Make a repository on GitHub (Ahmad)

Make a Box folder (Ahmad)

Simple task for each session (Everyone for their session)

Have people install the packages (Natalia looks at YouTube)

**Day 1: Introduction to R Programming**

Ahmad

* Introduction to R and RStudio: Installation, interface overview, and basics of RStudio.
* R Data Types and Structures: Vectors, matrices, lists, and data frames.
* Some commonly used functions such as head, tail, str, class, table, colnames, row.names, sort, ...
* Basic Operations in R: Arithmetic, logical operations, and assignment.
* Regular expression.
* Data Import and Export: Reading/writing CSV, Excel, and other file formats.
* Sasha
* Basic Data Manipulation: Subsetting, filtering, and sorting with base R functions.
* Control Structures: if-else, for and while loops, and functions.
* Intro to Packages: Installing and loading packages (e.g., dplyr, ggplot2).
* Data Wrangling with dplyr: Filtering, grouping, summarizing, and joining datasets.

**Day 2: Statistics and Visualizations in R**

Sasha (Statistics)

* Descriptive Statistics: Mean, median, standard deviation, and summary statistics.
* Basic Hypothesis Testing: t-tests, ANOVA, Mann-Whitney, ...
* Introduction to Linear and Logistic Regression: Model fitting and interpretation.
* Ahmad (visualization)
* Data Visualization with ggplot2: Creating basic plots (histograms, bar charts, scatter plots, boxplots, etc.).
* Advanced Visualizations: Scatter plots with trend lines, multi-faceted plots, and customizing aesthetics.

**Day 3: Introduction to Bioinformatics in R**

* Natalia and Hridya
* Introduction to Bioinformatics Tools in R: Overview of common bioinformatics packages for scRNA-seq and CyTOF (e.g., Seurat, CATALYST, …). Make a list
* Biological data format
* Hridya
* CyTOF Data Analysis: Reading CyTOF data, preprocessing, clustering, and visualizations.
* Natalia
* Introduction to scRNA-seq Analysis:
  + Review of tutorials on the Seurat package
  + Loading and exploring a Seurat object
  + Example of visualizing the marker expression (heatmap, violin plot, and featureplot)