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Precise modeling and prediction of cancer progress based on computationally-calculated of a large number of amino acid characteristics

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Much attention has been paid to the prediction of function based on nucleic acid sequence or modelling 3D structure of protein from its nucleic acid sequence. The general belief is that structural amino acid characteristics which are an intermediate stage between DNA/RNA and advanced protein structure are too simple and restricted for precise modelling of protein function. Opposite to the general belief, we demonstrated the possibility of estimating accurate amino acid-based models by improving the following steps: (1) Extraction of a large number of amino acid characteristics trough computational biology, (2) Selection of the important amino acid characteristics trough attribute weighting, and (3) Testing different combinations of machine learning with attribute weighting algorithms to find the best model. Our procedure showed high performance in different biological examples such as prediction of protein thermostability and halostability, prediction of different influenza types, as well as monitoring breast and lung cancers progress. This finding has the potential to be efficiently used in protein genetic engineering, discovery of amino acid based-biomarkers, increasing the accuracy 3D protein prediction, and developing websites/softwares for prediction of the result of amino acid mutation. In addition, important discovered amino acid features can be employed as clues for discovering key DNA mutations in cancer research.

Biography

Esmaeil Ebrahimie has completed his Ph.D at the age of 31 years from Tehran University and postdoctoral studies from The University of Adelaide. He is Adjunct Lecturer at the School of Molecular and Biomedical Science, at The University of Adelaide. He has published more than 30 papers in reputed. His major interest is application of novel bioinformatics, data mining, and molecular network analysis at infectious diseases and cancer research.