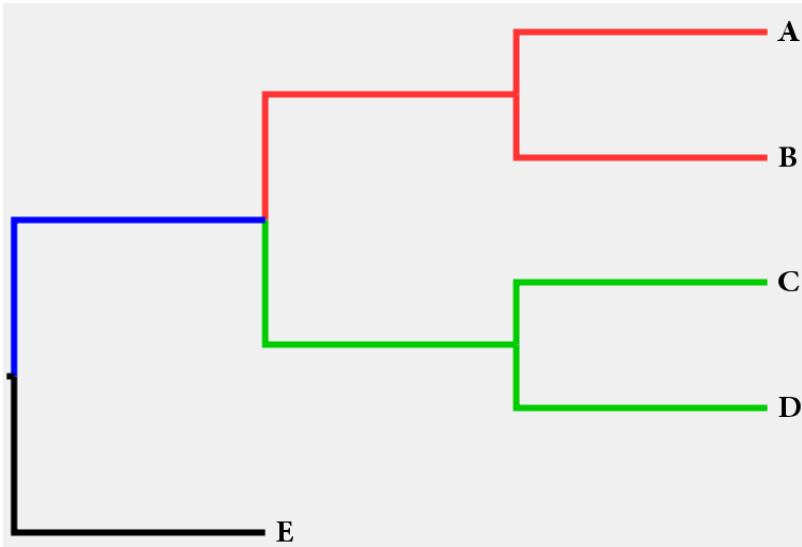
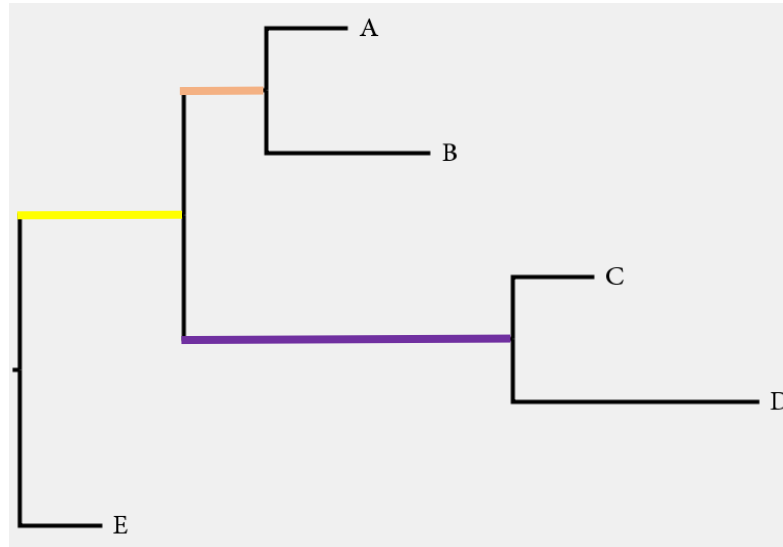


NEWICK tree format



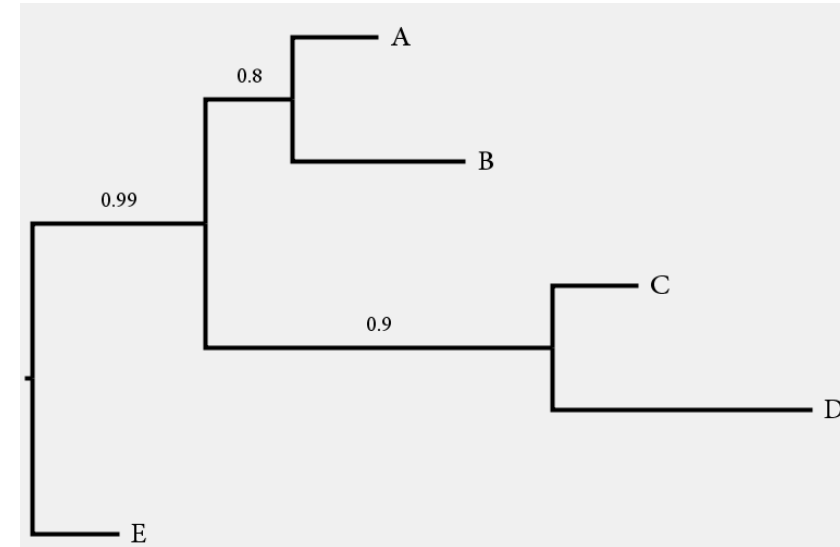
`((A,B),(C,D)),E;`

topology



`(((A:1,B:2):1,(C:1,D:3):4):2,E);`

branch lengths

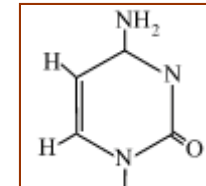
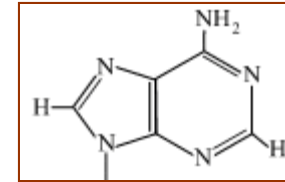
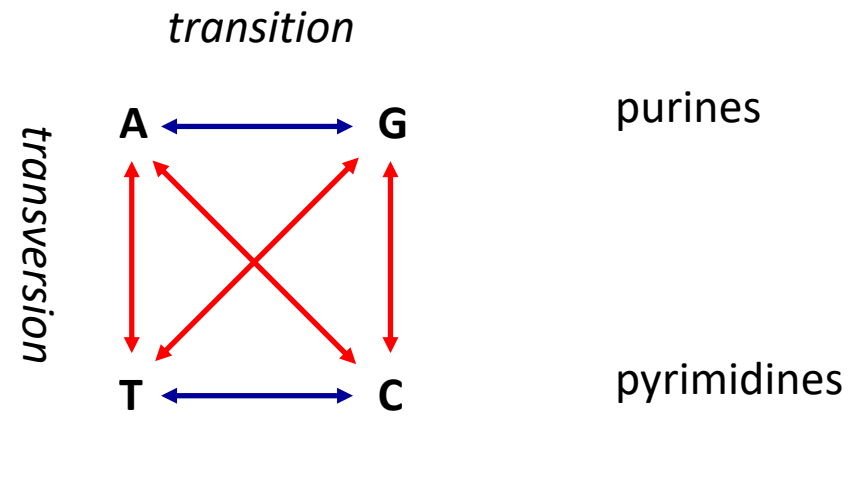


`(((A:1,B:2)0.8:1,(C:1,D:3)0.9:4)0.99:2,E);`

support values

Evolutionary models for DNA sequences

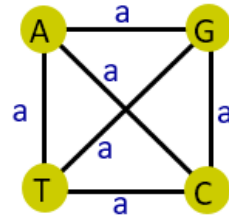
- models for sequence changes



- parameters
 - base frequencies
 - substitution types (transitions, transversions)
 - heterogeneity in substitution rates (G)
 - proportion of invariant sites (I)

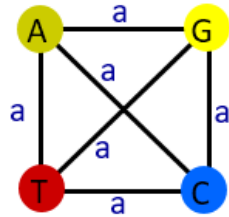
Substitution models for DNA sequences

Increasing number of parameters



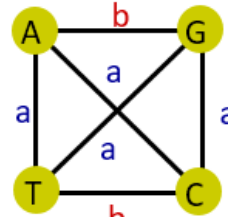
JC (Jukes-Cantor 1969)

- same substitution rates
- same base frequencies



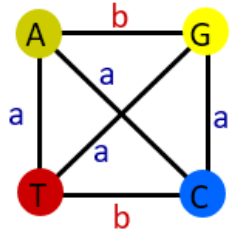
F81 (Felsenstein 1981)

- same substitution rates
- different base frequencies



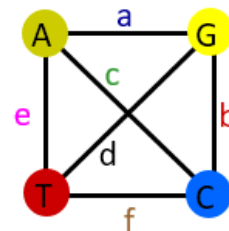
K2P (Kimura 2 parameter 1980)

- two different substitution rates
- same base frequencies



HKY (Hasegawa, Kishino & Yano 1985)

- two different substitution rates
- different base frequencies



GTR (General time-reversible model)
(Tavaré et al. 1986)

- six different substitution rates
- different base frequencies

[illegible]