How to use raxml-GUI to access CIPRES

First register as a CIPRES REST user. Go to http://www.phylo.org/restusers

Click Register, and complete the form.

Next, download the raxml-GUI package from CIPRES and unzip in a convenient location. It is convenient to choose a location where the folder does not have a blank space in the name.

In the folder where you place the application code, navigate to the scripts/scripts folder

Initiate the program by clicking raxmlGUI.py (you must have Python installed).

The interface will open, as well as a command line window

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Go to Utilities/Configure CIPRES ID. Enter your credentials, then save and close. This will create a file called raxmlgui_cipres.conf in your home directory, which will contain your credentials.

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Now configure your job run as you would normally. If you are new to raxmIGUI, consult the manual.

https://sourceforge.net/projects/raxmlgui/files/raxmlGUI1.5b1 manual.pdf/download

A test data set (combi.phy) can be found at File/raxmlgui/combi.phy

Once you are ready to submit, make sure the Resource field says CIPRES-RAxML in background, as in the images above.

Click Run. A dialogue will appear that allows you to enter a name for your job. You can choose to receive an email when the job completes. Then click "Submit"

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The application will acknowledge your submission:



Once the job is completed, you can view your results, download, or delete your results. Click to Utilities/Check CIPRES Jobs. This will spawn a dialogue box, and you can choose where you wish your results to appear.

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Please contact us with any questions.