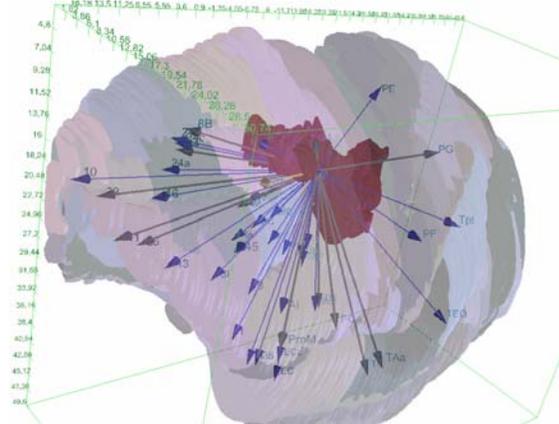# CoCoMac-Paxinos3D Visualization Tool v.2.2.1[©] User Manual

Gleb Bezgin, Andrew T. Reid, Rolf Kötter
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1. System requirements

The software is fully tested on MS Windows XP platform. Several components are compatible with Linux and Macintosh OS. To use the Paxinos3D visualization tool (version 2.2.1), the following must be installed:

- **Java Runtime Environment, JRE** (1.6 or later) – available at
  http://java.sun.com/javase/downloads/index.jsp
- **Java3D API** (1.3 or later) – available at
  http://java.sun.com/products/java-media/3D/download.html

NOTE: if you have updated your JRE to a new version, make sure Java3D is reinstalled after that. This is necessary because reinstallation of JRE removes previously installed APIs, including Java3D.

An internet connection is also required to enable access to the online connectivity database CoCoMac, although viewing of data files is possible offline. It is also possible to display connectivity data from CoCoMac graphically without internet connection, since for these purposes the *.mdb file located in the `data` folder is used.

This version was designed and tested for Java SE 1.6 from Sun Microsystems, which is freely available at the above URL. Small problems may arise as a result of using earlier versions, in particular, with viewing the "About" screen.

2. Software installation

Unzip the archive which contains the software (`CP3D_v2.2.1_080808.zip`) to an appropriate location on your hard disk (e.g., `Program Files` for Windows users). This should result in the creation of a folder called `CP3D_v2.2.1_080808`, and two subfolders: `bin` and `data`. The `bin` folder contains Java archive folders which constitute the executable code for CoCoMac-Paxinos3D tool. The `data` folder contains atlas data files (Paxinos *et al*., 2000), consisting of:

- An Excel file encoding RGB patterns into structure acronyms: `!Paxinos_StructureList+_080123.xls`
- 151 Scalar Vector Graphic (`svg`) files containing digitized atlas data
- the CoCoMac database file (`CoCoMac_online.mdb`) used by the software to display connectivity data graphically

To launch the Paxinos3D tool in Windows XP, run the batch file `CP3D.bat` from the main directory. To run on other platforms, it is necessary to run the main file `uk.ac.ed.paxinos3d.Main` class from the file `paxinos3d.jar`, including all `jar` files in the classpath. See the contents of the `CP3D.bat` file for an example.

3. Features

The software interface contains four main features: **buttons**, the **structures tree**, the **Java3D panel**, and the **information bar**, as is illustrated below.
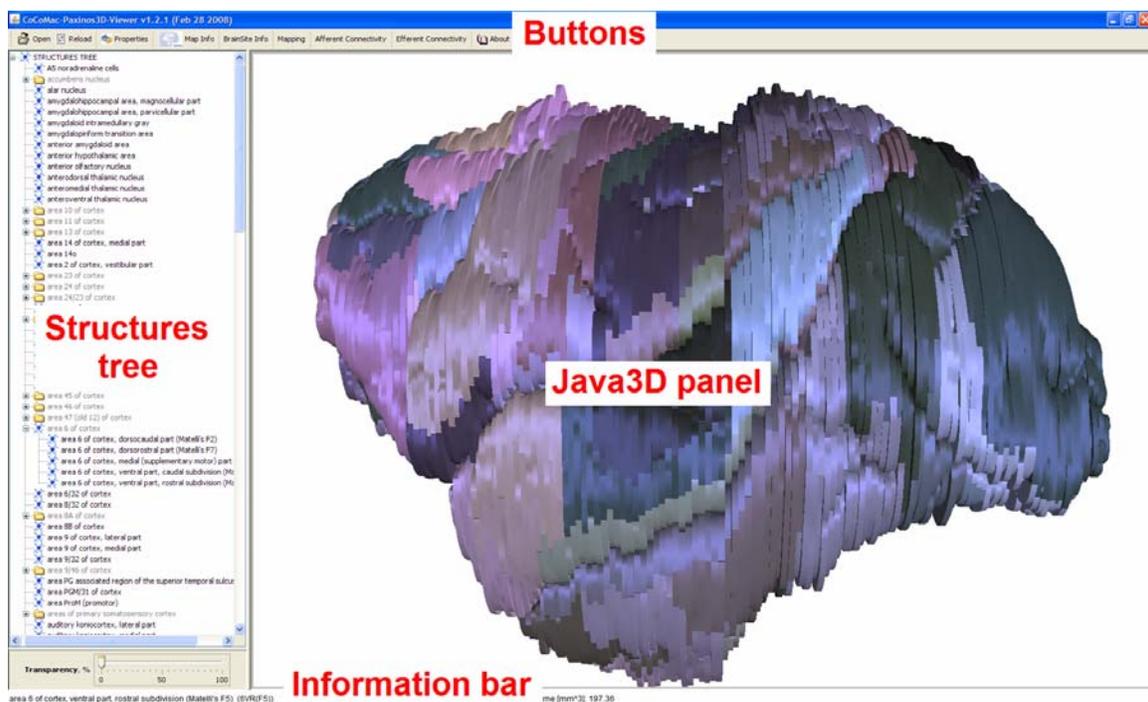
Paxinos3D interface features

2

Just below the structures tree, there is a transparency slider allowing the user to adjust transparency parameters for clearer data display.
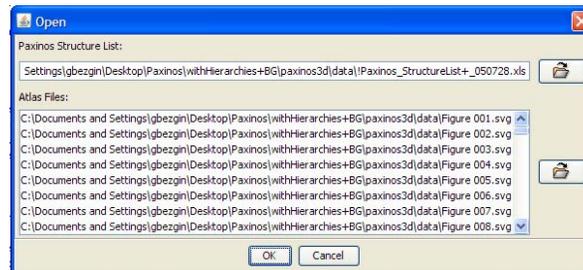
The following sections describe the features of this interface.

3.1 Buttons

Open file

This button allows the user to load the atlas data. Clicking the button will bring up the following dialog:

Use this dialog to load data from the data directory. Both the structure file (`!Paxinos_StructureList+_080123.xls`), and some or all of the individual sections (`svg` files) can be selected. Note that the `svg` files, numbered 1 through 151, correspond to individual sections in the Paxinos *et al*. atlas.

Reload data

Use this button to reload the data from file. All the meta-info retrieved from the database (e.g., graphical representation of the connectivity data) will be removed by clicking this button.
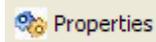
Set properties for the viewer

This button displays an options dialog which allows the user to specify settings.

- **Re-orient atlas on feature selection**. When selected, will alter the camera position in the Java3D display window to best display the structure selected from the structures list (see **Structures List**, below).
- **Show stereotaxic grid**. When selected, displays the stereotaxic grid relative to bregma, as represented in the original paper atlas.
- **Set background colour**. A combo box, where the items represent three different options for background colour: white, grey or black.

Map Info   **Various CoCoMac buttons**

The buttons labelled **Map Info**, **BrainSite Info**, **Mapping**, **Afferent Connectivity**, and **Efferent Connectivity**. They operate in a following way. Each of the buttons **Map Info**, **BrainSite Info**, **Mapping**, sends a query to the CoCoMac database (http://cocomac.org) in order to display the relevant information about the selected structure. The information is displayed in the system default web browser, using the online CoCoMac interface. It includes the mapping scheme in which the selected structure is represented and the connectivity patterns for this structure, as exist in the literature and are collated in the CoCoMac database. By contrast, **Afferent Connectivity**, and **Efferent Connectivity** buttons provide additional capabilities of displaying the connectivity data retrieved from the CoCoMac database as graphics. Each of these two buttons brings a dialog window with checkboxes enabling the user to choose whether the connectivity information should be displayed in the same way as it is done by the previous three buttons, shown graphically, or both.

About   **About CoCoMac-Paxinos3D viewer v2.2.1**

Displays a dialog containing the version number of the current product, a license agreement, a list of credits, and buttons linking to both http://cocomac.org and this document.

3.2 Structures Tree

This tree, located at the left of the screen, contains all currently loaded structures. Any structure may be selected by clicking on its text. A selected structure will appear in the Java3D panel coloured red and opaque (regardless of the transparency setting). The structure name will also appear highlighted in the list, as illustrated below. Some structures include substructures – those are designated on the tree by a folder icon. Clicking on such structure will highlight all the substructures which serve as children for this superstructure. Clicking on "+" sign will browse all those children, which can be selected separately from their parent structure. Those children who have the same name as their parent structure are indicated by "*unassigned subvolume*" mark, which means that they do not have an appropriate representation in CoCoMac, due to an inconsistency with its ontology, which implies strictly hierarchical representation of structures. This concept, along with the current software, will be described in detail in forthcoming publication (Bezgin *et al*., submitted).
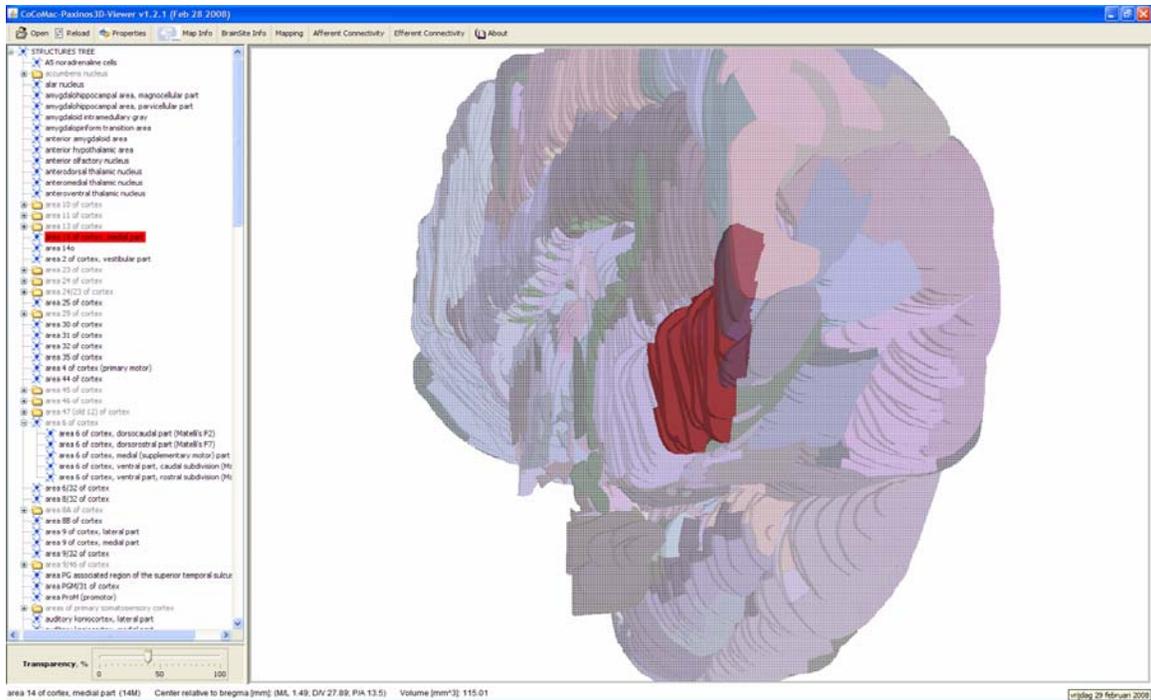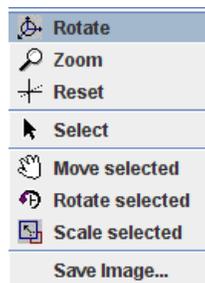
Selecting a structure from the `Structures Tree`

Right-clicking on a structure in the list also gives the user an option to show or hide the particular structure. A structure which is hidden will not be rendered in the Java3D window. This is useful for removing large overlying structures, in particular when transparency equals zero.

The user can also choose to hide all structures and show only a few select ones. To do this, right-click on the root node at the top of the tree, labelled "Morphology", and select **hide**. The Java3D panel will appear empty. Now it is possible to display only individual structures, by right-clicking their names on the tree and selecting **show**.

3.3 Java3D Panel

The Java3D panel is where the rendering of atlas structures occurs. Users can interact with the 3D model in a number of ways. The interaction mode can be specified by right-clicking on the panel, which brings up the following menu.

The modes are described below.

- **Select mode.** This is the default mode, which allows users to click on particular structures and select them. This is equivalent to clicking a structure name in the structures list, except that no change in camera position occurs. It is useful for identifying structures graphically.
- **Rotate.** This mode allows the user to rotate the camera around the model by dragging the mouse, and thus examine it from various orientations.
- **Zoom.** This allows the camera distance to be altered, which occurs by dragging the mouse in a particular direction. It is useful for adjusting the scope of the viewing panel.
- **Reset.** This resets the camera to its default zoom and orientation, which is a lateral view displaying the entire model.
- **Move/Rotate/Scale selected.** These options enable the user to manipulate single structures apart from the entire model. This allows a structure to be removed from the model, and inspected on its own. While there is currently no intuitive means of returning the structure to its original size and orientation, this can be done by hiding the structure using the structures list and then showing it again (see **Structures Tree**, above).
- **Save image.** This allows the current model view to be saved as an image file in `png` format. Note: in order to save the file properly, make sure that the extension `png` is specified: `myfile.png`.
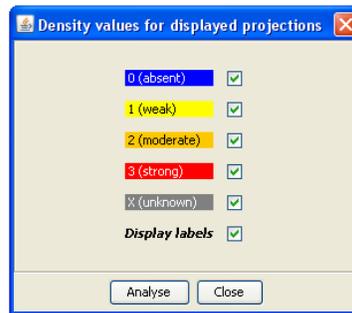
3.4 Information Bar

The information bar located at the bottom of the screen provides information about selected structures and (when displayed) connectivity data. This information includes the structure name and acronym, its center of mass expressed in stereotaxic coordinates relative to bregma (mm), and its estimated volume (mm^3). It is shown below. When connectivity data are displayed graphically, the information bar provides the hash table in a format {target (source) site *X*=density of connection to (from) target (source) site *X*} (the "=" sign here does not mean "equals", it indicates a mapping between hash table components).

| area 3a of cortex (somatosensory) (3a) | CENTRE COORDINATES RELATIVE TO BREGMA [mm]: (M/L 14.14; D/V 15.64; P/A -10.35) | VOLUME ESTIMATE [mm^3]: 231.11 |

3.5. CoCoMac interface features

As shown above, the buttons **Afferent Connectivity** and **Efferent Connectivity** provide two options each for displaying the connectivity data from the CoCoMac database, related to the brain structures currently loaded into the atlas: to display these data either as text in a default system browser, or graphically. If the latter option is chosen and confirmed by the **OK** button, the user will be asked to choose one of three types of queries, namely:

1. Query based on *primary projections*, i.e. those connectivity statements extracted from the literature, based on explicitly specified acronyms from the Paxinos *et al*. atlas.
2. *Integrated primary projections* are primary projections with redundant and contradictory data being filtered out.
3. Connectivity data retrieved from the database by obtaining so-called *mapping paths*, i.e. sequences of mapping statements derived from the literature. They allow, in particular, to map the data from the Paxinos *et al*. atlas, to which no connectivity data are attributed, to other database resources containing those connectivity data. Therefore this type of query provides greater reliability than the first two. Note that it might take up to several minutes to process this query, depending on the amount of mapping data available in the database for a particular brain region.

When this choice is made, it will be indicated in the information bar that the query is being processed. When the data are displayed, and the information bar displays query results, the following dialog will also appear:

For each connection datum entered into the CoCoMac, the density (connection strength) information is specified. The dialog allows making the connections of particular density invisible, if they are of no interest for the user. Usually, this is the case for absent (zero-density, colour coded blue) connections, which are not essential for most users to be seen. Note that if the atlas is reloaded, these graphical data are no longer displayed.

Clicking the **Analyse** button brings a table containing all the optimal connection paths for areas being queried, based on Dijkstra's single source shortest path algorithm, like shown below:

Source	Target	Path	Euclidean distance, [mm]	Cost based on minimal density along the path
	temporal parietooccipital associated area in sts	[8A->TPO]	57.86	0
area 9/46 of cortex	area 29a-c of cortex	[9/46->29a-c]	69.35	0.33
	area 29d of cortex	[9/46->29d]	70.07	0.33
	area 31 of cortex	[9/46->31]	69.44	0.33
	area 8B of cortex	[9/46->8B]	22.05	0.33
	area 23 of cortex	[9/46->23]	75.08	0.33
	area 46 of cortex	[9/46->46]	14.73	0.33
parietal area PG	area 23a of cortex	[PG->V3A->8A->23a]	178.6	0.67
	area 23b of cortex	[PG->V3A->8A->23b]	176.8	0.67
	area 23c of cortex	[PG->23c]	46.78	0.33
	area 24a of cortex	[PG->V3A->8A->24a]	157.56	0.67
	area 31 of cortex	[PG->31]	42.13	0.33
	area 32 of cortex	[PG->PGa->32]	137.7	0.33
	area 8B of cortex	[PG->8B]	72.58	0.33
	basal nucleus (Meynert)	[PG->V3A->8A->B]	172.97	0.33
	centrolateral thalamic nucleus	[PG->V3A->8A->CL]	173.37	0.33
	central medial thalamic nucleus	[PG->V3A->8A->CM]	176.36	0.33
	caudate nucleus	[PG->V3A->V2->Cd]	120.55	0.33
	fundus of superior temporal sulcus	[PG->FST]	43.81	0.33
	intraparietal sulcus associated area in the superior temporal sulcus	[PG->IPa]	71.8	0.33
	parietal area PEa	[PG->PEa]	26.16	0.33
	area PG associated region of the superior temporal sulcus	[PG->PGa]	59.82	0.33
	parieto-occipital area	[PG->PO]	47.74	0.33
	parietooccipital associated area in the intraparietal sulcus	[PG->POa]	21.87	0
	reticular thalamic nucleus	[PG->V3A->V2->R]	104.26	0.33
	temporal area TAa	[PG->TAa]	62.98	0.33

The first two columns of this table display full names of source and target, respectively; the third column provides the optimal path between source and target (displayed in an abbreviated form), the corresponding Euclidean distance is shown in the fourth column. The fifth column introduces a measure associated with minimal projection strength (density) along the specified path; the values are distributed in a range [0, 1] and are higher for lower density projections and vice versa. Zero cost indicates that all the projections in the path are of the highest density.

4. Contact

For feedback please send a message to g.bezgin@science.ru.nl.

5. References

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