- 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 $p \le 0.05$, 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 HIV-sets.fas
```