

Computational method for predicting protein function

Sequence-based software predicts GO functions for proteins—even with weak homology—more accurately than conventional methods.

Researchers at Purdue University have developed a software, Protein Function Prediction (PFP), to predict the biological function of a protein from its amino acid sequence. The software applies a data mining tool to sequence and gene ontology data to provide the most probable annotation for the query sequence in its associated biological process, molecular function, and cellular component. The software provides a list of protein functions ranked by likelihood that the function belongs to the input protein. PFP compares favorably to PST-BLAST, more accurately assigning function in weakly similar sequences. PFP was benchmarked with a set of 2000 nonredundant protein sequences randomly selected from UniProt and has been employed for five test sequences provided at the assessment of function prediction servers at the Automated Function Prediction Special Interest Group meeting at ISMB 2005. This software has both industrial and research applications in the biomedical and pharmaceutical sectors.

Technology Validation:

This technology has been validated through testing of the software product.

Advantages:

- Capable of making predictions about proteins that aren't in the database
- Functional for greater number of proteins than alternate solutions

Applications:

- Pharmaceuticals
- Biomedical Research/Industry

Related Publication:

Technology ID

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Category

Biotechnology & Life
Sciences/Bioinformatics &
Computational Biology
Artificial Intelligence & Machine
Learning/AI Model Optimization
& Acceleration Tools
Pharmaceuticals/Drug Discovery
& Development

Further information

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Enhanced automated function prediction using distantly related sequences
and contextual association by PFP

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