| | |
|---|---|
| **COURSE TITLE** | **SCRNA ANALYSIS** |
| **COURSE CODE** | **01CB0709** |
| **COURSE CREDITS** | **2** |

**Objective:**

1. To introduce students to single-cell RNA sequencing (scRNA-Seq) and teach them how to analyze this data using R.
2. The course focuses on practical skills using real datasets and popular tools like Seurat and Monocle.

**Course Outcomes:** After completion of this course, student will be able to:

1. Apply computational tools such as R to load, preprocess, and perform quality control of scRNA-Seq datasets.
2. Analyze scRNA-Seq data to identify cell types and determine marker genes using statistical and computational methods.
3. Analyze differential gene expression patterns to compare cellular populations and interpret biological variations across conditions.
4. Evaluate visualization techniques and analytical workflows for effective representation of single-cell data insights.
5. Design reproducible reports and visualizations for scRNA-Seq analysis using computational tools with clear scientific communication.

**Pre-requisite of course:**Basic Knowledge of R

**Teaching and Examination Scheme**

| Theory Hours | Tutorial Hours | Practical Hours | ESE | IA | CSE | Viva | Term Work |
|---|---|---|---|---|---|---|---|
| 0 | 2 | 0 | 0 | 0 | 0 | 50 | 50 |

| Contents : Unit | Topics | Contact Hours |
|---|---|---|
| **Total Hours** | | |

**Suggested List of Experiments:**

| Contents : Unit | Topics | Contact Hours |
|---|---|---|
| 1 | **Experiment 1**<br>Introduction to the concept of Single-Cell analysis: overview and applications. | 1 |
| 2 | **Experiment 2**<br>To explore scRNA-Seq Technologies & major sequencing platforms. | 1 |

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**Digitally signed by (Name of HOD)**

DR. RAJENDRASINH BAHADURSINH JADEJA
**Digitally signed by (Name of Dean/ Principal)**

**Suggested List of Experiments:**

| Contents : Unit | Topics | Contact Hours |
|---|---|---|
| 3 | **Experiment 3**<br>To install and configure tools for R Environment Setup, packages & Data Acquisition. | 2 |
| 4 | **Experiment 4**<br>Application of Data import, loading & quality check. | 2 |
| 5 | **Experiment 5**<br>Exploratory analysis of scRNA Data Structures | 2 |
| 6 | **Experiment 6**<br>Quality Control of raw sequencing scRNA Data | 2 |
| 7 | **Experiment 7**<br>To apply thresholds for data cleaning and Filtering. | 2 |
| 8 | **Experiment 8**<br>Execution of scRNA Data Normalization | 2 |
| 9 | **Experiment 9**<br>Identification highly variable genes (feature selection) in scRNA dataset | 2 |
| 10 | **Experiment 10**<br>Execution of scRNA data scaling | 2 |
| 11 | **Experiment 11**<br>To apply the concept of Dimensionality Reduction using PCA | 2 |
| 12 | **Experiment 12**<br>Visualization of clusters using UMAP | 2 |
| 13 | **Experiment 13**<br>To detect cluster-specific marker genes | 2 |
| 14 | **Experiment 14**<br>To implement Clustering of Cells | 2 |
| 15 | **Experiment 15**<br>Annotation of cell type for assigning biological identities. | 2 |
| 16 | **Experiment 16**<br>Mastering scRNA sequencing: Unveiling insights through RNA-sequencing Analysis using real datasets | 2 |
| **Total Hours** | | **30** |

**Textbook :**


1 A guide to single-cell RNA-sequencing analysis, Stephanie C. Hicks et al., Nature Reviews Genetics, 2021


**References:**


1 Comprehensive Integration of Single-Cell Data, Comprehensive Integration of Single-Cell Data, Rahul Satija et al., Cell, 2019

2 Exponential scaling of single-cell RNA-seq in the past decade, Exponential scaling of single-cell RNA-seq in the past decade, Valentine Svensson et al., Nature Protocols, 2018

**References:**

3 Massively parallel digital transcriptional profiling of single cells, Massively parallel digital transcriptional profiling of single cells, Zheng et al., Nature Communications, 2017

**Suggested Theory Distribution:**

The suggested theory distribution as per Bloom's taxonomy is as follows. This distribution serves as guidelines for teachers and students to achieve effective teaching-learning process

| Distribution of Theory for course delivery | | | | | |
|---|---|---|---|---|---|
| **Remember / Knowledge** | **Understand** | **Apply** | **Analyze** | **Evaluate** | **Higher order Thinking / Creative** |
| 0.00 | 0.00 | 35.00 | 35.00 | 30.00 | 0.00 |

**Instructional Method:**

1 The course delivery method will depend upon the requirement of content and need of students. The teacher in addition to conventional teaching method by black board, may also use any of tools such as demonstration, role play, Quiz, brainstorming, MOOCs etc

2 The internal evaluation will be done on the basis of continuous evaluation of students in the laboratory and class-room.

3 Practical examination will be conducted at the end of semester for evaluation of performance of students in laboratory.

**Supplementary Resources:**

1 https://www.sc-best-practices.org/introduction/analysis_tools.html#single-cell-analysis-frameworks-and-consortia

2 https://satijalab.org/seurat/articles/essential_commands

3 https://github.com/hbctraining/Intro-to-scRNAseq/blob/master/lessons/03_quality_control-setup.qmd