DR Biosciences

Scientific Bio-Minds
Life begins here...

Scientific Bio-Minds in association with DR Biosciences is organizing
Hands on Training in

National Workshop in
Next-Generation Sequencing Data Analysis
Decode genome with AI & ML

Duration: 3 Days

📅 28th – 30th March, 2024

About the workshop
The Next-Generation Sequencing (NGS) Data Analysis workshop is designed to provide hands-on training on various bioinformatics tools and techniques for analyzing large-scale genomic data generated by next-generation sequencing technologies.

Aim
The workshop also aims to provide participants with advanced knowledge and skills in NGS data analysis. The ultimate goal of the workshop is to enable participants to apply these techniques to solve complex research questions and make meaningful scientific discoveries in the field of genomics.

Course Objectives:

1. To provide participants with a solid understanding of the principles and methods used in NGS data analysis, including quality control, read alignment, variant calling, and annotation.
2. To enable participants to apply NGS techniques to solve complex research questions and make meaningful scientific discoveries in the field of genomics.
3. To provide participants with hands-on experience in working with real-world datasets and using popular bioinformatics tools and pipelines for NGS data analysis.
4. To foster collaboration and networking among participants and instructors, providing valuable insights and feedback.
5. To prepare participants for a range of careers in genomics research and bioinformatics, including academia, industry, and government.
6. To enable participants to think critically and solve complex problems related to NGS data analysis, preparing them to apply these skills in real-world research settings.

What you will learn?

Days	Content
Day-1	Introduction to NGS Technology Overview of NGS data formats Accessing NGS data using SRA tool kit Quality control (FastQC) of reads
Day-2	Processing of raw reads, adapter clipping, quality trimming Read mapping (BWA, BWA-MEM, HISAT2) to reference sequence Mapping output (SAM/BAM format) Visualization and evaluation of mapping quality Read count generation, Differential gene expression analysis
Day-3	Bacterial whole genome assembly using SPADES Assessment of genome assembly using BUSCO, QUAST Genome Annotation Functional annotation and enrichment analysis: EGG-NOG mapper

Registration Fees

Registration fees	INR
UG/PG Students	2500/-
PhD Scholars	3000/-
Teaching Professionals	5000/-
Industrial Professionals	5000/-

Registration link:
https://forms.gle/RczeigedaZgYeScP6
Please send a copy of the transaction ID and your details to info@scientificbiominds.in

Last Date for Registration: 20th March, 2024
(Limited Seats)
No refund for cancellation of registration.

Computer Support
Participants should bring a laptop with Wi-Fi support able to boot from USB keys. In case we fail to boot your computer into Linux from the USB keys, you will need to agree to install a Virtual Box and run Linux UBUNTU from within your current operating system. Instructions and software will be provided at the workshop. Participants can bring their laptops if you have laptop with 8GB RAM, 500GB hard disk, 32/64 core i5/i7 processor and Ubuntu or above operating systems. for this option, and that you can safely and completely remove the software after the course. (Note: If the student is not having a Laptop, We will provide the working computer to get practice)

Venue: #17, KK Chambers, 1st Floor, Bettahalasur, Bengaluru - 562157, Karnataka, India