PAMLX 1.2: A Brief User Guide

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PAMLX is a graphical user interface for the PAML program package (Yang 1997; 2007). It allows the user to create, open, edit, save and print control files for the paml programs, as well as launching jobs. The current version works with PAML 4.7 (and hopefully later versions), and incorporates the following PAML programs: BASEML, CODEML, MCMCTREE, PAMP, YN00, and EVOLVER (the options of simulating nucleotide, amino acid and codon sequence alignments). PAMLX is written using the Qt library and communicates with PAML programs through files. Compiled executables for Windows, Linux, and Mac OSX are provided.

To cite the program,
Xu B, Yang Z. 2013. PAMLX: a graphical user interface for PAML. Mol Biol Evol. 30:2723-2724.

How to install and run PAMLX

(1) Download and unpack the most up-to-date version of PAML. If you use Mac OSX or linux, you may have to recompile the PAML programs yourself. Go to the src/ folder, modify the Makefile file before typing make. Then move the compiled executables from src/ into bin/.
(2) Copy (and unpack if necessary) pamlX. Start pamlX. Go to Tools-Configuration (pamlX-Preferences on the Mac) to set the folder name for the paml files. Suppose you have the paml programs unpacked into the folder C:\Users\me\Programs\paml4.7. Then you specify this folder name C:\Users\me\Programs\paml4.7 inside pamlX, and then pamlX expects to find the executables in C:\Users\me\Programs\paml4.7\bin\, the documentation in C:\Users\me\Programs\paml4.7\doc\, and the examples in C:\Users\me\Programs\paml4.7\examples.

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References

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