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Binary Encoding and Genome Rearrangement Analysis

Genome rearrangements have been widely used in phylogenetic reconstruction. Compared to sequence data, analyzing these events is mathematically more difficult. To overcome this problem, encoding genomes into binary sequences was proposed with limited success. We revisited the idea of encoding by using maximum-likelihood and a model that better fits the evolution of gene orders. Similar to the model first proposed by Dr. Sankoff, our model is biased as adjacencies can be easily broken than being restored. Our new approach achieved very good performance in both speed and accuracy, and can cope with datasets which no existing methods can handle.