Kristu Jayanti College

AUTONOMOUS Bengaluru

Reaccredited A++ Grade by NAAC | Affiliated to Bengaluru North University

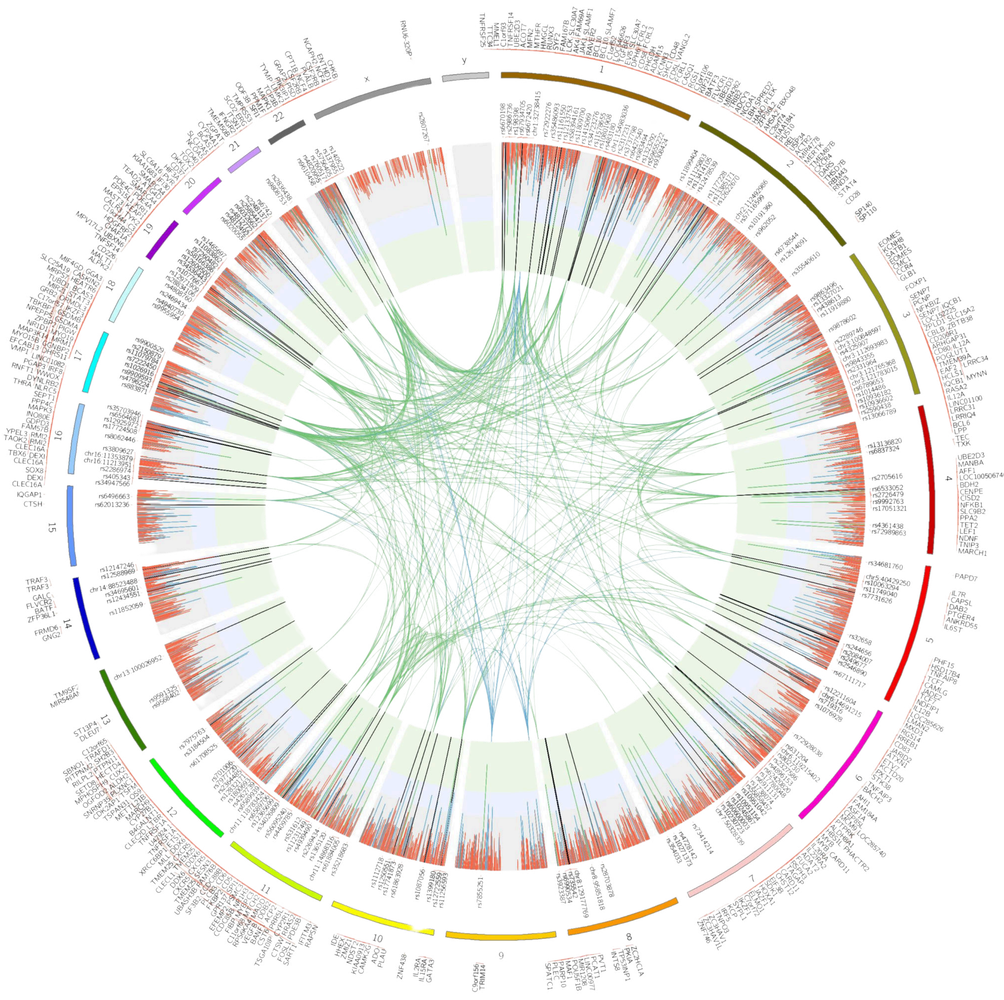
Department of Life Sciences

Light & Prosperity

Kristu Jayanti College

1999 - 2024

Empowering Visions, Enriching Lives



Workshop on

Computational Omics

Edition 2

October 19-21 & 26-27, 2024

Resource Persons

Dr. Nitish Malhotra
Dept. of Ecology
& Evolutionary Biology
University of California,
Irvine, CA

Ms. Akshara Dubey
Dept. of Bioinformatics
NCBS
Bengaluru

Dr. Anurag K. Singh
Dept. of Bioinformatics
NCBS
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Dr. Kushi Anand
Dept. of Life Sciences
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Dr. Dileep Francis
Dept. of Life Sciences
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Bengaluru

Key Take Away Skills

- Proficiency in R and Python
- Extracting meaningful insights from sequence data
- Understanding NGS workflows
- Competency in phylogenomic analysis
- Skills for mutation characterisation from DNA sequencing data
- Competency in transcriptomic analysis (RNA-sequencing)
- Hands-on proficiency in Computer Aided-Drug Design

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Kristu Jayanti College, Autonomous, Bengaluru, Karnataka-560077

About the Workshop

Advanced omics technologies have revolutionized and transformed our understanding of biological machinery in different physiological conditions. However, the wealth of data generated in modern omics and the fast-evolving technologies poses significant challenges. For meaningful interpretation, sophisticated computational strategies and advanced bioinformatics expertise is required. This motivates us to organize the **Second Edition** of intensive five-day hands-on workshop on computational Omics. This training will help the participants to develop the required skills to comprehend the latest computational techniques used to analyse high throughput data that support toward understanding of the biological processes, evolution, and diagnosis. After successful completion of all the session they will be proficient in analysing different types of Next genome sequencing (NGS) data and answering biological research questions. The workshop will bring together students, trainees, early-stage investigators, and expert faculty in bioinformatics, and omics technologies.

Selection & Eligibility

- Target Audience: Faculty Members, PhD Scholars, Researchers, Postgraduate Students, & Final Year Undergraduate Students
- Maximum Intake: 45 Only
- Mode of Selection: First-cum First-Served Basis

Registration & General Guidelines

Register online using the following link:
https://portal.kristujayanti.edu.in/event-workshop-on-computational-omics-edition-2
or by scanning the QR code

After successful registration and payment, selected participants will be informed by 18. 10. 2024
Last date to apply: **16. 10. 2024 before 7: 30 pm**
Dates: **October 19th - 21st &, 26th & 27th, 2024**
Timing: **09:15 am – 05:15 pm**
Venue: **Computer Lab, Kristu Jayanti College, Autonomous**

Registration Fees (INR)

UG and PG students (Internal) : 2000
UG and PG students (External) : 2500 + GST
Research Scholars: 2500 + GST
Faculty members : 3000 + GST

General Guidelines:

Registration fees once paid will not be returned in any case
Participants are eligible for a Certificate only if they attend all the sessions of the workshop
Registration fees do not include lodging
Working lunch will be provided

For more details, contact conference convenors:

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Dr. Dileep Francis
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Workshop Schedule

Day 1: *19. 10. 2024*

Theory Session I

- Introduction to drugs, targets and drug discovery
- Computer Aided Drug Discovery: Structure based and ligand based drug discovery
- Docking & Molecular DynamicsTheory

Hands-on Training Session I

- Molecular Visualisation using Pymol
- Molecular Docking using Autodock Vina, Schrodinger Maestro
- Virtual Screening Using Glide
- Molceular Dynamics & MMGBSA using Desmond

Day 2: *20. 10. 2024*

Hands-on Training Sesion II

- Introduction to R and Python
- Introduction to interface
- Basic syntax
- Types of data formats
- Reading, writing and interconverting different types of data
- Introduction to basic packages and modules
- Reading and processing NGS data

Theory Session II

- Basics of DNA and its organisation in the nucleus
- Next Generation Sequencing (NGS), history and its basics
- Types of NGS applications. What questions can be answered through NGS
- Understanding the NGS data and file formats
- Introduction to publicly available dataset repositories and how to access them.
- How do we identify an organism? 16S metagenome and other methods

Day 3: *21. 10. 2024*

Hands-on Training Session III

- From sequence to the organism: genome assembly, annotating the genome and identifying the organism (bacterial species), tools used and its description
- Finding relationships between species based on genome sequences
  - Aligning sequences, description of different methods and their benefits
  - Assessing conservation and diversity
  - Creating a phylogenetic tree
  - Identifying phylogenetic relationships between species

Theory Session III

- Alterations in the DNA sequences, a recipe for disease and evolution?
  - Mutations and chromosomal variations: types and how to identify them
  - What leads to the generation of these DNA alterations
  - Examples of the devastating effects of these mutations
- Inferences and applications of understanding evolution
  - How do mutations/ variations in the genome lead to evolution
  - Example cases of species diversification through mutations
- Mutations associated with cancer
- Personalised therapy for cancer patients?

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Workshop Schedule

Day 4: *26. 10. 2024*

Hand-on Training Session IV

- Identifying variations from NGS data
- Basics for the software used
- Downloading the data and its processing, formats of data
- Running the mutation finder software
- Filtering of mutations
- Visualization of mutations
- Predicting the effect of mutations found through our analysis.

Theory Session IV

- Principles of Central Dogma and its violations
- Understanding gene regulation and transcription
- How and why to study gene transcription
- Experimental setup for RNA-seq
- Potential use cases of RNA-seq in diseases and medicine

Day 5: *27. 10. 2024*

Hands-on Training Session V

- Analysing RNA-seq data from scratch
- Downloading data and understanding the file formats
- Description of software used for the RNA-seq analysis
- Basics of the reference genome
- Alignment of the reads to reference genome, split alignment?
- Gene annotation and count data generation
- Identification of differentially expressed genes: DGE analysis
- Filtering of gene candidates
- Identifying functions affected by drug treatment: pathway enrichment analysis

Post-Workshop Assessment

- MCQ test
- Group discussion (4 students per group) about real-life application of learnt themes and invoking the thought process on new techniques to tell them the possibilities
- Closing Remarks and Prize distribution

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