

# 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

Contrast-FEL **found evidence** of

Found 0 sites with different dN/dS

with q-value threshold of 0.2

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

Navigation buttons: <<, <, >, >>

Site	Partition	alpha	beta (background)	beta (Delta)	beta (Alpha)	subs (Delta)	subs (Alpha)	P-value (overall)	Q-value (overall)	Permutation p-value
1118	1	0.000	3.764	0.553	281.807	0.000	1.000	0.005	1.000	1.000
1191	1	0.091	8.275	0.280	275.724	0.000	1.000	0.071	1.000	-1.000
70	1	4.841	23.558	0.000	869.606	0.000	1.000	0.081	1.000	-1.000

```
hyphy contrast-fel --alignment data/AlphaDeltaSpike.fas --tree data/AlphaDeltaSpike.tree --branch-set Alpha --branch-set Delta
```