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A novel prediction model for different post-translational modifications: GEARS (genetic evolution of classifier by learning residues rules of sequences)

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Functional switching of proteins is an important challenge in proteomics and genomics. Information about structural dynamics of proteins regulating different functional modulations is helpful in predicting the multi-functionality of the proteins. The function of the protein depends on all levels of conformation (primary-3D) and post-translational modifications. The primary sequence and 3D structure information of the proteins has been utilized to evolve different prediction models by using various machine learning methods. The evolution of the prediction model by using information about the significant residues in surrounding of the modified residues as well as biophysical and biochemical properties of the amino acids are not considered yet. MAPRes (Mining Association Patterns among preferred amino acid residues in the vicinity of amino acids targeted for post-translational modifications) is a useful computational tool to find significant residues in surrounding of modified amino acids and for the development of the association patterns of these significant residues. The information about the primary sequence of the proteins and the association rules for the significant residues are considered to evolve the new dataset. These evolved datasets can play an important role for the development of a reliable prediction model. The current study proposes a classifier rule learning model named as GEARS (Genetic Evolution of CLAssifier by Learning Residues Rules of Sequences). This classifier considered artificial neural network (ANN), hidden Markov model (HMM) and MAPRes to train modified protein dataset. The capacity of the predication of the GEARS model will show improved results by the combination of different evolution models.

Biography

Zeeshan Iqbal has completed his MPhil from GC University, Lahore. He is the senior research associate at Institute of Molecular Sciences and Bioinformatics, Lahore. He has published 14 papers in reputed journals and serving as an Editorial Board Member of repute.

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