Short Read Workshop Day 6
Introduction to R and RStudio

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Day 6 Overview

1. Running `R` in the terminal
2. Running `R` in `RStudio`
3. Submitting `R script` as an sbatch job

Goal of the day

Learn how to run R code!

Practice installing packages, tidying data, saving files and plotting.

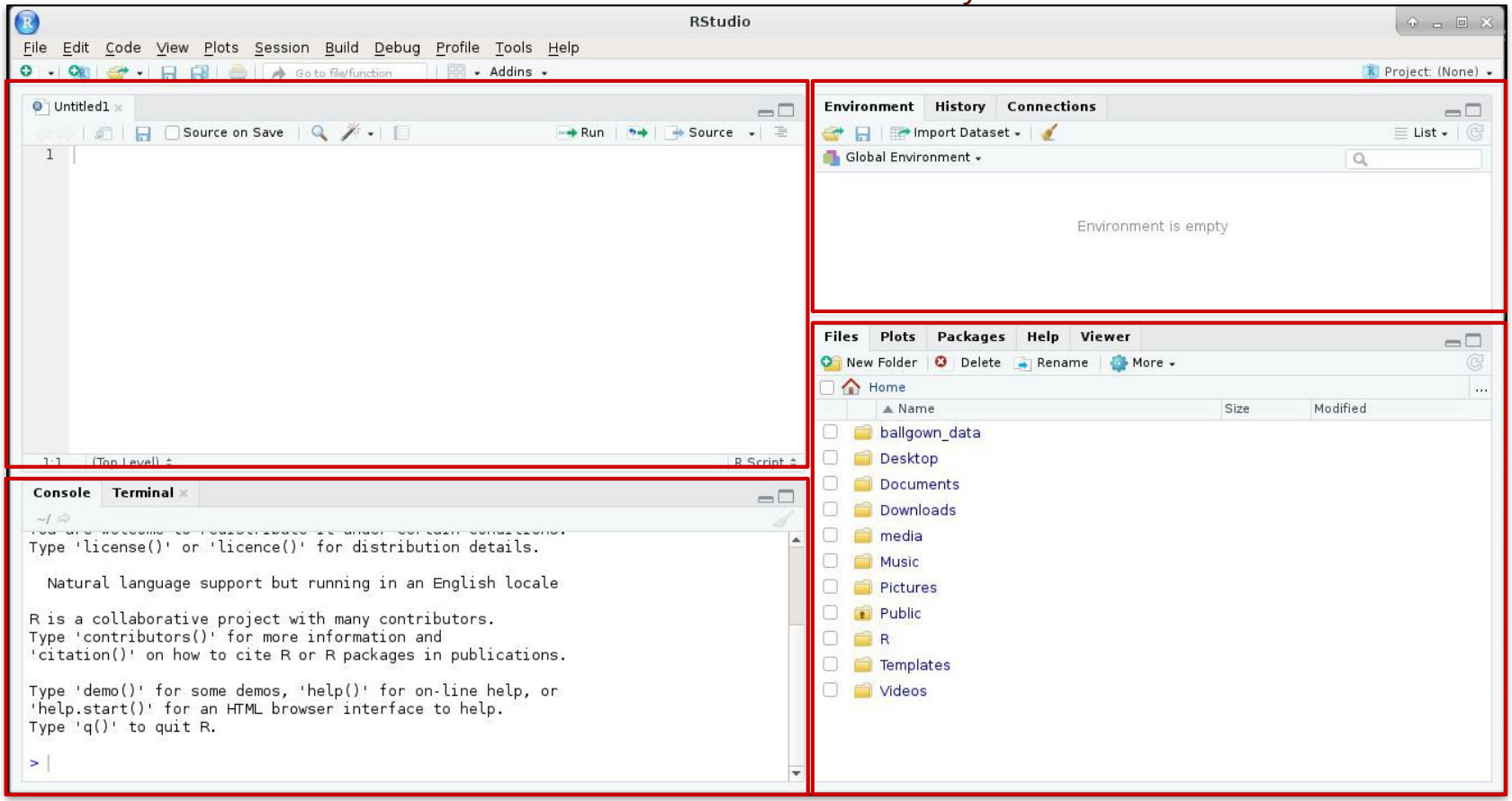
What is R?

- R is a free statistical computing and graphing software
- Can be installed from their website https://www.r-project.org/
- R can be run in a few environments:
  - RStudio
  - Jupyter

Summary of RStudio

R scripts, R markdown, R notebooks

Summary of all the data loaded in Rstudio



R console, Terminal

Directories, Plots, Packages...

There are different ways to interact with R

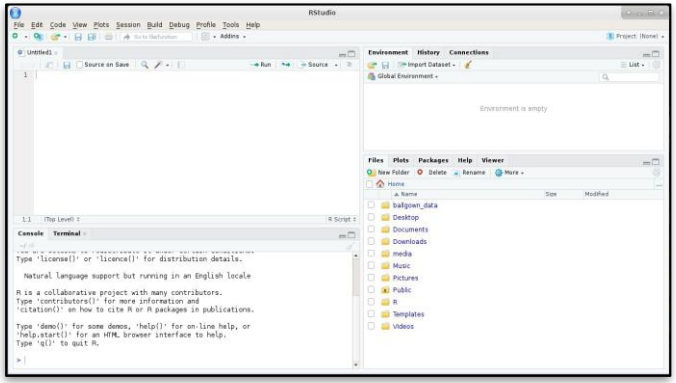
R console

```
(base) cu-biot-14-10:~ rutendo$ R

R version 3.6.3 (2020-02-29) -- "Holding the Windsock"
Copyright (C) 2020 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin15.6.0 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[Previously saved workspace restored]

>
```

Enter **R code** here

Interactive

R Studio



Enter **R code** and **visualize plots**

More interactive

Submit an R script as a job

```
#!/bin/bash
#
#SBATCH --job-name=feature_counts                    # Job name
#SBATCH --mail-type=ALL                              # Mail events (NONE, BEGIN, END, FAIL, ALL)
#SBATCH --mail-user=email@colorado.edu               # Where to send mail
#SBATCH --nodes=1                                    # Number of cores job will run on
#SBATCH --ntasks=4                                   # Number of CPU (processers, tasks)
#SBATCH --time=1:00:00                               # Time limit hrs:min:sec
#SBATCH --partition compute                          # Job queue
#SBATCH --mem=4gb                                    # Memory limit
#SBATCH --output=/scratch/Users/rutendos/e_and_o/%x_%j.out
#SBATCH --error=/scratch/Users/rutendos/e_and_o/%x_%j.err

################## SET VARIABLES #####################################

FEATURECOUNTS=/scratch/Users/rutendos/day6/featureCounts/scripts/d6_featureCounts.R

######################################################################
################ PRINT JOB INFO ######################################

printf "Sample ID: $ROOTNAME"
printf "\nDirectory: $PROJECT"
printf "\nRun on: $(hostname)"
printf "\nRun from: $(pwd)"
printf "\nScript: $0\n"
date

printf "\nYou've requested $SLURM_CPUS_ON_NODE core(s).\n"

######################################################################

Rscript $FEATURECOUNTS
```

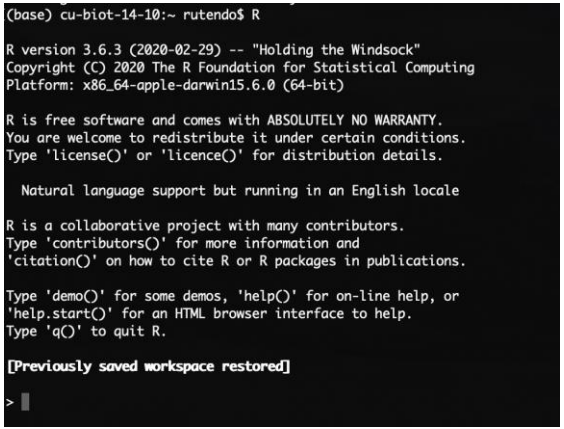
Run **R script** here

Least interactive

For more compute intensive scripts

R you ready to learn some R?

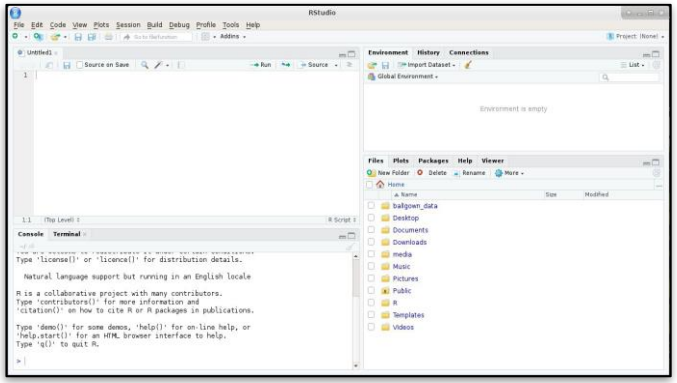
- Let us go over the `Day6_worksheet_learning_r` worksheet:
  - Introduction to R in the terminal
  - Learn basic R commands



R console

Learning R in RStudio

- Let us go over the `Learning_R.R` worksheet in R Studio:
  - Introduction to R and R Markdown
  - Introduction to the iris dataset
  - Installing and loading libraries
    - tidyverse
  - Generating summary statistic in R
  - Making plots with ggplot2
  - Manipulating data.frames



R Studio

Challenge Question

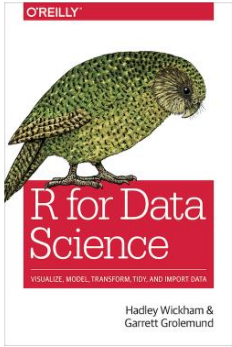
- How would you perform a computationally intensive R job?
  - i.e. Requires more memory than on your personal computer.

Writing an R script to submit on a supercomputer

- Create a new R script based on the `Learning_R.R` script
  - Include the *“Manipulating mtcars”* section in to a script called `Learning_R_submit_aws.R`
  - Save plots and tables to a working directory in the script
- Run the R script as a job on AWS
  - Use the `RScript` command to call your script

More resources for R

- ggplot2 website https://ggplot2.tidyverse.org/
- R-bloggers https://www.r-bloggers.com/
- Quick-R https://www.statmethods.net/
- R for Data Science (by Hadley Wickham & Garrett Grolemund) http://r4ds.had.co.nz/



Homework

1. Complete the `Learning_R_Additional_Practice.R`

This homework will go over most of the topics covered today, but on a different dataset. There will be more advanced questions that build on what was in the inclass session.

1. Install `rsubread`

A library for counting reads from bam files over genome features such as genes. *Install this in the R on AWS*.

1. Install `DESeq2`

This library takes in counts as input and performs differential gene expression analyses on the input features. You will be using this library in Day7. *Install this on your local machine*.

This takes a long time, so get this installed before Day7.