

Online Hands-on Workshop on RNA Seq Data Analysis

13-16 April 2026, 6:30 PM IST

About the Workshop

The RNA-seq Data Analysis for Differential Gene Expression (DEG) course is designed to equip participants with the knowledge and practical skills needed to analyze transcriptomic data effectively. Over three days, participants will explore the principles of RNA-seq technologies, focusing on data preprocessing, differential expression analysis, and visualization techniques. Through a combination of theoretical discussions and hands-on activities, participants will learn how to conduct quality control, preprocess data, calculate differentially expressed genes (DEGs) using statistical methods, and visualize their findings. The course will also cover best practices for data interpretation and reproducibility, ensuring that participants can apply their knowledge to real-world biological questions.

Target Audience

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

Workshop Fee and Features

Rs 1199 (India) | \$75 (International)

• Hands-on Workshop • Live Sessions • e-Certificate • Recordings • Software & Installation Support • Protocols (PDF) • Lecture PPTs

Event Date: 13-16 April, 2026

Time: India – 6:30 PM IST, Paris – 3:00 PM, Dubai – 5:00 PM, Sydney – 12:00 PM, New York – 9:00 PM, Saudi Arabia – 4:00 PM



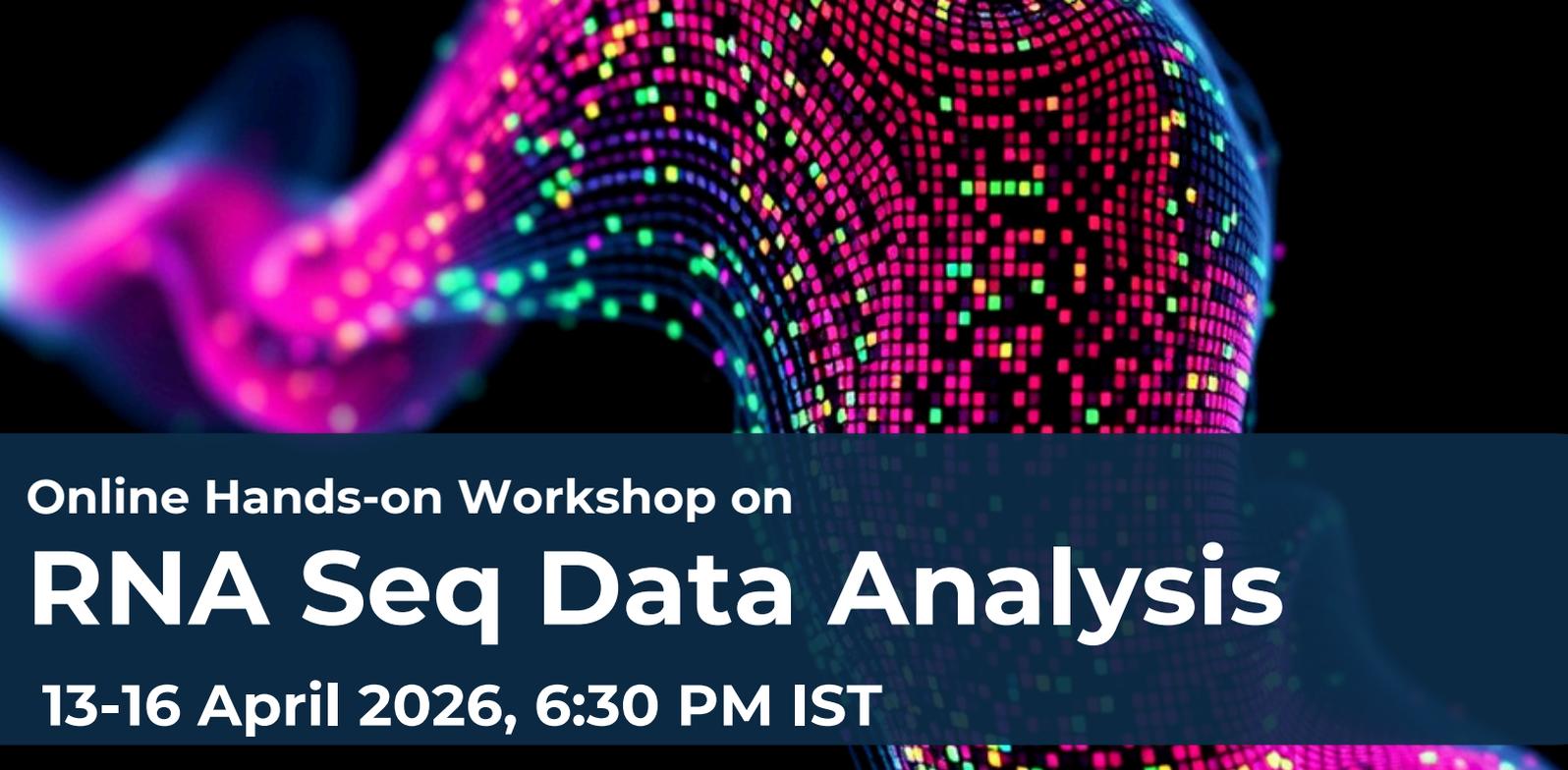
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Workshop Module

Session 1: Introduction to RNA-Seq and Overview of Data

Overview of RNA-Seq:

- What is RNA-Seq? Applications in differential expression and transcript discovery.
- Overview of the RNA-Seq data analysis workflow.

Introduction to Raw Data:

- FASTQ format and quality scores.
- Common challenges: low-quality reads, adapter contamination.

Session 3: Alignment and Transcript Quantification

Read Alignment:

- Reference genome vs. transcriptome alignment.

Transcript Quantification:

- Gene-level vs. transcript-level quantification.

Hands-On:

- Align reads to a reference genome using HISAT2.
- Perform transcript quantification with feature Counts.

Session 2: Preprocessing and Quality Control

Quality Assessment:

- Quality assessment using FastQC.

Trimming and Filtering Reads:

- Trimming and filtering reads with Trimmomatic.

Hands-On:

- Run FastQC on a sample dataset.
- Perform trimming and check results.

Session 4 & 5: Differential Expression Analysis and Visualization

Normalization and Statistical Testing:

- Need for normalization (e.g., TPM, FPKM, counts per million).
- Differential expression analysis using DESeq2.

Visualization of Results:

- Volcano plots and heatmaps.
- Functional enrichment analysis (e.g., GO/KEGG).

Hands-On:

- Conduct differential expression analysis with DESeq2.
- Generate a volcano plot and a heatmap.