

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.

Contrast-FEL results summary

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

Export

ContrastFEL found evidence of

Found 5 sites with different Overall dN/dS

with p-value threshold of 0.01.

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

Please cite [PMID 15703242](#) if you use this result in a publication, presentation, or other scientific work.

ContrastFEL Table

Showing entries 1 through 20 out of 1273.

Export Table to CSV

Site	Partition	alpha	beta (Delta)	beta (Alpha)	beta (background)	subs (Delta)	subs (Alpha)	P-value (overall)	Q-value (overall)	Permutation p-value	To branch length
70	1	6.145	11.989	710.847	2.892	3.000	2.000	0.000	0.325	-1.000	30.000
157	1	7.355	73.889	0.000	0.445	5.000	0.000	0.001	0.623	-1.000	4.000
950	1	0.037	54.713	0.000	740.108	6.000	0.000	0.003	1.000	-1.000	3.000
142	1	0.000	40.094	7.705	460.016	6.000	1.000	0.004	1.000	-1.000	2.000
77	1	0.000	41.101	0.000	0.835	6.000	0.000	0.009	1.000	-1.000	2.000

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hyphy contrast-fel --alignment AlphaDeltaSpike.fas --tree AlphaDeltaSpike.nwk --branch-set Alpha --branch-set Delta
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