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

Datamonkey recommends that you use...

GARD

GARD (**Genetic Algorithm** for **Recombination Detection**) is a method to screen a multiple sequence analysis for the presence of recombination and is extremely useful as a pre-processing step for selection inference. Because recombinant sequences cannot be adequately described with a single phylogenetic history, selection inference on recombinant data often leads to a significant increase in false positives. GARD alleviates this concern by comprehensively screening an alignment for recombination breakpoints and inferring a unique phylogenetic history for each detected recombination block.

For more information, please see the summary on hyphy.org or see Kosakovsky Pond, SL et al. "Automated Phylogenetic Detection of Recombination Using a Genetic Algorithm." Mol. Biol. Evol. 23, 1891–1901 (2006).