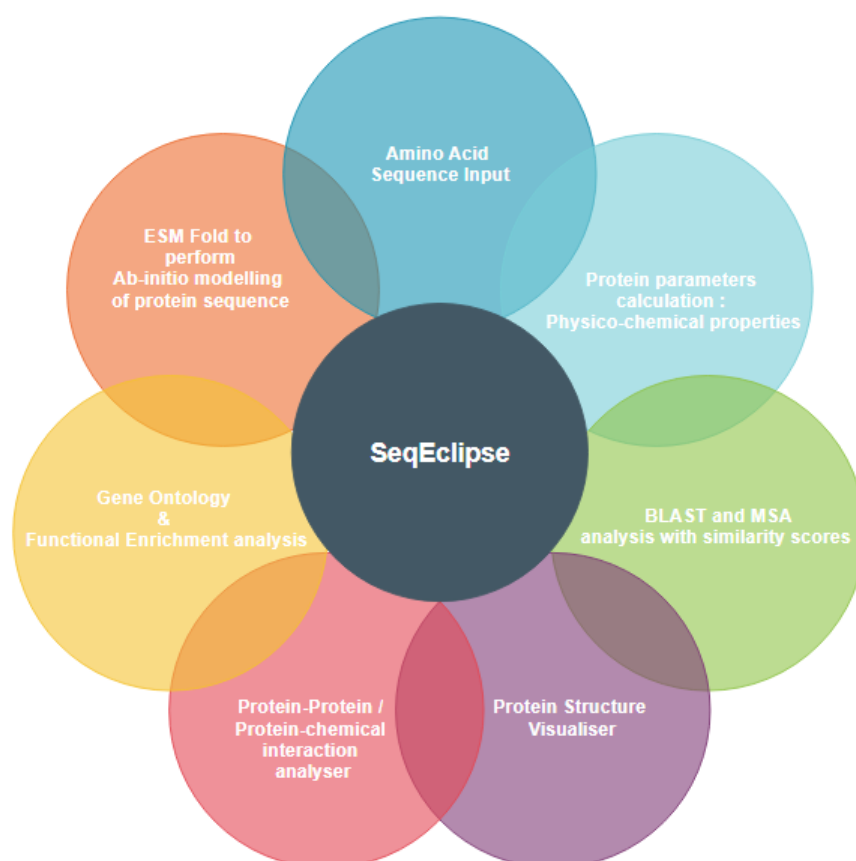


SeqEclipse : The bioinformatics server built with python web development

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In this document we present the python based web server for bioinformatics which has been built using Biopython library which is the python library for biological analysis of nucleotide or protein sequence analysis. Functionalities like protein parameter calculations to compute the physico-chemical properties of the protein sample input by user and BLAST analysis to obtain biologically and evolutionary similar sequences from the NCBI databases. We have also included the API from STRING database which will enable the functionalities to fetch the Protein-Protein or Protein-Chemical interactions based on the target protein/gene input by the user which will obtain us with the network graph of all possible interactions along with the Gene Ontology terminologies and functional enrichment analysis with biological localisations of the target and its interactions. We also leveraged the functionality of stmol and Py3DMol to program a protein structure visualiser where the user will input the PDB 4 letter code and the desired visualisation format for the molecule and submit on which the server will return the user with the complete structure from biological databases. The user will also be able to label desired amino acid residues which will be labelled onto the result structure. Ultimately we utilise the API from ESMFold which is an Ab-initio modelling technique for protein structures from their sequences which return the crystallised structured by comparing the query against similar proteins from the database. The user will be asked to input their desired amino acid sequence along with the similar options mentioned in the protein structure visualiser functionality previously after which the server will provide the user the possible predicted structure for the query amino acid sequence.



Link for the video explanation of the server : https://drive.google.com/file/d/1Dju2FPmN0i_NRvWt-AKD7aNFqWtw6LV/view?usp=sharing