

Simona Grusea

Measures for the exceptionality of gene order in conserved genomic regions.

Abstract:

The goal of this work is to find "good" measures for quantifying the exceptionality of the order of the orthologs in conserved genomic regions between two different species. Here "good" means both biologically relevant and computationally accessible. We propose three measures based on the transposition distance in the permutation group for measuring the gene order conservation in orthologous gene clusters found by the reference region approach. We obtain analytic expressions for their distribution in the case of a random uniform permutation, i.e. under the null hypothesis of random gene order. Our results can be used to increase the power of the significance tests for gene clusters which take into account only the proximity of the orthologous genes, and not their order.