



TI2BioP: Topological Indices to BioPolymers

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Abstract: TI2BioP (Topological Indices to BioPolymers) is a software to estimate topological indices (TIs) from two-dimensional (2D) graphical approaches for the natural biopolymers DNA, RNA and proteins. The methodology mainly turns long biopolymeric sequences into 2D artificial graphs such as Cartesian and four-color maps but also reads other 2D graphs from the thermodynamic folding of DNA/RNA strings inferred from other programs. The topology of such 2D graphs is either encoded by node or adjacency matrixes for the calculation of the spectral moments as TIs. These numerical indices were used to build up alignment-free models to the functional classification of biosequences and to calculate alignment-free distances for phylogenetic purposes. We released the version 2.0 of the software that can be freely downloaded from <http://ti2biop.sourceforge.net/>.

Keywords: 2D graphs; Topological indices; Alignment-free models; phylogenetics

1. TI2BioP software

TI2BioP was mainly developed from the TOPS-MODE methodology [1] for the estimation of the spectral moments series as TIs, but it takes advantage of the MARCH-INSIDE program platform [2]. It was built up on object-oriented Free Pascal IDE Tools (Lazarus)

running on either a Windows or Linux operating system. TI2BioP has a friendly interface allowing users to introduce multiple fasta files containing either DNA or protein sequences to select the biopolymer 2D representation type and the calculation of TIs. We released version 2.0 of

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