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Nota di contenuto	Genetic Processing -- Generalized Hultman Numbers and the Distribution of Multi-break Distances -- Implicit Transpositions in Shortest DCJ Scenarios -- Constraint-Based Genetic -- Compilation -- Molecular Recognition/Prediction P2RANK: Knowledge-Based Ligand Binding Site Prediction Using Aggregated Local Features -- StreamM - A Stream-Based Algorithm for Counting Motifs in Dynamic Graphs -- Convolutional LSTM Networks for Subcellular Localization of Proteins -- Phylogenetics -- Hybrid Genetic Algorithm and Lasso Test Approach for Inferring Well Supported Phylogenetic Trees Based on Subsets of Chloroplastic Core Genes -- Constructing and Employing Tree Alignment Graphs for Phylogenetic Synthesis -- A More Practical Algorithm for the Rooted Triplet Distance -- Likelihood-Based Inference of Phylogenetic Networks from Sequence Data by PhyloDAG -- Constructing Parsimonious Hybridization Networks from Multiple

