Exercise 2 help file: This file also contains an annotated portion of the results output by codeml for a pairwise ML analysis. This file annotates the additional information required to complete exercise 2.

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pairwise comparison, codon frequencies: Fequal. ← Note that the user-specified model for codon frequencies is indicated here.

2 (Sim) ... 1 (Mel)
lnL = -926.280300
   0.10533   1.88371   0.32004 ← The middle value in this line is the ML estimate of kappa (ts/tv)

t= 0.1053   S=   165.8   N=   434.2   dN/dS= 0.3200   dN= 0.0221   dS= 0.0691

This is the ML estimate of branch length (t) between the pair of sequences. It is measured as the mean number of substitutions per codon site.

N is the number of non synonymous sites

S is the number of synonymous sites.

dN is the nonsynonymous substitution rate

dS is the synonymous substitution rate