

# Nanopore Sequencing and data analysis: opportunities for rapid biodiversity and biosurveillance programs and local capacity building

[16 March, 2023 to 29 March, 2023]

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## Overview

This workshop covers basic and applied aspects of next generation sequencing including sequencing technologies with special emphasis on nanopore sequencing, sequencing applications, nanopore-based on site DNA barcoding, clinical genomics, metagenomics, whole shotgun metagenomics and meta-transcriptomics. Sequencing technologies cover from Sanger to NGS, second generation sequencing technologies: from 454 to Element biosciences and third generation sequencing technologies (single molecules). Sequencing applications include whole genome resequencing, targeted capture methods for exome and gene panels, De novo assembly and Pan-genomes, RNA Sequencing, and Methylome analysis. Clinical genomics consists of primary analysis (FASTQ, filtering/trimming reads based on quality score, demultiplexing, adapters trimming), and Secondary analysis (Alignment of reads on the reference genome, De-duplication, variant calling on aligned reads, Filtering of variants based on quality of variants call). Nanopore-based on site DNA barcoding contains from “samples to the lab” to “lab to the samples”: an overview, and protocols and instruments for on-site DNA barcoding. Metagenomics analysis comprises quality control, filtering and assembly/clustering to taxonomic classification, functional assignment and comparative metagenomics. Both community analysis of amplicon sequencing data as well as analysis of whole genome shotgun sequencing data will be covered including methods for statistical comparisons of multiple metagenomics samples.

Transcriptome sequencing and informatics concepts provide training on analyses of RNA-Seq data including the use of different analytical tools, relevant file formats, reference genomes, transcriptome annotations, quality control measures, reference-based alignment, gene expression, and differential gene and isoform analyses.

You will be briefly introduced into the Linux operating system and in this environment you will analyze sequencing data using various publicly available tools. The course would consist of lecture and practical sessions to familiarize students with the theory and practice of phylogenetic studies, structural and functional genomics. Furthermore it will also provide a clear understanding about Next Generation Sequencing concepts and data analysis especially nanopore sequencing, clinical genomics, metagenomics and transcriptomics. These tutorials will be accompanied by hands-on exercises using complete analytical pipelines on test datasets.

<b>Modules</b>	<p style="text-align: center;"><b>16 March, 2023 to 29 March, 2023</b></p> <p><b>Module: Theory and Practice of Next Generation Sequencing, metagenomics, transcriptomics, and Data Analysis</b></p> <p>Number of participants for the course will be limited to Thirty (<b>30 Nos.</b>).</p>
<b>You Should Attend If...</b>	<p>Postgraduate students, scholars, and researchers from universities, research institutions, government organizations, and R&amp;D laboratories who are interested in research.</p>
<b>Registration</b>	<p><b>No registration fee.</b> Participants are requested to register with Global Initiative of Academic Networks (GIAN) portal <a href="https://gian.iitkgp.ac.in">https://gian.iitkgp.ac.in</a> And select the course No. 194017C01.</p>
<b>Boarding and Lodging</b>	<p><b>Boarding and lodging will be met by the participants.</b> The participants will be provided single/shared accommodation in the Institute Guest house/Guest Rooms/ student hostel on payment basis.</p>

# Modules

16 March, 2023 to 29 March, 2023

## **Module 1: Sequencing technologies (4 hours)**

- From Sanger to NGS
- Second generation sequencing technologies: from 454 to Element biosciences
- Third generation sequencing technologies (single molecules)

## **Module 2: Sequencing applications (4 hrs)**

- Whole genome resequencing
- Targeted Capture Methods for exome and gene panels
- De novo assembly and Pan-genomes
- Metabarcoding and RNA Sequencing and Methylome Analysis

## **Module 3: Nanopore-based on site DNA barcoding (4h)**

- On site sequencing: an overview
- Protocols and instruments for on-site DNA barcoding

## **Module 4: (Meta)barcoding (practical, 8 hours)**

- MinION library preparation
- Sequencing, Base calling and Blast analysis

## **Module 5: Molecular Phylogeny and Bioinformatics (Theory & practical, 6 hours)**

## **Module 6: Metagenomics data analysis (Theory & Practical – 16 hrs)**

- Amplicon sequencing of marker genes
- Analysis of marker genes – practical part
- Data preparation (sequence trimming, quality filtering, OTU clustering)
- OTU table construction and OTUs classification
- Evaluation of results from meta-taxonomic analysis

## **Module 7: Open Source Scientific Tools and Computing Languages (Theory & Practical – 6 hrs)**

- R Statistical Computing Language for biologists
- Scientific Computing for Rare Disease Genomics
- Introduction to LINUX

## **Module 8: Open Source Reproducible Research (Theory & Practical – 2 hrs)**

- Open Source Reproducible Research

## **Module 9: R and Bioconductor (Theory & Practical – 4 hrs)**

- Introduction to R & Bioconductor for Cancer Genomics
- Open Source Data Visualization for Cancer Genomics

## **Module 10: R Statistical Computing (Practical – 6 hrs)**

- Programming with R Statistical Computing Language - Beginner Level

## **Module 11: R Statistical Computing (Practical – 6 hrs)**

- Programming with R Statistical Computing Language - Advanced Level

## **Module 12: Genomics & Computational Biology (Theory & Practical – 6 hrs)**

- Statistical Genomics with R & Bioconductor Level 0,1 and 2

## **Module 14: Transcriptomic Profiling - I (Theory & Practical – 10 hrs)**

- RNAseq: From raw reads to count matrix - Part 1-5

## **Module 15: Transcriptomic Profiling - II (Theory & Practical – 9 hrs)**

- RNAseq: From count matrix to differential expression analysis - Part 1 & 2
- RNAseq: Differential expression analysis to enrichment analysis - Part 1 & 2
- RNAseq data visualization - Part 1 & 2

## International Course Coordinator



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**Prof. Massimo Delledonne** received his Ph.D. from Università Cattolica del S. C. in 1994. During 1995-1998 he visited Chris Lamb at the Salk Institute for Biological Studies in California, discovering the function of nitric oxide in plant disease resistance. In 2001, he joined the University of Verona as Associate Professor of Plant Genetics (SSD Agr/07). Together with his colleague Mario Pezzotti, in January 2007 founded the Center of Functional Genomics. This center is dedicated to the development and use of the new tools that the new genomic technologies are offering to microbial, plant, animal and human biologists. Massimo Delledonne is currently Full Professor of Genetics (SSD Bio/18). He manages a vigorous research program that emphasizes interdisciplinary approaches to understanding plant and human biology. His own expertise is in the areas of genetics, molecular biology and genomics, and collaborates with researchers in diverse fields, including bioinformatics, microbiology and plant genomics, and medicine. He is co-founder of Personal Genomics S. R. L., a former spin-off of University of Verona established in 2011 that operates in the field of human genomics and personalized medicine, now part of the SOL group. He has published more than 400 research publications and his H index is 73 with 25600 citations to his credit.

## Invited Speakers



**Dr. Sandip Paul**  
*Associate Professor, Centre for Health Science and Technology,  
JIS Institute of Advanced Studies and Research Kolkata*

Dr. Sandip Paul is a computational biologist having more than 15 years' experience with analysis and understanding of the diverse adaptive evolutionary mechanisms in microbes through the use and development of different software tools. His work has provided important insights to explore the adaptive evolutions necessary for phenotypic diversification of human commensal and pathogenic microorganisms.

## Course

## Coordinator

**Prof. Guruswami  
Gurusubramanian**

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## Invited Speakers



**Dr. Rintu Kutum** *Faculty Fellow, Department of Computer Science, Faculty, Trivedi School of Biosciences, Data Scientist, Mphasis Lab for Machine Learning & Computational Thinking, Ashoka University, Sonipat, Haryana, India.*

Dr. Rintu Kutum is a faculty fellow/data scientist at the Department of Computer Science, Ashoka University. He was the project coordinator of “AL/ML for Health care” theme under the “City Knowledge Innovation Cluster – Delhi Research Implementation and Innovation” Project at the Center for Excellence in Healthcare, IIT, Delhi. He is expertise in the areas of machine learning, genomics and gene regulatory networks. His long term interest is to train and nurture transdisciplinary scholars for doing collective research on Computational Health Sciences: Cellular Ecosystem to Public Health.



**Dr. Aakansha Rai**

*Postdoctoral Fellow, Cell Biology Lab, IIT-Delhi, Sonipat Campus, Haryana*

Dr. Aakansha Rai is working as a research associate at the IIT Delhi Sonipat Campus. She did her PhD from CSIR-Institute of Genomics and Integrative Biology (IGIB) and her Masters in the field of Plant Molecular Biology was from University of Delhi, South Campus. She has extensive training in cell and molecular Biology. Despite being from an experimental background she learnt to use R programming, with the help of peers and friends, to derive insights from publicly available datasets like TCGA, applying basic statistics to her experimental data and through participating in the renowned DREAM challenges.



**Ms. Himani Balutia**

*Project Associate - Rare Disease Genomics, Centre for Computational Biology & Bioinformatics, Ashoka University, Sonipat, Haryana, India.*

Ms. Humani Balutia is a Project Associate at the Centre for Computational Biology & Bioinformatics at Ashoka University. She did her master's in the area of Pharmaco Informatics from NIPER, Kolkata. Currently she is involved in various projects at Ashoka University such as Understanding Regulatory Logics in Rare Disease Genomics, Harmonization of Unstructured EHR for Machine Learning Ready EHR data etc. She uses R programming extensively for her ongoing research.

**Course**

**Coordinator**

**Prof. Guruswami  
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## Local Course Coordinator



G. Gurusubramanian is Professor of Zoology, School of Life Sciences in the Department of Zoology at Mizoram Central University, Mizoram, India. He earned his UG and PG degree from Madurai Kamaraj University, Tamilnadu and received his Ph.D. from the University of Madras, Chennai. He is a recipient of the Humboldt fellow, INSA

Visiting fellow, UGC visiting fellow, International Visiting Scientist, DBT Overseas Associateship, and Fellow of International Society of Ecological Communication, Poland. In his assignment as a Humboldt fellow from Biologische Bundesanstalt fur land & Forstwirtschaft, Institut fur biologischen pflanzenchutz, Germany involved in the industrial production of neem pesticides and *Bacillus thuringiensis* against forest and agricultural pests. In 1993, he joined the Goodricke R&D, London, UK and managed the international Tea Research operations in India, Zambia, Papua New guinea and Sri Lanka and dedicated to the development and practice of organic farming, Biocontrol and Bio-pesticides. He is an author/co-author of more than 250 peer-reviewed Scopus indexed Q1 publications with high impact factor, 25 book chapters and 13 patents, he presented 65 invited or keynote lectures, and was the supervisor of 25 Ph.D. students. His H index is 25 with 2509 citations to his credit. He is a life member of the several associations and societies and acts as a peer reviewer for several Elsevier, Springer and nature communications Journals. His own expertise is in the areas of molecular entomology, IPM, Organic farming, Insect-plant-Microbe interactions, Stress Biology, and collaborates with researchers in diverse fields, including animal model studies, phyto-medicine, Metagenomics, Transcriptomics, Metabarcoding, Molecular phylogeny, Molecular medicine, drug designing and Toxicogenomics. He manages a vigorous research programs as a project leader or co-investigator on several research projects funded by the UGC, SERB, CSB, DST, DBT, CSIR, DRDO, and numerous industrial projects.

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