

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

| 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.nwk --branch-set Alpha --branch-set Delta
```