Advanced Transcriptomics and RNA-Seq Data Analysis Training Course

Professional Development Training Course Outline

Category	Biotechnology and Pharmaceutical Development	**Duration**	10 Days
Base Fee	$4,000 USD	**Delivery Mode**	Online / On-site Hybrid

Course Introduction

Advanced Transcriptomics and RNA-Seq Data Analysis Training Course offers an immersive, hands-on experience in Advanced Transcriptomics and RNA-Sequencing (RNA-Seq) Data Analysis, moving beyond foundational concepts to explore the cutting-edge of genomic research. The Next-Generation Sequencing (NGS) revolution has made RNA-Seq the gold standard for gene expression profiling, allowing researchers to measure mRNA, non-coding RNA, and alternative splicing with unprecedented resolution. However, translating vast quantities of raw sequencing data into robust, biologically meaningful insights requires mastery of complex bioinformatics pipelines and advanced statistical methods. This training bridges, the critical gap between data generation and actionable biological discovery, focusing on highly sought-after skills like single-cell RNA-Seq, spatial transcriptomics, and multi-omics integration. We empower participants to independently manage and interpret large-scale transcriptome datasets, a crucial capability for accelerating research in precision medicine, drug target identification, and molecular diagnostics.

The curriculum emphasizes practical application using industry-standard tools and the command-line interface, ensuring immediate applicability to real-world research projects. Through a series of comprehensive modules and real-world case studies, attendees will learn to execute reproducible research workflows, from rigorous quality control (QC) and read alignment to sophisticated differential expression analysis (DGE) and pathway interpretation. The focus on reproducible bioinformatics and cloud-based computing prepares participants for the technical demands of modern, high-throughput science. By mastering these advanced analytical skills, scientists can unlock the full potential of their transcriptomic data, leading to deeper mechanistic understanding and driving innovation in life sciences

Programme Curriculum

Advanced Transcriptomics and RNA-Seq Data Analysis Training Course

Introduction

Advanced Transcriptomics and RNA-Seq Data Analysis Training Course offers an immersive, hands-on experience in Advanced Transcriptomics and RNA-Sequencing (RNA-Seq) Data Analysis, moving beyond foundational concepts to explore the cutting-edge of genomic research. The Next-Generation Sequencing (NGS) revolution has made RNA-Seq the gold standard for gene expression profiling, allowing researchers to measure mRNA, non-coding RNA, and alternative splicing with unprecedented resolution. However, translating vast quantities of raw sequencing data into robust, biologically meaningful insights requires mastery of complex bioinformatics pipelines and advanced statistical methods. This training bridges, the critical gap between data generation and actionable biological discovery, focusing on highly sought-after skills like single-cell RNA-Seq, spatial transcriptomics, and multi-omics integration. We empower participants to independently manage and interpret large-scale transcriptome datasets, a crucial capability for accelerating research in precision medicine, drug target identification, and molecular diagnostics.

The curriculum emphasizes practical application using industry-standard tools and the command-line interface, ensuring immediate applicability to real-world research projects. Through a series of comprehensive modules and real-world case studies, attendees will learn to execute reproducible research workflows, from rigorous quality control (QC) and read alignment to sophisticated differential expression analysis (DGE) and pathway interpretation. The focus on reproducible bioinformatics and cloud-based computing prepares participants for the technical demands of modern, high-throughput science. By mastering these advanced analytical skills, scientists can unlock the full potential of their transcriptomic data, leading to deeper mechanistic understanding and driving innovation in life sciences.

Course Duration

10 days

Course Objectives

1. Master the complete RNA-Seq data analysis pipeline from raw FASTQ files to final biological interpretation.
2. Perform rigorous Next-Generation Sequencing (NGS) Quality Control (QC) and preprocessing using industry-standard tools like FastQC and Trimmomatic.
3. Execute read alignment and transcript quantification using pseudo-alignment and alignment-based methods
4. Conduct robust Differential Gene Expression analysis using statistical packages like DESeq2 and edgeR in R/Bioconductor.
5. Apply advanced statistical methods to correct for batch effects and confounding factors in complex experimental designs.
6. Perform comprehensive Functional Enrichment Analysis and Pathway Analysis to interpret DGE results.
7. Analyze and visualize complex data from Single-Cell RNA-Seq experiments, including clustering, cell type annotation, and trajectory inference.
8. Understand the principles and initial analysis of Spatial Transcriptomics datasets.
9. Investigate Alternative Splicing and Differential Exon Usage (DEU) to uncover regulatory mechanisms beyond simple gene expression.
10. Integrate RNA-Seq data with other multi-omics data for a systems-level perspective.
11. Develop reproducible bioinformatics workflows using the Command Line Interface (CLI) and workflow managers like Nextflow or Snakemake.

12. Generate publication-quality data visualizations for effective scientific communication.
13. Design and execute an independent transcriptomics research project, applying best practices in computational biology.

Target Audience

1. Post-Doctoral Researchers and PhD Students in Molecular Biology, Genomics, and Genetics.
2. Computational Biologists and Bioinformaticians.
3. Research Scientists and R&D Staff in Biotechnology and Pharmaceutical Companies utilizing NGS technologies.
4. Principal Investigators (PIs) and Lab Managers.
5. Biostatisticians looking to apply advanced statistical models to RNA-Seq data.
6. Core Facility Staff involved in advising on or performing transcriptomics analysis.
7. Molecular Pathologists and Clinical Researchers.
8. Computer Scientists.

Course Modules

Module 1: Introduction to Advanced Transcriptomics and RNA-Seq Workflows

- Review of NGS platforms and RNA-Seq assay types
- Principles of Experimental Design for robust transcriptomics studies.
- Introduction to the Command Line Interface and HPC environments.
- Setup of the analysis environment.
- Case Study: Evaluating the impact of biological and technical replicates on statistical power in a bulk RNA-Seq cancer study.

Module 2: Raw Data Quality Control and Preprocessing

- Assessing raw read quality with FastQC and multi-sample summaries.
- Adapter and quality trimming using tools like Trimmomatic or fastp.
- Understanding common sequencing artifacts and batch effect indicators.
- File formats and data storage best practices.
- Case Study: Troubleshooting a low-quality sequencing run to identify and filter a contaminated library.

Module 3: Read Alignment and Quantification

- Principles of genome-guided and transcriptome-guided alignment.
- Alignment with high-performance tools like STAR and HISAT2.
- Pseudo-alignment for rapid quantification and their advantages.
- Generating read counts/TPM/FPKM matrices for downstream analysis.
- Case Study: Comparing count concordance and speed between Salmon and STAR/FeatureCounts on a large gene expression panel.

Module 4: Foundations of Differential Gene Expression

- Statistical distributions for count data
- Data normalization methods and their biological relevance.
- Using DESeq2 for simple two-group comparisons.
- Fold Change, p-values, and False Discovery Rate
- Case Study: Identifying differentially expressed genes in a control and treated cell line experiment.

Module 5: Advanced DGE with Complex Designs

- Accounting for time-points, multiple tissues, and paired samples.
- Handling confounding variables and applying linear models in DESeq2 and edgeR.
- Methods for Batch Effect Correction
- Likelihood Ratio Test for comparing complex models and identifying significant factors.
- Case Study: Analyzing a human clinical trial dataset with multiple variables and correcting for a known lab batch effect.

Module 6: Functional Annotation and Pathway Analysis

- Gene Ontology enrichment analysis and interpretation.
- Using KEGG and Reactome for pathway analysis.
- Applying GSEA to rank-ordered gene lists.
- Visualizing pathway results
- Case Study: Linking a list of DGEs from a disease model to activated or suppressed biological pathways.

Module 7: Single-Cell RNA-Seq Introduction

- Overview of scRNA-Seq technologies
- Pre-processing scRNA-Seq data.
- Quality control for single cells
- Introduction to the Seurat and Scanpy analysis frameworks.
- Case Study: Initial QC and filtering of a 10x Genomics PBMC dataset.

Module 8: scRNA-Seq Clustering and Visualization

- Dimensionality reduction techniques.
- Unsupervised clustering algorithms for cell population identification.
- Visualizing cell clusters and gene expression on dimensionally reduced plots.
- Marker gene identification for cluster annotation.
- Case Study: Identifying and annotating major immune cell types in a complex tissue sample.

Module 9: Advanced scRNA-Seq Analysis I: DGE and Trajectory

- Differential expression testing between identified cell clusters.
- Pseudotime analysis and trajectory inference
- Analyzing cell state transitions and differentiation paths.
- Integration of multiple scRNA-Seq samples
- Case Study: Tracking the differentiation of progenitor cells into mature cell types in a developmental biology experiment.

Module 10: Advanced scRNA-Seq Analysis II: Cell-Cell Communication

- Ligand-Receptor analysis to predict cell-cell interactions.
- Tools for analyzing communication networks
- Identifying key signaling pathways across different cell types.
- Visualization of interaction networks and communication strength.
- Case Study: Mapping potential communication pathways between tumor cells and the surrounding immune microenvironment.

Module 11: Spatial Transcriptomics (ST) Analysis

- Principles of Spatial Transcriptomics
- Alignment and data processing for spatial data.
- Integrating ST data with H&E or fluorescence images.
- Identifying spatially variable genes and tissue domain deconvolution.
- Case Study: Mapping gene expression to histological features in a brain tissue section to identify novel spatial patterns.

Module 12: Alternative Splicing and Isoform Analysis

- Methods for detecting Alternative Splicing events.
- Tools for Differential Exon Usage
- Quantifying and visualizing isoform expression changes.
- Linking AS events to protein function and disease mechanisms.
- Case Study: Identifying a specific isoform switch in a drug-resistant cell line.

Module 13: Multi-omics Data Integration and Network Biology

- Strategies for integrating RNA-Seq with genomics, epigenomics, and proteomics.
- Correlative analysis and identifying causal relationships.
- Introduction to Gene Regulatory Network inference.
- Principles of network visualization and centrality analysis.
- Case Study: Integrating ATAC-Seq and RNA-Seq data to link chromatin accessibility changes with differential gene expression.

Module 14: Reproducible Bioinformatics and Scalable Workflows

- Principles of reproducible research.
- Automating pipelines with workflow managers
- Introduction to containerization with Docker and Singularity.
- Best practices for running and optimizing large-scale analyses on cloud computing platforms.
- Case Study: Converting a manual RNA-Seq analysis script into a containerized, version-controlled Nextflow pipeline.

Module 15: Final Project and Scientific Communication

- Applying all learned skills to a novel, publicly available transcriptomics dataset.
- Designing appropriate analysis steps and setting up the computational environment.
- Generating a comprehensive analysis report with high-quality figures.
- Tips for scientific writing, data interpretation, and presentation of NGS results.
- Case Study: Independent execution and presentation of a complete bulk or scRNA-Seq analysis project.

Training Methodology

The training employs an Active Learning approach combining didactic lectures with extensive, Hands-On Practical Sessions.

- Lectures.
- Live Coding Demonstrations.
- Guided Practical Exercises.
- Case Study Deep Dives.
- Group and Peer Discussion.

Register as a group from 3 participants for a Discount

Send us an email: info@fineskilltrainingcenter.org or call +254769199797

Certification

Upon successful completion of this training, participants will be issued with a globally- recognized certificate.

Tailor-Made Course

We also offer tailor-made courses based on your needs.

Key Notes

a. The participant must be conversant with English.

b. Upon completion of training the participant will be issued with an Authorized Training Certificate

c. Course duration is flexible and the contents can be modified to fit any number of days.

d. The course fee includes facilitation training materials, 2 coffee breaks, buffet lunch and A Certificate upon successful completion of Training.

e. One-year post-training support Consultation and Coaching provided after the course.

f. Payment should be done at least a week before commence of the training, to Fineskill Training Center account, as indicated in the invoice so as to enable us prepare better for you.

Upcoming Scheduled Sessions

Start Date	End Date	Location	Price
23 Nov 2026	04 Dec 2026	Online	$2,000
23 Nov 2026	04 Dec 2026	Physical	$3,000
23 Nov 2026	04 Dec 2026	Physical	$6,000
23 Nov 2026	04 Dec 2026	Physical	$6,000
23 Nov 2026	04 Dec 2026	Physical	$12,000
23 Nov 2026	04 Dec 2026	Physical	$9,000
23 Nov 2026	04 Dec 2026	Physical	$12,000
23 Nov 2026	04 Dec 2026	Physical	$12,000

Ready to enroll or request a customized program? Book online or contact us:

Register Online Now

Email: info@fineskilltrainingcenter.com | Website: www.fineskilltrainingcenter.com