

# Detection of Related Species by Denoising Phylogenetic Trees

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## Abstract

One of the popular methods to summarize a molecular data set is clustering; in this way, related species can be detected. There are many classification indices proposed in the literature, but the performance of these indices decreases if different species share similar features. In addition, these methods may need user defined thresholds. We propose a new algorithm which automatically detects related species at phylogenetic trees by denoising lifting transformation of trees.

Our algorithm estimates its own threshold, so it removes the manual intervention on the choice of a threshold. In addition, the nature of our algorithm can deal with cases where there is no clear separation between different species. We compare the performance of our algorithm with some other available indices in the literature using some simulated and real data sets.

**Key Words:** Phylogenetic trees, hierarchical clustering, cluster validity indices, wavelets, lifting

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