Biocomputing with R

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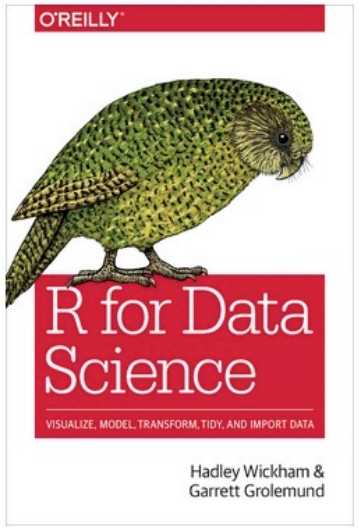
21 June 2022

Genetic Diversity Centre (GDC)
Bioinformatics
ETH Zurich

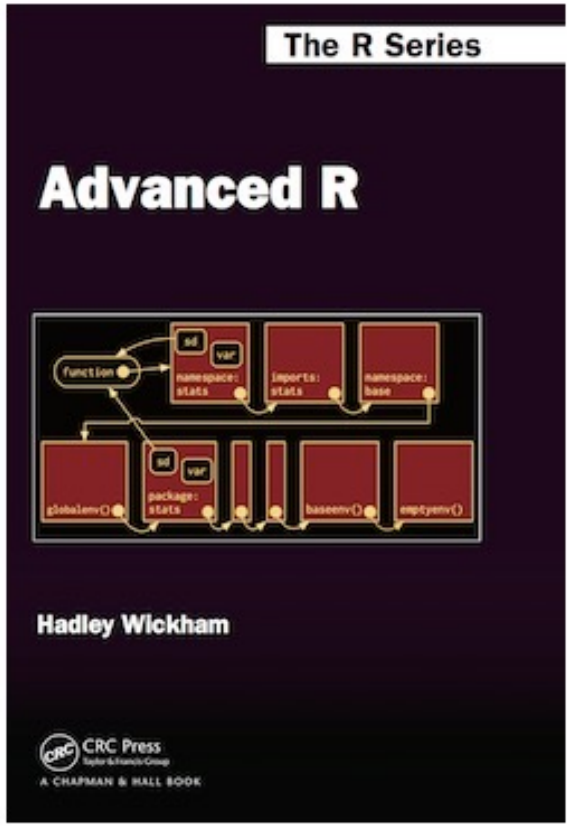
Resources

Many many tutorials, forum, YouTube videos posts and books available



R-bloggers

R news and tutorials contributed by (750) R bloggers



Packages

Available Packages

Currently, the CRAN package repository features 18607 available packages.

Table of available packages, sorted by date of publication

Table of available packages, sorted by name

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Rstudio

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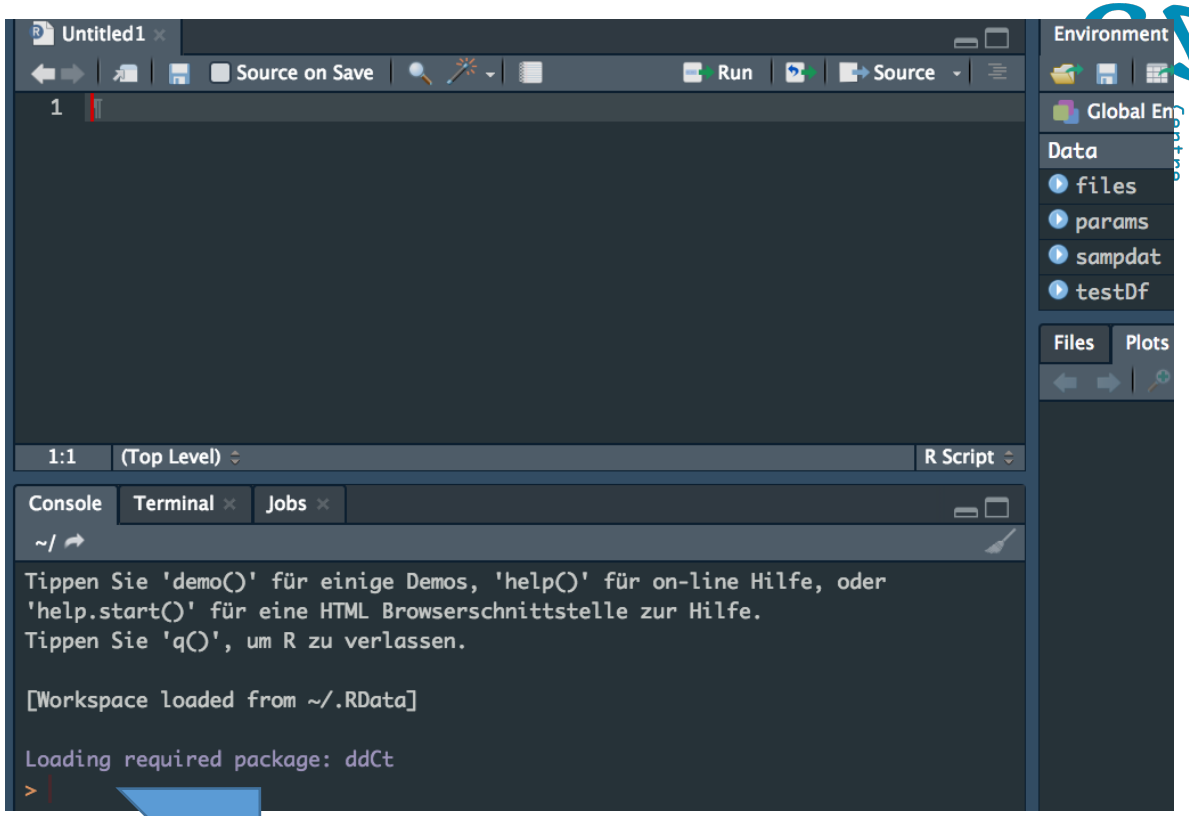
urse Webpage

art
equirements
nux 1 - Local Terminal
nux 2 - Remote Terminal
ocomputing
ocomputing with R
ocomputing on a HPC cluster
eproducible Research
PS (NGS)

Biocomputing with R




```
### set working directory
setwd("~/Desktop")

### generate folder
dir.create("Demo")
setwd("Demo")

### download scripts for Demo
utils::download.file("https://www.gdc-docs.ethz.ch/GeneticDiversityAnalysis/GDA
utils::download.file("https://www.gdc-docs.ethz.ch/GeneticDiversityAnalysis/GDA

### open R scripts
file.edit("My_functions.R")
file.edit("Demo.R")
```

Copy-paste

R-scripts

```
##·set·working·directory¬
setwd("~/Desktop")¬
¬
#·Prepare·workplace·----¬
##install·library¬
install.packages("tidyverse")¬
¬
##·remove·all·variables¬
rm(list·=·ls())¬
¬
##·set·seed¬
set.seed(1000)¬
¬
##·load·library¬
library(tidyverse)¬
##·source¬
source("My_functions.R")¬
¬
```

```
4  ¬
5  sessionInfo()¬
```

Import tables

```
dat <- read.csv("http://gdc-web.ethz.ch/gdc-analysis-course/2019/data/Students19.txt", header = T, sep="\t")

dat <- read_tsv("http://gdc-web.ethz.ch/gdc-analysis-course/2019/data/Students19.txt")
```

data.table::fread

R Objects

- Data frames
- Lists
- Vectors
- Matrixes

as.logical	TRUE, FALSE, TRUE	Boolean values (TRUE or FALSE).
as.numeric	1, 0, 1	Integers or floating point numbers.
as.character	'1', '0', '1'	Character strings. Generally preferred to factors.
as.factor	'1', '0', '1', levels: '1', '0'	Character strings with preset levels. Needed for some statistical models.

```
str(iris)
```

```
## 'data.frame':    150 obs. of  5 variables:
##  $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
##  $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
##  $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
##  $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
##  $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...
```

R Objects

tibble

```
as_tibble(iris)
```

```
## # A tibble: 150 x 5
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           <dbl>       <dbl>        <dbl>       <dbl> <fct>
##  1          5.1         3.5          1.4         0.2 setosa
##  2          4.9         3            1.4         0.2 setosa
##  3          4.7         3.2          1.3         0.2 setosa
##  4          4.6         3.1          1.5         0.2 setosa
##  5          5           3.6          1.4         0.2 setosa
##  6          5.4         3.9          1.7         0.4 setosa
##  7          4.6         3.4          1.4         0.3 setosa
##  8          5           3.4          1.5         0.2 setosa
##  9          4.4         2.9          1.4         0.2 setosa
## 10          4.9         3.1          1.5         0.1 setosa
## # … with 140 more rows
```

Data Manipulation

```
iris.df <- data.frame(iris$Sepal.Length, iris$Sepal.Width, iris$Species)
```

Replace patterns

```
iris.df$Species2 <- gsub("setosa", "Setosa", iris.df$iris.Species)
```

subset

```
iris.df.sub <- subset(iris.df, iris.df$iris.Species == "setosa")
```

order table

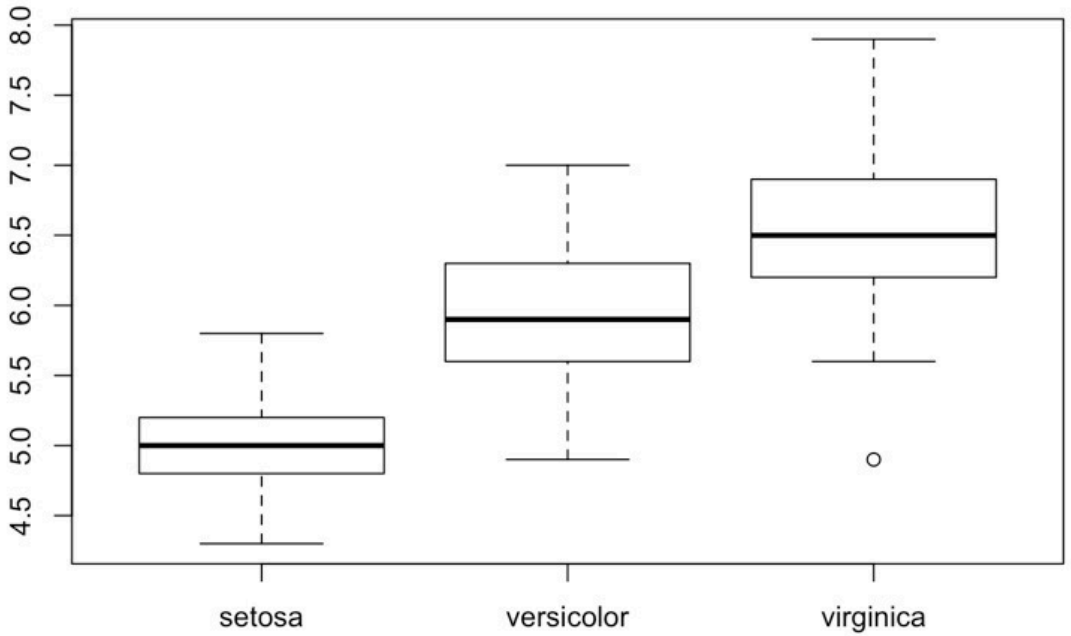
```
iris.df.orderd <- iris.df[order(iris.df$iris.Sepal.Length), ]
```

Data Manipulation

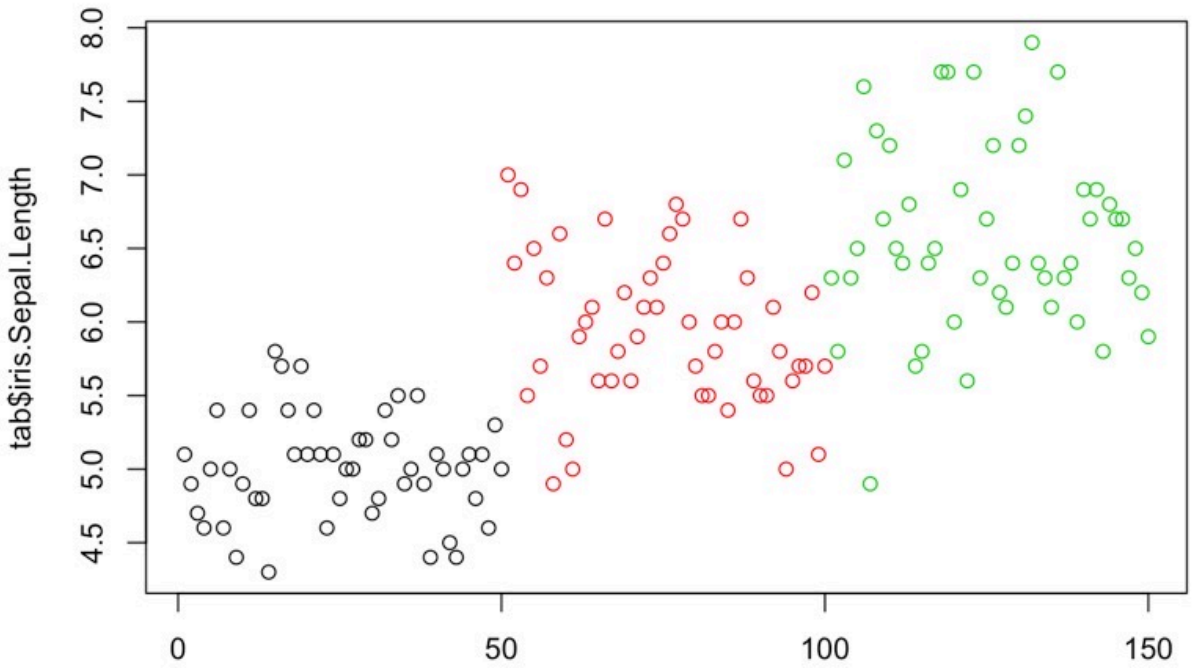
```
iris.tb <- as_tibble(iris) %>%
           select(Species, Sepal.Length, Sepal.Width, Petal.Length) %>%
           dplyr::filter(Species != "setosa") %>%
           mutate(Species2 = gsub("versicolor", "Versicolor", Species)) %>%
           arrange(., Sepal.Length)
```

Data visualization

```
boxplot(tab$iris.Sepal.Length~tab$iris.Species)
```

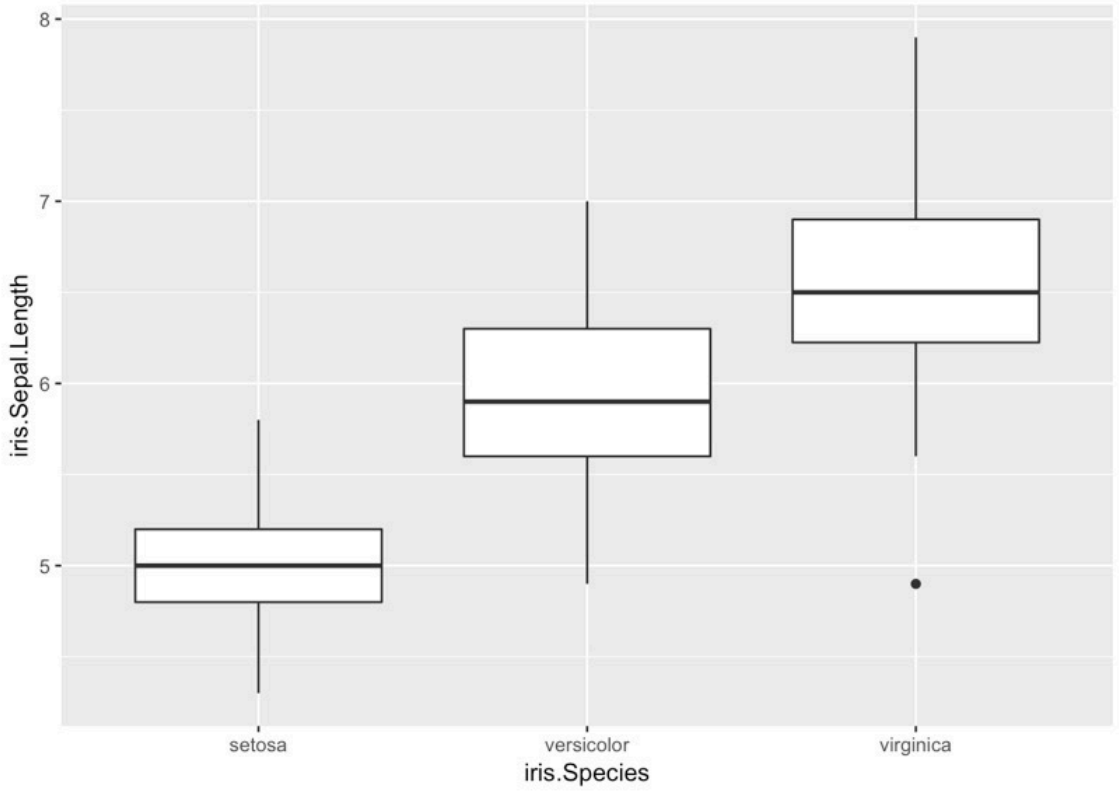



```
plot(tab$iris.Sepal.Length, col=tab$iris.Species)
```

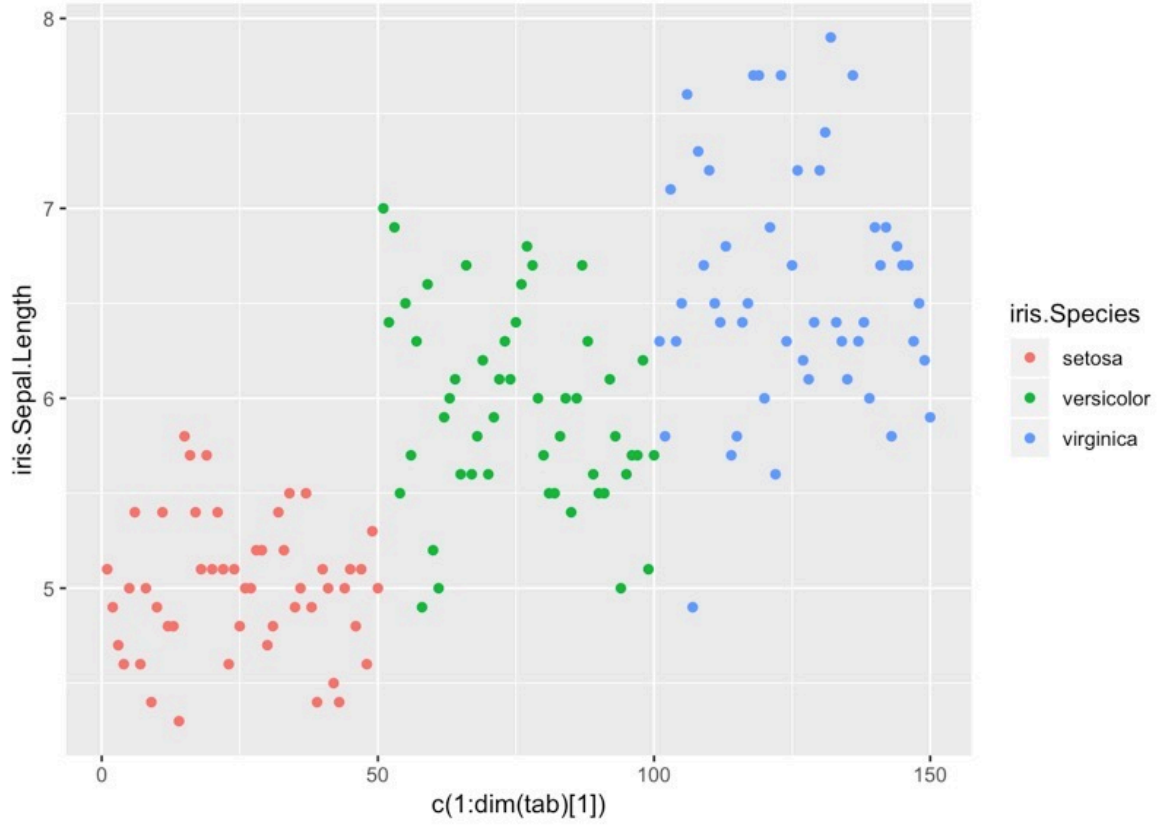


Visualization-ggplot2

```
library(ggplot2)
ggplot(tab, aes(x=iris.Species,y=iris.Sepal.Length))+
  geom_boxplot()
```

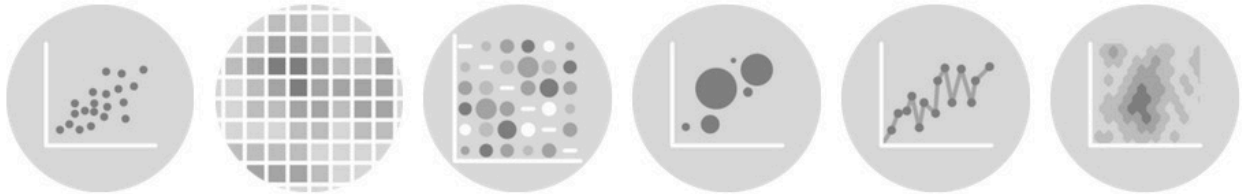



```
ggplot(tab, aes(x=c(1:dim(tab)[1]),y=iris.Sepal.Length, colour=iris.Species))+
  geom_point()
```



Distribution

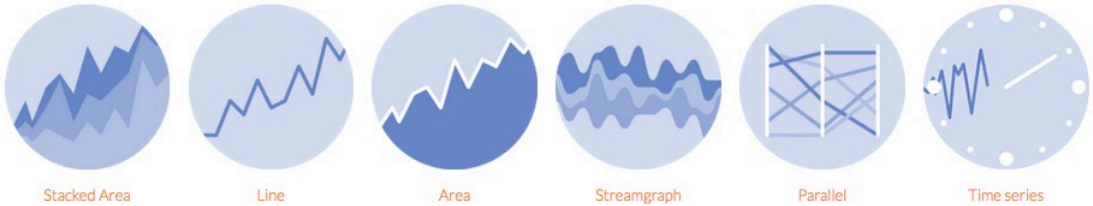
Correlation



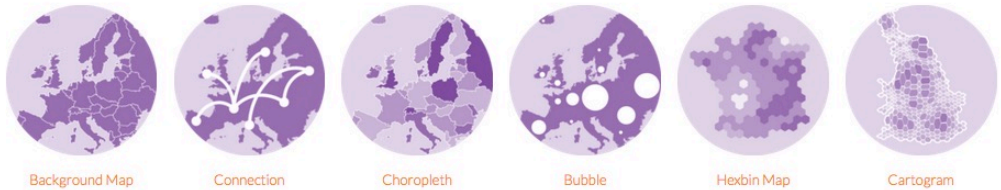
Rankings

Part of a whole

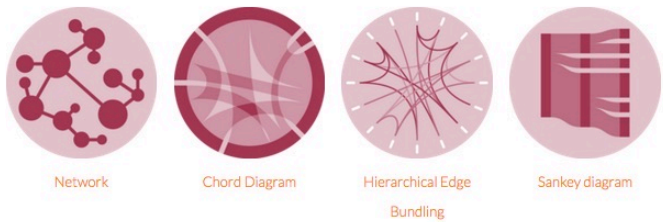
Evolution



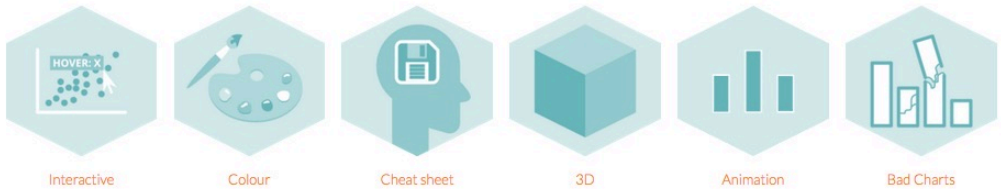
Maps



Flow

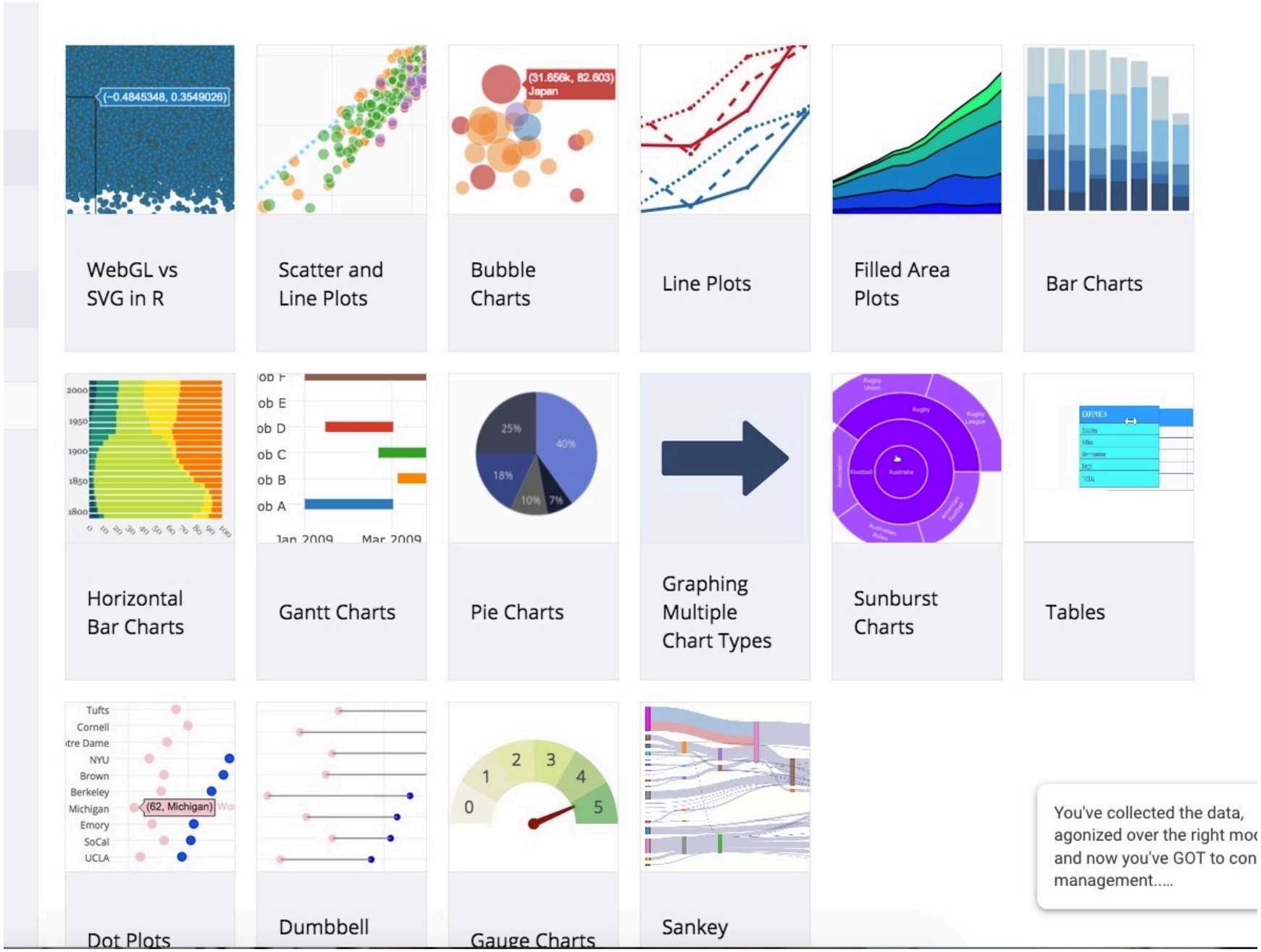


Other



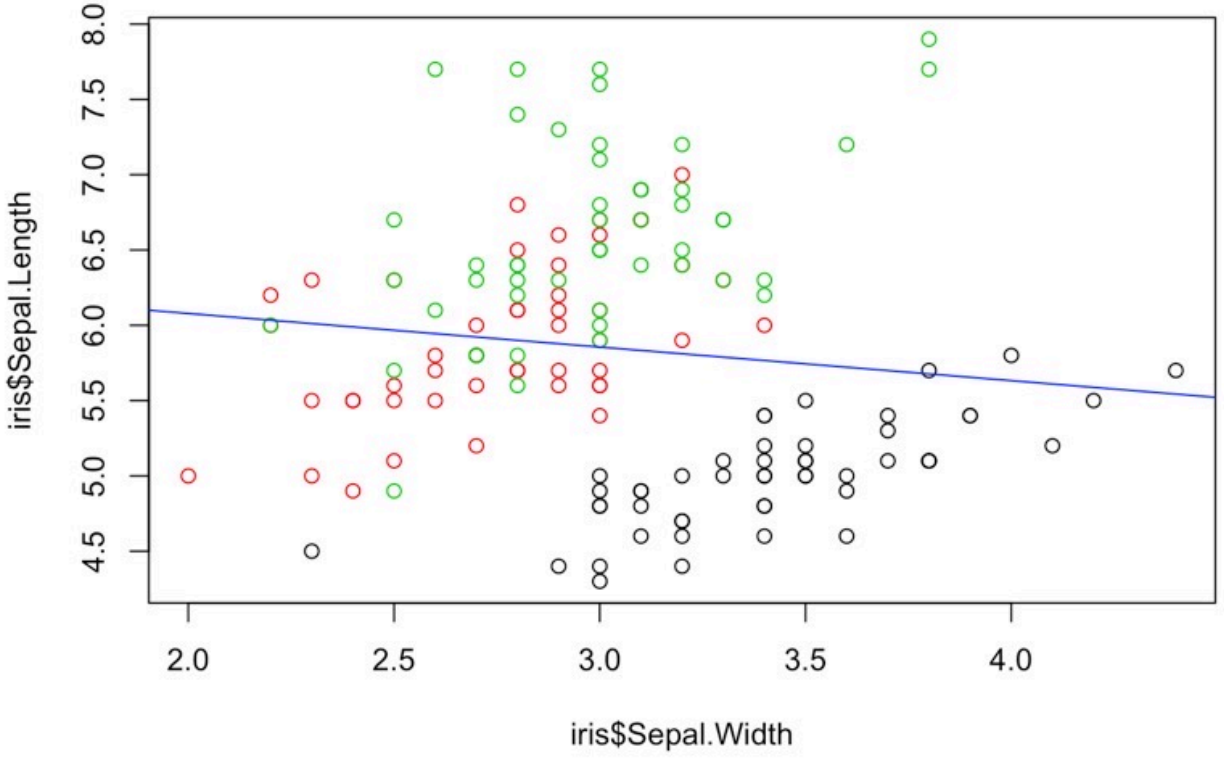
https://www.r-graph-gallery.com/

Plotly

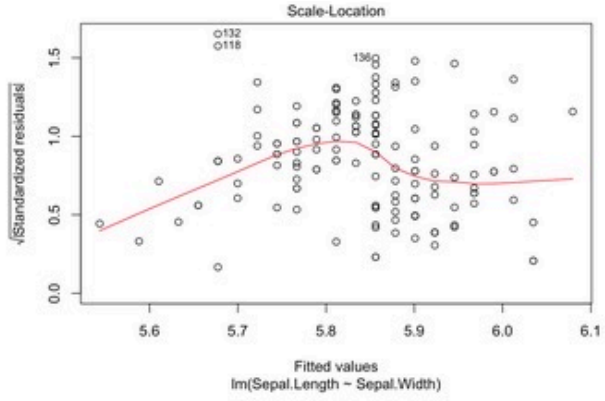

(−0.4845348, 0.3549026)
WebGL vs SVG in R
Scatter and Line Plots
(31.656k, 82.603)
Japan
Bubble Charts
Line Plots
Filled Area Plots
Bar Charts
Horizontal Bar Charts
ob E
ob D
ob C
ob B
ob A
Jan 2009
Mar 2009
Gantt Charts
25%
40%
18%
10%
7%
Pie Charts
Graphing Multiple Chart Types
Sunburst Charts
Tables
Tufts
Cornell
NYU
Brown
Berkeley
Michigan
Emory
SoCal
UCLA
(62, Michigan)
Dot Plots
Dumbbell
0
1
2
3
4
5
Gauge Charts
Sankey
You've collected the data,
agonized over the right mod
and now you've GOT to con
management.....

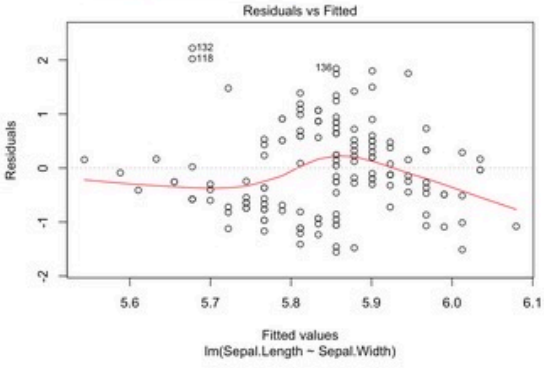
Statistics using R-Linear models

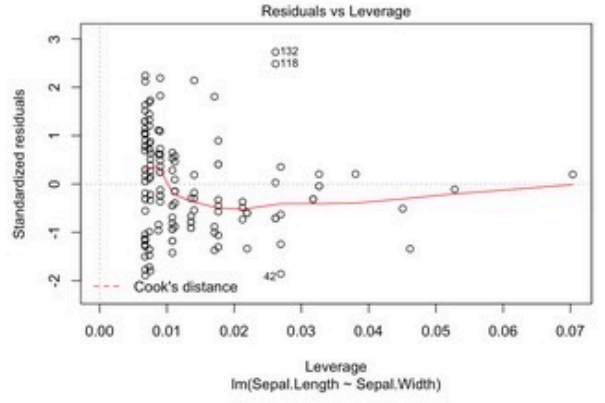
```
m1<-lm(Sepal.Length~Sepal.Width,data=iris)

plot(iris$Sepal.Length~iris$Sepal.Width, col=iris$Species)
abline(m1$coefficients, col="blue")
```

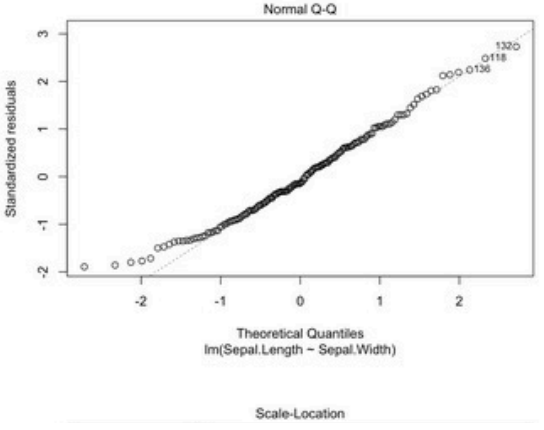



```
plot(m1)
```









Keep data

save specific objects to a file

```
save(iris,file="iris.RData")
```

load object

```
load("iris.RData")
```

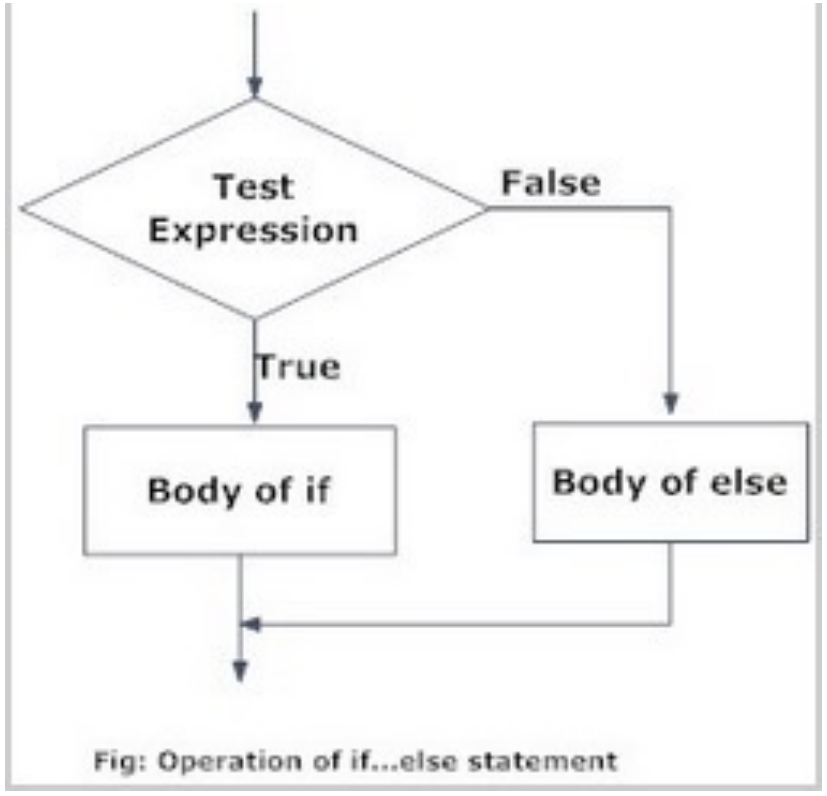
save workspace

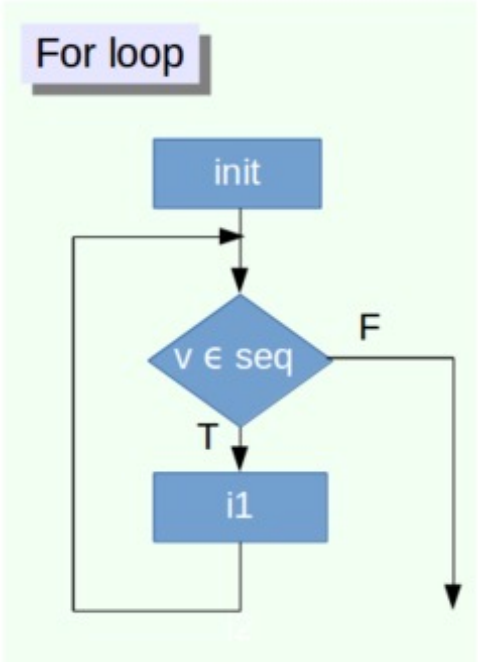
```
save.image(file='image.RData')
```

load workspace

```
load("image.RData")
```

Programming in R

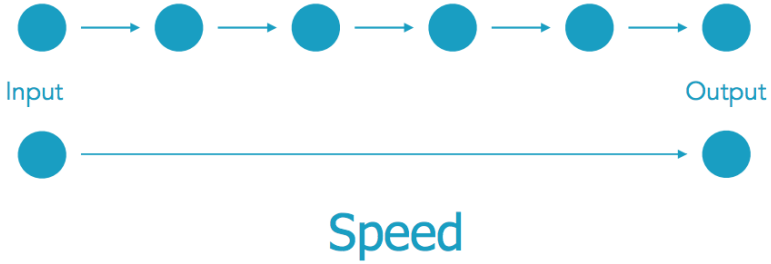




Hands-On Programming with R

https://rstudio-education.github.io/hopr/

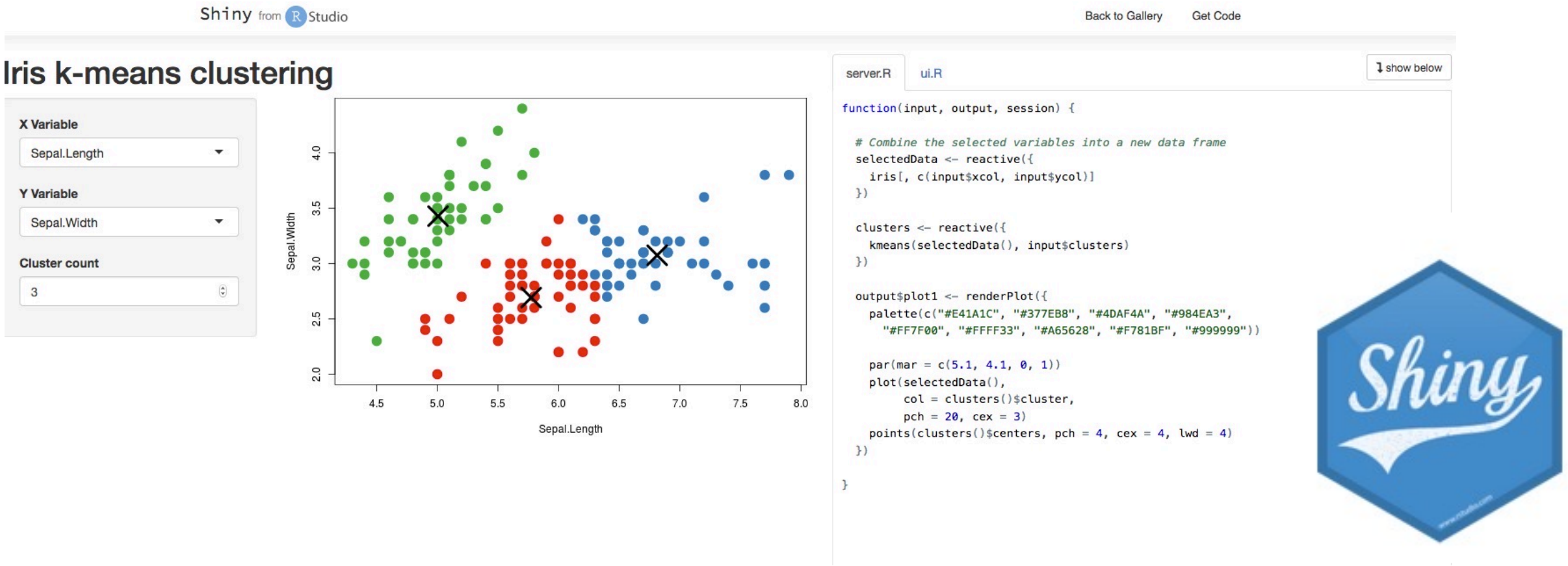
Customized functions



Myfunction <- function(variables) {
Function1
Function2
value/plot
}

```
ploting <- function(n_samples) {
  dat <- rnorm(n_samples, 100, 5)
  plot(dat)
}

ploting(10000)
```

Shiny Apps



https://shiny.rstudio.com/gallery/kmeans-example.html

Customized packages

Take home massage

- Fastly developing
- Many resources for biologists
- Also suitable for programming