

# RELAX(ed selection test) results summary

INPUT DATA | AlphaDeltaSpike.fas | 133 sequences | 1273 sites

Export

Test for selection **intensification** ( $K = 1.31$ ) was **not significant** ( $p = 0.558$ ,  $LR = 0.34$ ).

See [here](#) for more information about this method.  
Please cite [PMID 123456789](#) if you use this result in a publication, presentation, or other scientific work.

## Model fits



Model	<i>log L</i>	#. params	$AIC_c$	Branch set	$\omega_1$	$\omega_2$	$\omega_3$
General descriptive	-8790.1	367	18315.9	Shared	0.00 (11.36%)	0.86 (88.62%)	1288.13 (0.02%)
RELAX alternative	-8876.3	199	18151.1	Reference	1.00 (97.76%)	1.00 (2.24%)	1450.96 (0.00%)
				Test	1.00 (97.76%)	1.00 (2.24%)	13744.44 (0.00%)
RELAX null	-8876.5	198	18149.4	Reference	1.00 (98.05%)	1.00 (1.95%)	11625.16 (0.00%)
				Test	1.00 (98.05%)	1.00 (1.95%)	11625.16 (0.00%)

```
hyphy relax --alignment data/AlphaDeltaSpike.fas --tree data/AlphaDeltaSpike.nwk --test Delta --reference Alpha --starting-points 5
```

# Which sites are evolving differentially?

- We have established that in the HIV example, donor, recipient, and transmission branches evolve differently.
- Can we identify specific sites where this may be occurring?
  - Why is this of interest?
- More generally, given a tree with  $N$  sets of branches, we wish to find sites where evolution is different between these  $N$  sets, with a degree of statistical significance.
- Solution: use a fixed effects method (Contrast-FEL)
  - For each branch set  $i$ , estimate a dN/dS ratio ( $N$  total ratios)
  - Test whether or not any of the ratios are different (group test)
  - For each pair of ratios, test if they are different [ up to  $N(N-1) / 2$  tests ]
- Can identify subtle differences among selective pressures.