

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...

SLAC

SLAC (**S**ingle-**L**ikelihood **A**ncessor **C**ounting) uses a combination of maximum-likelihood (ML) and counting approaches to infer nonsynonymous (dN) and synonymous (dS) substitution rates on a per-site basis for a given coding alignment and corresponding phylogeny. Like FEL, 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 \(2005\).](#)



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