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Abstract

The importance of bioinformatics methods in different branches of biotechnology

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Abstract:

In the recent era of science, the researchers are facing a considerable amount of raw biological information on different aspects of life science. Processing this information could be of great importance for predicting the outcome of biological interactions. One of the advantages of the in silico methods is to reduce the cost of laboratory work, project expenses, and the unnecessary sacrifice of animals. One of the applications for computers in life science is for classifying the structures of proteins based on their pseudo amino acid composition; such as classification of laccase enzymes from bacterial and fungal sources, or classification of Glutathione S-transferases from various sources by using different machine learning algorithms, such as Support vector machine (SVM), Random Forests (RF), Covariance Discrimination (CD) and Optimized Evidence-Theoretic K-nearest Neighbor (OET-KNN). In silico methods could also be used for predicting the structures of proteins that their tertiary structures have not been identified by crystallography methods, such as predicting the structure of Alcohol Dehydrogenase from Cyanobacterium Synechocystis sp. PCC 6803, which is a critical enzyme for biofuel production, or the Glutamate Dehydrogenase (GDH) from this Cyanobacterium. In this regard, different protein structure prediction methods, including denovo, template-based or a combination of them could be used by researcher's choice, based on the available information on protein. Another application of bioinformatics methods on structure analysis is the phylogenetic tree analysis, which demonstrates highly valuable information, that indicates the relationship of the similar structures from different species. Such information will be very useful for predicting the structure of a homology modeled protein, or perhaps the activity of a protein, based on its amino acid sequence.

Another practical use for these in silico methods is to predict the interaction of the receptors and their potential ligands (including both co-enzymes, or substrates. In this regard, examples include predicting the substrates and co-enzymes for Alcohol Dehydrogenase from Cyanobacterium Synechocystis sp.

Biography:

Mohammad Moradi has accomplished a master degree in medical biotechnology at Iranian center for blood transfusion organization, and is currently a Ph.D. candidate of microbial biotechnology in University of Isfahan, Iran. During his master degree, he has gained some insights from various application of biotechnology in medicine, but he believed that biotechnology is having more potential in other aspects of life, such as the impact of biotechnology in industry. He started his Ph.D. in the field of microbial biotechnology in 2018 at University of Isfahan. There he has worked on different aspects of using microbial biotechnology to improve the quality of human life. In 2018, he started to learn about the application of in silico methods in the field of biotechnology and life science. After that, he has been trying to use bioinformatics in different area of biotechnology.

Publication of speakers:

1. Behbahani M, Nosrati M, Moradi M, Mohabatkar H. Using Chou's general pseudo amino acid composition to classify laccases from bacterial and fungal sources via Chou's five-step rule. Applied Biochemistry and Biotechnology. 2020;190(3):1035-48.

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