ARTIFICIAL INTELLIGENCE SYSTEM FOR BIOINFORMATICS ANALYSIS

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Soft computing approaches have already been exploited to a great extent for applications in various fields of Bioinformatics. Our approach is based on the design and development of a rule-based Expert System (ES) for the purpose of automation of various analytical tasks in Bioinformatics. This system has a domain-specific knowledgebase, complete with its own inferencing system and an interface for Bioinformatics tools.

Based on the domain-specific input provided by the user, the system is capable of performing complete analysis of the data, by using Bioinformatics tools which are specific for the selected domain, and take decisions based on the automated inferencing of the results of these tools for supporting nature and course of further analysis. The system has currently been applied to prediction of 3D structures of proteins. Based on the statistics of the query sequence provided by the user, the system is capable of dynamically deciding the modeling approach, ie. Homology based, Threading based or the Ab-initio approach. The system then executes a set of Bioinformatics tools for structure prediction and validation of predicted structures, under the control of the inferencing system, which accesses the knowledge-base for its operation. This system is different from the existing ones (Swiss-model and I-Tasser) on the basis that it is not limited to a single modeling approach but weighs the chances of success of all three, before deciding the course of action.

Other fields of Bioinformatics to which the system is being applied are gene prediction and in analysis of gene expression data.