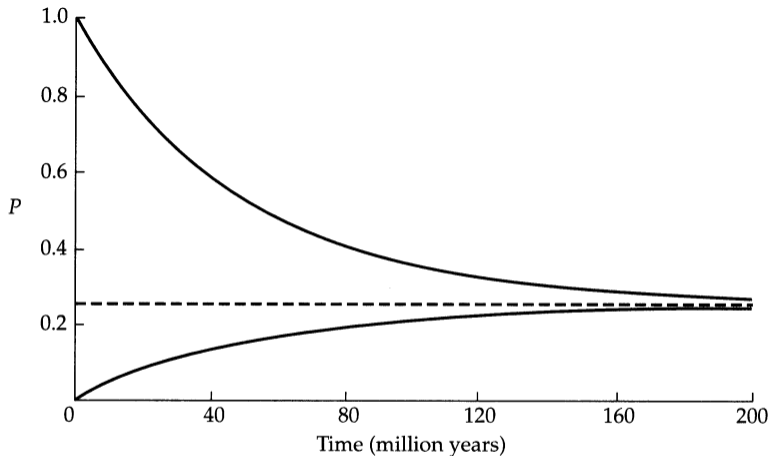
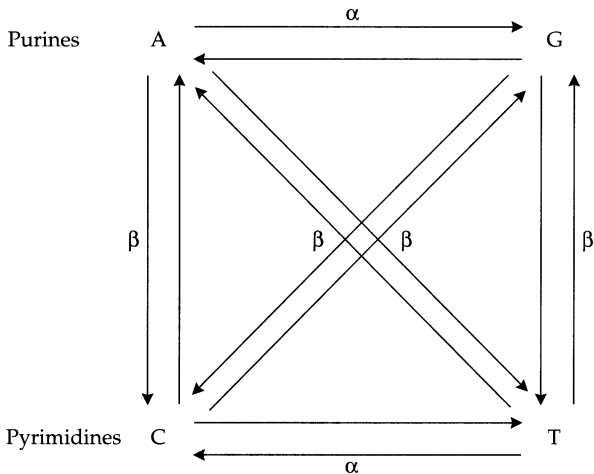


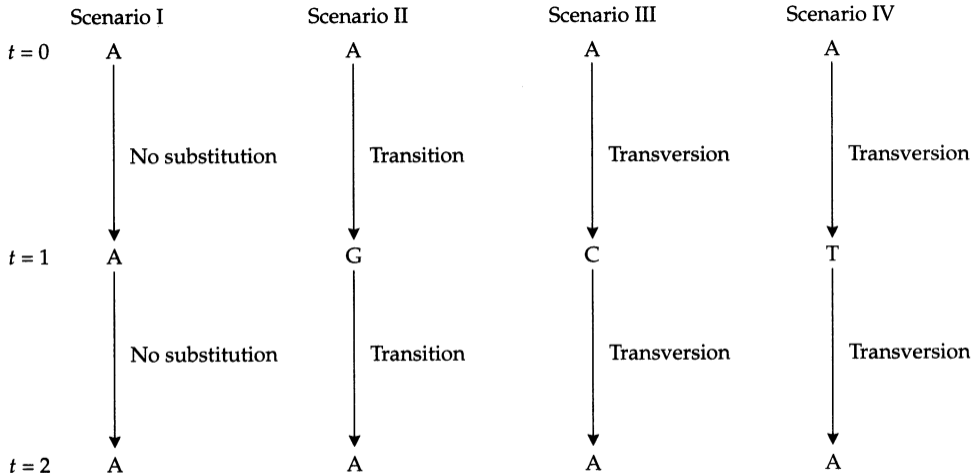
**FIGURE 3.1** One-parameter model of nucleotide substitution. The rate of substitution in each direction is  $\alpha$ .



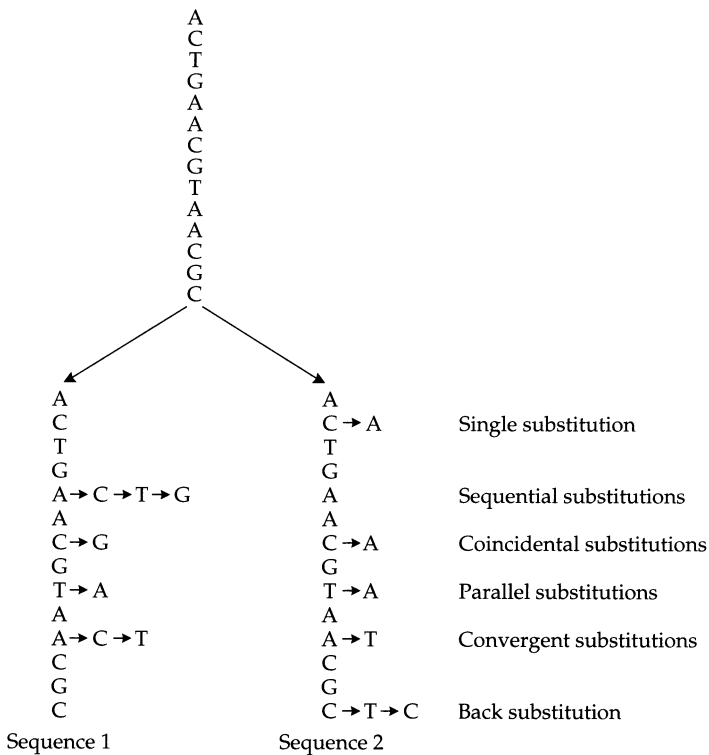
**FIGURE 3.3** Temporal changes in the probability,  $P$ , of having a certain nucleotide at a position starting with either the same nucleotide (upper line) or with a different nucleotide (lower line). The dashed line denotes the equilibrium frequency ( $P = 0.25$ ).  $\alpha = 5 \times 10^{-9}$  substitutions per site per year.



**FIGURE 3.4** Two-parameter model of nucleotide substitution. The rate of transition ( $\alpha$ ) may not be equal to the rate of transversion ( $\beta$ ).



**FIGURE 3.5** Four possible scenarios, according to Kimura's (1980) two-parameter model, for having A at a site at time  $t = 2$ , given that the site had A at time 0.



A A  
C-A  
T T  
G G  
G-A  
A A  
G-A  
G G  
A A  
A A  
T T  
C C  
G G  
C C

**FIGURE 3.6** Two homologous DNA sequences that descended from an ancestral sequence have accumulated mutations since their divergence from each other. Note that although 13 mutations have occurred, differences can be detected at only three nucleotide sites (-). Note further that "sequential substitutions," "coincidental substitutions," "parallel substitutions," "convergent substitutions," and "back substitutions" all involve multiple substitutions at the same site, though perhaps in different lineages.