

Assessing the Accuracy of Parsimony Methods in Some Genome Evolution Models

Nafisa Raisa (Mentors: Dr. Poly Hannah da Silva, Dr. Arash Jamshidpey, 2023 IICD SRP)

Parsimony methods are widely employed in biology to infer the evolutionary trajectory of genomes. These methods aim to reconstruct the most likely evolutionary history, often as a phylogenetic tree, by minimizing the number of selected steps from a relatively small collection of genomic operators such as inversions, reciprocal translocations, and double-cut-and-joins. The minimization principle used in these methods makes them maximum parsimony. Various studies show the effectiveness of the parsimony methods for moderately evolved genomes when the genomes follow the most parsimonious paths during their evolution. However, it is essential to note that genomes do not necessarily evolve along the fastest evolutionary paths, cf. M. Meghdari Miardan, A. Jamshidpey, D. Sankoff (2023). More precisely, in the case of more significant divergence from its original state, the evolutionary path traversed by the evolving genome deviates from the parsimonious path. In such cases, parsimony methods underestimate the actual time required for genome evolution, indicating that they may not always be perfectly suitable for accurately inferring the true evolutionary history.

In this study, our goal is to assess the validity of parsimony methods in certain models of genome evolution. Specifically, we focus on linear and/or circular multi-chromosomal genomes with possible duplicated genes. Considering various genomic operations such as double-cut-and-join, indel (insertions and deletions), and copy number variation, which is particularly useful in cancer studies, we study the speed of escape of a random genome evolution process from parsimony. The findings from this research will contribute to a better understanding of the benefits and restrictions of the parsimony methods in capturing the dynamics of genome evolution.

Reference

M. Meghdari Miardan, A. Jamshidpey, and D. Sankoff. "Escape from Parsimony of a Double-Cut-and-Join Genome Evolution Process." *Journal of Computational Biology*, 30:2, (2023): 118-130.