

A NOVEL SOFTWARE FOR ORGANELLE GENOME-BASED BARAMINOLOGY STUDIES

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ABSTRACT

The genomes of different organelles make molecular baraminology studies easier and much more high-throughput, due to the abundance of organelles in the cell and the small size of their DNA. The different classes of plastid and mitochondrial DNA can be used to delineate several apobaramins. Differences in gene order, organelle genome size, GC%, codon usage, and gene repertoire can help delineate holobaramins in some cases. In this paper existing organelle genome baraminology studies will be reviewed, as well as resources and algorithms for organelle genome-based molecular baraminology studies. Two new software will be presented in this paper, the Organelle DNA Analysis script (ODA), and an app called the Molecular Baraminology Analysis Tool (MBAT) suite. Both tools perform sequence download, alignment, and cluster analysis. The first software is a command line script written in Python, which downloads a list of sequences via Entrez, then performs alignment of these sequences, calculates a sequence similarity matrix, and then performs k-means clustering on the matrix. The software outputs a heatmap, the sequence similarity matrix, baraminic trees of each cluster, and also several plots. This script can be automated on the command line in Linux. The second software is a shiny app written in R, and I accessible online. It allows the user to download a set of sequences from the NCBI database, and then align these sequences to produce a sequence similarity matrix, either using third-party tools or using the app itself. The user can then run a clustering method to calculate putative clusters (baramins), as well as statistics on these clusters. Molecular baraminology-based software can be used to complement morphology-based tools.

KEYWORDS

organelle, genome, baraminology, software

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Matthew Cserhati has published 45 technical level articles in creation science. His specialty is bioinformatics and molecular baraminology. He has also led a team that assembled the whole genome sequence of Neanderthal and Denisovan. He has a PhD in bioinformatics, a BSc in software development, and an MA in theology. He has taught several college level courses on bioinformatics.