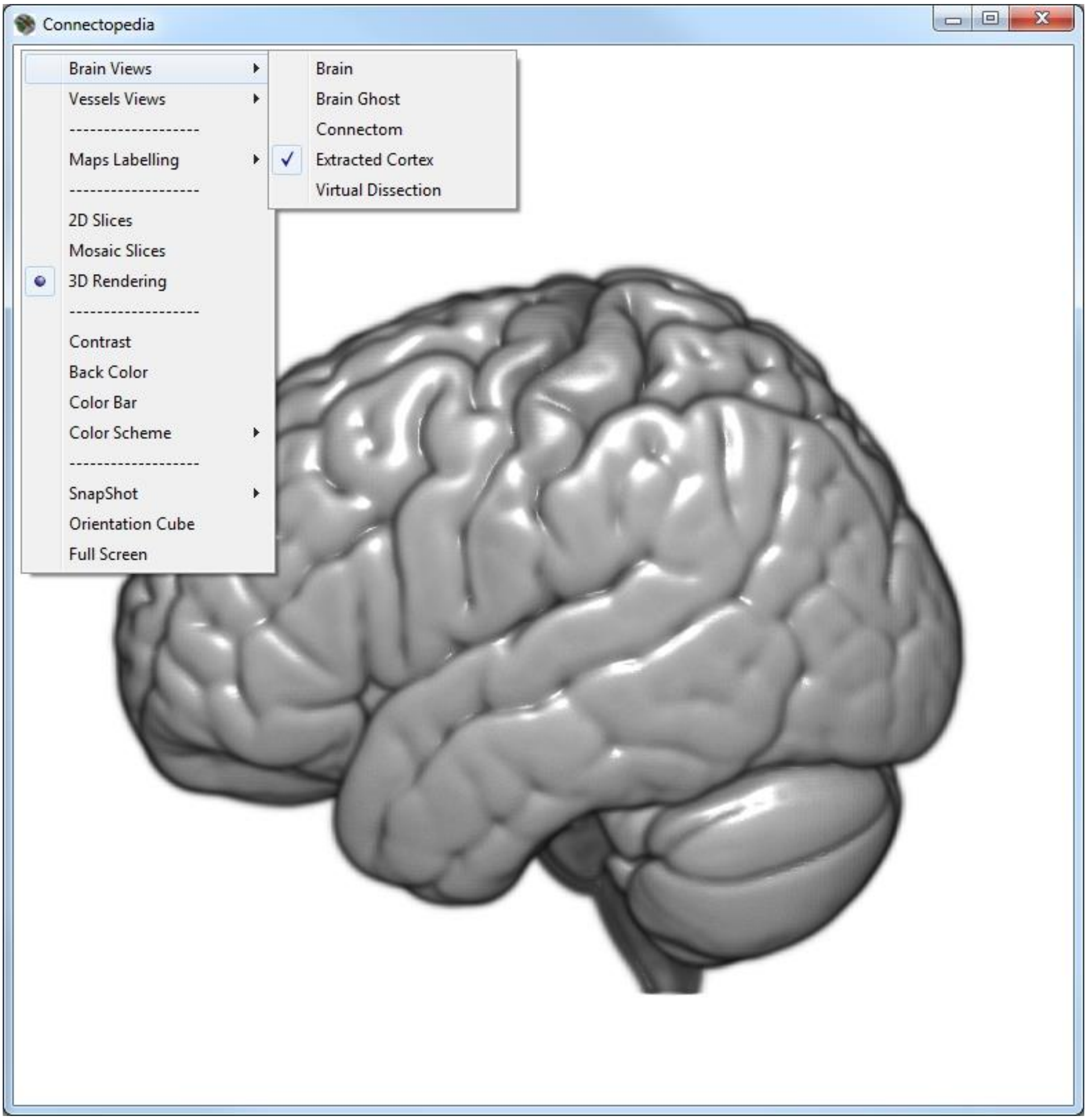
II.II OSX Installation:

Download the software "XConnectopedia.zip" on the web site. When downloaded, double-click on it where it was downloaded (e.d. "Downloads" folder) to unarchive "XConnectopedia", then run the software by double-clicking on it.

Users of OSX 10.8 and Mavericks (10.9) should change the OSX Gatekeeper properties to be able to run XConnectopedia (see the "Troubleshootings" section of this manual).

III. How to use it ?

Menus are available using the Right button of the mouse (Right Click, RC) in the **3D Rendering Area**, the **Connectoms Path Selector**, the **Clipping Tool Panel** and the **Movie Selector**.

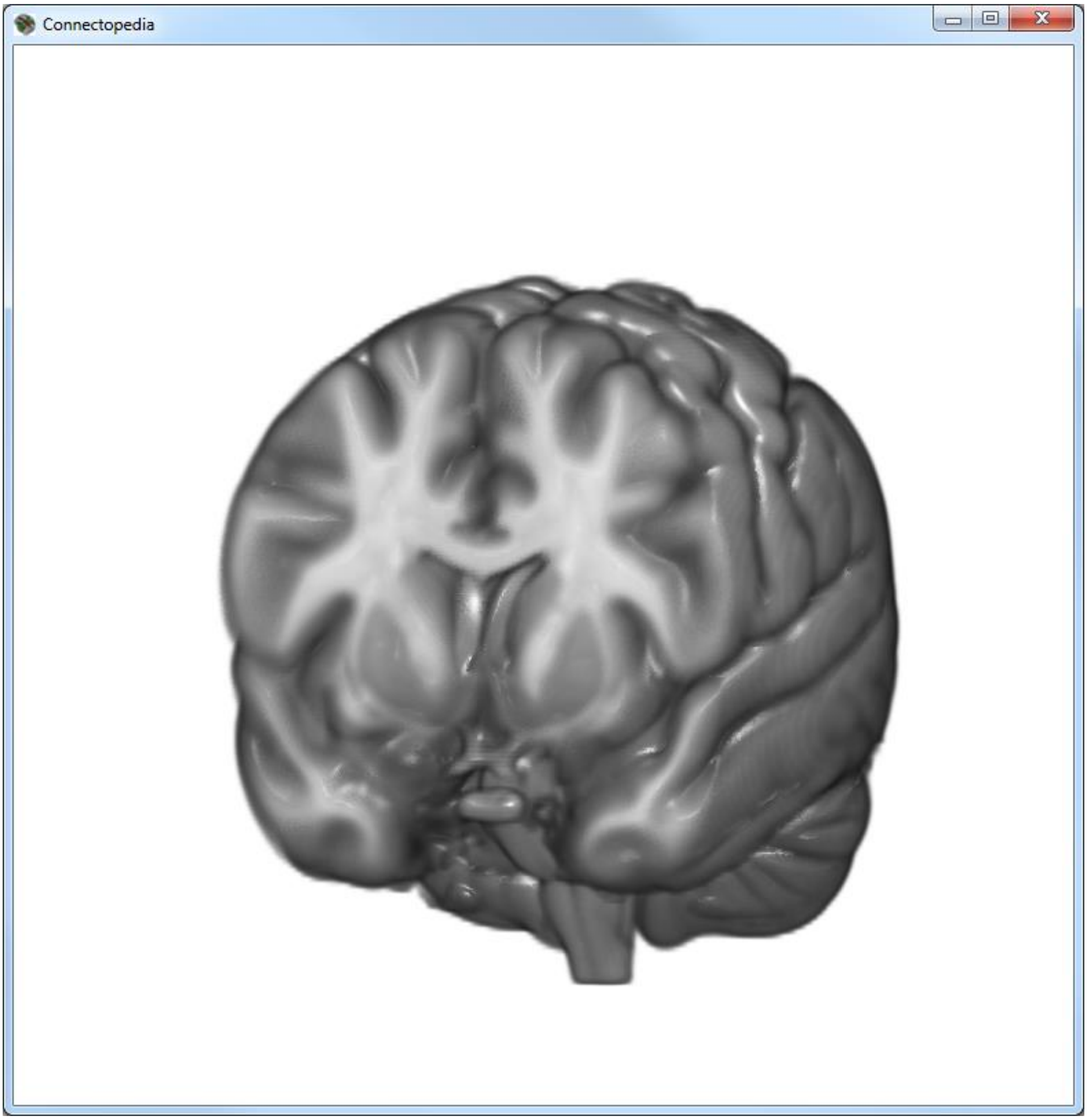


By RC on the **3D Render Window**, you can select either "Brain Views" with "Brain", "Brain Ghost", "Connectom", "Extracted Cortex" or "Virtual Dissection" sub-menus, "Vessels Views" with "Arteries" and "Veins" sub-menus reconstructions Templates, in 3D, 2D MPR Slices, or 2D mosaic slices.

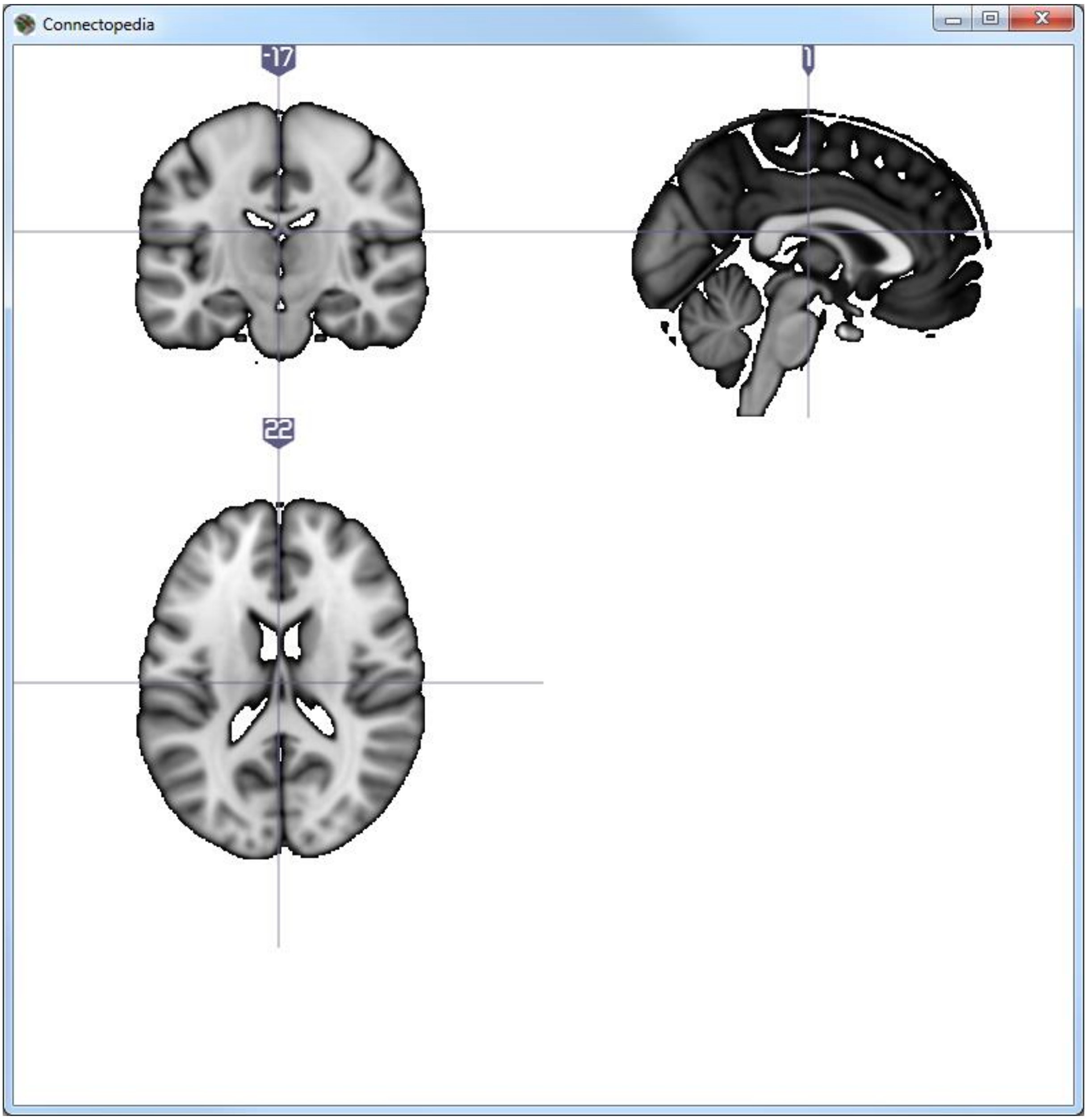
RC is also used to Zoom the 3D rendered view.

Using the Clipping bars below the Display area in Display Tab of the Selector Window, user can perform 2D or 3D clipping reconstructions of the selected Template.

Here is a **3D Cut** using the “Brain” Template:

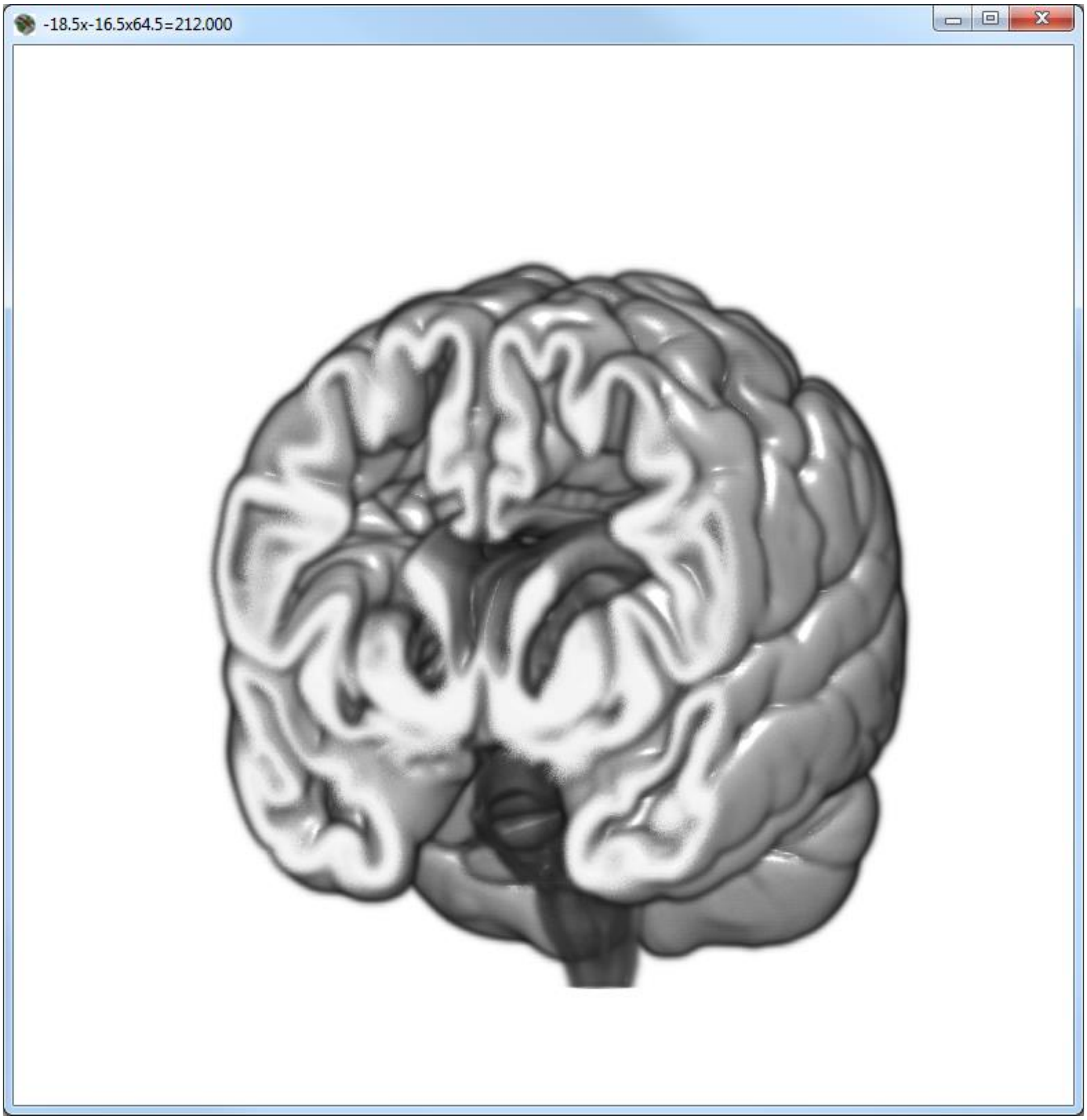


The matching **2D MPR** reconstruction:



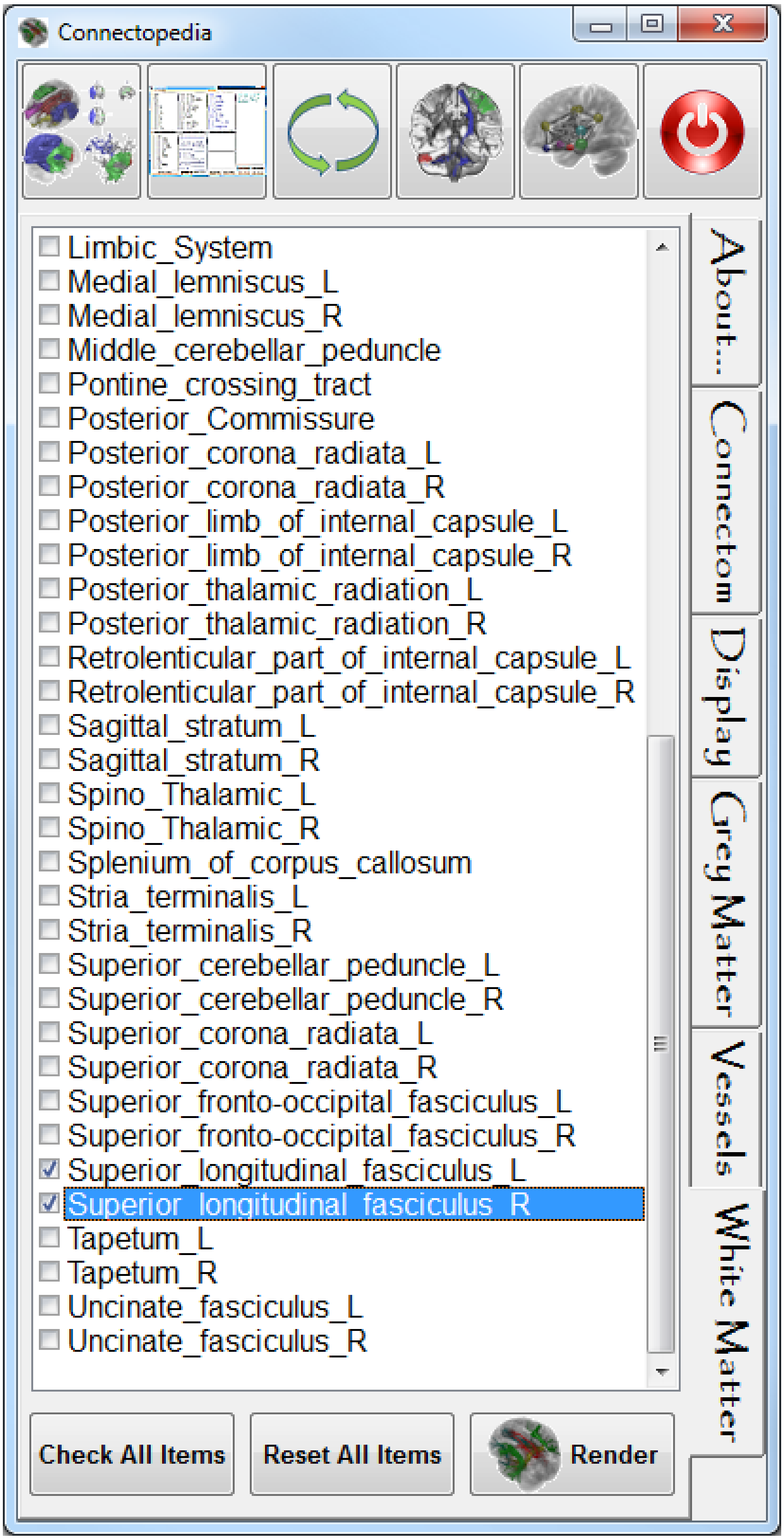
Note that given coordinates in 2D reconstructions are in true MNI coordinates.

Here is a **3D Cut** using the “Cortex” Template (in this template, only grey matter is reconstructed):



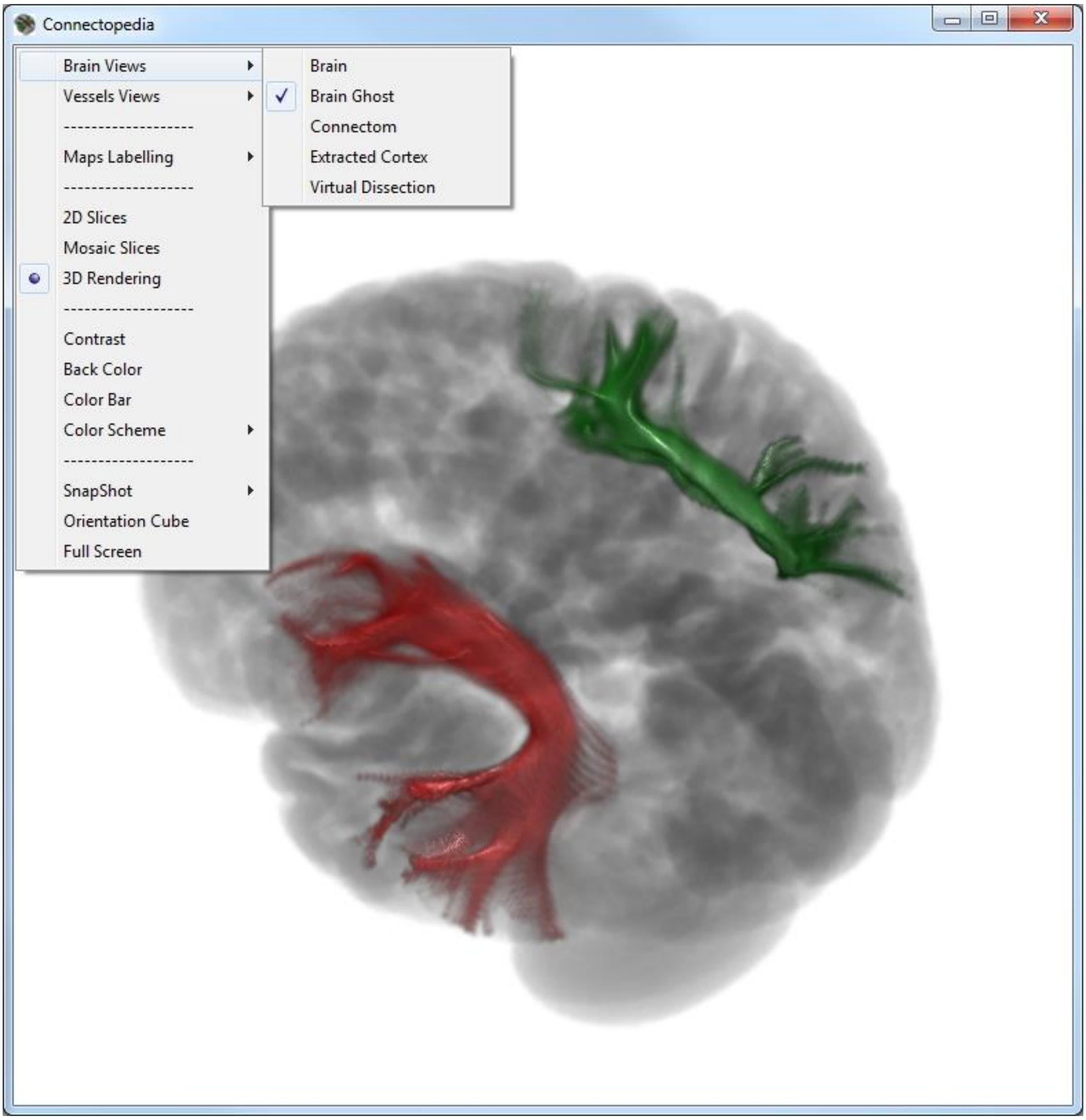
IV. First exercise: Bundles selection

Let's study the both Superior Longitudinal Fasciculi, especially the Arcuate bundles.



First select in the White Matter Tab Selector the matching bundles (« Superior_Longitudinal_Fasciculus_L and _R ») by LC on the small empty square (to deselect it, just reclick), then set the "Brain Views" Template using RC on the 3D rendering area, then press the Render Button.

Choose the "Brain Ghost" sub-menu item by RC on the 3D Render window.

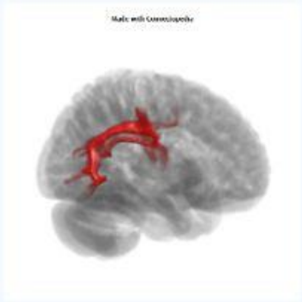


When selected, the KDB Window displays anatomo-functional informations related to the selected bundle or cortical area.

Connectopedia

CONNECTOPEDIA OFFLINE KNOWLEDGE DATABASE

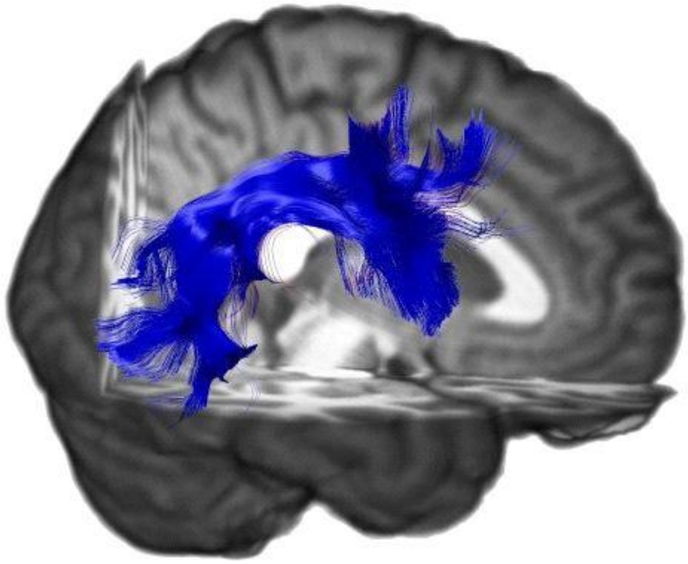
SUPERIOR LONGITUDINAL FASCICULUS



SUPERIOR LONGITUDINAL FASCICULUS AXIAL SLICES

Made with Connectopedia

SUPERIOR LONGITUDINAL FASCICULUS



The superior longitudinal fasciculus (also called the superior longitudinal fascicle or SLF) is a pair of long bi-directional bundles of neurons connecting the front and the back of the cerebrum. Each association fiber bundle is lateral to the centrum ovale of a cerebral hemisphere and connects the frontal, occipital, parietal, and temporal lobes. The neurons pass from the frontal lobe through the operculum to the posterior end of the lateral sulcus where numerous neurons radiate into the occipital lobe and other neurons turn downward and forward around the putamen and radiate to anterior portions of the temporal lobe.

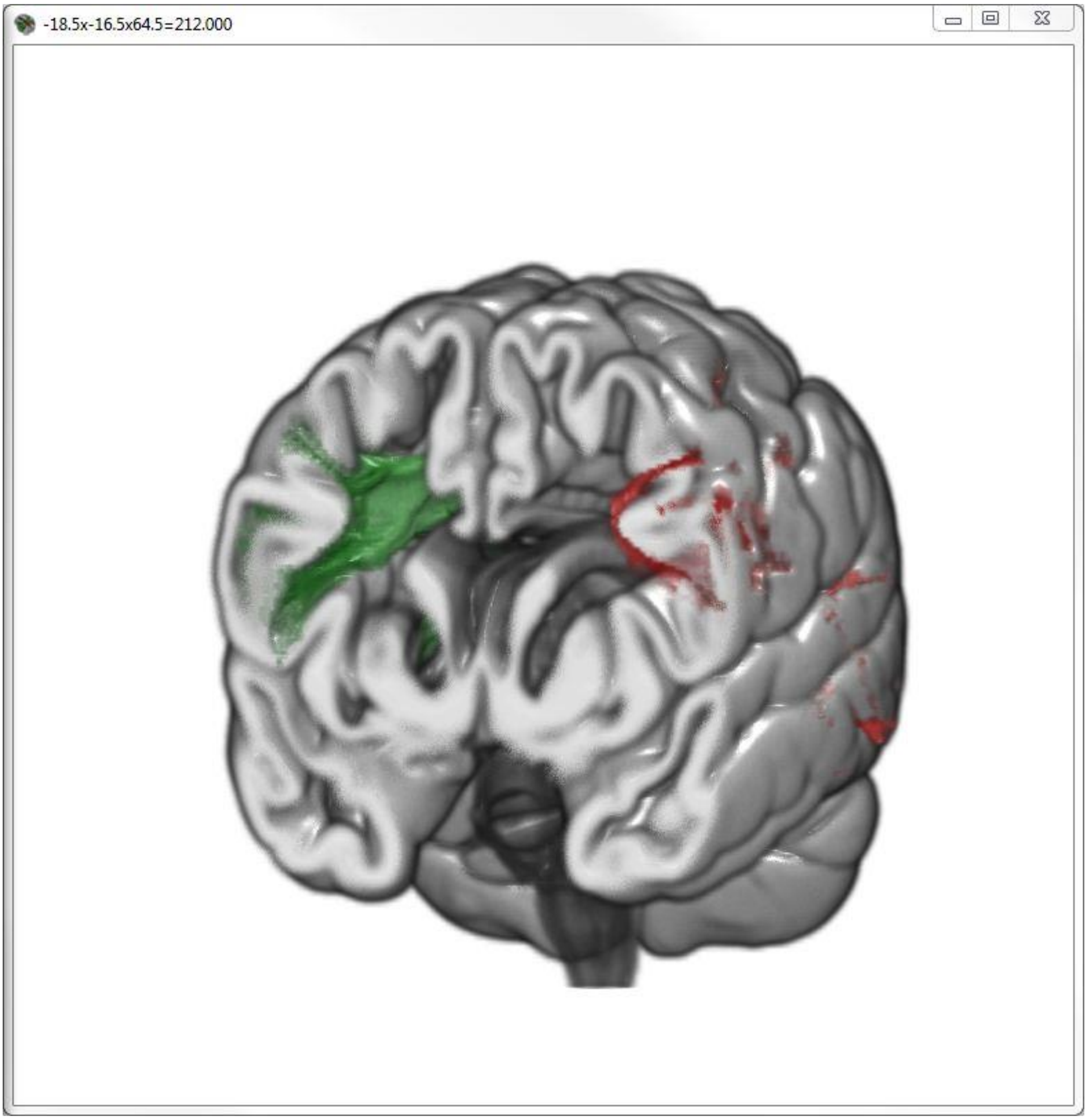
Anatomy

The SLF is composed of four distinct components SLF I, SLF II, SLF III, and arcuate fascicle (AF). In humans, these four components are bundled together although they are functionally separate. In non-human primates, the SLF and AF are anatomically separate and have separate trajectories.

SLF I

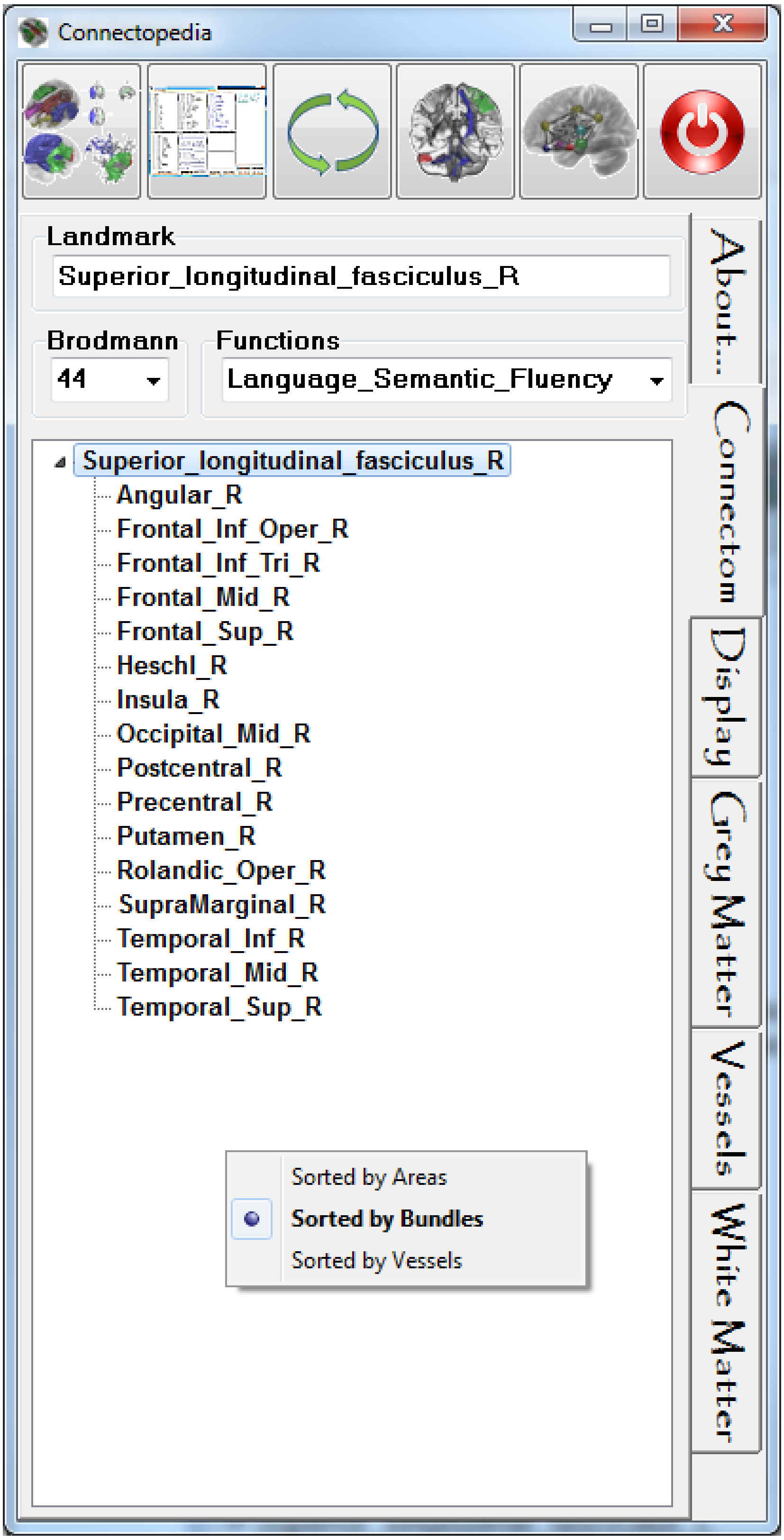
SLF I is the dorsal component and originates in the superior and medial parietal cortex, passes around the cingulate sulcus and in the superior parietal and frontal white matter, and terminates in the dorsal and medial cortex of the frontal lobe (Brodmann 6, 8, and 9) and in the supplementary motor cortex (M II).

The selected bundles can be viewed with the “Extracted Cortex” Template in 3D VR mode using a **3D Cut** clipping:



By LC in the Connectom Tab Selector on a cortical area (e.g. « Frontal_Oper_Inf_L »), Brodmann areas referring to the selected cortical area are displayed in the BA selector.

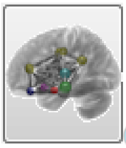
You can select between all the displayed BA by Left Clicking on the **BA Selector**:



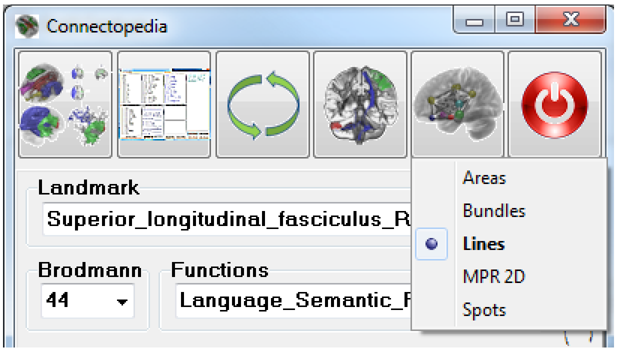
Informations in the **Connectom Tab** are restricted to the selected bundle.

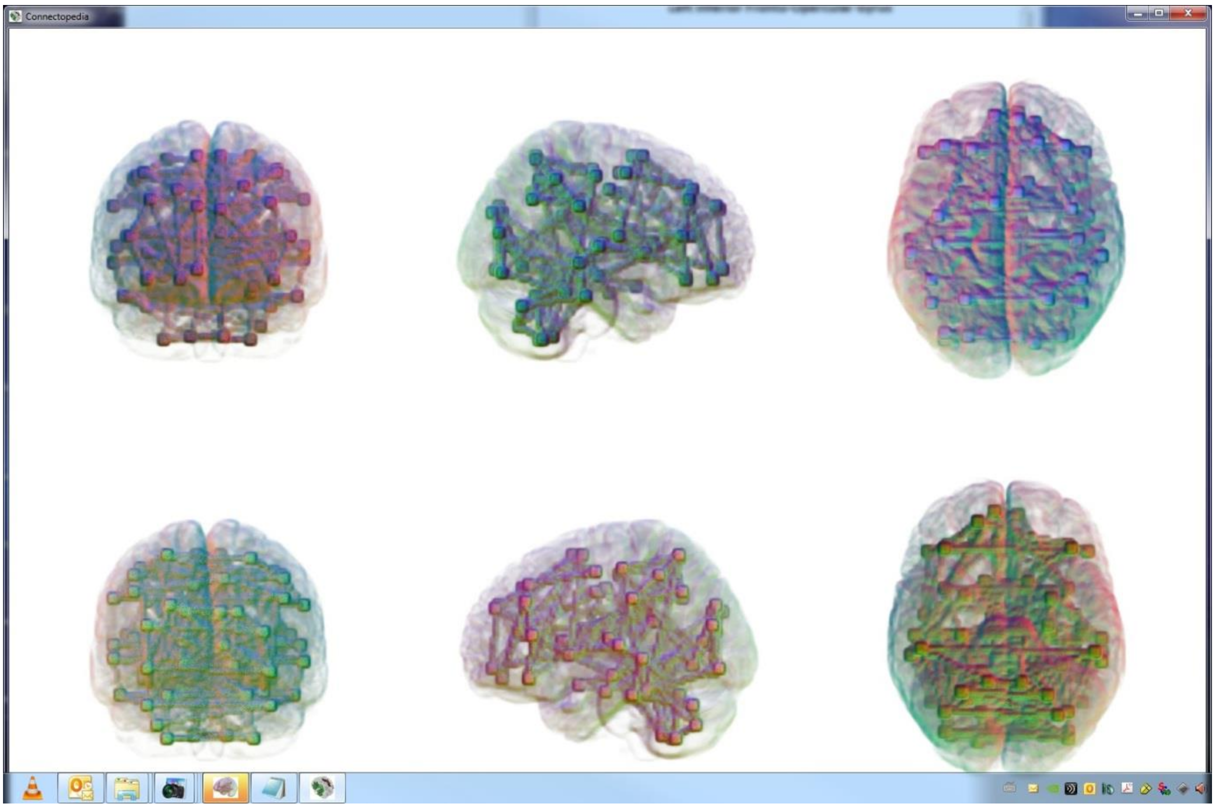
By LC on the triangle ◢, a Connectoms Treeview displays all the cortical areas linked to each other by the selected bundle. You can sort these either by Areas, Bundles or Vessels by RC on the Connectom Path Selector and selecting the menu item.

On the right side of the **BA Selecto**r is the **BF Selector**. When selecting a specific BA, functions are listed in the **BF Selector**, and can be selected by LC on it (here BA « 44 », and Function: « Language_Semantic_Fluency »).

When the function is selected, movies showing the real time activation of the brain can be displayed by LC on the **Movie Viewer Button** 

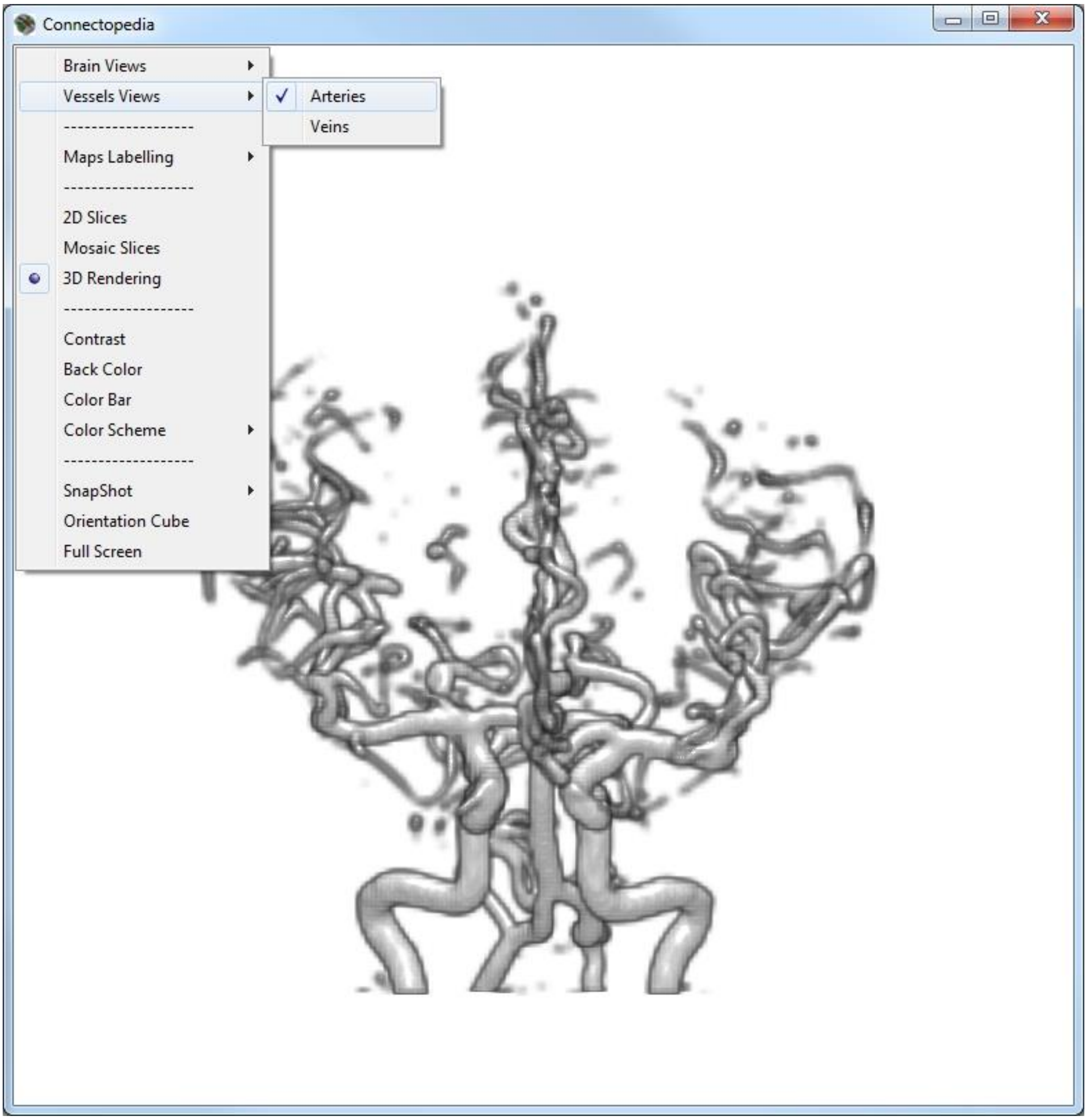
User can choose between “Areas”, “Lines”, “Bundles”, “Spots”, and “MPR 2D” movies, showing the brain connectivity in real time:



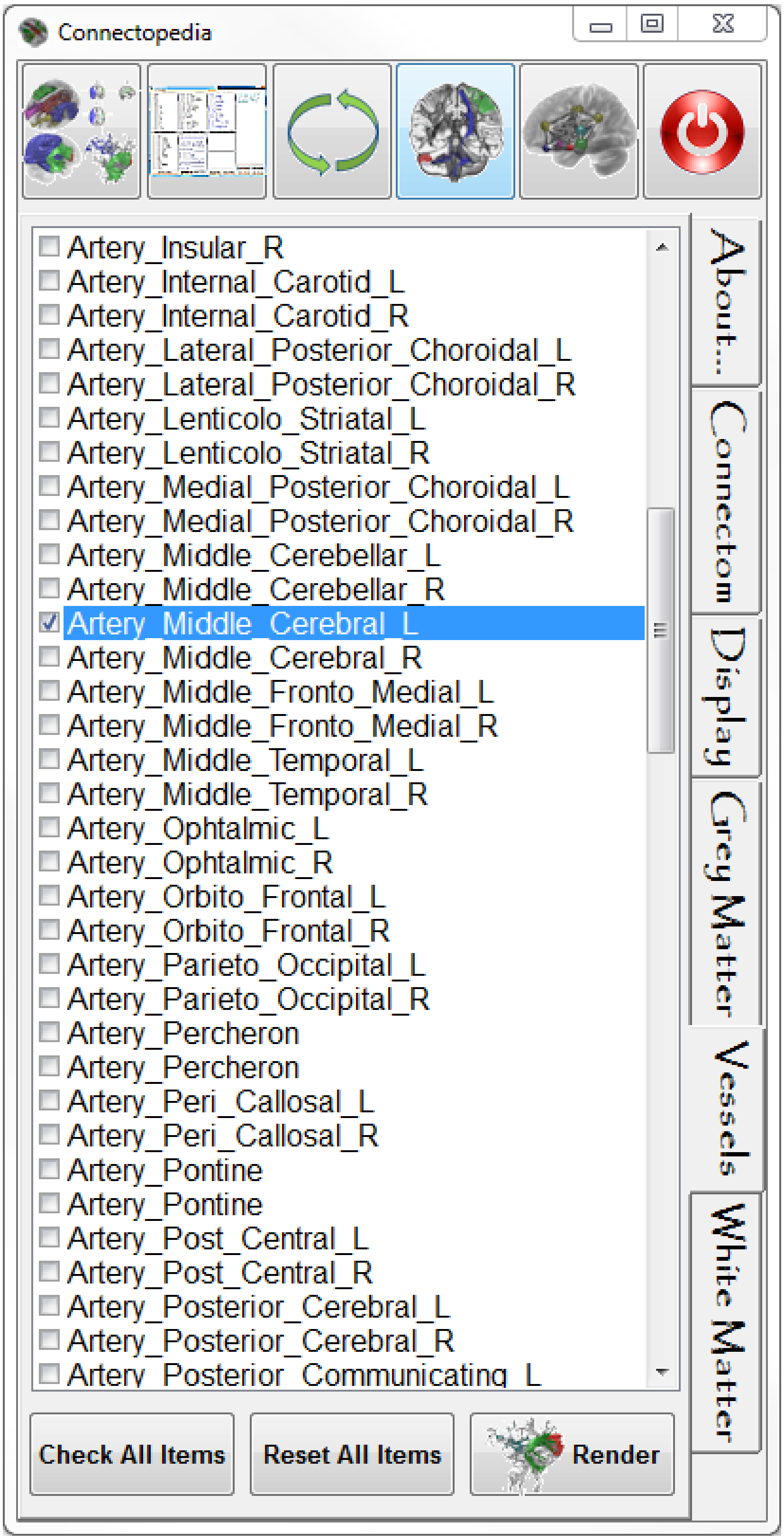


V. Second exercise: Bundles and Arteries

Connectopedia includes a vascular knowledge database of arterial and venous structures. User can reconstruct brain arteries using the "Arteries" Template in the "Vessels Views" menu of the 3D rendering window:

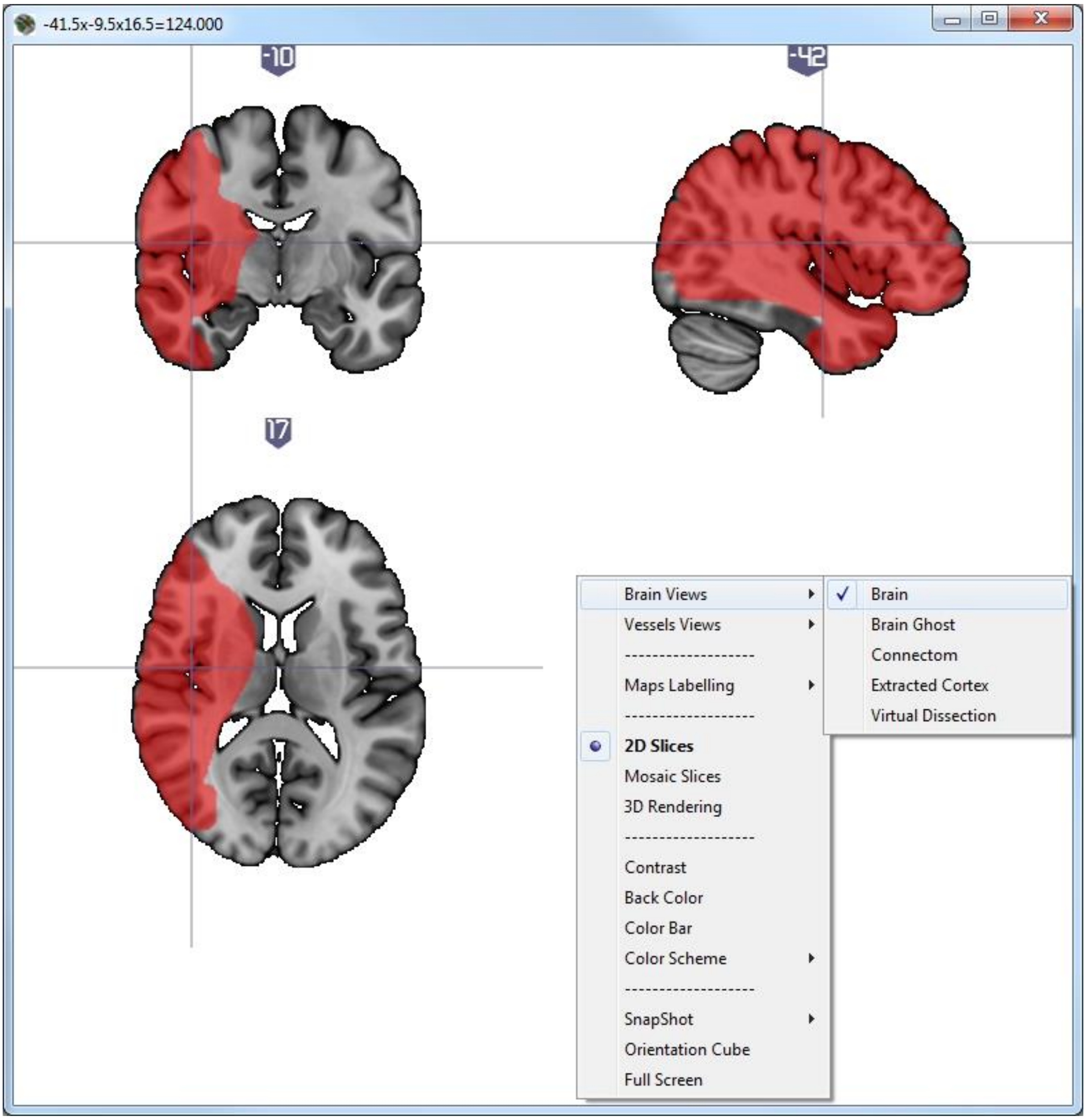


Let's now study the Left Middle Cerebral Artery combined with the Right Superior Longitudinal Fasciculus.

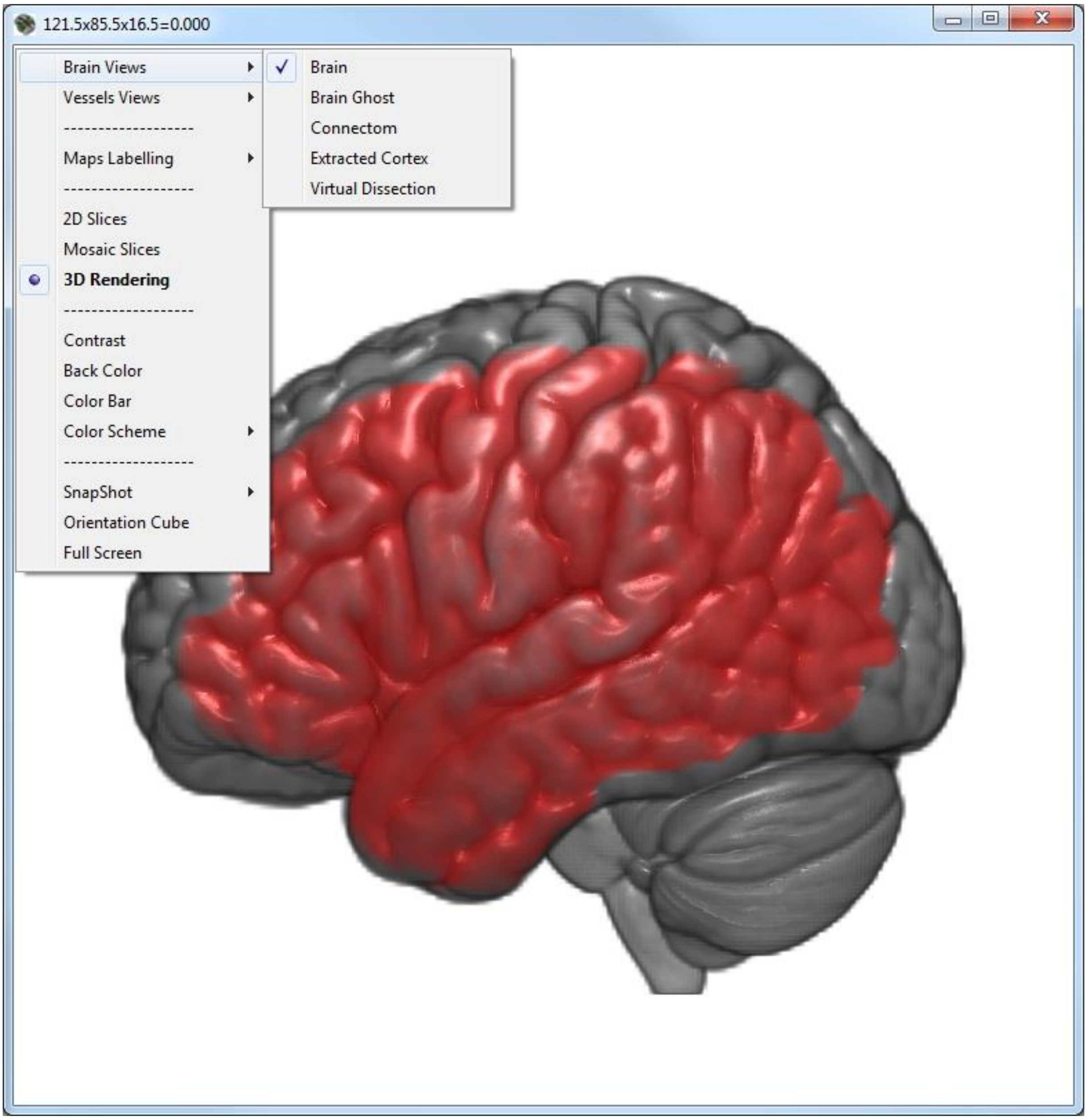


First select in the **Vessels Tab Selector** the matching artery (« Artery_Middle_Cerebral_L ») by LC on the small empty square (to deselect it, just LC again), then set the "Arteries" Template using RC on the 3D rendering area, then press the Render Button.

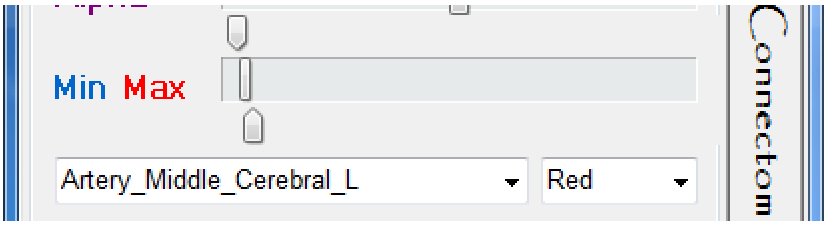
Let’s now have a look at the 2D Slices of the Left MCA arterial territory. RC on the 3D Rendering area, select « 2D Slices » and also select the « Brain » Template in the “Brain Views” menu:

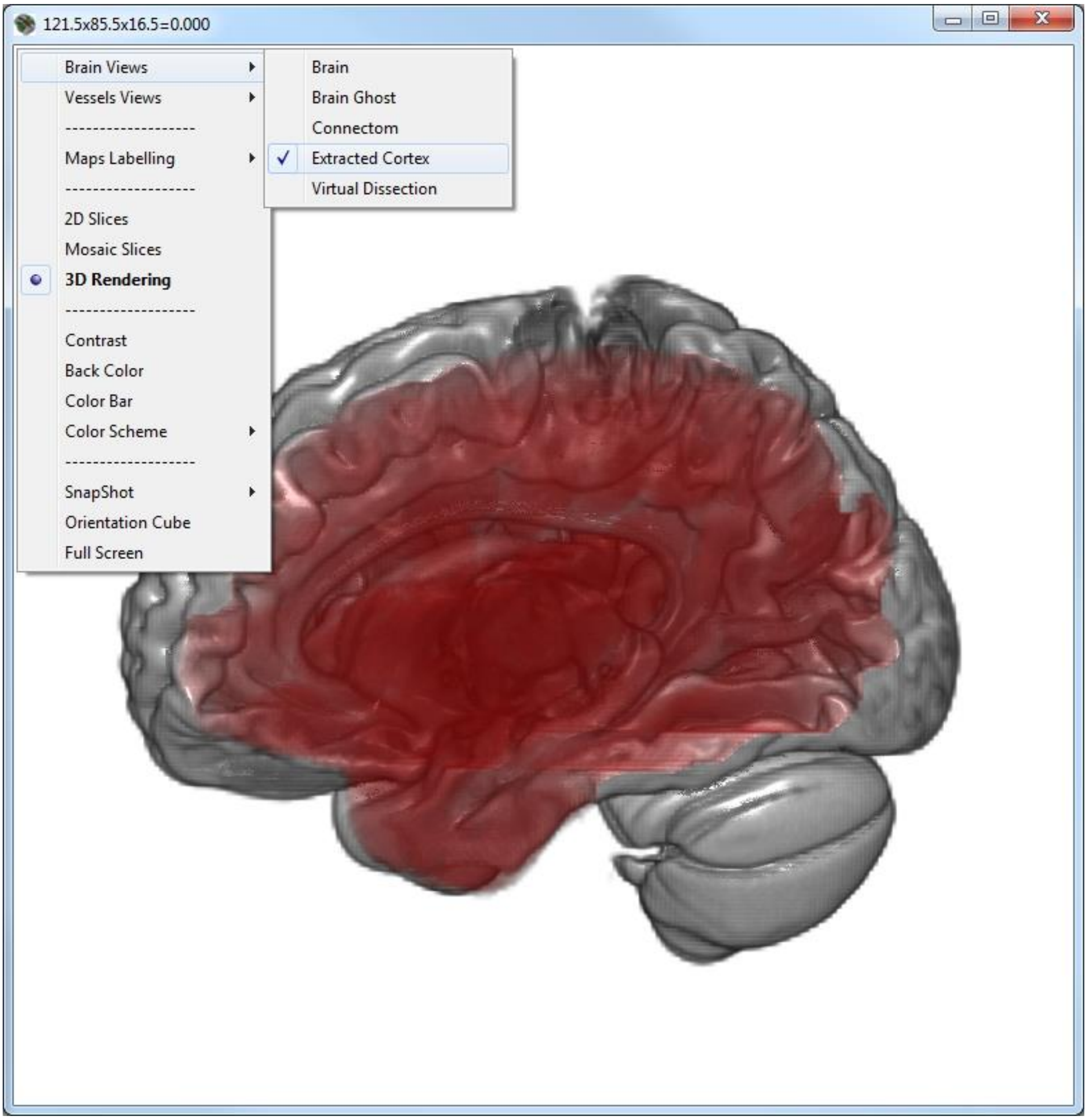

-41.5x-9.5x16.5=124.000
-10
-42
17
Brain Views
Vessels Views
Maps Labelling
2D Slices
Mosaic Slices
3D Rendering
Contrast
Back Color
Color Bar
Color Scheme
SnapShot
Orientation Cube
Full Screen
Brain
Brain Ghost
Connectom
Extracted Cortex
Virtual Dissection

Now have a look at the 3D VR reconstruction of this arterial territory:

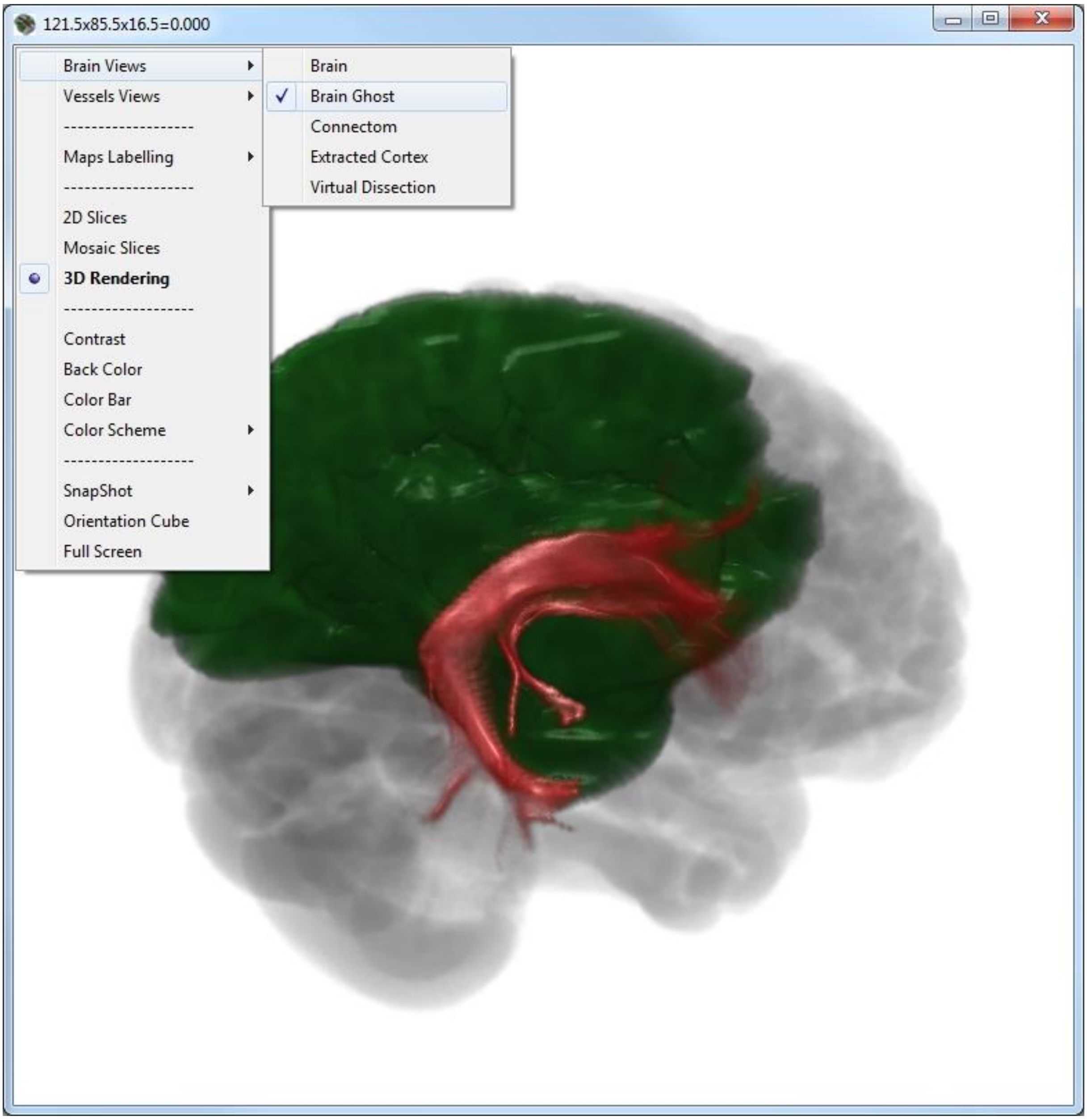


In the "Extracted Cortex" sub-menu item of the "Brain Views" Template, with "Display Settings" set to High Min and Low Max, some transparent view of the arterial territory:



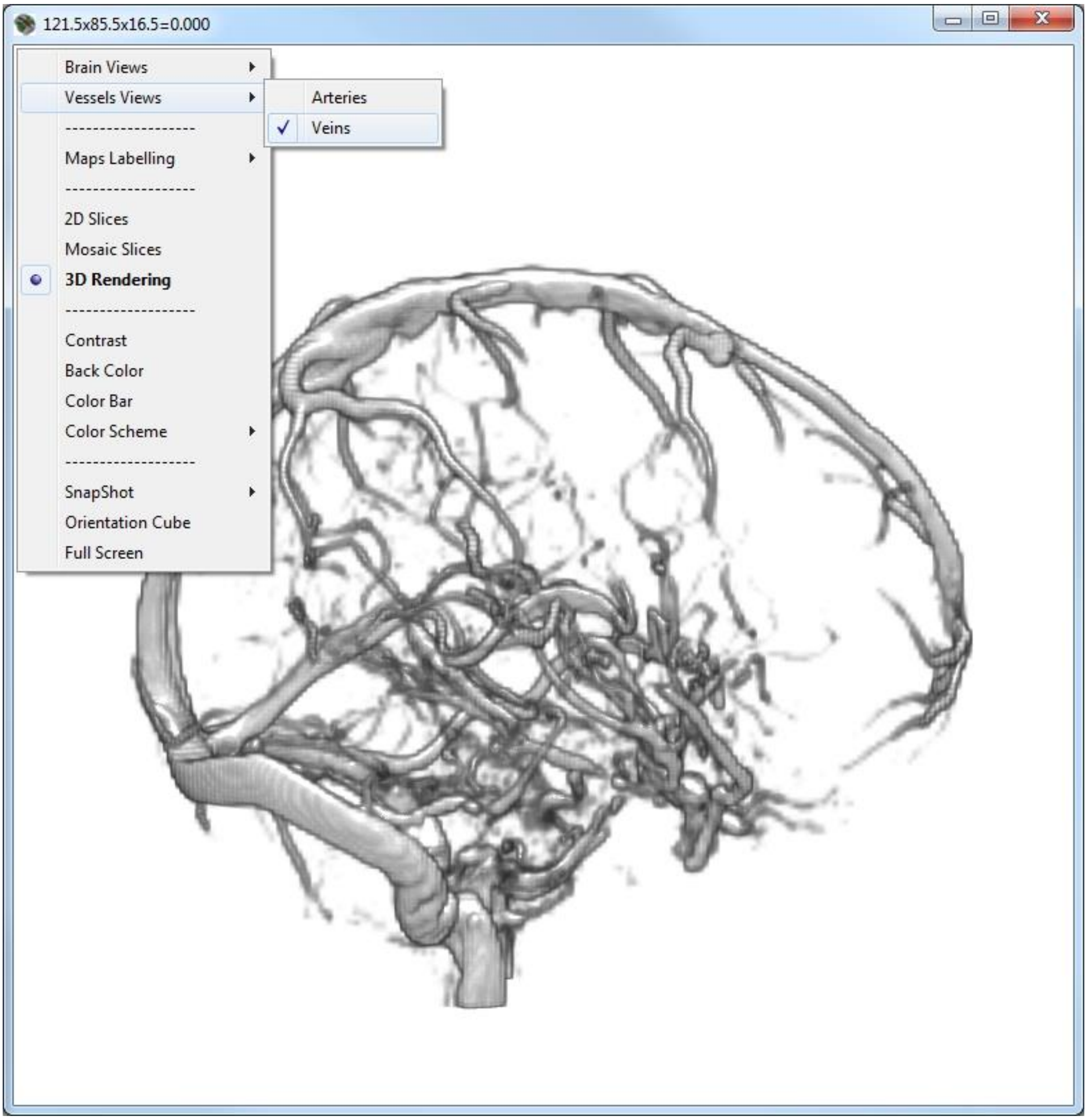


At last, combine this artery with the Right Superior Longitudinal Fasciculus by LC on the matching empty square in the **White Matter Tab Selecto**r and display these selected items using the "Brain Ghost" sub-menu of the "Brain Views" 3D VR Template (by RC on the 3D rendering area):

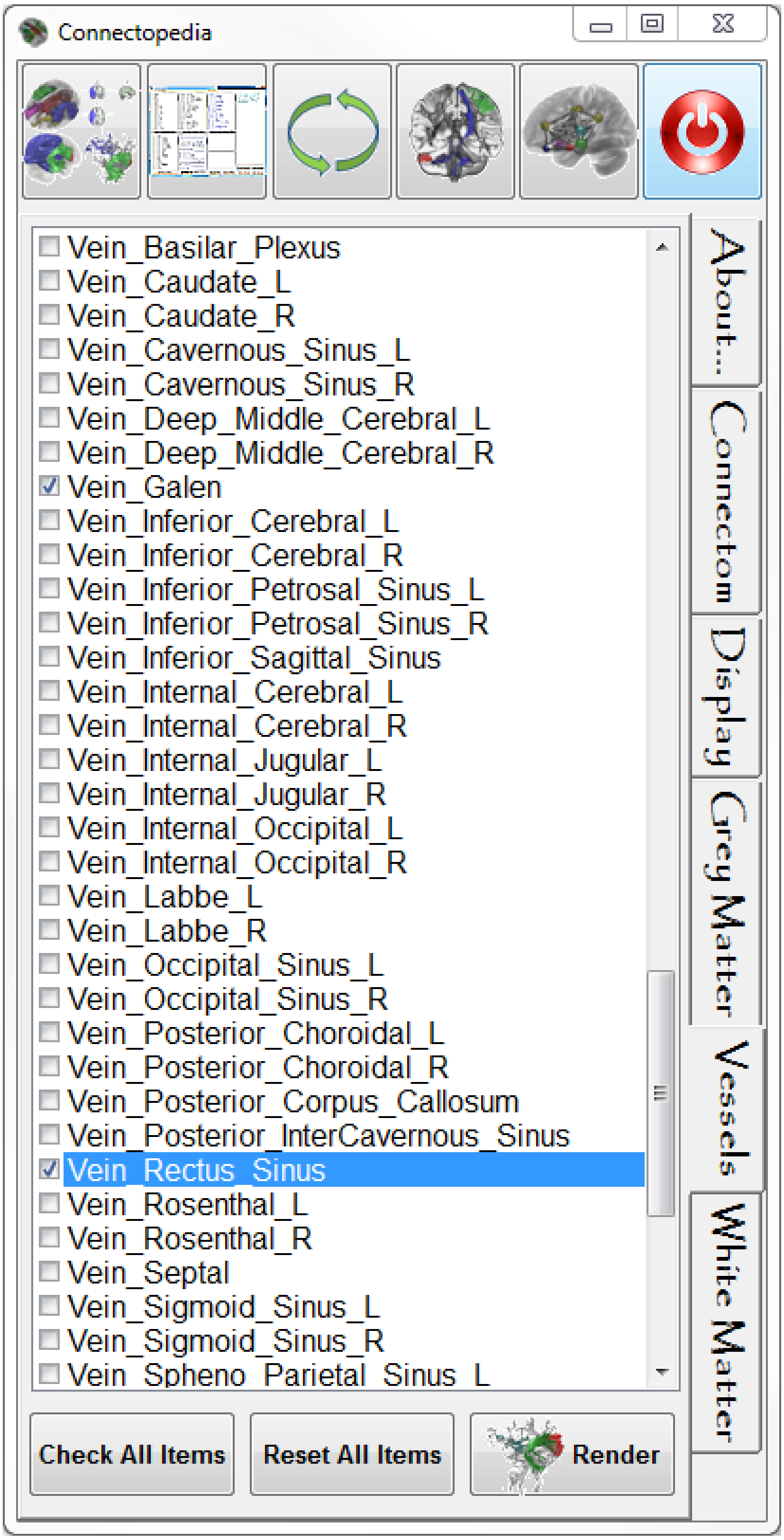


VI. Third exercise: Grey Matter Structures and Veins

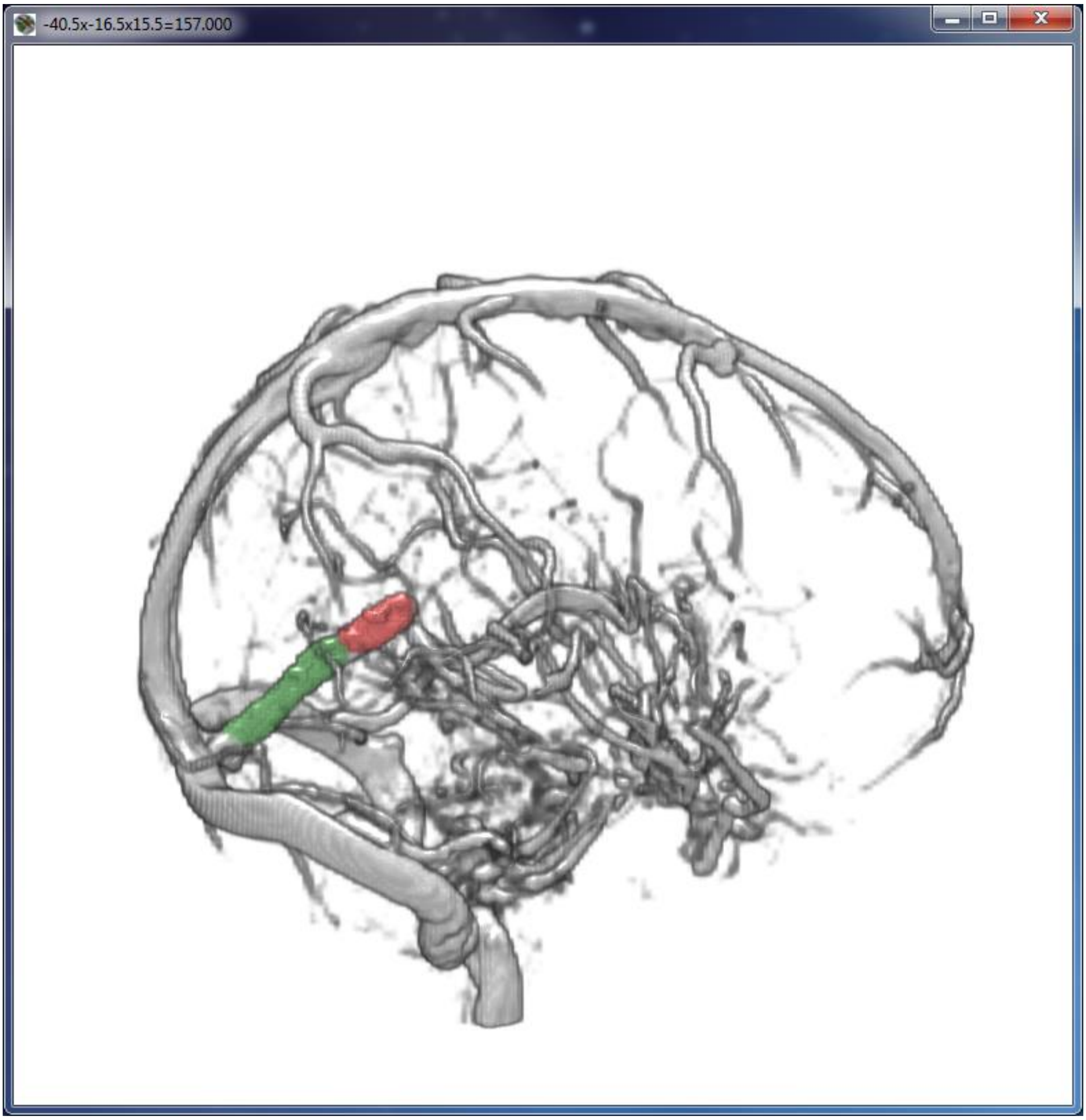
User can also reconstruct brain veins and venous sinuses using the “Veins” Template of the 3D rendering window:



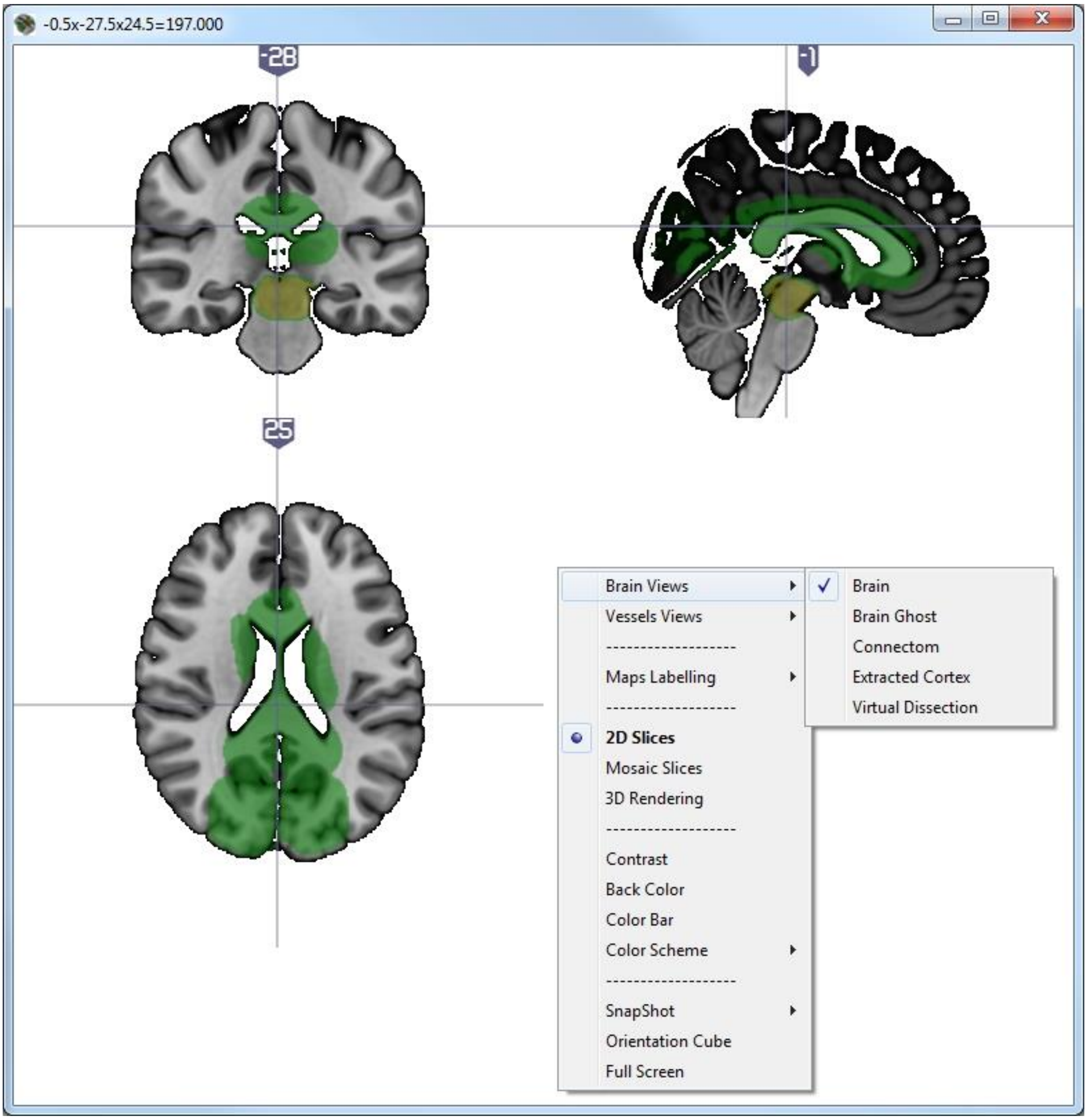
Let’s now study the both Thalami combined with the Galen Vein and the Straight Sinus (e.g. in case of deep venous thrombosis).



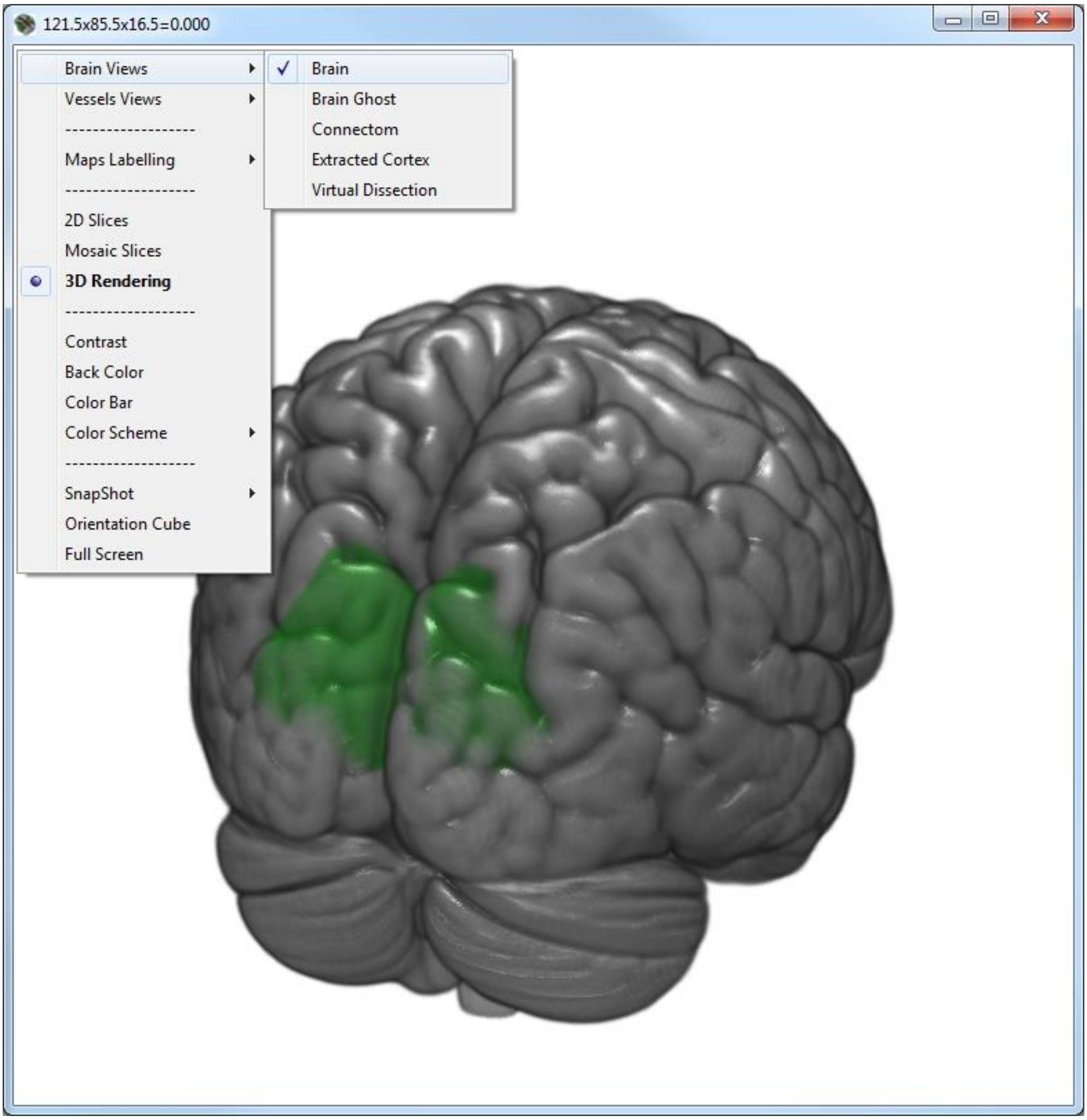
First select in the **Vessels Tab Selector** the matching venous structures (« Vein_Galen » and « Vein_Rectus_Sinus ») by LC on the small empty square (to deselect it, just LC again), then set the “Veins” Template in the “Vessels Views” menu using RC on the 3D rendering area, then press the Render Button.


-40.5x-16.5x15.5=157.000

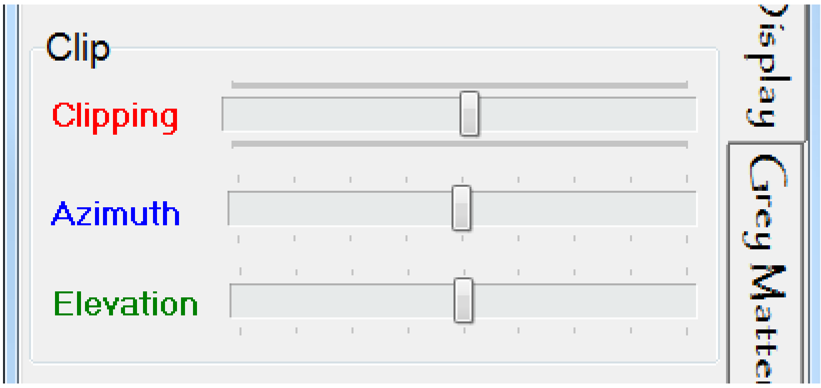
Now let's see how are these venous territories in 2D (RC on the 3D Rendering area, and select the « Brain » Template in the "Brain Views" menu , then the « 2D Slices »):

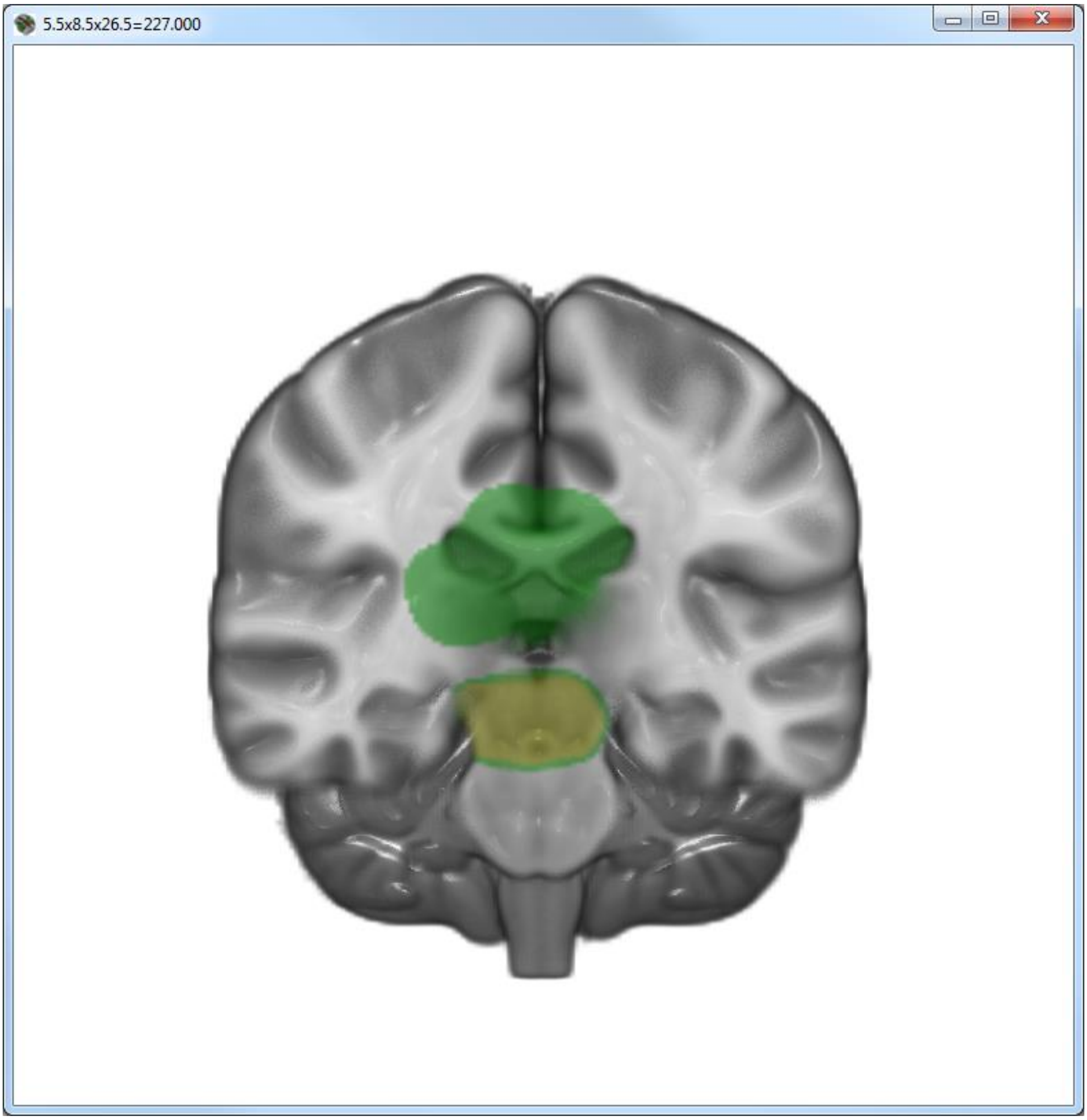


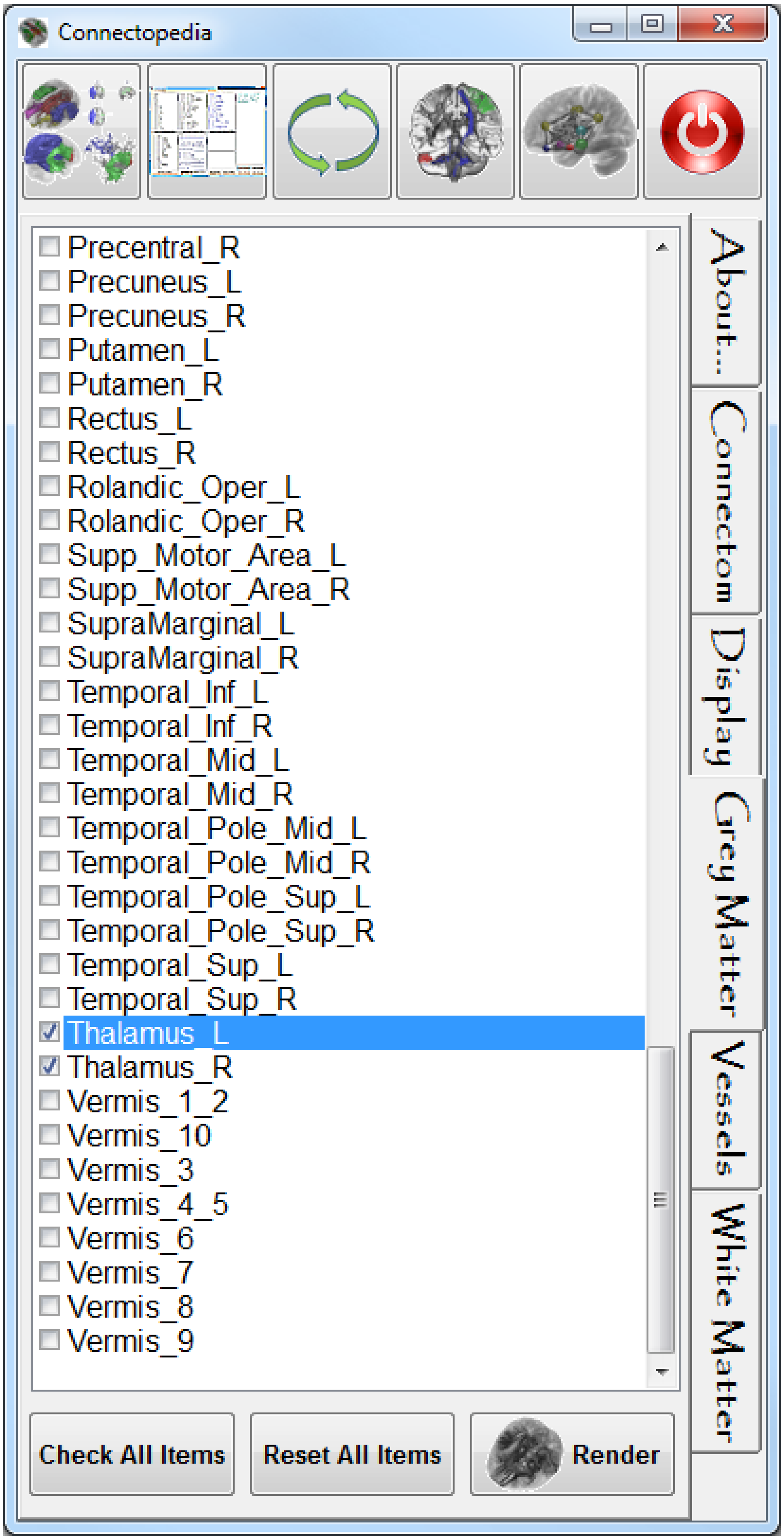
Let's see them in 3D (RC on the 3D Rendering area and select « 3D Rendering »):



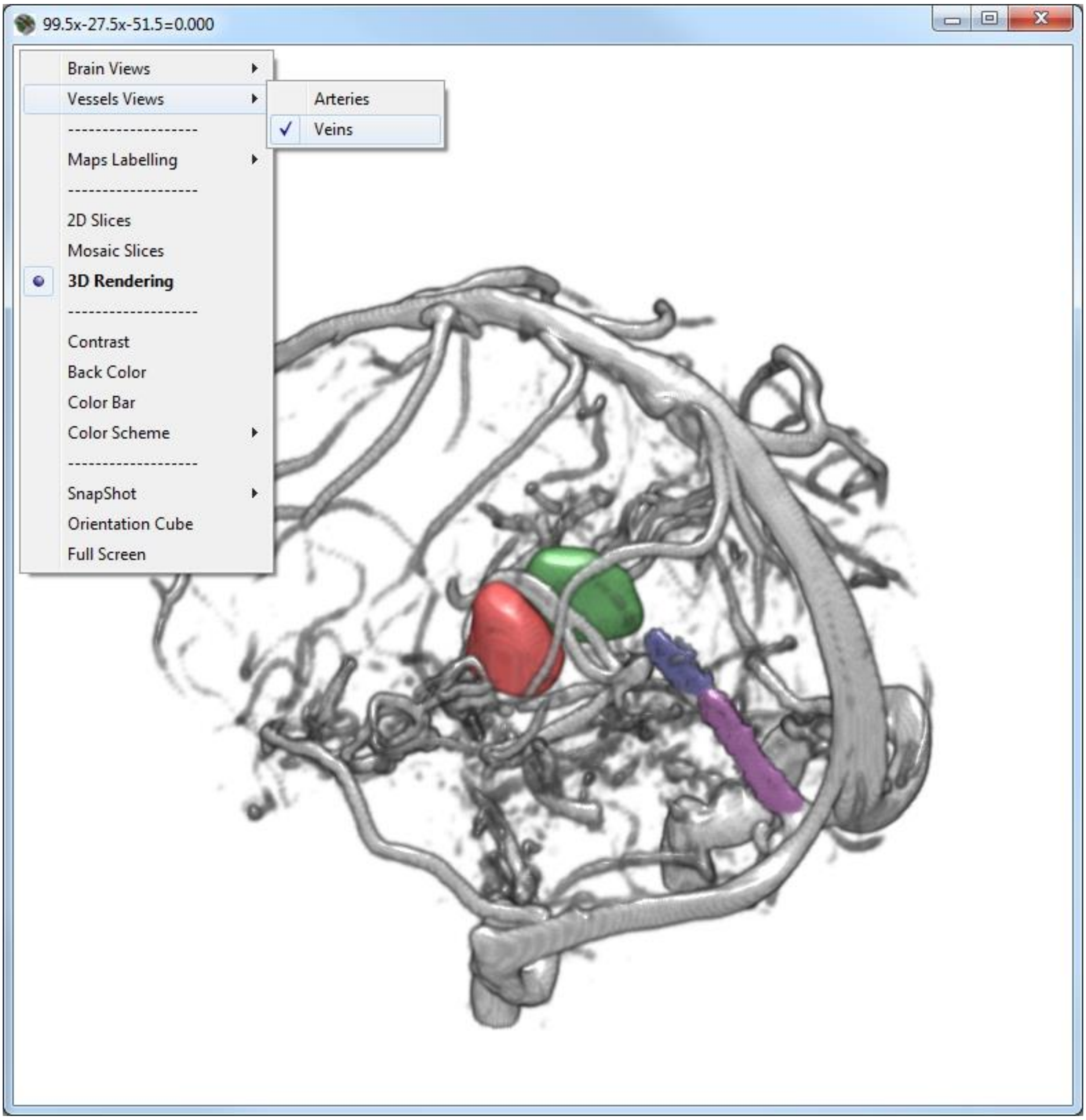
And inside the brain when applying the **3D Cut** Clipping Tool:



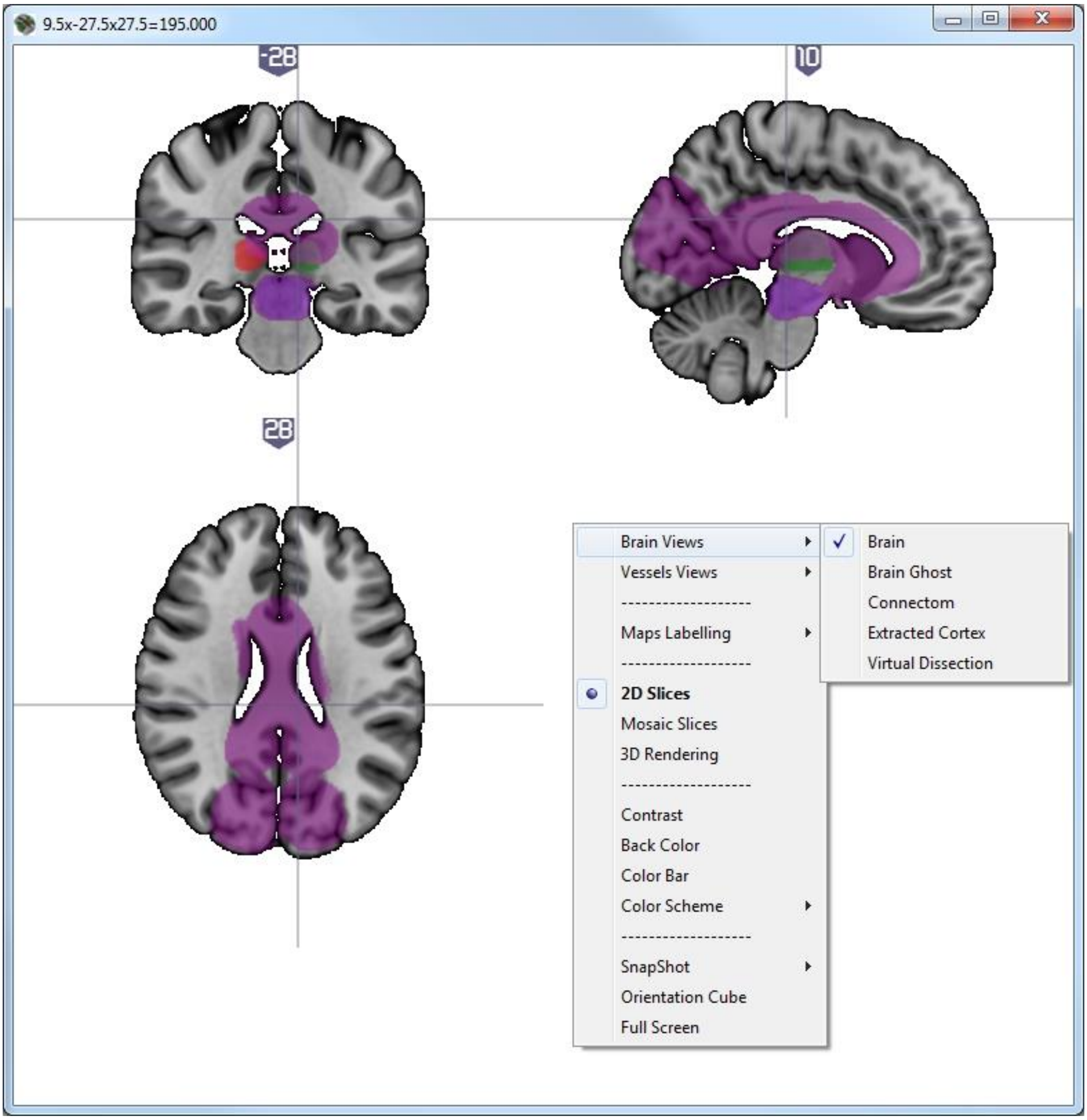




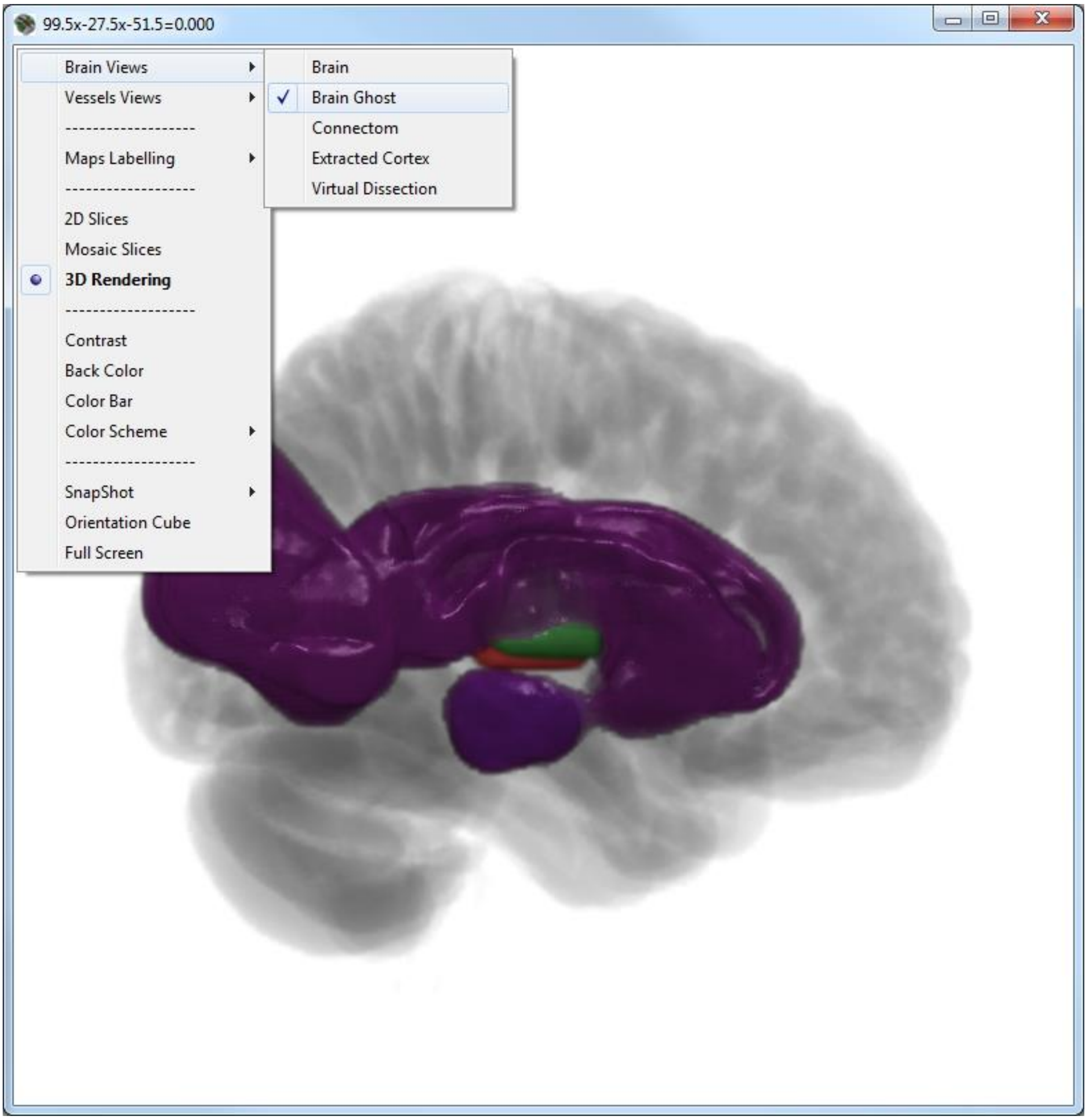
Now select the « Thalamus_R » and « Thalamus_L » by LC on the empty square in the Gery Matter Tab Selector, and RC on the 3D Rendering area to select the « Veins » Template of the "Vessels Views" menu again, showing venous and grey matter structures, then press the Render Button:


99.5x-27.5x-51.5=0.000
Brain Views
Vessels Views
Arteries
Veins
Maps Labelling
2D Slices
Mosaic Slices
3D Rendering
Contrast
Back Color
Color Bar
Color Scheme
SnapShot
Orientation Cube
Full Screen

Let's see how these structures are each other intermingled in « 2D Slices » by RC on the 3D Rendering area and selecting the "Brain" Template of the "Brain Views" menu:



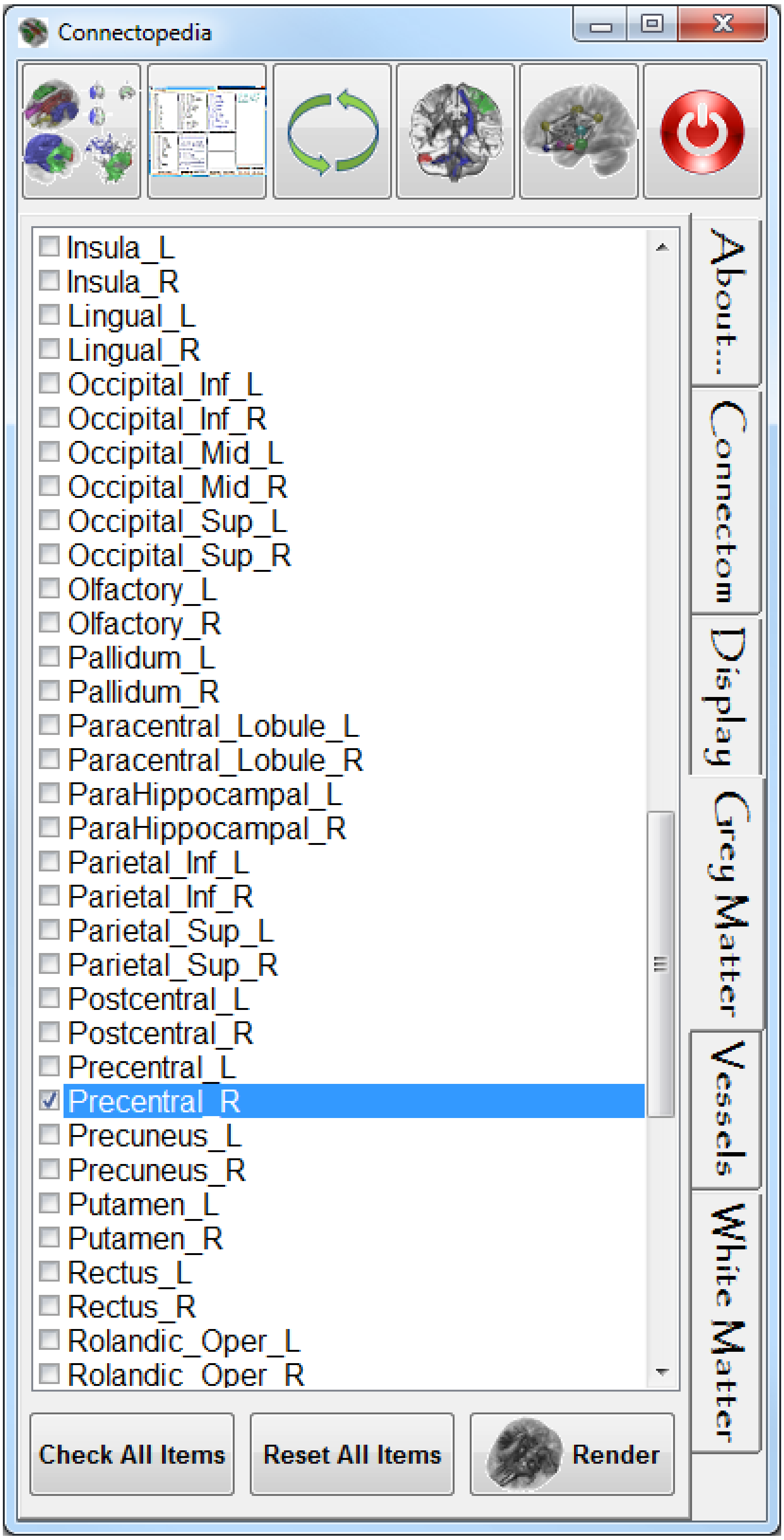
Now have a look at the 3D VR reconstruction of these structures by RC on the 3D Rendering area and selecting the “Brain Ghost” sub-menu of the “Bundles” Template:

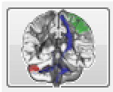


Venous drainages are overlapping the both Thalami, as you can see.

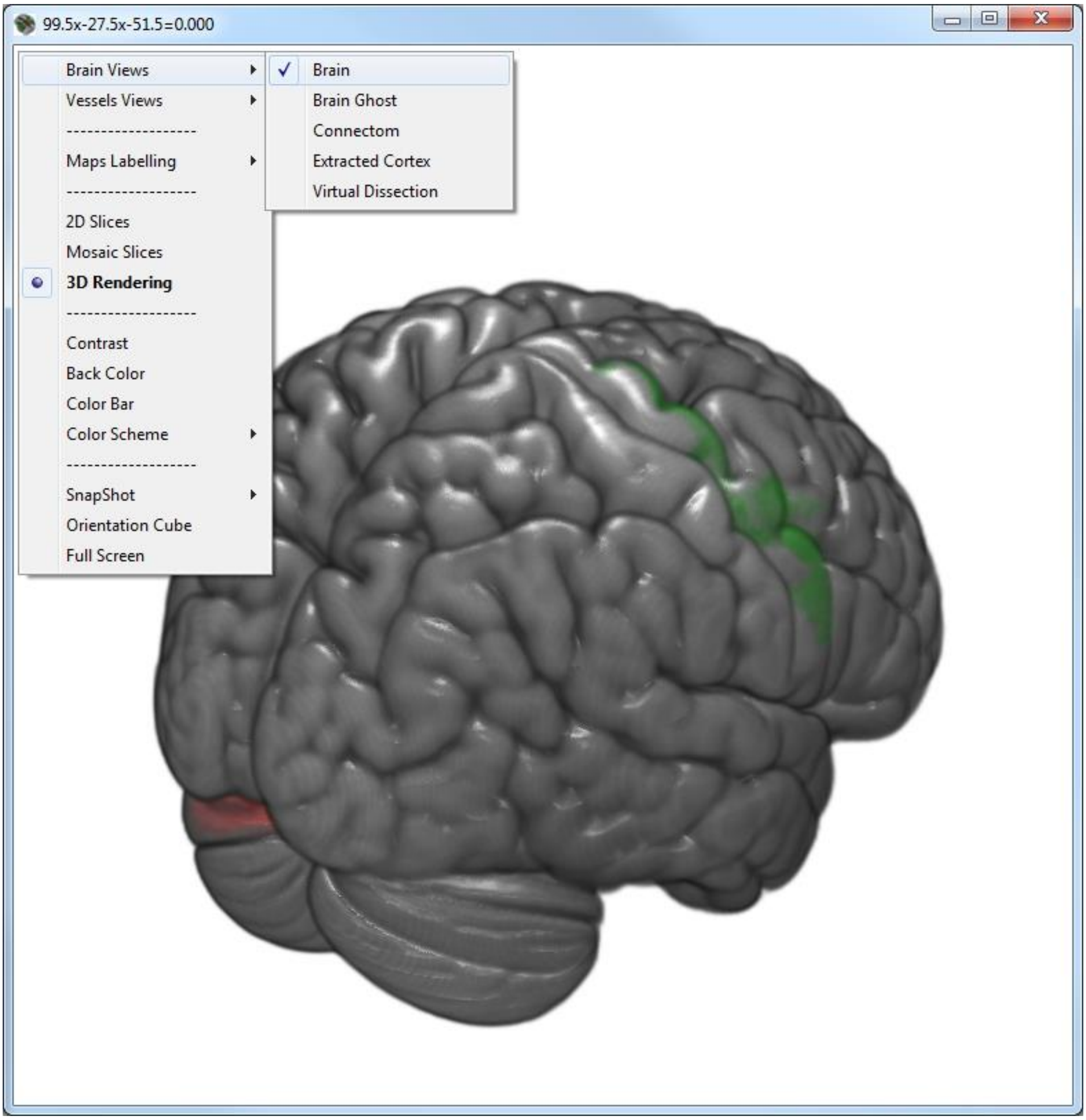
VII. Fourth exercise: Tracking fiber pathways between two cortical areas

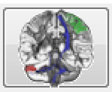
Connectopedia includes an algorithm involved in automated identification of linked grey matter structures by white matter fiber bundles.



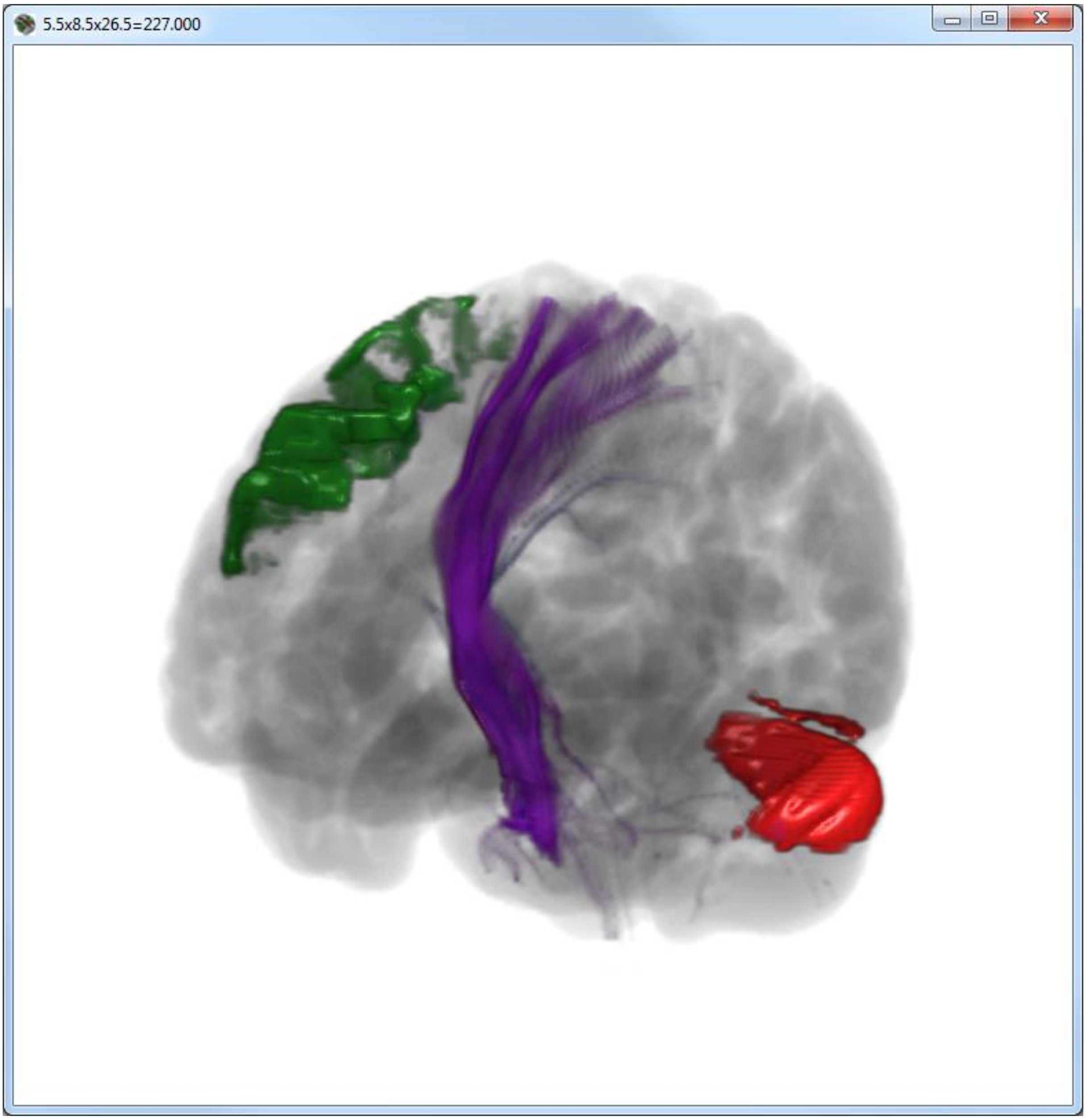
User can check the relations existing between grey matter areas using the "Tracking Pathways" Button  in the **Selector** window.

Let's see which fibers bundle(s) is (are) linking the "Right Pre-Central" cortical area and the "Left Cerebellum Crus 1". First select the cortical areas by LC on the empty square in the Grey Matter Tab Selector, then select the "Brain" Template of the "Brain Views" menu.



Then LC on the “Track Pathways” Button : 

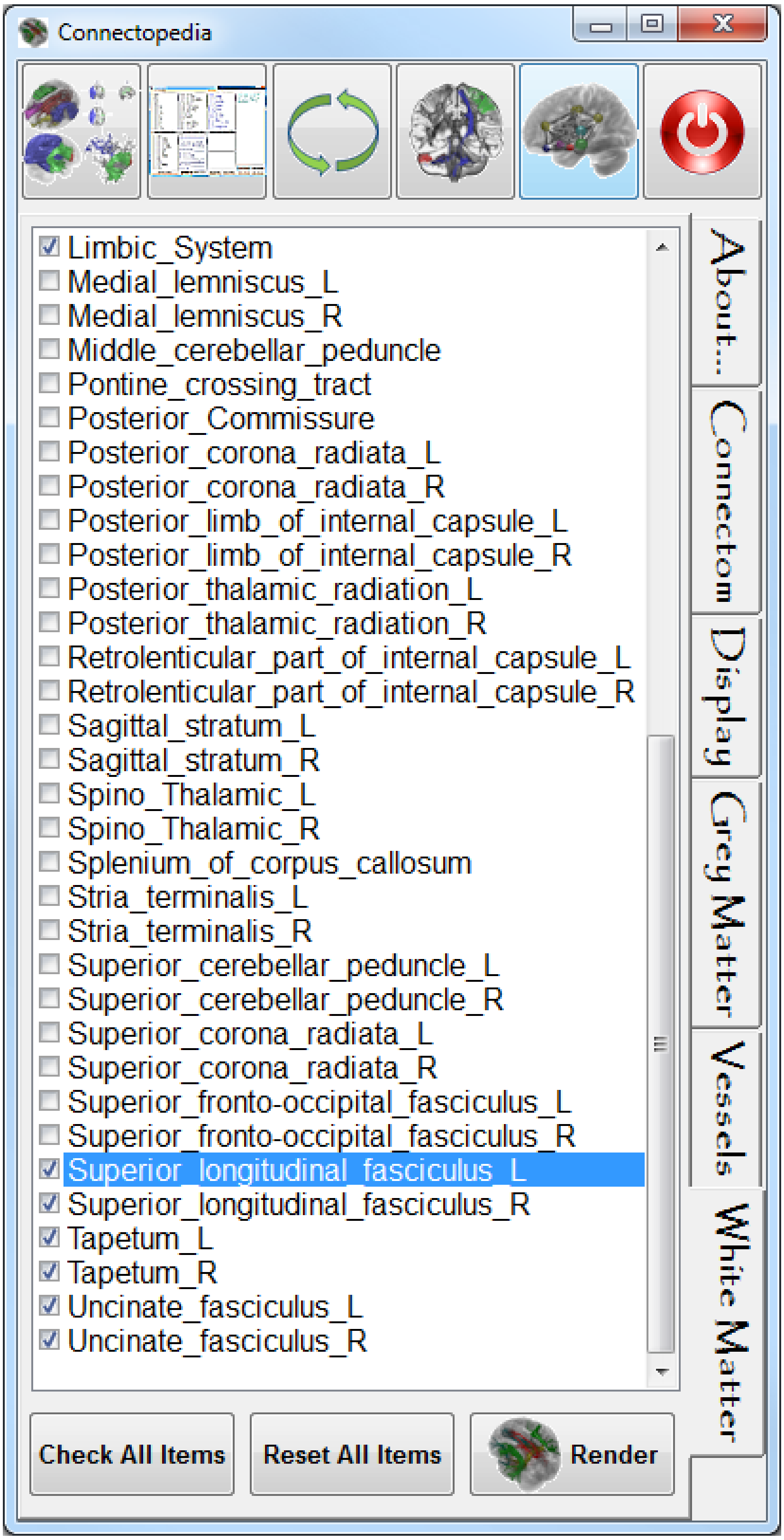
Connectopedia will detect the fiber bundles that are linking these two areas, here the “Cerebral_Peduncle_R” and the “Posterior_Limb_Internal_Capsule_R” by the cortico-ponto-cerebellar tract, and will display the found bundle(s) in the “Brain Ghost” sub-menu of the “Brain Views” Template 3D VR mode :



User can select from 2 to 116 cortical areas, but the more you select, the less you have chance to detect commun bundles (inclusive arithmetics).

VIII. Fifth exercise: Virtual Dissection with "Anatomist" Drawings Rendering

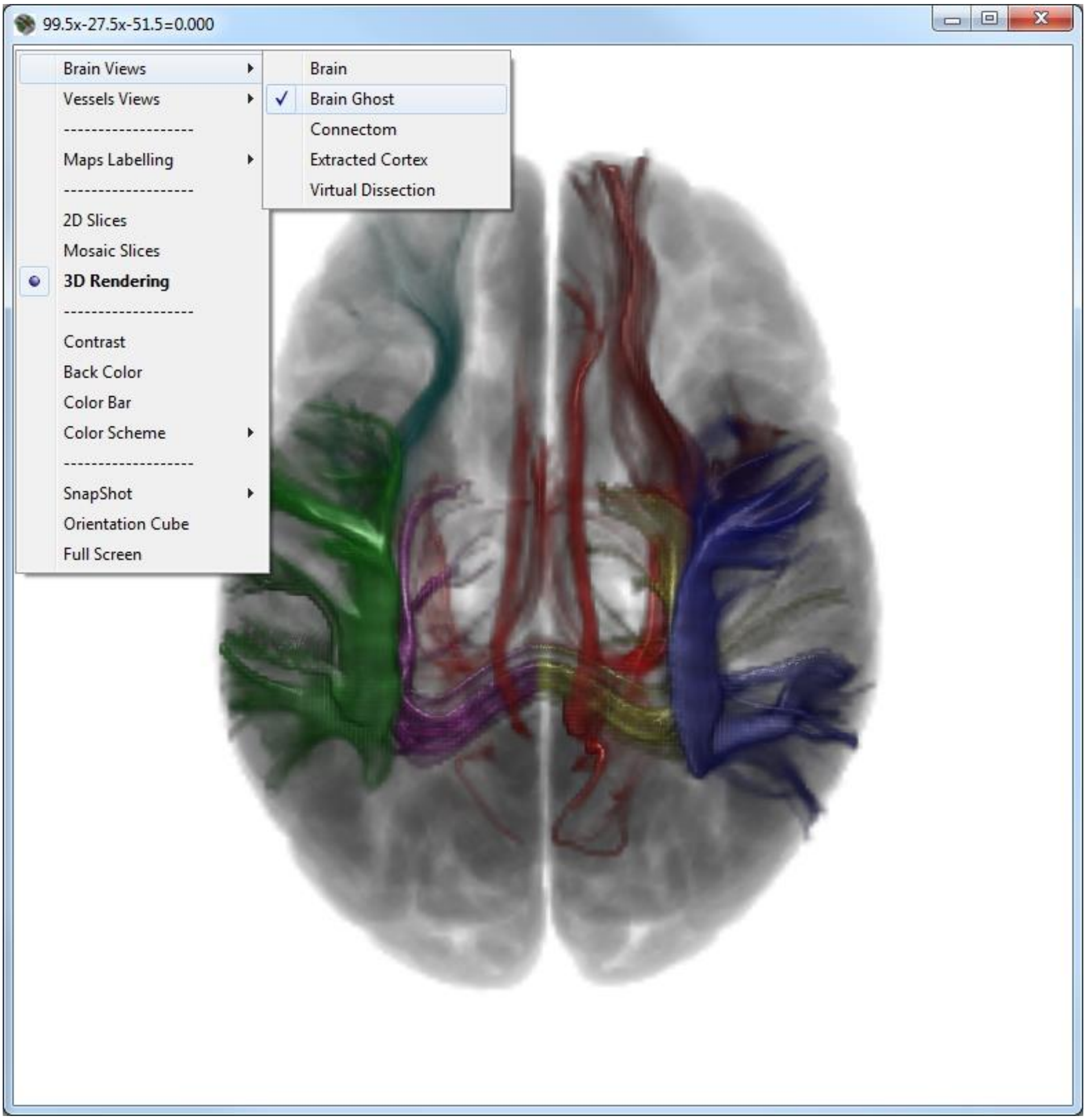
Connectopedia includes a tool to perform virtual dissection in the "19th century anatomists" drawings fashion, either in color or black and white.



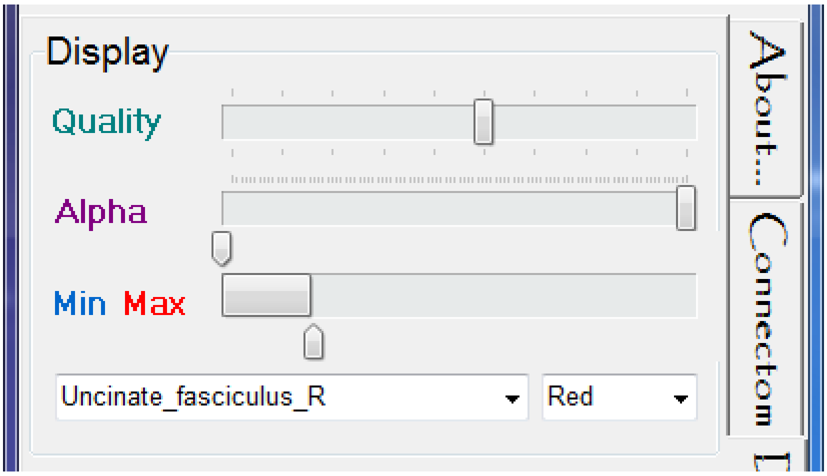
Let's start using the following White Matter Tracts, selected in the **White Matter Selector Tab** by LC on the empty square:

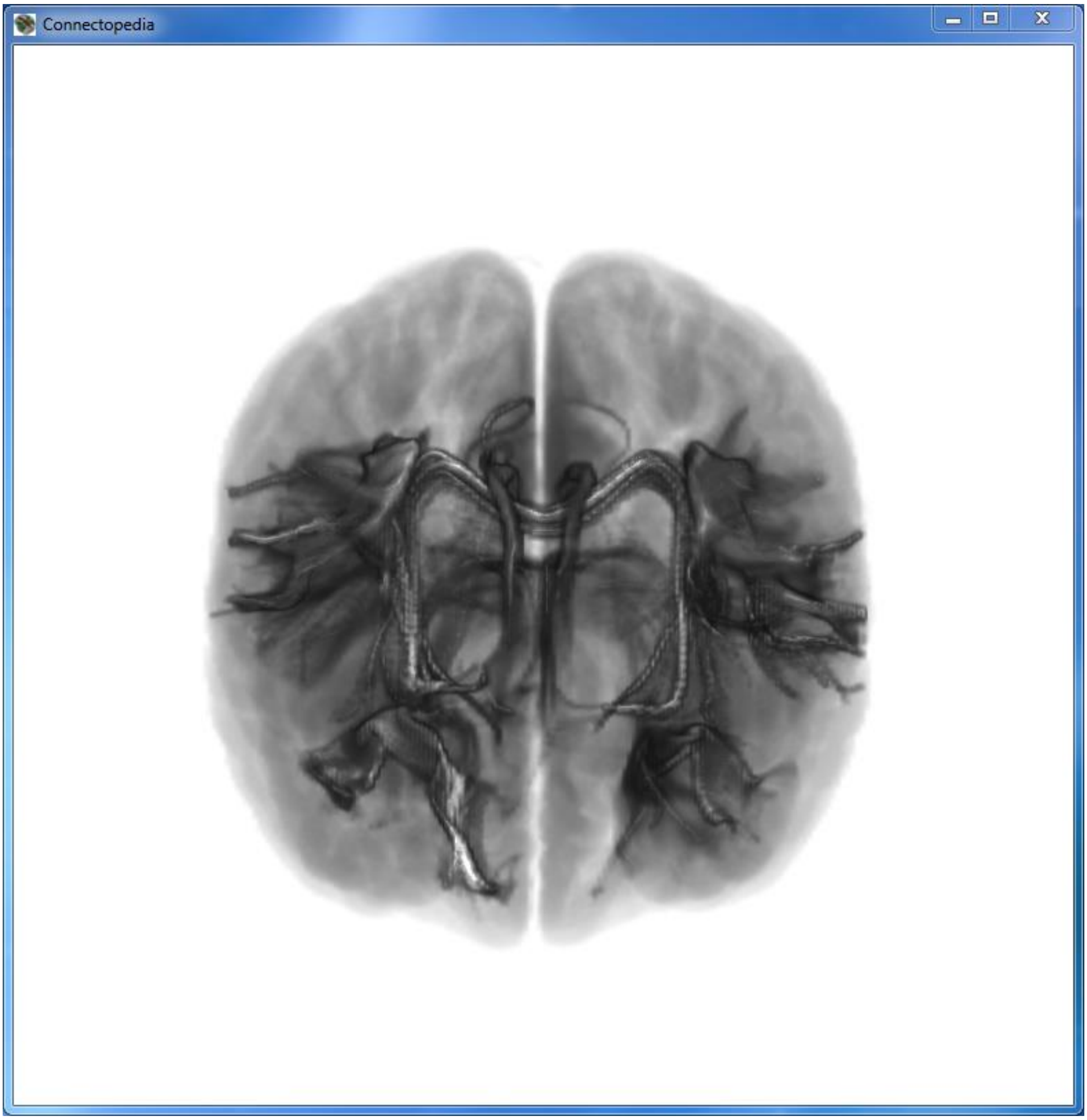
- Limbic System
- Superior Longitudinal Fasciculus R
- Superior Longitudinal Fasciculus L
- Tapetum R
- Tapetum L
- Uncinate Fasciculus R
- Uncinate Fasciculus L

Set the 3D Render window property to "Brain Ghost" sub-menu of the "Brain Views" menu Template, and press the Render button.

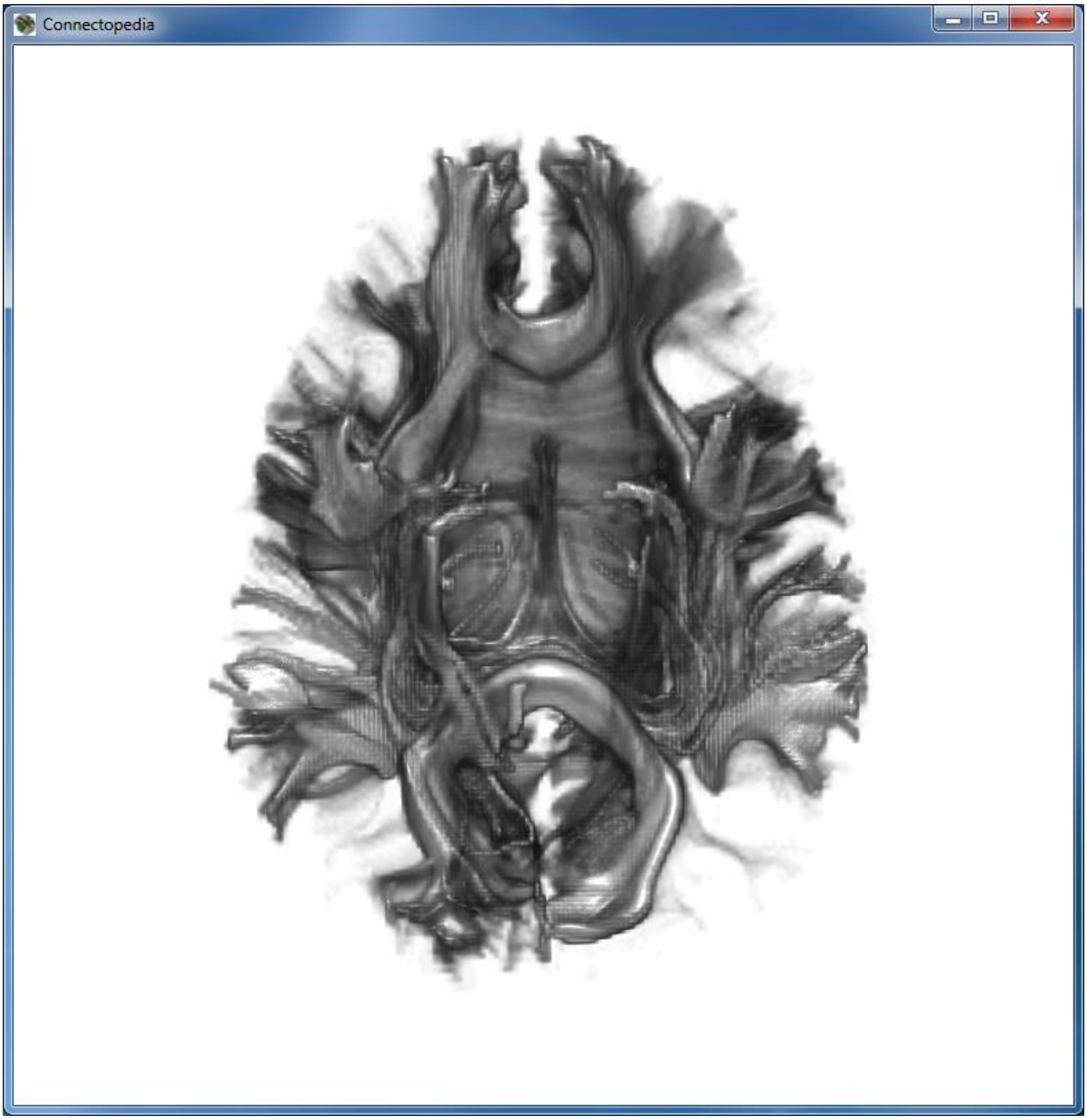


In the **Display Tab** of the **Selector**, set the “Alpha” property to 100 to render the selected bundles in Black and White.

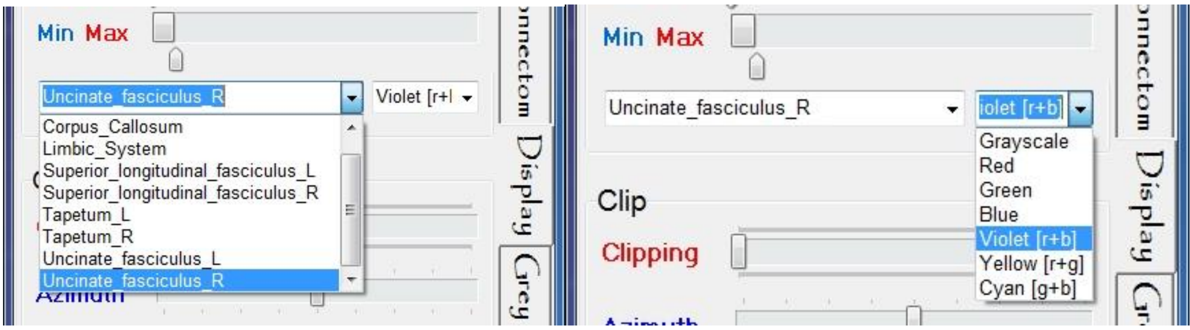

Display
Quality
Alpha
Min Max
Uncinate_fasciculus_R
Red
About...
Connectom

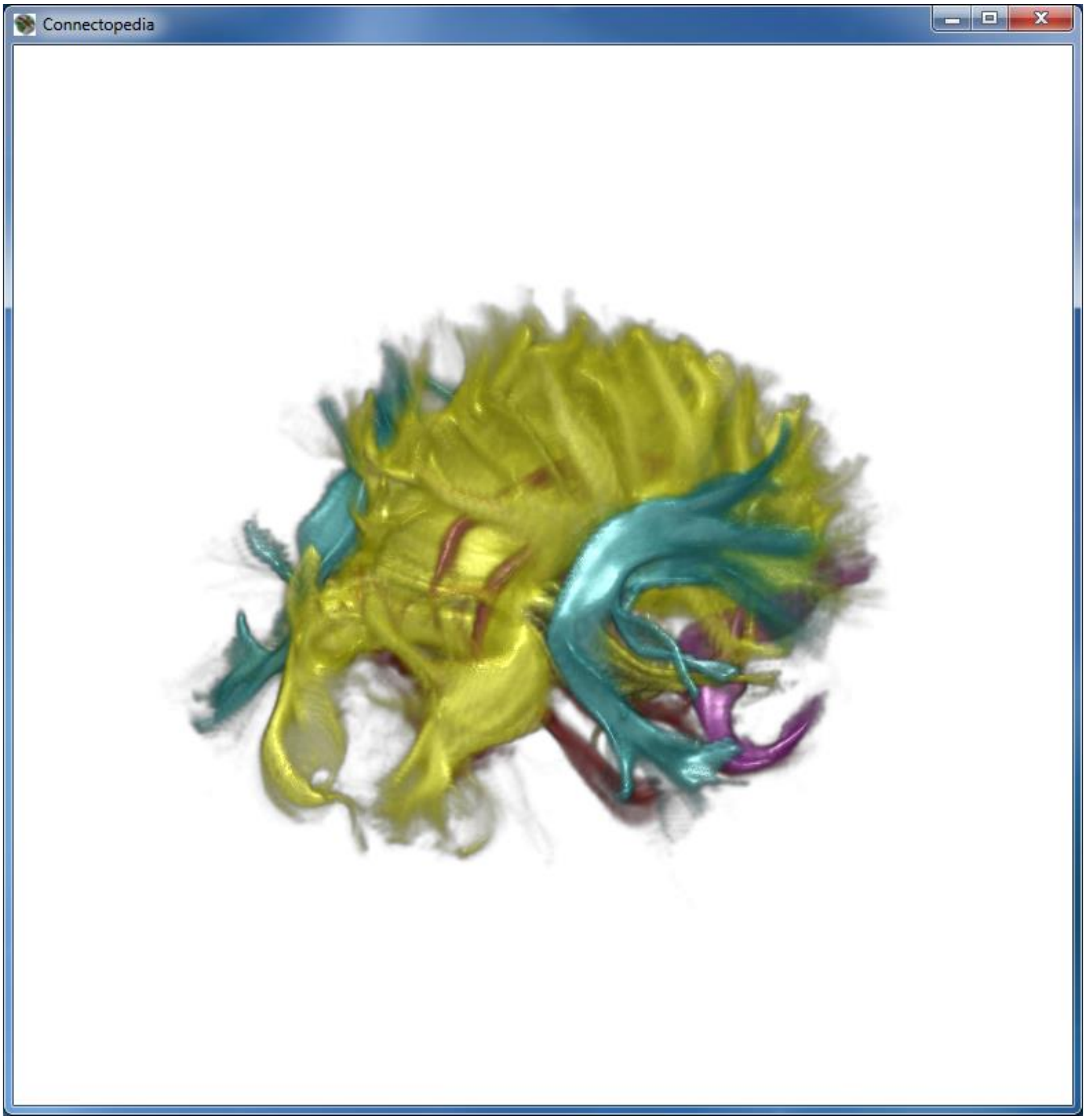

Connectopedia

Then select the “Virtual Dissection” sub-menu of the “Brain Views” menu Template in the **3D Render** window to see the selected items without the outside brain. After the rendering, add the “Corpus Callosum” item by LC on the empty square in the **White Matter Tab** Selector, press the Render button, and set the “MinMax” property in the Display to to have a good quality rendering:



Set the “Alpha” property of the **Display Tab** to 50, and change the rendered color by selecting the reconstructed item and choosing the appropriate color:

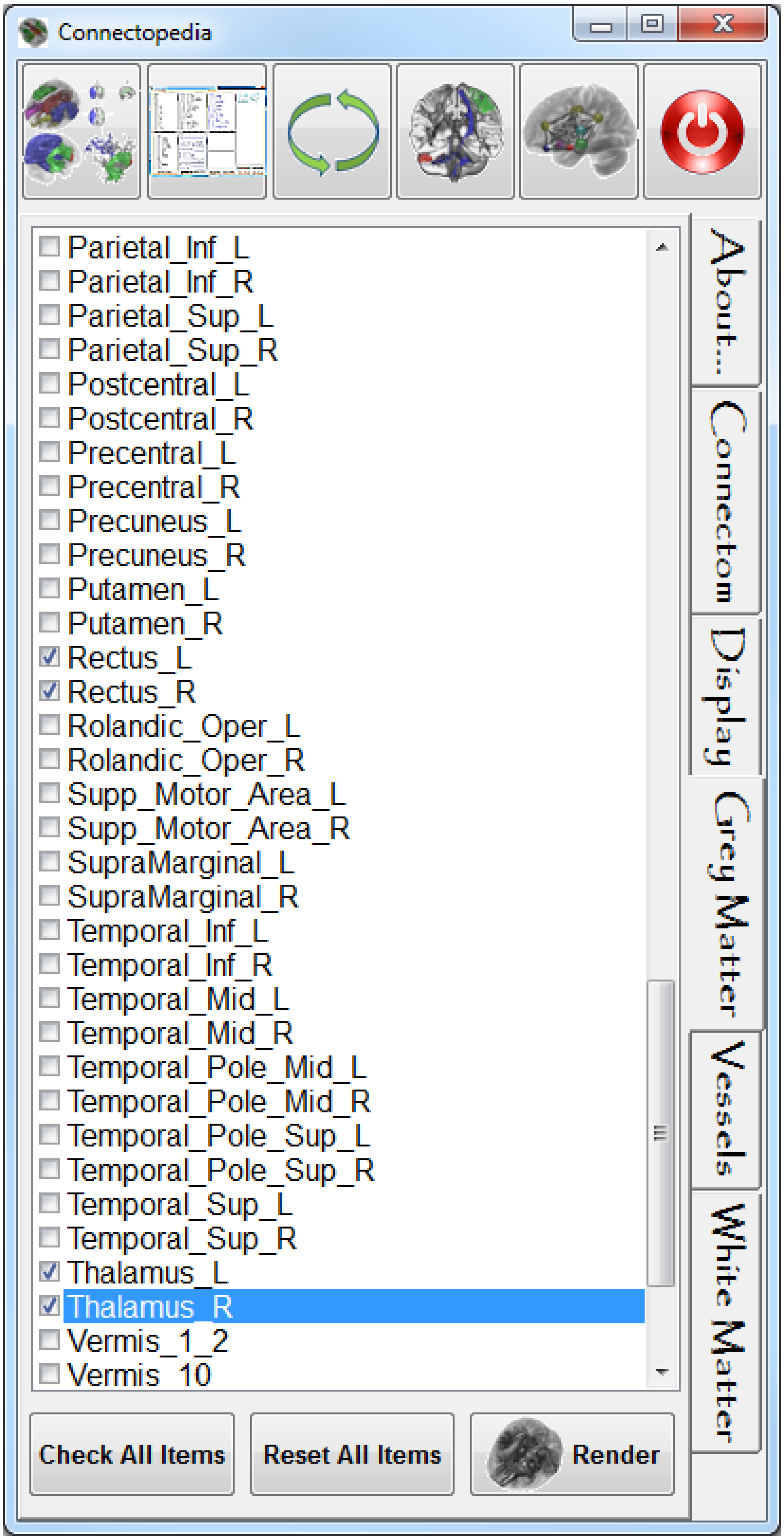

Min Max
Uncinate_fasciculus_R
Violet [r+l
Corpus_Callosum
Limbic_System
Superior_longitudinal_fasciculus_L
Superior_longitudinal_fasciculus_R
Tapetum_L
Tapetum_R
Uncinate_fasciculus_L
Uncinate_fasciculus_R
Display
Grey
Min Max
Uncinate_fasciculus_R
iolet [r+b]
Grayscale
Red
Green
Blue
Violet [r+b]
Yellow [r+g]
Cyan [g+b]
Clip
Clipping
Display


Connectopedia

IX. Sixth exercise: Connectom Rendering

Connectopedia includes a tool to assess and render the brain functional and structural connectoms, based on its database entries.

Let's see which are the functional and structural connexions of the Limbic System.



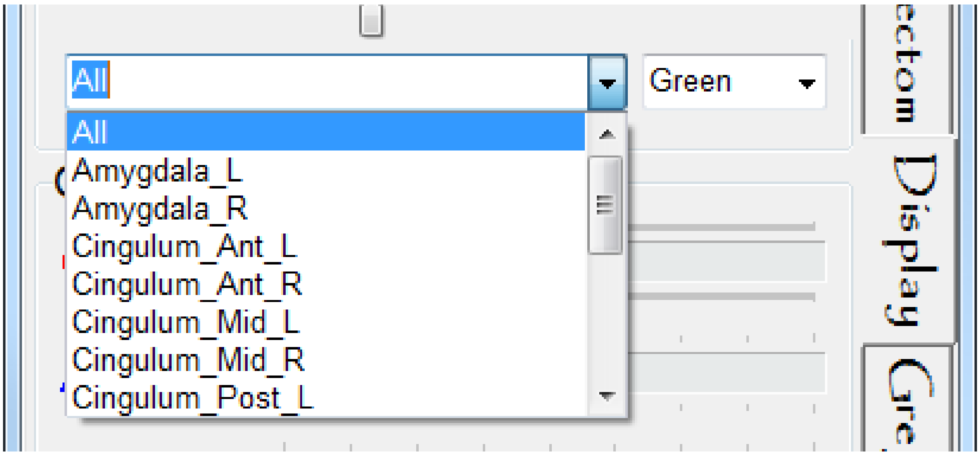
In the **Grey Matter Selector Tab**, select by LC on the empty square:

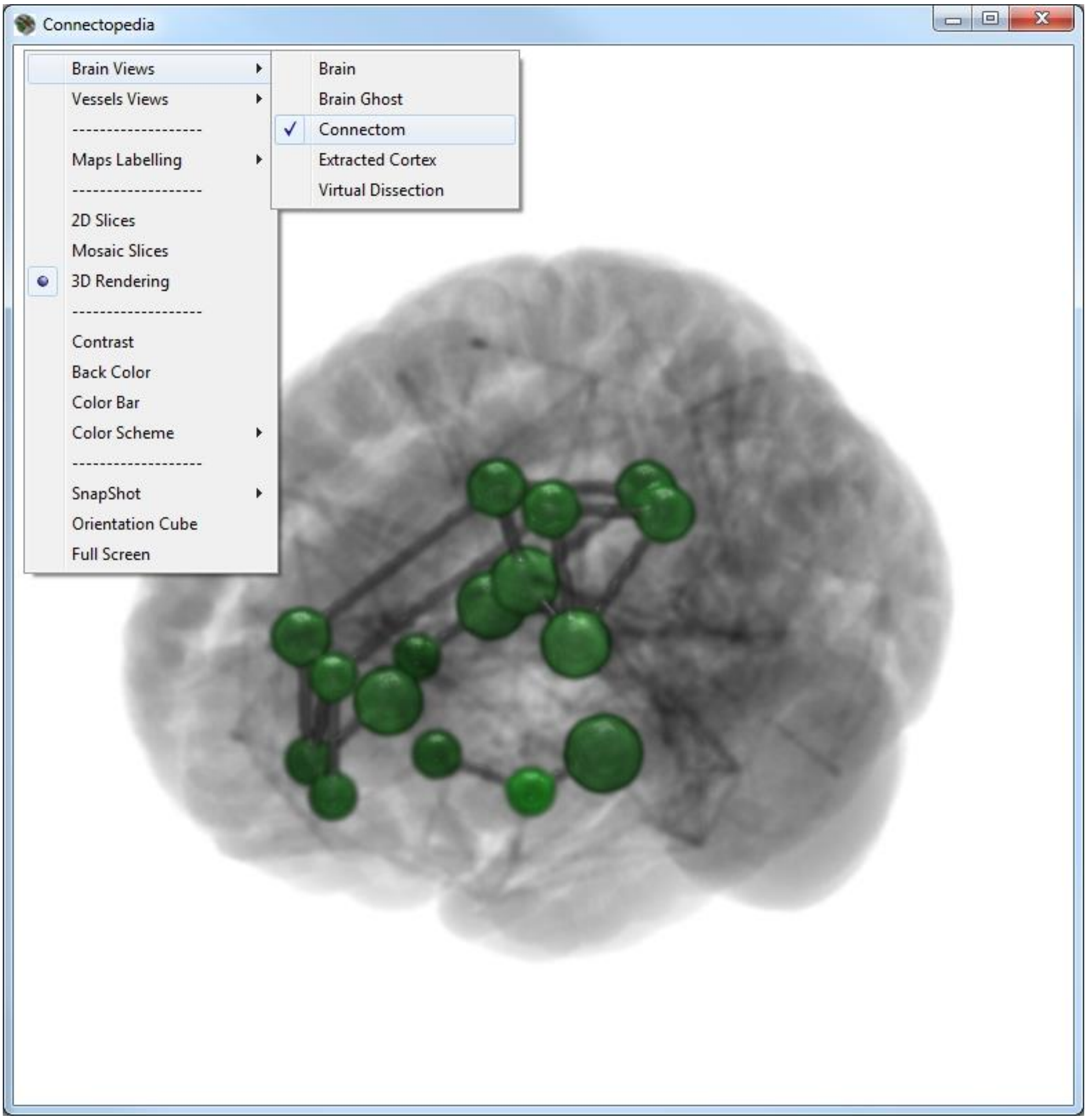
- Amygdala R and L
- Cingulum Ant, Mid, and Post R and L
- Hippocampus R and L
- Olfactory R and L
- Rectus R and L
- Thalamus R and L

Set the 3D Render window property to "Connectom" sub-menu of the "Brain Views" menu Template, and press the Render button.

In the "Display" Tab, select the Color Selector to "All" then "Green", to render the connectoms in green.

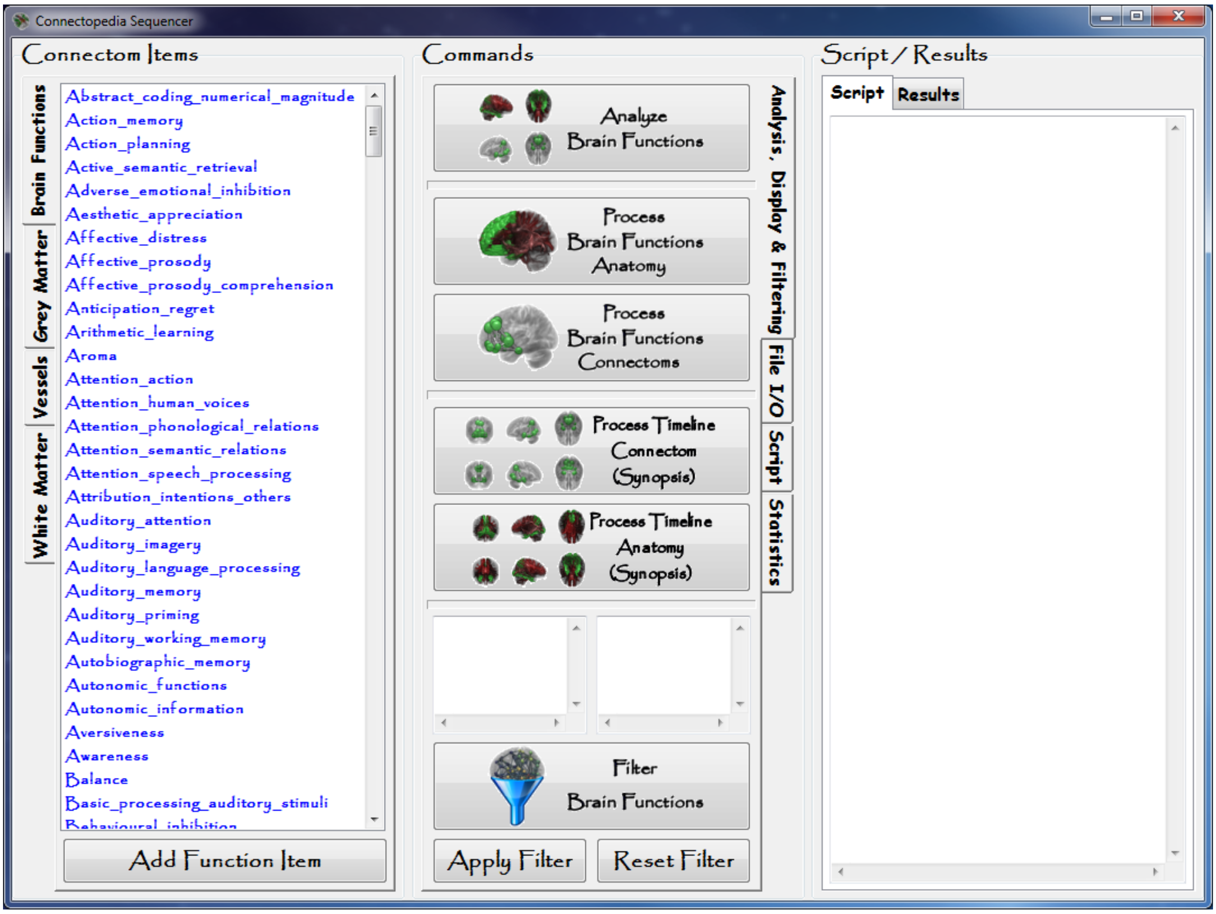
Whole brain structural connexions are shown in a skeleton line shape:


All
Green
All
Amygdala_L
Amygdala_R
Cingulum_Ant_L
Cingulum_Ant_R
Cingulum_Mid_L
Cingulum_Mid_R
Cingulum_Post_L
Display


Connectopedia
Brain Views
Vessels Views
Maps Labelling
2D Slices
Mosaic Slices
3D Rendering
Contrast
Back Color
Color Bar
Color Scheme
SnapShot
Orientation Cube
Full Screen
Brain
Brain Ghost
Connectom
Extracted Cortex
Virtual Dissection

XI. Seventh exercise: Script and Brain Functions Analyses

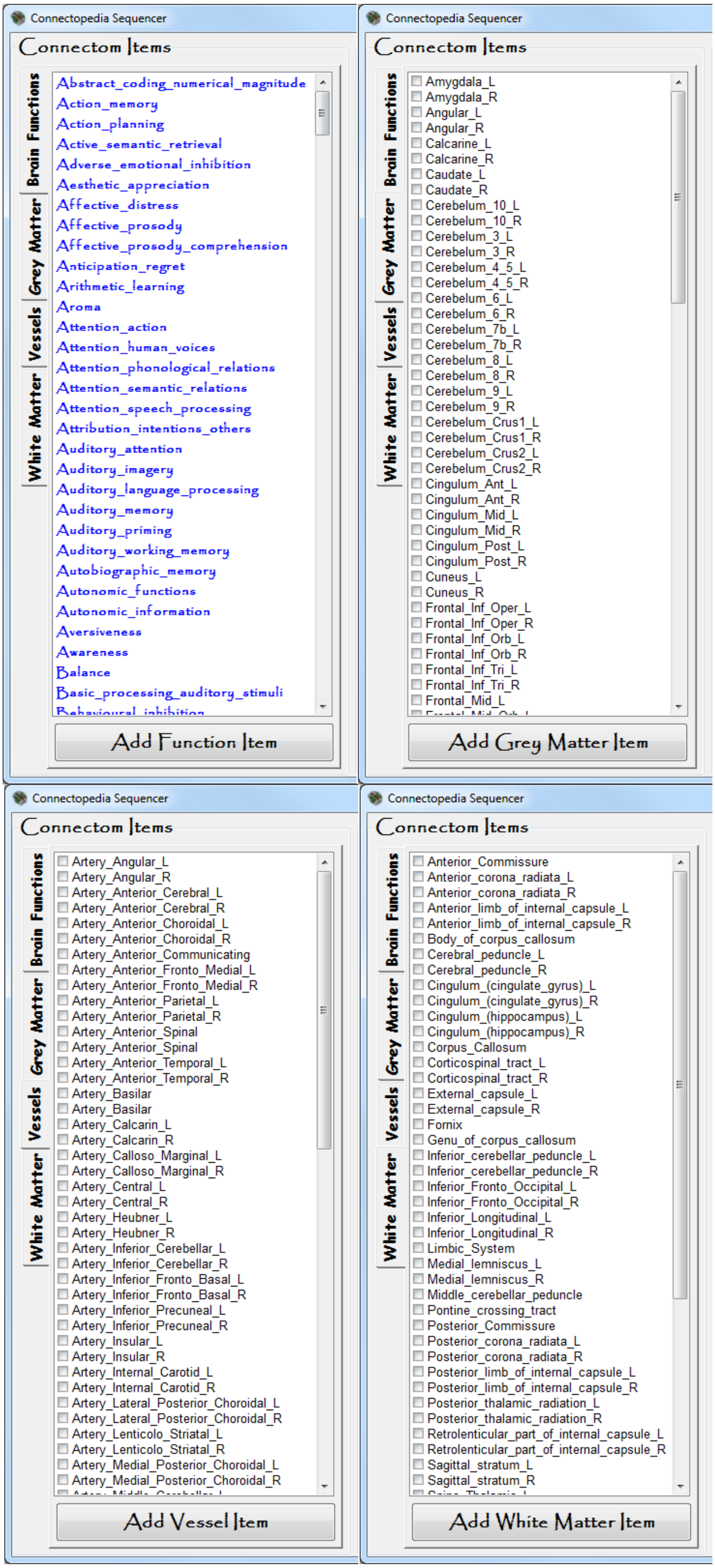
The **Connectopedia Sequencer** window lets users drive Connectopedia to script 3D reconstructions of the Brain Structures and to analyze Brain Functions.



There are Selector Tabs for Grey and White Matter, and Vessels structures, Brain Functions for filtering the analysis and Script Commands that can be batch processed or added to the “Script” window in the right part of the **Sequencer**.

By **RC** on the Buttons, users can choose between adding Structures to Script, or Functions to filter (inclusive “Add” or exclusive “Not”).

Filters are applied or reset by **LC** on the appropriate Button, and Scripts can be Loaded, Saved, Cleared or Run also by **LC** on their respective Button in the ‘**Script**’ Selector Tab.



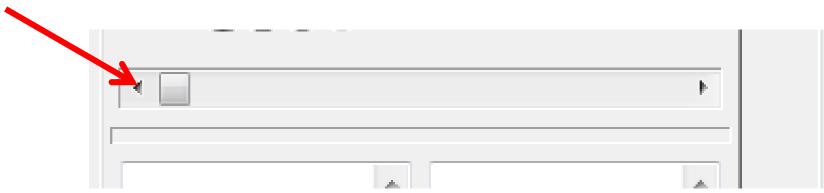
Connectopedia Sequencer
Connectom Items
Brain Functions
Grey Matter
Vessels
White Matter
Abstract_coding_numerical_magnitude
Action_memory
Action_planning
Active_semantic_retrieval
Adverse_emotional_inhibition
Aesthetic_appreciation
Affective_distress
Affective_prosody
Affective_prosody_comprehension
Anticipation_regret
Arithmetic_learning
Aroma
Attention_action
Attention_human_voices
Attention_phonological_relations
Attention_semantic_relations
Attention_speech_processing
Attribution_intentions_others
Auditory_attention
Auditory_imagery
Auditory_language_processing
Auditory_memory
Auditory_priming
Auditory_working_memory
Autobiographic_memory
Autonomic_functions
Autonomic_information
Aversiveness
Awareness
Balance
Basic_processing_auditory_stimuli
Add Function Item
Connectopedia Sequencer
Connectom Items
Brain Functions
Grey Matter
Vessels
White Matter
Amygdala_L
Amygdala_R
Angular_L
Angular_R
Calcarine_L
Calcarine_R
Caudate_L
Caudate_R
Cerebelum_10_L
Cerebelum_10_R
Cerebelum_3_L
Cerebelum_3_R
Cerebelum_4_5_L
Cerebelum_4_5_R
Cerebelum_6_L
Cerebelum_6_R
Cerebelum_7b_L
Cerebelum_7b_R
Cerebelum_8_L
Cerebelum_8_R
Cerebelum_9_L
Cerebelum_9_R
Cerebelum_Crus1_L
Cerebelum_Crus1_R
Cerebelum_Crus2_L
Cerebelum_Crus2_R
Cingulum_Ant_L
Cingulum_Ant_R
Cingulum_Mid_L
Cingulum_Mid_R
Cingulum_Post_L
Cingulum_Post_R
Cuneus_L
Cuneus_R
Frontal_Inf_Oper_L
Frontal_Inf_Oper_R
Frontal_Inf_Orb_L
Frontal_Inf_Orb_R
Frontal_Inf_Tri_L
Frontal_Inf_Tri_R
Frontal_Mid_L
Add Grey Matter Item
Connectopedia Sequencer
Connectom Items
Brain Functions
Grey Matter
Vessels
White Matter
Artery_Angular_L
Artery_Angular_R
Artery_Anterior_Cerebral_L
Artery_Anterior_Cerebral_R
Artery_Anterior_Choroidal_L
Artery_Anterior_Choroidal_R
Artery_Anterior_Communicating
Artery_Anterior_Fronto_Medial_L
Artery_Anterior_Fronto_Medial_R
Artery_Anterior_Parietal_L
Artery_Anterior_Parietal_R
Artery_Anterior_Spinal
Artery_Anterior_Spinal
Artery_Anterior_Temporal_L
Artery_Anterior_Temporal_R
Artery_Basilar
Artery_Basilar
Artery_Calcarin_L
Artery_Calcarin_R
Artery_Calloso_Marginal_L
Artery_Calloso_Marginal_R
Artery_Central_L
Artery_Central_R
Artery_Heubner_L
Artery_Heubner_R
Artery_Inferior_Cerebellar_L
Artery_Inferior_Cerebellar_R
Artery_Inferior_Fronto_Basal_L
Artery_Inferior_Fronto_Basal_R
Artery_Inferior_Precuneal_L
Artery_Inferior_Precuneal_R
Artery_Insular_L
Artery_Insular_R
Artery_Internal_Carotid_L
Artery_Internal_Carotid_R
Artery_Lateral_Posterior_Choroidal_L
Artery_Lateral_Posterior_Choroidal_R
Artery_Lenticolo_Striatal_L
Artery_Lenticolo_Striatal_R
Artery_Medial_Posterior_Choroidal_L
Artery_Medial_Posterior_Choroidal_R
Add Vessel Item
Connectopedia Sequencer
Connectom Items
Brain Functions
Grey Matter
Vessels
White Matter
Anterior_Commissure
Anterior_corona_radiata_L
Anterior_corona_radiata_R
Anterior_limb_of_internal_capsule_L
Anterior_limb_of_internal_capsule_R
Body_of_corpus_callosum
Cerebral_peduncle_L
Cerebral_peduncle_R
Cingulum_(cingulate_gyrus)_L
Cingulum_(cingulate_gyrus)_R
Cingulum_(hippocampus)_L
Cingulum_(hippocampus)_R
Corpus_Callosum
Corticospinal_tract_L
Corticospinal_tract_R
External_capsule_L
External_capsule_R
Fornix
Genu_of_corpus_callosum
Inferior_cerebellar_peduncle_L
Inferior_cerebellar_peduncle_R
Inferior_Fronto_Occipital_L
Inferior_Fronto_Occipital_R
Inferior_Longitudinal_L
Inferior_Longitudinal_R
Limbic_System
Medial_lemniscus_L
Medial_lemniscus_R
Middle_cerebellar_peduncle
Pontine_crossing_tract
Posterior_Commissure
Posterior_corona_radiata_L
Posterior_corona_radiata_R
Posterior_limb_of_internal_capsule_L
Posterior_limb_of_internal_capsule_R
Posterior_thalamic_radiation_L
Posterior_thalamic_radiation_R
Retrolenticular_part_of_internal_capsule_L
Retrolenticular_part_of_internal_capsule_R
Sagittal_stratum_L
Sagittal_stratum_R
Add White Matter Item

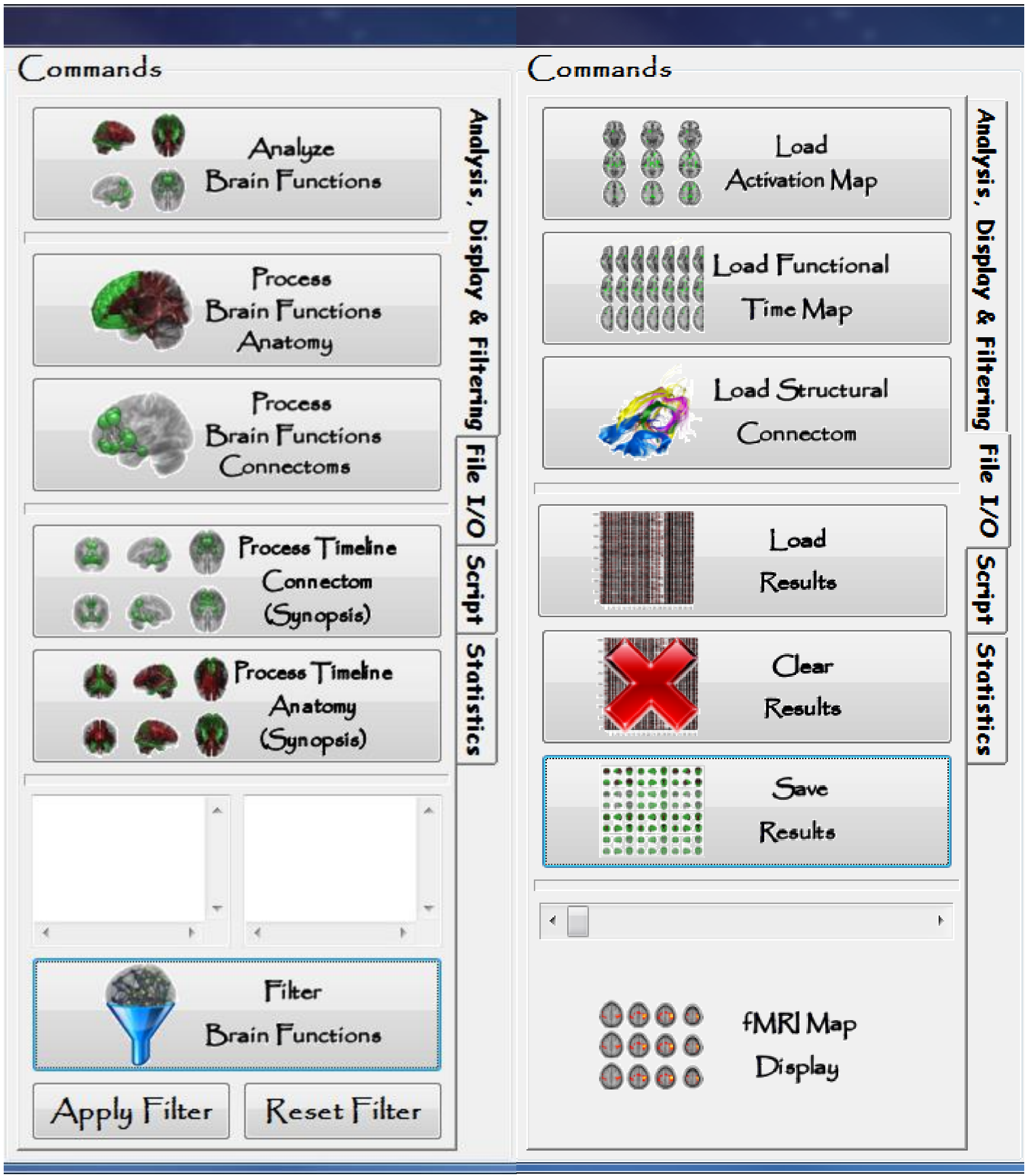
XI.I Batch Commands

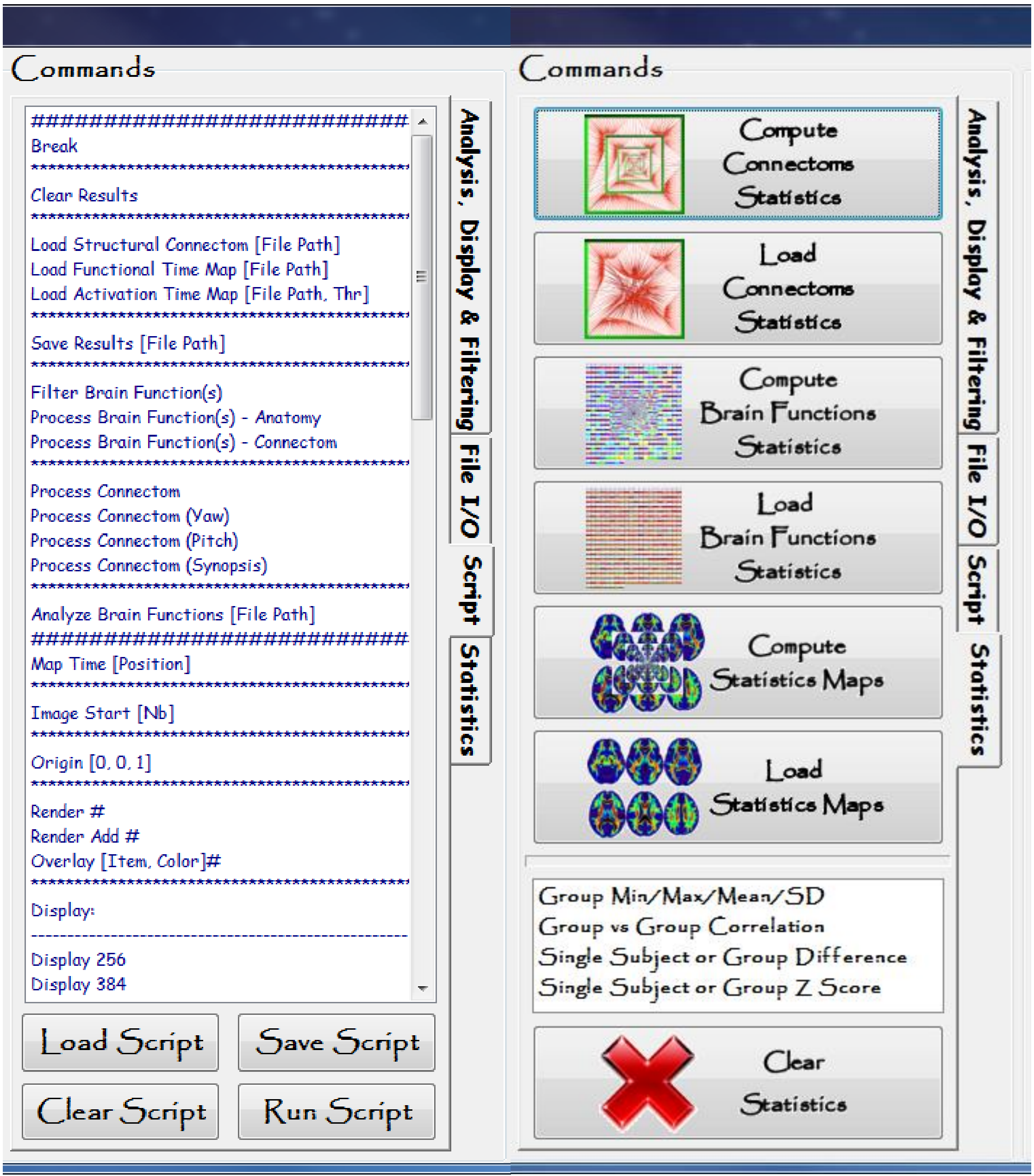
The ‘Sequencer Window’ has batch commands to Analyze Brain Functions, to Process Connectoms either of Brain Functions or from the Timeline fMRI acquisition, to Filter the Brain Functions using Grey and/or White Matter selected (checked) items, and Input/Output commands to Load or Save maps and results, and Scripts Commands further described.

- ***Analysis, Display and Filtering Tab:***
  - ‘Analyze Brain Functions’ requires a Structural Connectom map file (.ctc) and a Functional Timeline Map file (.tta) created in DPTools (in the ‘Connectomics’ tab, by **LC** on ‘Structural’ or ‘Functional’ connectomic button).
  - ‘Process Brain Functions Anatomy’, ‘Process Brain Functions Connectoms’ require a selected Brain Function in the ‘Connectoms’ Tab
  - ‘Process Timeline Connectoms (Synopsis)’, ‘Process Timeline Anatomy (Synopsis)’, require a Functional Timeline Map file (.tta) created in DPTools
  - ‘Filter Brain Functions’ will search for all Grey and/or White Matter Structures involved in different functions.
- ***File I/O Tab:***
  - ‘Load Results’, ‘Save Results’, ‘Clear Results’ will load, save or clear the ‘Results’ Tab
  - ‘fMRI Map Display’ will display a previously loaded fMRI .ima file (-PST.ima) processed using DPTools
  - ‘Load Activation Map’ will load a fMRI .ima file (-PST.ima) processed using DPTools
- ***Script Tab:***
  - Script to be executed, saved, clear or loaded.
- ***Statistics Functions :***
  - ‘Compute Connectoms Statistics’, ‘Compute Brain Functions Statistics’, ‘Compute Statistics Maps’ to compute Min/Max/Mean/SD, Correlation, ZScore, Difference of Single Subject or Group data.
  - ‘Load Connectoms Statistics’, ‘Load Brain Functions Statistics’, ‘Load Statistics Maps’ to load previously computed statistics.

In the ‘File I/O & Filter’ Tab, there are also Memoboxes for Boolean filter selections, and a scrollbar to scroll between the different timelines of a .tta file, showing all the Grey And White Matter items detected along the acquisition time.






Commands
###########################
Break
Clear Results
Load Structural Connectom [File Path]
Load Functional Time Map [File Path]
Load Activation Time Map [File Path, Thr]
Save Results [File Path]
Filter Brain Function(s)
Process Brain Function(s) - Anatomy
Process Brain Function(s) - Connectom
Process Connectom
Process Connectom (Yaw)
Process Connectom (Pitch)
Process Connectom (Synopsis)
Analyze Brain Functions [File Path]
###########################
Map Time [Position]
Image Start [Nb]
Origin [0, 0, 1]
Render #
Render Add #
Overlay [Item, Color]#
Display:
Display 256
Display 384
Load Script
Save Script
Clear Script
Run Script
Analysis, Display & Filtering
File I/O
Script
Statistics
Commands
Compute Connectoms Statistics
Load Connectoms Statistics
Compute Brain Functions Statistics
Load Brain Functions Statistics
Compute Statistics Maps
Load Statistics Maps
Group Min/Max/Mean/SD
Group vs Group Correlation
Single Subject or Group Difference
Single Subject or Group Z Score
Clear Statistics
Analysis, Display & Filtering
File I/O
Script
Statistics

XI.II Scripting

Scripts commands are:

- *Break*: to stop the running script
- *Clear Results*: to clear the Results
- *Load Structural Connectom [File Path]*: to load the Structural Connectom, File Name and Path have to be provided
- *Load Functional Time Map [File Path]:* to load the Functional Connectom, File Name and Path have to be provided
- *Load Activation Time Map [File Path, Thr]:* to load the fMRI Activation Map in GIS format, either Global or in Real-Time ; File Name, Path and Threshold Value have to be provided
- *Save Results [File Path]:* to save to results of an analysis
- *Process Brain Function(s):* to generate a script for the Function Analysis dropped in the ‘And Filter Box’
- *Process Connectom:* to generate a script for the Connectom Analysis
- *Process Connectom (Yaw):* to generate a script for the Connectom Analysis with Yaw rotations
- *Process Connectom (Pitch)):* to generate a script for the Connectom Analysis with Pitch rotations
- *Process Connectom (Synopsis):* to generate a script for the Connectom Analysis with Synopsis Six views
- *Map Time [Position]:* to set the first Time Point of a fMRI activation map ; Integer value has to be provided (in number of TR)
- *Image Start [Nb]:* to set the number of the first image to be saved in the Movie Reconstructions ; Integer value has to be provided
- *Origin [0, 0, 1]:* to set the 3D rendering at the Origin view
- *Render #:* To Render the Grey, White Matter or Vessels structures ; Structures have to be added after the “Render #” and before the last “#” sign
- *Render Add #:* To Render the Grey, White Matter or Vessels structures in an “Additive” way ; Structures have to be added after the “Render #” and before the last “#” sign

- *Overlay [Item, Color]#:* to set the color of a rendered item ; Structures have to be added after "*Overlay [Item, Color]#*", followed by the selected Color ("*Gray*", "*Red*", "*Blue*", "*Cyan*", "*Yellow*", "*Violet*", "*Green*"), and before the last "#" sign
- *Display 256*: set the rendered display size to 256x256
- *Display 384*: set the rendered display size to 384x384 (default size for Synopsis Views)
- *Display 512*: set the rendered display size to 512x512
- *Display 720p*: set the rendered display size to 720p (1280x720)
- *Arteries*: to set the 3D rendering to the "Arteries" Template of the "Vessels Views" menu
- *Brain*: to set the 3D rendering to the "Brain" Template of the "Brain Views" menu
- *Brain Ghost*: to set the 3D rendering to the "Brain Ghost" Template of the "Brain Views" menu
- *Connectom*: to set the 3D rendering to the "Connectom" Template of the "Brain Views" menu
- *Cortex*: Brain: to set the 3D rendering to the "Extracted Cortex" Template of the "Brain Views" menu
- *Veins*: to set the 3D rendering to the "Veins" Template of the "Vessels Views" menu
- *Virtual Dissection*: to set the 3D rendering to the "Virtual Dissection" Template of the "Brain Views" menu
- Mosaic [Row, *Col, Orient, SlcNb]*: to set the 2D rendering Mosaic View of the selected Template ; Row number, Col number, Orientation (Axial, Coronal, Sagittal+, Sagittal-), Slice Labeling (0 or 1) values have to be provided
- *MPR*: to set the 2D rendering MPR view of the selected Template
- *Blue, Cyan, Gray, Green, Red, Violet, Yellow* colors for the Overlay [Item, Color]# script command
- *Rotation&Alpha #:* Command to set the Rotations (Yaw, Pitch, Yaw and Pitch, Synopsis) and Alpha variations of the 3D rendering reconstructions, with values:

  -**Yaw [Start, End, Nb Img]*

  **Start*: Starting value of the Yaw Rotation

  **End*: Ending value of the Yaw Rotation

  **Nb Img*: Number of images for one rotation

  - **Pitch [Start, End, Nb Img]*

Start: Starting value of the Pitch Rotation

End: Starting value of the Pitch Rotation

Nb Img: Number of images for one rotation

-*Distance [Nb Img]*

Nb Img: Number of images for the distance variation

- *Alpha [Start, End, Nb Img]*

Start: Starting value the Alpha intensity

End: Ending value of the Alpha intensity

Nb Img: Number of images in between the intensity variation

#: Ending of the Rotation&Alpha # command

NB: if number of images rotations and number of images alpha variation are identical, the Alpha variation occurs during the rotation

- *Snapshot:* To take a single picture of the 3D Renderer Window
- *Alpha 3, Alpha 6, Alpha 12, Alpha 24*: Preset values for Alpha variation (3, 6, 12, 24 images)
- *Yaw 90, Yaw 180, Yaw 270, Yaw 360*: Preset values for Yaw rotations (90, 180, 270, 360 degrees)
- *Pitch 90, Pitch 180, Pitch 270, Pitch 360*: Preset values for the Pitch rotations (90, 180, 270, 360 degrees)
- *Yaw&Pitch 90, Yaw&Pitch 180, Yaw&Pitch 270, Yaw&Pitch 360*: Preset values for the Yaw and Pitch rotations (90, 180, 270, 360 degrees)
- *Single Bmp*: to save image into a single picture
- *Synopsis Bmp*: to save image to a six views Synopsis picture
- *Gif*: Video format for Animated GIF movies
- *MP4:* Video format for MP4 codec movies
- *Create Movie [Path]* : to create a movie ; File Name and Path have to be provided

Here is the script example for the Limbic System 3D reconstruction:

```
Origin [0, 0, 1]
Display 512
Single Bmp
Brain Ghost
Render #
Olfactory_L
Olfactory_R
#
Overlay [Item, Color]#
Olfactory_L
Green
Olfactory_R
Green
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
```

0
30
#
Render Add #
Rectus_L
Rectus_R
#
Overlay [Item, Color]#
Rectus_L
Green
Rectus_R
Green
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Anterior_Commissure
#
Overlay [Item, Color]#
Anterior_Commissure
Red
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Hippocampus_L
Hippocampus_R
#
Overlay [Item, Color]#
Hippocampus_L
Green
Hippocampus_R
Green
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Amygdala_L
Amygdala_R
#
Overlay [Item, Color]#
Amygdala_L
Green
Amygdala_R
Green
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Limbic_System
#
Overlay [Item, Color]#
Limbic_System
Red
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Thalamus_L
Thalamus_R
#
Overlay [Item, Color]#
Thalamus_L
Green
Thalamus_R
Green
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Stria_terminalis_L
Stria_terminalis_R
Tapetum_L
Tapetum_R
#
Overlay [Item, Color]#
Stria_terminalis_L
Red
Stria_terminalis_R
Red
Tapetum_L
Red
Tapetum_R
Red
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
ParaHippocampal_L
ParaHippocampal_R
#
Overlay [Item, Color]#
ParaHippocampal_L
Green
ParaHippocampal_R
Green
#

Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Uncinate_fasciculus_L
Uncinate_fasciculus_R
#
Overlay [Item, Color]#
Uncinate_fasciculus_L
Red
Uncinate_fasciculus_R
Red
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Cingulum_Ant_L
Cingulum_Ant_R
#
Overlay [Item, Color]#
Cingulum_Ant_L
Green
Cingulum_Ant_R
Green
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Cingulum_Mid_L
Cingulum_Mid_R
#
Overlay [Item, Color]#
Cingulum_Mid_L
Green
Cingulum_Mid_R
Green
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Cingulum_Post_L
Cingulum_Post_R
#
Overlay [Item, Color]#
Cingulum_Post_L
Green
Cingulum_Post_R
Green
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Corpus_Callosum
#
Overlay [Item, Color]#
Corpus_Callosum
Red
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Frontal_Inf_Oper_L
Frontal_Inf_Oper_R
#
Overlay [Item, Color]#
Frontal_Inf_Oper_L
Green
Frontal_Inf_Oper_R
Green
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Superior_longitudinal_fasciculus_L
Superior_longitudinal_fasciculus_R
#
Overlay [Item, Color]#
Superior_longitudinal_fasciculus_L
Red
Superior_longitudinal_fasciculus_R
Red
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30
*Alpha [Start, End, Nb Img]
100
0
30
#
Render Add #
Heschl_L
Heschl_R
Angular_L
Angular_R
#

Overlay [Item, Color]#
Heschl_L
Green
Heschl_R
Green
Angular_L
Green
Angular_R
Green
#
Rotation&Alpha #
*Yaw [Start, End, Nb Img]
0
360
30

*Alpha [Start, End, Nb Img]
100
0
30
#
MP4
Create Movie [Path]
X:\Temp3\Limbic-Circuit-Yaw

-
-

****
****

Analyze Brain Functions [File Path]

Sequence Type:
Single Bmp
Synopsis Bmp
****
****
Video Format:

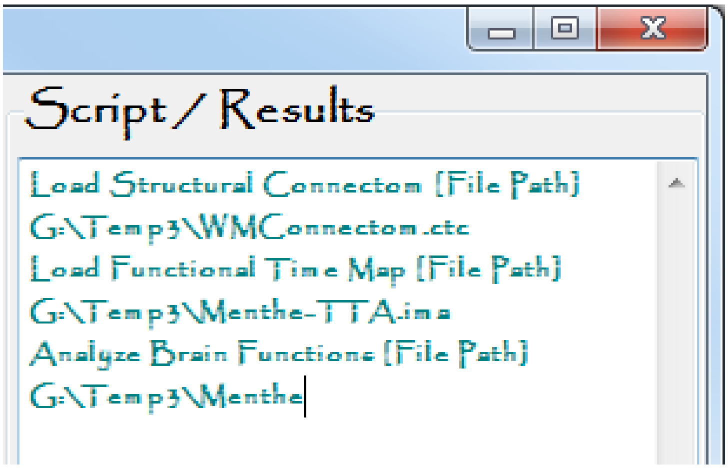
Gif
MP4
****
****
Create Movie [Path]
****
****

XI.III Brain Functions Analysis

To analyze the Brain Functions of a specific task, user has to provide:

- The Structural Connectom map (.ctc file from DPTools processing)
- The Functional Timeline map (.tta file from DPTools processing)

And either to set the script command: ‘Analyze Brain Functions [File Path]’ or ‘Analyze & Render Brain Functions [File Path]’ (far longer…) to the appropriate File Name and Path:

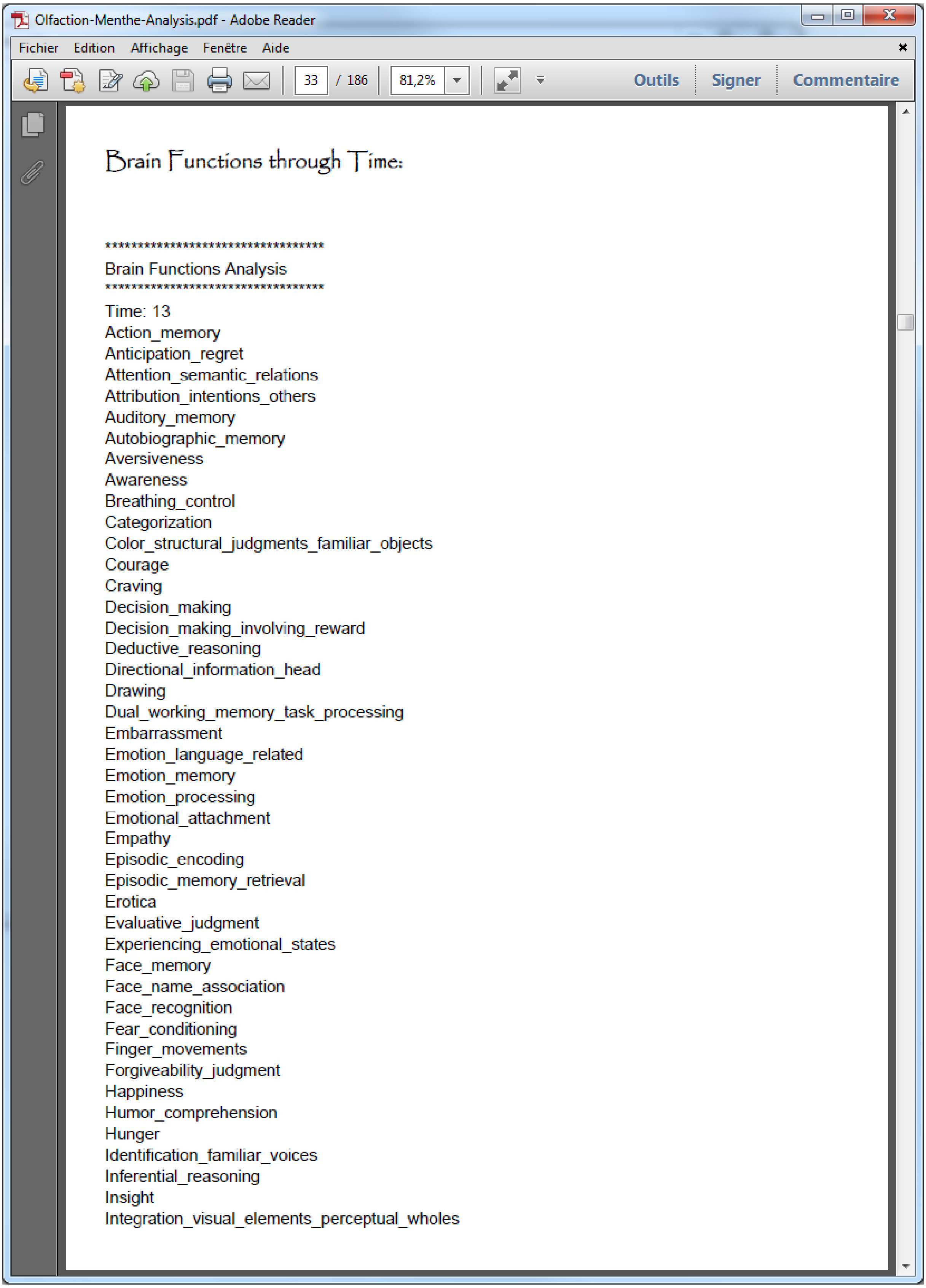


Or by LC on the ‘Analyze Brain Functions’ / ‘Analyze & Render Brain Functions’ buttons in the ‘Commands’ ‘Analysis & Processing’ Tabs.

To focus on specific functions, user can add Functions to Filter by selecting them on the appropriate window, and LC on the “Add Function to Filter” Button.
Then to press the “Run Script” Button.

A pdf file will be generated with Major and Minor Brain Functions Occurences, and Timeline Brain Functions patterns:


Olfaction-Menthe-Analysis.pdf - Adobe Reader
Fichier
Edition
Affichage
Fenêtre
Aide
1
/ 186
81,2%
Outils
Signer
Commentaire
Brain Analysis for file: Olfaction-Menthe
Occurence(s):
Working_memory: 2.756 %
Smelling_familiar_odors: 1.551 %
Executive_control_behavior: 1.551 %
Verbal_fluency: 1.448 %
Attribution_intentions_others: 1.710 %
Phonological_processing: 1.374 %
Novelty_discrimination: 1.573 %
Navegational_skills: 1.573 %
Emotion_processing: 1.573 %

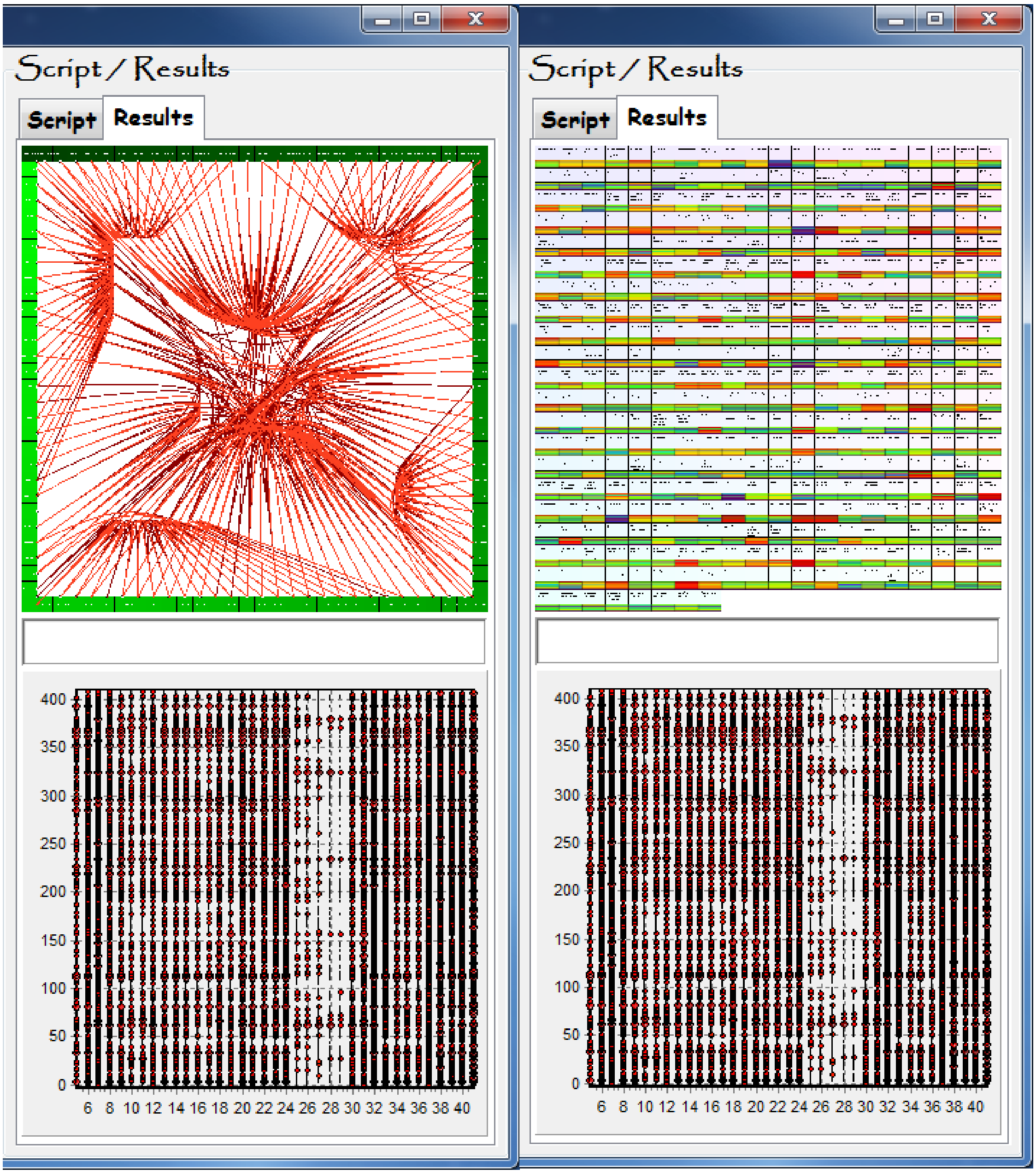


Brain Functions through Time:

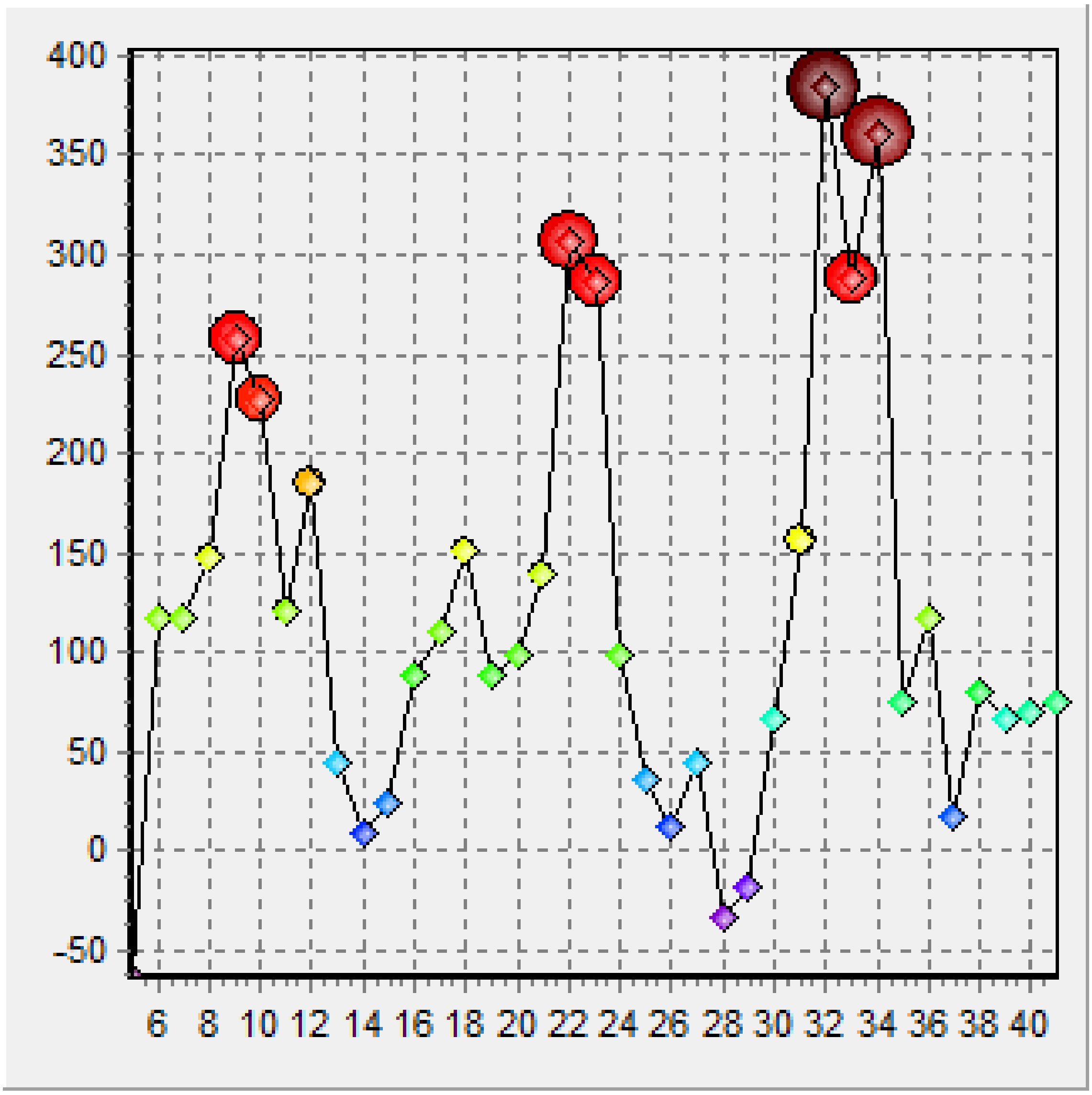
****
Brain Functions Analysis
****
Time: 13
Action_memory
Anticipation_regret
Attention_semantic_relations
Attribution_intentions_others
Auditory_memory
Autobiographic_memory
Aversiveness
Awareness
Breathing_control
Categorization
Color_structural_judgments_familiar_objects
Courage
Craving
Decision_making
Decision_making_involving_reward
Deductive_reasoning
Directional_information_head
Drawing
Dual_working_memory_task_processing
Embarrassment
Emotion_language_related
Emotion_memory
Emotion_processing
Emotional_attachment
Empathy
Episodic_encoding
Episodic_memory_retrieval
Erotica
Evaluative_judgment
Experiencing_emotional_states
Face_memory
Face_name_association
Face_recognition
Fear_conditioning
Finger_movements
Forgiveability_judgment
Happiness
Humor_comprehension
Hunger
Identification_familiar_voices
Inferential_reasoning
Insight
Integration_visual_elements_perceptual_wholes

Other data are available in PDF or .xls files, and on graphs.

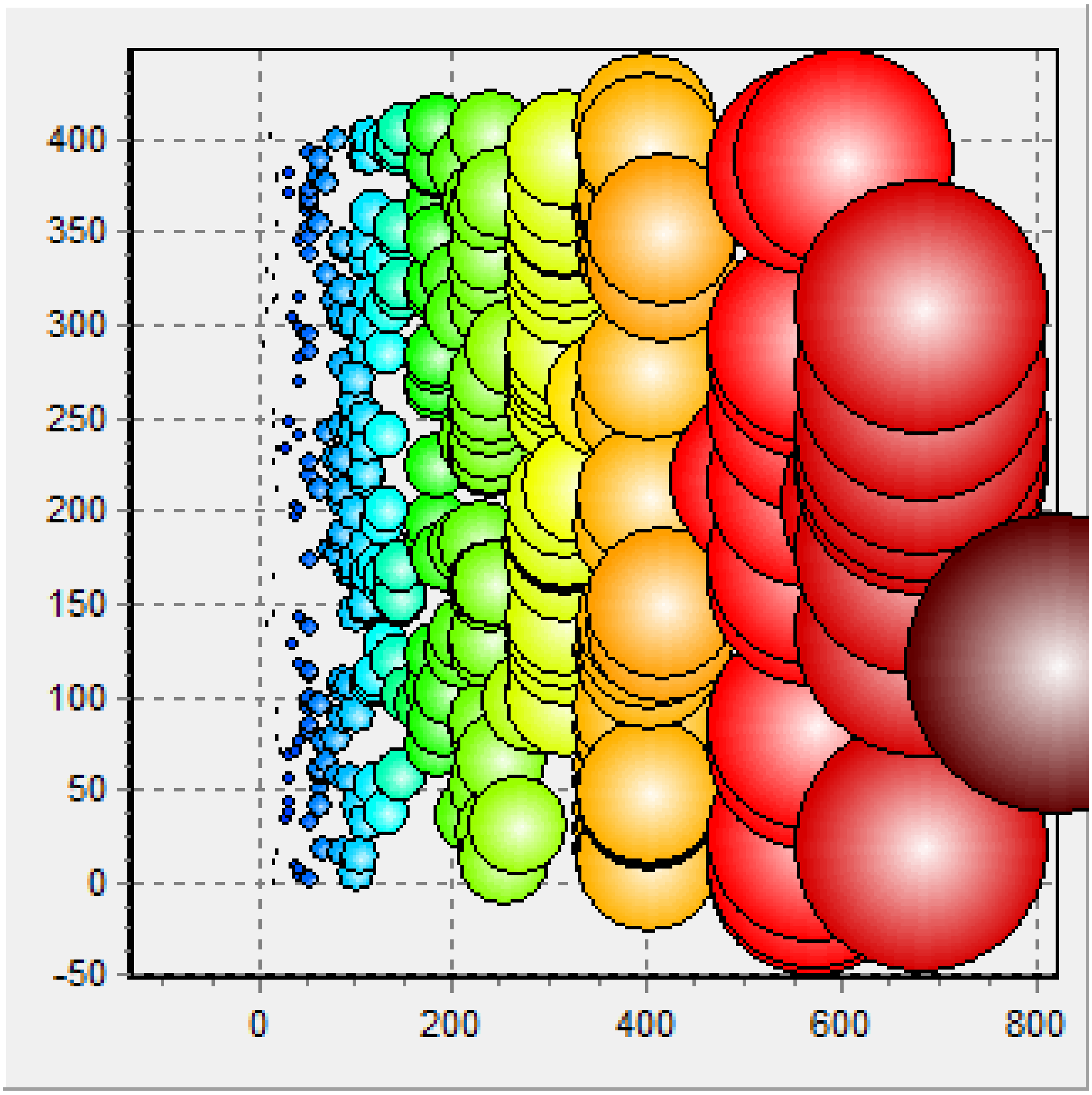
By Double Click on the Graph, user changes from Structural Connectomic View to Brain Function Usage:

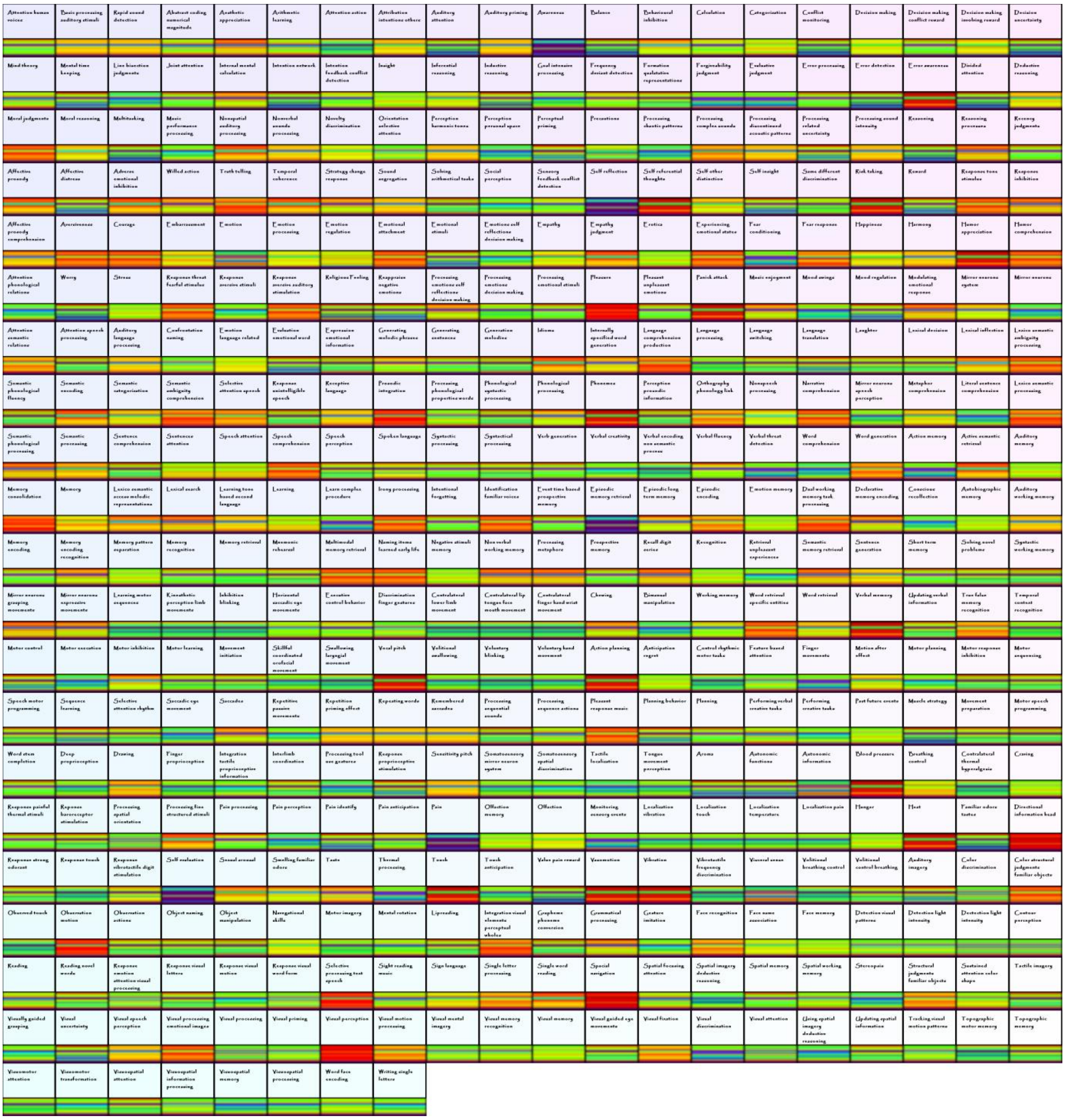


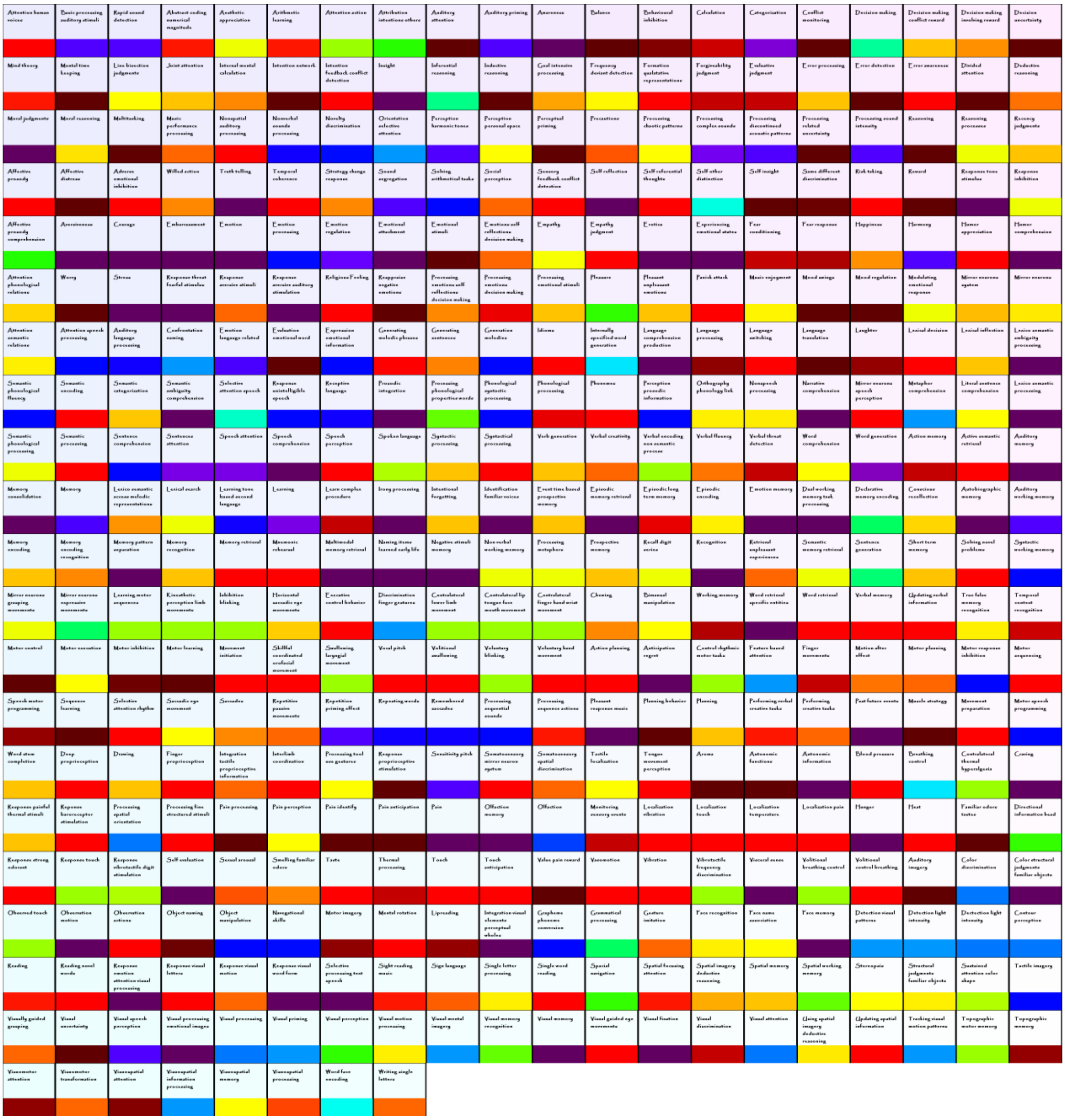
When analysis is performed, by LC on either Grey Matter Item or Brain Function, Statistics of Function or Grey Matter Usage is displayed:



400
350
300
250
200
150
100
50
0
-50
6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40


400
350
300
250
200
150
100
50
0
-50
0
200
400
600
800



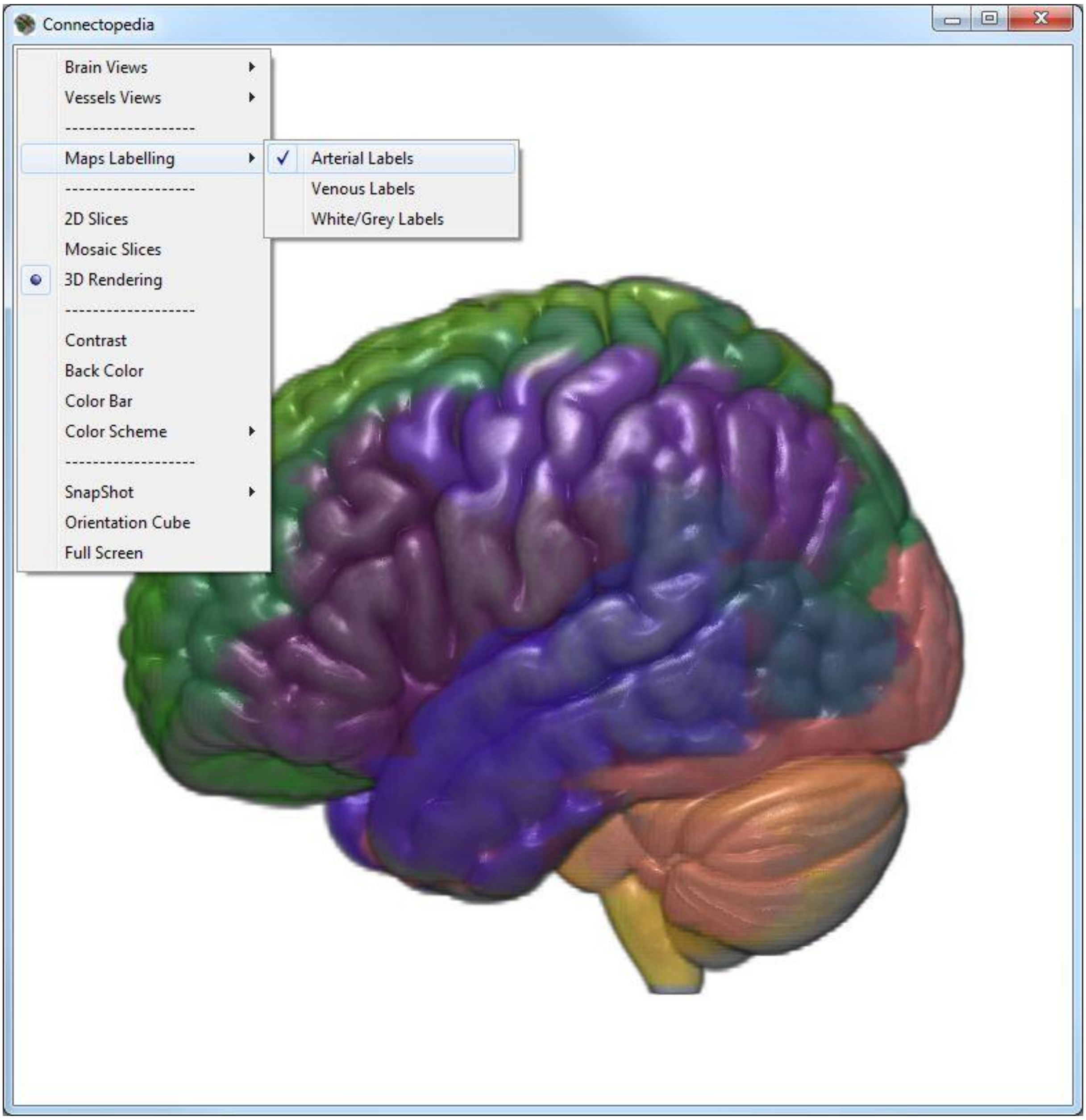


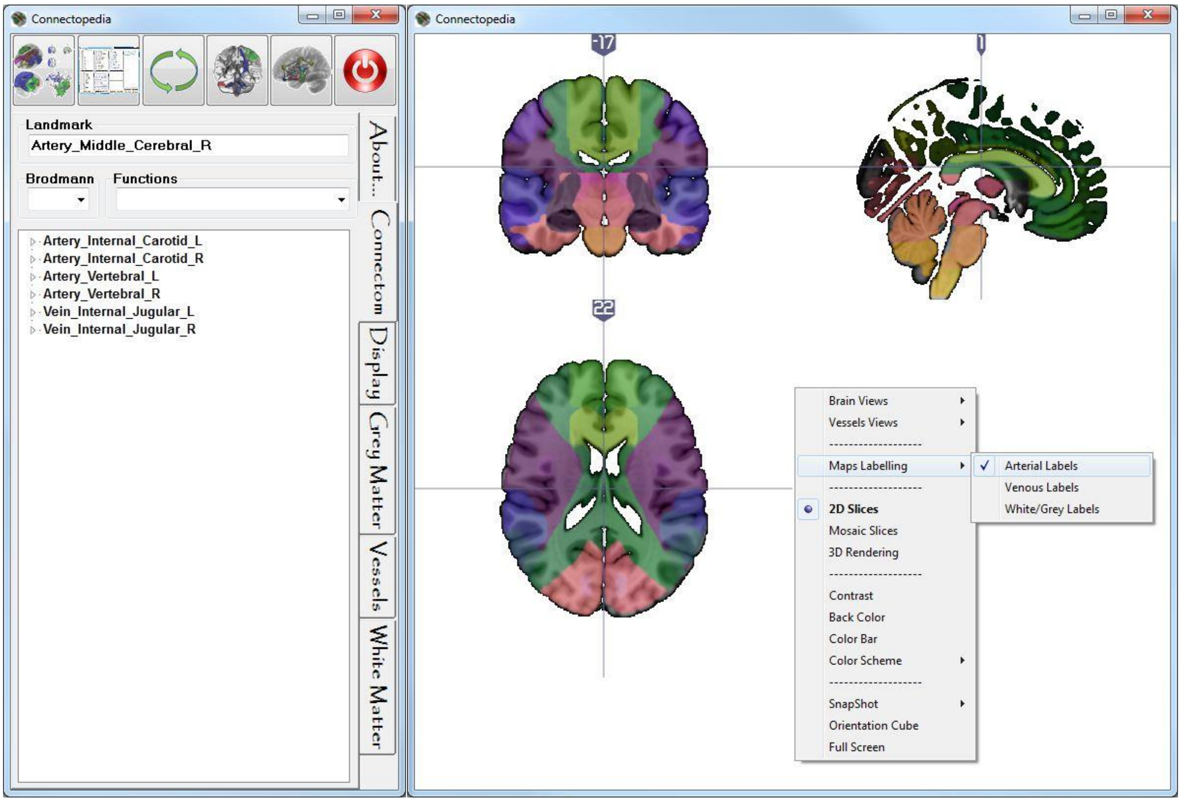
XII. Eighth exercise: Labeling Anatomy, Arteries and Veins

The 3D Renderer window has a ‘Map Labelling’ menu with arterial, venous and grey/white matter structures maps which can be explored using the ‘2D Slices’ menu.

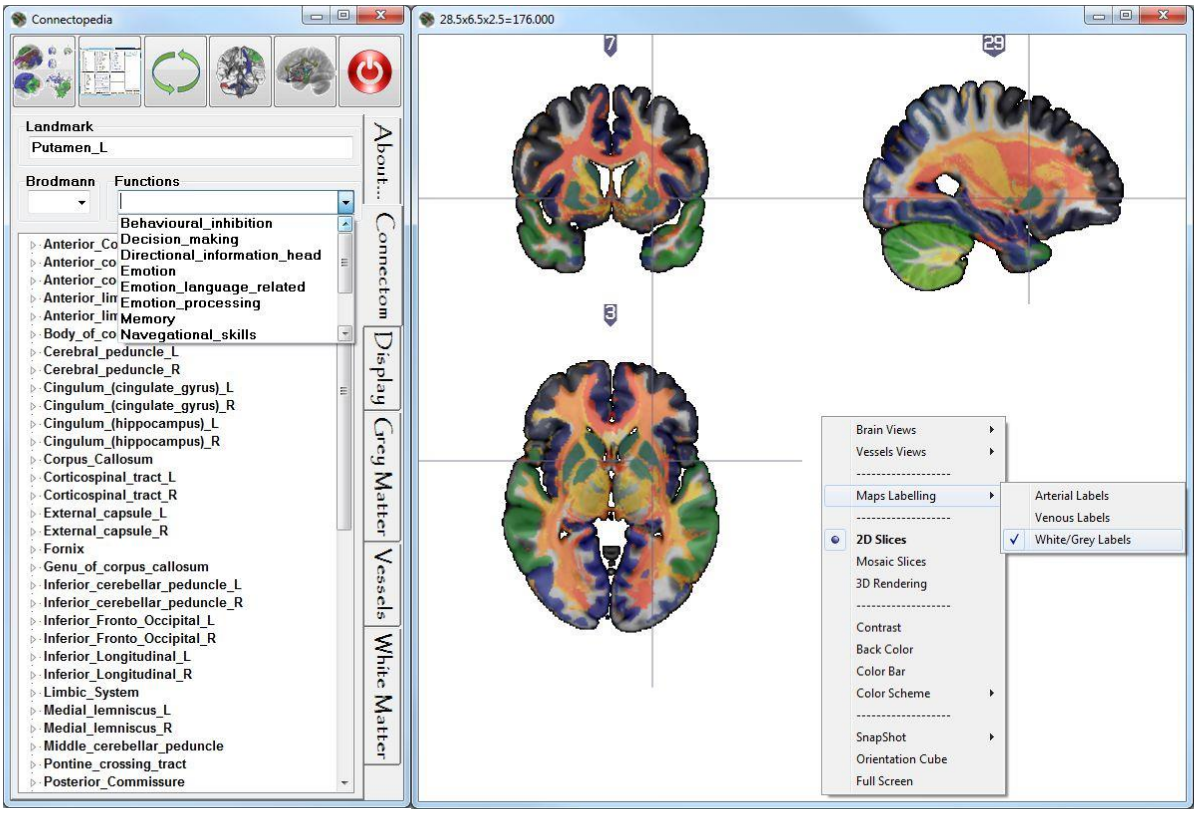
First, LC on the ‘Arterial Labels’ sub-menu of the ‘Maps Labelling’ menu item, then LC on ‘2D Slices’ and display the ‘Connectom Tab’ in the ‘Selector’ window.

Then LC on a MPR reconstructed area in the 2D window ; the ‘Landmark’ label in the ‘Connectom’ tab will display the name of the pointed out structure.





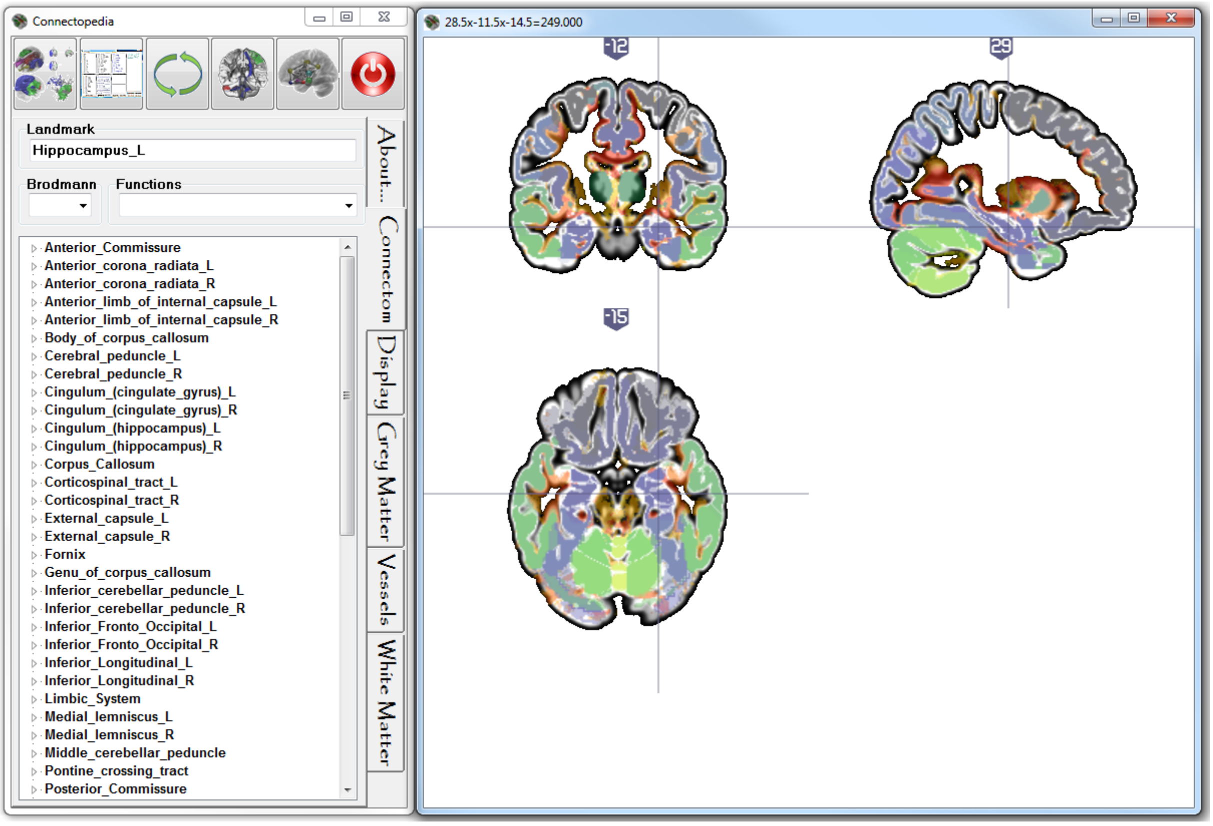
When 'White/Grey Labels' is selected, the structure name is displayed as well as all the Brodmann areas and the Brain Functions where the pointed out structure is involved.



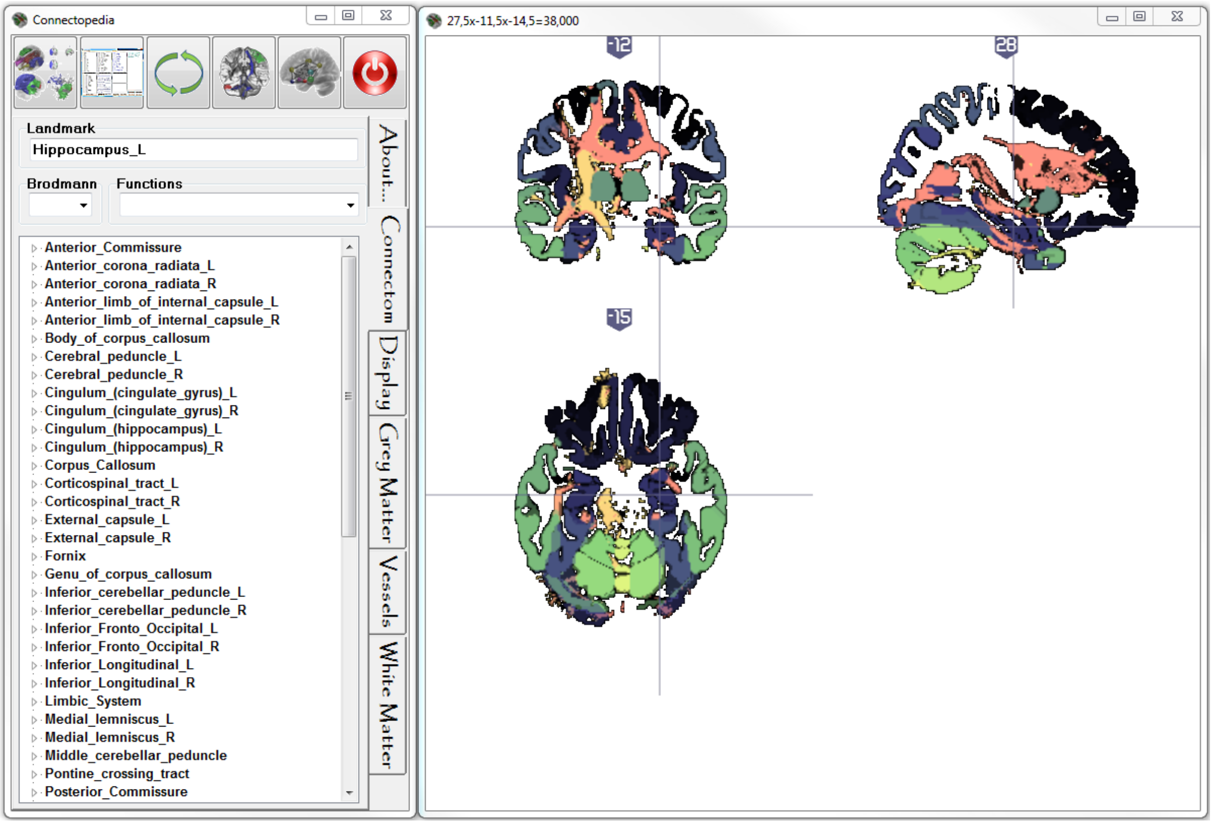
XIII. Ninth exercise: Extracting Connectoms / Anatomy Pathways

The 2D Slices Menu using the ‘White/Grey Labels’ map template has a feature that enables the rendering of Anatomy or Connectoms pathways from a starting point Grey Matter area. By LC + hitting a special key on a grey matter area, all the structures that are connected to this area are displayed in an anatomic shape (key: ‘CTRL’) or in a connectomic shape (keys ‘CTRL’ + ‘Left Shift’ together).

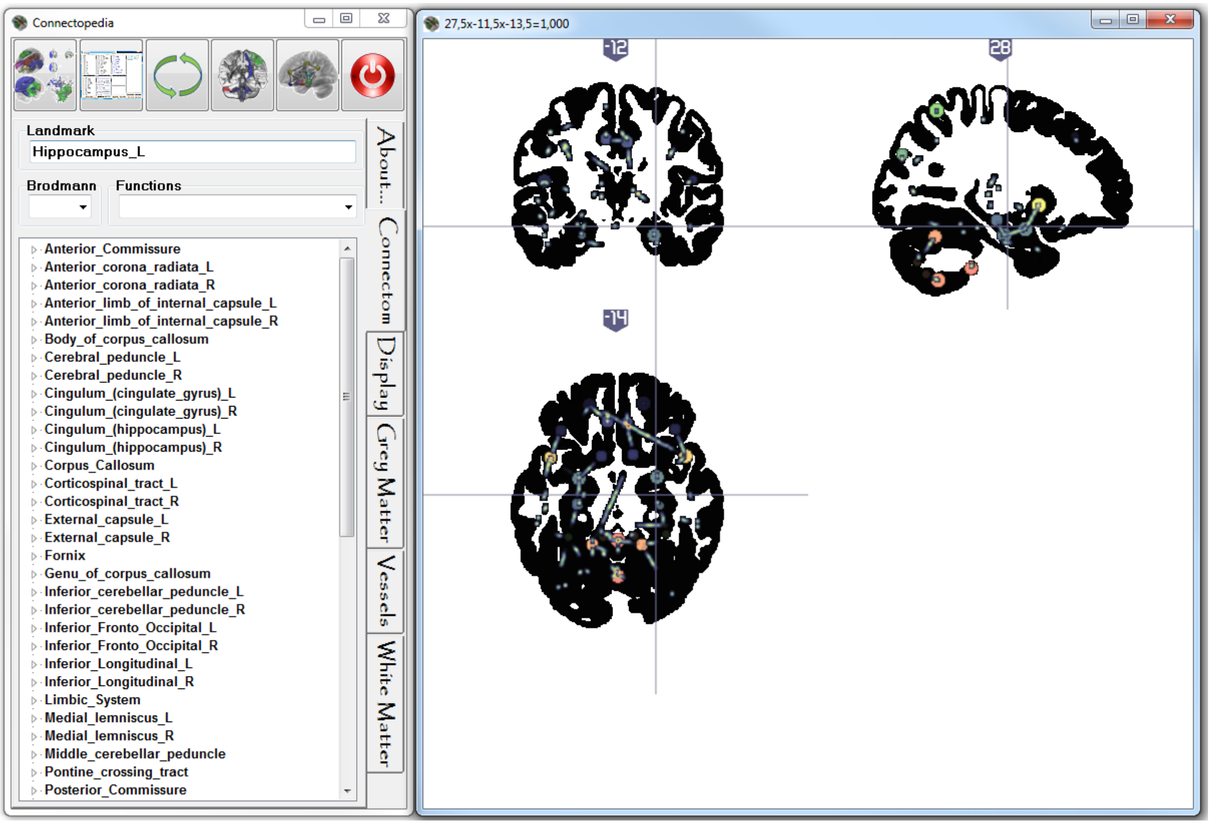
First select the ‘Brain Ghost’ template, then LC on ‘2D Slices’ then ‘White/Grey Labels’, and LC on the Left Hippocampus (Label displayed in the ‘Connectom’ Tab:



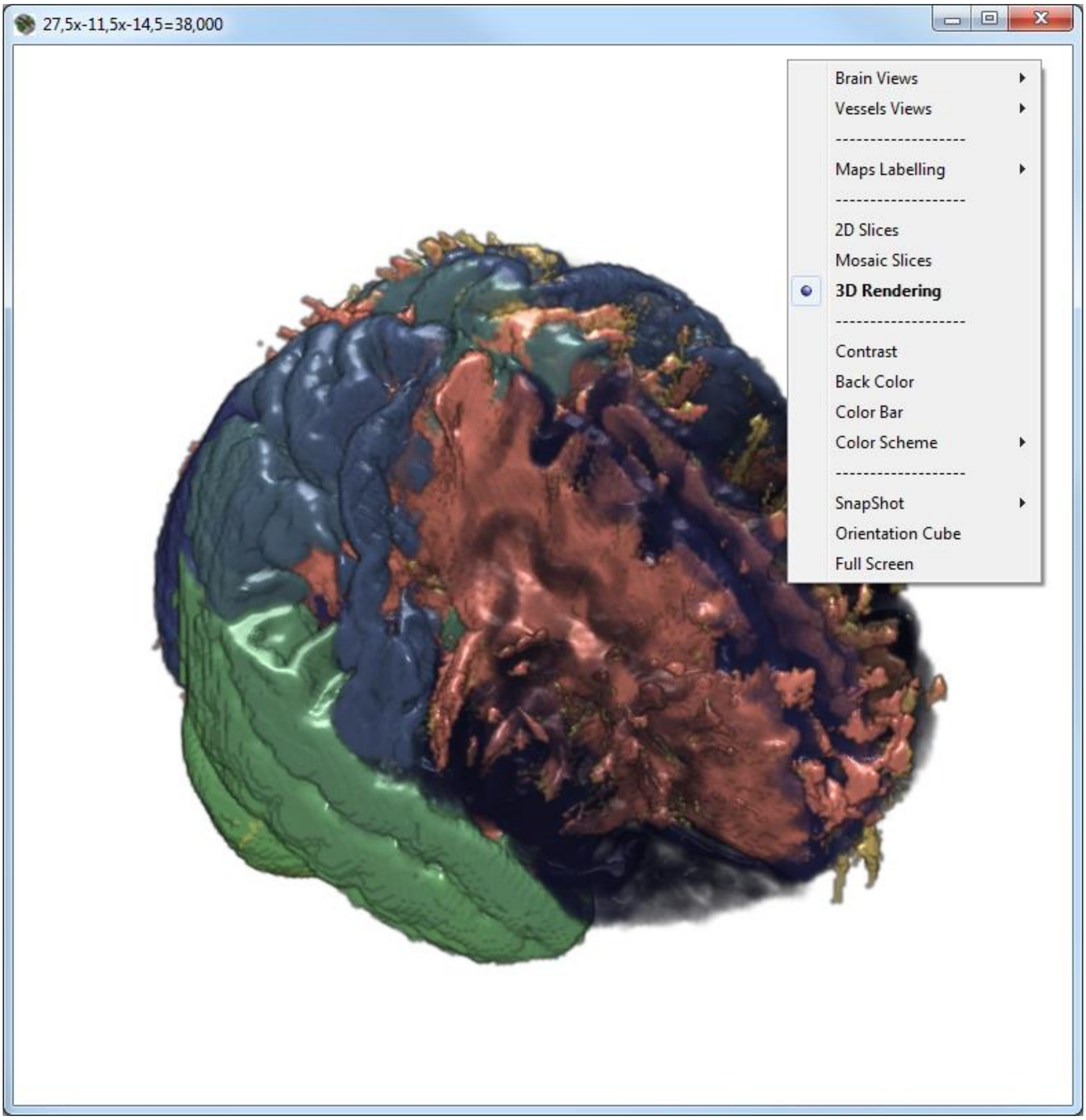
Then combine LC + ‘CTRL’ key on the same Grey Matter Structure to see the Anatomy Rendering of the connexions in 2D:



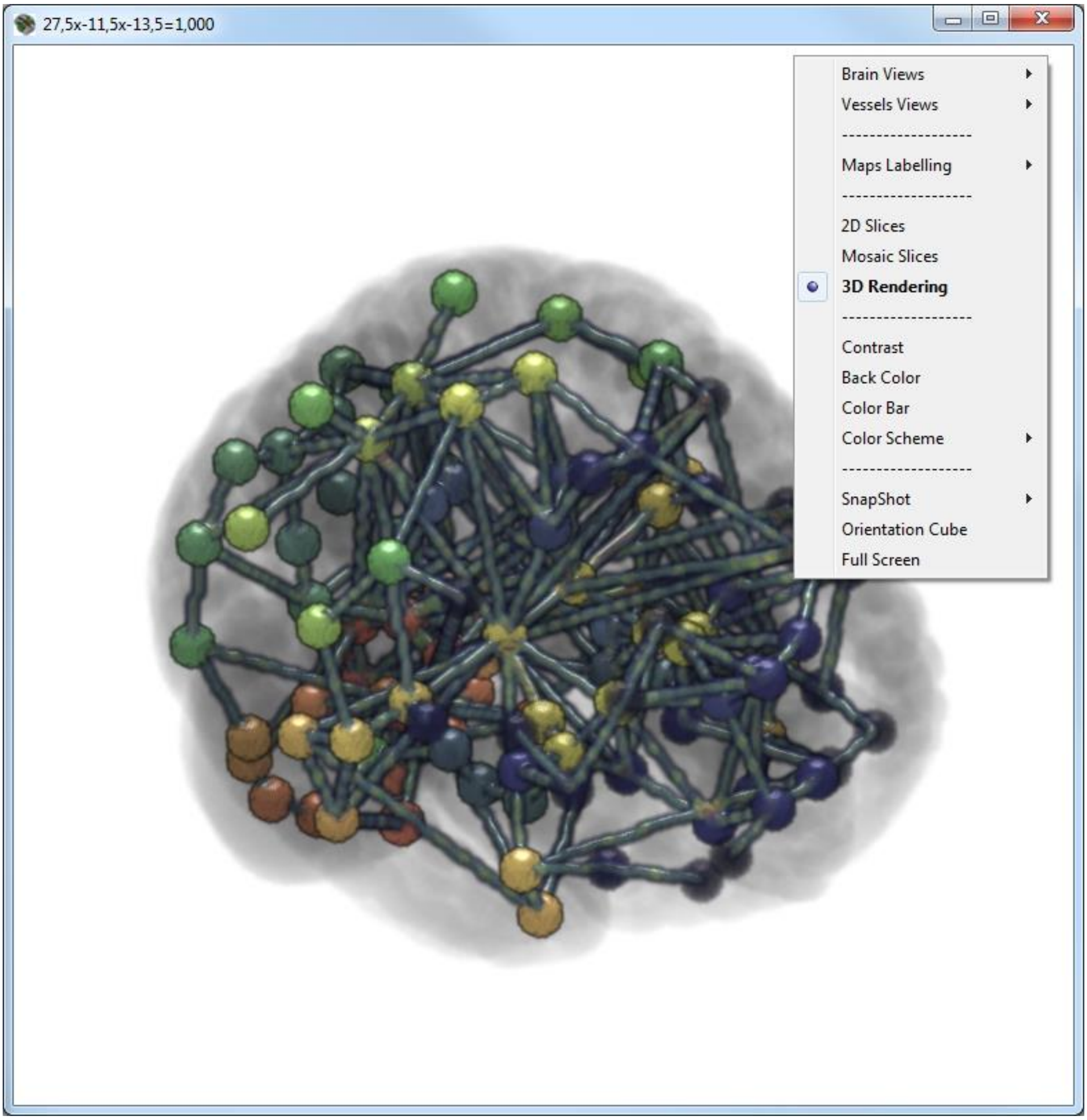
Or LC + ‘CTRL’ + ‘Left Shift’ to see the Connectoms rendering of the connections:



By LC on ‘3D Rendering’ these reconstructions can be viewed in 3D mode, either for the Anatomy Rendering of the connections:



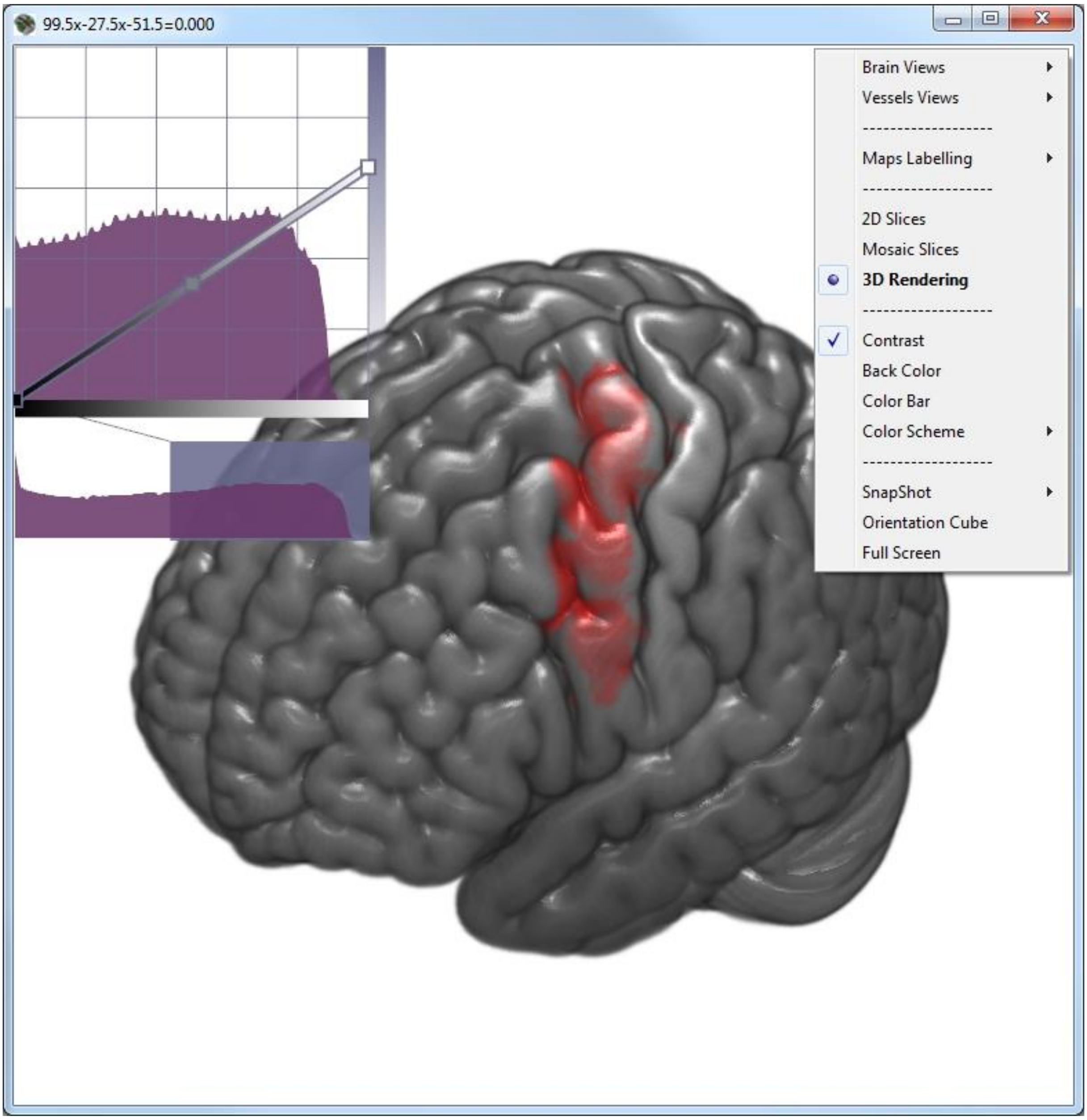
Or for the Connectoms Rendering of the connections :



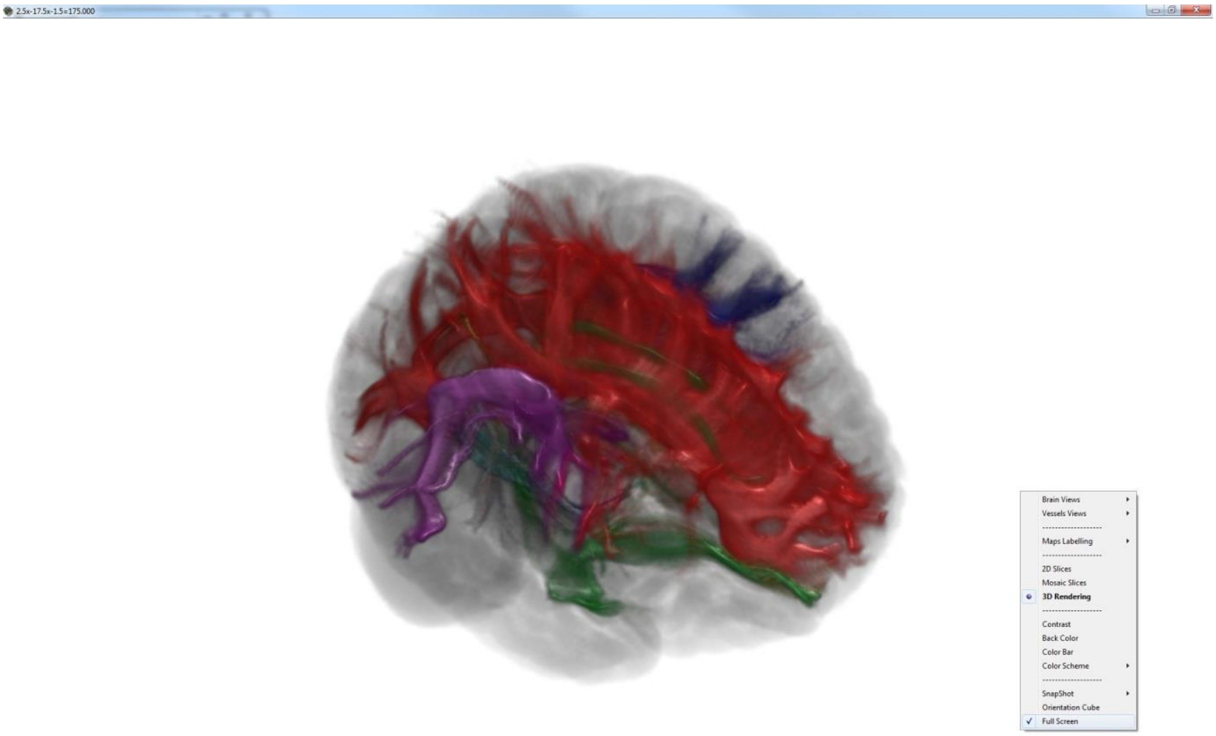
XIV. Other functions :

By LC on the 3D rendering area, user can:

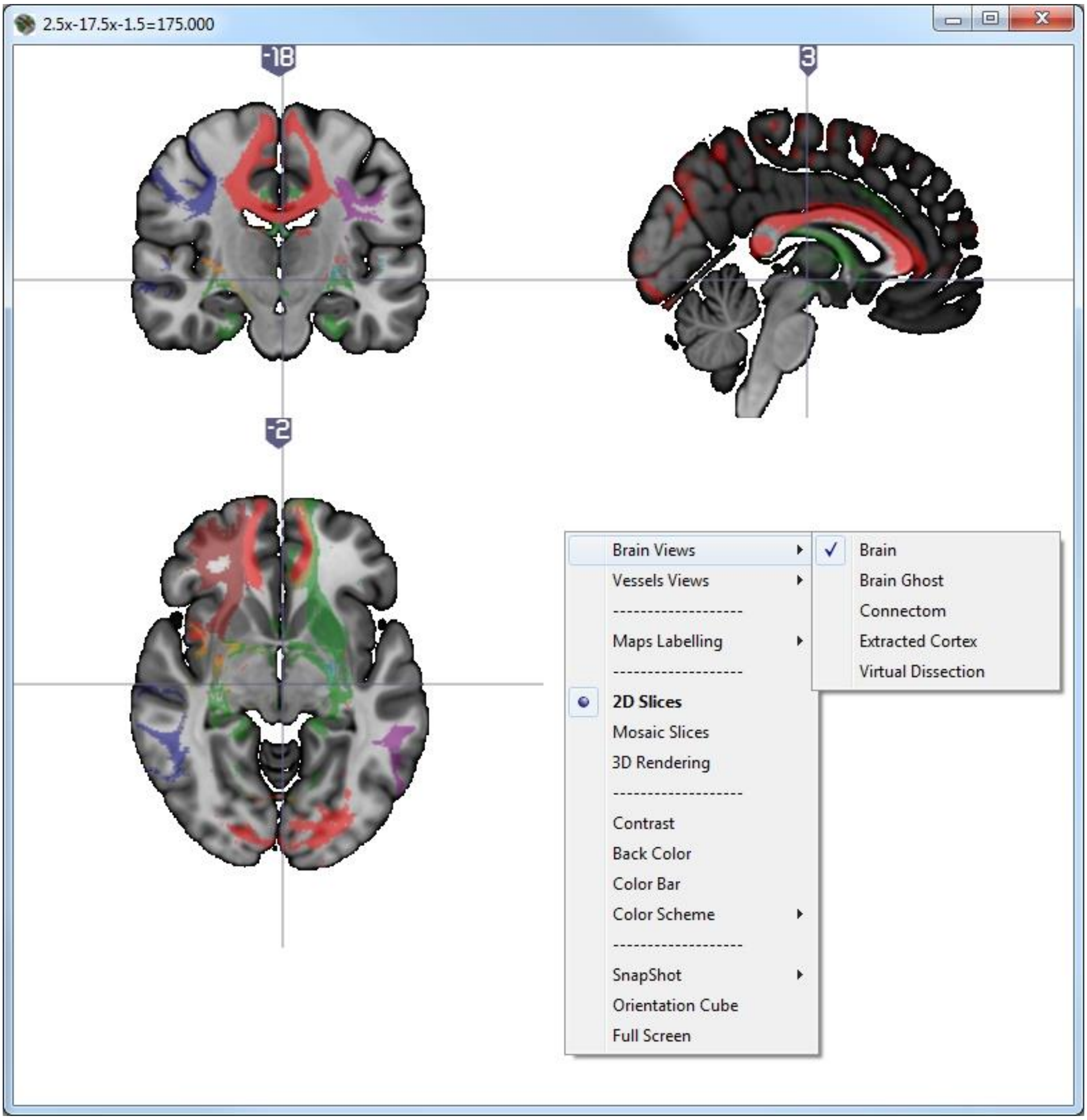
- Set Contrast (by LC on it)
- Set Back Color (here white)
- Set Color Bar visible
- Orientation Cube visible
- Take a snapshot of the 3D Rendering area



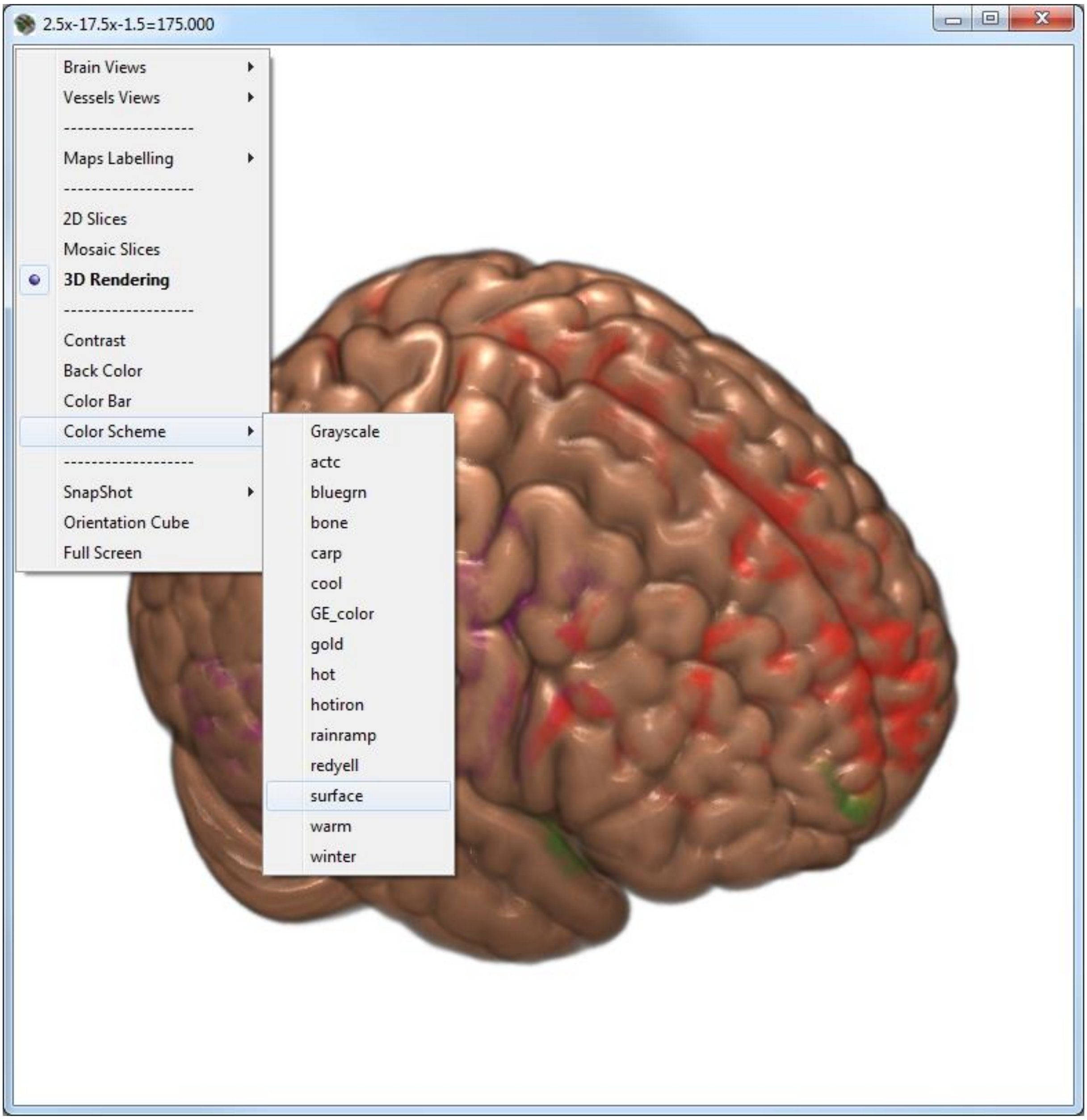
User can view 3D Rendering area in « Full Screen »:



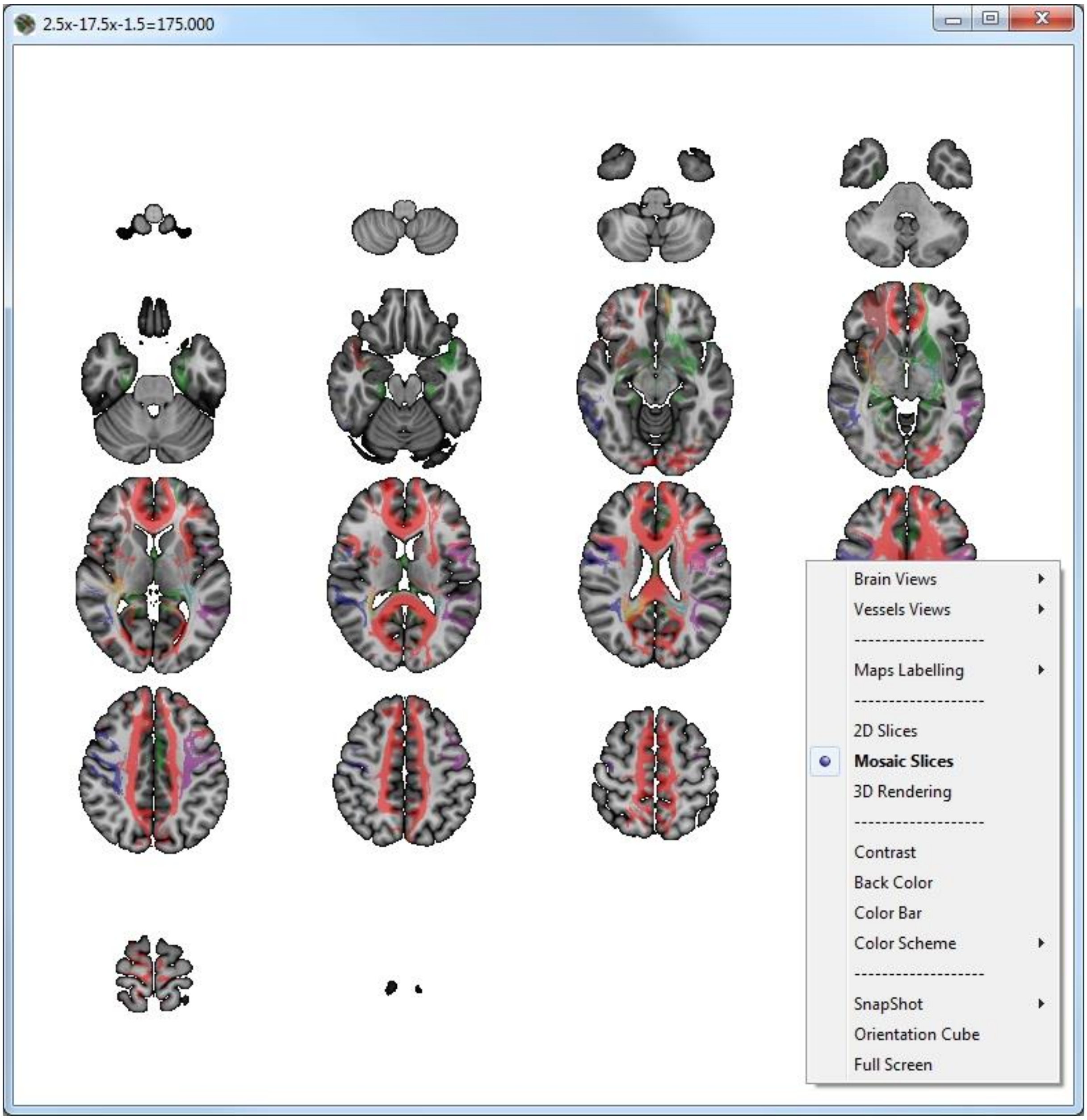
User can view in 2D MPR slices the selected items (WM, GM, and Vasculature):

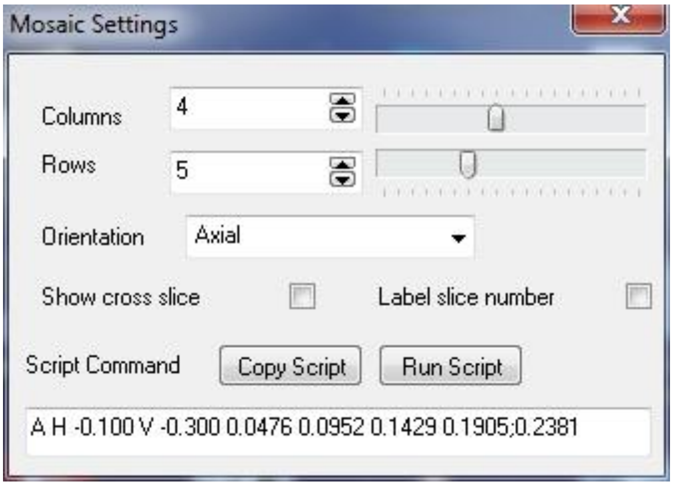


User can set the 3D Rendering color reconstruction set by LC on « Color Scheme »:



User can view mosaic slices of the selected Bundles / Areas / Vessels by LC on « Mosaic Slices »:





User can select axial, sagittal, coronal reconstructions, and the number / pattern of the displayed slices.

XV. Troubleshooting's

User might have some problems in installing or running Connectopedia. Here are some clues.

XV.I Connectopedia Windows Version:

XV.I.I Installation Shortcut

After install, the link created in the "Start Program" menu of Windows might be erroneous.
Explore the files using "Windows Explorer" to see where Connectopedia have been installed (by defaut, "C:\DPTools\bin\Connectopedia"), then locate the "Connectopedia.exe" file. Create a symbolic link to the Desktop by Right-Click on it, then select "Send to…", then "Desktop (Create Shortcut)".
You should be able now to run Connectopedia by Double-Clicking on the link created on the Desktop.

XV.I.II Running issues

When Shortcut are erroneous, running Connectopedia can generate error messages at launch time, and Connectopedia can not be used.
Correcting the Connectopedia Shortcut (see section IX.I.I) generally solves this issue.

XV.II Connectopedia OSX Version:

Main issue with the OSX version is related to Mavericks GateKeeper, because Connectopedia is not signed as "Apple Approved" software yet.

Let's see how to overcome this issue (here "Onyx" software taken for example).

Starting with OS X Mountain Lion, Apple introduced a data execution prevention routine called Gatekeeper, which will block the automatic execution of programs that are either unsigned by an Apple Developer, or not issued through the App Store.

This routine prevents potentially malicious programs from running and harming the system or your data. However, while beneficial, it can also prevent legitimate programs from running, where it issues a warning that the program is not signed and will not allow it to run.

Warnings such as this will show when you attempt to open apps that are not signed, if you have Gatekeeper enabled on your Mac.

If you regularly use third-party programs that give this warning, then one option is to turn off Gatekeeper in the Security System Preferences, but this will prevent the service from helping secure your **Mac**.

To overcome this, there are two options. The first is to right-click the program and use the "Open" contextual menu item to initially launch such programs. The use of this menu suggests you explicitly intend to open the program, instead of perhaps inadvertently launching it with a double-click. When you do this, a warning message will still appear; however, if you choose the option to open the program, then a Gatekeeper exception will be made for it.

This message and button will appear in the Security & Privacy system preferences when you encounter an unsigned program.

If you have installed **OS X Mavericks** on your system, Apple has introduced another means for bypassing Gatekeeper. If you open a program that issues a Gatekeeper warning, then even if you have dismissed the warning, you can go to the Security pane of System Preferences, where you will see a message under the Gatekeeper settings about the recently blocked program. Next to this message is a button titled "Open Anyway," which if clicked, will launch the program and make an exception for it in the Gatekeeper database.

Even though the extra steps to use this new feature make it less convenient than using the contextual menu, it is still a new option for those using OS X Mavericks.

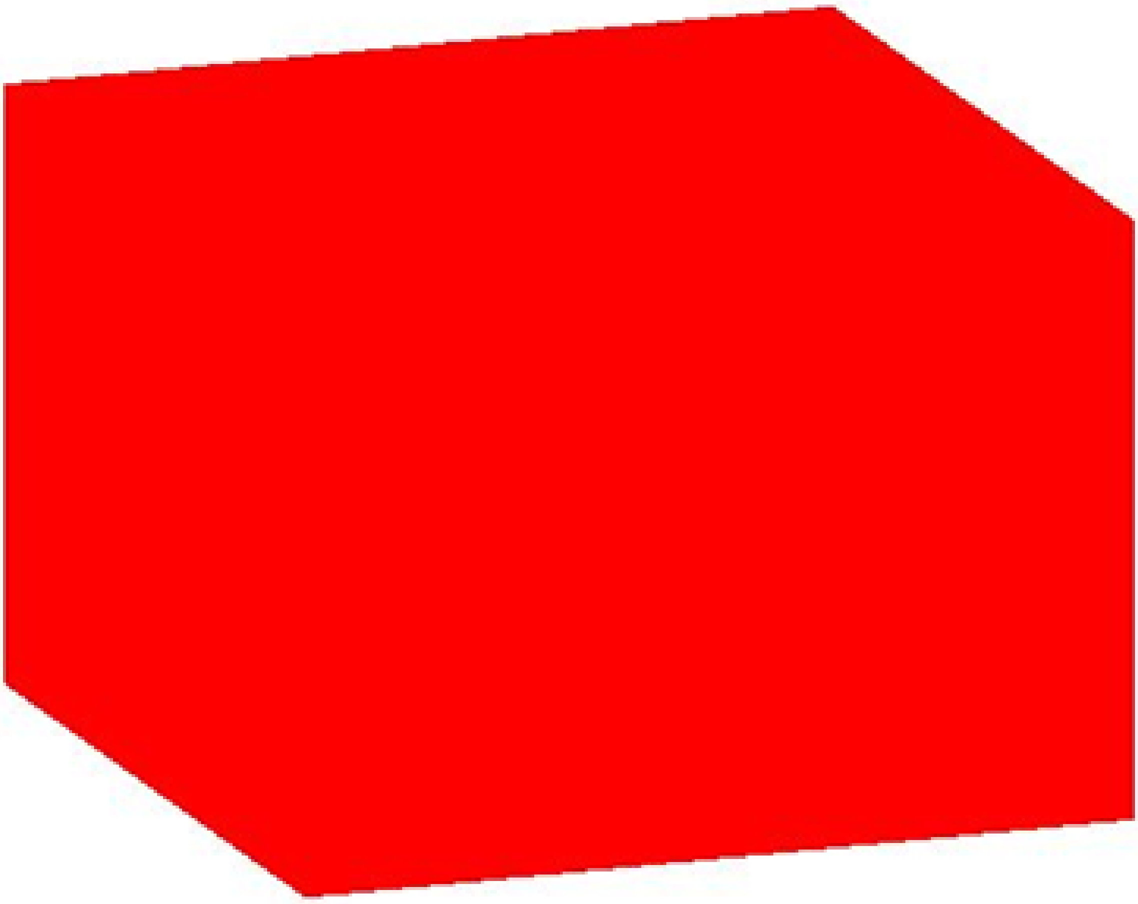
XV.III OpenGl issues with Connectopedia Windows and OSX Version:

Both Windows and OSX versions of Connectopedia can be affected by a strange OpenGL issue due to the way OpenGl Shaders are rendered by the Video Card.

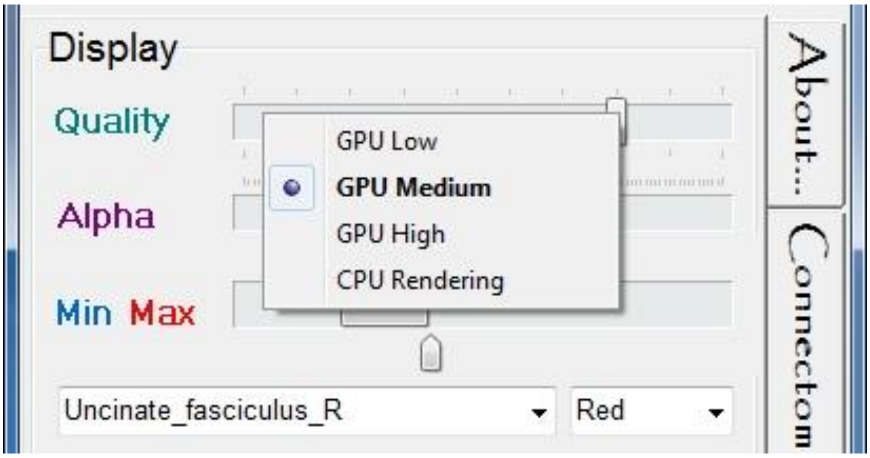
Brain can be rendered “deformed” such as:

When user encounters this issue, closing then running Connectopedia again should correct this.

Other issues might also be encountered when the OpenGl drivers of the Video Card are incompletely implemented, e.g. when using VMWare Fusion on OSX for virtualization of the DPTools or Windows Standalone distribution of Connectopedia:



To overcome this issue, user can select different Rendering Quality, from “GPU Low” to “High Quality”, and “CPU Rendering” by Right-Clicking on “Shader Quality” in the **Display Panel**.



All these issues are not exhaustive. If you have any pitfall or comment, please send an email to: denis.ducreux@fmritools.org

Visit http://www.fmritools.org to see Teaching Files and Videos related to Connectopedia.

Enjoy !