

Non random DNA evolution

Valenzuela, Carlos Y.

A model for testing molecular evolution is proposed. Randomness of recurrent mutation is defined based on isotropy and zero covariance among nucleotide sites. Assuming an equal rate of mutation for the bases A, T, G, and C, in both DNA strands, a mutational matrix of transformation A, T, G, and C proportions (F) of the bases are $F(A) = F(T) = (D + E) / [2(D + E + H + J)]$ and $F(G) = F(C) = (H + J) / [2(D + E + H + J)]$, D, E, H, J being 4 of the 6 matrix parameters. Thus the expected $(F(A) + F(T)) / (F(G) + F(C))$ ratio can also be tested. If the average rate of mutation is 10^{-8} per nucleotide site and cell replication, the equilibrium for every site, in most species, is reached in 108 years. Eight DNA segments from human, bacteria, fungus and insect genomes were chosen to test these proportions and their heterogeneity among coding and non coding subsegments. While $F(G)$ was similar to $F(C)$ as expected $F(A)$ was highly different from $F(T)$. Huge heterogeneities were found between coding and non