

MrModeltest2

C program for selecting DNA substitution models using PAUP*.

MrModeltest 2.3 README, May 22 2008 (minor updates 2018)

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Description

For performing hierarchical likelihood ratio tests and calculating approximate AIC and/or very approximate AICc values of the nucleotide substitution models currently implemented in both PAUP*4 and MrBayes v3. Version 2.3 also does some model averaging of the parameter estimates obtained by PAUP.

MrModeltest 2.3 is a modified version of David Posada's Modeltest 3.6 (see Modeltest homepage). "Modified version" means that it was rewritten to compare 24 instead of 56 models of nucleotide substitution (basically a Modeltest version 1.0). On the other hand, all of the 24 models can be implemented in MrBayes version 3. Furthermore, MrModeltest uses (by default) four different hierarchies for the likelihood ratio tests. The hierarchies are described in detail in *Posada, D. and K. A. Crandall. 2001. Selecting the best-fit model of nucleotide substitution. Systematic Biology, 50:580-601 (Fig. 4a-d)*. The hierarchies implemented in MrModeltest are also depicted in the files hLRT1.jpg, hLRT2.jpg, hLRT3.jpg, and hLRT4.jpg.

Suggested reference

Nylander, J. A. A. 2004. MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University.

Quick instructions

Installing the pre-build program on Windows or MacOSX

1. Find the appropriate binary file for your operating system (in the 'bin' folder) and use directly (see Running MrModeltest2 below) or, preferably, copy it to a location included in your PATH.

Note: The windows version is compiled and tested on Win XP.

Installing from source (on UNIX/MacOSX)

1. cd into the distribution src directory:
`cd MrModeltest2/src`
2. Compile by typing (try `make -f Makefile.MACOSX` if `make` fails on the Mac):
`make`
3. The binary file `mrmodeltest2` can then be run in the same directory or be moved somewhere on your system where you have access to it (i.e., in your PATH).

Before using MrModeltest2

1. Execute your data file in PAUP*:

```
exe datafile.nex;
```

2. Execute the file `MrModelblock` in PAUP*. A file called `mrmodel.scores` will appear in the current directory:

```
exe MrModelblock;
```

Important note to users of PAUP alpha (test) versions: The default output format have changed in the test version of PAUP*. If you want to use `MrModeltest2.3` on the `model.scores` generated by a PAUP test version (> v.4.0a154), you need to execute the file `MrModelblock.newpaup` instead:

```
exe MrModelblock.newpaup;
```

3. This file (`mrmodel.scores`) is the input for `mrmodeltest2`.

Running MrModeltest2

`MrModeltest2` does not have a graphical user interface. Therefore, UNIX/Win/MacOSX users need to open a terminal ("Terminal", "Console", "DOS window") and type:

```
mrmodeltest2 < mrmodel.scores > out
```

The results are written in the 'out' file.

Note: If `mrmodeltest2` is not in your PATH, you can try to run the program by first `cd` in to the same directory where the binary and the `mrmodel.scores` are located and then type:

```
./mrmodeltest2 < mrmodel.scores > out
```

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