

Protein Prediction II

Exercise 1

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Keywords

Machine Learning
Bootstrapping
BLAST
Standard error
Ribosome
Support Vector Machine
Globular proteins
Sequence motif
High-Throughput Sequencing
UniProt
Protein Function
Translation
Hydrophobicity
Cross-validation
Cytoplasm
The Central Dogma of MB
In silico
Eukaryote
De novo method
E-value
Cellular Sorting
PSI-BLAST
Signal patch
Signal peptide
Multiple Alignment
RNA
HSSP-curve

The 'Big' Project



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Develop a novel homology-based method for protein localization prediction

Compare it to current most popular *de novo* localization prediction methods

Show that your method is better than any other (homology-based) method out there

The Plan (preliminary)

