An Introduction to R

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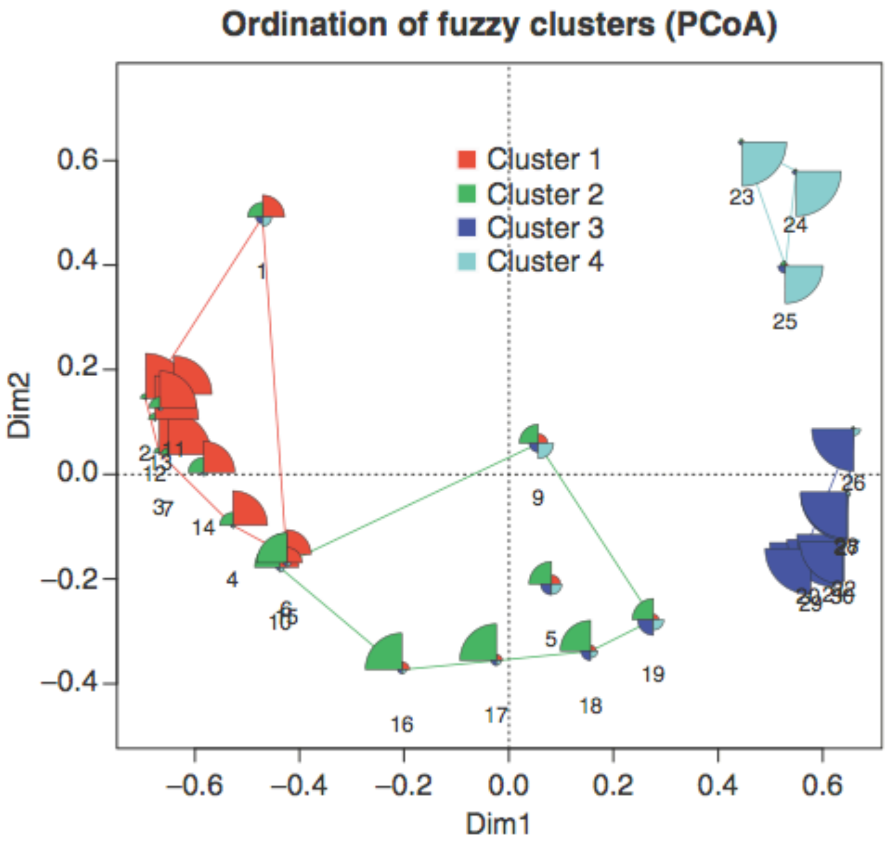
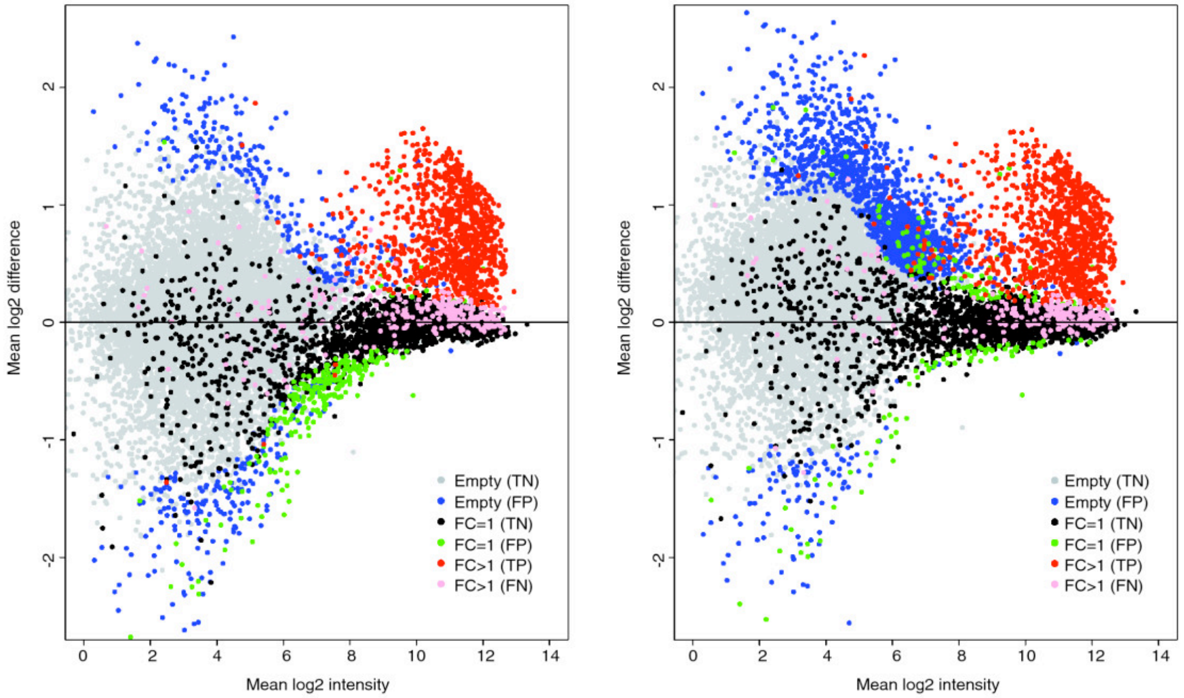


What is R?

A free software environment for statistical computing and graphics



Why is R useful?

- Data management and manipulation
- Well established system of packages and documentation
- Support for rich statistical simulation and modeling
- Active development and dedicated community
- Cutting-edge graphical data visualization
- Free!

Where to learn more about R

- The R Project Homepage: http://www.r-project.org
- Quick R Homepage: http://www.statmethods.net
- Bioconductor: http://www.bioconductor.org
- An Introduction to R (long!): http://cran.r-project.org/doc/manuals/R-intro.html
- Google - there are tons of tutorials, guides, demos, packages and more

R for Biologists

- Bioconductor (http://bioconductor.org)
    - 1560 packages (07-10-2018):
        - Variant detection: coding changes, PolyPhen database
        - Annotation: pathway analysis, access GO, KEGG, NCBI and many others
        - High-throughput assays: flow cytometry, mass spec
        - Transcription factor binding detection
- Ecology (see: http://cran.r-project.org/web/views/Environmetrics.html)
        - Ordination
        - Cluster Analysis
        - Ecological Theory
        - Population Dynamics
        - Spatial Data Analysis
- Phylogenetics and Evolution (see: http://cran.r-project.org/web/views/Phylogenetics.html)
    - Ancestral State Reconstruction
    - Phylogenetic Inference
    - Trait Evolution

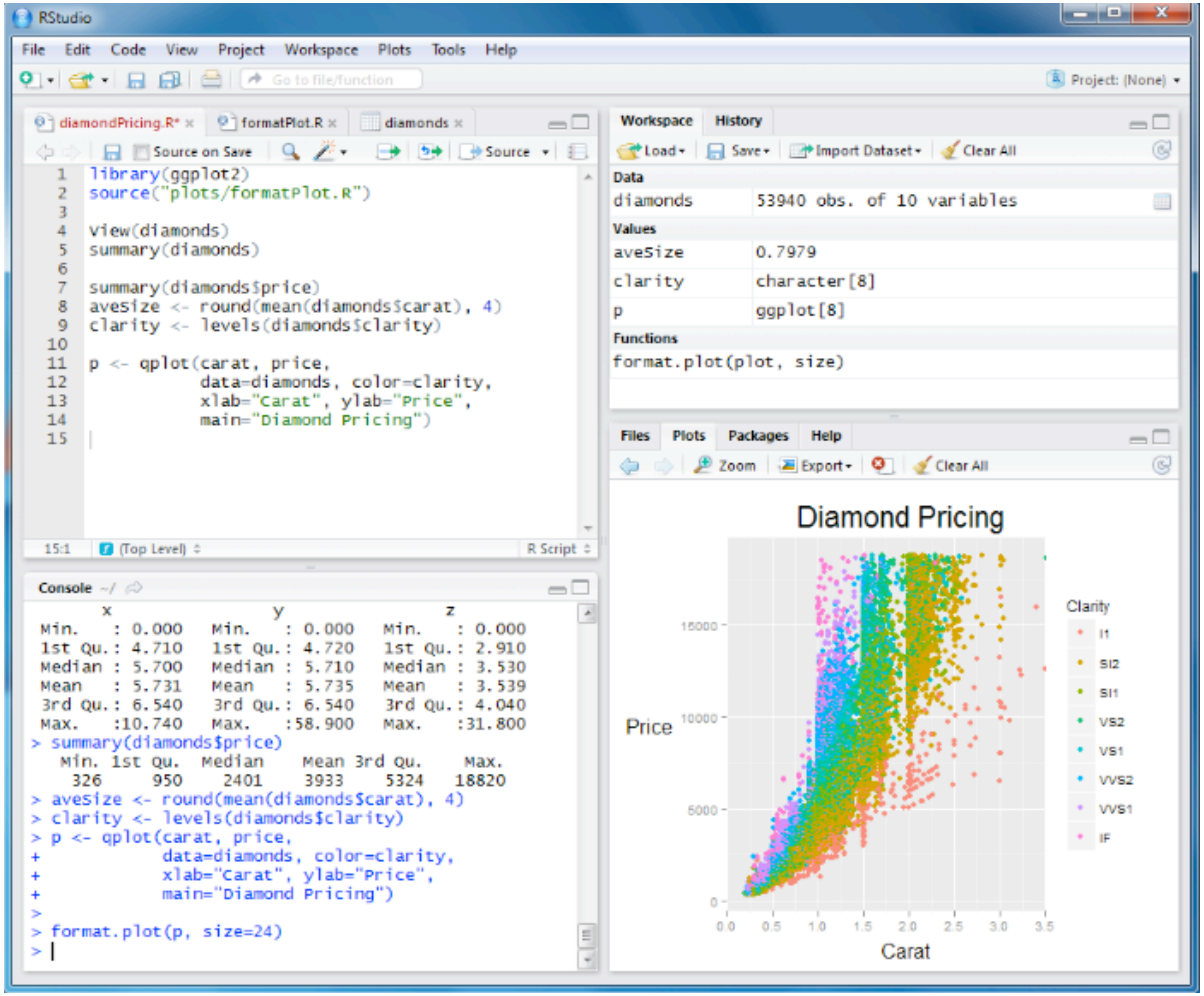
Obtaining R

- Windows, Mac or Linux OS: https://www.r-project.org

Running R

- Install a R Integrated Development Environment (IDE)
    - RStudio: http://www.rstudio.com
    - Makes working with R much easier, particularly for a new R user
    - Run on Windows, Mac or Linux OS
- Or from the command line, type R

R Studio



```
library(ggplot2)
source("plots/formatPlot.R")

view(diamonds)
summary(diamonds)

summary(diamonds$price)
avesize <- round(mean(diamonds$carat), 4)
clarity <- levels(diamonds$clarity)

p <- qplot(carat, price,
           data=diamonds, color=clarity,
           xlab="Carat", ylab="Price",
           main="Diamond Pricing")
```

Data

diamonds   53940 obs. of 10 variables

Values

aveSize   0.7979

clarity   character[8]

p   ggplot[8]

Functions

format.plot(plot, size)

```
       x                 y                 z
 Min.   : 0.000   Min.   : 0.000   Min.   : 0.000
 1st Qu.: 4.710   1st Qu.: 4.720   1st Qu.: 2.910
 Median : 5.700   Median : 5.710   Median : 3.530
 Mean   : 5.731   Mean   : 5.735   Mean   : 3.539
 3rd Qu.: 6.540   3rd Qu.: 6.540   3rd Qu.: 4.040
 Max.   :10.740   Max.   :58.900   Max.   :31.800
> summary(diamonds$price)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    326     950    2401    3933    5324   18820
> avesize <- round(mean(diamonds$carat), 4)
> clarity <- levels(diamonds$clarity)
> p <- qplot(carat, price,
+            data=diamonds, color=clarity,
+            xlab="Carat", ylab="Price",
+            main="Diamond Pricing")
>
> format.plot(p, size=24)
> 
```

Basic R functionality

Calculator

- +, -, /, *, ^, log(), exp(), sqrt(), abs(), cos(), sin(), tan(), ...

```
(4+5^2)/3.14
[1] 9.235669
```

Set Variables / Vectors

```
y=13.4          y=c(1,2,3,4,5)
>y              >y
[1] 13.4        [1] 1 2 3 4 5
```

Sequences

```
y=rep(2,10)   [1] 2 2 2 2 2 2 2 2 2 2

y=2:8         [1]  2 3 4 5 6 7 8
```

Statistics

```
t.test(7:34, 5:29)
```

```
t = 1.6348, df = 50.999, p-value = 0.1082
alternative hypothesis: true difference in means is not
equal to 0
95 percent confidence interval:
 -0.797982  7.797982
sample estimates:
mean of x mean of y
     20.5      17.0
```

Manipulation I

```
n=c(3, 7, 12, 50, 103)

n[4]                                [1] 50

n[-2]                               [1] 3 12 50 103

n[1:3]                              [1] 3 7 12

n[c(1,3,5)]                         [1] 3 12 103

n[n<50]                             [1] 3 7 12

n[n>8 & n!=50]                      [1] 12 103
```

Manipulation II

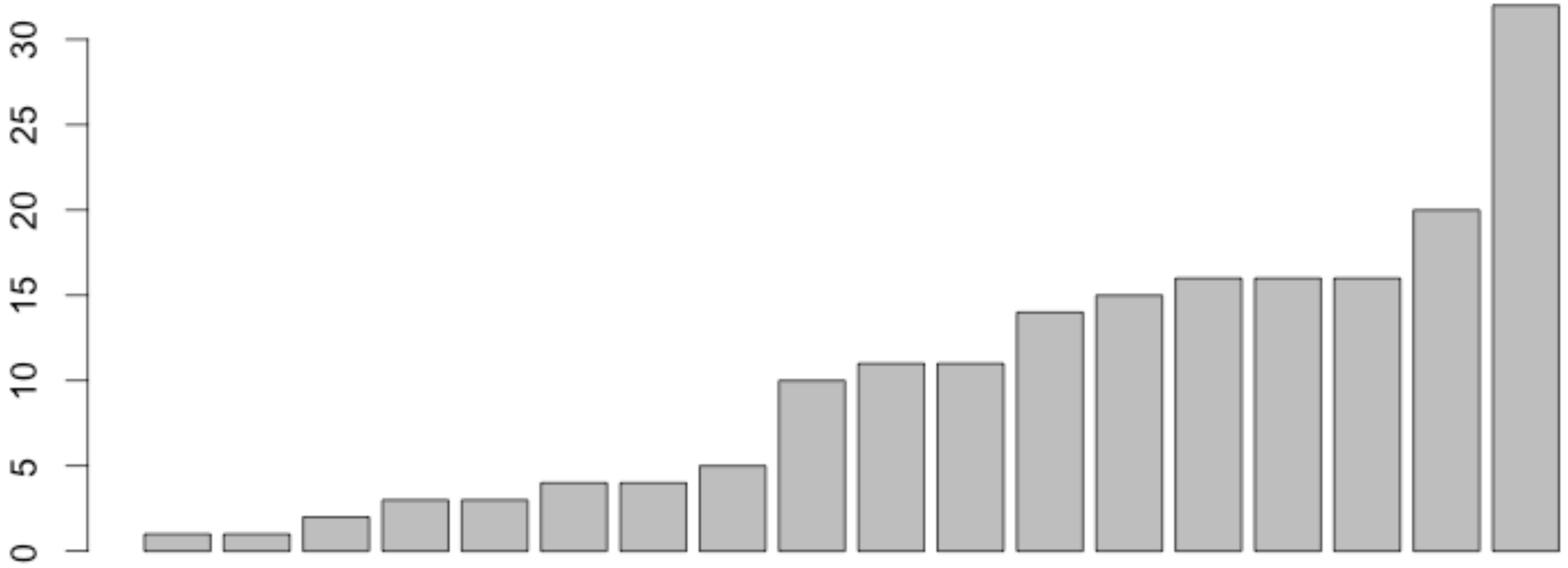
```
n=c(3, 7, 12, 50, 103)
```

```
n+1                          [1] 4 8 13 51 104

sum(n)                       [1] 175

mean(n)                      [1] 35

var(n)                       [1] 1796.5

min(n)                       [1] 3

max(n)                       [1] 103
```

Basic Visualization I

```
y=c(1,1,2,3,3,4,4,5,10,11,11,14,15,16,16,16,20,32)
```

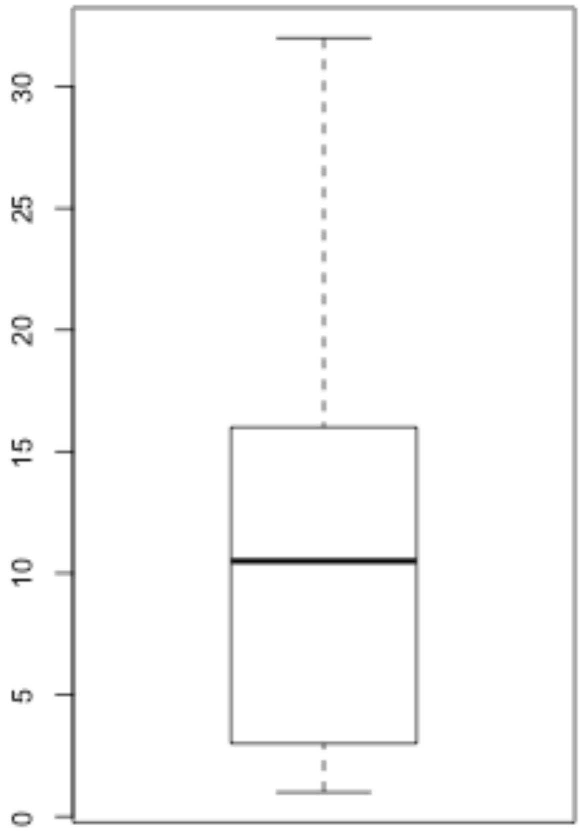
```
barplot(y)
```



Basic Visualization II

```
y=c(1,1,2,3,3,4,4,5,10,11,11,14,15,16,16,16,20,32)
```

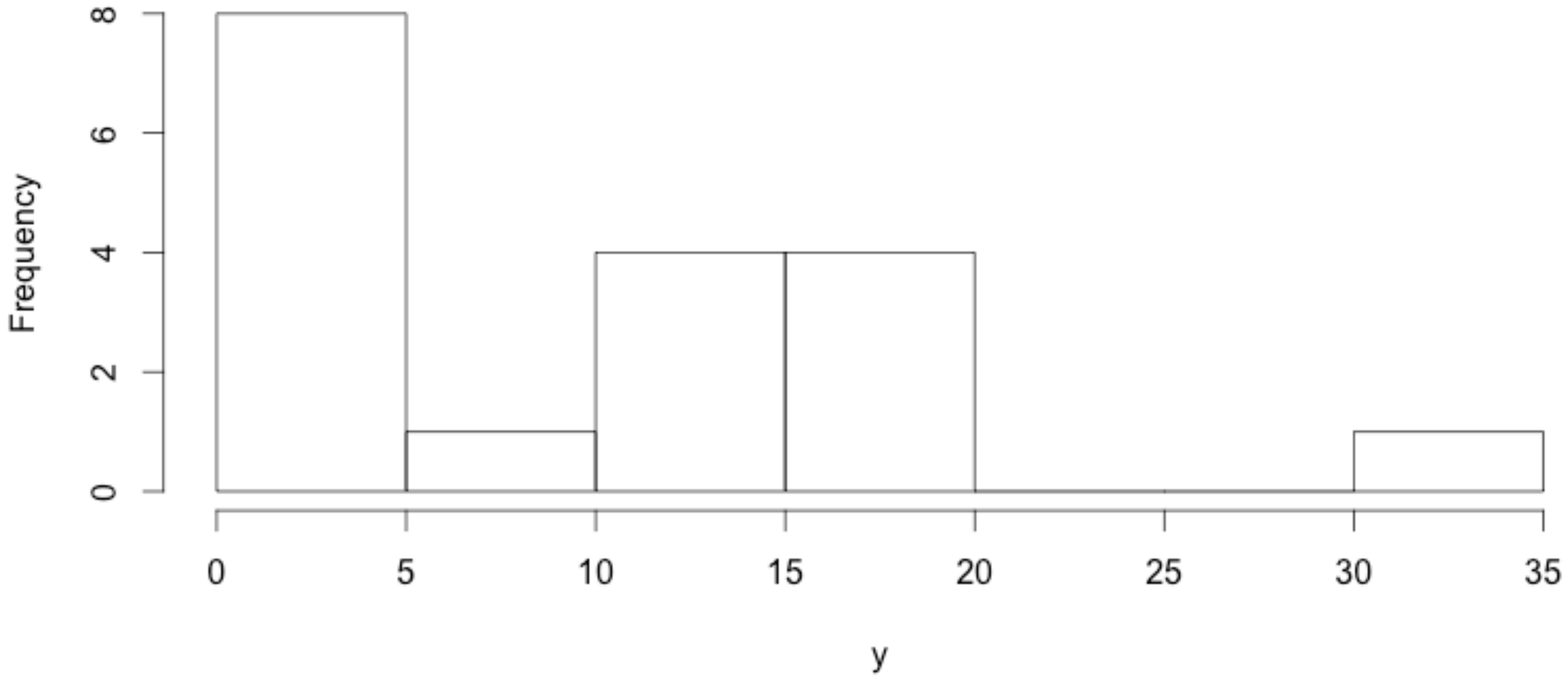
```
boxplot(y)
```



Basic Visualization III

```
y=c(1,1,2,3,3,4,4,5,10,11,11,14,15,16,16,16,20,32)
```

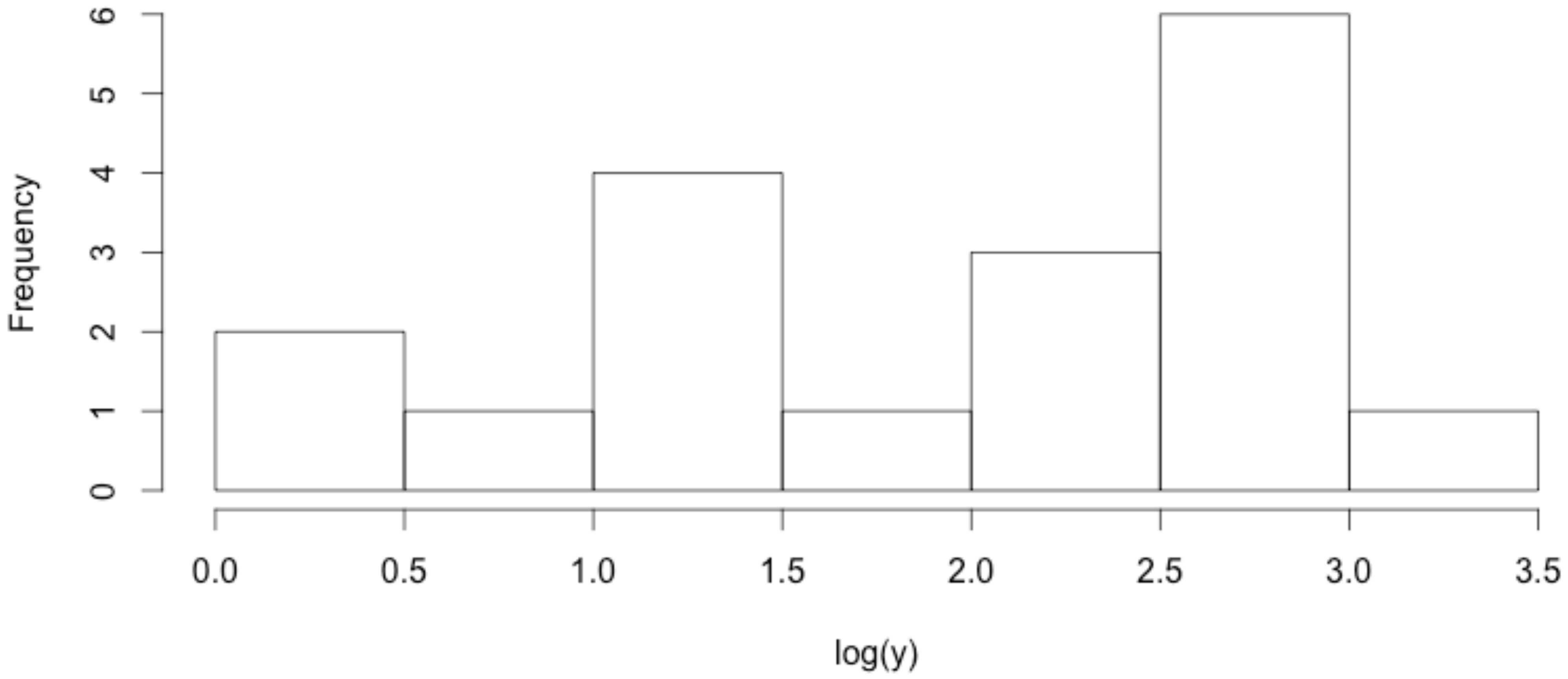
```
hist(y)
```



Basic Visualization III.i

```
y=c(1,1,2,3,3,4,4,5,10,11,11,14,15,16,16,16,20,32)
```

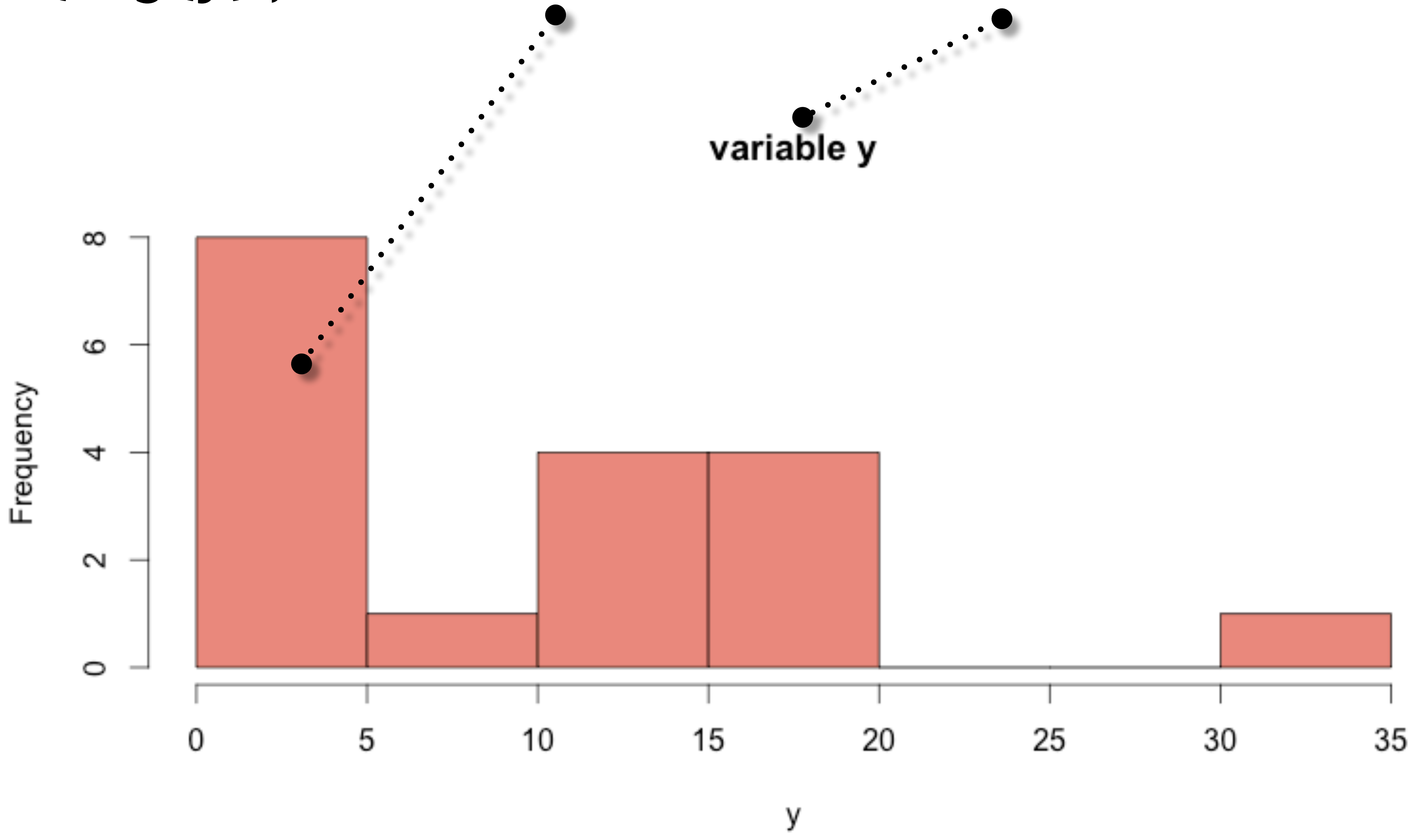
```
hist(log(y))
```



Basic Visualization III.ii

```
y=c(1,1,2,3,3,4,4,5,10,11,11,14,15,16,16,16,20,32)
```

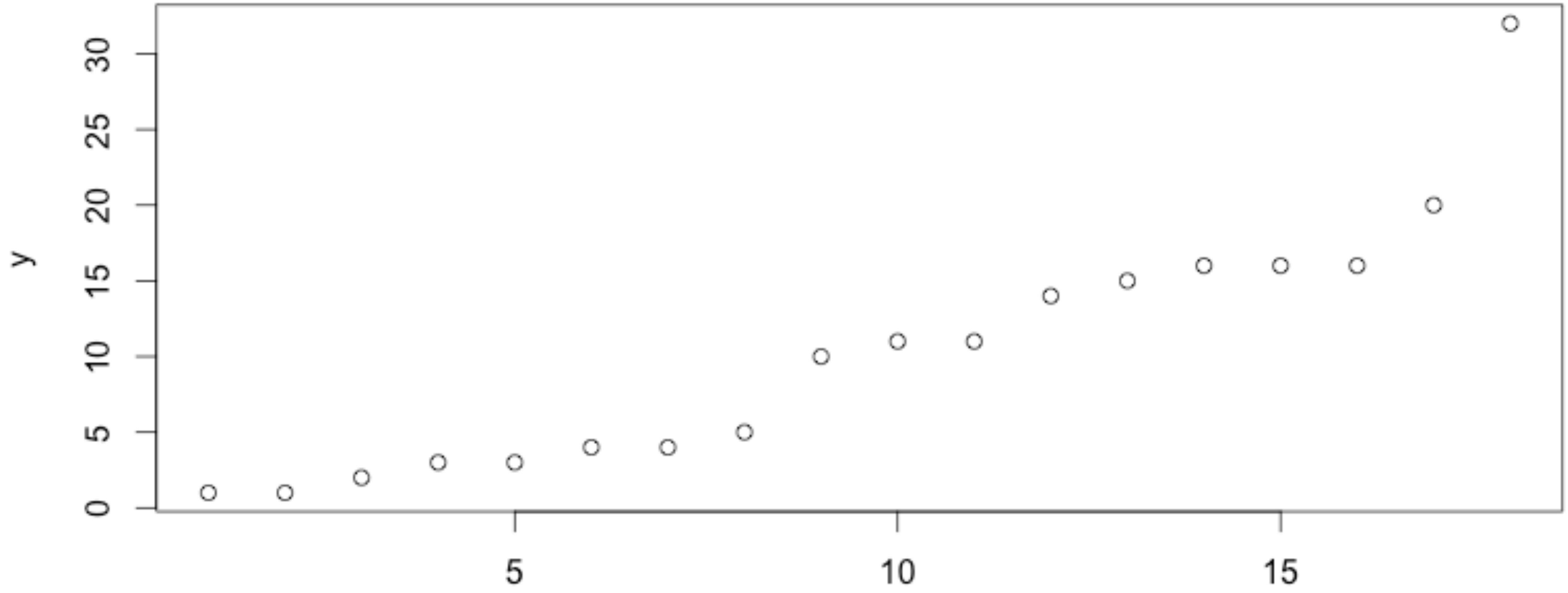
```
hist(log(y),
```



Basic Visualization IV

```
y=(1,1,2,3,3,4,4,5,10,11,11,14,15,16,16,16,20,32)
```

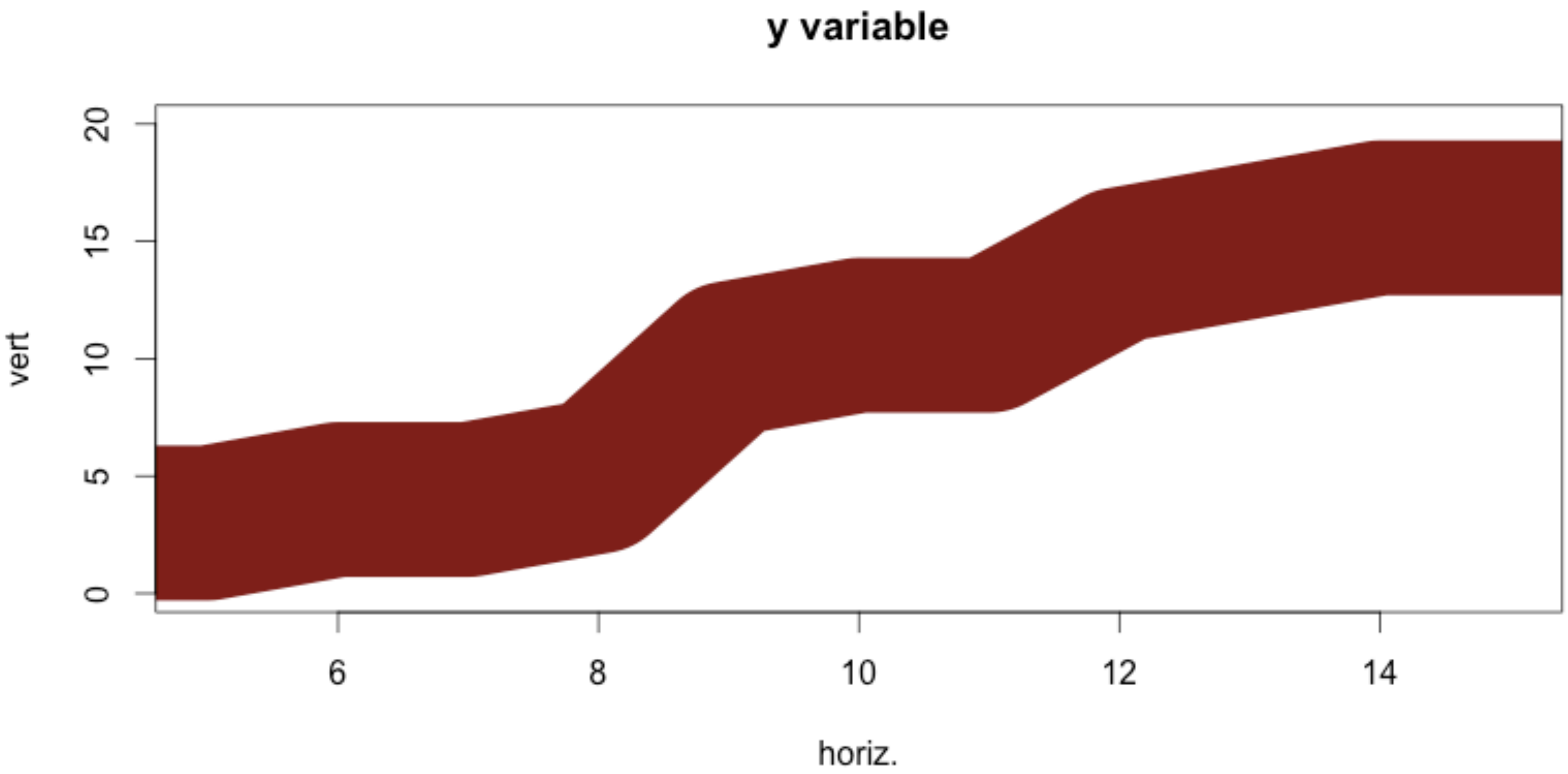
```
plot(y)
```



Basic Visualization IV.ii

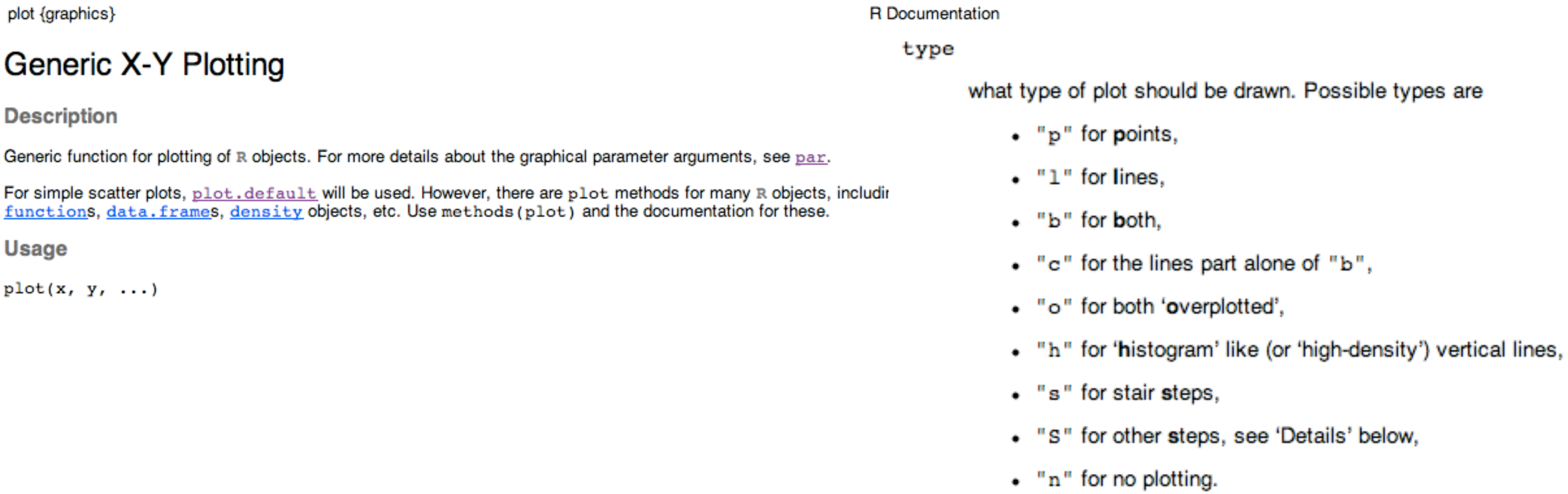
```
y=(1,1,2,3,3,4,4,5,10,11,11,14,15,16,16,16,20,32)
```

```
plot(y, type="l", col="dark red", lwd=100, main="y
variable", ylim=c(0,20), xlim=c(5,15), ylab="vert",
xlab="horiz.")
```



Help

- Do you need to remember all of the variables?
- ? is your friend
- ?plot



plot {graphics} R Documentation

Generic X-Y Plotting

Description

Generic function for plotting of R objects. For more details about the graphical parameter arguments, see par.

For simple scatter plots, plot.default will be used. However, there are plot methods for many R objects, includi functions, data.frames, density objects, etc. Use methods(plot) and the documentation for these.

Usage

```
plot(x, y, ...)
```

`type`

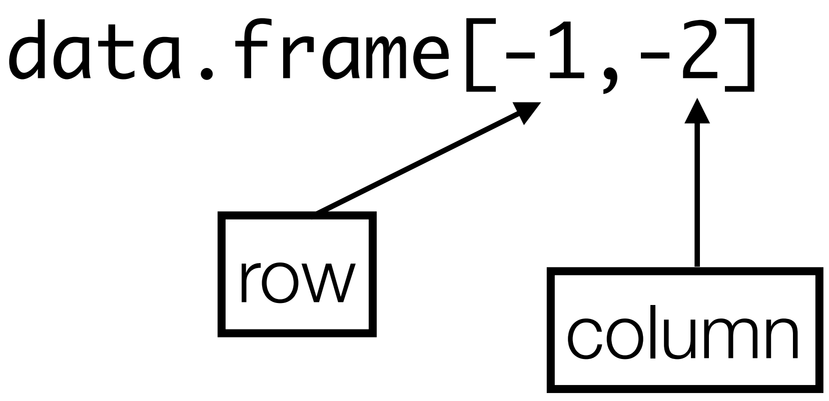
what type of plot should be drawn. Possible types are

- "p" for **p**oints,
- "l" for **l**ines,
- "b" for **b**oth,
- "c" for the lines part alone of "b",
- "o" for both '**o**verplotted',
- "h" for '**h**istogram' like (or 'high-density') vertical lines,
- "s" for stair **s**teps,
- "S" for other **s**teps, see 'Details' below,
- "n" for no plotting.

Data Frames

- A data.frame is essentially a table
- columns can be mixed types
  - numeric, text strings
- rows must be same type

	clostridia	proteobacteria	bacteroides
01_healthy	22	54	245
02_healthy	26	65	265
03_healthy	34	66	262
01_sick	32	32	116
02_sick	12	24	101
03_sick	9	18	87



```
data.frame[-1,-2]
```

	clostridia	bacteroides
02_healthy	26	265
03_healthy	34	262
01_sick	32	116
02_sick	12	101
03_sick	9	87

Data Frame Manipulations

	clostridia	proteobacteria	bacteroides
01_healthy	22	54	245
02_healthy	26	65	265
03_healthy	34	66	262
01_sick	32	32	116
02_sick	12	24	101
03_sick	9	18	87

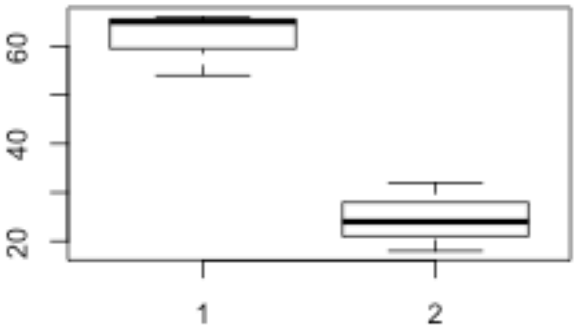
```
data.frame$proteobacteria
```

```
[1] 54 65 66 32 24 18
```

```
t.test(data.frame$proteobacteria[1:3],
data.frame$proteobacteria[4:6])
```

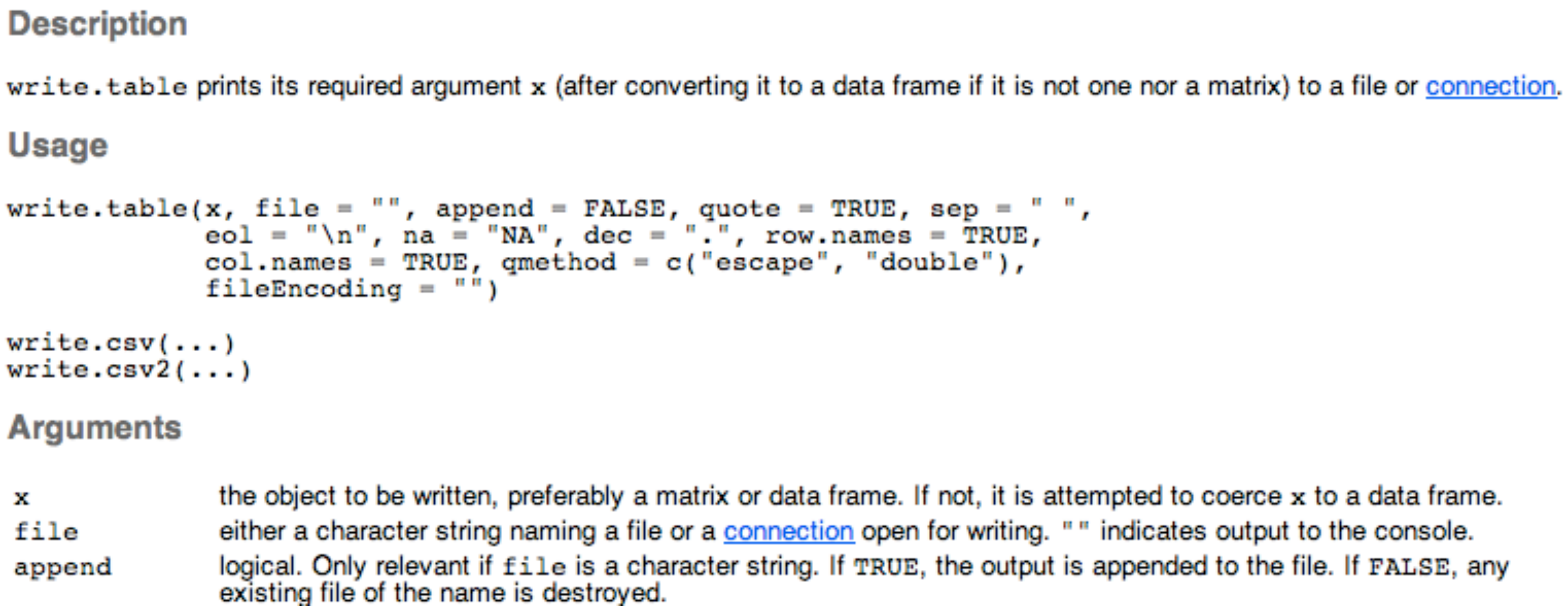
p-value = 0.002725

```
boxplot(data.frame$proteobacteria[1:3],
data.frame$proteobacteria[4:6])
```



Getting Help in R

```
?write.table
```



Description

`write.table` prints its required argument `x` (after converting it to a data frame if it is not one nor a matrix) to a file or connection.

Usage

```
write.table(x, file = "", append = FALSE, quote = TRUE, sep = " ",
            eol = "\n", na = "NA", dec = ".", row.names = TRUE,
            col.names = TRUE, qmethod = c("escape", "double"),
            fileEncoding = "")

write.csv(...)
write.csv2(...)
```

Arguments

`x` the object to be written, preferably a matrix or data frame. If not, it is attempted to coerce `x` to a data frame.

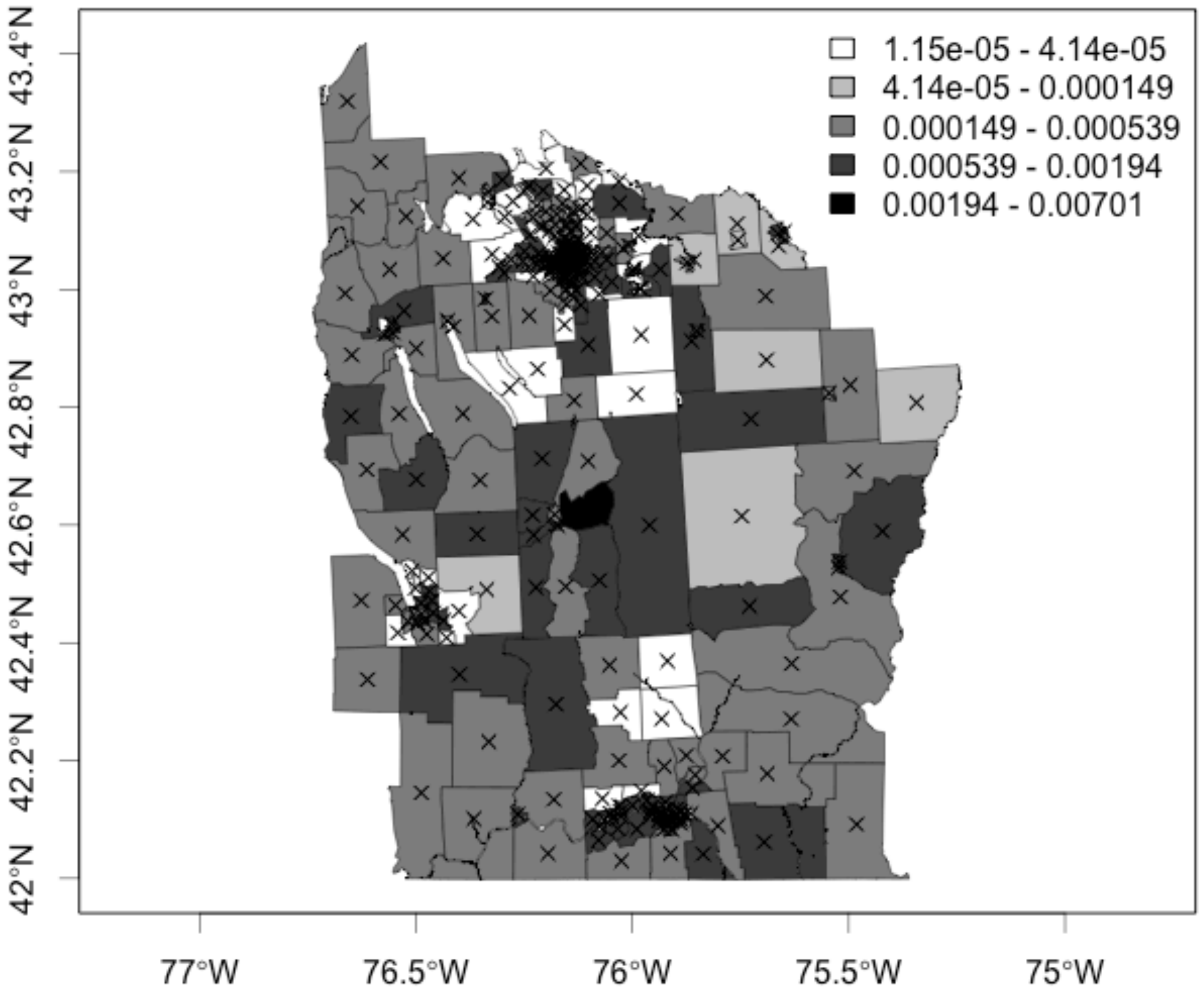
`file` either a character string naming a file or a connection open for writing. `""` indicates output to the console.

`append` logical. Only relevant if `file` is a character string. If `TRUE`, the output is appended to the file. If `FALSE`, any existing file of the name is destroyed.

Advanced and Other Applications in R

Spatial Epidemiology and Maps

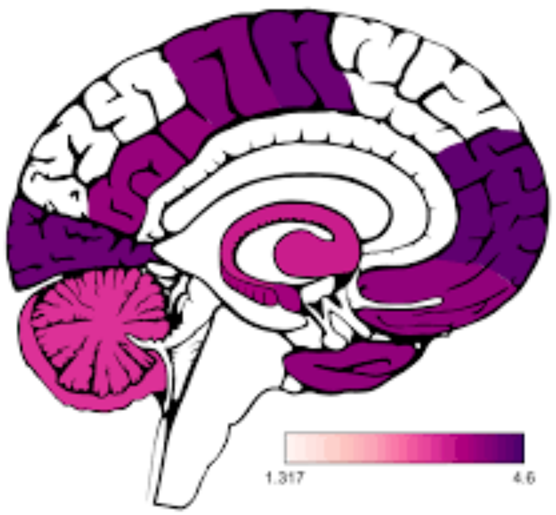
```
library(SpatialEpi)

data(NYleukemia)
sp.obj <- NYleukemia$spatial.polygon
centroids <- latlong2grid(NYleukemia$geo[, 2:3])
population <- NYleukemia$data$population
cases <- NYleukemia$data$cases

plotmap(cases/population, sp.obj, log=TRUE, nclr=5)
points(grid2latlong(centroids), pch=4)
```

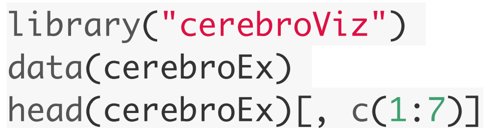


Anatomical Mapping

CerebroViz

https://github.com/ethanbahl/cerebroViz

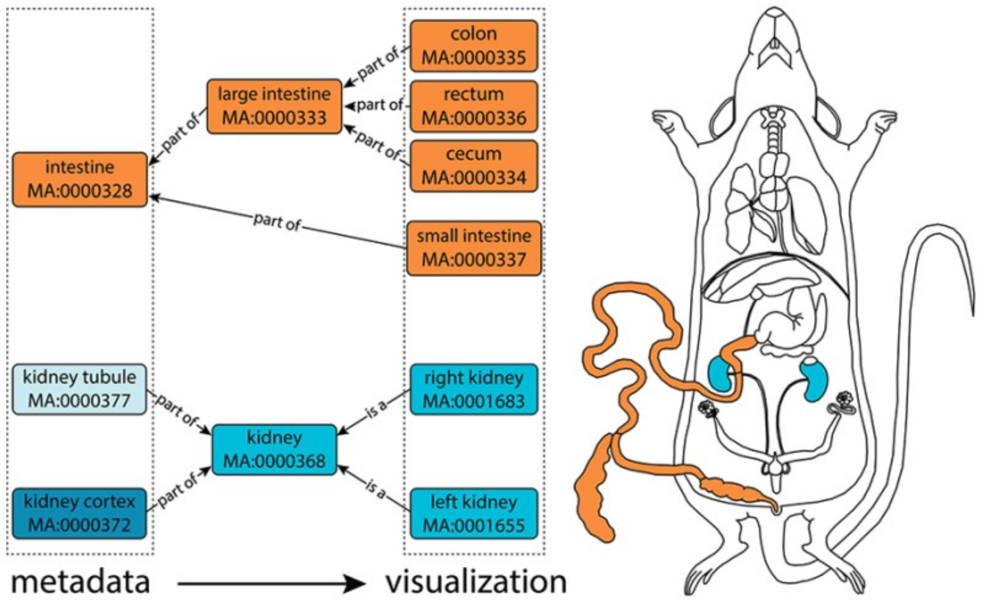




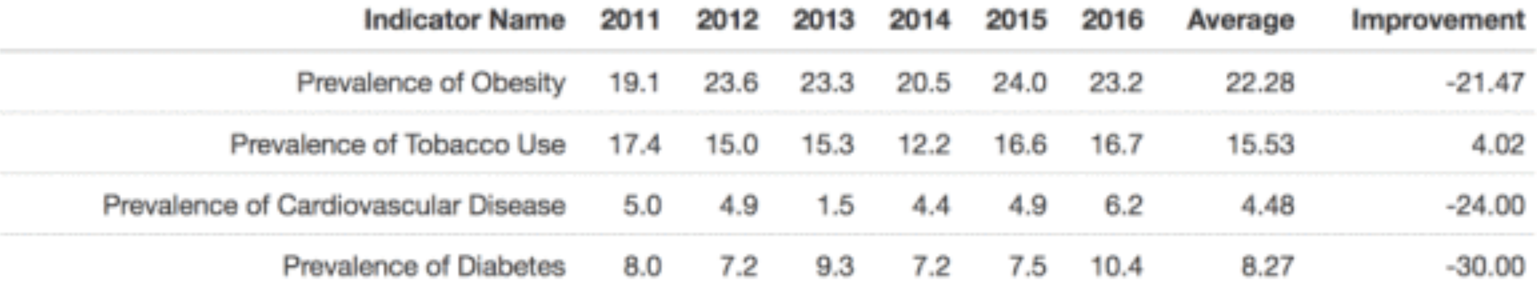
```
library("cerebroViz")
data(cerebroEx)
head(cerebroEx)[, c(1:7)]
```

COMICS

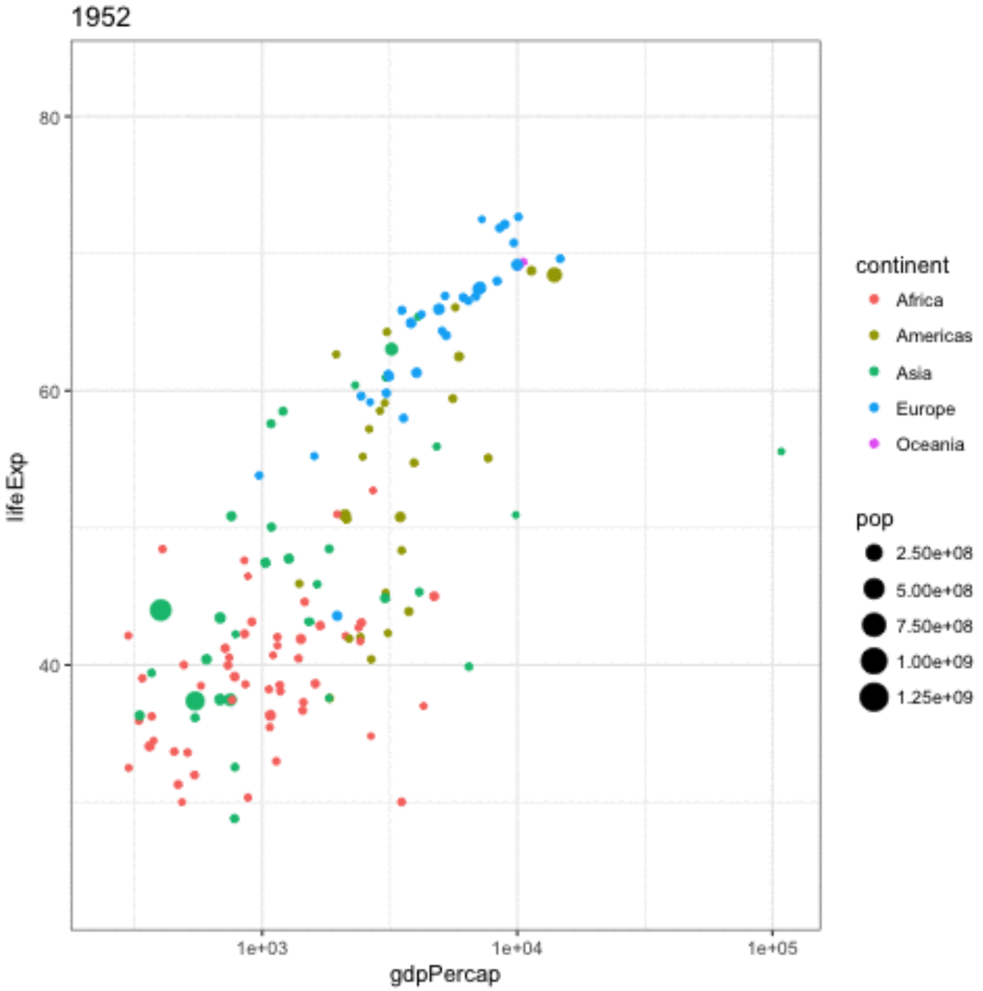
https://github.com/y-popov/COMICS



Animation / Interactivity



Indicator Name	2011	2012	2013	2014	2015	2016	Average	Improvement
Prevalence of Obesity	19.1	23.6	23.3	20.5	24.0	23.2	22.28	-21.47
Prevalence of Tobacco Use	17.4	15.0	15.3	12.2	16.6	16.7	15.53	4.02
Prevalence of Cardiovascular Disease	5.0	4.9	1.5	4.4	4.9	6.2	4.48	-24.00
Prevalence of Diabetes	8.0	7.2	9.3	7.2	7.5	10.4	8.27	-30.00



Tidyverse

dplyr
ggplot2
TIBBLE
readr
tidyr
purrr

What is the tidyverse

The tidyverse is an opinionated collection of R packages designed for data science. All packages share an underlying design philosophy, grammar, and data structures.

- ggplot2: a system for creating graphics (**G**rammar of **G**raphics)
- dplyr: a system for data manipulation
- tidyr: functions for tidying data
- readr: a system for reading in data
- purrr: functional programming in R
- string: system for working with strings
- forcats: system for working with factors (categorical

ggplot

Step 1: Initiate your data and aesthetics

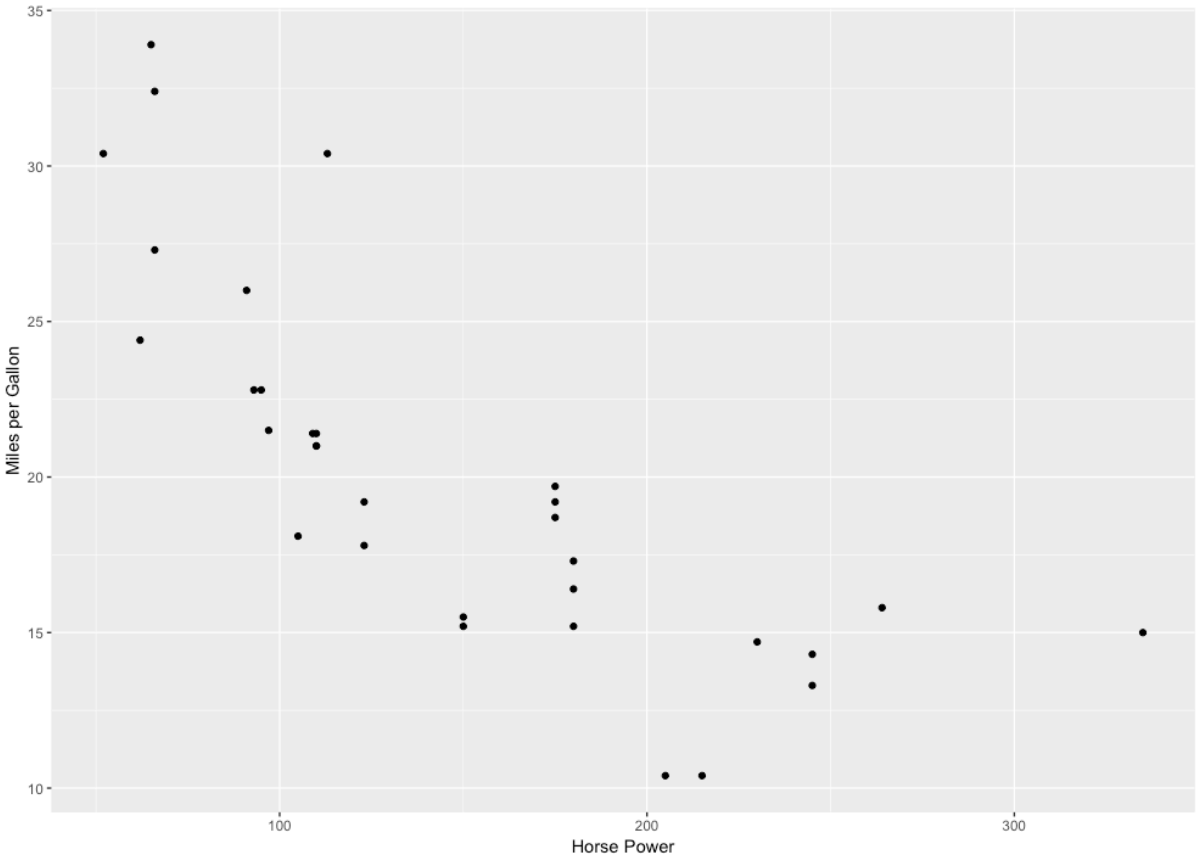
```
ggplot(mtcars, aes(x=hp, y=mpg))
```

Step 2: Apply geometry

```
geom_point()
```

Step 2: Refine

```
labs(y="Miles per Gallon", x = "Horse Power")
```

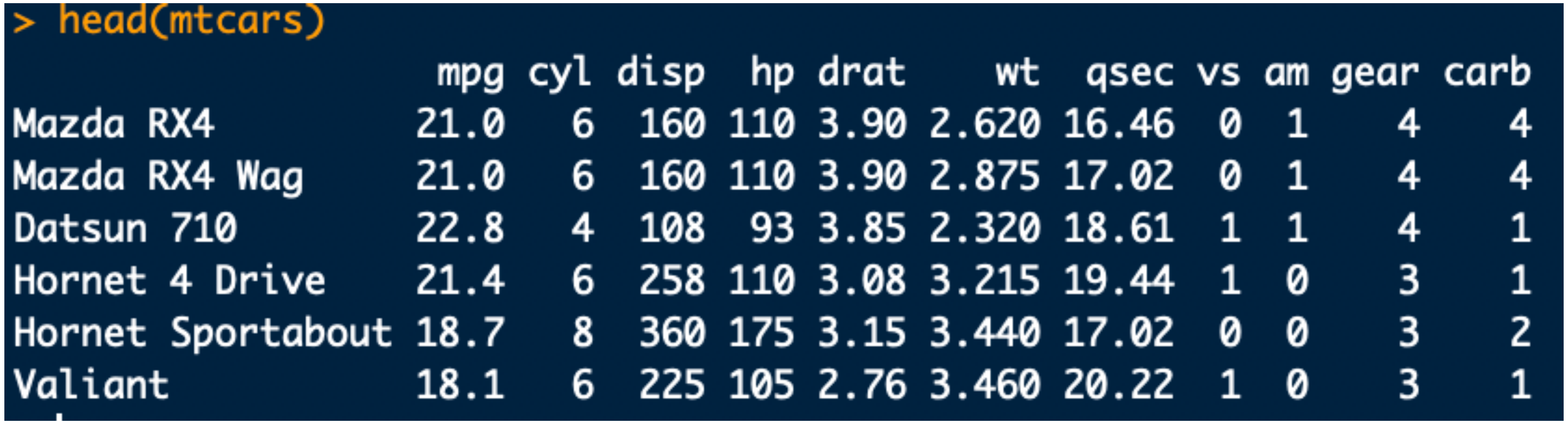


```
ggplot(mtcars, aes(x=hp, y=mpg)) +
   geom_point() +
   labs(y="Miles per Gallon", x = "Horse Power")
```

dplyr

- **mutate()** adds new variables that are functions of existing variables
- **select()** picks variables based on their names
- **filter()** picks cases based on their values
- **summarise()** reduces multiple values down to a single summary
- **arrange()** changes the ordering of the rows

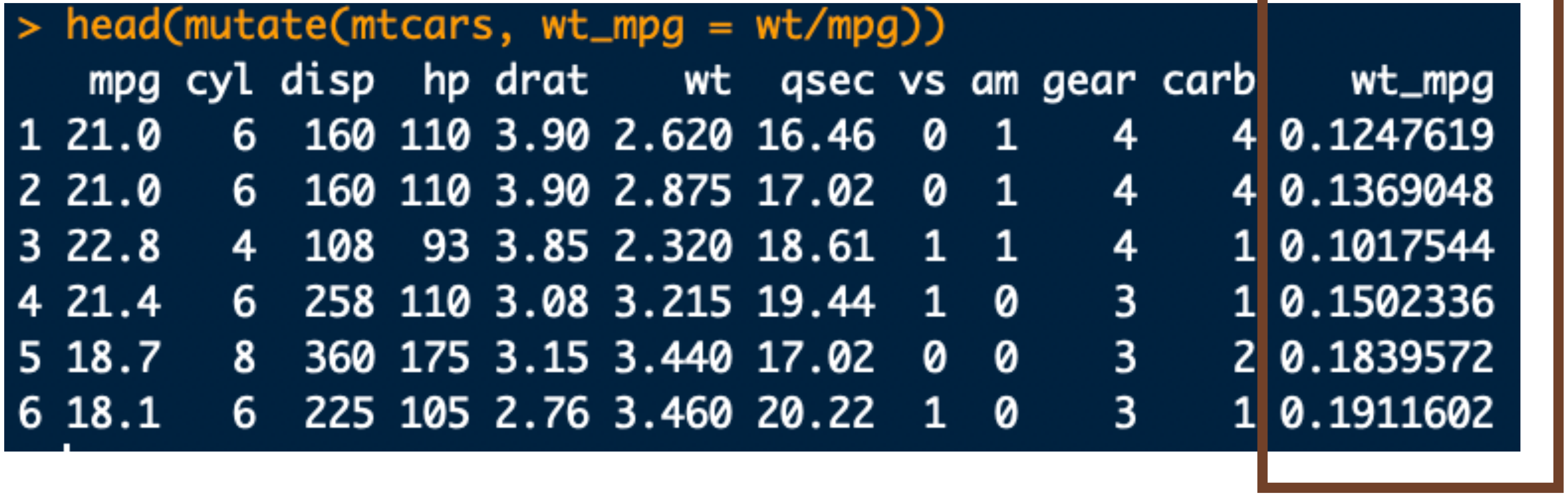
dplyr::mutate



```
> head(mtcars)
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

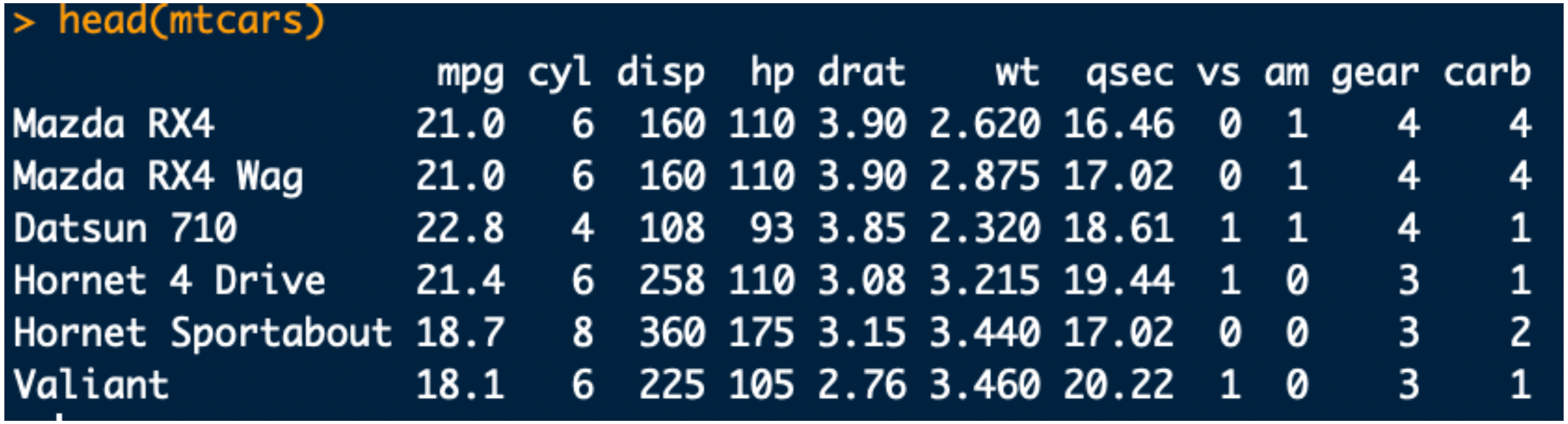
mutate

mutate(mtcars, wt_mpg = wt/mpg)



```
> head(mutate(mtcars, wt_mpg = wt/mpg))
   mpg cyl disp  hp drat    wt  qsec vs am gear carb    wt_mpg
1 21.0   6  160 110 3.90 2.620 16.46  0  1    4    4 0.1247619
2 21.0   6  160 110 3.90 2.875 17.02  0  1    4    4 0.1369048
3 22.8   4  108  93 3.85 2.320 18.61  1  1    4    1 0.1017544
4 21.4   6  258 110 3.08 3.215 19.44  1  0    3    1 0.1502336
5 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2 0.1839572
6 18.1   6  225 105 2.76 3.460 20.22  1  0    3    1 0.1911602
```

dplry::select

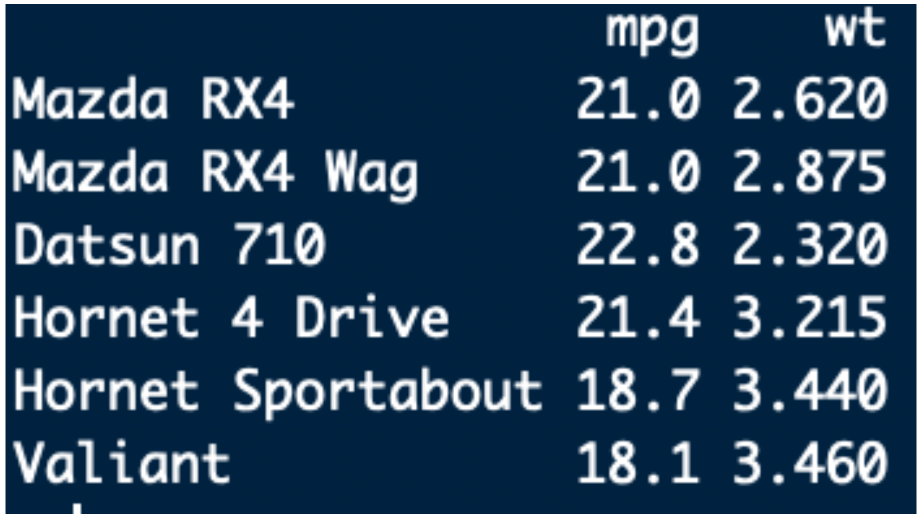


```
> head(mtcars)
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

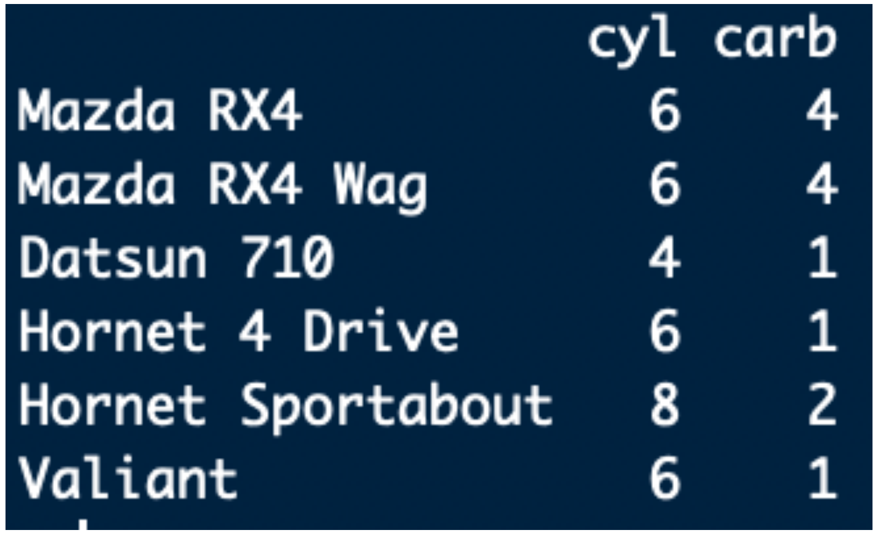
select

select(mtcars, mpg, wt)

select(mtcars, starts_with(c))

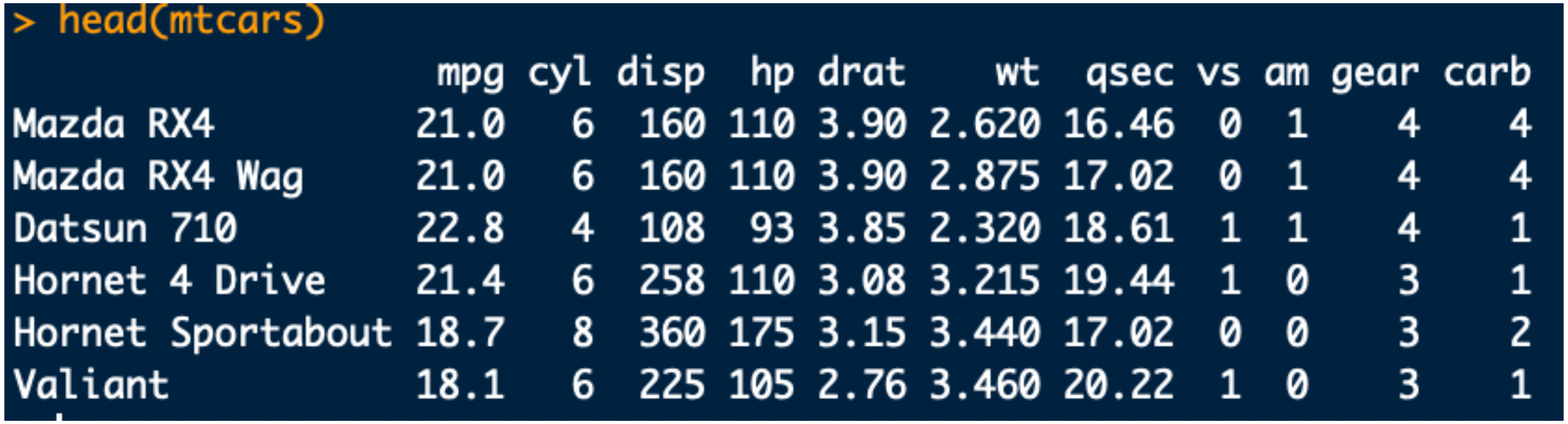


```
                   mpg    wt
Mazda RX4         21.0 2.620
Mazda RX4 Wag     21.0 2.875
Datsun 710        22.8 2.320
Hornet 4 Drive    21.4 3.215
Hornet Sportabout 18.7 3.440
Valiant           18.1 3.460
```



```
                  cyl carb
Mazda RX4           6    4
Mazda RX4 Wag       6    4
Datsun 710          4    1
Hornet 4 Drive      6    1
Hornet Sportabout   8    2
Valiant             6    1
```

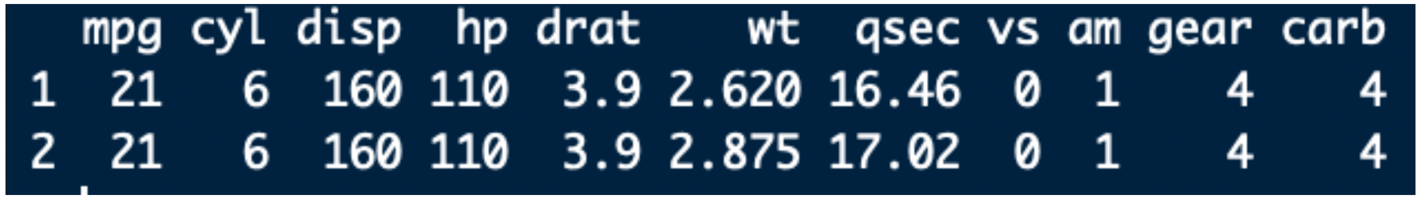
dplyr::filter



```
> head(mtcars)
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

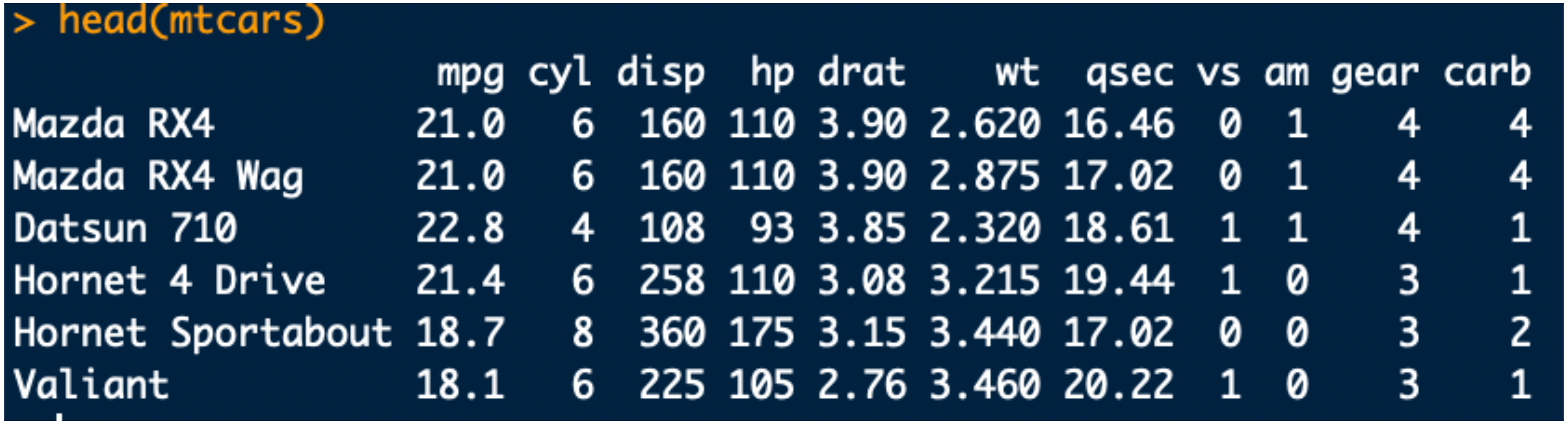
filter

filter(mtcars, mpg > 20 & carb == 4)



```
  mpg cyl disp  hp drat    wt  qsec vs am gear carb
1  21   6  160 110  3.9 2.620 16.46  0  1    4    4
2  21   6  160 110  3.9 2.875 17.02  0  1    4    4
```

dplyr::summarise

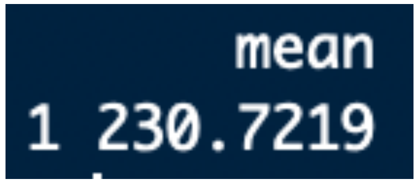


```
> head(mtcars)
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

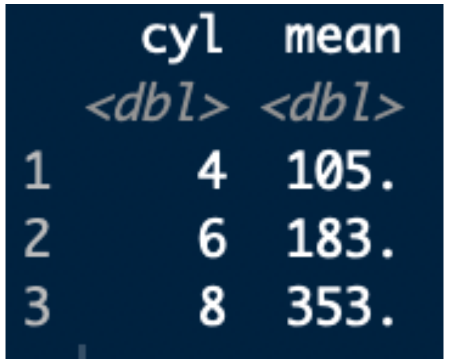
summarise

summarise(mtcars, mean = mean(disp))

```
mtcars %>%
    group_by(cyl) %>%
    summarise(mean = mean(disp))
```



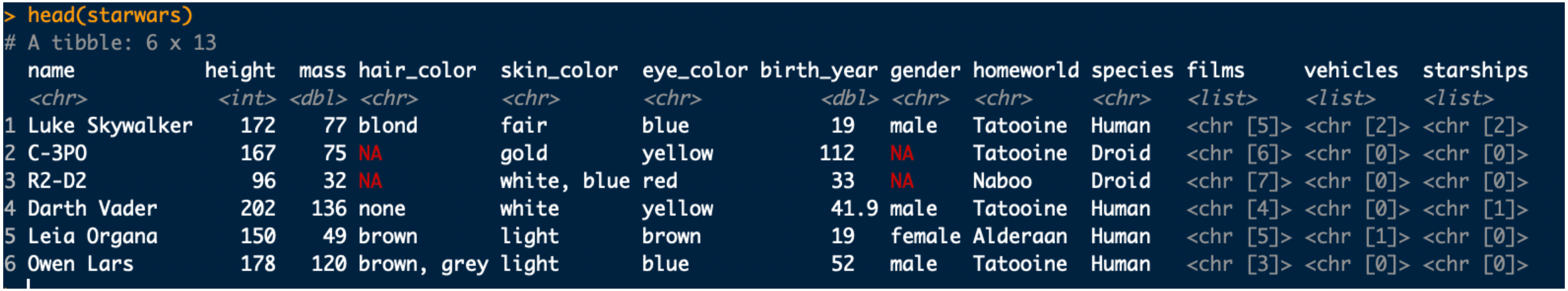
```
      mean
1 230.7219
```



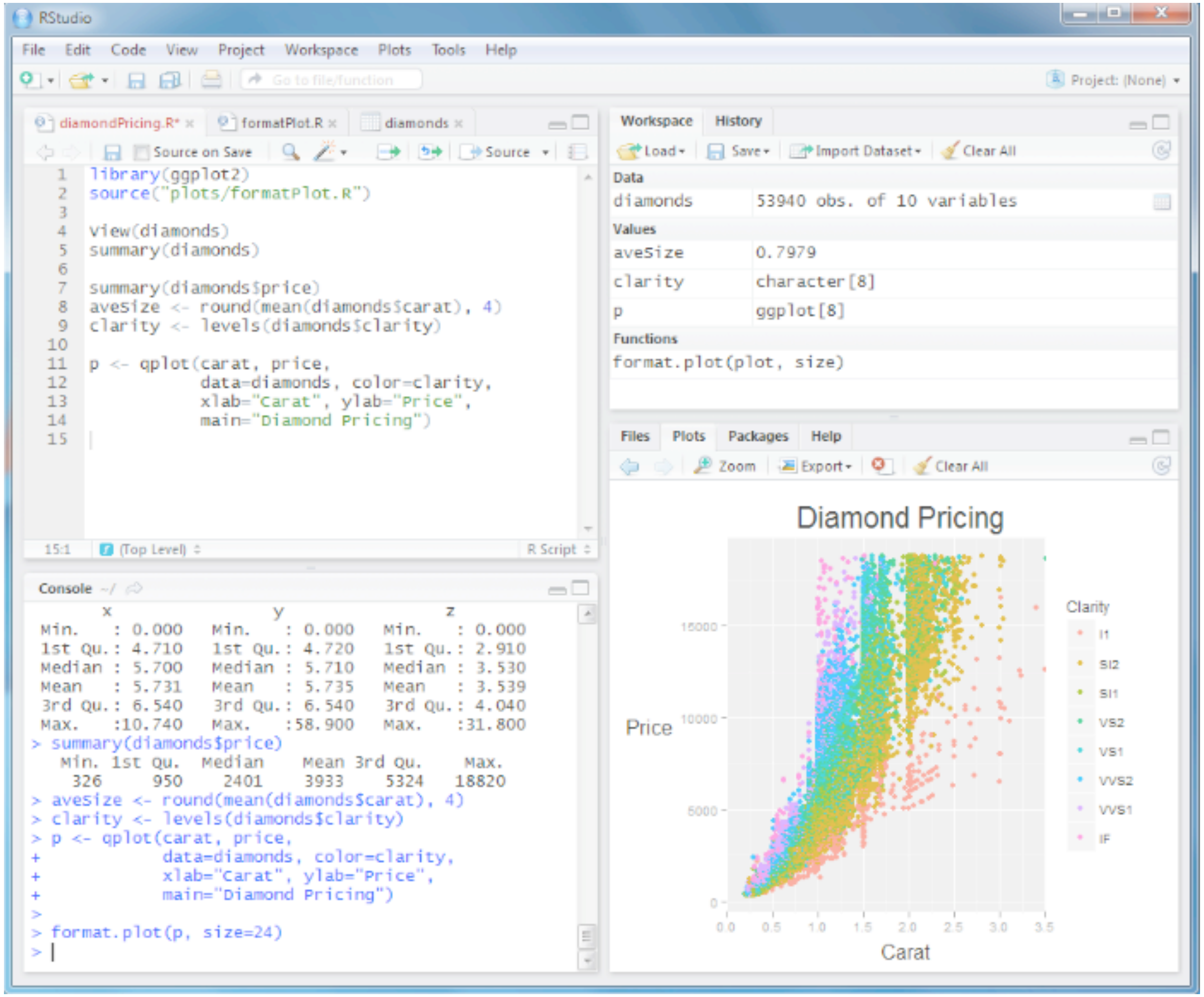
```
    cyl  mean
  <dbl> <dbl>
1     4  105.
2     6  183.
3     8  353.
```

tidyverse example

- Starwars data set



```
> head(starwars)
# A tibble: 6 x 13
  name           height  mass hair_color skin_color  eye_color birth_year gender homeworld species films     vehicles  starships
  <chr>           <int> <dbl> <chr>      <chr>       <chr>          <dbl> <chr>  <chr>     <chr>   <list>    <list>    <list>
1 Luke Skywalker    172    77 blond      fair        blue            19   male   Tatooine  Human   <chr [5]> <chr [2]> <chr [2]>
2 C-3PO             167    75 NA         gold        yellow         112   NA     Tatooine  Droid   <chr [6]> <chr [0]> <chr [0]>
3 R2-D2              96    32 NA         white, blue red             33   NA     Naboo     Droid   <chr [7]> <chr [0]> <chr [0]>
4 Darth Vader       202   136 none       white       yellow          41.9 male   Tatooine  Human   <chr [4]> <chr [0]> <chr [1]>
5 Leia Organa       150    49 brown      light       brown           19   female Alderaan  Human   <chr [5]> <chr [1]> <chr [0]>
6 Owen Lars         178   120 brown, grey light       blue            52   male   Tatooine  Human   <chr [3]> <chr [0]> <chr [0]>
```



```r
library(ggplot2)
source("plots/formatPlot.R")

View(diamonds)
summary(diamonds)

summary(diamonds$price)
aveSize <- round(mean(diamonds$carat), 4)
clarity <- levels(diamonds$clarity)

p <- qplot(carat, price,
           data=diamonds, color=clarity,
           xlab="Carat", ylab="Price",
           main="Diamond Pricing")
```

Data

diamonds	53940 obs. of 10 variables

Values

aveSize	0.7979
clarity	character[8]
p	ggplot[8]

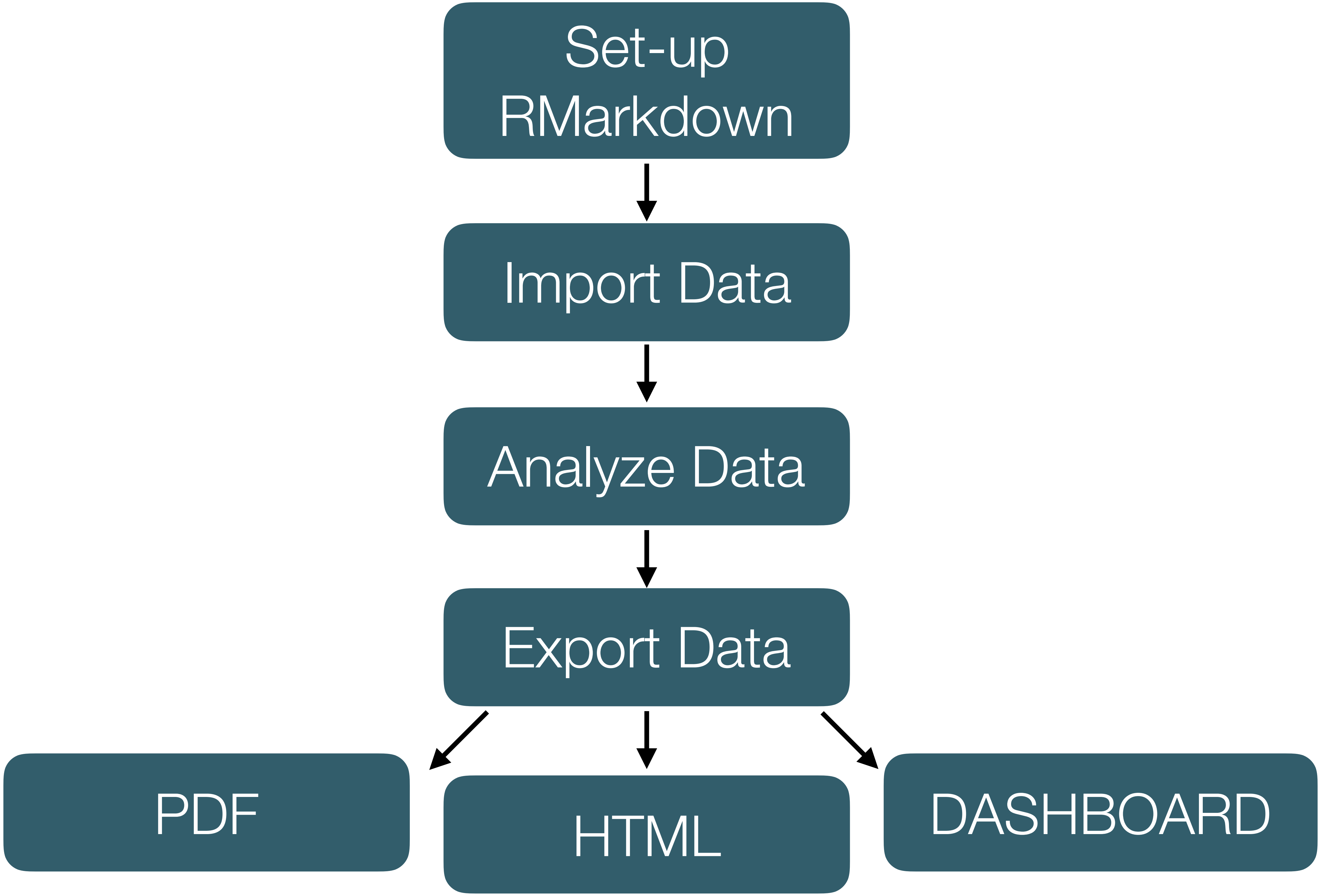
Functions

format.plot(plot, size)

```
       x                y                z
 Min.   : 0.000   Min.   : 0.000   Min.   : 0.000
 1st Qu.: 4.710   1st Qu.: 4.720   1st Qu.: 2.910
 Median : 5.700   Median : 5.710   Median : 3.530
 Mean   : 5.731   Mean   : 5.735   Mean   : 3.539
 3rd Qu.: 6.540   3rd Qu.: 6.540   3rd Qu.: 4.040
 Max.   :10.740   Max.   :58.900   Max.   :31.800
> summary(diamonds$price)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    326     950    2401    3933    5324   18820
> aveSize <- round(mean(diamonds$carat), 4)
> clarity <- levels(diamonds$clarity)
> p <- qplot(carat, price,
+            data=diamonds, color=clarity,
+            xlab="Carat", ylab="Price",
+            main="Diamond Pricing")
>
> format.plot(p, size=24)
> |
```

Basic Data Science Workflow with R and RStudio

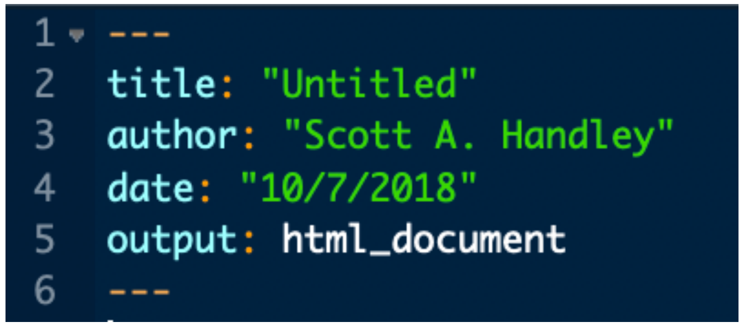
R Analysis Workflow Overview



RMarkdown

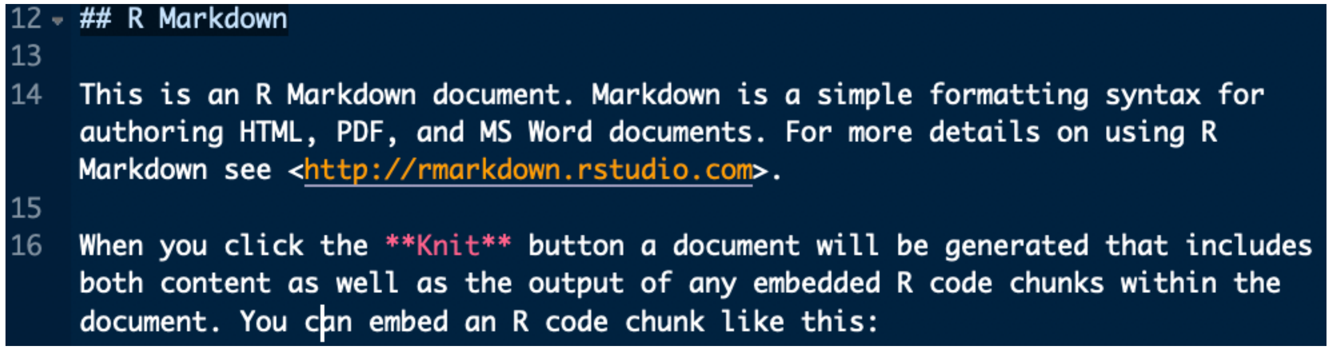
YAML

Yet **A**nother **M**arkdown **L**anguage



```
---
title: "Untitled"
author: "Scott A. Handley"
date: "10/7/2018"
output: html_document
---
```

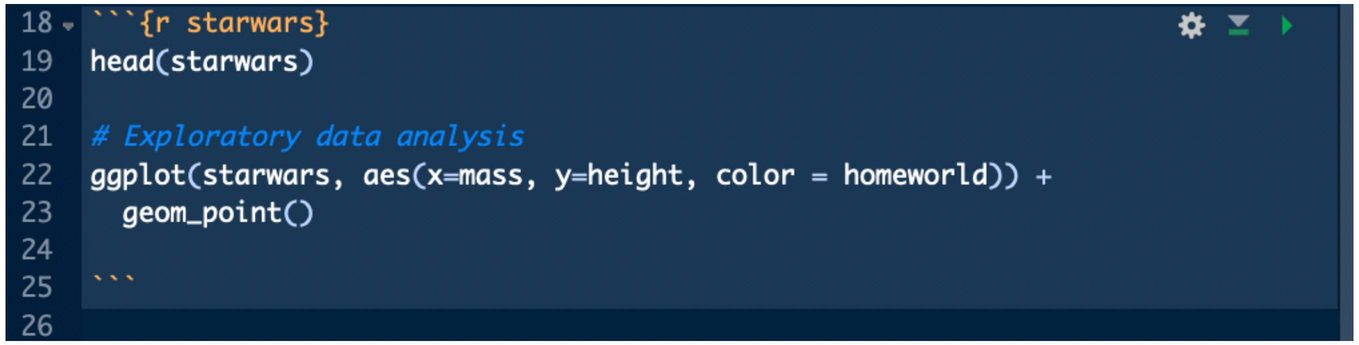
TEXT



```
## R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:
```

CHUNK

```{r title}

contents

```



~~~
```{r starwars}
head(starwars)

# Exploratory data analysis
ggplot(starwars, aes(x=mass, y=height, color = homeworld)) +
  geom_point()

```
~~~

CHUNK

TEXT

. . .

EXAMPLE: Star Wars Data