

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 **S** is unusually low (positive selection) or unusually high (negative selection), using the binomial distribution given p_e from step 2.

A method for detecting positive selection at single amino acid sites

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>500 citations

