

"Introduction to R" series

Aug.30: Part 1 – Data Wrangling

Sep.06: Part 2 – Data Visualization

Sep.13: Part 3 – Data Analysis

Sep.20: Part 4 – Real-world Data Analysis Using R



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Bioinformatics and Computational Biosciences Branch (BCBB)

- **My background:** Biomedical Statistical Specialist in the Bioinformatics and Computational Biosciences Branch in the Office of Cyber Infrastructure and Computational Biology
- Check us out: <https://www.niaid.nih.gov/research/bioinformatics-computational-biosciences-branch>
- Do you conduct research involving genomics (clinical, meta and microbial), imaging, data science and biostatistics, or structural biology?
 - We offer collaboration opportunities to address research questions at no direct cost to the NIAID research community and collaborators

What is R?

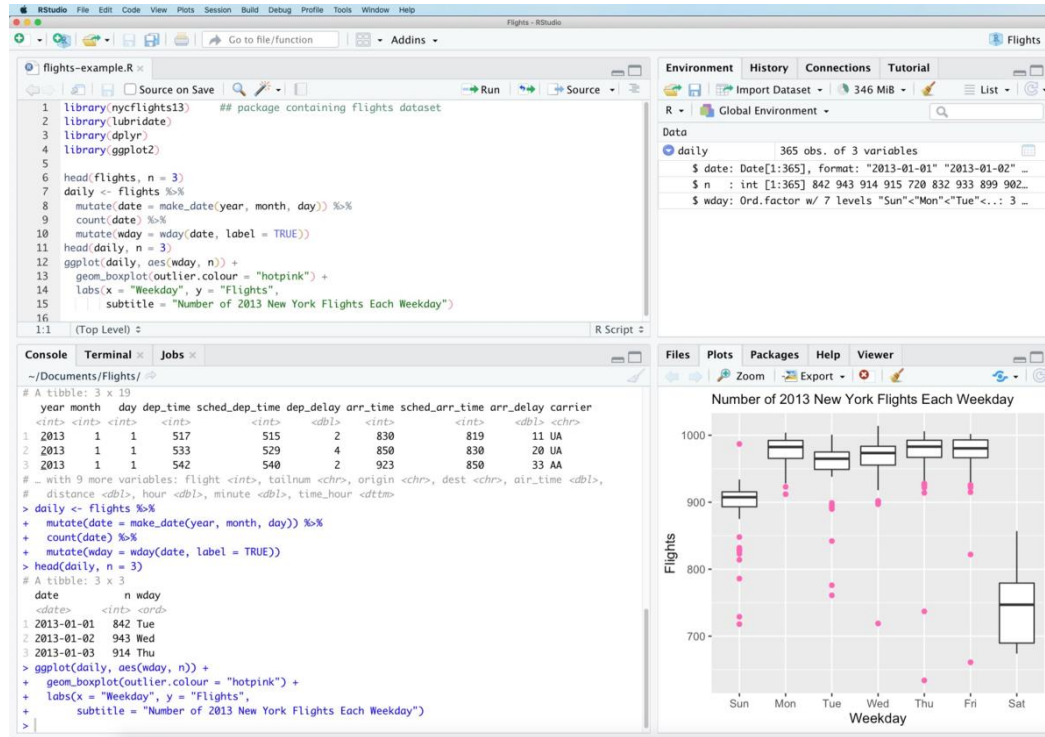
- Created by Ross Ihaka and Robert Gentleman – the name derived from the first letter of each of their names
- First released in March of 1995
- More than 2 million people use the programming language worldwide
- Over 18,000 packages in CRAN repository that do various tasks and analyses
- FOSS (free and open-source) software

Why learn R?

- Top 20 programming language according to TIOBE index and top 10 language in PYPL list (Aug 2024)
- Significant usage within biomedical research community as well as a high demand skill from employers
- It is specially suited for data analysis, statistics, visualization, machine learning, and other tasks within data science
- Useful tool especially with complement of another language like python if focused on data science as a career path

How does one use R?

- Can be used on the command line
- Better used within an IDE (integrated development environment) such as Rstudio
- Load data, install R packages, and then interactively explore, visualize, analyze, and report results



Where to find R?

- Within NIAID, you can use self-service:
 - Windows Software Center: <https://inside.niaid.nih.gov/it-equipment/installing-scientific-software-using-software-center>
 - Mac self-service: <https://inside.niaid.nih.gov/it-equipment/installing-scientific-software-mac-self-service>
- Within NIH, you can use the Biowulf HPC cluster: <https://hpc.nih.gov/>
- Download and install R and Rstudio:
 - R: <https://www.r-project.org/>
 - Rstudio: <https://www.rstudio.com/>

Tutorial overview

- I will provide a tutorial of using R in the next part of the seminar
- Next slides will cover the pre-requisites and the set-up if you would like to follow along
- I will keep advancing during the tutorial to ensure we complete it and will try to keep a reasonable pace
- If you simply want to listen and complete the tutorial later or if you get stuck, no worries...
 - You can go back to the material and complete later
 - Goal today is to introduce the material and demonstrate its use

Pre-requisites for tutorial

- You will need to have R and RStudio installed, and the course materials downloaded from GitHub
 - R version 4.2.1+ (<https://cran.r-project.org/>)
 - Rstudio (<https://www.rstudio.com/products/rstudio/>)
 - Location of course materials: https://github.com/niaid/2024_Introduction-to-R
- If within NIAID, consider self-service for R and Rstudio install:
 - Windows self-service: <https://inside.niaid.nih.gov/it-equipment/installing-scientific-software-using-software-center>
 - Mac self-service: <https://inside.niaid.nih.gov/it-equipment/installing-scientific-software-mac-self-service>
- We will be using the R script file (2024_Part 1_Intro to R_Data wrangling.R)

Tutorial Set Up

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Local Codespaces

Clone

HTTPS SSH GitHub CLI

https://github.com/niaid/2024_Introduction-to-R

Clone using the web URL.

Open with GitHub Desktop

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yuyanyinh Add files via upload

Dataset Add files via upload

Part 1_Data wrangling Add files via upload

README.md Update README.md

README

2024_Introduction-to-R

The goal of this repository is to provide a series of course materials that is used for online seminars to introduce R programming. Each subfolder in the repository provides materials for a specific course in the seminar series.

About

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Readme

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Releases

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Packages

Tutorial Set Up

- Unzip the downloaded file in your downloads folder
- Open the subfolder “Part 1_Data wrangling” and then the “2024_Part 1_Intro to R_Data wrangling.R” file
- If Rstudio is installed, then this should open the project in RStudio