

## Workshop Structure

### Tracks

- Complete Workshop Pass – Observer Track A (Lectures + Demonstrations)  
Includes access to all theory sessions, video demonstrations, and bioinformatics training (Days 1–3)  
No wet lab participation
- Complete Workshop Pass – Hands-on Track B  
Includes full access to all lectures (Days 1–3) + wet lab participation (Days 1–2, Track B) + bioinformatics sessions (Day 3)

### TENTATIVE AGENDA

## Day 1 – Foundations & Neural Applications

Time	Session
08:30 – 09:00	Registration
09:00 – 09:30	Opening Remarks
09:30 – 10:15	Overview of Sequencing Technologies & Research Applications
10:15 – 11:00	Neurovirology & Brain Models
11:00 – 11:15	Tea Break
11:15 – 12:00	RNA Barcoding & Memory
12:00 – 13:00	Clinical Genomics Ecosystem
13:00 – 13:45	Lunch

### PARALLEL TRACKS

<b>Track A – Observer Track (Lectures + Demonstrations)</b>	<b>Track B – Hands-on Track (Wet Lab Participation)</b>
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Time	Session	Time	Session
13:45 – 14:45	Brain Tissue to Single Cells Workflow (Video Demo)	13:45 – 14:45	Lab Entry, Safety Briefing & Orientation
14:45 – 15:45	Library Preparation Workflow (Step-by-step walkthrough)	14:45 – 15:15	Brain Tissue to Single Cells Workflow-Live Demo
15:45 – 16:45	Neuro-immunology in Brain Disorders (scRNA perspective)	15:15 – 17:45 <b>Lab Session 1</b>	RNA-Seq Library Preparation
16:45 – 17:30	Open Q&A and Discussion on Key Checkpoints & Troubleshooting		RNA Quality Assessment (QC & Quantification) RNA Enrichment / Selection Strategies cDNA Synthesis

		17:45 – 18:00	Open Q&A and Discussion on Key Checkpoints & Troubleshooting
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## Day 2 – Dual Track

<b>Track A – Observer Track (Lectures + Demonstrations)</b>	<b>Track B – Hands-on Track (Wet Lab Participation)</b>
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Time	Session	Time	Session
09:00 – 10:00	Isoform Sequencing: Long-read Technologies & Transcript Diversity	09:30 – 10:15 (Lab Session 2)	Library Preparation: End Processing
10:00 – 11:00	Host–Pathogen Multi-omics: Integrating Genomics, Transcriptomics & Proteomics	10:15 – 11:00	Adapter Ligation & Indexing Concepts
11:00 – 11:15	Tea Break	11:00 – 11:30	Post-ligation Processing & Clean-up
11:15 – 12:15	Immune–Brain Axis: Neuroinflammation & Cellular Crosstalk	11:30 – 13:00	Library Amplification
12:15 – 13:15	Lunch	13:00 – 14:00	Working Lunch
13:15 – 14:15	CNS Signalling Pathways: Molecular Networks in Brain Disorders	14:00 – 15:30	Library Quality Control (Size & Quantification)
14:15 – 15:15	Single-cell Applications in Neurological Diseases (Case Studies & Design)	15:30 – 16:30	Library Pooling & Normalization
15:15 – 15:30	Tea Break	16:30 – 17:15	Sequencing Workflow Overview & Readiness
15:30 – 16:30	Translating Multi-omics to Clinical Research: Feasibility & Study Planning	17:15 – 18:00	Open Q&A and Discussion
16:30 – 17:30	Open Q&A and Discussion		

## Day 3 – Bioinformatics & Data Analysis

Time	Session
09:00 – 10:00	Spatial Transcriptomics: Concepts, Platforms & Study Design
10:00 – 11:00	NGS Data Processing Pipeline: From FASTQ to Count Matrix
11:00 – 11:15	Tea Break
11:15 – 12:15	Quality Control & Pre-processing of Single-cell Data
12:15 – 13:00	Lunch
13:00 – 14:00	Clustering & Denoising using R (Workflow Overview)
14:00 – 15:00	Seurat Basics: Data Integration & Feature Selection
15:00 – 15:15	Tea Break

15:15 – 16:15	UMAP Visualization & Interpretation of Cell Populations
16:15 – 17:00	Open Q&A and Discussion
17:00 – 17:30	Valedictory Session & Certificate Distribution