

Abstract

Palindromic Symmetry in Genomes and Evolution [†]

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Any genome is a symbol sequence from a four-letter alphabet. A lot can be retrieved from the studies of frequency distribution in ensembles of considerably short strings, of a given length. A palindrome is two strings that read equally in opposite directions; a complementary palindrome is two strings that read equally in opposite directions with respect to Chargaff's substitution rule ($A \leftrightarrow T$ and $C \leftrightarrow G$). The symmetry observed over a genome manifests in a proximal equivalence of the strings comprising a complementary palindrome; it should be stressed that the frequencies are counted over a single strand. Thus, it seems that a duality exists between the symmetry and the double helix structure. The frequency equality is not exact, but shows some deviations. We studied a number of genomes of various taxa to determine the deviation figures in order to learn the relation between the deviation figure, and taxonomy of a genome bearer. The deviation figures have been studied for the strings that range from 1 to 8 in length. Also, a theoretical estimation of the deviation figures has been obtained, for various models of a genetic sequence. A dependence of deviation figures from taxonomy has been observed for high taxa ranks, only. Besides, an inhomogeneity of a genome in terms of the figures has been studied for a number of organisms. A new inner structuredness manifesting in divergence of the deviation figures observed for various genome regions was found in all the genomes.

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