



#### **Canadian Bioinformatics Workshops**

#### Introduction to R Programming for Bioinformatics

Day 1- Module 1A: Inturoduction to R programming Language

Mohamed Helmy, PhD

Principal Scientist and Adjunct Professor Bioinformatics and Systems Biology Lab VIDO, University of Saskatchewan

6-7October 2025, VIDO, Saskatoon



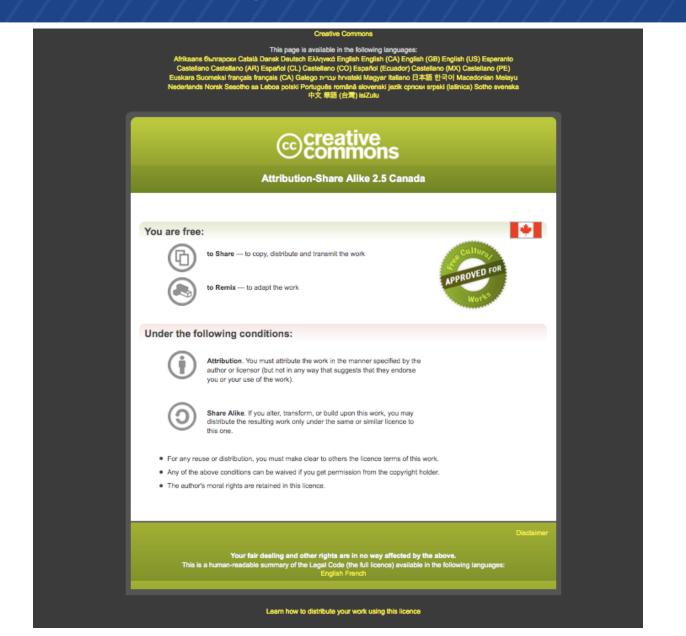


## Land Acknowledgement

"As we gather here today, we acknowledge we are on Treaty 6 Territory and the Homeland of the Métis. We pay our respect to the First Nations and Métis ancestors of this place and reaffirm our relationship with one another."

- University Council, University of Saskatchewan

# CBW and CBH Open Contents



# House Keeping Rules

**Bathrooms** 

**Coffee breaks** 

Lunches

Internet access

### Workshop Objectives

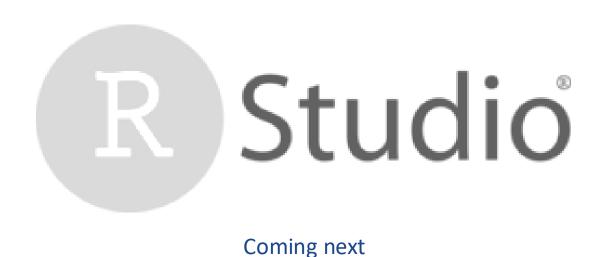
By the end of this workshop, participants will be able to:

- Navigate the R environment: Install, load, and manage R packages.
- Apply core programming concepts: Variables, data structures, loops, and functions.
- Organize and manipulate data: Import, subset, reshape, and prepare datasets.
- Visualize biological data: Generate and customize plots for exploration and communication.
- Work with Bioconductor: Access and explore omic datasets using specialized data structures.
- Preprocess and analyze omics data: Perform normalization, basic visualization (PCA, heatmaps), and annotation.
- Build confidence in R for bioinformatics: Apply learned skills to real-world biological datasets.

## Module 1: Getting to Know R

The environment, syntax, data types, and data handling





#### What is R?



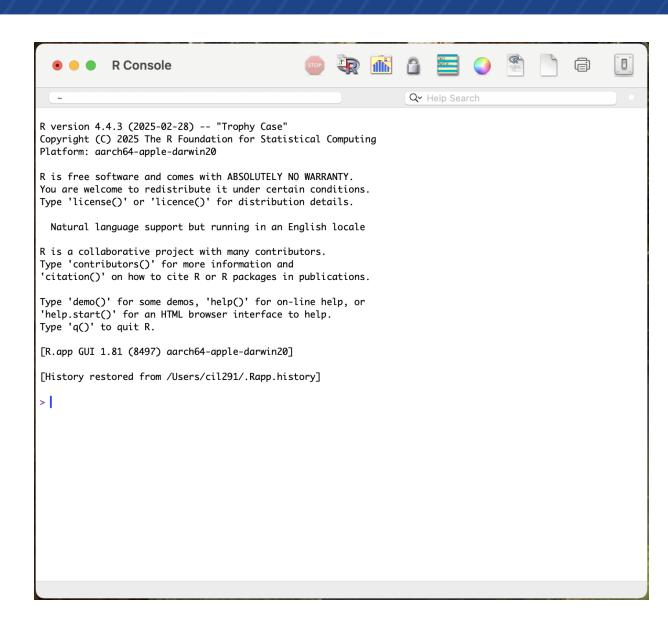
 Open-source programming language for statistics, visualization, and bioinformatics

Widely used in biology, medicine, and data science

Supported by a large community and thousands of packages

• Free, cross-platform (Windows, Mac, Linux)





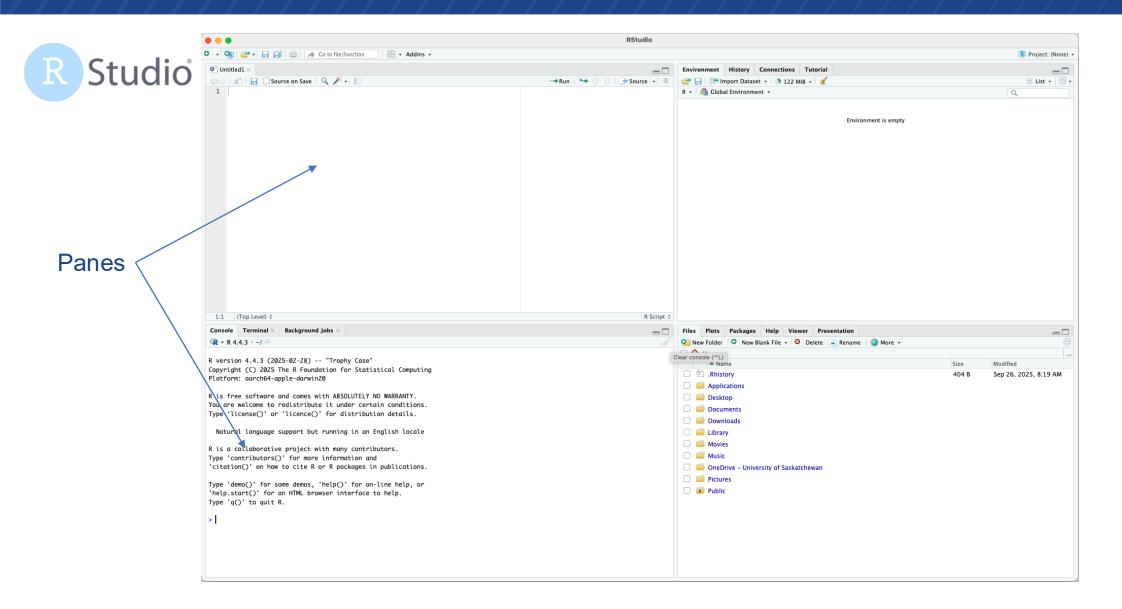


Integrated development environment (IDE)

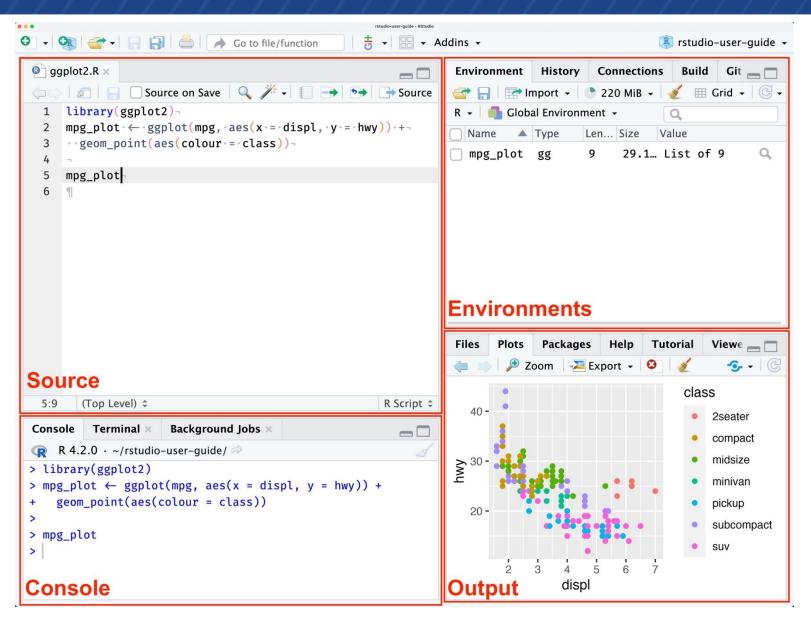
- Execute both R and Python code
- Syntax highlighting and code completion
- Manage multiple projects

Another popular environment are Jupyter notebooks and Google CoLab:





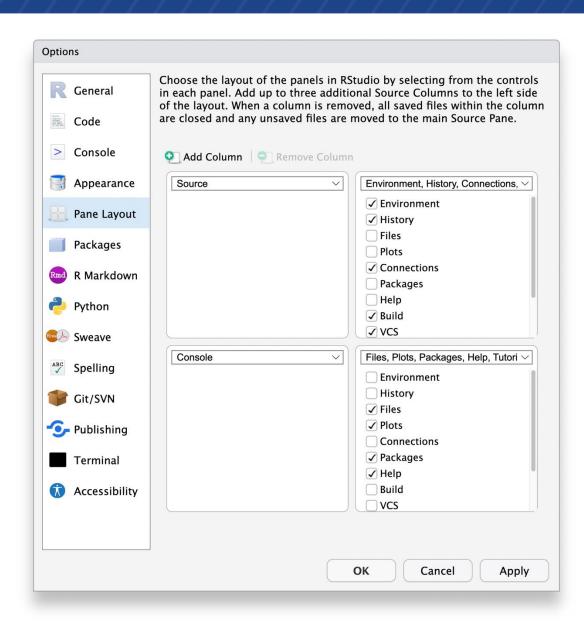
R Studio



Source: RStudio IDE User Guide



#### Pane layout



### First Steps in R

• We talk with R through a Syntax (grammar)

• It is as simple as using a Calculator

```
Source on Save Q > - | 1
2 # A simple calculation
3 2 + 3
4
5 # Calcualte the square root
6 sqrt(16)
```

 And we add comments to make our code easy to understand

### Variables and Assignments

Variables are places to store Values

Values are assigned to Variable

The assignment in R is = or <- signs.</li>

### Scripts and Projects in RStudio

#### Scripts

- ○Save your code in .R files → easy to re-run and share
- Use comments (#) to explain steps

#### Projects

- Keep files, data, and scripts organized in one folder
- Makes your work reproducible

#### Workspaces

Save variables and reload sessions (.RData)

## Basic Data Types in R

• **Numeric:** x <- 42

- Character (string): name <- "Alice", "Mike\_123"</li>
- Logical (TRUE/FALSE): flag <- TRUE, T</li>
- Factor (categorical): group <- factor(c("control", "treated"))</li>
- Date/Time: Sys.Date()

### Data Structures in R

Vector: 1D collection of elements

Matrix: 2D numeric data

Dataframe: like a table with rows and columns

List: collection of different objects

#### Data Structures in R

• **Vector**: v <- c(1, 2, 3)

• **Matrix**: m <- matrix(1:6, nrow=2)

Dataframe: df <- data.frame(age=c(25,30), group=c("A","B"))

List: lst <- list(numbers=v, info=df)</li>

# Saving & Loading Work

- Save your script (.R file) to keep your code.
- Save your workspace (.RData) to reload objects later.
- Use save.image() and load() commands.
- Tip: Best practice is to save code, not just the workspace.

# THANK YOU





