

## **An Accurate Method for Phylogeny Tree Reconstruction Based on a Modified Wild Dog Algorithm**

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**Abstract :** This study solves a phylogeny problem by using modified wild dog pack optimization. The least squares error is considered as a cost function that needs to be minimized. Therefore, in each iteration, new distance matrices based on the constructed trees are calculated and used to select the alpha dog. To test the suggested algorithm, ten homologous genes are selected and collected from National Center for Biotechnology Information (NCBI) databanks (i.e., 16S, 18S, 28S, Cox 1, ITS1, ITS2, ETS, ATPB, Hsp90, and STN). The data are divided into three categories: 50 taxa, 100 taxa and 500 taxa. The empirical results show that the proposed algorithm is more reliable and accurate than other implemented methods.

**Keywords :** least square, neighbor joining, phylogenetic tree, wild dog pack

**Conference Title :** ICBBCB 2016 : International Conference on Bioinformatics, Biomedicine, Biotechnology and Computational Biology

**Conference Location :** Boston, United States

**Conference Dates :** April 25-26, 2016