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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 sel	ection across branches, indi	vidual sites, or an entire gene?	
Branches	Sites	Gene	

Are you concerned about biases introduced by multinucleotide substitutions and variation in synonymous substitution rates?

No	Yes

## Datamonkey recommends that you use...

## <u>BUSTED-MH</u>

BUSTED-MH is a sophisticated extension that incorporates Multinucleotide Substitutions (MH) into evolutionary analyses. By accommodating this source of evolutionary complexity, this method can enhance the accuracy of natural selection detection and minimize the risk of false-positive inferences of diversifying episodic selection. It is especially suitable for scenarios where traditional models fail due to their inability to consider such evolutionary complexities. It can be enabled by selecting it via the BUSTED method under "Include support for multiple nucleotide substitutions?".

For more information, please see the <u>summary on hyphy.org</u> or see <u>Alexander G Lucaci, Jordan D Zehr, David Enard, Joseph W Thornton, Sergei L Kosakovsky Pond. "Evolutionary Shortcuts via Multinucleotide Substitutions and Their <u>Impact on Natural Selection Analyses." Molecular Biology and Evolution, Volume 40, Issue 7, July 2023.</u></u>

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https://datamonkey.org