SYLLABUS DEL CORSO

Single-cell RNA sequencing data preprocessing and analysis

2425-117R-RNACell

Title

Single-cell RNA Sequencing Data Preprocessing and Analysis

Teacher(s)

Chiara Damiani

Language

English

Short description

This course provides theoretical and practical training on the analysis of single-cell RNA sequencing (scRNA-seq) data, focusing on sequencing-based methods. Participants will learn the key steps of preprocessing, including quality control, normalization, and feature selection, and gain practical experience in clustering, dimensionality reduction, and differential expression analysis. At the end of the course, participants will demonstrate their proficiency by completing a practical evaluation, analyzing a dataset of their choice.

Learning Objectives

• Understand the preprocessing steps for single-cell RNA sequencing data, including quality control, normalization,

and feature selection.
- Perform clustering, dimensionality reduction, and differential expression analysis on scRNA-seq datasets.
- Gain hands-on experience with tools and workflows for scRNA-seq data analysis.
- Demonstrate the ability to independently analyze and interpret scRNA-seq data through a practical evaluation.

Course Materials

Participants will receive:
- Lecture slides and notes
- Sample datasets for practice
- Code templates for preprocessing and analysis

Course Schedule

Day 1:

Morning (Theoretical):
- Introduction to scRNA-seq Data Analysis
- Overview of sequencing-based methods
- Key concepts: raw counts, quality control, and data normalization
- Introduction to popular tools (Seurat, Scanpy)

Afternoon (Practical):
- Hands-on Session: Preprocessing scRNA-seq Data
- Quality control: filtering low-quality cells and features
- Data normalization and handling batch effects
- Saving preprocessed data for downstream analysis

Day 2:

Morning (Theoretical):
- scRNA-seq Analysis Workflows
- Dimensionality reduction techniques (PCA, t-SNE, UMAP)
- Clustering and cell-type identification
- Differential expression analysis for marker discovery

Afternoon (Practical):
- Hands-on Session: Data Analysis and Visualization
- Performing clustering and dimensionality reduction
- Visualizing results with feature plots, heatmaps, and UMAP projections
- Conducting differential expression analysis and interpreting findings

Evaluation

At the end of the course, participants will analyze a single-cell RNA sequencing dataset of their choice using the tools and methods covered. Successful completion of this practical evaluation will demonstrate proficiency in scRNA-seq data analysis.

Software and Tools
- Google Colab: A browser-based platform for running Python scripts without the need for local installation. Participants need a Google account to access Colab.
- Galaxy: A web-based platform for bioinformatics analyses, accessible through any modern browser. No local installation required.

CFU / Hours

8 hours

Teaching period

January 27-28, 2025

Sustainable Development Goals