# Human Genomics: Computational Methods and Applications

## Overview

The course will cover recent advancements in the fields of Human Genomics with a wide coverage on computational studies, and introduction to real-life practical applications. The goal of lectures is to introduce participants to basic theoretical ideas of computational genomics with the special focus on algorithms. Lectures will be accompanied by tutorials and training that will allow participants to perform simple genomics tasks, including programming/statistical data processing at the scale of the whole Human genome.

The main objective of the course is to study the three-dimensional structure of the human genome, and its relationship with the genomic diversity of human populations, both natural and pathological. The participants will learn the use of structural information to enrich the sequential genomic analysis to better define the function of selected genomic regions that are important in the context of personalized medicine. For this purpose, firstly we propose to introduce to the participants a variety of large-scale computational tools for analysis of whole genome sequences, the identification of structural variants, determining the statistical significance of the observed number of copies of genomic regions in selected cohorts of patients etc. Secondly, we will show their uniqueness in comparing the observed changes with typical and natural genomic diversity that has been catalogued, for example, in the 1000 Genomes Project Consortium. Thirdly, we may infer the biological functions of these genomic regions using publicly available databases. Fourthly, we will identify unique local three-dimensional environment for selected sites, eg. regulatory ones. In the fifth step, we will analyze the impact of structural re-arrangements of those local neighborhoods on the gene expression profiles, which is related to the presence of transcription factories.

Course participants will learn these topics through lectures and hands-on experiments. Also case studies and assignments will be shared to stimulate research motivation of participants.

**Modules**

**Course Duration : December 11 to December 16, 2017**

**Course details:**

***Day#1:***

- ***Lecture 1*****:** Introduction to Human Genome.
- ***Lecture 2*****:** Introduction to Systems Biology and its applications in Human Genomics.

***Day#2:***

- ***Lecture 3:*** Introduction to Computational Genomics Methods and Algorithms.
- ***Lecture 4*****:** Next Generation Sequencing methods, genome sequence assembly algorithms
- ***Tutorial 1*****:** Introduction to Bioinformatics tools and databases, systems biology methods.

***Day#3:***

- ***Lecture 5:*** Identification of structural variants in Human Genome.
- ***Lecture 6*****:** DNA sequence motifs analysis and identification.
- ***Tutorial 2:*** Problem solving session with examples: Introduction to Bio-Python.

***Day#4:***

- ***Lecture 7* :** Protein structure prediction: theory and applications
- ***Lecture 8* :** Protein function prediction: theory and applications
- ***Tutorial 3*****:** Problem solving session with examples: Clustering and Classification; phylogenetic tree analysis.

***Day#5:***

***Lecture 9:*** Genomics tools, resources and databases.

***Lecture 10*:** Recent advances in human genome three-dimensional structure identification.

***Tutorial 4:*** 1000 Genomes web resources, ENCODE database, WashU genome browser: case studies.

**Number of participants for the course will be limited to fifty.**

## You Should Attend If…

- You are a scientist or researcher from bioinformatics and computational biology domains from Government organizations, R&D laboratories or other institutions.
- You are a student at of B.Sc./B.Tech./M.Sc./M.Tech./Ph.D.
- You are a faculty member from a reputed academic institution or technical institution.

## Fees

**Step 1: GIAN Registration**

Mandatory registration fee of Rs.500/- to be paid through the GIAN website (http://www.gian.iitkgp.ac.in/GREGN). The registration on GIAN is a one-time affair, i.e. once you are registered on GIAN portal you may apply for any GIAN course.

**Step 2: Course registration**

*Participants from abroad :* ***US $200***
*Industry/ Research Organizations:* ***Rs.5000/-***
*Academic Institutions:* ***Rs.2000/-***
*Students:* ***Rs.1000/-***

The above fee must be paid over and above the GIAN registration fee and includes all instructional materials, tutorials and laboratory usage charges.

Course Registration website: https://goo.gl/forms/2vTJEB3hLUgPefs03
Contact email: gian.genomics@gmail.com

# The Faculty

**Dariusz Plewczynski** is a Professor at the University of Warsaw in the Center of New Technologies CeNT, Warsaw, Poland, and head of the Laboratory of Functional and Structural Genomics. His recent achievements cover qualitative and quantitative biological data analysis, the general systems theory and interdisciplinary problems in the context of bioinformatics, genomics, drug design, and systems biology; ensemble learning systems, meta-clustering techniques and computational modelling to various interdisciplinary problems in Human genomics.

**Mita Nasipuri** received her B.E.Tel.E., M.E.Tel.E, and Ph.D. (Engg.) degrees from Jadavpur University, in 1979, 1981 and 1990, respectively. Prof. Nasipuri has been a faculty member in the Department of Computer Science and Engineering, Jadavpur University, since 1987. Her current research interest includes bioinformatics, image processing, pattern recognition, and multimedia systems. She is a senior member of the IEEE, U.S.A., Fellow of I.E. (India) and W.B.A.S.T, Kolkata, India.

**Subhadip Basu** received his Ph.D. degree from Jadavpur University in 2006 and did his Post-Doctoral research from University of Iowa, USA in 2010-11 and from University of Warsaw, Poland during 2012-14. Dr. Basu is a faculty member of the Computer Science and Engineering Department of Jadavpur University since 2006, where he is currently serving as an Associate Professor. He is also an Honorary Research Scientist in the Department of Electrical and Computer Engineering, University of Iowa, USA since 2016. His current research interests include bioinformatics, biomedical image analysis, handwritten text analysis, character recognition etc. He has worked in many international institutes of repute, including Hitachi Central Research Laboratory, Japan, Bournemouth University, UK, University of Lorraine, France, Nencki Institute of Experimental Biology, Poland, etc. He is the recipient of the Research Award from UGC, Govt. of India, BOYSCAST and FASTTRACK young scientist fellowships from DST, Govt. of India, HIVIP fellowship from Hitachi, Japan and EMMA fellowships from the European Union. He is a senior member of IEEE and life member of IUPRAI (Indian unit for IAPR).

## Course Co-ordinators

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**GIAN Registration Link:**
http://www.gian.iitkgp.ac.in/GREGN

**Course Registration website:**
https://goo.gl/forms/2vTJEB3hLUgPefs03