

Online Hands-on Workshop on

NGS Data Analysis using Linux & R

Next Generation Sequencing, Conda Environment Setup, R Programming, Linux, DNA/RNA Alignment, Gene Expression and Pathway Analysis

08-12 April 2026, 7:15 PM IST

ABOUT THE WORKSHOP

This course provides a comprehensive, hands-on introduction to transcriptomics and bioinformatics, equipping participants with both theoretical knowledge and practical skills for analyzing gene expression data. Over five days, you will learn to utilize essential tools such as Linux and R to establish your working environment, process RNA-seq data, and conduct advanced analyses. The curriculum includes setting up Conda environments, aligning data using HISAT2, quantifying gene expression with FeatureCount, and performing differential expression analysis with DESeq2. Additionally, you will explore dimensionality reduction techniques like PCA and investigate pathway analysis tools such as GSEA and KEGG. By the conclusion of this workshop, you will be well-prepared to handle complex transcriptomic data and apply these competencies to your research in genomics, bioinformatics, and molecular biology.

ABOUT THE CATR

Centre for Advanced Training and Research (CATR) was established with the vision of providing transformative learning experiences to students globally. It has been duly registered with the Government and has achieved ISO and IAF certification. It is a distinguished digital platform for educational purposes and career progression, providing individuals across the globe with the chance to participate in online and offline learning within the realm of science and technology.

FEATURES OF THE COURSE

- e-Certificate to Participants
- Online by Google Meet Platform
- Hands-on Live Sessions
- Interaction with Resource Person
- Software and Protocols to participants
- Lecture PPTs and Recordings to Participants

WHO CAN JOIN?

Graduate / Postgraduate / Research scholars/ Faculty/ Industrialist in the field of Life Sciences (ZBC, Biotech, BioChem, MicroBio etc.), MBBS/MD/MS, Pharmacy, Chemical Sciences, Medicine, Medical Professionals etc.

DATE AND TIME

08-12 April 2026

India	7:15 PM	Paris	2:45 PM
Saudi /Qatar	4:45 PM	UAE /Oman	5:45 PM
Netherlands	2:45 PM	New York	8:45 AM
United Kingdom	1:45 PM	Sydney	00:45AM
Italy/ Nigeria	2:45 PM	London	1:45 PM

WORKSHOP FEE

For India Participants ₹1499
For Other Participants \$ 100 US

REGISTER NOW

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WORKSHOP MODULE

Day 1: NGS Basics & Conda Environment Setup

Introduction to NGS

- Overview of NGS technology
- Common NGS workflows (DNA-seq, RNA-seq)

Conda Environment Basics (Hands On)

- Installing and setting up Conda
- Creating, activating, and managing environments

Linux Basics (Hands On)

- Essential Linux commands (navigation, file operations)

Day 3: Alignment Theory & Hands-on

Alignment Theory

- Basics of alignment (DNA/RNA alignment)
- Tools: BWA, Bowtie, STAR
- Understanding reference genomes and indexes

Hands-on Alignment

- Aligning sample data to a reference genome using a tool like STAR or BWA

Day 5: Dimensionality Reduction & Pathway Analysis

Dimensionality Reduction & PCA

- Theory of PCA for dimensionality reduction
- Hands-on PCA in R

Pathway Analysis (Hands On)

- Basics of downstream pathway analysis (GSEA, KEGG)
- Practical hands-on example using pathway analysis tools

Day 2: R Basics & Command Line

R Basics (Hands On)

- R installation and setup
- Basic R syntax and data structures (vectors, data frames)
- Command-line usage with R (installing packages, running scripts) with basics of ggplot2 (Histogram, Boxplot, Violin-Plot)

Linux Command Line (Hands On)

- Using the command line for file manipulation
- Scripting basics in Linux (bash scripting)

Day 4: FeatureCount & Differential Expression in DESeq2

FeatureCount Theory & Hands-on

- Understanding read counting and gene expression quantification
- Hands-on with FeatureCount for counting reads

Differential Expression with DESeq2 (Hands On)

- Introduction to DESeq2
- Running a basic differential expression analysis using DESeq2

REGISTER NOW

