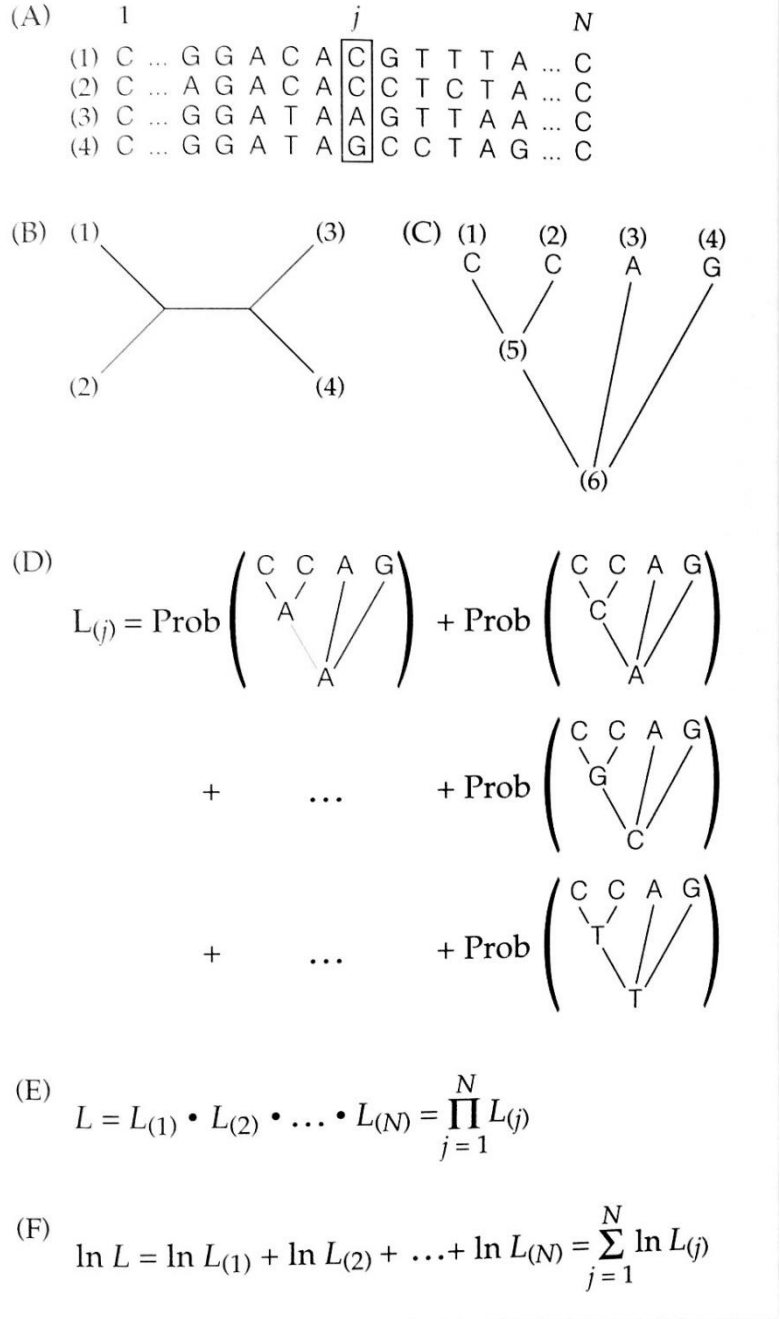

Swofford, Olsen, Waddell & Hillis
Ch. 11 in Hillis *et al*. 1996
Molecular Systematics

Calculation of likelihood for ancestral states:

Given position *j* in an alignment (A), the likelihood of rooted topology (C) is the sum of the probabilities of that topology for all possible ancestral sites.

The likelihoods are calculated for all informative sites and multiplied (E).

Adding the logarithms of the likelihoods (F) is equivalent.

Similar calculations are done on the individual branch lengths and combined with ancestry likelihoods.