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.

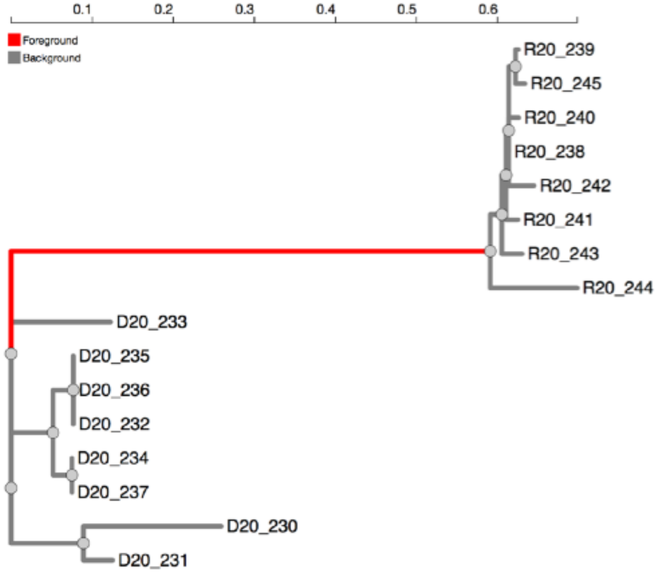
Export Table to CSV

Site	Partition	alpha	beta (background)	beta (Delta)	beta (Alpha)	subs (Delta)	subs (Alpha)	P-value (overall)	Q-value (overall)	Permutation p-value	b
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
```

Branch testing; exploratory vs *a priori*

- aBSREL and BUSTED can test all branches for selection (exploratory), or apply the test to a set of branches defined *a priori* (e.g. defining a particular biological hypothesis).
- For BUSTED, *a priori* partitioning of branches can increase power, especially if selective regimes are markedly different on different parts of the tree.
- For example, BUSTED applied to the HIV dataset where the transmission branch is designated as foreground, found a greater proportion sites under stronger selection on this branch that the rest of the tree (8% vs 1%), and a lower **`p-value`**.



	Background	Foreground
Class 1	ω = 0.51 p = 0.08	ω = 0.00 p = 0.92
Class 2	ω = 0.72 p = 0.91	
Class 3	ω = 116 p = 0.01	ω = 510 p = 0.08