Introduction to R

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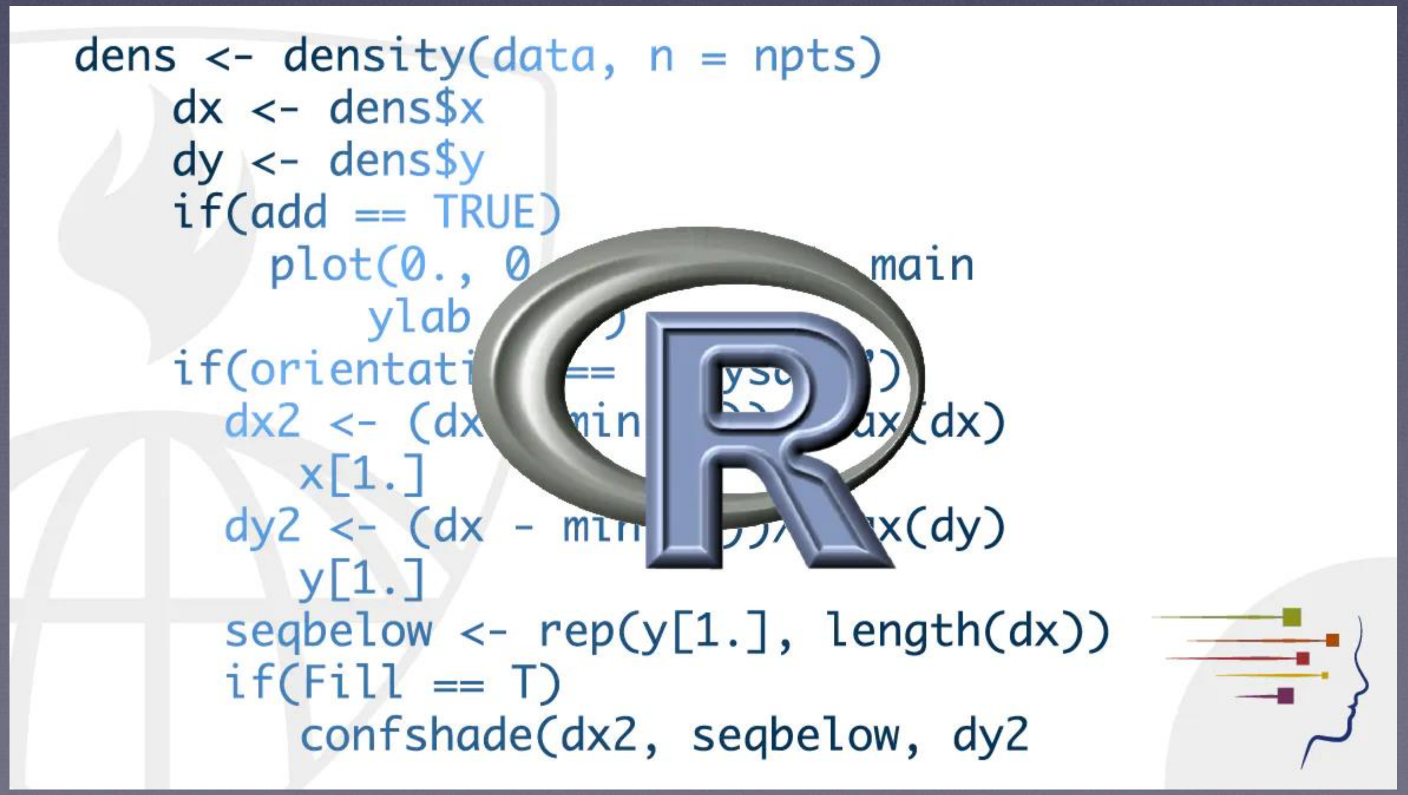
Borrowed from: Ramiro Logares (ICM-CSIC, Barcelona)

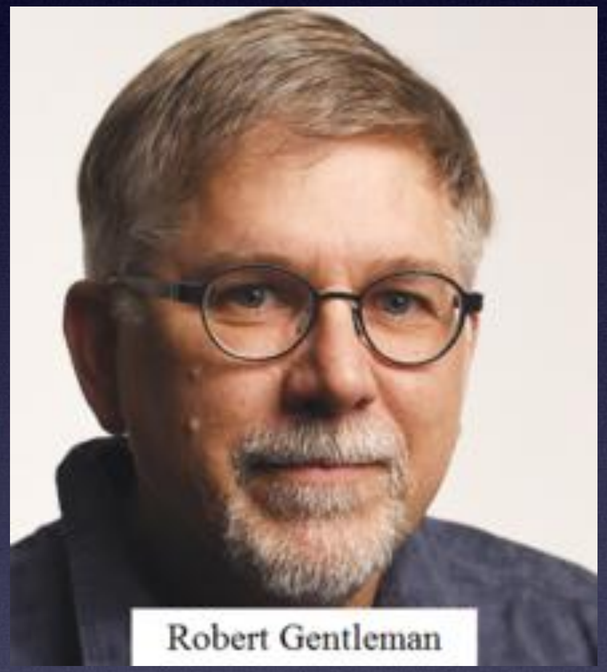


```
dens <- density(data, n = npts)
    dx <- dens$x
    dy <- dens$y
    if(add == TRUE)
        plot(0., 0            main
            ylab    )
    if(orientati   ==   ysc   ')
      dx2 <- (dx   min        ax(dx)
        x[1.]
      dy2 <- (dx - min     )/   x(dy)
        y[1.]
      seqbelow <- rep(y[1.], length(dx))
      if(Fill == T)
        confshade(dx2, seqbelow, dy2
```

History

- Originated from S
  - Statistical programming language developed by John Chambers at Bell Labs in the 70s
  - Developed at the same times as Unix
  - Closed source
- First version of R: developed by Robert Gentleman and Ross Ihaka in the mid-1990s
  - Aimed for better statistics software in their Mac teaching labs
  - Open Source alternative
- R 1.0.0 released in 2000
  - Current version 4.1.1
- Developers: international R-core developing team

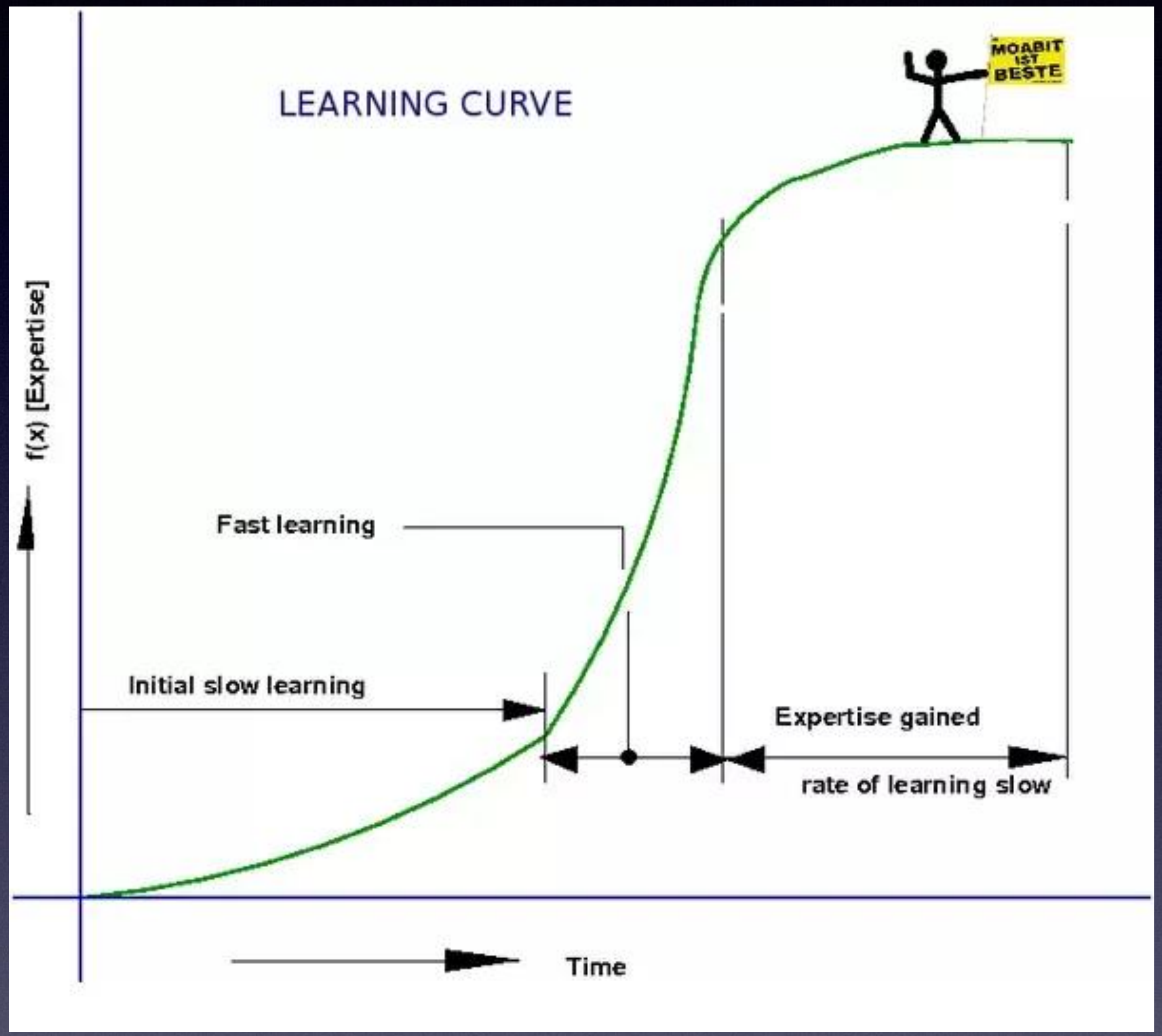
John Chambers



Ross Ihaka

Why learn R?

- Language and environment for statistical computing and graphics
- Open Source (free)
- Cross-platform compatibility
- Community supported
- Great flexibility to do what you want
- Many packages available: ecology, metabarcoding, networks
- Amazing publication quality graphs

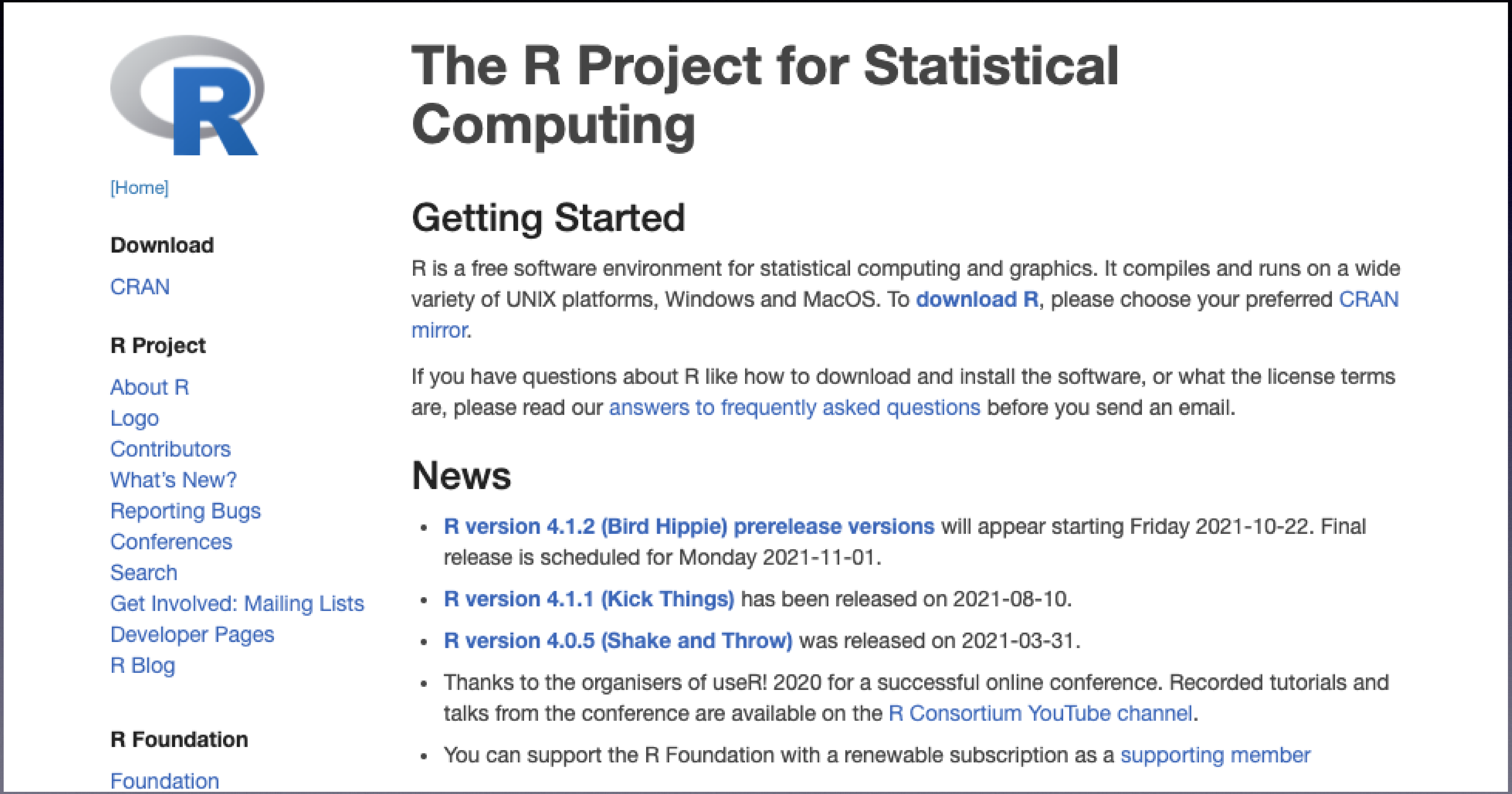


okay, I want R

- https://cran.uib.no: Linux, Mac, Windows…
- We will use an Integrated Development Environment (IDE): *R-Studio*
    - *https://www.rstudio.com/*
  - Set of tools designed to help and be more productive with R
  - Includes a console and syntax-highlighting editor that supports code execution
  - Allows having several open sessions
  - Includes a Unix terminal

Installing R

R version 4.1.1 (2021-08-10) -- "Kick Things"



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Foundation

The R Project for Statistical Computing

Getting Started

R is a free software environment for statistical computing and graphics. It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS. To **download R**, please choose your preferred CRAN mirror.

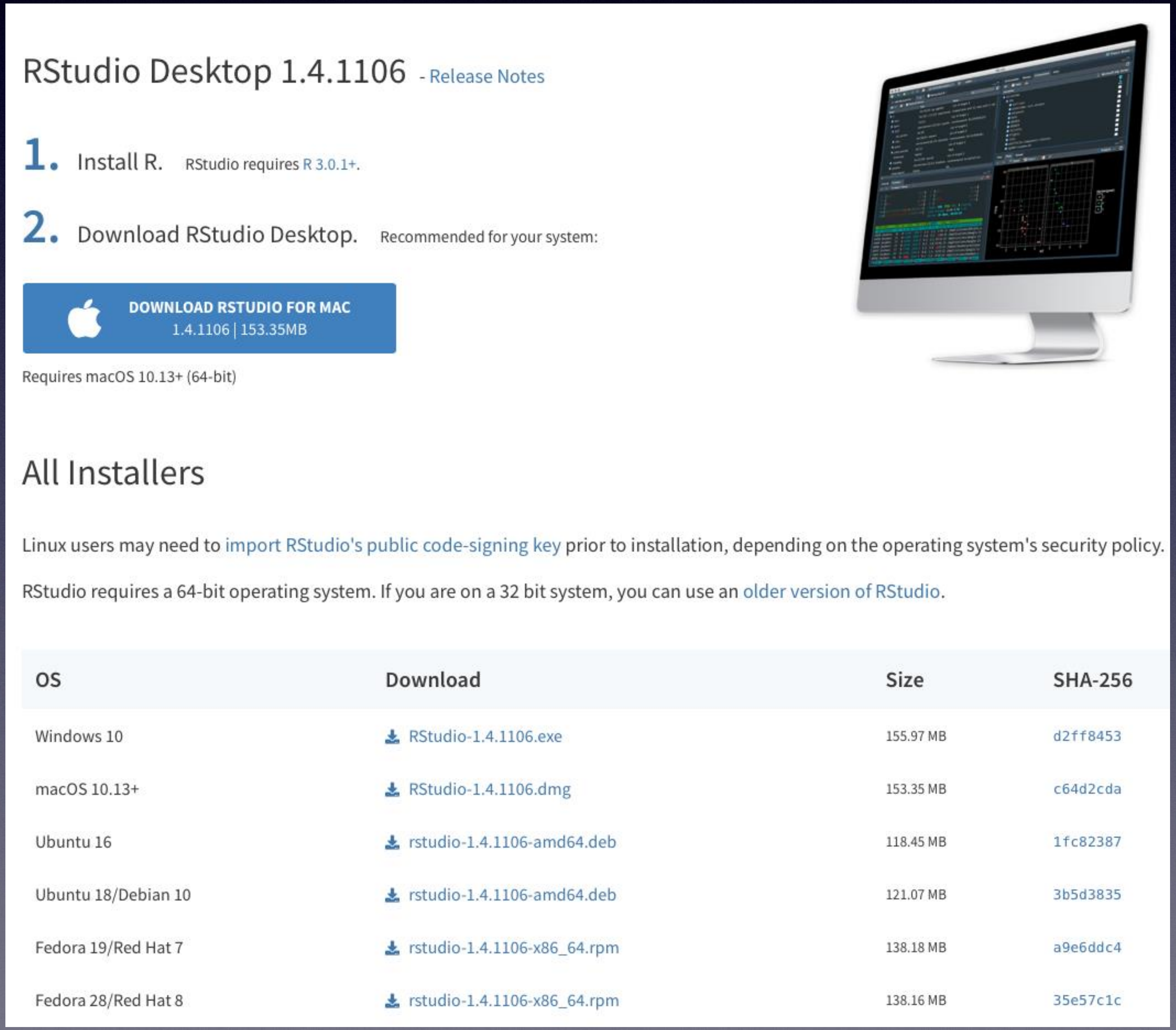
If you have questions about R like how to download and install the software, or what the license terms are, please read our answers to frequently asked questions before you send an email.

News

- **R version 4.1.2 (Bird Hippie) prerelease versions** will appear starting Friday 2021-10-22. Final release is scheduled for Monday 2021-11-01.
- **R version 4.1.1 (Kick Things)** has been released on 2021-08-10.
- **R version 4.0.5 (Shake and Throw)** was released on 2021-03-31.
- Thanks to the organisers of useR! 2020 for a successful online conference. Recorded tutorials and talks from the conference are available on the R Consortium YouTube channel.
- You can support the R Foundation with a renewable subscription as a supporting member

Installing R-Studio

https://www.rstudio.com



RStudio Desktop 1.4.1106 - Release Notes

1. Install R. RStudio requires R 3.0.1+.

2. Download RStudio Desktop. Recommended for your system:

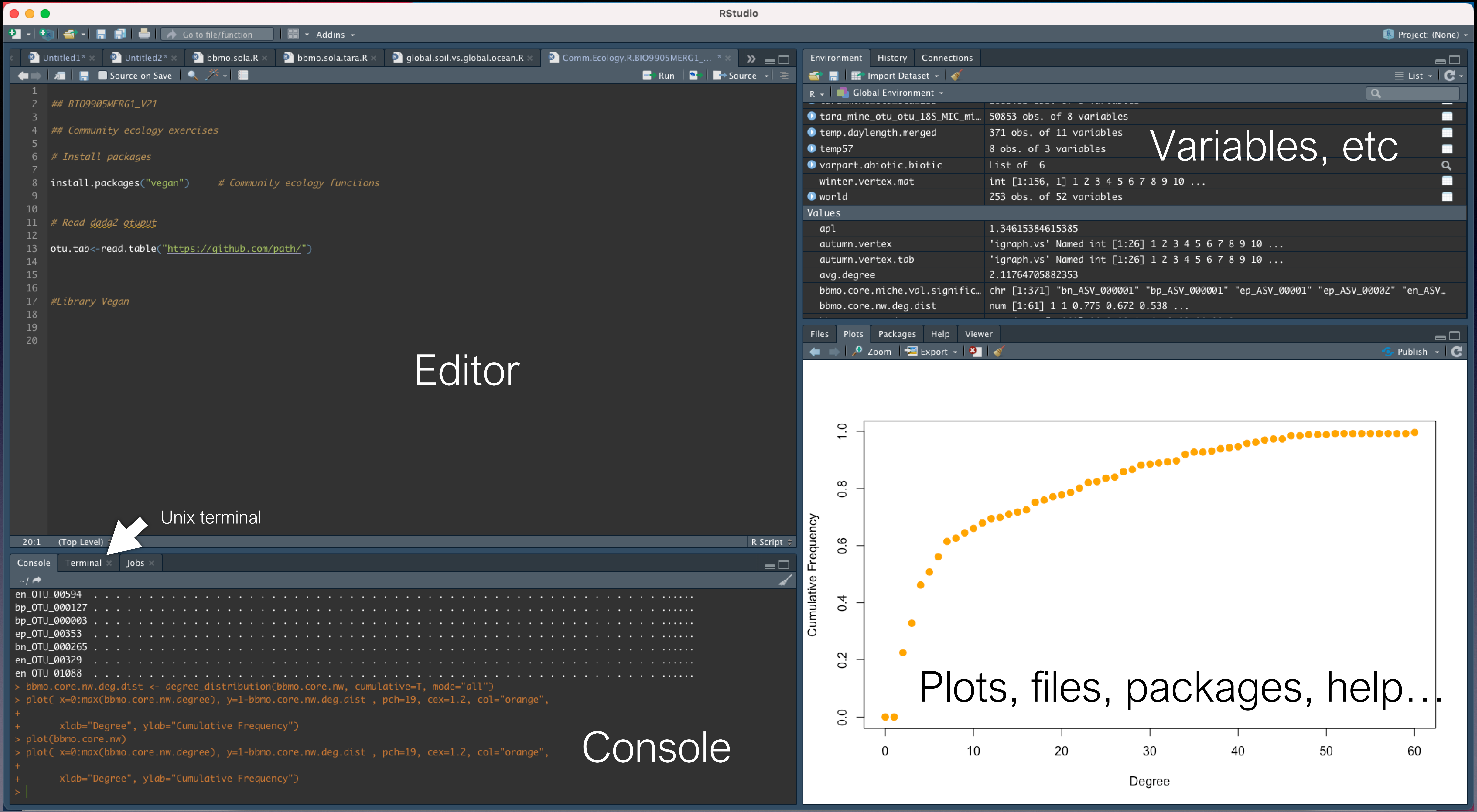
Requires macOS 10.13+ (64-bit)

All Installers

Linux users may need to import RStudio's public code-signing key prior to installation, depending on the operating system's security policy.

RStudio requires a 64-bit operating system. If you are on a 32 bit system, you can use an older version of RStudio.

OS	Download	Size	SHA-256
Windows 10	RStudio-1.4.1106.exe	155.97 MB	d2ff8453
macOS 10.13+	RStudio-1.4.1106.dmg	153.35 MB	c64d2cda
Ubuntu 16	rstudio-1.4.1106-amd64.deb	118.45 MB	1fc82387
Ubuntu 18/Debian 10	rstudio-1.4.1106-amd64.deb	121.07 MB	3b5d3835
Fedora 19/Red Hat 7	rstudio-1.4.1106-x86_64.rpm	138.18 MB	a9e6ddc4
Fedora 28/Red Hat 8	rstudio-1.4.1106-x86_64.rpm	138.16 MB	35e57c1c



```
## BIO9905MERG1_V21

## Community ecology exercises

# Install packages

install.packages("vegan")      # Community ecology functions


# Read dada2 otuput

otu.tab<-read.table("https://github.com/path/")



#Library Vegan
```

```
tara_mine_otu_otu_18S_MIC_mi…  50853 obs. of 8 variables
temp.daylength.merged          371 obs. of 11 variables
temp57                         8 obs. of 3 variables
varpart.abiotic.biotic         List of  6
winter.vertex.mat              int [1:156, 1] 1 2 3 4 5 6 7 8 9 10 ...
world                          253 obs. of 52 variables
Values
apl                            1.34615384615385
autumn.vertex                  'igraph.vs' Named int [1:26] 1 2 3 4 5 6 7 8 9 10 ...
autumn.vertex.tab              'igraph.vs' Named int [1:26] 1 2 3 4 5 6 7 8 9 10 ...
avg.degree                     2.11764705882353
bbmo.core.niche.val.signific…  chr [1:371] "bn_ASV_000001" "bp_ASV_000001" "ep_ASV_00001" "ep_ASV_00002" "en_ASV…
bbmo.core.nw.deg.dist          num [1:61] 1 1 0.775 0.672 0.538 ...
```

```
en_OTU_00594   . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . ......
bp_OTU_000127  . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . ......
bp_OTU_000003  . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . ......
ep_OTU_00353   . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . ......
bn_OTU_000265  . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . ......
en_OTU_00329   . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . ......
en_OTU_01088   . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . ......
> bbmo.core.nw.deg.dist <- degree_distribution(bbmo.core.nw, cumulative=T, mode="all")
> plot( x=0:max(bbmo.core.nw.degree), y=1-bbmo.core.nw.deg.dist , pch=19, cex=1.2, col="orange",
+
+       xlab="Degree", ylab="Cumulative Frequency")
> plot(bbmo.core.nw)
> plot( x=0:max(bbmo.core.nw.degree), y=1-bbmo.core.nw.deg.dist , pch=19, cex=1.2, col="orange",
+
+       xlab="Degree", ylab="Cumulative Frequency")
>
```

Variables, etc

Editor

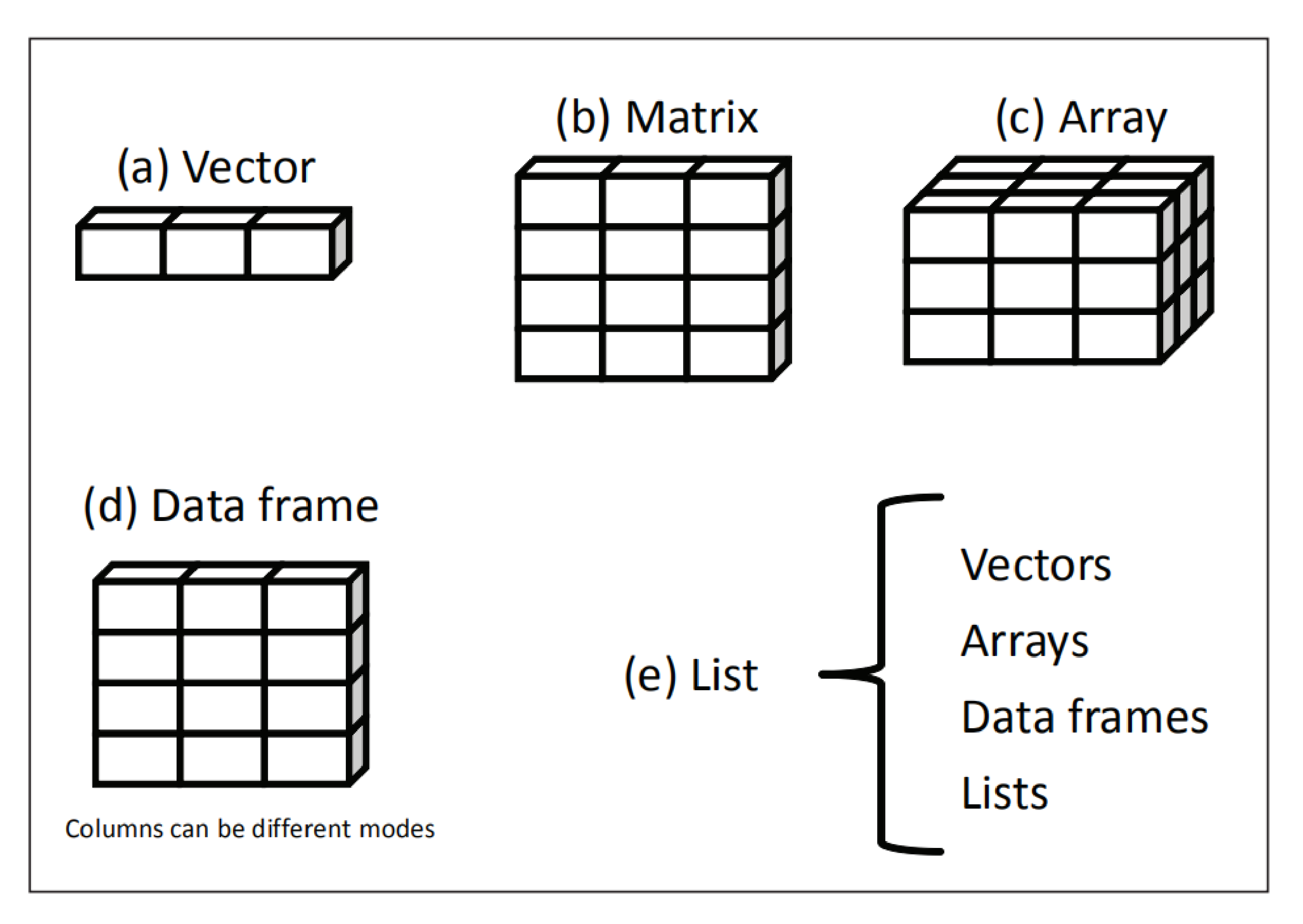
Unix terminal

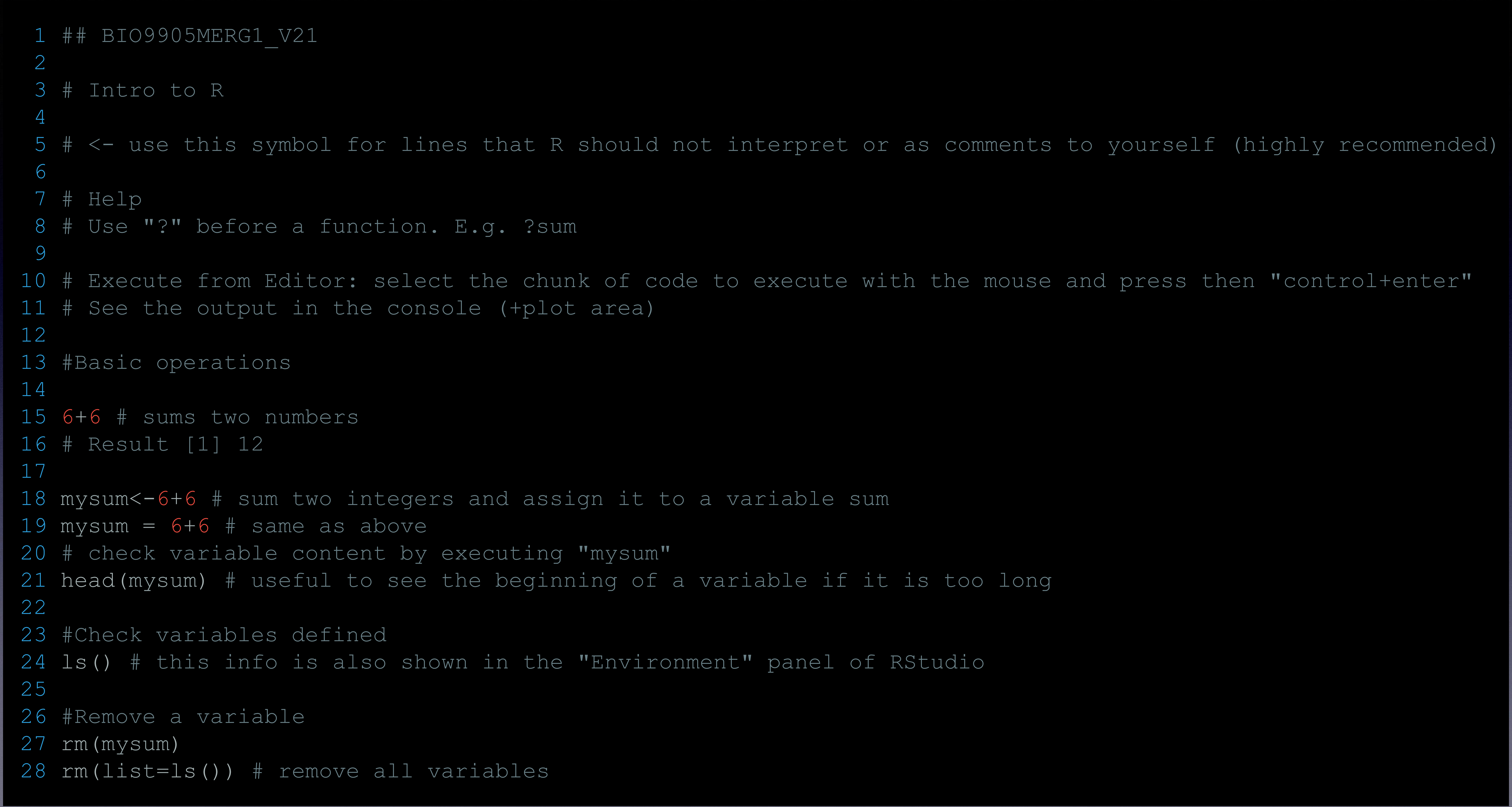
Plots, files, packages, help...

Console

Objects and data-types

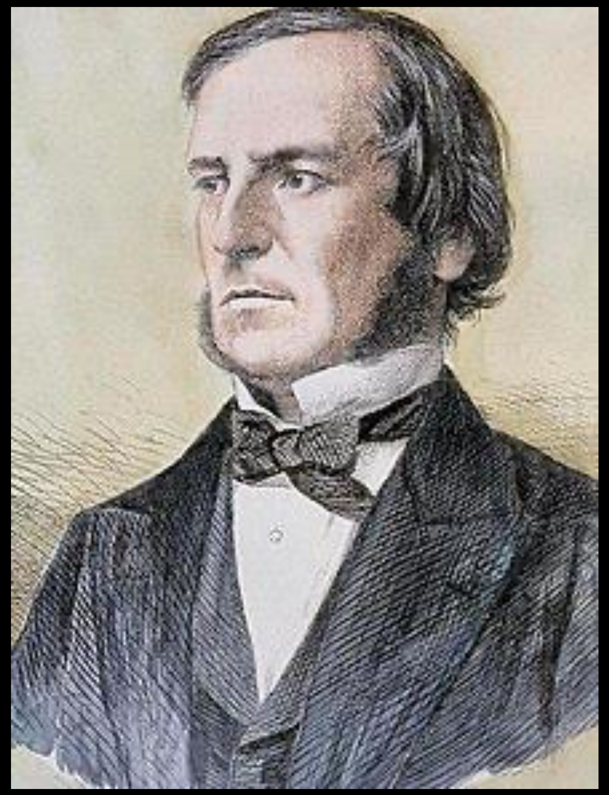
- Fundamental structures in R
- Objects: Vectors, Matrices, Arrays, Factors, Data frames, Lists,
- Data types: numeric, integer, character, logical





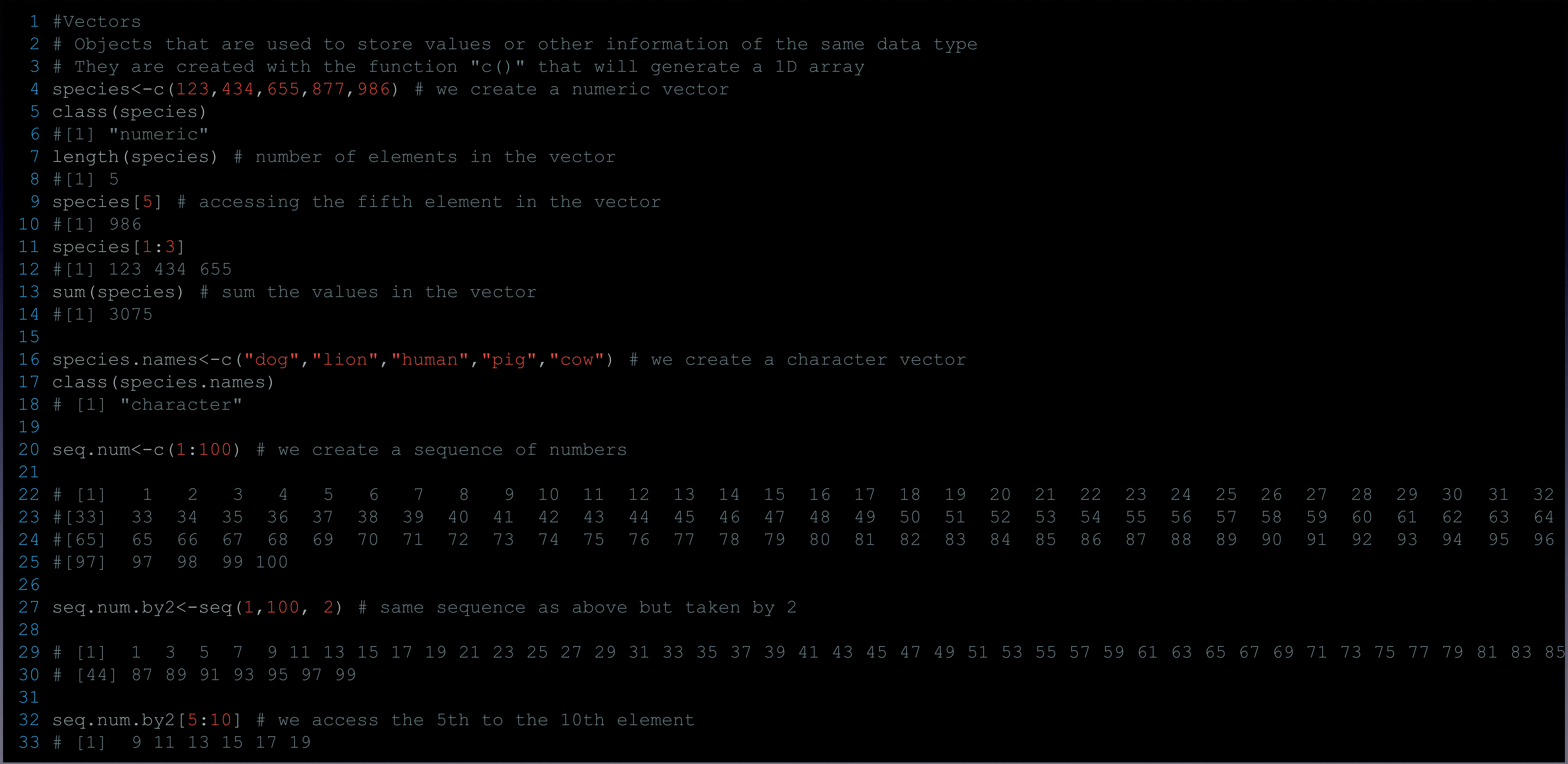
```r
## BIO9905MERG1_V21

# Intro to R

# <- use this symbol for lines that R should not interpret or as comments to yourself (highly recommended)

# Help
# Use "?" before a function. E.g. ?sum

# Execute from Editor: select the chunk of code to execute with the mouse and press then "control+enter"
# See the output in the console (+plot area)

#Basic operations

6+6 # sums two numbers
# Result [1] 12

mysum<-6+6 # sum two integers and assign it to a variable sum
mysum = 6+6 # same as above
# check variable content by executing "mysum"
head(mysum) # useful to see the beginning of a variable if it is too long

#Check variables defined
ls() # this info is also shown in the "Environment" panel of RStudio

#Remove a variable
rm(mysum)
rm(list=ls()) # remove all variables
```

```r
#Objects or data structures : Vectors, Lists, Matrices, Arrays, Factors, Data frames
#Let’s have a look to basic datatypes on which R objects are built

#Numeric: numbers with decimals
mynumber<-66.6
print(mynumber)
# [1] 66.6
class(mynumber) # use it to know what is the data type
# [1] "numeric"

#Integer: numbers with no decimals
mynumber.int<-as.integer(mynumber)
# [1] 66
class(mynumber.int)
# [1] "integer"

#Character: can be a letter or a combination of letters enclosed by quotes
mychar<-"bioinfo course"
print(mychar)
# [1] "bioinfo course"
class(mychar)
#[1] "character"

#Logical: a variable that can be TRUE or FALSE (boolean)
im.true<-TRUE
print(im.true)
#[1] TRUE
class(im.true)
# [1] "logical"
```



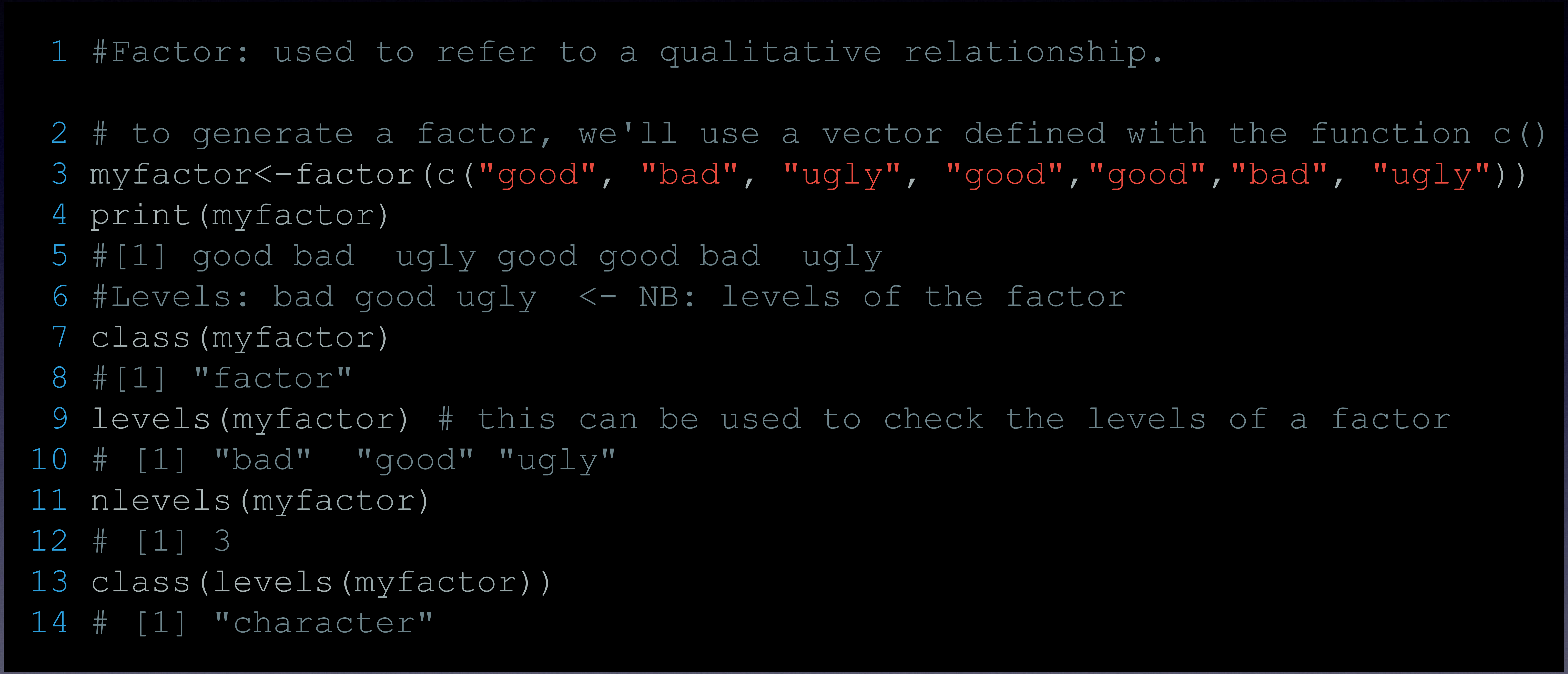
George Boole

Vectors



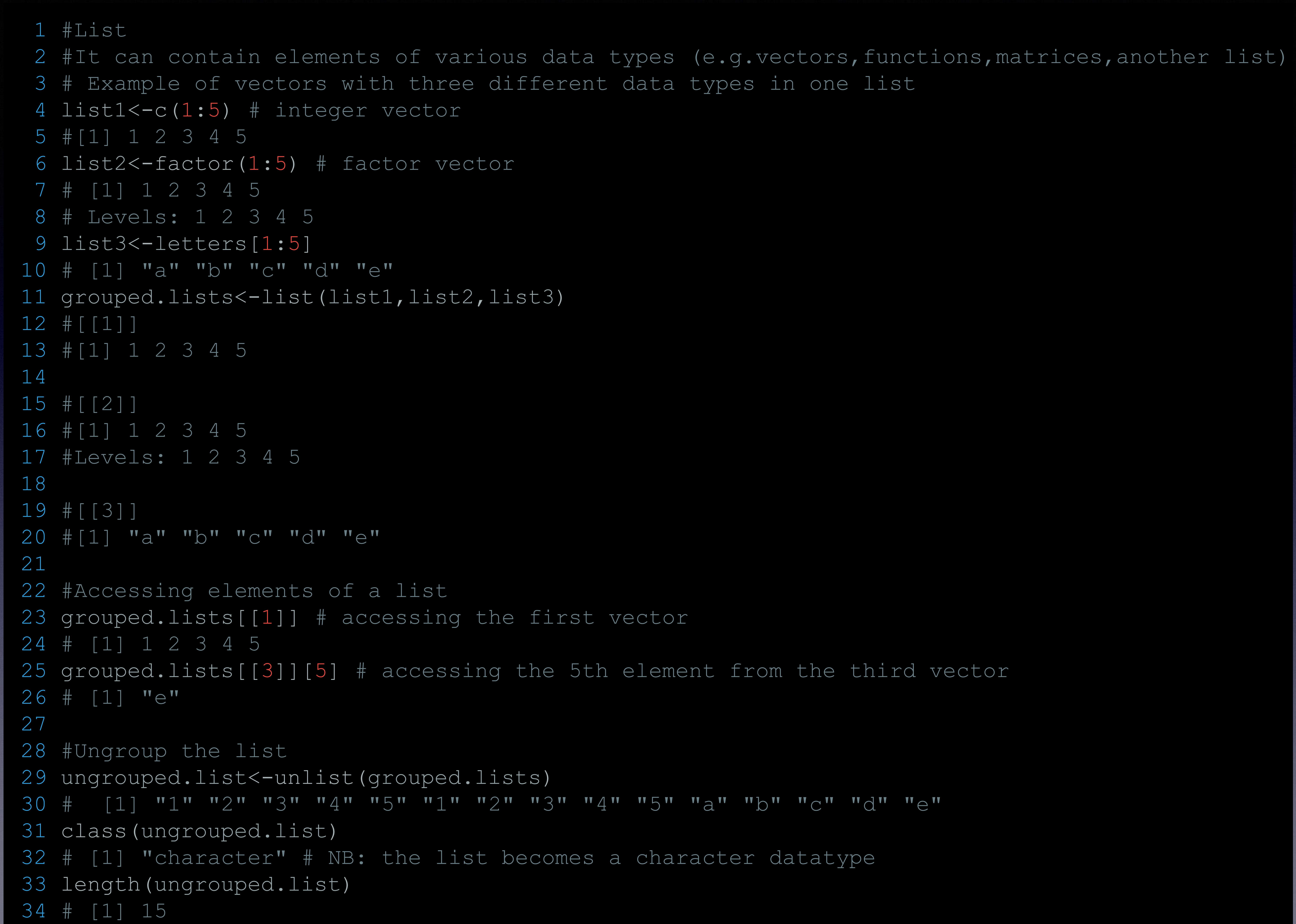
```
#Vectors
# Objects that are used to store values or other information of the same data type
# They are created with the function "c()" that will generate a 1D array
species<-c(123,434,655,877,986) # we create a numeric vector
class(species)
#[1] "numeric"
length(species) # number of elements in the vector
#[1] 5
species[5] # accessing the fifth element in the vector
#[1] 986
species[1:3]
#[1] 123 434 655
sum(species) # sum the values in the vector
#[1] 3075

species.names<-c("dog","lion","human","pig","cow") # we create a character vector
class(species.names)
# [1] "character"

seq.num<-c(1:100) # we create a sequence of numbers

# [1]   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20  21  22  23  24  25  26  27  28  29  30  31  32
#[33]  33  34  35  36  37  38  39  40  41  42  43  44  45  46  47  48  49  50  51  52  53  54  55  56  57  58  59  60  61  62  63  64
#[65]  65  66  67  68  69  70  71  72  73  74  75  76  77  78  79  80  81  82  83  84  85  86  87  88  89  90  91  92  93  94  95  96
#[97]  97  98  99 100

seq.num.by2<-seq(1,100, 2) # same sequence as above but taken by 2

# [1]  1  3  5  7  9 11 13 15 17 19 21 23 25 27 29 31 33 35 37 39 41 43 45 47 49 51 53 55 57 59 61 63 65 67 69 71 73 75 77 79 81 83 85
# [44] 87 89 91 93 95 97 99

seq.num.by2[5:10] # we access the 5th to the 10th element
# [1]  9 11 13 15 17 19
```

Factors



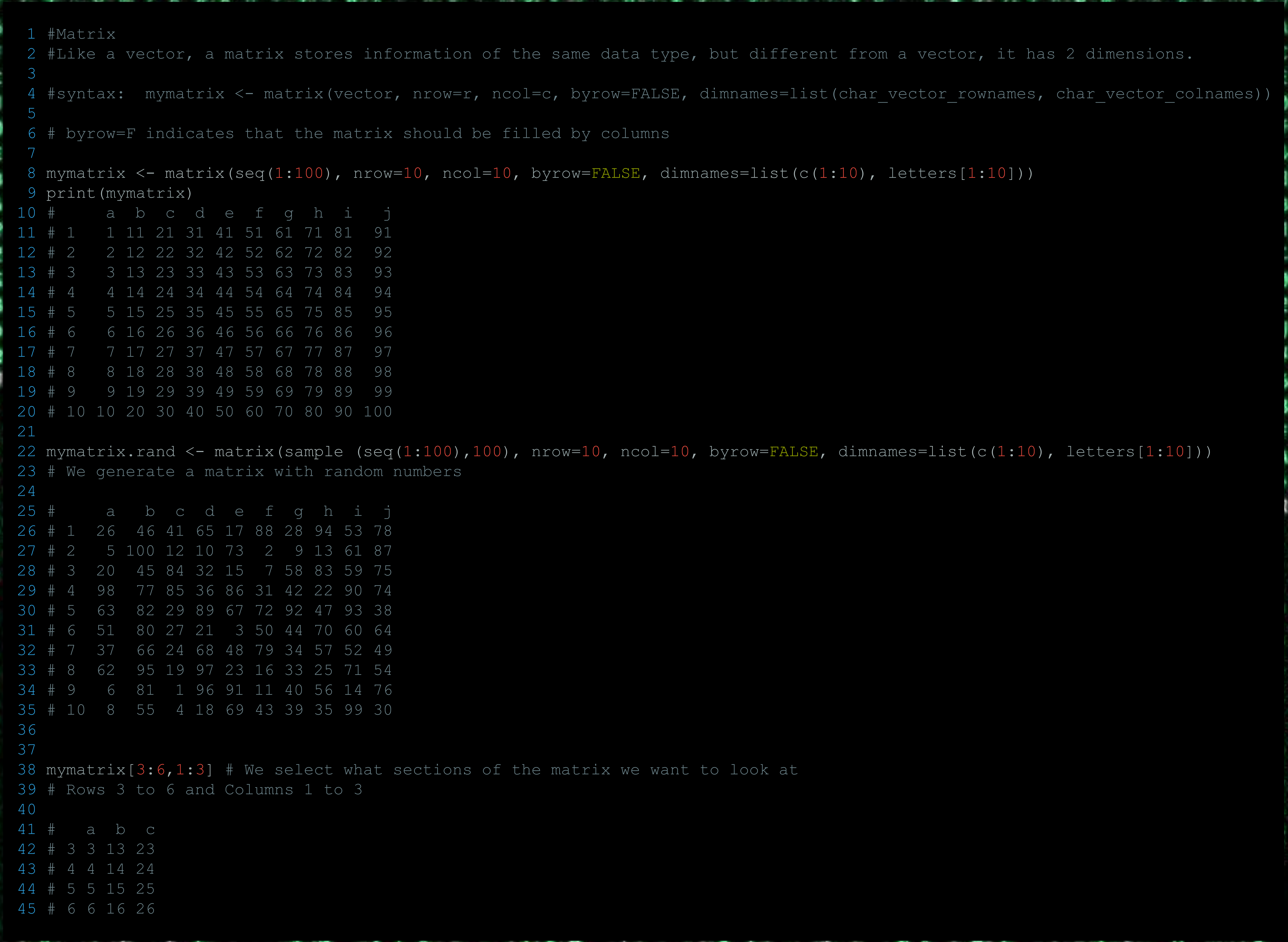
```
#Factor: used to refer to a qualitative relationship.

# to generate a factor, we'll use a vector defined with the function c()
myfactor<-factor(c("good", "bad", "ugly", "good","good","bad", "ugly"))
print(myfactor)
#[1] good bad  ugly good good bad  ugly
#Levels: bad good ugly  <- NB: levels of the factor
class(myfactor)
#[1] "factor"
levels(myfactor) # this can be used to check the levels of a factor
# [1] "bad"  "good" "ugly"
nlevels(myfactor)
# [1] 3
class(levels(myfactor))
# [1] "character"
```

List



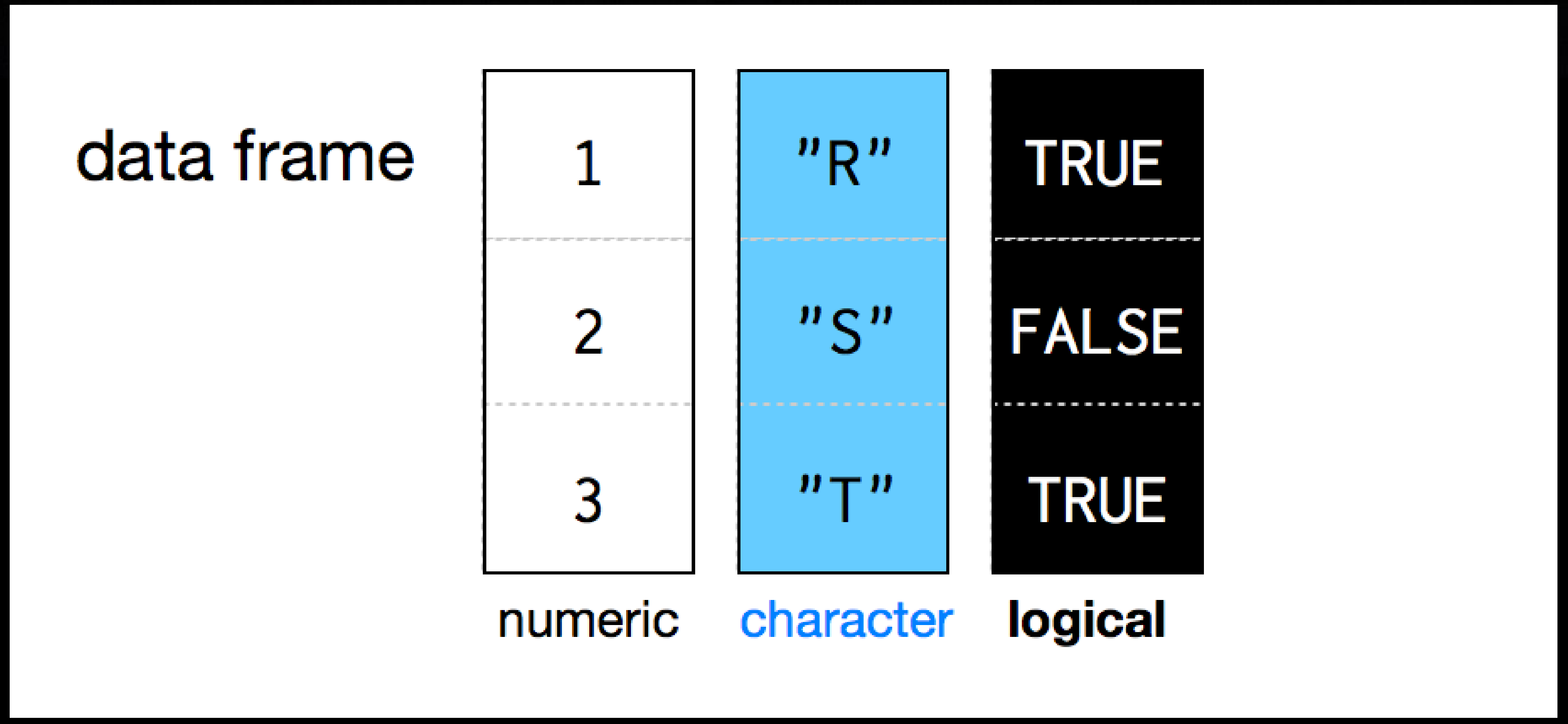
```
#List
#It can contain elements of various data types (e.g.vectors,functions,matrices,another list)
# Example of vectors with three different data types in one list
list1<-c(1:5) # integer vector
#[1] 1 2 3 4 5
list2<-factor(1:5) # factor vector
# [1] 1 2 3 4 5
# Levels: 1 2 3 4 5
list3<-letters[1:5]
# [1] "a" "b" "c" "d" "e"
grouped.lists<-list(list1,list2,list3)
#[[1]]
#[1] 1 2 3 4 5

#[[2]]
#[1] 1 2 3 4 5
#Levels: 1 2 3 4 5

#[[3]]
#[1] "a" "b" "c" "d" "e"

#Accessing elements of a list
grouped.lists[[1]] # accessing the first vector
# [1] 1 2 3 4 5
grouped.lists[[3]][5] # accessing the 5th element from the third vector
# [1] "e"

#Ungroup the list
ungrouped.list<-unlist(grouped.lists)
#  [1] "1" "2" "3" "4" "5" "1" "2" "3" "4" "5" "a" "b" "c" "d" "e"
class(ungrouped.list)
# [1] "character" # NB: the list becomes a character datatype
length(ungrouped.list)
# [1] 15
```

Matrix



```
#Matrix
#Like a vector, a matrix stores information of the same data type, but different from a vector, it has 2 dimensions.

#syntax:  mymatrix <- matrix(vector, nrow=r, ncol=c, byrow=FALSE, dimnames=list(char_vector_rownames, char_vector_colnames))

# byrow=F indicates that the matrix should be filled by columns

mymatrix <- matrix(seq(1:100), nrow=10, ncol=10, byrow=FALSE, dimnames=list(c(1:10), letters[1:10]))
print(mymatrix)
#     a  b  c  d  e  f  g  h  i   j
# 1   1 11 21 31 41 51 61 71 81  91
# 2   2 12 22 32 42 52 62 72 82  92
# 3   3 13 23 33 43 53 63 73 83  93
# 4   4 14 24 34 44 54 64 74 84  94
# 5   5 15 25 35 45 55 65 75 85  95
# 6   6 16 26 36 46 56 66 76 86  96
# 7   7 17 27 37 47 57 67 77 87  97
# 8   8 18 28 38 48 58 68 78 88  98
# 9   9 19 29 39 49 59 69 79 89  99
# 10 10 20 30 40 50 60 70 80 90 100

mymatrix.rand <- matrix(sample (seq(1:100),100), nrow=10, ncol=10, byrow=FALSE, dimnames=list(c(1:10), letters[1:10]))
# We generate a matrix with random numbers

#     a   b  c  d  e  f  g  h  i  j
# 1  26  46 41 65 17 88 28 94 53 78
# 2   5 100 12 10 73  2  9 13 61 87
# 3  20  45 84 32 15  7 58 83 59 75
# 4  98  77 85 36 86 31 42 22 90 74
# 5  63  82 29 89 67 72 92 47 93 38
# 6  51  80 27 21  3 50 44 70 60 64
# 7  37  66 24 68 48 79 34 57 52 49
# 8  62  95 19 97 23 16 33 25 71 54
# 9   6  81  1 96 91 11 40 56 14 76
# 10  8  55  4 18 69 43 39 35 99 30


mymatrix[3:6,1:3] # We select what sections of the matrix we want to look at
# Rows 3 to 6 and Columns 1 to 3

#   a  b  c
# 3 3 13 23
# 4 4 14 24
# 5 5 15 25
# 6 6 16 26
```

Dataframes

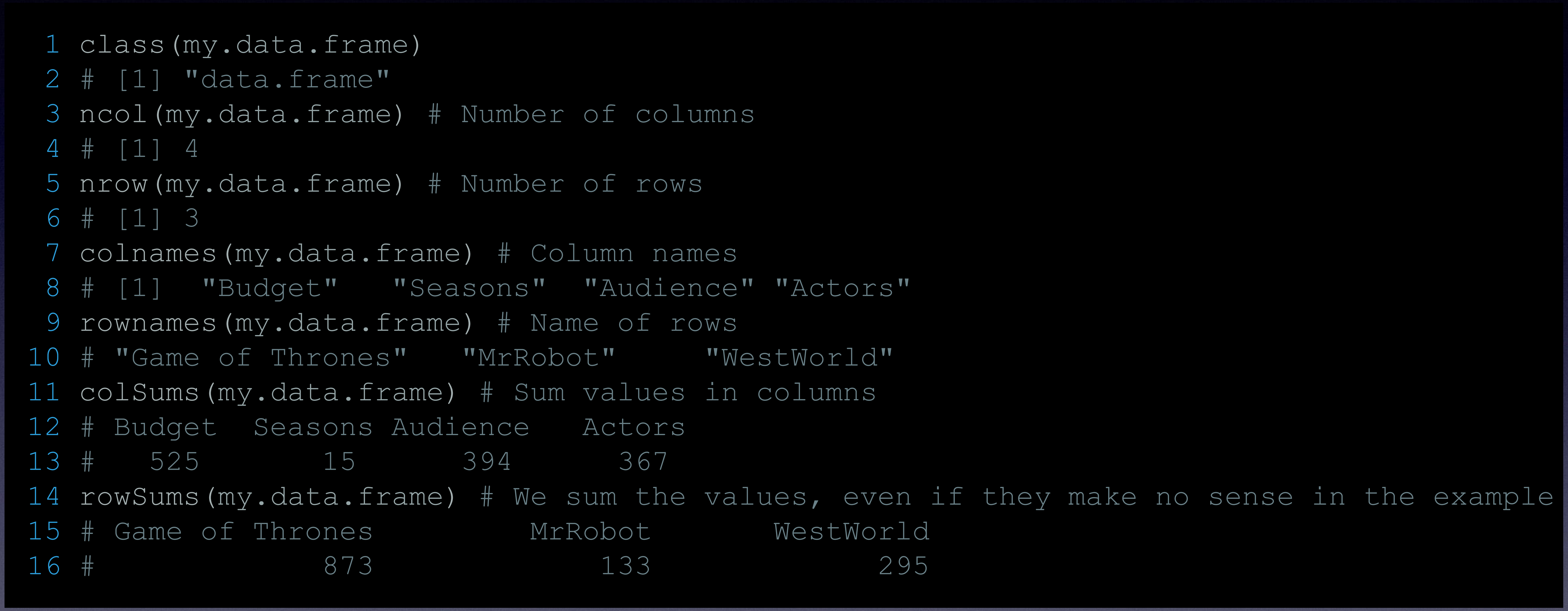


data frame

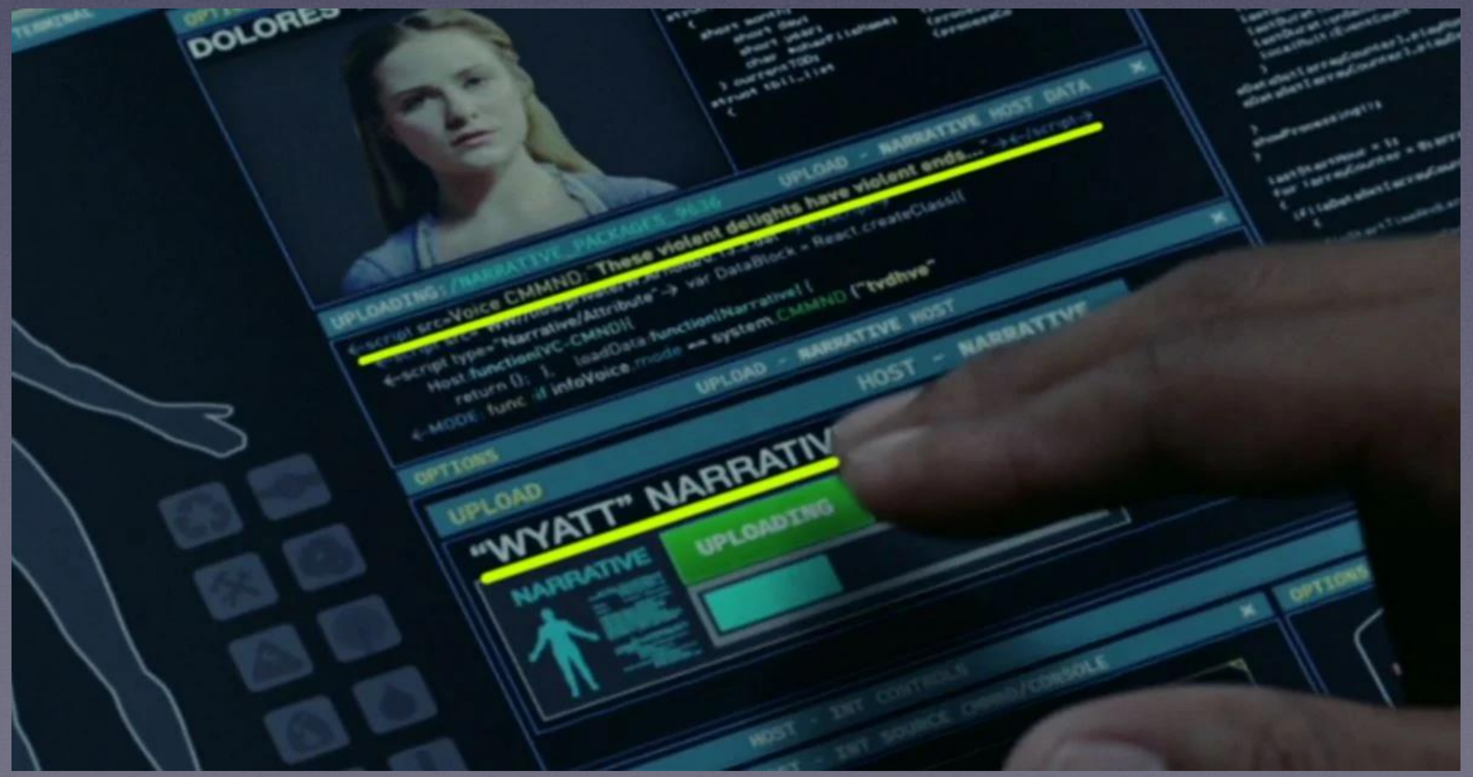
numeric	character	logical
1	"R"	TRUE
2	"S"	FALSE
3	"T"	TRUE

```r
#Dataframes
# More general than a matrix and can contain different data types
# Variables or features are in columns, while observations are in rows
# =>NB: this is one of the most common objects in metabarcoding analyses<=
# Generated with the data.frame() function

my.data.frame<-data.frame(
 Name=c("Game of Thrones","MrRobot","WestWorld"),
 Budget=c(344,59,122),
 Seasons=c(8,4,3),
 Audience=c(300,14,80),
 Actors=c(221,56, 90)
)
print(my.data.frame)
#              Name Budget Seasons Audience Actors
#1  Game of Thrones    344       8      300    221
#2          MrRobot     59       4       14     56
#3        WestWorld    122       3       80     90

row.names(my.data.frame)<-my.data.frame[,1] # Assign to the row names the names in the first column
my.data.frame<-my.data.frame[,-1] # Remove the fisrt column
print(my.data.frame) # By clicking this object in the "Environment" panel on the right, you'll see a window with the dataframe

#                  Budget Seasons Audience Actors
# Game of Thrones     344       8      300    221
# MrRobot              59       4       14     56
# WestWorld           122       3       80     90
```

Dataframes

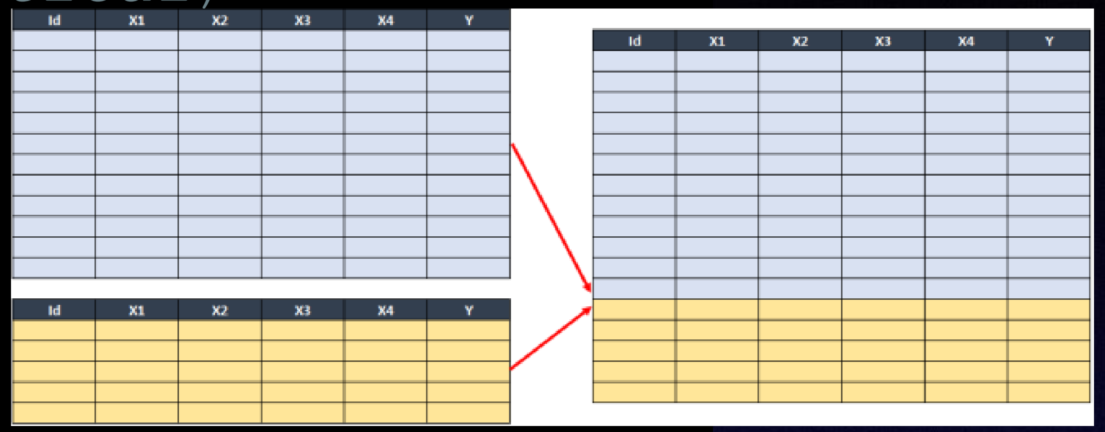


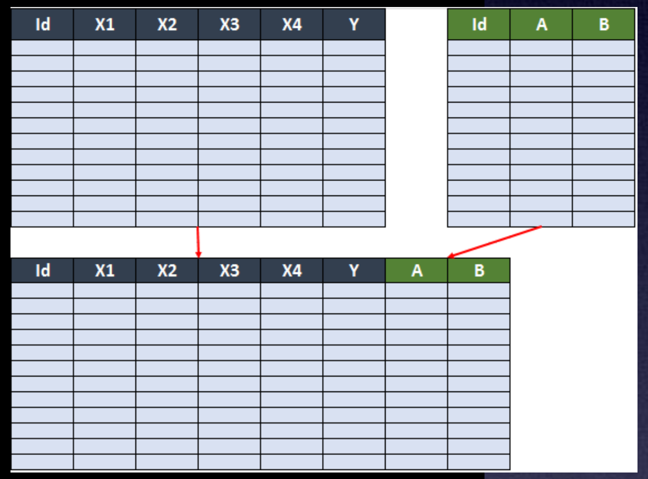
```
class(my.data.frame)
# [1] "data.frame"
ncol(my.data.frame) # Number of columns
# [1] 4
nrow(my.data.frame) # Number of rows
# [1] 3
colnames(my.data.frame) # Column names
# [1] "Budget"   "Seasons"  "Audience" "Actors"
rownames(my.data.frame) # Name of rows
# "Game of Thrones"   "MrRobot"     "WestWorld"
colSums(my.data.frame) # Sum values in columns
# Budget  Seasons Audience   Actors
#   525       15      394      367
rowSums(my.data.frame) # We sum the values, even if they make no sense in the example
# Game of Thrones        MrRobot       WestWorld
#             873            133             295
```



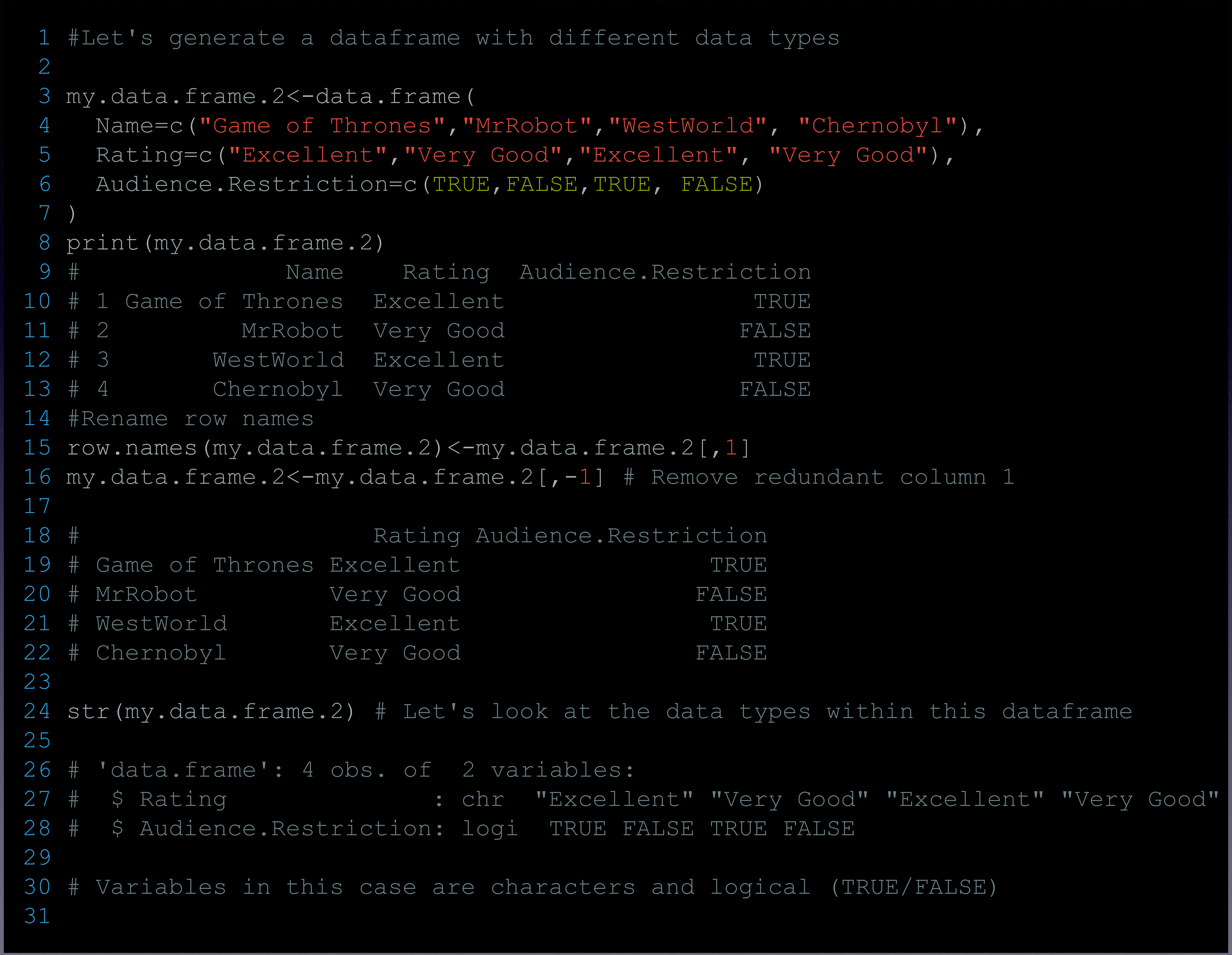
Dataframes

```
rbind(my.data.frame,my.data.frame) #  appends dataframes one below the other (column names identical)
#                  Budget Seasons Audience Actors
# Game of Thrones     344       8      300    221
# MrRobot              59       4       14     56
# WestWorld           122       3       80     90
# Game of Thrones1    344       8      300    221
# MrRobot1             59       4       14     56
# WestWorld1          122       3       80     90

cbind(my.data.frame,my.data.frame) # appends dataframes one next to the other (row names identical)
#                  Budget Seasons Audience Actors Budget Seasons Audience Actors
# Game of Thrones    344       8      300    221    344       8      300    221
# MrRobot             59       4       14     56     59       4       14     56
# WestWorld          122       3       80     90    122       3       80     90

head(my.data.frame, 2) # Useful to have a look to the beginning of the dataframe (specially useful in big tables)
# Here asking to print only 2 rows
#                 Budget Seasons Audience Actors
# Game of Thrones    344       8      300    221
# MrRobot             59       4       14     56

my.data.frame[1:2,2:4] # Useful to look at specific sections of the dataframe
#                 Seasons Audience Actors
# Game of Thrones       8      300    221
# MrRobot               4       14     56
```



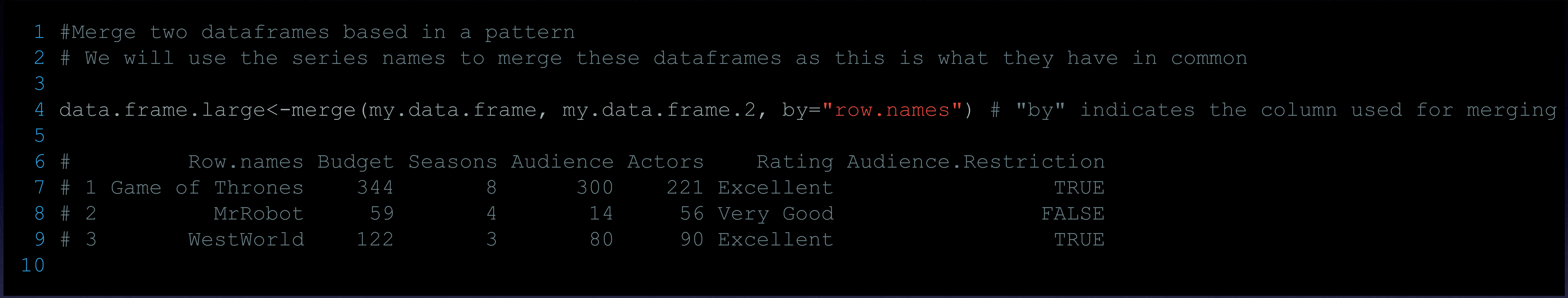


Dataframes



```
#Let's generate a dataframe with different data types

my.data.frame.2<-data.frame(
  Name=c("Game of Thrones","MrRobot","WestWorld", "Chernobyl"),
  Rating=c("Excellent","Very Good","Excellent", "Very Good"),
  Audience.Restriction=c(TRUE,FALSE,TRUE, FALSE)
)
print(my.data.frame.2)
#               Name    Rating  Audience.Restriction
# 1 Game of Thrones Excellent                   TRUE
# 2         MrRobot Very Good                  FALSE
# 3       WestWorld Excellent                   TRUE
# 4       Chernobyl Very Good                  FALSE
#Rename row names
row.names(my.data.frame.2)<-my.data.frame.2[,1]
my.data.frame.2<-my.data.frame.2[,-1] # Remove redundant column 1

#                    Rating Audience.Restriction
# Game of Thrones Excellent                 TRUE
# MrRobot         Very Good                FALSE
# WestWorld       Excellent                 TRUE
# Chernobyl       Very Good                FALSE

str(my.data.frame.2) # Let's look at the data types within this dataframe

# 'data.frame': 4 obs. of  2 variables:
#  $ Rating              : chr  "Excellent" "Very Good" "Excellent" "Very Good"
#  $ Audience.Restriction: logi  TRUE FALSE TRUE FALSE

# Variables in this case are characters and logical (TRUE/FALSE)

```

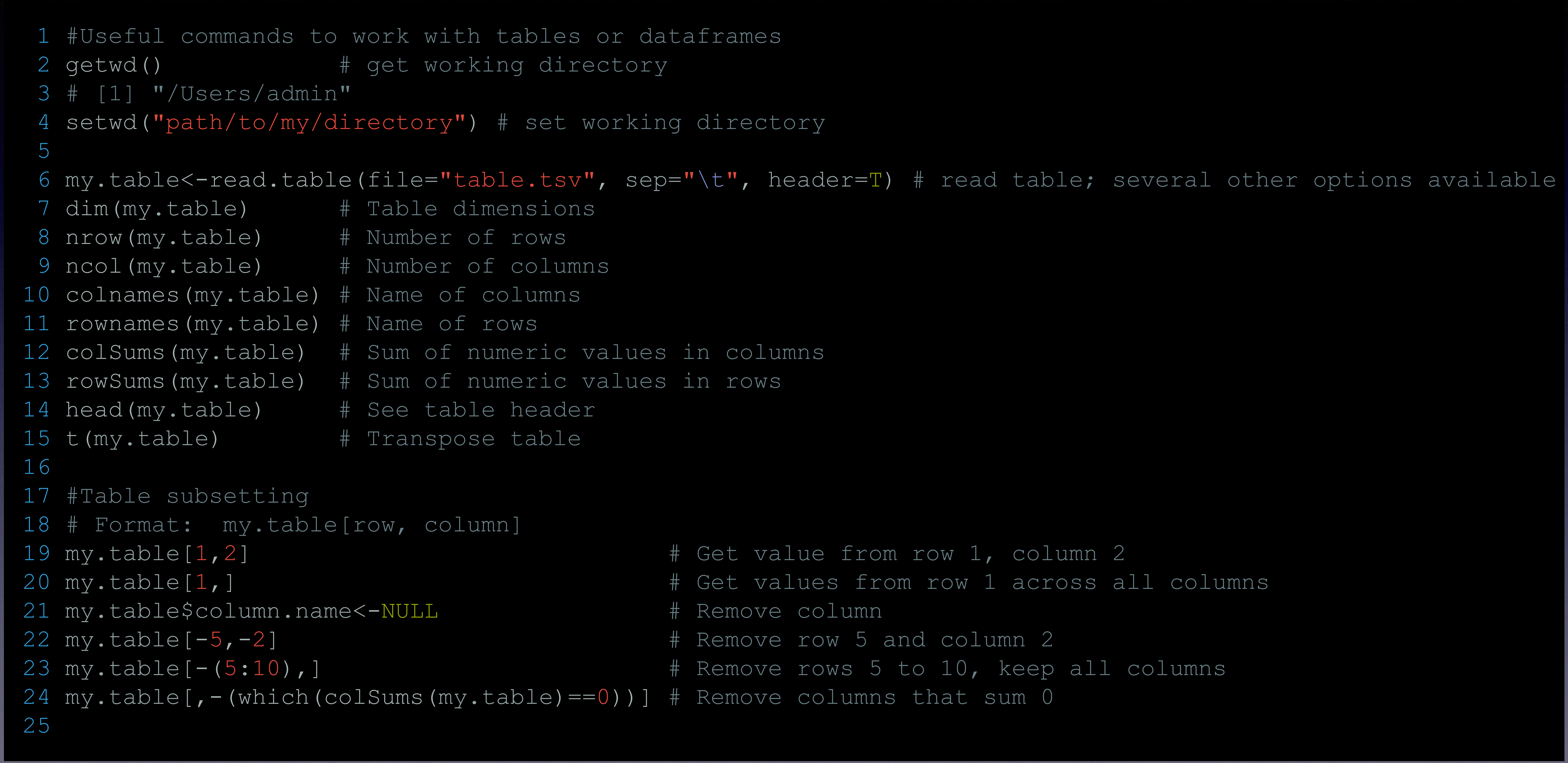
Dataframes



```
#Merge two dataframes based in a pattern
# We will use the series names to merge these dataframes as this is what they have in common

data.frame.large<-merge(my.data.frame, my.data.frame.2, by="row.names") # "by" indicates the column used for merging

#         Row.names Budget Seasons Audience Actors    Rating Audience.Restriction
# 1 Game of Thrones    344       8      300    221 Excellent                 TRUE
# 2         MrRobot     59       4       14     56 Very Good                FALSE
# 3       WestWorld    122       3       80     90 Excellent                 TRUE

```

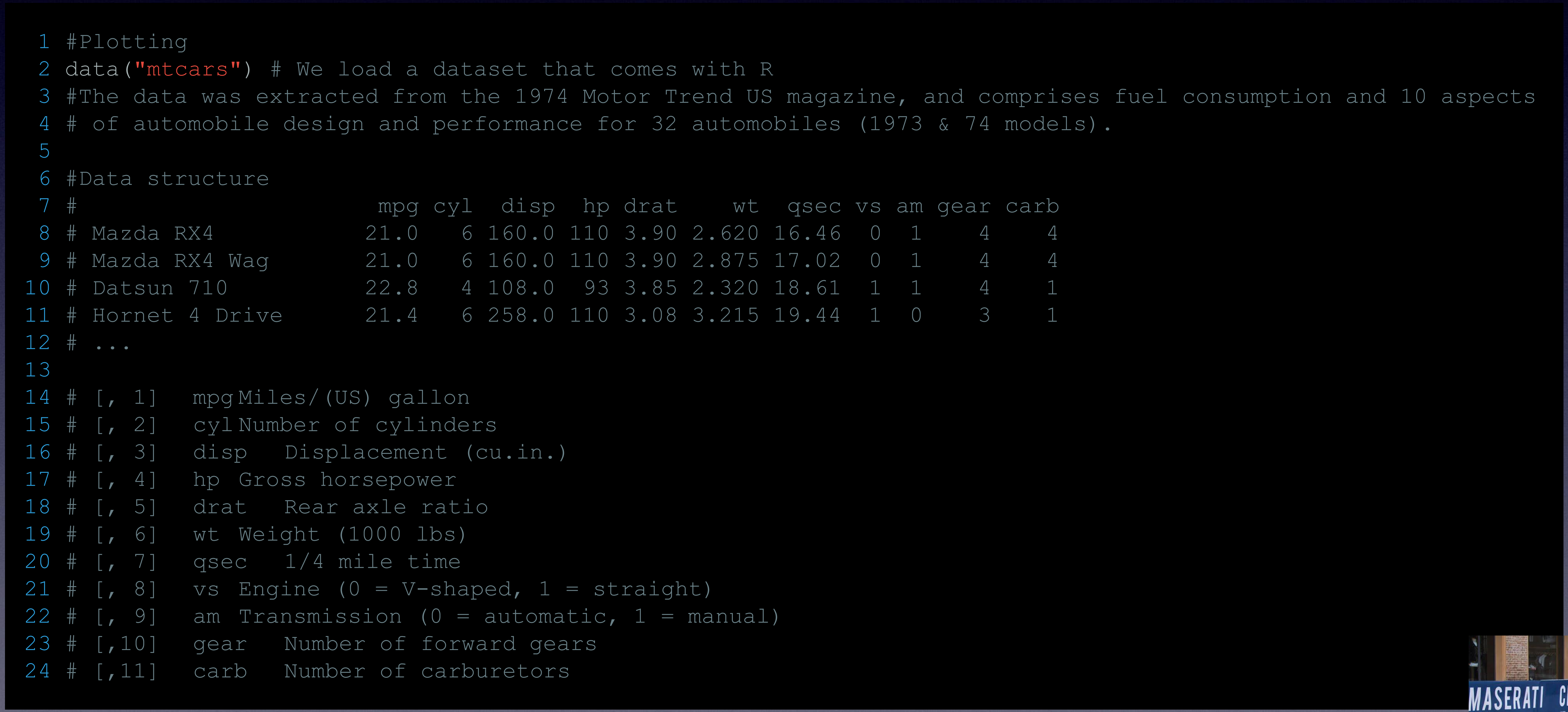
NB: “Chernobyl” was not used, as it was only present in one data frame, but this could be modified

Working with tables or data frames

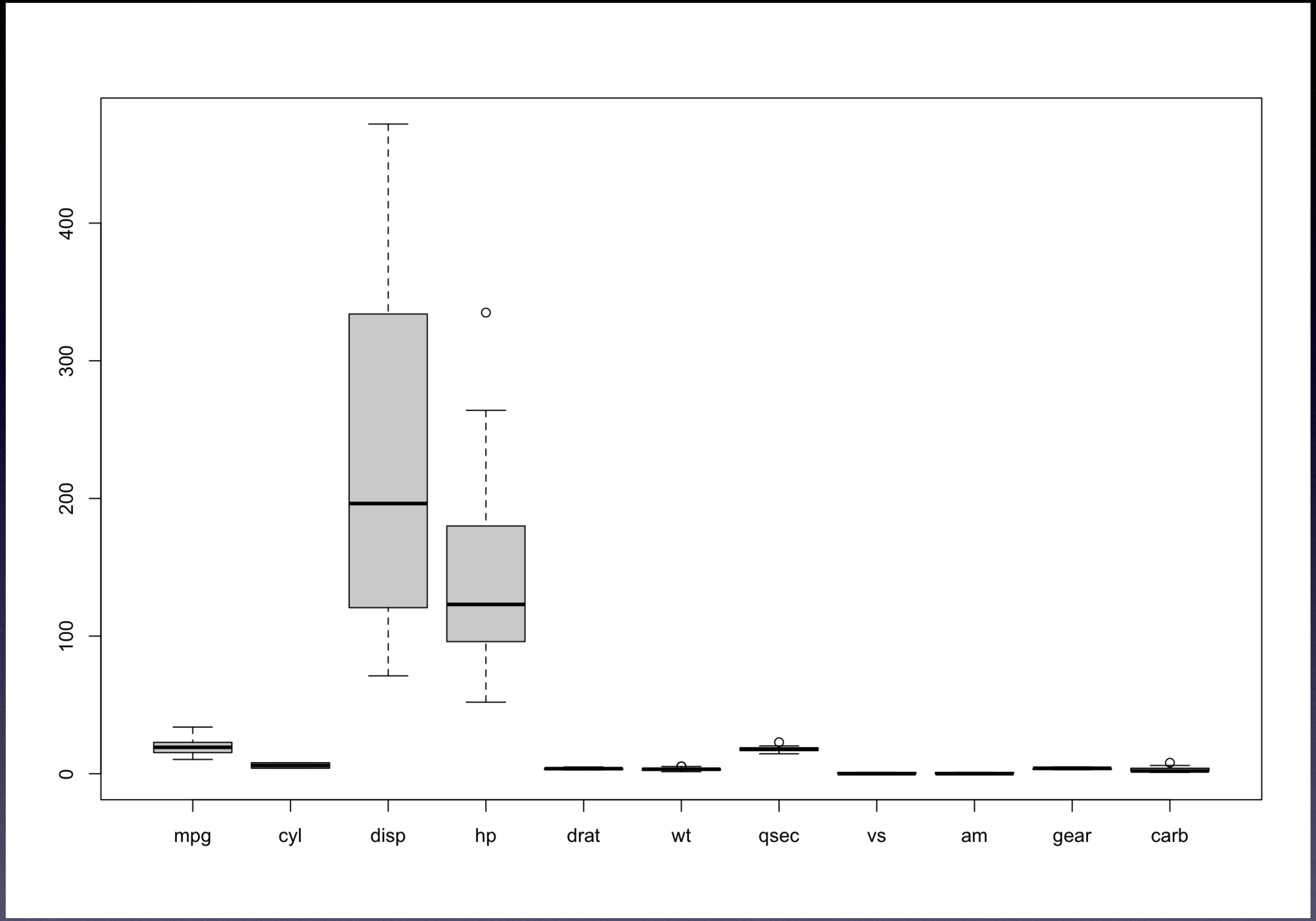


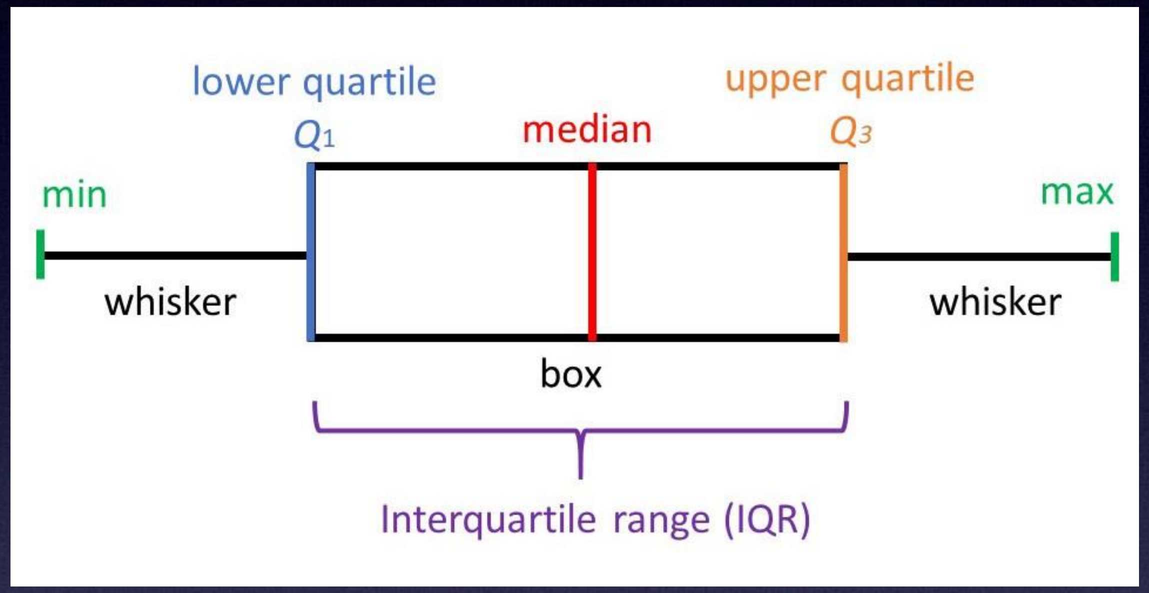
```
#Useful commands to work with tables or dataframes
getwd()            # get working directory
# [1] "/Users/admin"
setwd("path/to/my/directory") # set working directory

my.table<-read.table(file="table.tsv", sep="\t", header=T) # read table; several other options available
dim(my.table)      # Table dimensions
nrow(my.table)     # Number of rows
ncol(my.table)     # Number of columns
colnames(my.table) # Name of columns
rownames(my.table) # Name of rows
colSums(my.table)  # Sum of numeric values in columns
rowSums(my.table)  # Sum of numeric values in rows
head(my.table)     # See table header
t(my.table)        # Transpose table

#Table subsetting
# Format:  my.table[row, column]
my.table[1,2]                             # Get value from row 1, column 2
my.table[1,]                              # Get values from row 1 across all columns
my.table$column.name<-NULL                # Remove column
my.table[-5,-2]                           # Remove row 5 and column 2
my.table[-(5:10),]                        # Remove rows 5 to 10, keep all columns
my.table[,-(which(colSums(my.table)==0))] # Remove columns that sum 0

```

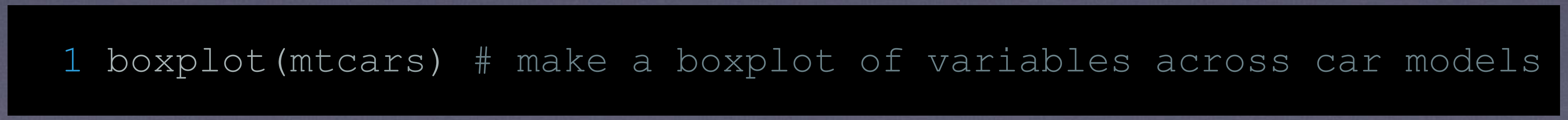
Simple plots



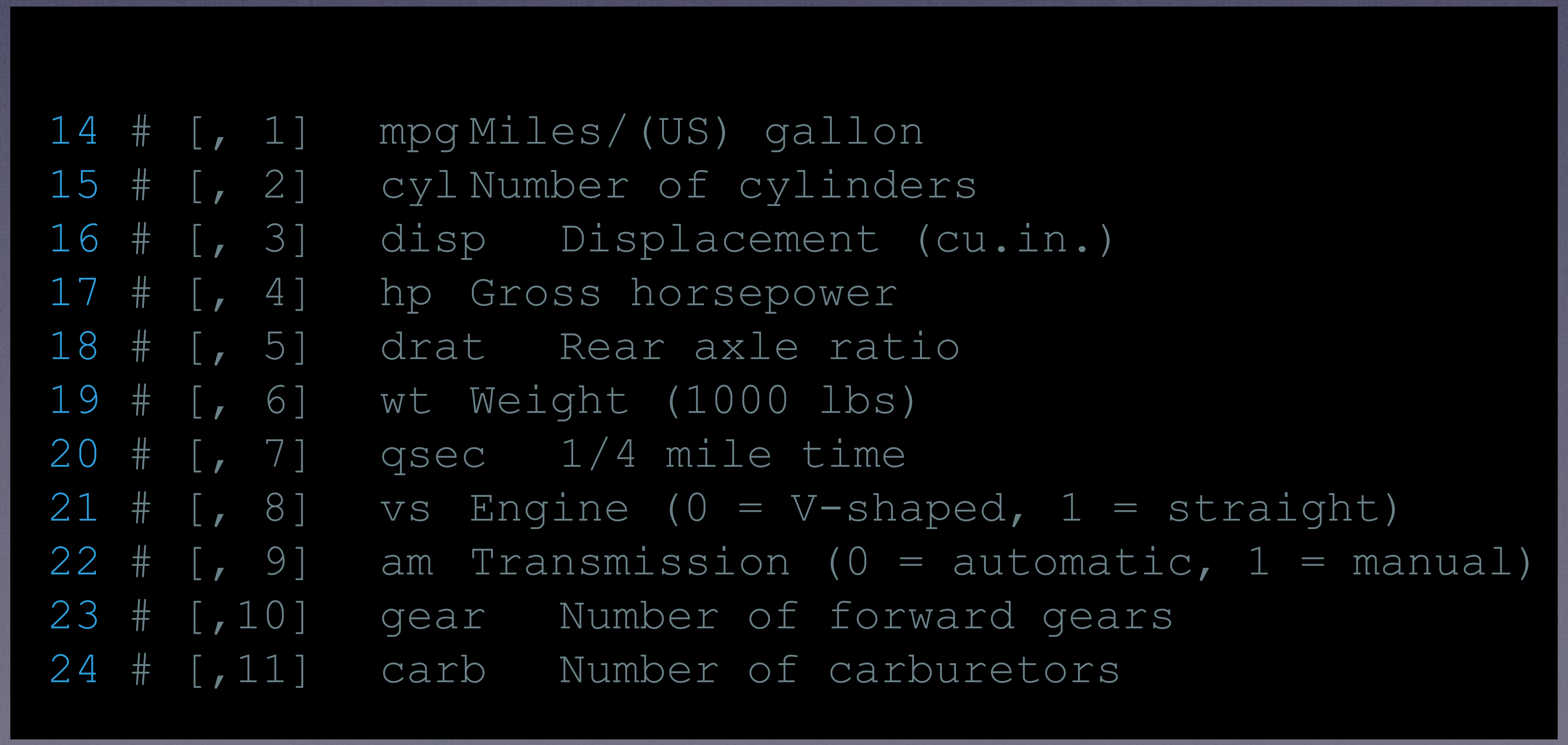
```
#Plotting
data("mtcars") # We load a dataset that comes with R
#The data was extracted from the 1974 Motor Trend US magazine, and comprises fuel consumption and 10 aspects
# of automobile design and performance for 32 automobiles (1973 & 74 models).

#Data structure
#                       mpg cyl  disp  hp drat    wt  qsec vs am gear carb
# Mazda RX4            21.0   6 160.0 110 3.90 2.620 16.46  0  1    4    4
# Mazda RX4 Wag        21.0   6 160.0 110 3.90 2.875 17.02  0  1    4    4
# Datsun 710           22.8   4 108.0  93 3.85 2.320 18.61  1  1    4    1
# Hornet 4 Drive       21.4   6 258.0 110 3.08 3.215 19.44  1  0    3    1
# ...

# [, 1]   mpg Miles/(US) gallon
# [, 2]   cyl Number of cylinders
# [, 3]   disp   Displacement (cu.in.)
# [, 4]   hp  Gross horsepower
# [, 5]   drat   Rear axle ratio
# [, 6]   wt  Weight (1000 lbs)
# [, 7]   qsec   1/4 mile time
# [, 8]   vs  Engine (0 = V-shaped, 1 = straight)
# [, 9]   am  Transmission (0 = automatic, 1 = manual)
# [,10]   gear   Number of forward gears
# [,11]   carb   Number of carburetors
```



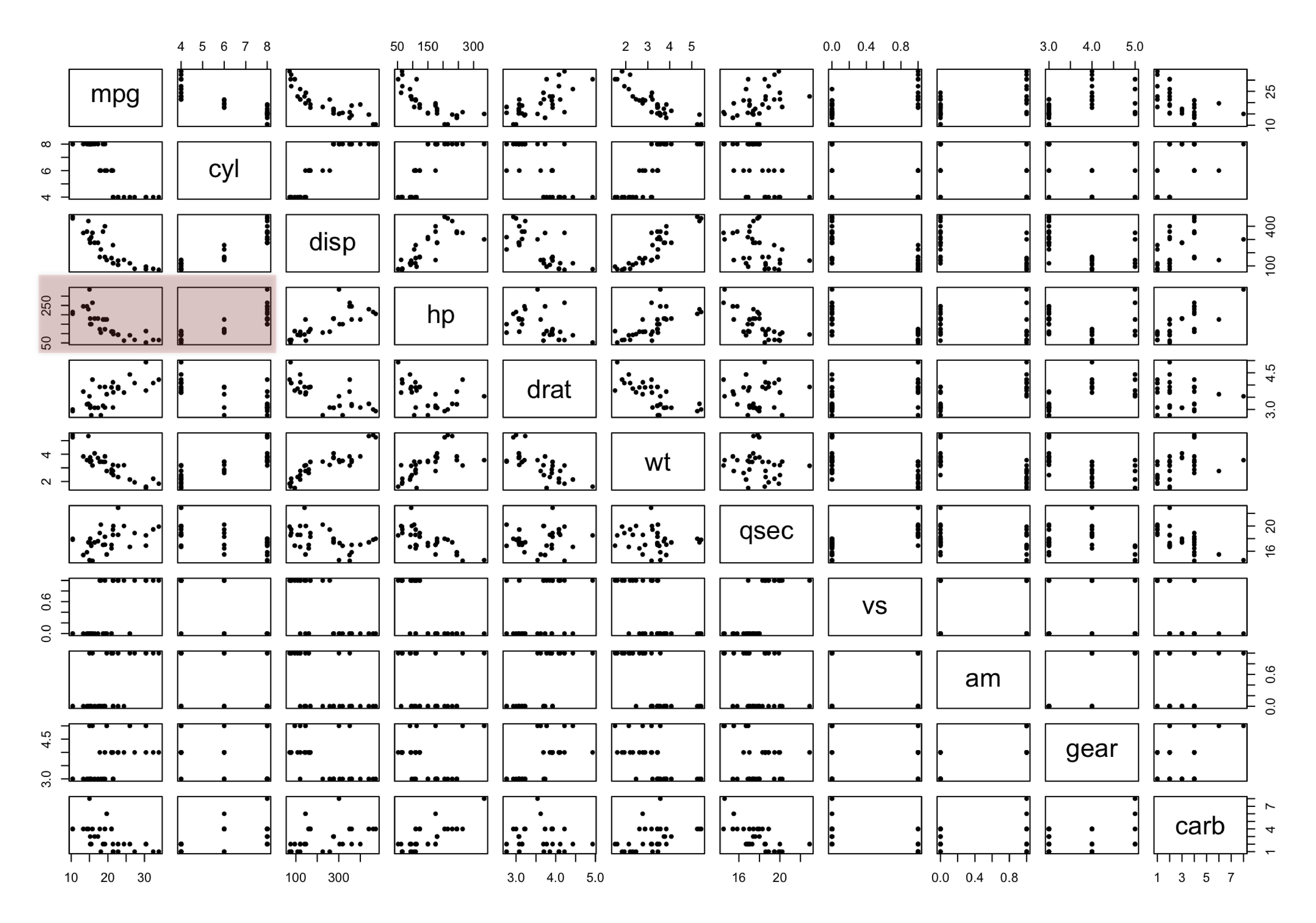




```
boxplot(mtcars) # make a boxplot of variables across car models
```

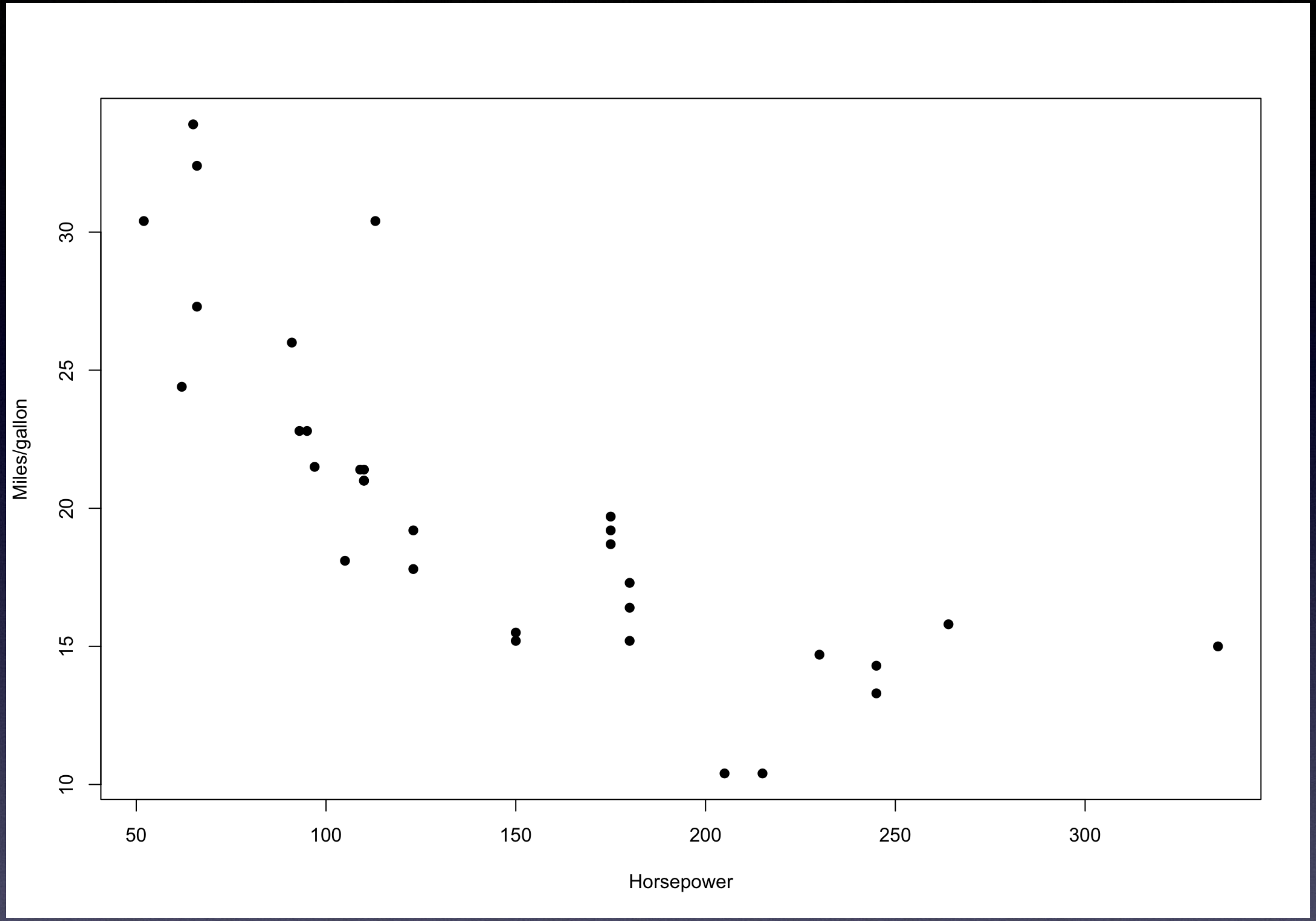


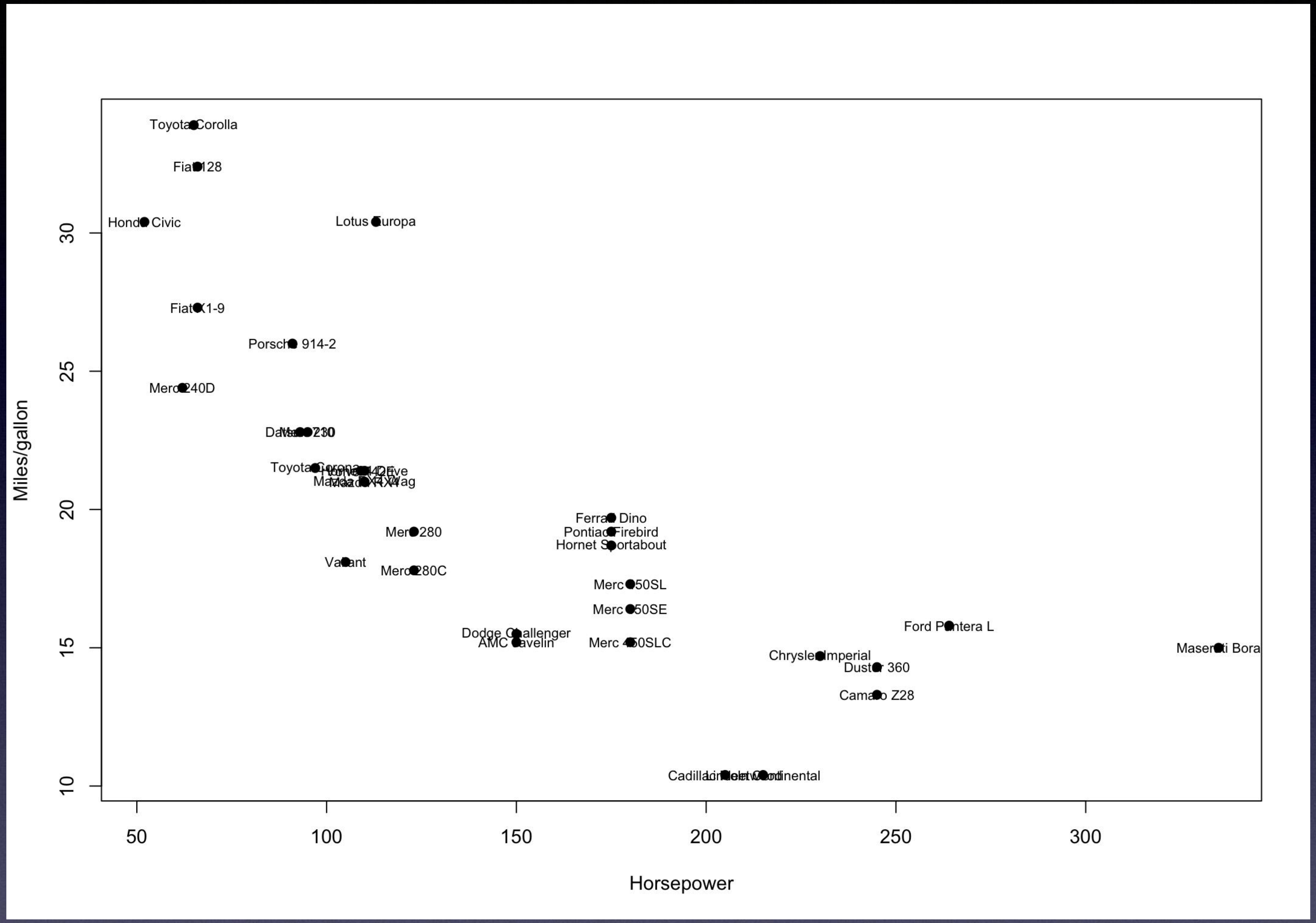
```
# [, 1]   mpg Miles/(US) gallon
# [, 2]   cyl Number of cylinders
# [, 3]   disp   Displacement (cu.in.)
# [, 4]   hp  Gross horsepower
# [, 5]   drat   Rear axle ratio
# [, 6]   wt  Weight (1000 lbs)
# [, 7]   qsec   1/4 mile time
# [, 8]   vs  Engine (0 = V-shaped, 1 = straight)
# [, 9]   am  Transmission (0 = automatic, 1 = manual)
# [,10]   gear   Number of forward gears
# [,11]   carb   Number of carburetors
```



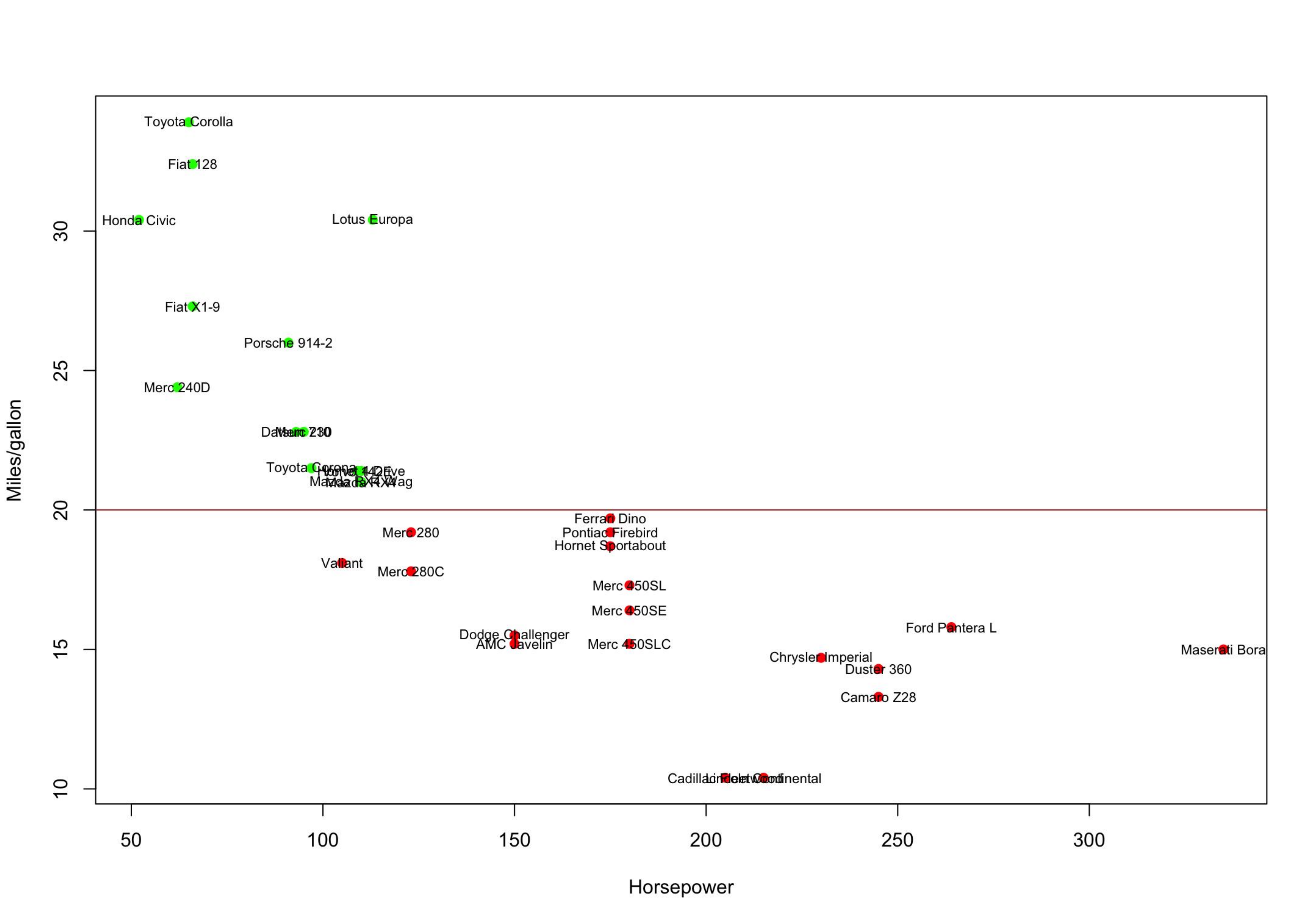
```
plot(mtcars, pch=19, cex=0.6) # make x-y plots for all variables
```

```
# [, 1]   mpg  Miles/(US) gallon
# [, 2]   cyl  Number of cylinders
# [, 3]   disp   Displacement (cu.in.)
# [, 4]   hp  Gross horsepower
# [, 5]   drat   Rear axle ratio
# [, 6]   wt  Weight (1000 lbs)
# [, 7]   qsec   1/4 mile time
# [, 8]   vs  Engine (0 = V-shaped, 1 = straight)
# [, 9]   am  Transmission (0 = automatic, 1 = manual)
# [,10]   gear   Number of forward gears
# [,11]   carb   Number of carburetors
```

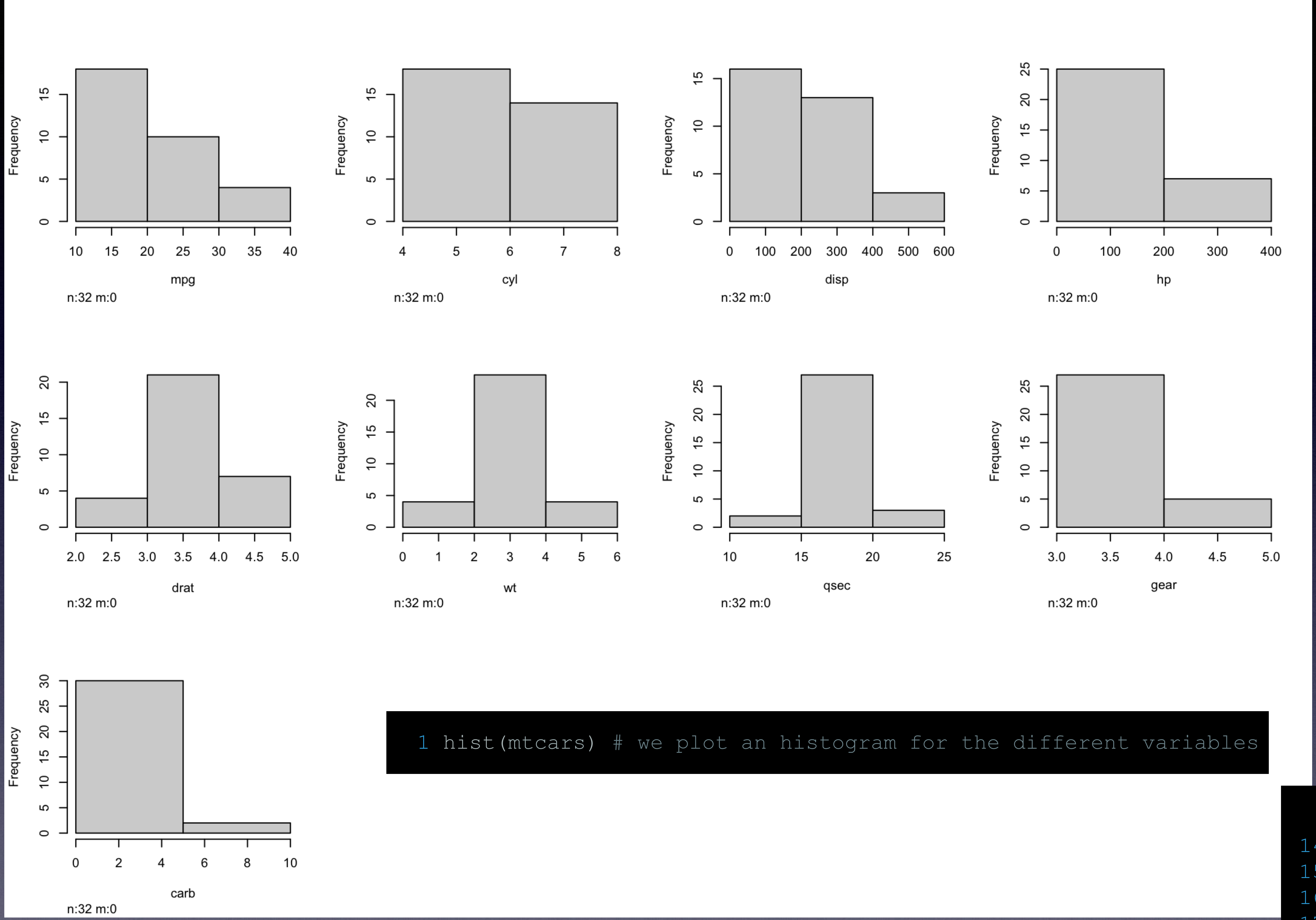




```
plot(mtcars$hp, mtcars$mpg, xlab="Horsepower", ylab="Miles/gallon", pch=19) # we plot horsepower vs. miles per gallon
text(mtcars$hp, mtcars$mpg, row.names(mtcars), cex=0.7) # we add the car model
```

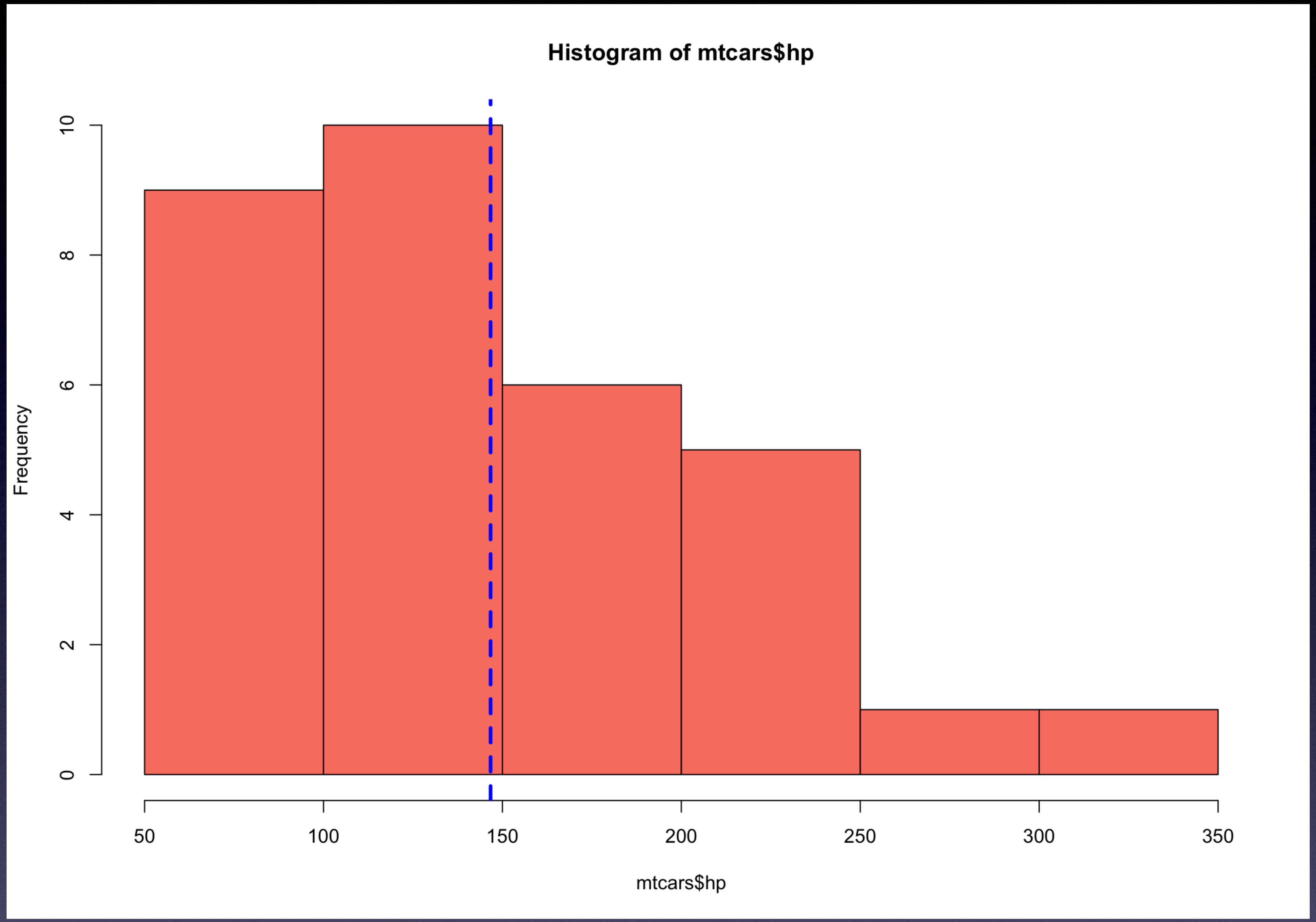


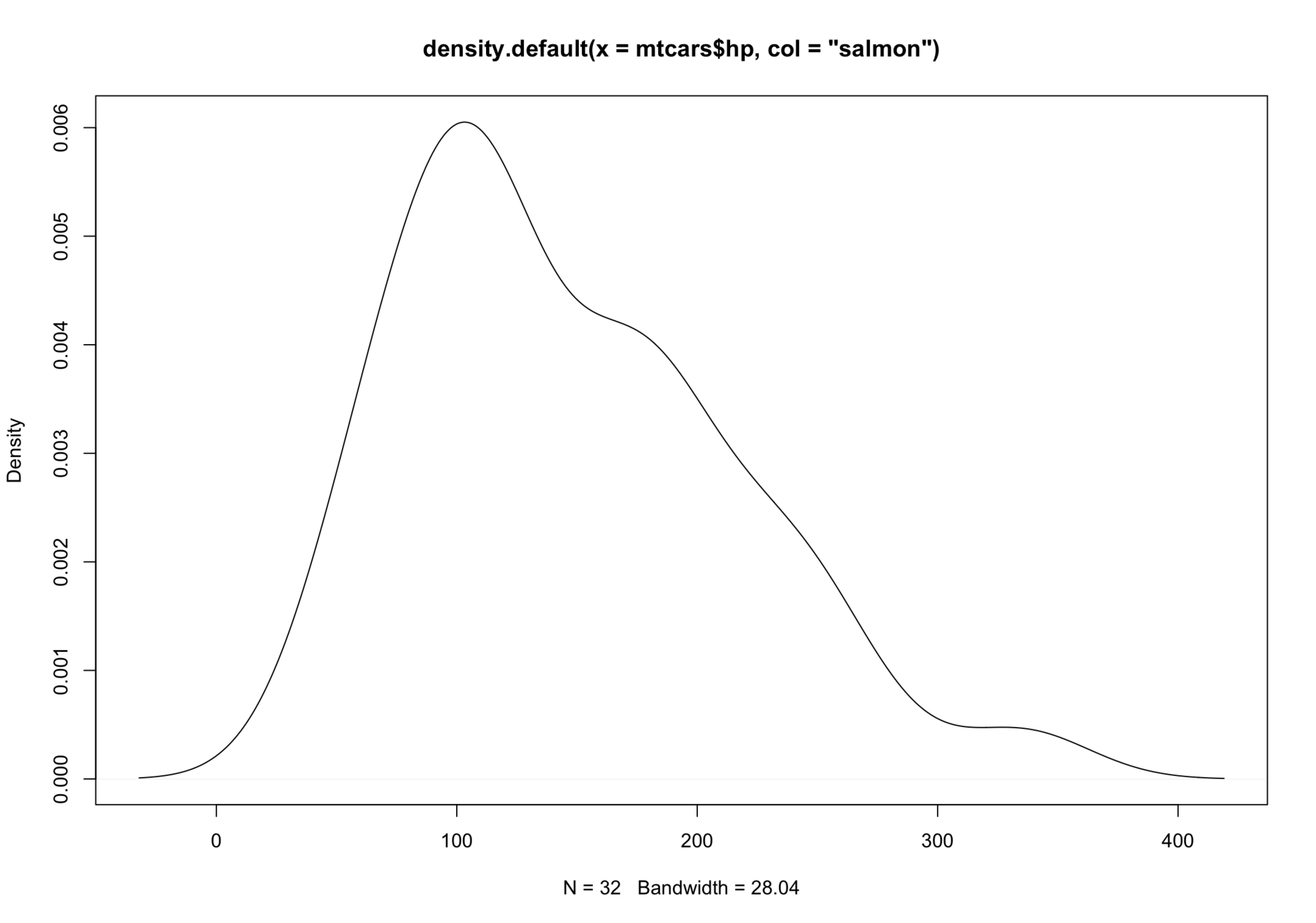
```
plot(mtcars$hp, mtcars$mpg, xlab="Horsepower", ylab="Miles/gallon", pch=19, col=ifelse(mtcars$mpg<20,"red", "green")) # We color dots according to
     a condition (20<x<20 mpg)
text(mtcars$hp, mtcars$mpg, row.names(mtcars), cex=0.7) # we add the car model
abline(h=20, col=“brown") # we add an horizontal line at “20”
```



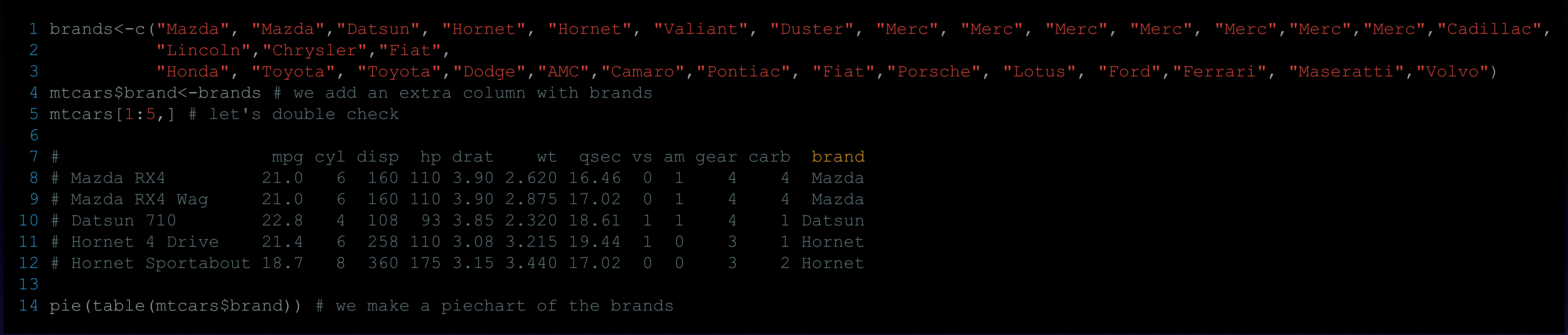
```
hist(mtcars) # we plot an histogram for the different variables
```

```
# [, 1]   mpg	Miles/(US) gallon
# [, 2]   cyl	Number of cylinders
# [, 3]   disp   Displacement (cu.in.)
# [, 4]   hp Gross horsepower
# [, 5]   drat   Rear axle ratio
# [, 6]   wt  Weight (1000 lbs)
# [, 7]   qsec   1/4 mile time
# [, 8]   vs  Engine (0 = V-shaped, 1 = straight)
# [, 9]   am  Transmission (0 = automatic, 1 = manual)
# [,10]   gear   Number of forward gears
# [,11]   carb   Number of carburetors
```

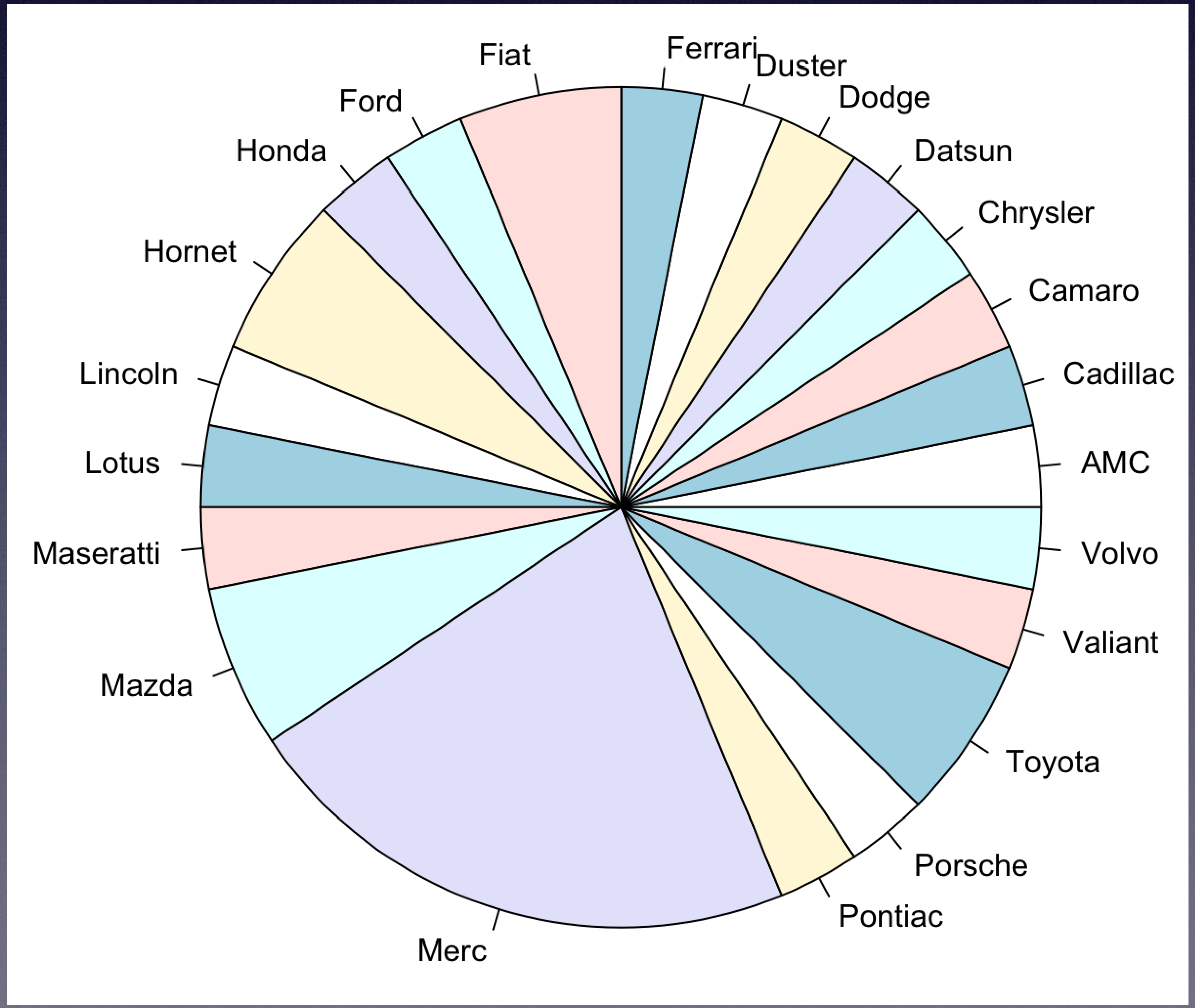




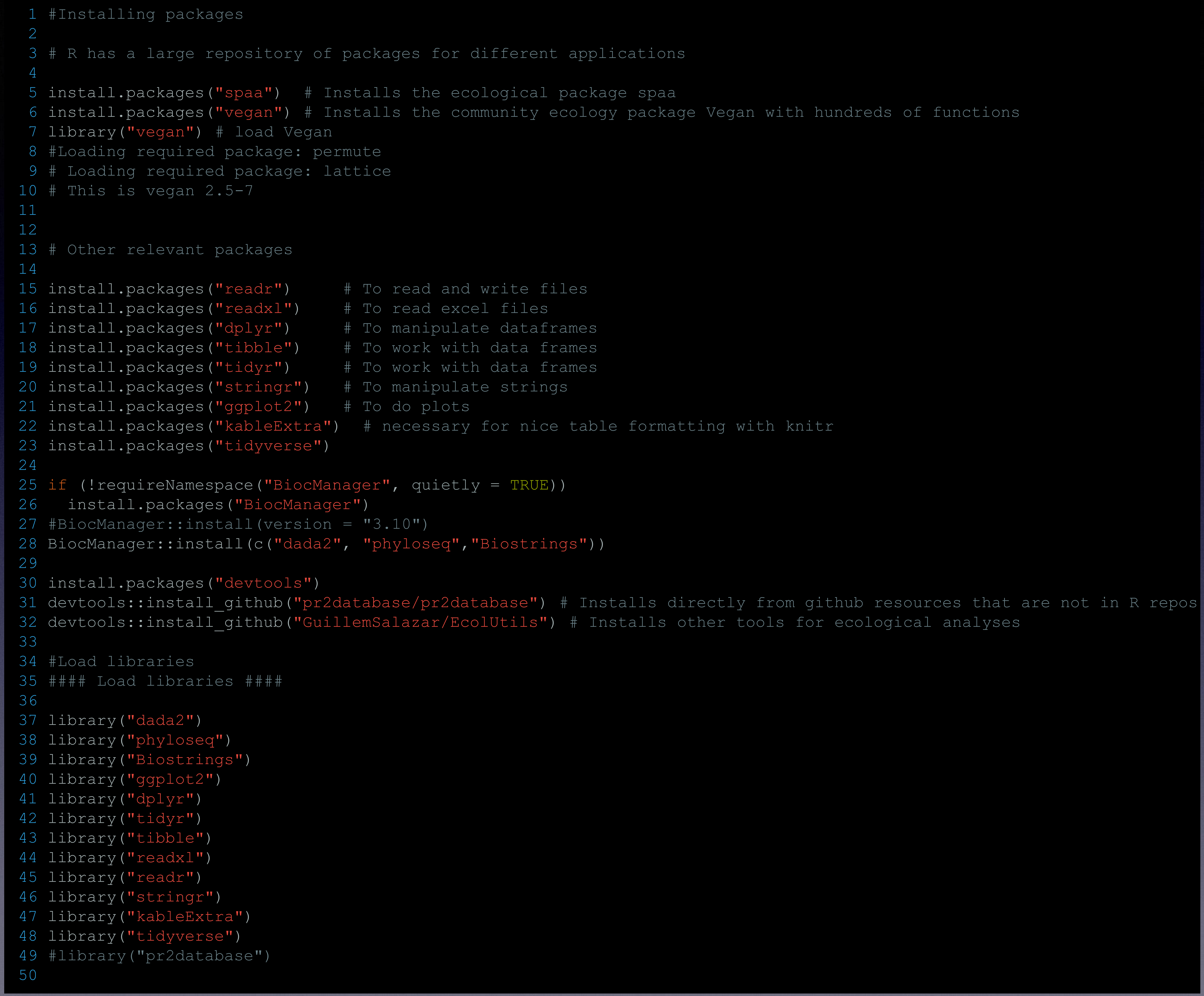
```
hist(mtcars$hp, col="salmon")
abline(v=mean(mtcars$hp), col="blue", lwd=3, lty=2)
plot(density(mtcars$hp))
```



```
brands<-c("Mazda", "Mazda","Datsun", "Hornet", "Hornet", "Valiant", "Duster", "Merc", "Merc", "Merc", "Merc", "Merc","Merc","Merc","Cadillac",
          "Lincoln","Chrysler","Fiat",
          "Honda", "Toyota", "Toyota","Dodge","AMC","Camaro","Pontiac", "Fiat","Porsche", "Lotus", "Ford","Ferrari", "Maseratti","Volvo")
mtcars$brand<-brands # we add an extra column with brands
mtcars[1:5,] # let's double check

#                    mpg cyl disp  hp drat    wt  qsec vs am gear carb  brand
# Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4  Mazda
# Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4  Mazda
# Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1 Datsun
# Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1 Hornet
# Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2 Hornet

pie(table(mtcars$brand)) # we make a piechart of the brands
```



Installing and loading packages



```r
#Installing packages

# R has a large repository of packages for different applications

install.packages("spaa")  # Installs the ecological package spaa
install.packages("vegan") # Installs the community ecology package Vegan with hundreds of functions
library("vegan") # load Vegan
#Loading required package: permute
# Loading required package: lattice
# This is vegan 2.5-7


# Other relevant packages

install.packages("readr")      # To read and write files
install.packages("readxl")     # To read excel files
install.packages("dplyr")      # To manipulate dataframes
install.packages("tibble")     # To work with data frames
install.packages("tidyr")      # To work with data frames
install.packages("stringr")    # To manipulate strings
install.packages("ggplot2")    # To do plots
install.packages("kableExtra")  # necessary for nice table formatting with knitr
install.packages("tidyverse")

if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
#BiocManager::install(version = "3.10")
BiocManager::install(c("dada2", "phyloseq","Biostrings"))

install.packages("devtools")
devtools::install_github("pr2database/pr2database") # Installs directly from github resources that are not in R repos
devtools::install_github("GuillemSalazar/EcolUtils") # Installs other tools for ecological analyses

#Load libraries
#### Load libraries ####

library("dada2")
library("phyloseq")
library("Biostrings")
library("ggplot2")
library("dplyr")
library("tidyr")
library("tibble")
library("readxl")
library("readr")
library("stringr")
library("kableExtra")
library("tidyverse")
#library("pr2database")

```

-Reproduce all steps shown in this presentation

-The code is available in:
https://github.com/krabberod/BIO9905MERG1_V21/blob/main/intro.to.r/Intro.to.R.BIO9905MERG1_V21.R

THE END