

numbers of gene substitutions and calculating genetic distances from gene sequence data are derived from population-genetic arguments. The molecular clock hypothesis, based on a population-genetic theorem, posits that neutral gene substitutions should occur at a rate equal to the mutation rate, which may be a linear function of time. This result provides a basis for the estimation of divergence times among major lineages in the absence of an adequate fossil record. Moreover, times of duplication of major gene functions (for instance, divergence times of members of the globin gene superfamily) can be estimated from sequence data.

The fifth chapter of the book develops the estimation of organismic relationships from molecular data. If genetic distance increases as a monotonic function of time then it should be possible to estimate the pattern (topology) of relationships from gene-sequence data (molecular phylogenies). This application of molecular data has given rise to a number of computational algorithms that can seem complicated and confusing to the novice. While molecular phylogenetics has reinvigorated the study of systematics in recent years, it has also yielded several contentious schools of thought on computational methodology. Molecular phylogenies are also providing an independent basis for the analysis of morphological evolution and for testing major issues like the hypothesis that mitochondria and chloroplasts had an endosymbiotic origin.

The remaining chapters deal with what might be called molecular phenomonology. For example, during the past quarter-century we have learned that eukaryotic genomes contain vast numbers of repeated DNA sequences whose functions are obscure; introns were discovered, as were overlapping genes; the molecular structure of transposable elements was documented; and these genetic entities were found to be ubiquitous in nature. In addition, retroviruses and their associated retrotransposons were described and their occasional horizontal transfer among species was documented. This wealth of empirical information has produced a kind of natural history of the genome. As with classical natural history, the natural history of the genome must be accounted for within a unified theoretical framework. The theory of evolution provides that framework. It is a testament to the power of evolutionary theory that it can easily accommodate observations that were not imagined a quarter of a century ago.

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