

- 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.









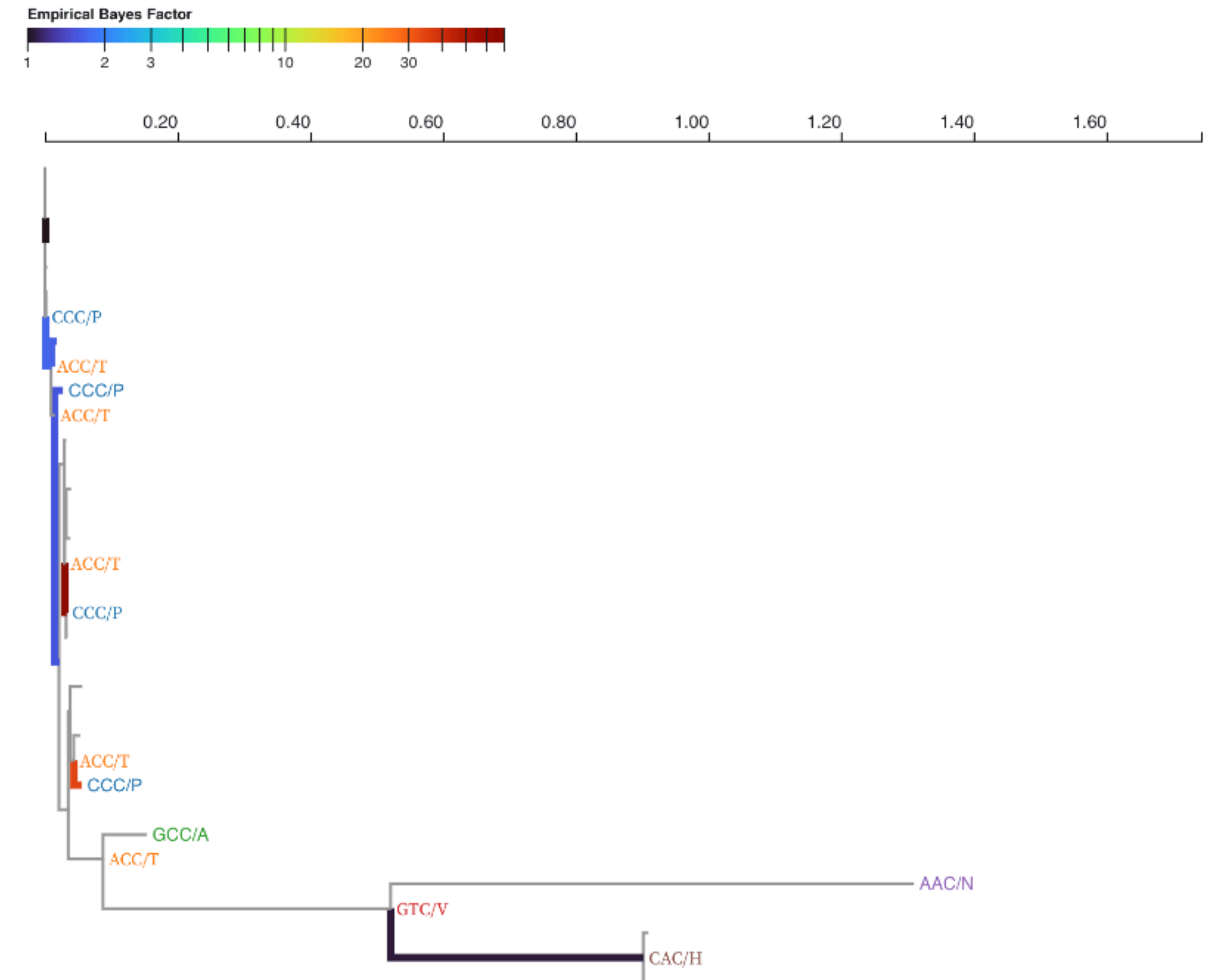
19 sequences in the alignment		619 codon sites in the alignment		1 partitions	
33 median branches/partition used for testing		N/A bootstrap replicates		4 sites subject to episodic diversifying selection	
0.75 median branches with support for selection/selected site		6 sites with variable ω across branches			

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

Part.	Codon	α	β^-	p^-	β^+	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.fna
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