

GIAN WORKSHOP ON GENOME INFORMATICS

(Data mining, systems biology, biomarker discovery, neural networks & protein modeling for functional analysis and designing of life forms)

Overview

Since the sequencing of the human genome, molecular techniques have grown into powerful technologies, with new approaches to study biology at genomic, epigenetic, proteomic and metabolomics levels. This has led to the generation of rapidly growing big data. Such data abodes the challenges of volume, resolution and complexity; plus the quality. Analysis of such data requires careful consideration, paying attention to the non-linearity and fluidity of biological systems, the interactions among molecular entities in pathways and the need for biological validation of the new entities, as these are discovered. These issues have never been fully addressed, nor have the data streams from multi-omics technologies integrated, utilising non-linear adaptive algorithms applied at systems biology level. As examples, molecular and bioinformatics techniques have been utilised in understanding and improving the structure and function of genes, promoters and life forms. These have been applied to develop new approaches to correct diseases and traits in all life forms. Yet the science of bio-informatics faces big gaps in analysing the information hidden in complex biological data. This course will teach the applications of computational methods, algorithms and neural networks for modeling systems in biology from the basics. It will include a broad basis of statistical methods, leading to robust algorithms for complexanalytics of nucleic acids, protein and pathways.

Modules	October 3 to October 8, inclusive of the weekend as working days. <hr/> The number of participants in the course will be limited to twenty. All participants will be given hands on training, involving problem solving. Hence, they must have their own laptops for participation in the workshop. The required software and LAN connectivity will be provided
You Should Attend If...	<ul style="list-style-type: none">• Researchers working on disease and trait- related biomarkers, networking and pathway construction, protein structure and systems analysis.• Biotechnology & molecular biology lab managers& biotech engineers and researchers from biotech, health and agriculture.• Computer science and IT faculty and students with interest in decoding the complexities of genetic coding language that determines the growth and development of biological forms.• Faculty and staff from government and private teaching organizations and R&D laboratories.• Students at all levels (BTech/MSc/MTech/PhD) or Faculty from reputed academic and technical institutions involved in genome assembly, comparative transcriptomics, genome editing, protein modeling.
Fees	The participation fees for taking the course is as follows: Participants from abroad : US \$500 Industry/ Research Organizations: INR5000 Academic Institutions: INR 2500 The above fee includes all instructional materials, laboratory equipment usage charges, 24 hr free internet facility. The participants will be provided with accommodation on payment basis.

The Faculty



Dr. Graham Roy Ball is Professor & Chair in Bioinformatics, School of Science & Technology, Nottingham Trent University, Nottingham, UK. He is Fellow of the Royal Society of Medicine and the Royal Society of Biology. He has special interest in the application of artificial neural networks to the modeling of plant and environmental systems. His work on the application of bio-informatic algorithms using ANN to the identification of biomarkers for human disease diagnostics, specially cancer and tuberculosis will be of special interest at the workshop. He is also Chief Scientific Officer of a company for strategic application of data mining, modeling and strategic development.



Dr. Rakesh Tuli is national J C Bose Fellow and Sr Research Advisor at Panjab University, Chandigarh. He has been Director of research laboratories in CSIR and DBT. He is Fellow of all major science academies in India. He has applied nucleic acids sequence analytics extensively to analyzing promoter function and gene designing. His group has been one of the pioneers in India to design and chemically synthesize novel genes and promoters for targeted functions in plants. He has guided research on transcriptomics, differential pathway analytics and gene editing and is known for the development of insect resistant transgenic crop plants.



Dr. Kashmir Singh is Associate Professor in the Department of Biotechnology at Panjab University, Chandigarh. He has guided a number of research projects involving coding and non coding RNA for functional genomic analysis in plants. He has guided work on secondary metabolism in medicinally important plants, and biotic as well as abiotic stress tolerance genes in crop plants. His expertise in genome assembly and comparative transcriptomics will be of special interest at the workshop.



Dr. Md. Ehesan Ali is an Associate Professor (Scientist-E) at Institute of Nano Science and Technology, Mohali. He is working on theory and simulations of various magnetic materials, bio-macromolecules and proteins to develop novel materials for spintronics, bioelectronics and also diagnostic techniques for diseases like malaria, cataract etc. His work is based on broad range of electronic structure theories including density functional theory, wave function based multi-configurational methods, transport calculations, *ab initio* and classical molecular dynamics simulations.

Course Co-ordinators

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Dr. Mamta Juneja is Assistant Professor in the Department of Computer Science Engineering, University Institute of Engineering. & Technology, Panjab University, Chandigarh. She is working on various research projects funded by MHRD and DeITY. Her research interests include Biomedical image processing, Medical devices and Restorative technologies, Data mining and Machine learning.

