









- Where in the tree is there evidence for selection?
- Can use exploratory Empirical Bayes Factor analysis to find “hotspots”
- Not a “strict” statistical test!

Based on the likelihood ratio test, *episodic diversifying selection* has acted on **4** sites in this dataset ( $p \leq 0.1$ ).

MEME analysis (v3.0) was performed on the alignment from /Users/sergei/Dropbox/Talks/VEME-current/data/WestNileVirus\_NS3.fas using HyPhy v2.5.40.

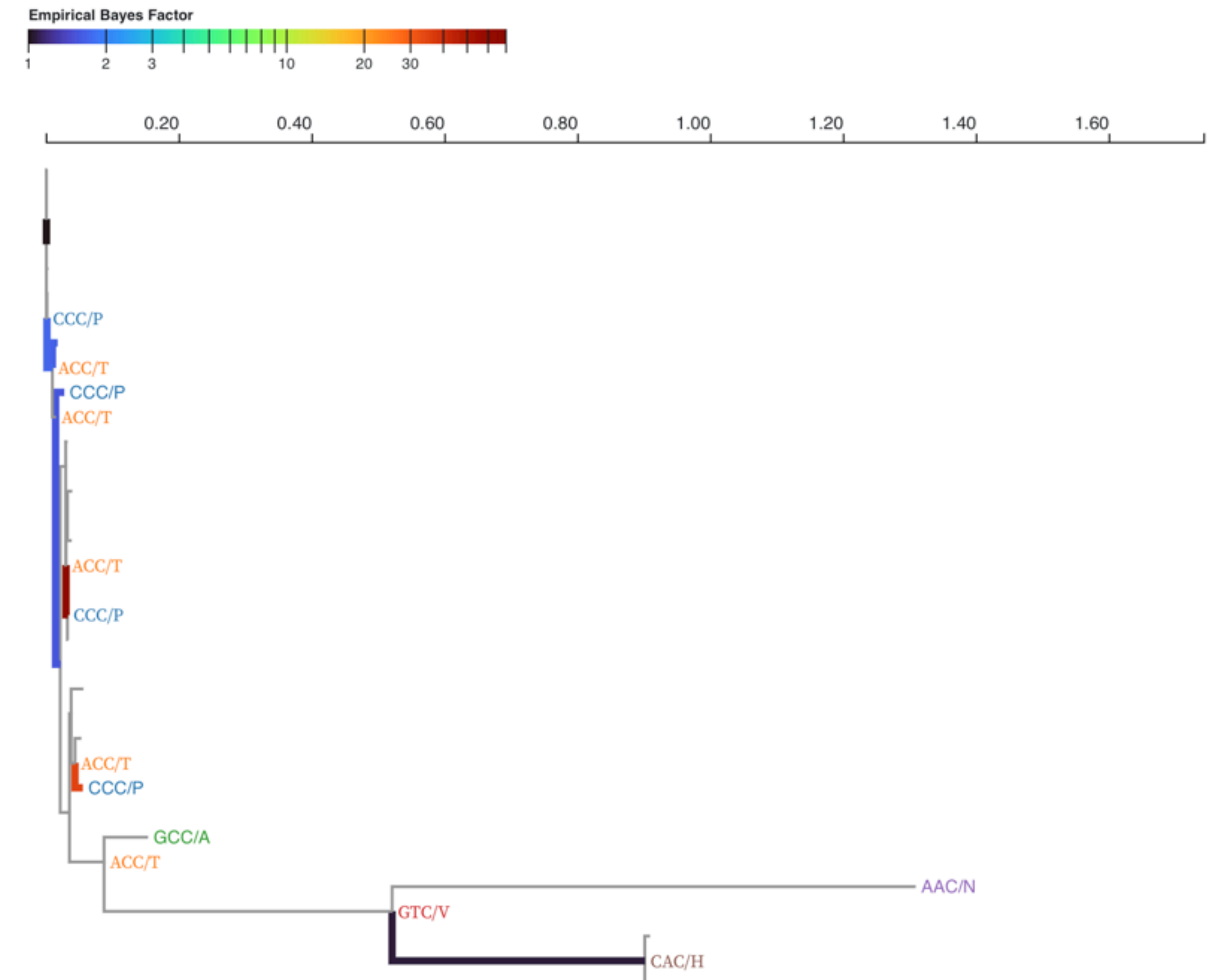
p-value threshold 0.1 Update

**Suggested citation:** Detecting Individual Sites Subject to Episodic Diversifying Selection. *PLoS Genet* 8(7): e1002764.

<b>19</b> sequences in the alignment		<b>619</b> codon sites in the alignment		<b>1</b> partitions	
<b>33</b> median branches/partition used for testing		<b>N/A</b> bootstrap replicates		<b>4</b> sites subject to episodic diversifying selection	
<b>0.75</b> median branches with support for selection/selected site		<b>6</b> sites with variable $\omega$ across branches			

**Table 1.** Detailed site-by-site results from the MEME analysis

Part.	Codon	$\alpha$	$\beta^-$	$p^-$	$\beta^+$	$p^+$	LRT	-p-value	# branches under selection	MEME LogL	FEL LogL	Variation p
1	249	0	0	0	2.708	1	7.883	0.009	0	-34.231	-34.232	1
1	557	0.234	0	0.965	140.484	0.035	5.517	0.029	1	-17.698	-14.167	0.029
1	521	0.922	0	0.961	103.466	0.039	3.6	0.078	1	-17.268	-14.308	0.052
1	87	1.972	0	0.948	29.804	0.052	3.455	0.084	1	-23.521	-16.735	0.001



```
hyphy meme --alignment data/WestNileVirus_NS3.fas
```