

# Exploring phylogenetic relationships in *Drosophila* using ciliate operations

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## Abstract

We studied the phylogenetic relationships among fly species using DNA-editing operations of ciliates. Phylogenetics is the study of evolutionary relationships among groups of organisms. Using a canonical reference species, the relative order of orthologous genes in another species is a scrambled version of the reference species. The ciliates are capable of unscrambling the DNA using merge, swap, and reverse operations. We create an algorithm to simulate DNA decryption using the three ciliate operations. The algorithm was implemented in Python and it determines distances among genomes via those operations in polynomial time ( $O(n^3)$ ). Using the algorithm, we found a correlation between the published evolutionary distances of the fly species and the number of reverse operations used. This correlation also held for the total number of operations used for all species but one.