

5th World Congress on **Biotechnology**

June 25-27, 2014 Valencia Conference Centre, Valencia, Spain

A novel AIS-MACAX classifier in bioinformatics

Pokkuluri Kiran Sree¹, Inampudi Ramesh Babu² and SSS N Usha Devi N³

¹Jawaharlal Nehru Technological University Hyderabad, India

²Acharya Nagarjuna University, India

³Jawaharlal Nehru Technological University Kakinada, India

This study aims at introducing a classifier named as AIS-MACAX (Artificial Immune System Based Multiple Attractor Cellular Automata) which can address major problems in bioinformatics. The proposed classifier can predict the protein coding regions from a given DNA sequence and promoters in eukaryotes. It can also predict the secondary and quaternary structure of protein. All these three problems are interrelated. If a DNA sequence has a promoter there is a chance of transcription. If the same sequence has protein coding regions it can possibly undergo translation phase to form protein. So understating and analyzing all these problems is the greater concern of Bioinformatics. This classifier AIS-MACAX can handle large data sets for training and testing. The average accuracy of prediction of protein structure, protein coding region and promoter are 78%, 84% and 89% respectively. This AIS-MACAX will work in an automated procedure and surely lay an important milestone in the field of Bioinformatics.

Biography

Pokkuluri Kiran Sree received his BTech in Computer Science & Engineering, from J.N.T.U and ME in Computer Science & Engineering from Anna University. He is pursuing PhD in Computer Science from J.N.T.U, Hyderabad. His areas of interests include Cellular Automata, Parallel Algorithms, Artificial Intelligence, and Compiler Design. He was the reviewer for many International Journals and IEEE Society Conferences on Artificial Intelligence & Image Processing. His bibliography was listed in Marquis Who's Who in the World, 29th Edition (2012), USA. He is the recipient of Bharat Excellence Award from Dr GV Krishna Murthy, Former Election Commissioner of India. He received Active Reviewer Award for International Journal of Information Technology. He is also selected for Glory of Education Excellence Award 2012. He is the Board of Studies member of VikramaSimhapuri University, Nellore in Computer Science & Engineering stream.

profkiranree@gmail.com

Molecular mosquito science and its relation to pesticide resistance

Mohamed Ahmed Ibrahim Ahmed

Assiut University, Egypt

Mosquitoes are, without a doubt, one of the most dangerous and annoying pests that you can encounter, and definitely a pest you think of when you hear the phrase pest control. Mosquitoes are known to spread a wide range of serious and deadly diseases such as dengue fever, malaria and west Nile virus. Having mosquitoes around not only is a nuisance but also represents a serious health issue. However, insecticide application is considered the most important component in the global mosquito control effort. Currently, Pyrethroid and neonicotinoid insecticides are the most widely used insecticides for controlling mosquitoes worldwide. However, mosquito-borne diseases are now once again becoming a problem, largely because of the insecticide resistance (one of the biggest problems related to health and the environment) that has developed in mosquito vectors. Insecticide resistance poses a severe threat to our efforts to control the insect vectors of many human and animal diseases. Furthermore, the last few years have witnessed a considerable expansion in the number of tools available to perform molecular and genetic studies on the genome of mosquitoes. As a consequence, knowledge of aspects of the biology of mosquitoes, such as immunity, reproduction and behaviour, that are relevant to their ability to transmit disease is rapidly increasing, and could be translated into concrete benefits for malaria control strategies. Genetic strategies for reducing populations of vector mosquitoes or replacing them with those that are not able to transmit pathogens benefit greatly from molecular tools that allow gene manipulation and transgenesis. Mosquito genome sequences and associated EST (expressed sequence tags) databases enable large-scale investigations to provide new insights into evolutionary, biochemical, genetic, metabolic, and physiological pathways. Additionally, comparative genomics reveals the bases for evolutionary mechanisms with particular focus on specific interactions between vectors and pesticide resistance.

maiaf2000@yahoo.com