

Organizers

Ms. Vijayalakshmi R
Ms. K. Sidhika
Mr. C. Narendran
Mr. P. Krishnamani Kumar
Mr. Paul X. Clinton

Workshop Tutor

Ms. Sowmya Pulapet

Patrons

Dr. Mariazeena Johnson, Chancellor
Dr. Marie Johnson, President
Mr. J. Arulselvan, Vice-President
Ms. Maria Bernadette Tamilarasi, Vice – President
Ms. Maria Catherine Jayapriya, Vice – President
Dr. T. Sasipraba, Vice – Chancellor

Refreshments and lunch will be provided
Certificates will be issued
Accommodation **will not be provided**

Candidates should bring their laptop with recent Windows version 10+ with 8GB RAM, Ubuntu or Wsh already installed if possible



SATHYABAMA

INSTITUTE OF SCIENCE AND TECHNOLOGY
(DEEMED TO BE UNIVERSITY)

Accredited with 'A++' grade by NAAC | 12B Status by UGC | Approved by AICTE
Jeppiaar Nagar, Rajiv Gandhi Road, Chennai-600119, Tamil Nadu, India



Sathyabama Institute of Science and Technology and Oneomics
jointly presents

3-Days Workshop on

From Sample to Insight: A Hands-on NGS and RNA-Seq Workshop



Venue: IRC 3rd Floor, Skill Development Centre
Sathyabama Institute of Science and Technology

About the Workshop

The purpose of this workshop is to get an understanding of Next-Generation Sequencing (NGS) and gain practical experience in RNA Sequencing data analysis. You will be trained to understand NGS data formats and handle potential problems/errors. The course layout has been adapted to beginners' needs in the NGS data analysis field. It allows anyone with no or little background in computer science to get a first hands-on experience in this new and fast-evolving research topic.

Workshop Outline

Essential Computing Skills: Introduce beginners to computing basics for NGS data analysis (e.g. Linux Command-line, tool installation).

NGS Analysis Algorithms and Data Formats: Understand read alignment and data formats used in NGS analysis.

Handling RNA-Seq Data: Learn to use bioinformatics tools for managing RNA-Seq data.

RNA-Seq Data Processing: Trim data, align it to a reference genome, and visualize alignments.

Expression Estimation: Estimate gene and transcript expression using different methods.

Differential Expression Analysis: Compare various approaches for analyzing differential gene expression.

Visualization in R: Visualize and summarize RNA-Seq analysis results using R.

Pathway Analysis: Perform pathway analysis to understand the biological context.

Schedule

Day 01

10:00 - 12:15	Intro-lecture on NGS and Data analysis Hands-on command line usage in Linux, Intro to RNA-seq and Workflow FASTA, FASTQ, and GTF - formats
12:15 - 13:00	Lunch
13:00 - 15:00	Tool installation and usage Data QC Data preprocessing

Day 02

10:00 - 12:15	RNA alignment concepts and file formats (SAM, BAM, and BED) Alignment vs Assembly vs K-mer approaches
12:15 - 13:00	Lunch
13:00 - 15:00	RNA-seq Alignment Visualization with IGV Quantification Data Normalization and DEG Analysis

Day 03

10:00 - 12:15	DE Visualization
12:15 - 13:00	Lunch
13:00 - 15:00	DE Pathway Analysis

Registration Fee: PG- 2000/- ; PhD- 2500/-

Seats limited to 25 nos

Eligibility: Post graduate, PhD

For Queries Contact:

98402 44450/ 70925 26805

Scan the QR code for registration

