Datamonkey

Methods and Tools ▾   Job Queue   Usage statistics   API ▾   Citations   Help   ⬀ Classic

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...

FEL

─────

FEL (**F**ixed **E**ffects**L**ikelihood) uses a maximum-likelihood (ML) 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 Kosakovsky Pond, SL and Frost, SDW. "Not So Different After All: A Comparison of Methods for Detecting Amino Acid Sites Under Selection." Mol. Biol. Evol. 22, 1208--1222 (2005).