



TRANSCRIPTOMICS

3-MONTH PROGRAM

Discover what genes are saying. Learn how to read the story.

Explore RNA-seq from gene-expression basics to analysing public datasets and presenting your findings in a guided research-style project.

WHAT IS TRANSCRIPTOMICS?

Every cell uses genes differently. Transcriptomics studies the RNA produced by cells and tissues to reveal which genes are active and how expression changes between conditions. RNA sequencing (RNA-seq) provides a genome-wide view of gene activity.

WHY LEARN TRANSCRIPTOMICS?

Understand gene activity

Explore how gene-expression patterns relate to biological questions.

Build analysis skills

Learn RNA-seq quality control, expression analysis and interpretation.

Create a project

Analyse public datasets and turn findings into plots, a report and presentation.

WHAT YOU WILL LEARN

Bulk RNA-seq

Compare expression profiles across samples or conditions.

Differential expression

Identify genes that change between groups using statistical analysis.

GO & KEGG pathways

Explore biological processes and pathways linked to gene lists.

Single-cell concepts

Understand how expression can be studied at individual-cell level.

Small RNA & miRNA

Learn how regulatory RNAs influence gene expression.

Data visualisation

Interpret volcano plots, heatmaps and PCA plots.

For students and early researchers in bioinformatics, biotechnology, life sciences, microbiology, genetics and related fields. Prior RNA-seq experience is not required; basic biology knowledge is helpful.

From RNA basics to biological insight

Each month builds on the last: understand the science, learn how sequencing data is generated, then use public datasets to conduct a guided analysis.

MONTH 1

FOUNDATIONS & EXPERIMENTAL DESIGN

Topics

- Transcriptome biology and the purpose of RNA-seq
- Research questions, comparison groups and study design
- RNA extraction principles and sample-quality concepts
- What Qubit, TapeStation and Bioanalyzer measure
- R and Python basics for transcriptomics

Outcome: Understand why study design, sample quality and replicates matter.

MONTH 2

RNA-SEQ WORKFLOW & DATA PREPARATION

Topics

- mRNA enrichment and its purpose
- cDNA synthesis and adapter ligation
- How sequencing reads are generated
- FASTQ files, base quality and demultiplexing
- Read quality assessment and trimming concepts

Outcome: Understand how sequencing data is produced and how quality issues are assessed.

MONTH 3

BIOINFORMATICS & RESEARCH PROJECT

Topics

- Find public RNA-seq datasets through NCBI SRA or GEO
- Read quality control and trimming
- Alignment and gene-expression quantification
- Differential expression analysis
- GO/KEGG enrichment, volcano plots, heatmaps and PCA
- Research report, figures and final presentation

Outcome: Build a guided transcriptomics analysis using a public dataset.

HOW A PUBLIC-DATA PROJECT WORKS

1. Choose a question

Which genes differ between two published conditions?

2. Find public data

Use NCBI SRA or GEO and review sample metadata.

3. Check read quality

Assess reads and decide whether trimming is needed.

4. Quantify expression

Align reads or use a suitable quantification workflow.

5. Compare groups

Run differential expression with appropriate statistics.

6. Interpret results

Create plots, explore pathways and present conclusions.

Dataset policy: The project uses publicly available online datasets. No original/in-house sequencing data or participant-generated sequencing run is included or promised.

What you can produce by the end

Depending on the selected dataset and project scope, you can develop a portfolio-style analysis showing how transcriptomics data is explored and interpreted.

PROJECT ITEM	WHAT IT SHOWS
Public dataset & metadata	Study source, sample groups and biological question.
Quality-control summary	Read-quality observations and preprocessing decisions.
Expression/count table	Gene-level values used for expression comparisons.
Differential-expression results	Genes with evidence of expression changes between groups.
Plots & pathway interpretation	Volcano plot, heatmap/PCA where appropriate, and GO/KEGG findings.
Research-style report	Methods, results, limitations and possible next steps.

PUBLIC DATA RESOURCES

NCBI SRA

Find sequencing read datasets deposited by researchers.

GEO

Explore published gene-expression studies and sample information.

Ensembl & UCSC

Reference genomes and annotations to support analysis.

SKILLS YOU WILL EXPLORE

Analysis: R and Python basics, FASTQ files, quality control, trimming, alignment/quantification and count tables.

Interpretation: differential expression, GO/KEGG enrichment, volcano plots, heatmaps and PCA.

Research practice: reading metadata, understanding study design, explaining limitations and communicating results.

WHO SHOULD JOIN?

BSc/MSc students, recent graduates and early researchers in Bioinformatics, Biotechnology, Life Sciences, Microbiology, Genetics and related fields who want to understand transcriptomics using public data.

START YOUR TRANSCRIPTOMICS JOURNEY

A guided 3-month learning experience at IBRI Noida.

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