

# A model of complete random molecular evolution by recurrent mutation

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A model for random molecular evolution based on recurrent mutation is proposed. Recurrent mutation replaces completely any original base in a nucleotidic site. This occurs if more than four times the number of reproductive cycles equal to the reciprocal of the mutation rate happen, no matter the population size, the number of nucleotides a genome has, or the taxa at which it belongs. The main results are: i) the expected distribution of DNA bases in a site is an isotetranomial distribution, where Adenine (A), Guanine (G), Cytosine (C) and Thymine (T) occur with probability equal to 0.25; ii) the distribution of bases in a site is independent from the distribution of bases in other sites. Several expected consequences that can be contrasted with actual data are generated. Species or operational taxonomic units (OTUs) that evolved in big populations should present distances equal to zero and similarities equal to one. OTUs evolving in small populations should present distances equal to 3