Suzuki-Gojobori (SG99): the penultimate extension of NG86

Uses a tree to compute dN/dS at a given site

- 1. Reconstruct ancestral sequences by nucleotide-level parsimony
- 2. Compute EN and ES using labeled branches; define $p_e = ES/EN$
- 3. Compute s and ns for each site (minimum evolution)
- 4. Estimate the probability that the number of synonymous substitutions \mathbf{S} is unusually low (positive selection) or unusually high (negative selection), using the binomial distribution given \mathbf{p}_{e} from step 2.

A method for detecting positive selection at single amino acid sites

Y. Suzuki and T. Gojobori Mol Biol Evol 16 1315-1328 (1999) >500 citations

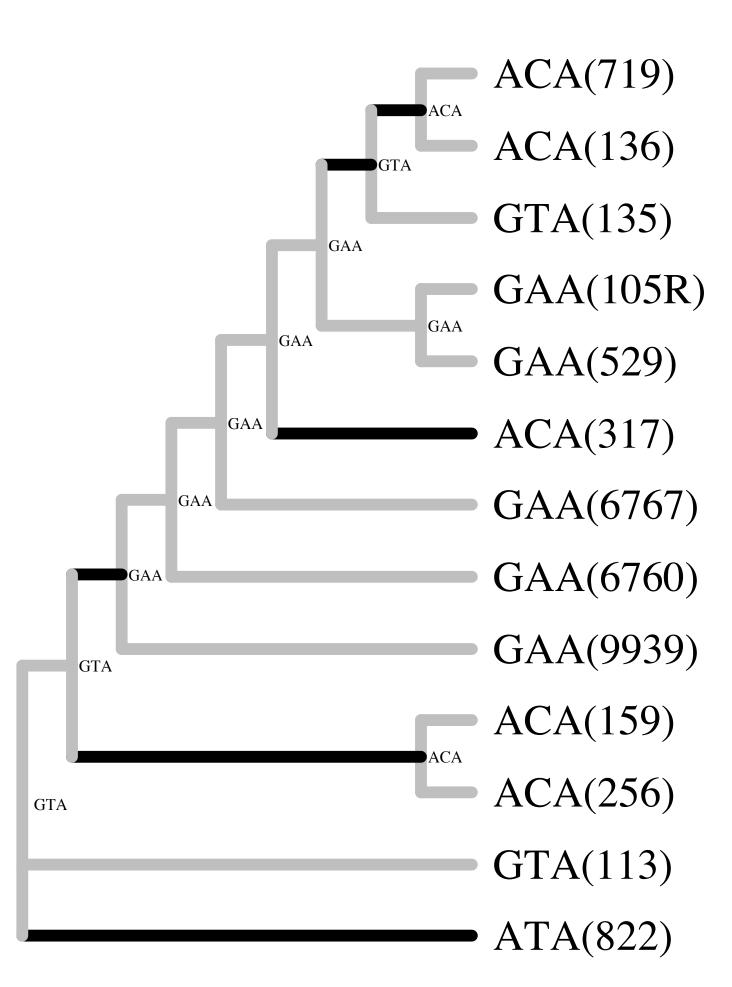


Fig. 1.6. An illustration of SLAC method, applied to a small HIV-1 envelope V3 loop alignment. Sequence names are shown in parentheses. Likelihood state ancestral reconstruction is shown at internal nodes. The parsimonious count yields 0 synonymous and 9 non-synonymous substitutions (highlighted with a dark shade) at that site. Based on the codon composition of the site and branch lengths (not shown), the expected proportion of synonymous substitutions is $p_e = 0.25$. An extended binomial distribution on 9 substitutions with the probability of success of 0.25, the probability of observing 0 synonymous substitutions is 0.07, hence the site is borderline significant for positive selection.