

MEGA: a biologist-centric software for evolutionary analysis of DNA and protein sequences.

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Abstract

The Molecular Evolutionary Genetics Analysis (MEGA) software is a desktop application designed for comparative analysis of homologous gene sequences either from multigene families or from different species with a special emphasis on inferring evolutionary relationships and patterns of DNA and protein evolution. In addition to the tools for statistical analysis of data, MEGA provides many convenient facilities for the assembly of sequence data sets from files or web-based repositories, and it includes tools for visual presentation of the results obtained in the form of interactive phylogenetic trees and evolutionary distance matrices. Here we discuss the motivation, design principles and priorities that have shaped the development of MEGA. We also discuss how MEGA might evolve in the future to assist researchers in their growing need to analyze large data set using new computational methods.

Keywords: [phylogenetics](#), [genome](#), [evolution](#), [software](#)

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