Datamonkey

A Collection of State of the Art Statistical Models and Bioinformatics Tools

What evolutionary process would you like to detect?

Selection | **Recombination**

Would you like to detect selection across branches, individual sites, or an entire gene?

Branches | Sites | **Gene**

Do you want to detect episodic or pervasive selection?

Episodic | Pervasive

Is your dataset small (less than this many sequences/sizes) or large?

Small | **Large**

Do you want to contrast selection pressures between two or more groups of branches?

No | Yes

Datamonkey recommends that you use...

Contrast-FEL

Contrast-FEL is a simple extension of the popular fixed effects likelihood method. It is suitable for identifying individual alignment sites where any among the K≥2 sets of branches in a phylogenetic tree have detectably different ω ratios, indicative of different selective regimes. This method is particularly useful when comparing selective pressures among sets of branches in a phylogenetic tree and identifying specific sites within genes that may be evolving differently.

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