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 <u>parsimony</u>

2. Compute **EN** and **ES** using labeled branches; define $\text{p}_\text{e} = \text{ES/EN}$

3. Compute **S** and **NS** for each site (minimum evolution)

4. Estimate the probability that the number of synonymous substitutions **S** is unusually low (positive selection) or unusually high (negative selection), using the binomial distribution given p_e from step 2.
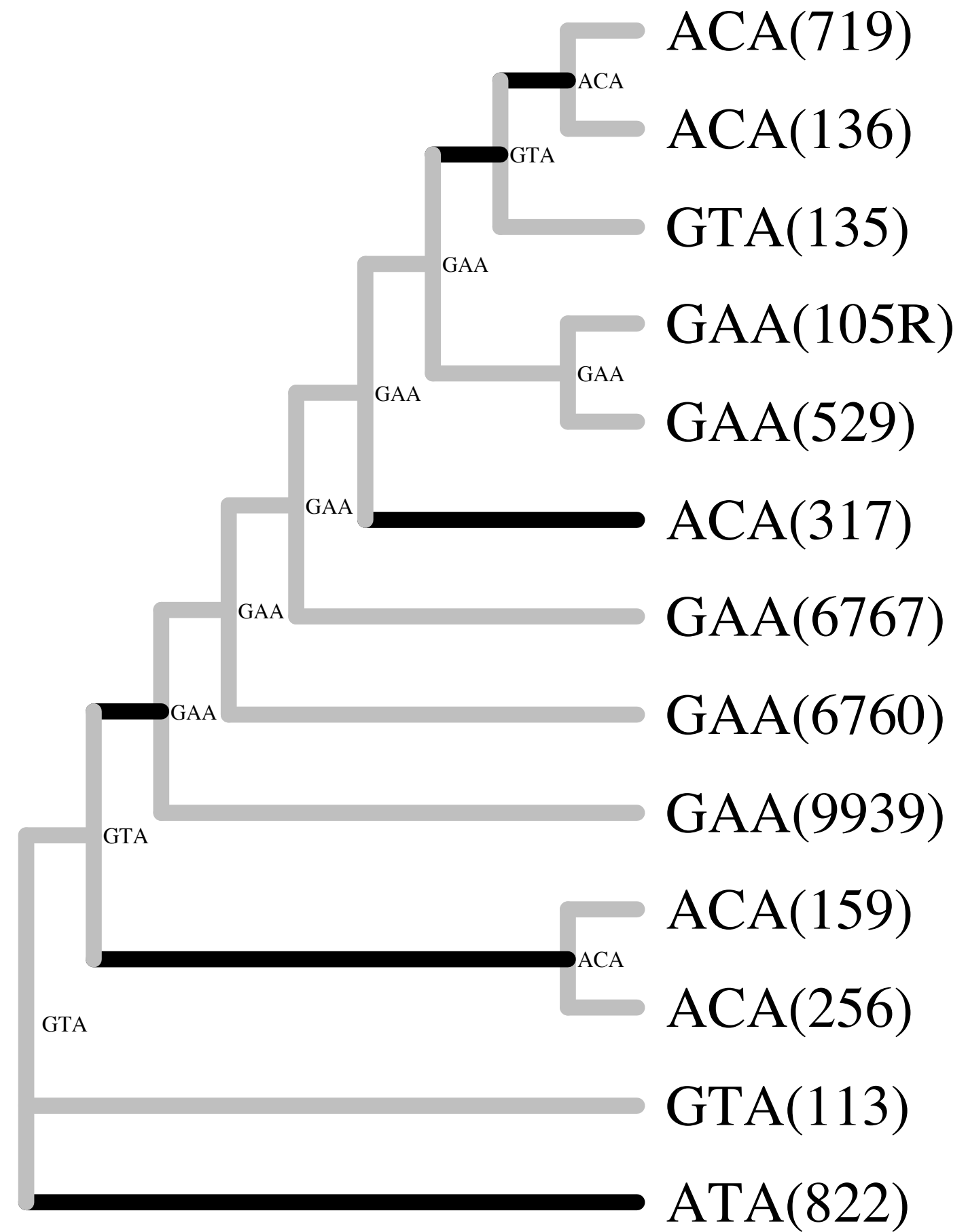
Fig. 1.6. An illustration of SLAC method, applied to a small HIV-1 envelope V3 loop alignment. Sequence names are shown in parentheses. Likelihood state ancestral reconstruction is shown at internal nodes. The parsimonious count yields 0 synonymous and 9 non-synonymous substitutions (highlighted with 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.