

Less Is More: An Adaptive Branch-Site Random Effects Model for Efficient Detection of Episodic Diversifying Selection

Martin D. Smith,¹ Joel O. Wertheim,² Steven Weaver,² Ben Murrell,² Konrad Scheffler,^{2,3} and Sergei L. Kosakovsky Pond^{*,2}


Mol. Biol. Evol. 32(5):1342–1353

- Fix the tree; estimate and fix some of the nuisance model parameters that are shared by all branches (GTR biases, frequency counts)
- Fit a simple baseline model (one ω per branch); use this model to get initial guesses for all other parameters
- **Perform a greedy step-up procedure** (like forward variable selection in regression models, but not as statistically bad)
 - For each branch (longest first) try two ω rate classes, then three ω rate classes etc, until no more goodness-of-fit improvement (AIC-c)
 - Fix the number of rates and move on to the next longest branch
 - Perform selection testing on the overall model (different number of ω classes on branches), using the likelihood ratio test
 - Each branch specified a priori (could be all branches)
 - Appropriate multiple testing correction

adaptive Branch Site REL results summary

INPUT DATA | HIV-sets.fas | 16 sequences | 288 sites

Export

aBSREL **found evidence** of episodic diversifying selection on **3** out of **26** branches in your phylogeny. 

A total of **26** branches were formally tested for diversifying selection. Significance was assessed using the Likelihood Ratio Test at a threshold of $p \leq 0.05$, after correcting for multiple testing. Significance and number of rate categories inferred at each branch are provided in the [detailed results](#) table.

See [here](#) for more information about this method.

Please cite [PMID 25697341](#) if you use this result in a publication, presentation, or other scientific work.

Tree summary

ω rate classes	# of branches	% of branches	% of tree length	# under selection
1	21	81%	0.49%	0
2	5	19%	100%	3

This table contains a summary of the inferred aBSREL model complexity. Each row provides information about the branches that were best described by the given number of ω rate categories.

```
hyphy absrel --alignment data/HIV-sets.nex
```