

Recombination

- Affects a large variety of organisms, from viruses to mammals (e.g. gene family evolution)
- Manifests itself by incongruent phylogenetic signal
- This can be exploited to detect which sequence regions recombined and which sequences were involved
- Recombination can influence or even mislead selection detection methods.
- Using an incorrect tree to analyze a segment of a recombinant analysis can bias **dS** and **dN** estimation
- The basic intuition is that an incorrect tree will generally break up identity by descent and hence make it appear as if more substitutions took place than did in reality.

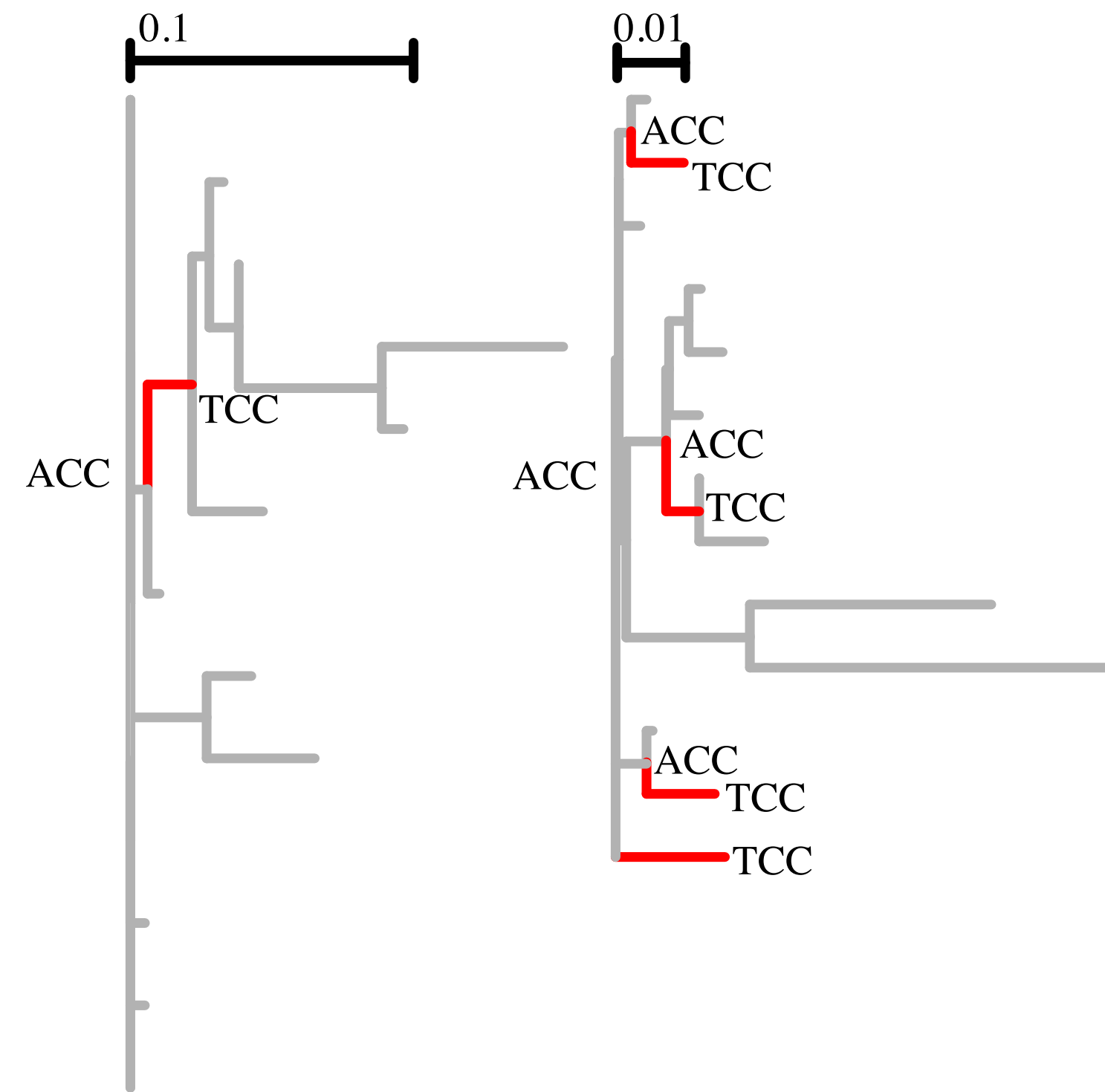


Figure 4.2: The effect of recombination on inferring diversifying selection. Reconstructed evolutionary history of codon 516 of the Cache Valley Fever virus glycoprotein alignment is shown according to GARD inferred segment phylogeny (left) or a single phylogeny inferred from the entire alignment (right). Ignoring the confounding effect of recombination causes the number of nonsynonymous substitutions to be overestimated. A fixed effects likelihood (FEL, Kosakovsky Pond and Frost (2005)) analysis infers codon 516 to be under diversifying selection when recombination is ignored ($p = 0.02$), but not when it is corrected for using a partitioning approach ($p = 0.28$).