Parkinson's Disease Gene Identification Using Physicochemical Properties of Amino Acids

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Abstract : Gene identification, towards the pursuit of mutated genes, leading to Parkinson's disease, puts forward a challenge towards proactive cure of the disorder itself. Computational analysis is an effective technique for exploring genes in the form of protein sequences, as the theoretical and manual analysis is infeasible. The limitations and effectiveness of a particular computational method are entirely dependent on the previous data that is available for disease identification. The article presents a sequence-based classification method for the identification of genes responsible for Parkinson's disease. During the initiation phase, the physicochemical properties of amino acids transform protein sequences into a feature vector. The second phase of the method employs Jaccard distances to select negative genes from the candidate population. The third phase involves artificial neural networks for making final predictions. The proposed approach is compared with the state of art methods on the basis of F-measure. The results confirm and estimate the efficiency of the method.