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]

- 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

HIV-1 *env*

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 ≤ 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.
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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
```

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