# Introduction to R for Biologists

Day 1 – Intro to R and the Tidyverse Ecosystem

## Day 1 Outline

- How to get set up using R
- 2. How and why to use RStudio & R Markdown (.Rmd)
- 3. Basics of programming
  - Data types
  - Functions
  - Troubleshooting
- 4. Intro to the Tidyverse
  - Tidy vs untidy data
  - Tidyverse-specific functions

# R: The premier data analysis and visualization platform

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



#### The Comprehensive R Archive Network

#### Download and Install R

Precompiled binary distributions of the base system and contributed packages, Windows and Mac users most likely want one of these versions of R:

- Download R for Linux
- Download R for (Mac) OS X
- Download R for Windows

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

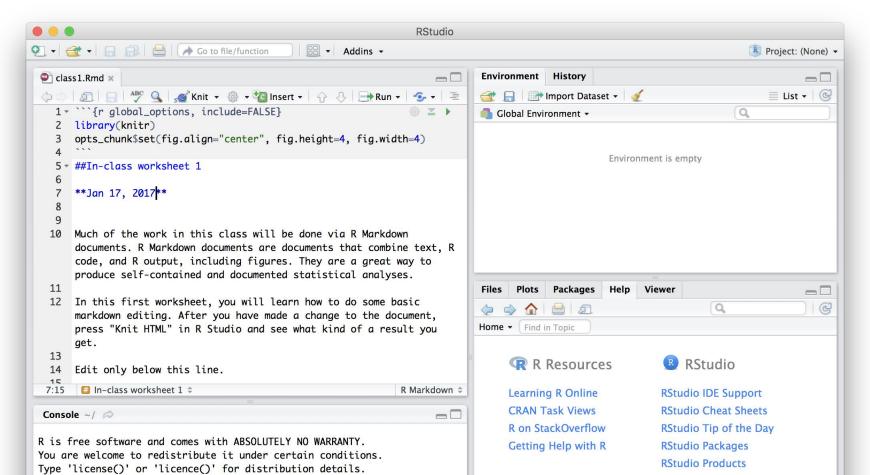
#### Source Code for all Platforms

Windows and Mac users most likely want to download the precompiled binaries listed in the upper

# R Studio: A nice user interface for R

https://www.rstudio.com/products/rstudio/download/

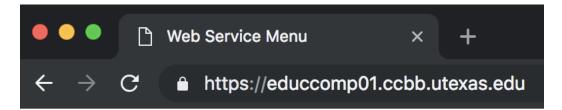




# Access R Studio through your web browser

- 1. <a href="https://gsafcomp01.ccbb.utexas.edu/">https://gsafcomp01.ccbb.utexas.edu/</a>
- 2. <a href="https://gsafcomp02.ccbb.utexas.edu/">https://gsafcomp02.ccbb.utexas.edu/</a>

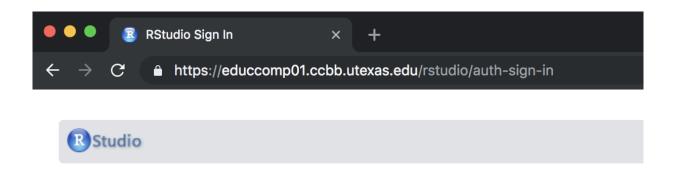
## Select RStudio



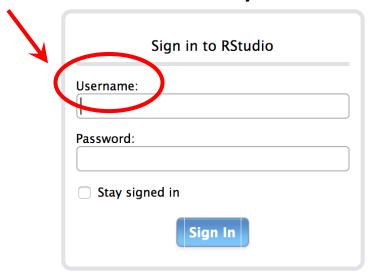
Please choose one of the following applications:

- RStudio
- <u>Jupyterhub</u>

# Sign in with your student# and password



#### Refer to class email for your individual username



# R Markdown

# R Markdown: Writing documents with embedded R code

```
🔎 class 1.Rmd 🛪
to Insert → 🔐 🕀 📑 Run → 🍜 →
 17 - ## 1. Basic Markdown editing
 18 Try out basic R Markdown features, as described
     [here.](http://rmarkdown.rstudio.com/authoring_basics.html) Write some text
     that is bold, and some that is in italics. Make a numbered list and a bulleted
     list. Make a nested list. Try the block-quote feature.
 19
 20 - ## 2. Embedding R code
 21
 22
     R code embedded in R chunks will be executed and the output will be shown.
 23 - ```{r}
 24 # R code goes here
 25 x <- 5
 26 y <- 7
 27 z <- x * v
 28
    Z
 29
 30
```

# R Markdown: Writing documents with embedded R code

## 1. Basic Markdown editing

Try out basic R Markdown features, as described here. Write some text that is bold, and some that is in italics. Make a numbered list and a bulleted list. Make a nested list. Try the block-quote feature.

## 2. Embedding R code

R code embedded in R chunks will be executed and the output will be shown.

```
# R code goes here
x <- 5
y <- 7
z <- x * y
z
```

```
## [1] 35
```

Play around with some basic R code. E.g., take the built-in data set cars, which lists speed and stopping distance for cars from the 1920. Plot speed vs. distance, and/or perform a correlation analysis. Then write a few sentences describing what you see.

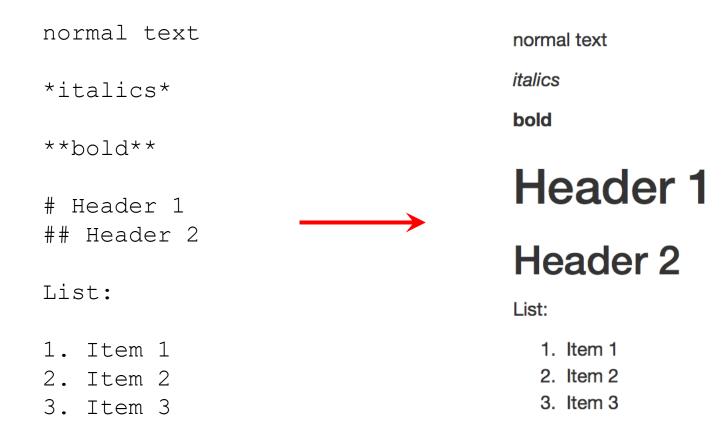
# We convert R Markdown to HTML by "knitting" the Markdown file

```
class 1.Rmd 🗱
                                             🚹 Insert 🕶 🔐 🕀 📑 Run 🕶

≪ Knit ▼
 17 - ## 1. Basic Markdown editina
 18 Try out basic R Markdown features, as described
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 23 + ```{r}
     # R code goes here
    x <- 5
 26
    y <- 7
    Z <- X * V
 28
     7
 29
 30
 31
     Play around with some basic R code. E.g., take the built-in data set `cars`,
     which lists speed and stopping distance for cars from the 1920. Plot speed vs.
                and/on nonform a connolation analysis. Then white a few contences
```

### Markdown basics

#### http://rmarkdown.rstudio.com/authoring basics.html



## Markdown basics

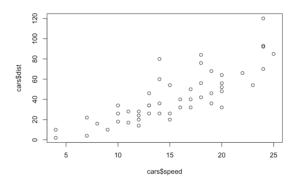
```
Embedded R code will be evaluated and printed
```

```
```{r}
head(cars)
plot(cars$speed, cars$dist)
```

## Embedded R code will be evaluated and printed

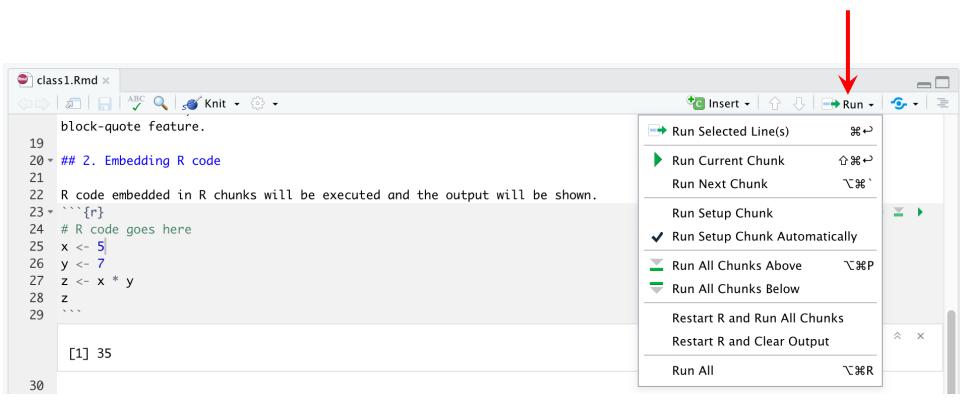
```
head(cars)
```

plot(cars\$speed, cars\$dist)





## Press the "Run" button



# Highlight code you want to execute and press ctrl+Enter (cmd+Enter on Macs)

```
R code embedded in R chunks will be executed and the output will be shown.
```{r}
# R code goes here
v <- 7
z \leftarrow x * y
         Terminal ×
Console
                     Jobs ×
 ~/Desktop/projects/
> x <- 5
> y <- 7
> Z <- X * V
> Z
Γ1] 35
```

# Place pointer on line of code you want to execute, press ctrl+Enter (cmd+Enter on Macs)

```
R code embedded in R chunks will be executed and the output will be shown.
```{r}
# R code goes here
x < -5
y <- 7
z <- x * y
         Terminal ×
Console
                    Jobs ×
 ~/Desktop/projects/
> Z <- X * V
```

# Use ctrl+Shift+Enter (cmd+Shift+Enter on Macs) to execute an entire code chunk

```
R code embedded in R chunks will be executed and the output will be shown.
```{r}
# R code goes here
x < -5
y <- 7
z <- x * y
Z
Console
         Terminal ×
                    Jobs ×
 ~/Desktop/projects/
> x <- 5
> y <- 7
> Z <- X * V
> Z
[1] 35
```

# Shortcuts for coding

- Ctrl+Shift+M (Cmd+Shift+M on Macs) produces a pipe operator %>% (will be used with the tidyverse)
- Ctrl+Shift+C (Cmd+Shift+C on Macs) will comment/uncomment a line or multiple lines
- Tab and Shift+Tab will indent and un-indent lines, respectively

# R Programming Basics

## Assignments, numbers, vectors

```
> x < -5
                      Assign number 5 to variable x
> x
[1] 5
> 5*x^2+7
                      Calculate 5*x<sup>2</sup>+7
[1] 132
> y < -c(1, 2, 3, 4, 5) Create vector, assign
                                 to variable y
[1] 1 2 3 4 5
                            Multiply each element
> x * y
                           in y with the number in x
[1] 5 10 15 20 25
```

## Strings

#### A string contains text:

```
> name <- "Rachael Cox"
> name
[1] "Rachael Cox"
```

#### A vector of strings:

```
> animals <- c("cat", "mouse", "mouse",
"cat", "rabbit")
> animals
[1] "cat" "mouse" "mouse" "cat"
"rabbit"
```

### **Factors**

Factors keep track of distinct categories (levels) in a vector:

```
> animals
[1] "cat" "mouse" "mouse" "cat"
"rabbit"

> factor(animals)
[1] cat mouse mouse cat rabbit
Levels: cat mouse rabbit
```

We use data frames to store data sets with multiple variables:

```
> pets <- data.frame(</pre>
    family = c(1, 2, 3, 4, 5),
    pet = animals
> pets
  family pet
             cat
           mouse
           mouse
             cat
```

We access individual columns in a data frame with \$ + the column name:

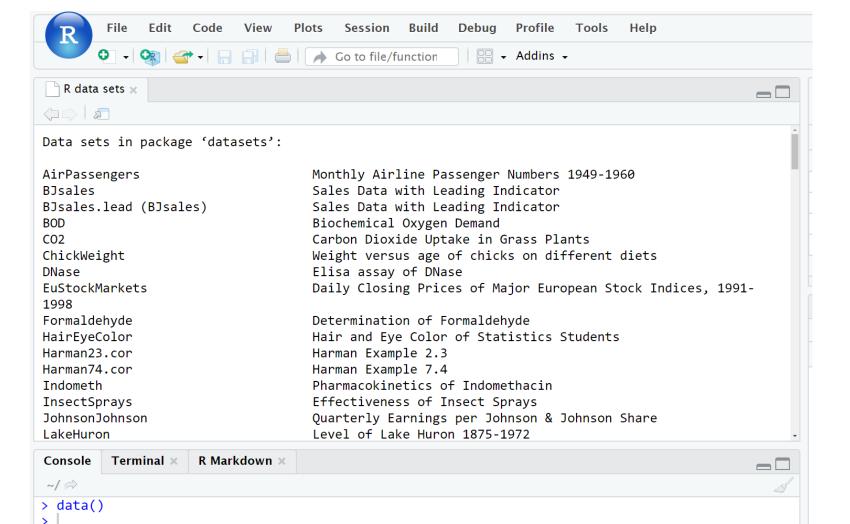
```
> pets$family [1] 1 2 3 4 5
```

```
> pets$pet
[1] cat mouse mouse cat rabbit
Levels: cat mouse rabbit
```

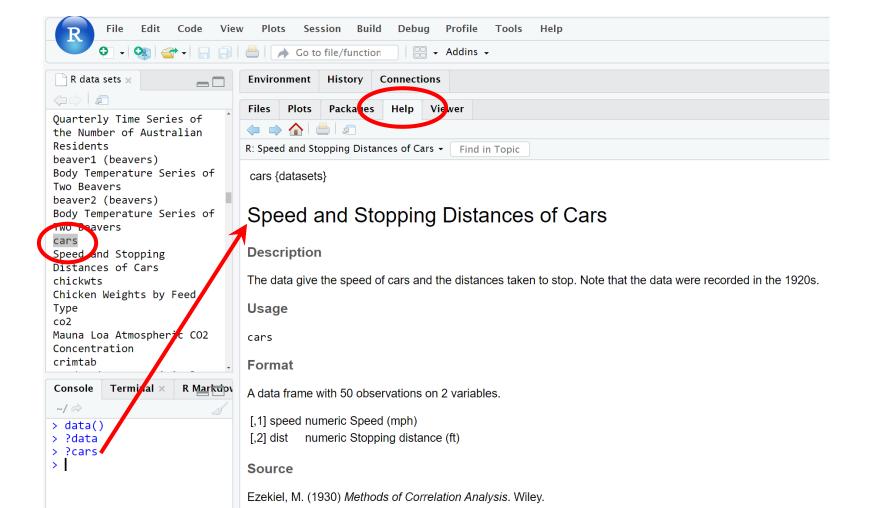
## R has many built-in data frames:

>	cars		>	chickwts	
	speed	dist		weight	feed
1	4	2	1	179	horsebean
2	4	10	2	160	horsebean
3	7	4	3	136	horsebean
4	7	22	4	227	horsebean
5	8	16	• •	• • •	• • •
6	9	10	11	. 309	linseed
7	10	18	12	229	linseed
8	10	26	13	181	linseed
9	10	34	14	141	linseed

#### Available built-in datasets can be accessed with data()



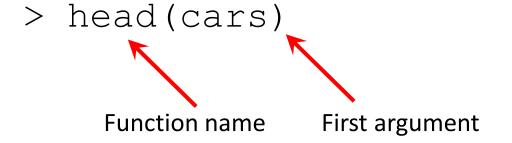
#### Data set information can be accessed with ?dataset



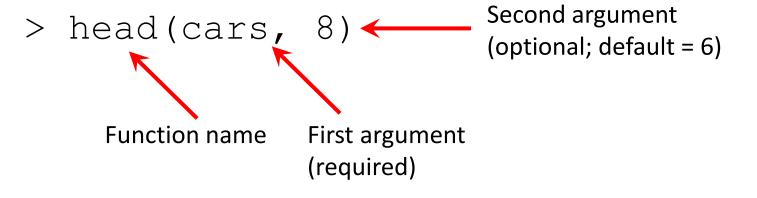
The head () function shows the first few lines of a data frame:

```
> head(cars)
  speed dist
2
      4
           10
3
4
      7 22
5
           16
6
           10
```

Functions are called in the format function (argument)



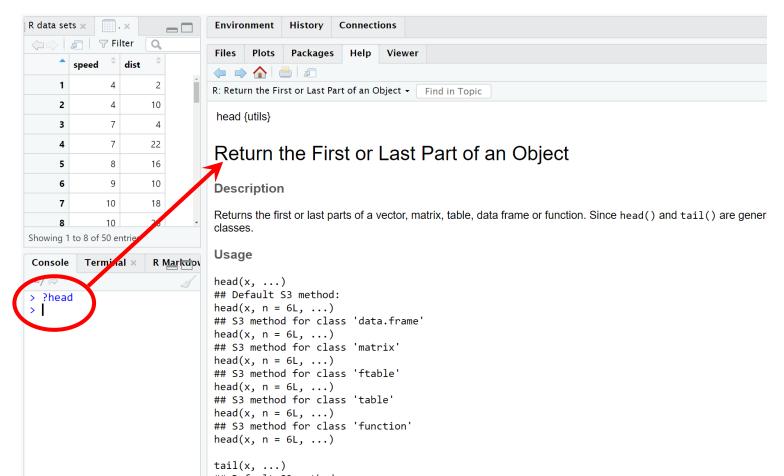
Functions can have any number of required arguments or optional arguments



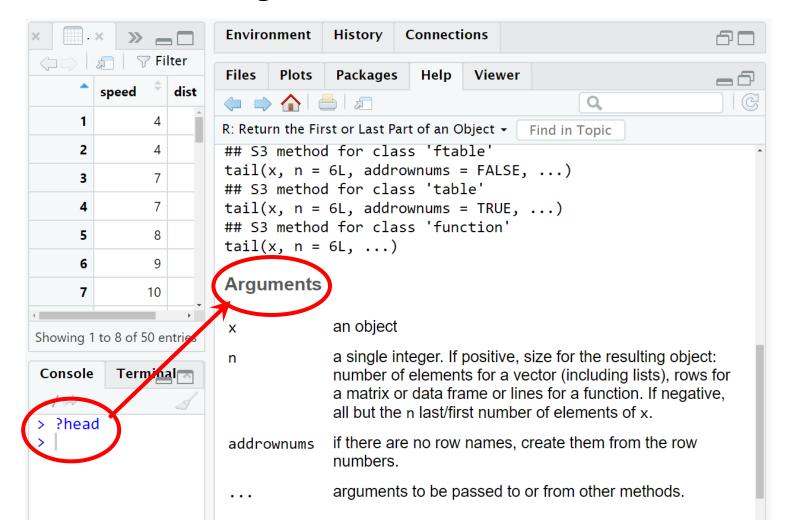
head (cars, 8) will show the first 8 lines of the data frame instead of the default 6:

```
> head(cars, 8)
  speed dist
      4 10
3
    7 22
5
          16
      8
          10
     10
          18
          26
```

# More information about what a function does and/or requires can be accessed with ?function



#### ?function has argument information



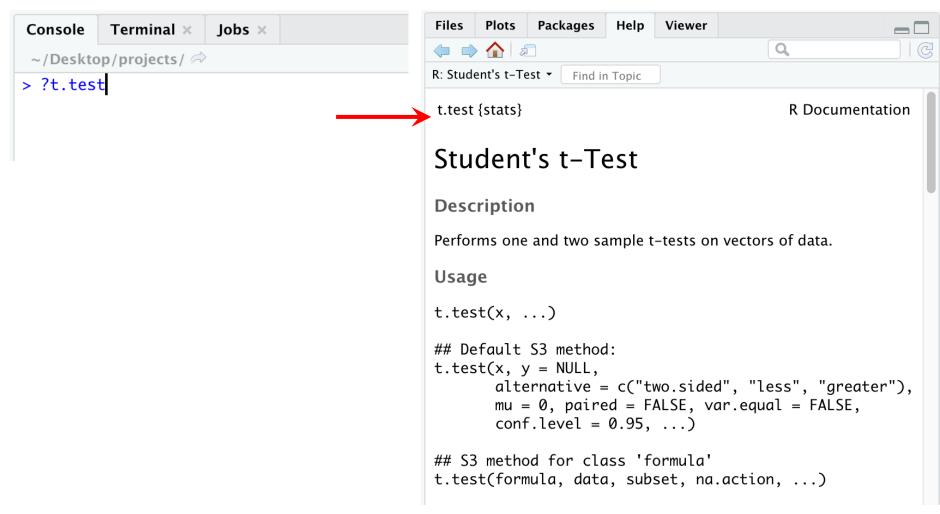
#### We can implicitly or explicitly pass arguments

```
head (x=cars, n=8)
> head(cars, 8)
  speed dist
                            speed dist
            10
                                     10
            22
                                     22
            16
                                     16
            10
                                     10
      10
            18
                               10
                                     18
            26
                                     26
                               10
```

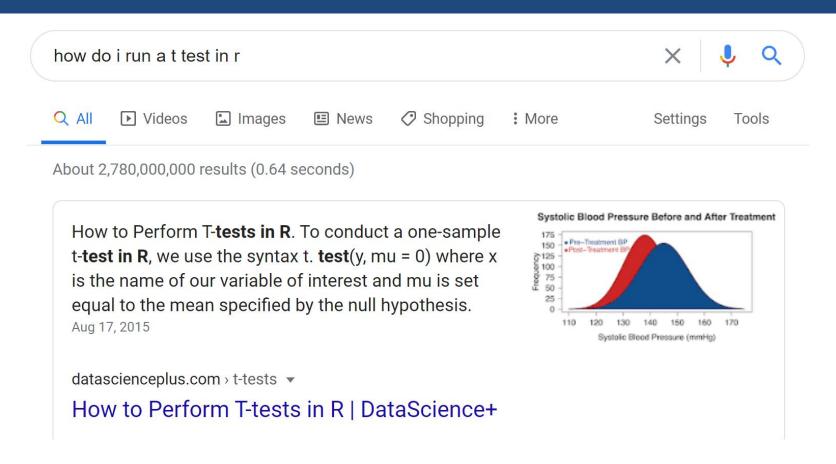
# Troubleshooting

## Ask RStudio for help

#### Type ?function into console

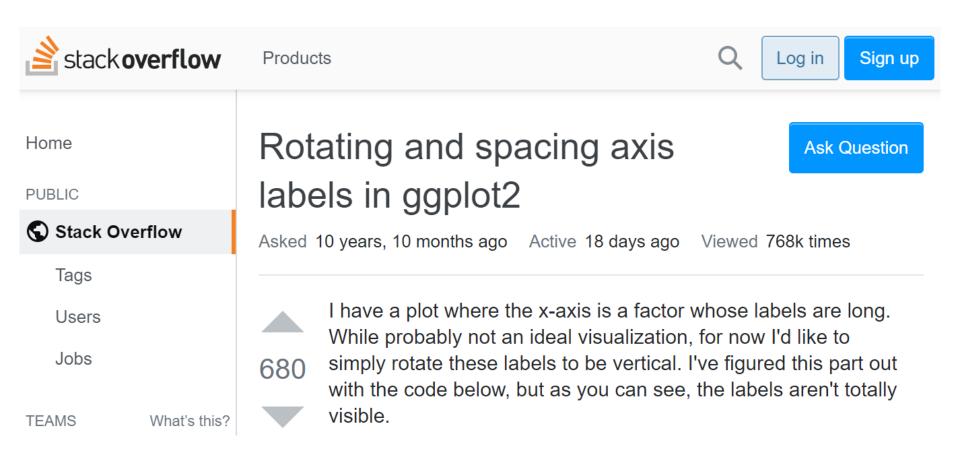


# Ask Google for help



- G Error in t.test.default(x, y) : not enough 'x' observations
- Q Error in t.test.default(x, y) : not enough 'x' observations Google Search

# Ask StackOverflow for help



# Extending R through packages: There's a package for everything

# R packages are available on CRAN (Comprehensive R Archive Network)



#### **Contributed Packages**

#### **Available Packages**

(+)

Currently, the CRAN package repository features 15364 available packages.

a cran.r-project.org

Table of available packages, sorted by date of publication

Table of available packages, sorted by name

#### Installation of Packages

Please type help("INSTALL") or help("install.packages") in R for information on how to install packages from this repository. The manual R Installation and Administration (also contained in the R base sources) explains the process in detail.

<u>CRAN Task Views</u> allow you to browse packages by topic and provide tools to automatically install all packages for special areas of interest. Currently, 41 views are available.

#### Package Check Results

All packages are tested regularly on machines running <u>Debian GNU/Linux</u>, <u>Fedora</u>, OS X, Solaris and Windows.

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# Bio-specific R packages are available on Bioconductor



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#### About Bioconductor

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

Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, and an active user community. Bioconductor is also available as an AMI (Amazon Machine Image) and Docker images.

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- Registration open for BioC2020.
- Core team job opportunities available, contact Martin.Morgan at RoswellPark.org
- Bioconductor F1000 Research Channel is

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   See posting for more information.
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