GLOBAL INITIATIVE OF ACADEMIC NETWORKS

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

[16 March, 2023 to 29 March, 2023]

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.

Modules	**16 March, 2023 to 29 March, 2023** **Module: Theory and Practice of Next Generation Sequencing, metagenomics, transcriptomics, and Data Analysis** Number of participants for the course will be limited to Thirty (**30 Nos.**).
You Should Attend If…	Students and Researchers from Universities, Research Institutions and government organizations including R&D laboratories.
Fees	The participation fees for taking the course is as follows: Participants from abroad : **US $ 1000** Research Scholars : **₹ 3000.00** Faculty Members : **₹ 6000.00** The above fee includes all instructional materials, computer use for tutorials and assignments, 24 h free internet facility. **Boarding, lodging, and meal charges are not included in the fees**. The participants will be provided single/shared accommodation in the Institute Guest house/Guest Rooms/ student hostel on payment basis.

Teaching Faculty

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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.

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G. Gurusubramanian is Professor of Zoology, School of Life Sciences in the Department of Zoology at Mizoram Central University. He earned his B.SC. in Chemistry and Zoology (Double Major) from Madura College, Madurai Kamaraj University, Madurai, Tamilnadu, M.Sc. from Ayya Nadar Janaki Ammal College, Madurai Kamaraj University, Madurai, Tamilnadu, Ph.D. in Zoology (Entomology – Interdisciplinary) from the University of Madras at Entomology Research Institute Loyola College, Chennai and post-doctoral experience from Biologische Bundesanstalt fur land & Forstwirtschaft, Institutfur biologischen pf lanzenschutz, Germany. His current research interests include Metagenomics, Transcriptomics, Metabarcoding, Molecular phylogeny, Molecular medicine and drug designing and Toxicogenomics. Over a period of 31 years, he has published over 200 research publications (H index 24 with 2402 citations) and 25 book chapters and served as project leader or co-investigator on several research projects funded by the UGC, SERB, CSB, DST, DBT, CSIR, DRDO, and numerous industries. 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.

Course Coordinator

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