An Introduction to R

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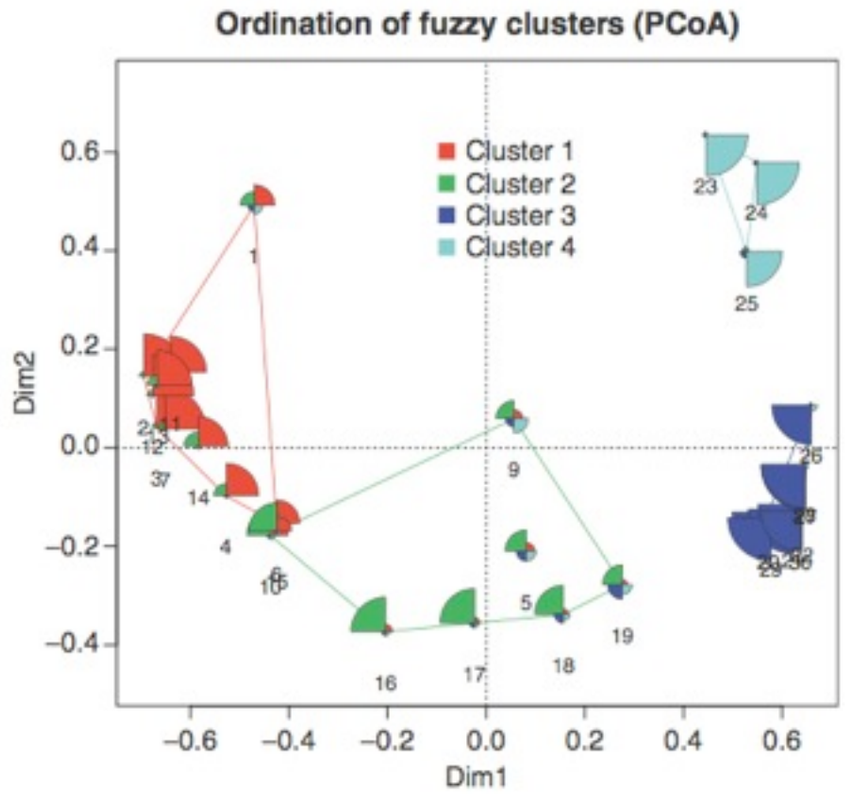
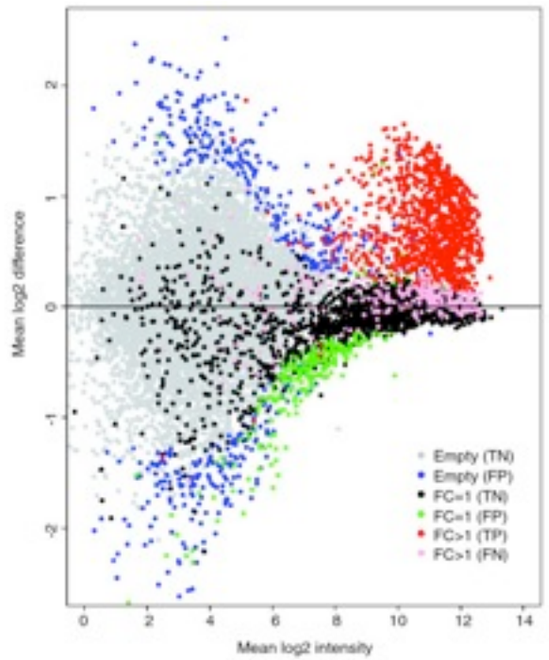
Goals

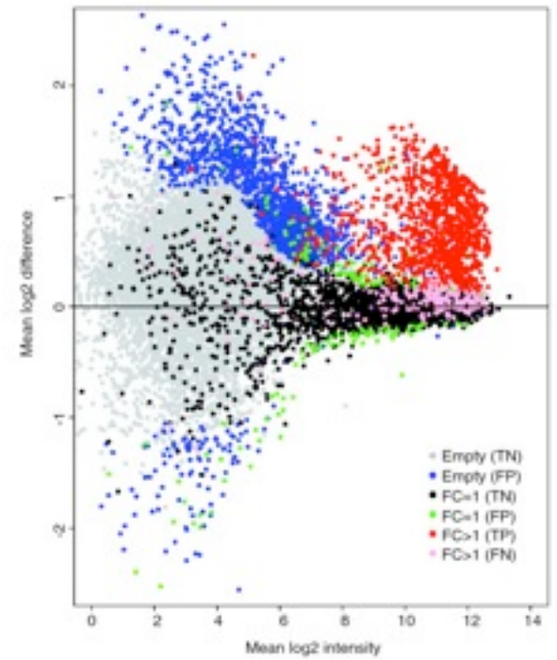
- Mechanical, not theoretical
- Upon leaving, you should be able to:
  - Get data into and out of R
  - Install specialized packages
  - Complete basic summary statistics on a set of data
  - Graph data

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
- Cutting-edge graphical data visualization
- Development
  - High-level interpreted language to prototype new computational methods
  - Active development and dedicated community
- 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
- Take an on-line course (https://www.coursera.org/course/compdata)

Why is R Useful for Biologists

- Bioconductor (http://bioconductor.org)
  - 671 packages (4/25/2013):
    - 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 (exploratory data analysis, not hypothesis testing. Ex. PCA, PCoA)
    - 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

- Ubuntu

```
sudo apt-get update
sudo apt-get install r-base r-base dev
```

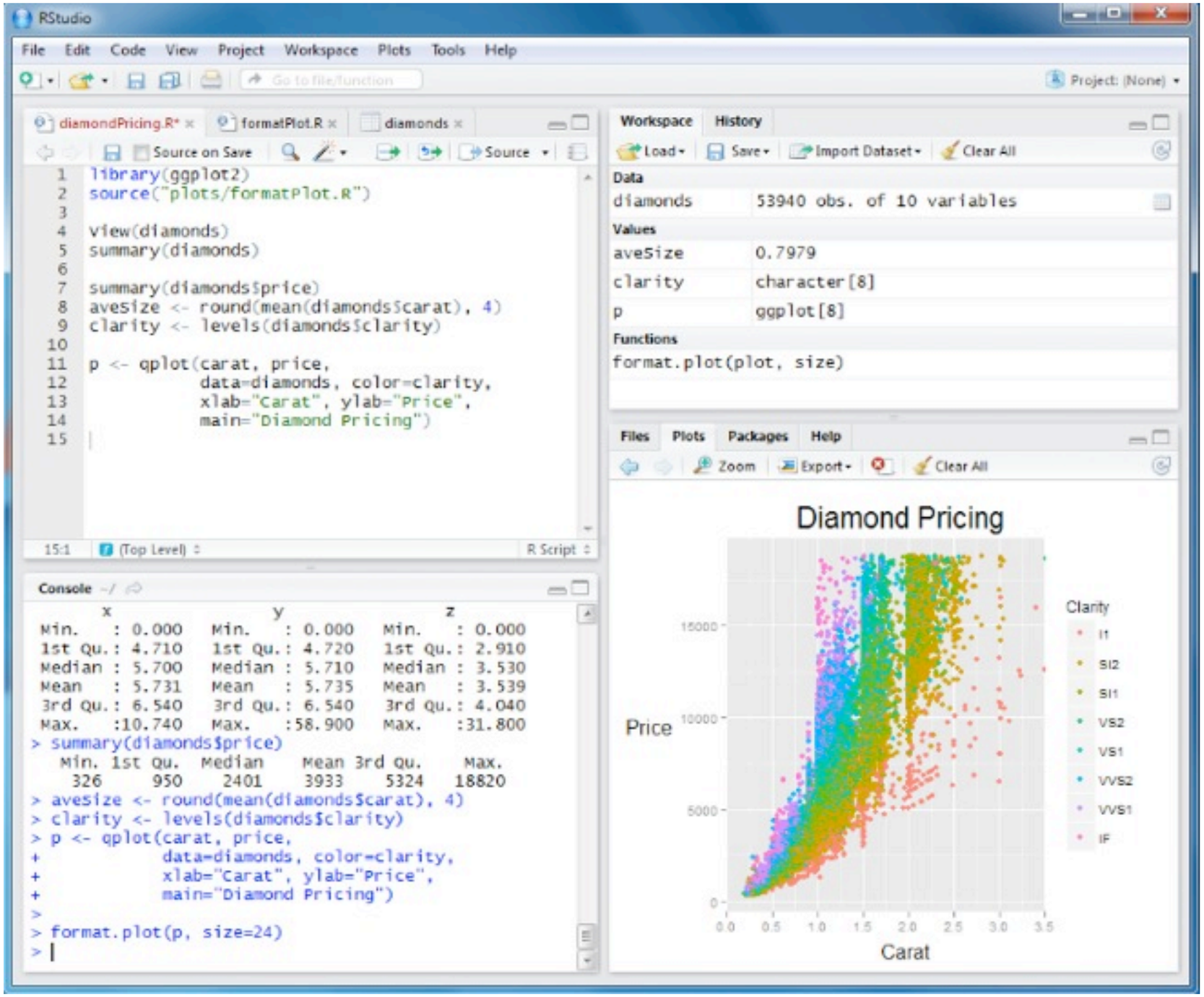
... or use the Ubuntu package manager

- Install directly from CRAN (The **C**omprehensive **R** **A**rchive **N**etwork)
  - http://cran.r-project.org/bin/macosx/

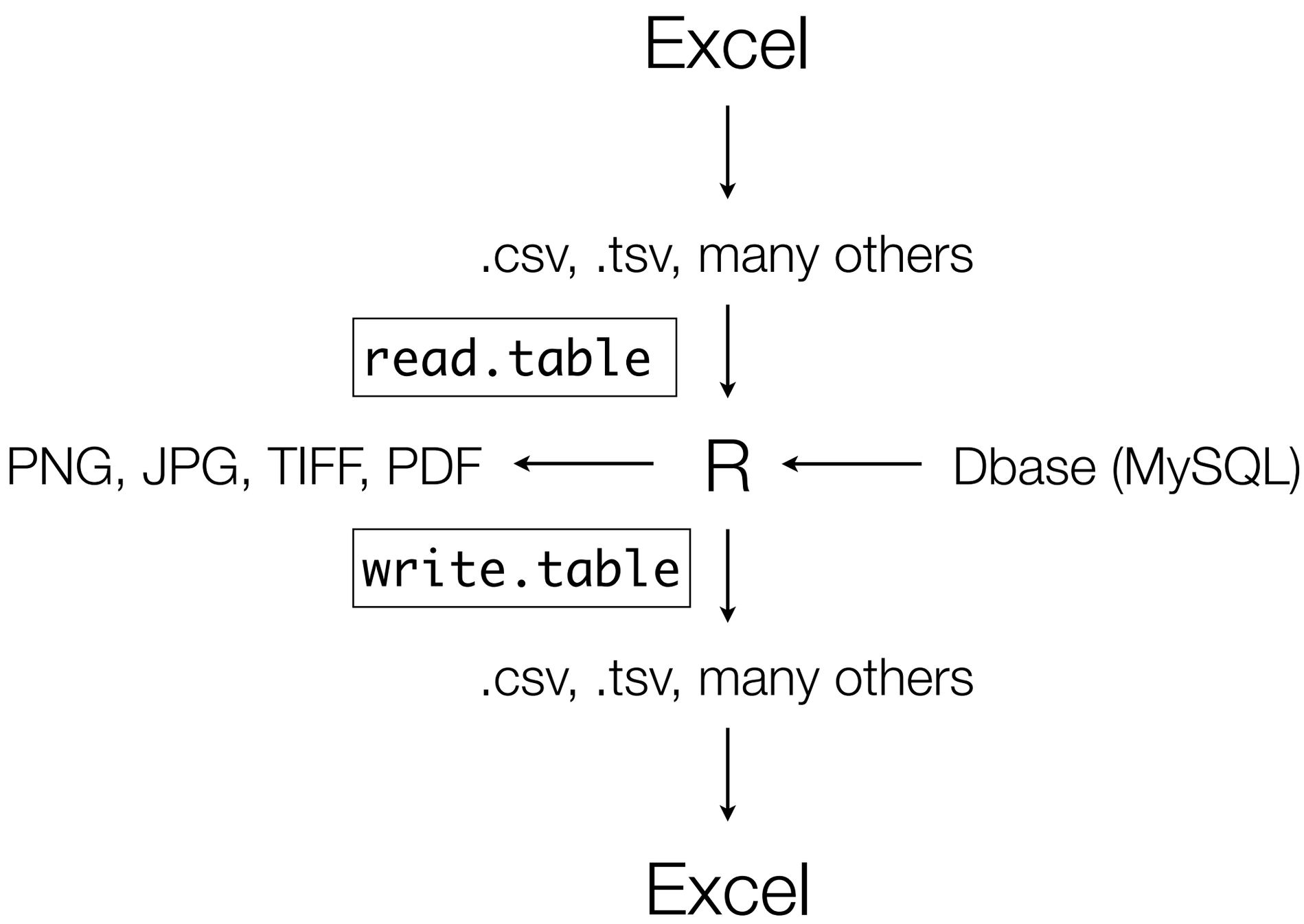
Running R

- Install a R Integrated Development Environment (IDE)
    - RStudio: http://www.rstudio.com
    - R Commander: http://socserv.mcmaster.ca/jfox/Misc/Rcmdr/
    - Both projects can make working with R much easier, particularly for a new R user
        - Both IDE's run on Windows, Mac or Linux OS
- Or from the command line, type R
    - Useful for scripting

R Studio


RStudio
File Edit Code View Project Workspace Plots Tools Help
Project: (None)
diamondPricing.R* formatPlot.R diamonds
Source on Save
Source
1 library(ggplot2)
2 source("plots/formatPlot.R")
3
4 view(diamonds)
5 summary(diamonds)
6
7 summary(diamonds$price)
8 avesize <- round(mean(diamonds$carat), 4)
9 clarity <- levels(diamonds$clarity)
10
11 p <- qplot(carat, price,
12 data=diamonds, color=clarity,
13 xlab="Carat", ylab="Price",
14 main="Diamond Pricing")
15
15:1 (Top Level) R Script
Console ~/
x y z
Min. : 0.000 Min. : 0.000 Min. : 0.000
1st Qu.: 4.710 1st Qu.: 4.720 1st Qu.: 2.910
Median : 5.700 Median : 5.710 Median : 3.530
Mean : 5.731 Mean : 5.735 Mean : 3.539
3rd Qu.: 6.540 3rd Qu.: 6.540 3rd Qu.: 4.040
Max. :10.740 Max. :58.900 Max. :31.800
> summary(diamonds$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)
>
Workspace History
Load Save Import Dataset Clear All
Data
diamonds 53940 obs. of 10 variables
Values
aveSize 0.7979
clarity character[8]
p ggplot[8]
Functions
format.plot(plot, size)
Files Plots Packages Help
Zoom Export Clear All
Diamond Pricing
Price
Carat
Clarity
I1
SI2
SI1
VS2
VS1
VVS2
VVS1
IF
15000
10000
5000
0
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5

Getting data into and out of R (one example)



Advanced Interactive Visualization Outputs

Interactive Scatterplot Matrix

http://healthviz.appspot.com/display/hs_43002

Interactive HeatMap

http://healthviz.appspot.com/display/hs_64003

Not R, but another great example

http://www.brown.edu/Faculty/Dunn_Lab/

Getting Started

1) Open RStudio
2) Get familiar with the interface
3) Set a working directory (setwd)

no_whitespace_

cAsE_seNsItive*

* You can have whitespace separating commands, just not within commands or filenames. Just don't do it. If something isn't working it is due to whitespace or the wrong case 75% of the time

Creating Data in R

Create a simple data frame

```
n = c(2,3,5)
s = c("aa", "bb", "cc")
b = c(TRUE, FALSE, TRUE)
df = data.frame(n,s,b)
df
```

```
> df
  n  s     b
1 2 aa  TRUE
2 3 bb FALSE
3 5 cc  TRUE
```

Note: *c* stands for *combine*

Calling Positions Within a Data Frame

Convention

```
data.frame[row,column]
df[1,1]
df[1,2]
df[1:3,1]
df[1,1:2]
df.2 <- df[-1,-2]
```

```
> df
  n  s     b
1 2 aa  TRUE
2 3 bb FALSE
3 5 cc  TRUE
```

Data in R

	taxon_1	taxon_2	taxon_3	taxon_4	taxon_5
control_1	10	43	143	506	6004
control_2	8	53	198	786	5647
exper_1	120	67	212	103	5674
exper_2	8	89	98	978	3012
exper_3	38	12	101	1005	4056

```
data.frame[1:2,3:5]
```

r comes with many example data frames (mtcars)

Core 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
[1] 13.4
```

```
y=c(1,2,3,4,5)
>y
[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 51 103
`sum(n)`	[1] 175
`mean(n)`	[1] 35
`var(n)`	[1] 1796.5
`min(n)`	[1] 3
`max(n)`	[1] 103

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

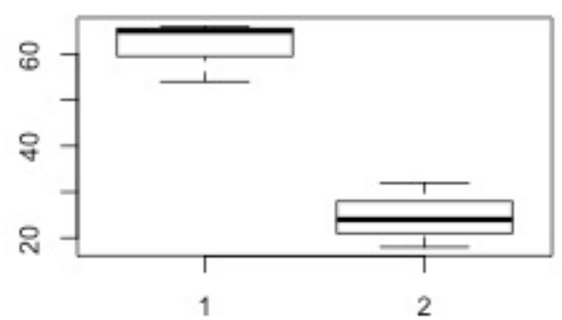
```
data.frame$proteobacteria
```

[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])
```



Functions Applied to Data Frames

tapply(): applies a function over a ranged array (data table)

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

Basic syntax:

- A **numeric** distribution
- A **factor** dividing the numeric distribution into groups
- A **function** (mean, var, sd, sum ...)

tapply()

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

What is the mean number of clostridia in Males? Females?

- numeric distribution
- factor dividing numeric distribution
- function

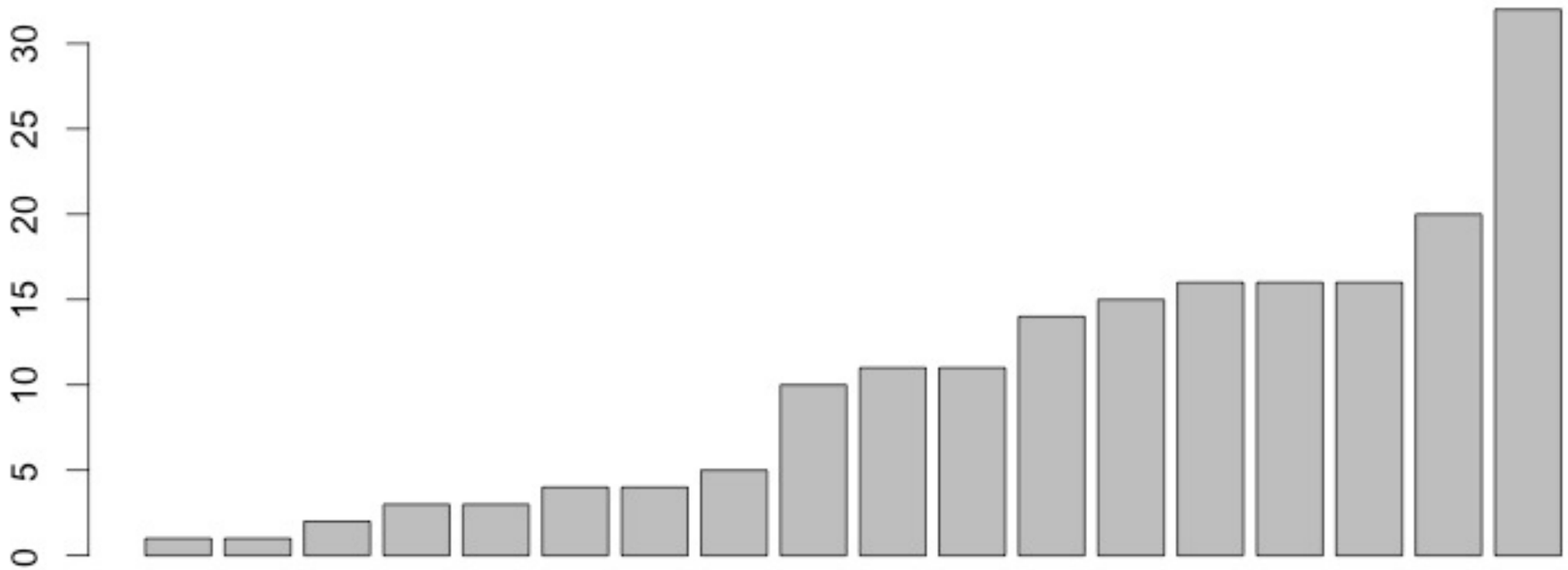
```
tapply(bac$clostridia, bac$sex, mean)
```

```
   F    M
29.00 19.25
```

Basic Visualization I

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

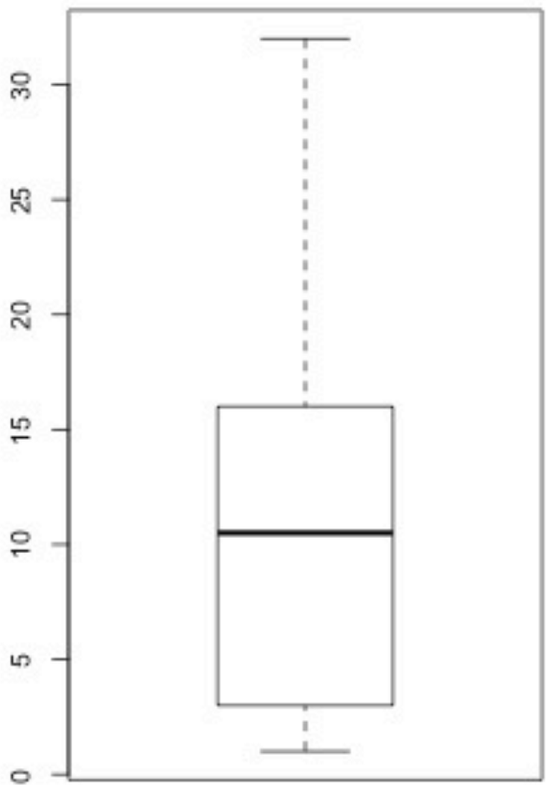
```
barplot(y)
```



Basic Visualization II

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

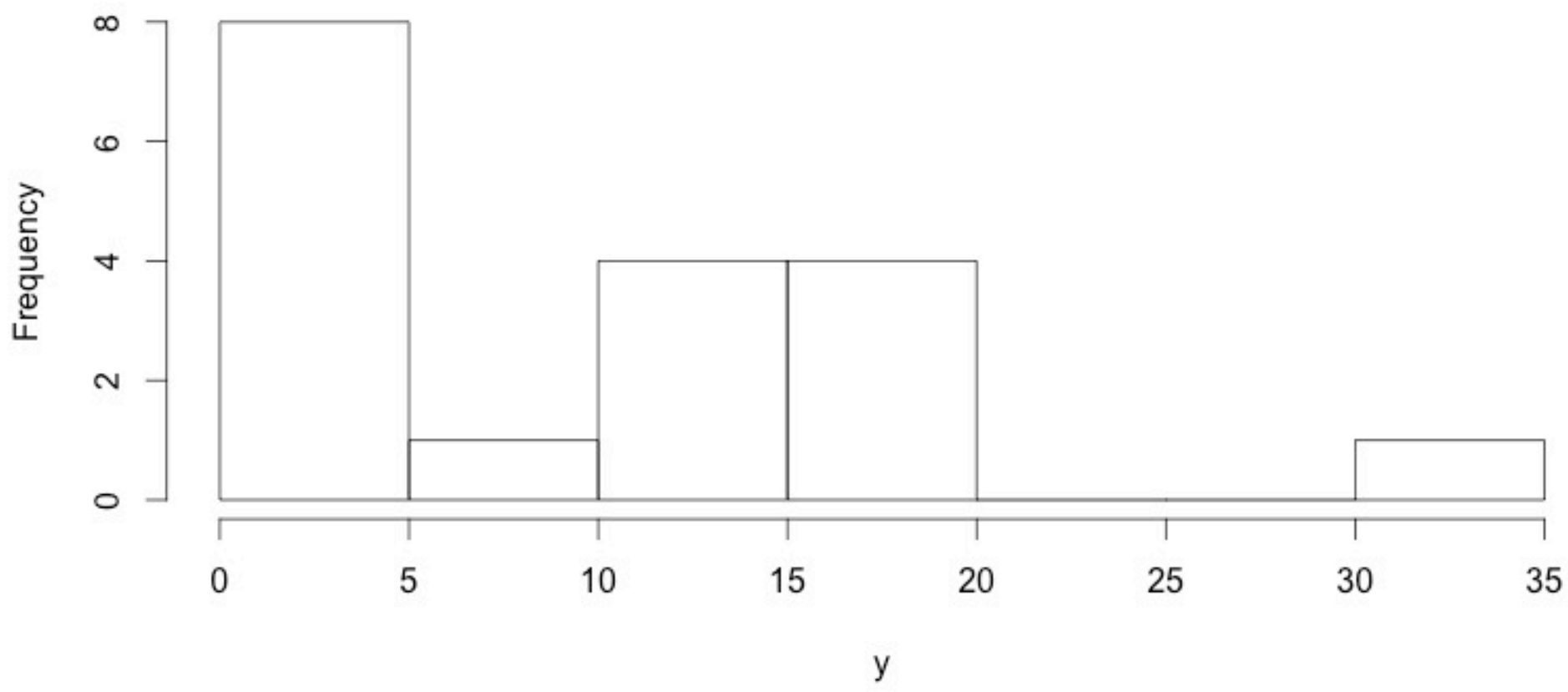
```
boxplot(y)
```



Basic Visualization III

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

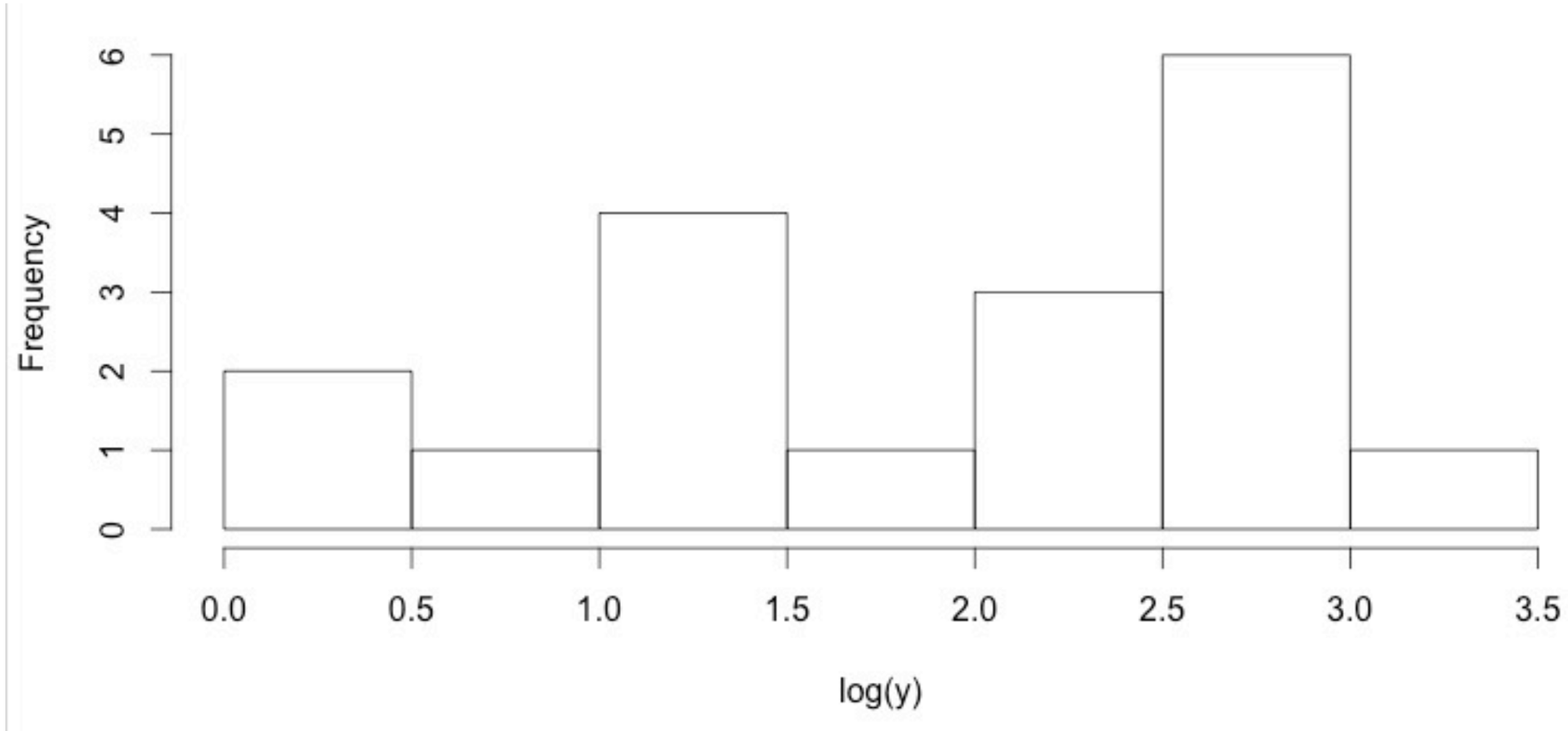
```
hist(y)
```



Basic Visualization III.i

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

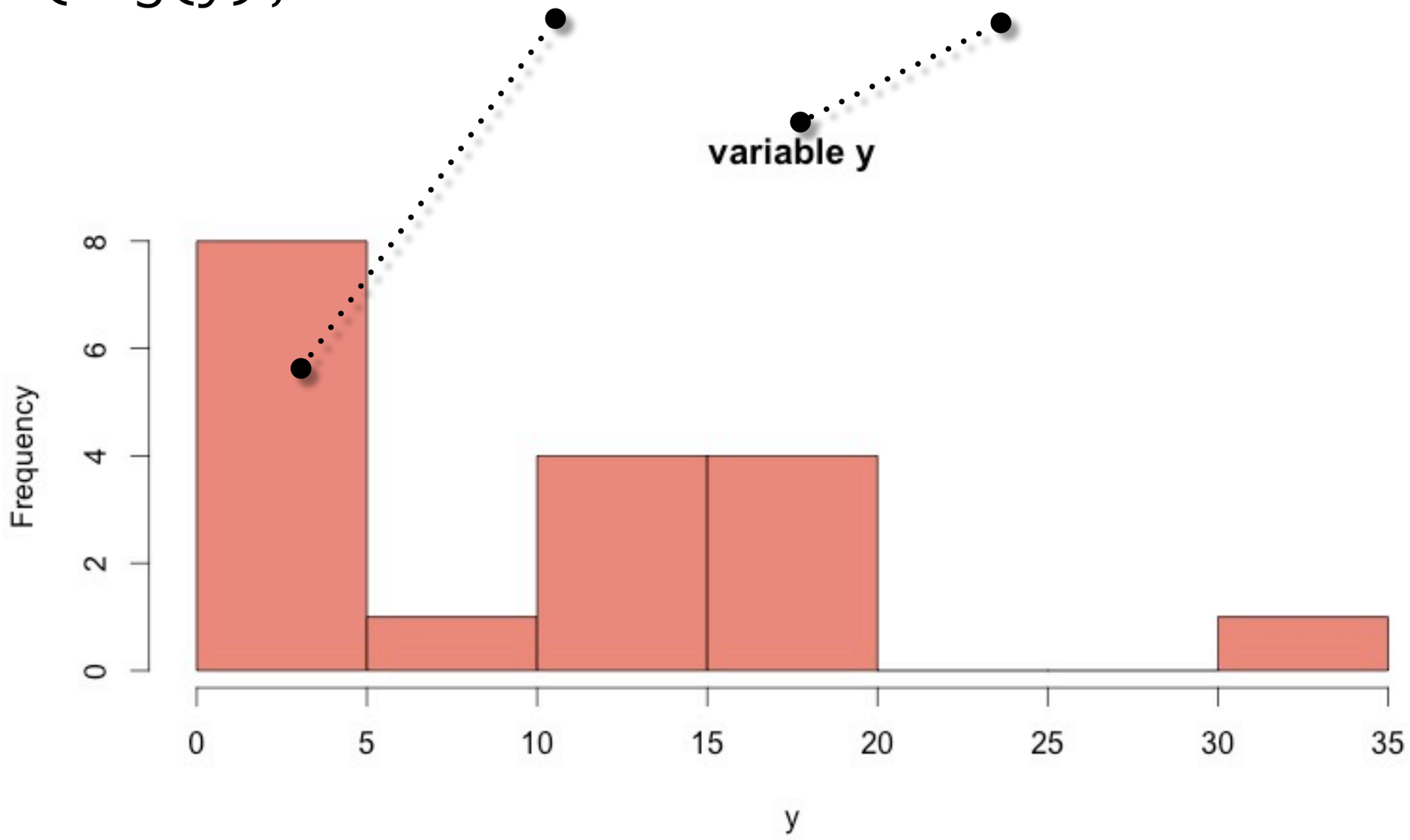
```
hist(log(y))
```



Basic Visualization III.ii

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

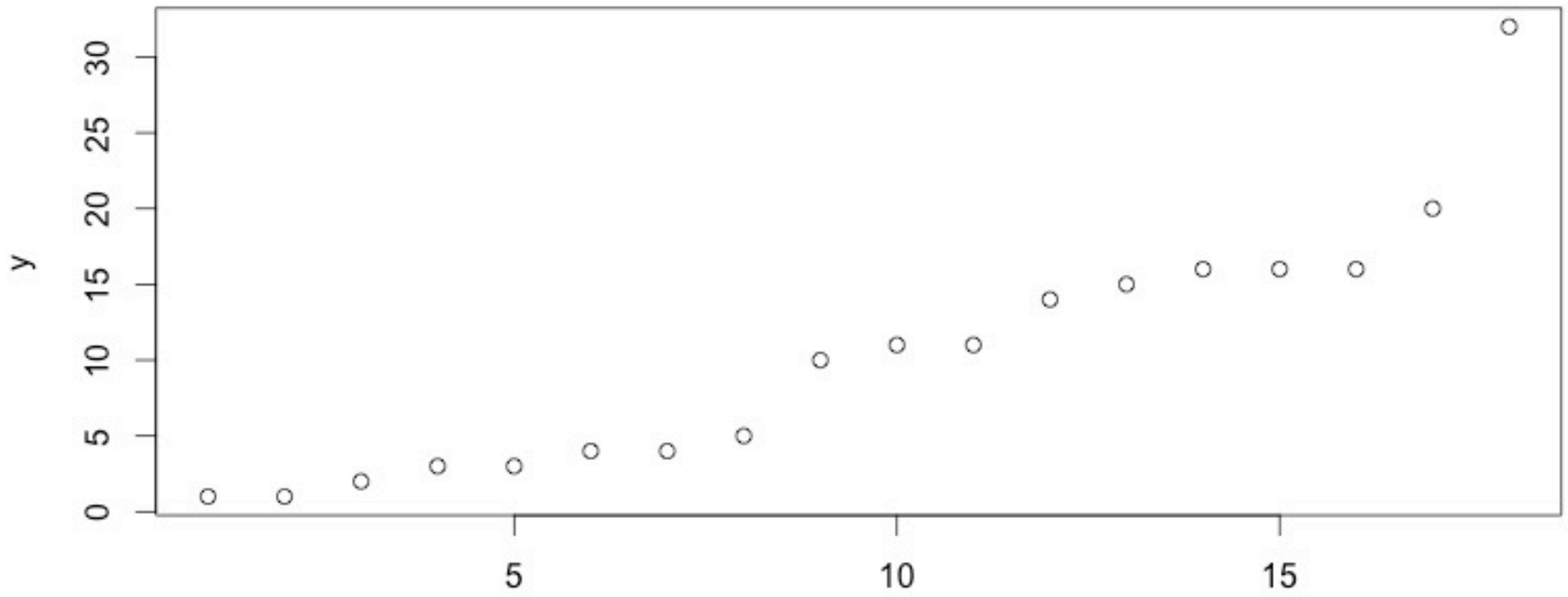
```
hist(log(y),
```



Basic Visualization IV

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

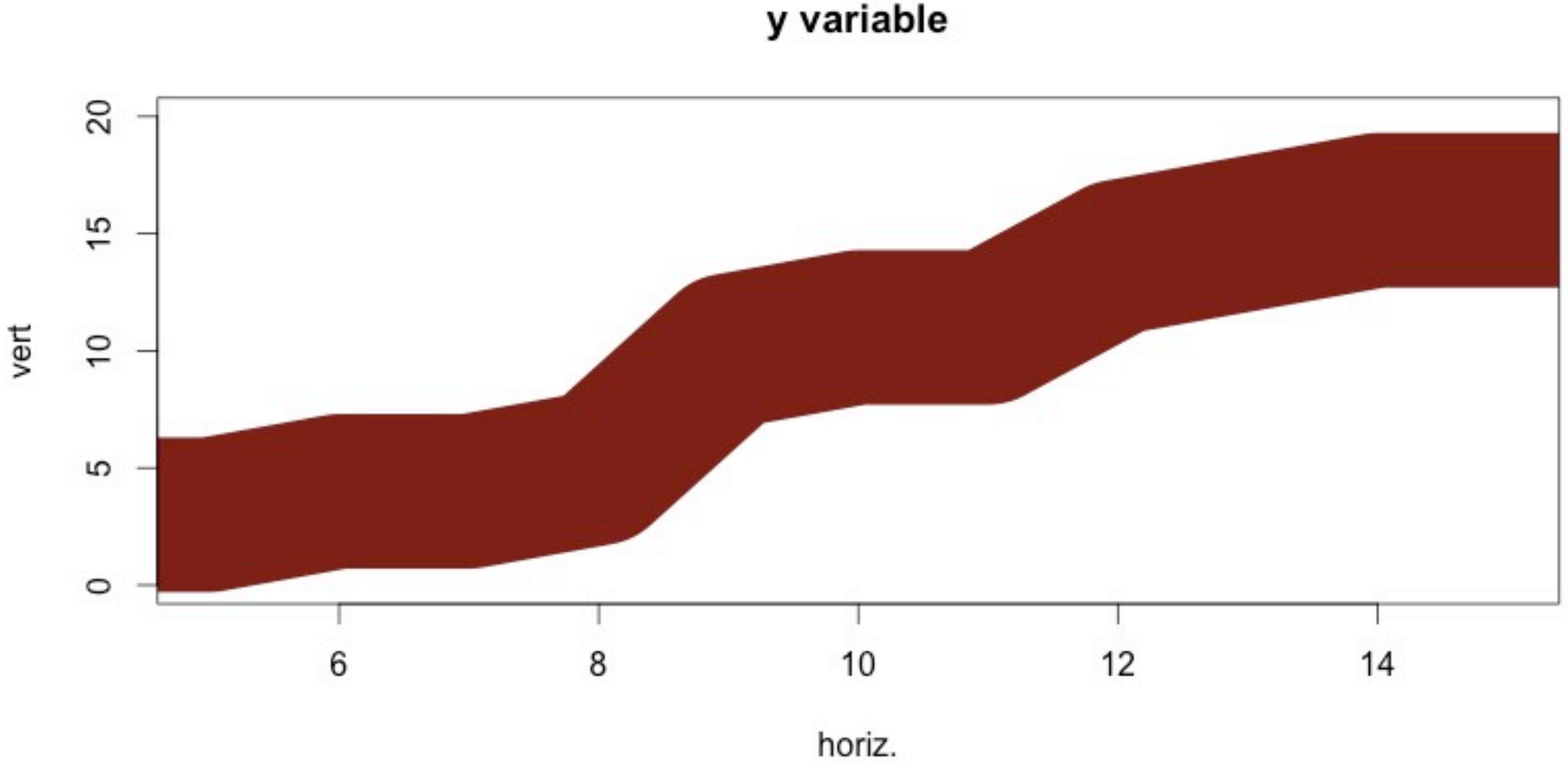
```
plot(y)
```



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}

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, ...)
```

R Documentation

`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.

Factors & Quick Summary Statistics

```
fac=as.factor(c("saint", "louis", "beer", "herpes",
"beer", "herpes"))
```

```
 levels(fac)
     [1] "beer" "herpes" "louis" “saint”
```

summary(fac)

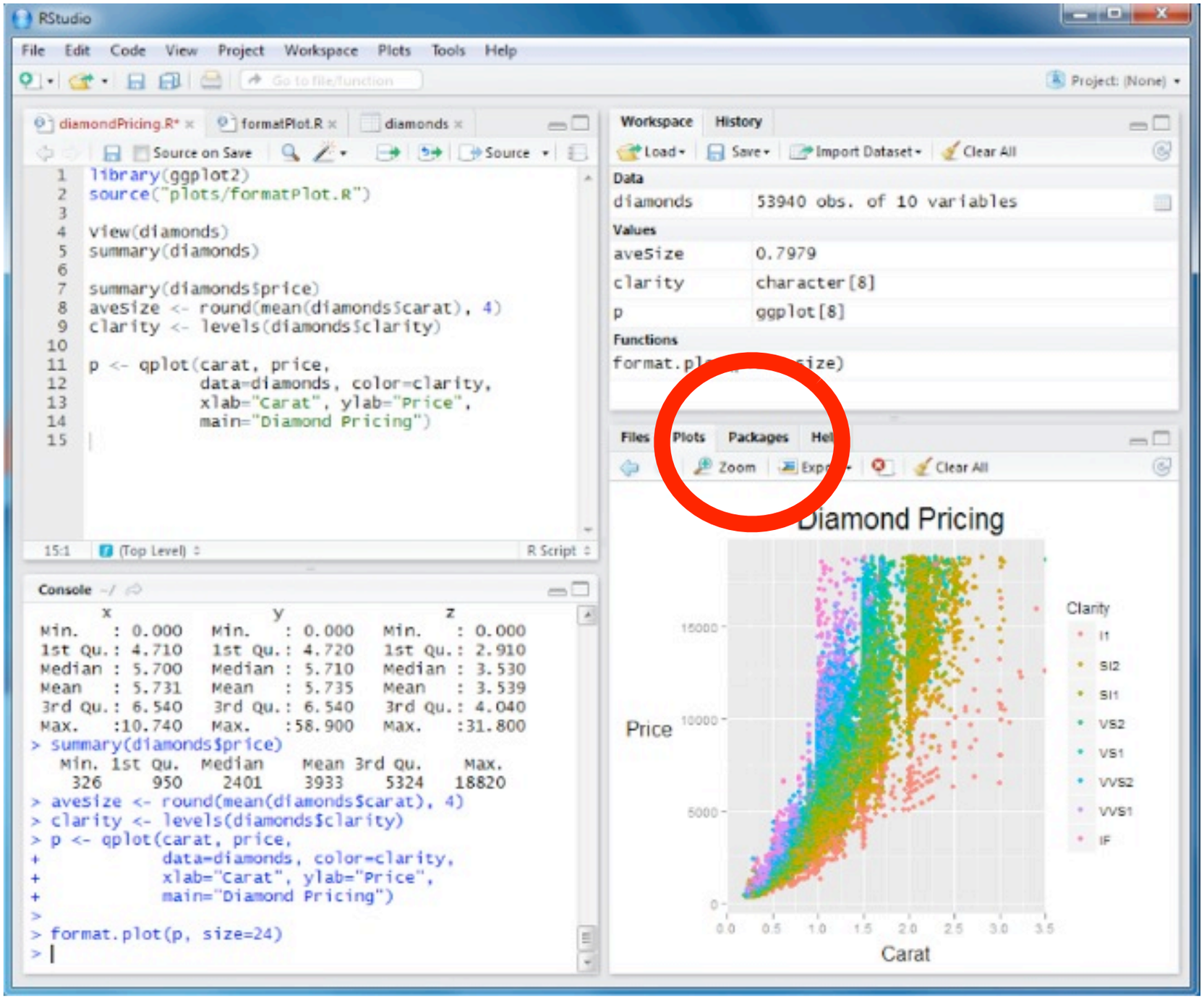
```
> summary(fac)
  beer herpes  louis  saint
     2      2      1      1
```

summary(y)

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
      1.00    3.25   10.50   10.22   15.75   32.00
```

Other Miscellaneous but Essential R Mechanics

R Mechanics - Installing Packages




```
install.packages("vegan")
```

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.

R Studio Overview

- http://evomics.org/learning/programming/introduction-to-r/