

BIOF 043: For True BeginRs | Hands-on R Training

R is a free, cross-platform – Windows, Mac, and Linux – programming language, designed specifically to facilitate data management, analysis, and visualization. Boasting vibrant development and support communities, R has become an indispensable tool for bioinformaticians, statisticians, and data scientists. Created with true beginRs in mind, this training will teach participants the fundamental, transferable skills needed to unleash R's full potential for producing publication-worthy analyses and visualizations.

Learning Objectives

- Interfacing with R using RStudio
- Using RStudio's built-in help function – ? – as well as resources for troubleshooting, including rdocumentation.org, cheat sheets, vignettes, YouTube channels, and stackexchange.com
- Creating project files; Working with the RStudio command line
- Identifying and changing the current working file directory
- Variables – local vs. global – naming conventions, and assignment operators
- Writing their first R script and how to properly document their code via commenting
- Using the '\$' accessor function
- The most common data types, including character strings, numerical, integers, and logicals
- How to access data entries using [] and [[]]; The most common data structure types, including vectors, lists, factors, data frames, and tibbles
- Package libraries and how to install them; Loading data into R and basic troubleshooting when importing data
- Data management, manipulation, subsetting, piping, and exploration using dplyr
- Creating and exporting highly customizable, publication-quality data visualizations with ggplot2
- Using R to perform statistical analyses, including simple linear regression, χ^2 contingency table analysis, t-tests, and analysis of variance

Class Type: Workshop

Prerequisites:

Participants should be comfortable with basic computer skills.

Program: Bioinformatics and Data Science