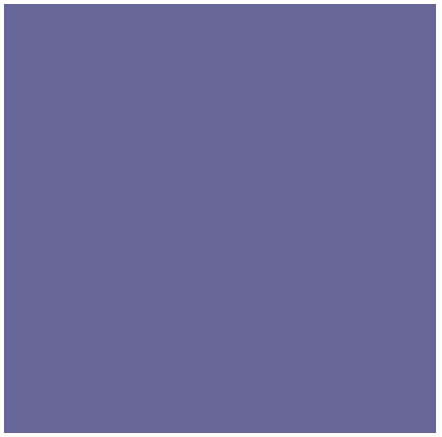
CREIGS 2020

Introduction to R

Lecture 5 Video 1



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Introduction

- If you have never learned programming before, DO NOT WORRY!!!
- The lecture will introduce you to the very basics of R programming and is thus perfect for begginers.
- Knowing these basics will allow you to apply many of the genomics tools and techniques covered later in the course.
- Once you understand the basics of R programming you will be able to teach yourself to any techniques you may need for your future research.

Lecture Overview

- This lecture will be split into 3 separate videos
- Video 1 (this video)
  - Will provide a very brief overview of R, including installation instructions.
- Video 2
  - Live demo, showing you how to read, write and manipulate data using R.
- Video 3
  - Live demo, showing you how to use functions in R, as well as some basic plots.

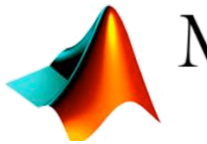
R Language

- R is a powerful language and environment for statistical computing and graphics that uses command-line scripting.
- R was initially written by Robert Gentleman and Ross Ihaka 1993 and version 1.0.0 came out in 2000.
- R is free and open-source (researchers like you and me can write out own R functions and make them available online)
- Thus, R includes virtually every type of data manipulation, statistical tool and plot type.

Facebook's Social Network Graph
Created using R!!!

http://www.r-bloggers.com/facebooks-social-network-graph/

Other Languages



MATLAB

python

Data Analysis — Software Development

User Friendly — Non-user Friendly

Memory Intensive — Memory Efficient

Installing R and RStudio

Install R

1. https://www.r-project.org/
2. Click download CRAN in the left bar
3. Choose a download site (pick closest location)
4. Choose your operation system
5. Select R version
6. Choose Download R v. (latest version)
7. Complete installation process
8. If you don't have admin rights for your computer, it is also possible to run R and RStudio from a USB stick instead of installing them

RStudio

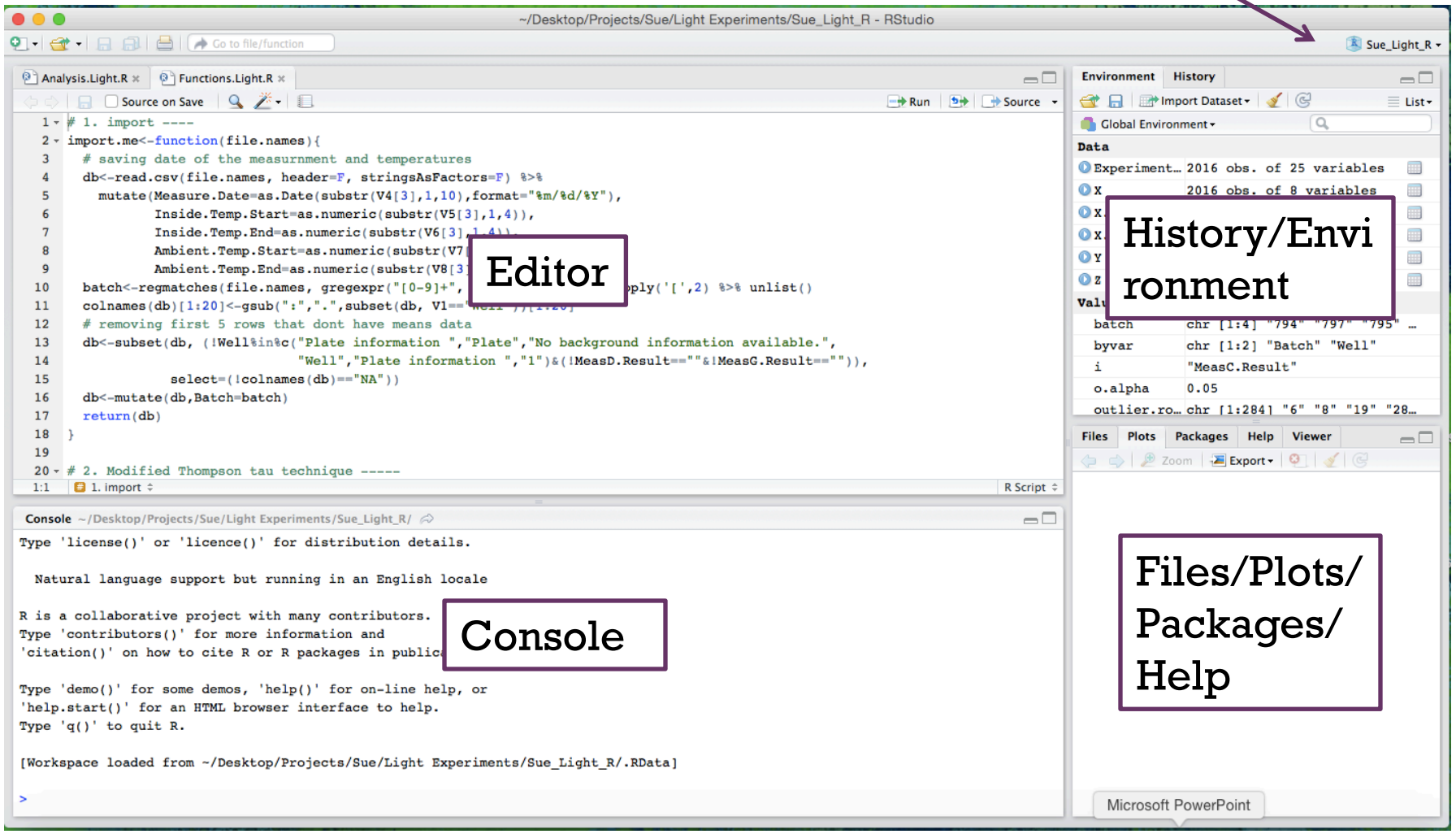
- RStudio is a powerful and productive user interface for R
- It's free and open-source
- Works great on Windows, Mac, and Linux

https://www.rstudio.com/

Install RStudio

1. https://www.rstudio.com/products/rstudio-desktop/
2. Download RStudio Desktop
3. Click on the Installer link for your platform (Mac/Windows/Linux)
4. Complete installation process
5. Open RStudio (no need to separately launch R)

Rstudio Layout



Functions & Packages

- Functions are are at the core of programming
- They take in 'arguments' (e.g data), and then process these inputs to return results (e.g data, plots etc).
- Example: The 'mean()' function, takes in a series of numbers and outputs their mean.

Functions & Packages

- Functions are organized in so-called packages or libraries
- CRAN Packages can be installed:
  - By point-and-click method: Rstudio->Packages->Install
  - Manually by running the code:

    install.packages("package name")
- GitHub Packages:
  1. require(devtools)
  2. install_github("project/package name")
- Bioconductor Packages:
  1. source("https://bioconductor.org/biocLite.R")
  2. biocLite("package name")
- After installing make package available by running either command:

  library("package name")

  require("package name")

CRAN

- The **C**omprehensive **R** **A**rchive **N**etwork

  https://cran.r-project.org/

- CRAN is a network of ftp and web servers around the world that store identical, up-to-date, versions of code and documentation for R

- Use CRAN to download versions of R and its packages

Bioconductor

- Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data

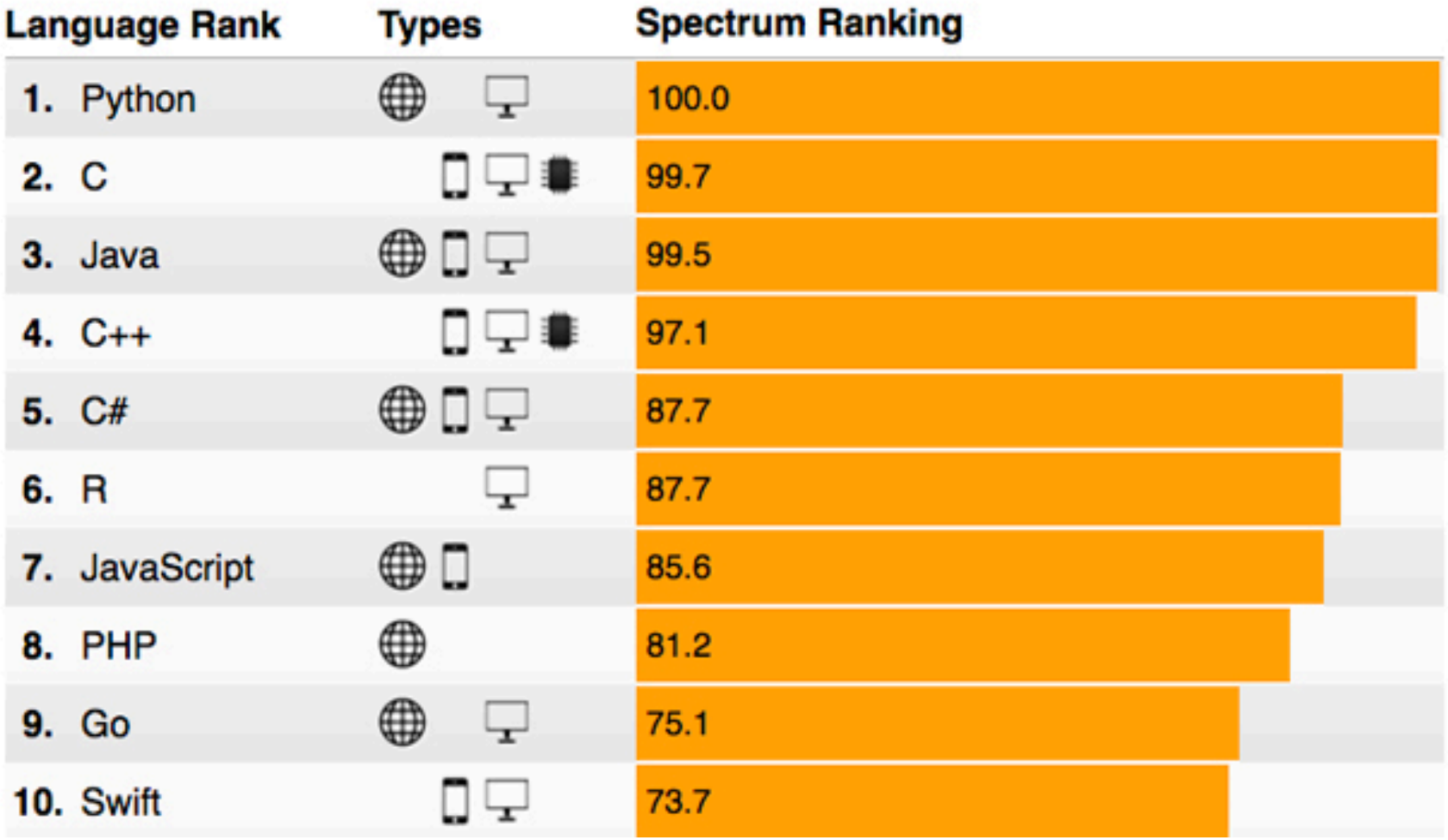
- Goals:
  - Provide widespread access to a broad range of powerful statistical and graphical methods for the analysis of genomic data
  - Facilitate the inclusion of biological metadata in the analysis of genomic data, e.g. literature data from PubMed, annotation data from LocusLink/Entrez
  - Further scientific understanding by producing high-quality documentation and reproducible research
  - Train researchers on computational and statistical methods for the analysis of genomic data

https://www.bioconductor.org/

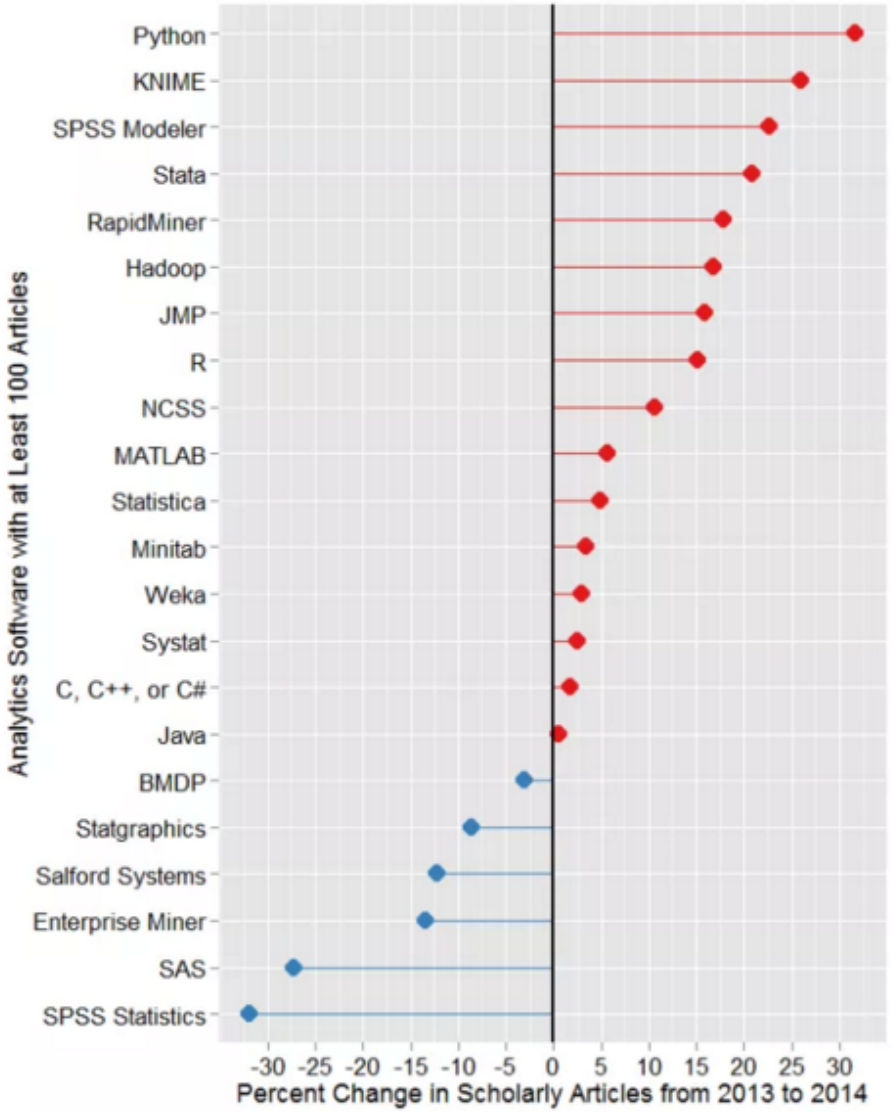
Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

Why R?

IEEE 2017 Top 10 Programming Languages (48 in total)



+ Fast acceptance among researchers



Great Community

- As a thriving open-source project, R is supported by a community of more than 2 million users and thousands of developers worldwide
- LinkedIn Group: "The R Project for Statistical Computing"
  - 67,340 members
- Meetups: "R User Group"
  - 233 groups with > 100k members
- Meetup in NYC: "New York Open Statistical Programming Meetup"
  - 6,348 members

R Help / Learning

R Help

A lot of ways to get help with R:

- Info about function ?function or help(function)
- Google: "R function"
- Most of the packages have extensive support pages and google groups
- Can post questions to get quick responses on:
  - LinkedIn Group "The R Project for Statistical Computing"
  - StackOverflow http://stackoverflow.com/
  - CrossValidated http://stats.stackexchange.com/

Learning R

Many free online resources:

- Coursera John Hopkins Data Science track

  https://www.coursera.org/specializations/jhu-data-science

- UCLA http://www.ats.ucla.edu/stat/r/
- CodeSchool http://tryr.codeschool.com/
- Programiz http://www.programiz.com/r-programming /