

An important task in molecular biology is the search for new proteins and the determination of their functions. Although experimental research on proteins remains irreplaceable, computational techniques allow us to obtain new insights much faster. Therefore, computer calculations are increasingly being used for predicting 3D structures and biological functions.

In this work, various methods for predicting functional annotations are discussed, including modern methods based on deep machine learning. Additionally, a new program called GOLizard is introduced, which can be used to visualize functions of similar proteins obtained through the BLAST and FoldSeek programs. It uses a hierarchical arrangement of Gene Ontology terms via a directed graph, showing the relationships between individual terms.