Datamonkey

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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 use a Bayesian (recommended) or counting based approach?

Bayesian	Counting

Datamonkey recommends that you use...

FUBAR

FUBAR (**F**ast, **U**nconstrained **B**ayesian **A**pp**R**oximation) uses a Bayesian approach to infer nonsynoymous (dN) and synonymous (dS) substitution rates on a per-site basis for a given coding alignment and corresponding phylogeny. This method assumes that the selection pressure for each site is constant along the entire phylogeny.

For more information, please see the summary on hyphy.org or see Murrell, B et al. "FUBAR: A Fast, Unconstrained Bayesian AppRoximation for inferring selection." Mol. Biol. Evol. 30, 1196–1205 (2013).