

R Statistics Essential Training



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Agenda

Module 1. Getting Started

- What is R
- Install R and RStudio
- Explore RStudio Interface
- Variables

Module 2. Data Types

- Numbers
- Text
- Vector
- Matrix
- Array
- Data Frame
- Factor
- List



Agenda

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- Packages
- Data Sets

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- Write data to file

Module 5. Charts

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- Line Plot
- Bar chart
- Boxplot
- Pie chart
- Histogram



Agenda

Module 6. Control Structures

- Conditional
- Loop
- Break & Next
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Module 7: Function

- Function syntax
- Function Example
- Function With Default Arguments
- Advanced Functions (Optional)



Agenda

Module 8. Statistical Application of R

- Basic Statistics
- Correlation
- Linear Regression
- Distributions
- Hypothesis Testing
- T - Test

Module 9. Intro to Advanced Statistics (Optional)

- ANOVA
- Chi-squared test
- Clustering



Module 1

Getting Started



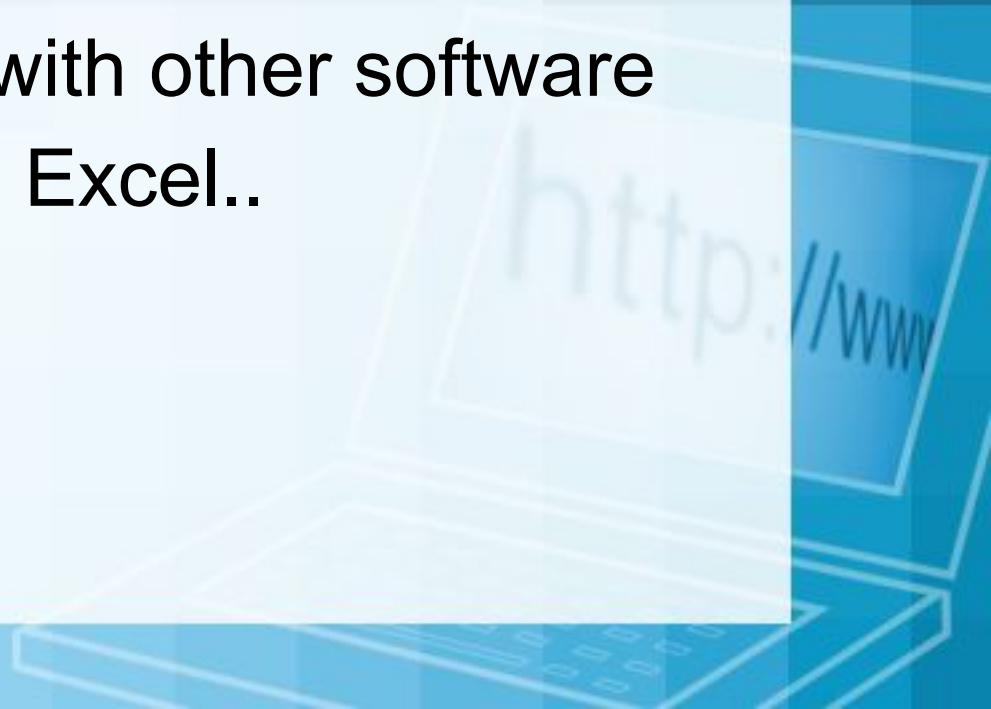
What is R?

- R was developed by Ross Ihaka and Robert Gentleman
- R is a language and environment for statistical computing and graphics
- R was developed based on S



Why R?

- R is open source and free!
- R is vector-based
- R is a programming language meant for statistics
- R can be integrated with other software such as SAS, SPSS, Excel..



R Development History



Install R

<http://cran.stat.nus.edu.sg/>



CRAN
[Mirrors](#)
[What's new?](#)
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About R
[R Homepage](#)
[The R Journal](#)

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[Manuals](#)
[FAQs](#)
[Contributed](#)

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 box, not the source code. The sources have to be compiled before you can use them. If you do not know what this means, you probably do not want to do it!

- The latest release (2015-12-10, Wooden Christmas-Tree) [R-3.2.3.tar.gz](#), read [what's new](#) in the latest version.
- Sources of [R alpha and beta releases](#) (daily snapshots, created only in time periods before a planned release).
- Daily snapshots of current patched and development versions are [available here](#). Please read about [new features and bug fixes](#) before filing corresponding feature requests or bug reports.
- Source code of older versions of R is [available here](#).
- Contributed extension [packages](#)

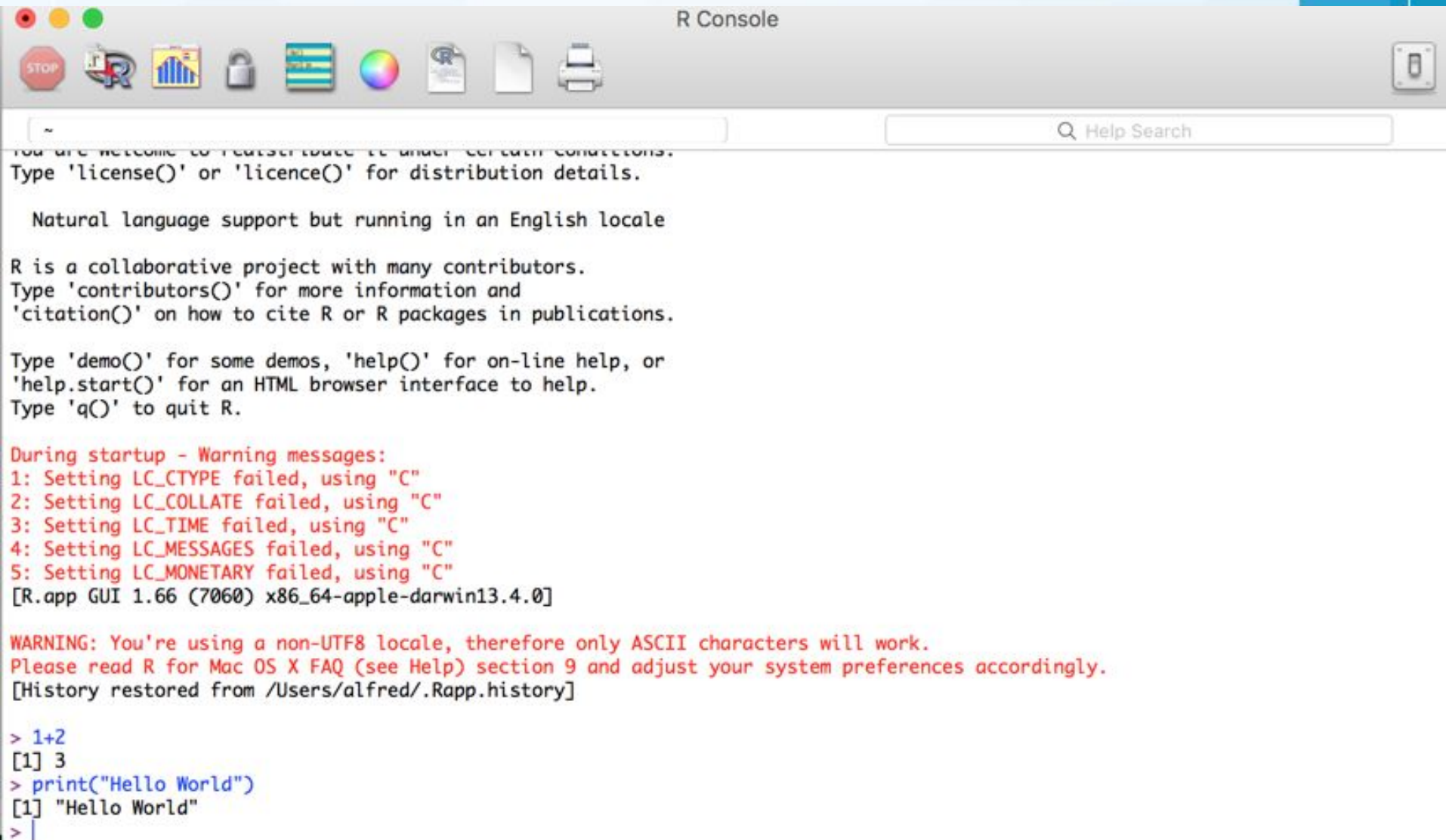
Questions About R

- 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.

What are R and CRAN?

R is 'GNU S', a freely available language and environment for statistical computing and graphics which provides a wide variety of statistical and graphical techniques: linear and nonlinear modelling, statistical tests, time series analysis, classification, clustering, etc. Please consult the [R project homepage](#) for further information.

Run R Console



```
R Console

~

You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

During startup - Warning messages:
1: Setting LC_CTYPE failed, using "C"
2: Setting LC_COLLATE failed, using "C"
3: Setting LC_TIME failed, using "C"
4: Setting LC_MESSAGES failed, using "C"
5: Setting LC_MONETARY failed, using "C"
[R.app GUI 1.66 (7060) x86_64-apple-darwin13.4.0]

WARNING: You're using a non-UTF8 locale, therefore only ASCII characters will work.
Please read R for Mac OS X FAQ (see Help) section 9 and adjust your system preferences accordingly.
[History restored from /Users/alfred/.Rapp.history]

> 1+2
[1] 3
> print("Hello World")
[1] "Hello World"
> |
```

Run R on Terminal

Type 'r' on the terminal/cmd to start r



Install R Studio IDE

<https://www.rstudio.com/>



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Blog



"The establishment of interactive feedback loops through Shiny allows us to continually optimize our decision processes."

- Marina Theodosiou, Risk Analytics Manager at [Funding Circle](#)

[Click to download the full story](#)



Powerful IDE for R

RStudio IDE is a powerful and productive user interface for R. It's free and open source, and works great on Windows,



R Packages

Our developers and expert trainers are the authors of several popular R packages, including ggplot2, plyr,



Bring R to the web

Shiny is an elegant and powerful web framework for building interactive reports and visualizations using R —

Explore RStudio Interface

RStudio File Edit Code View Plots Session Build Debug Tools Window Help 38% Mon 11 Jan 10:16 PM Alfred Ang

RStudio

Project: (None)

Environment History

Global Environment

WORKSPACE

Files Plots Packages Help Viewer

Zoom Export Publish

Histogram of Annual Canadian Lynx Trappings 1821-1934

Frequency

Number of Lynx Trapped

PACKAGE/ PLOTS/HELP

```
1 data(lynx) # Annual Canadian Lynx trappings 1821-1934
2 hist(lynx)
3
4 # Modify histogram
5 h <- hist(lynx, # Save histogram as object
6         breaks = 13, # "Suggests" 11 bins
7         breaks = seq(0, 7000, by = 100),
8         breaks = c(0, 1000, 2000, 3000, 4000, 5000, 6000, 7000),
9         freq = FALSE,
10        col = "thistle", lty = 1, las = 1, main = "Histogram of Annual Canadian Lynx Trappings\n1821-1934",
11        xlab = "Number of Lynx Trapped")
12
13 rm(list = ls()) # Clean up
```

1:1 (Top Level) R Script

Console

```
> rm(list = ls()) # Clean up
> lynx
Time Series:
Start = 1821
End = 1934
Frequency = 1
[1] 269 321 585 871 1475 2821 3928 5943 4950 2577 523 98 184 279 409 2285 2685 3409 1824 409
[21] 151 45 68 213 546 1033 2129 2536 957 361 377 225 360 731 1638 2725 2871 2119 684 299
[41] 236 245 552 1623 3311 6721 4254 687 255 473 358 784 1594 1676 2251 1426 756 299 201 229
[61] 469 736 2042 2811 4431 2511 389 73 39 49 59 188 377 1292 4031 3495 587 105 153 387
[81] 758 1307 3465 6991 6313 3794 1836 345 382 808 1388 2713 3800 3091 2985 3790 674 81 80 108
[101] 229 399 1132 2432 3574 2935 1537 529 485 662 1000 1590 2657 3396
> ?lynx
> #
```

SCRIPT

CONSOLE

Comments and Help

Single line comment

#

Help

?....

help(...)



Variables

`a <- 1` (Most common)

`a = 1`

`1 -> a`



List all variables

ls()



Clean Up the Variables

```
rm(x)
```

```
rm(a, b)
```

```
rm(list = ls())
```



Module 2

Data Types



Data Types

- Numbers
- Text
- Vector
- Matrix
- Array
- Data Frame
- Factor
- List



Numbers



Working With Numbers

2^4

`abs(-3.2)`

`round(3.4), round(5.24, digits = 1), round(5.24, 1)`

`sqrt(4)`

`cos(pi/2), factorial(3)`

`3/0`

`Inf/Inf`

`NaN` : Not a Number



Text



Splitting Text

```
a <- "Today is a good day"
```



Splitting & Joining Text

```
a <- "Today is a good day"
```

```
strsplit(a, " ")
```

```
strsplit(a, "is ")
```

```
a<-"angch"
```

```
b<-"tertiaryinfotech.com"
```

```
paste(a,b,sep="@")
```



Sorting Text

```
v <- c("Red","Blue","yellow","violet")
```

```
sort(v)
```

```
sort(v, decreasing=TRUE)
```



Vector



Create Vector Using : Operator

```
a <- 0:10
```

```
a <- 5:13
```

```
a <- 10:-4
```

`class(a)` - check the type of a

`str(a)` - check the structure of a

Create Vector Using c Operator

```
c(1,2,4)
```

```
c(1,7:9)
```

```
c('red','green',"yellow")
```

```
c(1:5, 10.5, "red")
```



Create Vector Using seq

`seq(10)`

`seq(3,20)`

`seq(3,20,3)`

`seq(1, 9, by = 2)`

`seq(from=4.5, to=2.5, by=-0.2)`

`seq(0, 1, length.out = 11)`



Application of seq

```
x<-seq(0,4*pi,length.out = 200);  
y <- sin(x);  
plot(x,y)
```



Creating Vectors Using rep -1

```
rep(3,10)
```

```
rep(1:3, 3)
```

```
rep(c(1,2,3),3)
```

```
rep(seq(3),3)
```

```
rep(seq(3),length.out=5)
```

```
rep(seq(3),len=5)
```

```
rep(1:4, each = 2)
```

```
rep(1:4, c(2,1,2,1))
```



Creating Vectors Using rep -2

```
rep(1:4, each = 2, len = 4)
```

```
rep(1:4, each = 2, len = 10)
```

```
rep(1:4, each = 2, times = 3)
```



Accessing Vector Elements

`a[5]`

`a[5:8]`

`a[5:3]`

`a[-2]` - take away the 2nd element

`a[-1:-4]`

`a[c(5, 6, 7, 8)]`



Tail and Head

tail(a)

tail(a,n=3)

tail(a,3)

head(a)

head(a,n=3)

head(a,3)



Logical Indexing

$c(1,2,3) = c(3,2,1)$

$1 \text{ \%in\% } c(3,4,5)$

$c(1,2) \text{ \%in\% } c(1,2,3,4)$



Challenge: Logical Indexing

```
a <-c(2,3,-1,3,5,2,-3,1)
```

find the sum of the positive elements of a

Hint: $a > 0$



Dropping NA values

```
a<-c(3,-2,4,NA,-1,8,-4,9,NA, 11,3,8,NA);  
a[!is.na(a)]
```

NA: Missing data



Manipulating Vectors

```
x <- c(1,2,1)
```

```
y <- c(3,2,4)
```

```
v <- x + y
```

```
v <- x - y
```



Vector Arithmetic

```
a <-c(2,3,4,2,5,6)
```

```
mean(a)
```

```
median(a)
```

```
sum(a), prod(a)
```

```
min(a). max(a)
```

```
cummin(a), cummax(a)
```

```
cumsum(a), cumprod(a)
```

```
diff(a)
```



Sorting Vector Elements

```
v <- c(3,8,4,5,0,11, -9, 304)
```

```
sort(v)
```

```
sort(v, decreasing=TRUE)
```



Sum Vector Elements

```
v <- c(3,6,2,NA,1)
```

```
sum(v)
```

```
sum(v, na.rm=TRUE)
```

```
sum(a[!is.na(a)])
```



Structure of Vectors

```
v <- c(3,8,4,5,0,11, -9, 304)
```

```
str(v)
```

```
v <- c("Red","Blue","yellow","violet")
```

```
str(v)
```



Matrix

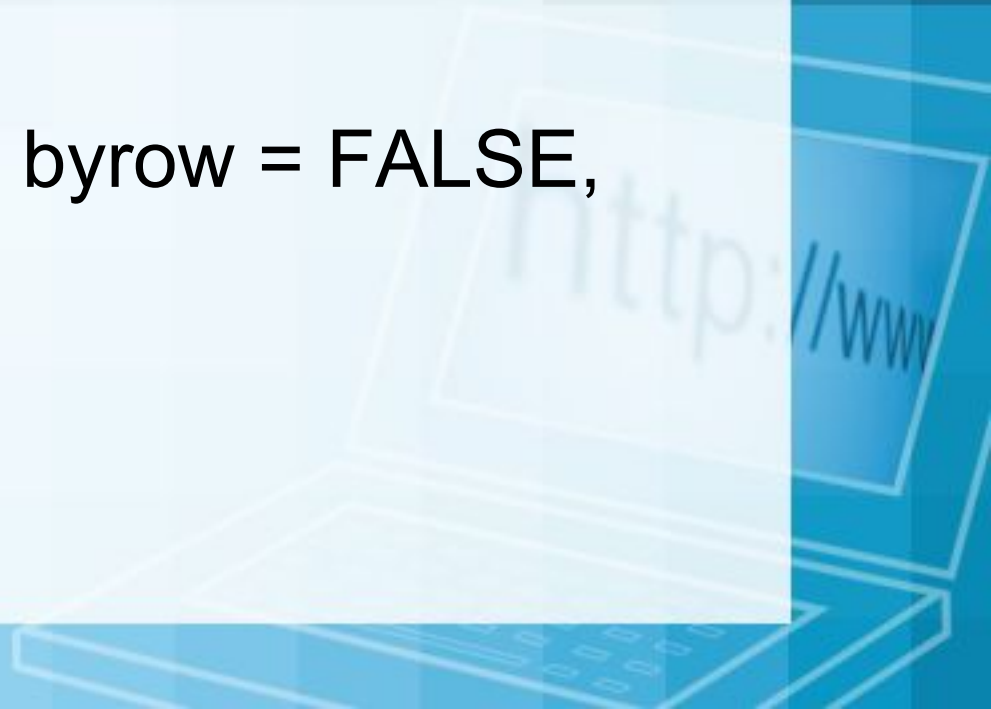


What is Matrix

Matrices are the R objects in which the elements are arranged in a two-dimensional rectangular layout.

Syntax:

```
matrix(data, nrow, ncol, byrow = FALSE,  
dimnames)
```



Creating Matrix

Usage: `matrix(data = NA, nrow = 1, ncol = 1, byrow = FALSE, dimnames = NULL)`

`matrix(1:12, ncol=4)`

`matrix(1:12, nrow=4)`

`matrix(c(3, 9, -1, 4, 2, 6), nrow=2)`

`matrix(1:12, ncol=4, byrow=TRUE)`

`matrix(1:12, nrow=4, byrow=TRUE)`

Convert Vector to Matrix

```
a <- c(1,1,1,1)
```

```
dim(a)<-c(2,2)
```



Combining Vectors to Matrix

```
a1 <- c(1,1,1,1)
```

```
a2 <- c(2,2,2,2)
```

```
rbind(a1,a2)
```

```
cbind(a1,a2)
```



Accessing Matrix Elements

- M[1,3] - row 1, col 3
- M[2,] - row 2
- M[,3] - col 3
- M[1:2,3:4] - row 1 to 2, col 3 to 4



Challenge: Matrix Elements

`a <- matrix(1:20,ncol=4)`. Extract the elements in **red**

	[,1]	[,2]	[,3]	[,4]
[1,]	1	6	11	16
[2,]	2	7	12	17
[3,]	3	8	13	18
[4,]	4	9	14	19
[5,]	5	10	15	20

Time: 5 mins

Manipulating Matrix Elements

```
M1 <- matrix(c(3, 9, -1, 4, 2, 6), nrow=2)
```

```
M2 <- matrix(c(5, 2, 0, 9, 3, 4), nrow=2)
```

```
M3 <- M1 + M2
```

```
M4 <- M1 + M2
```



Row and Column Names

```
matrix(c(3, 9, -1, 4, 2, 6), nrow=2)  
rownames(M)<-c("row1","row1")  
colnames(M)<-c("col1","col2","col3")
```

```
M["row2",]
```

```
M[, "col3"]
```



Matrix Arithmetic

rowSums(M)

- sum of each row

colSums(M)

- sum of each col

colMeans(M)

- mean of each col

t(M1)

- transpose

solve(M1)

- invert

*

- element-wise multiple

%*%

- matrix multiplication

Array



What is Array?

Arrays are the R data objects which can store data in more than two dimensions



Creating Array

```
a <- array(c(11:14,21:24,31:34),dim=c(2,2,3))
```



Accessing Array Elements

`a[:,1]` - 1st matrix

`a[1,:,1]` - 1st row, 1st matrix



Data Frame



What is Data Frame?

A data frame is a table or a two-dimensional array-like structure in which each column contains values of one variable and each row contains one set of values from each column.

- The column names should be non-empty.
- The row names should be unique.
- The data stored in a data frame can be of numeric, factor or character type.
- Each column should contain same number of data items.

Creating Data Frame

Usage: `data.frame(..., row.names = NULL,...)`

```
gender <- c('Female','Female','Male')
```

```
height <- c(162,169,170)
```

```
weight <- c(40,50,60)
```

```
age <- c(21,22,23)
```

```
name <- c('Ally','Belinda','Alfred')
```

```
a <- data.frame(gender, height, weight, age,  
row.names= name)
```

Creating Data Frame - Compact

```
a <- data.frame(  
  gender = c("Male", "Male", "Female"),  
  height = c(152, 171.5, 165),  
  weight = c(81, 93, 78),  
  age = c(42, 38, 26),  
  row.names = c('Ally', 'Belinda', 'Alfred')  
)
```

Note: there is only 1 variable generated

Create Data Frame from Matrix

from matrix to data frame

```
a <- matrix(1:20, nrow=4)
```

```
b <- as.data.frame(a)
```

from data frame to matrix

```
c <- as.matrix(b)
```



Create DF from Vectors

```
gender = c("Female", "Male", "Female")
```

```
height = c(155, 171.5, 155)
```

```
weight = c(71, 93, 68)
```

```
x4 = cbind(gender, height, weight)
```

Catch: Everything is converted to text

Columns & Rows Names

`rownames(x)`

`colnames(x)` or `names(x)`



Rows & Column Numbers

`nrow(x)` : Number of Rows

`ncol(x)` : Number of Columns



Subset Operators

\$: Select a single component from the data

[[: Select single component by name or position

[: Select multiple components



Accessing Single Component

Using \$ operator

x\$gender

x\$height

Using [[operators]]

x[["gender"]]

x[[1]]



Accessing Multiple Components

Using [operator

`a[1]`

`a["gender"]`

`a[-2]`

`a[1:2,]`

`a[c(1,4)]`

`a[,2]`

`a[c(2,3),c(1,2)]`



Filter Data using subset

```
subset(a, select = c("gender", "age"))
```

```
subset(a, subset = height > 163, select = c  
("gender", "height", "age"))
```



Add Column to Data Frame

```
a$name =c('Ally','Belinda','Jane')
```



Add Rows to Data Frame

```
b <- data.frame(  
  gender = c("Female", "Male", "Female"),  
  height = c(155, 171.5, 155),  
  weight = c(71, 93, 68),  
  age = c(42, 38, 26),  
  row.names = c('SC', 'Alfred', 'TC')  
)
```

```
c <- rbind(a, b)
```

Summary of Data Frame

summary(a)



Factor



What is Factor?

Factors are the data objects which are used to categorize the data and store it as levels. They can store both strings and integers

```
data <- factor(c("male","female","female","male"))  
is.factor(data)  
is.factor(sleep$group)  
is.factor(sleep$extra)
```

List



What is List?

Lists are the R objects which contain elements of different types like – numbers, strings, vectors and another list inside it.



Unnamed List

```
a <-list(1:10, matrix(1:4,ncol = 2),"r" )
```



Named List

List groups different objects

```
a <-list('A'=1:10, 'B'=matrix(1:4,ncol = 2),'C'="r"  
)
```



Accessing List Element

Using [[]] operator

`a[[1]]`

`a[['A']]`

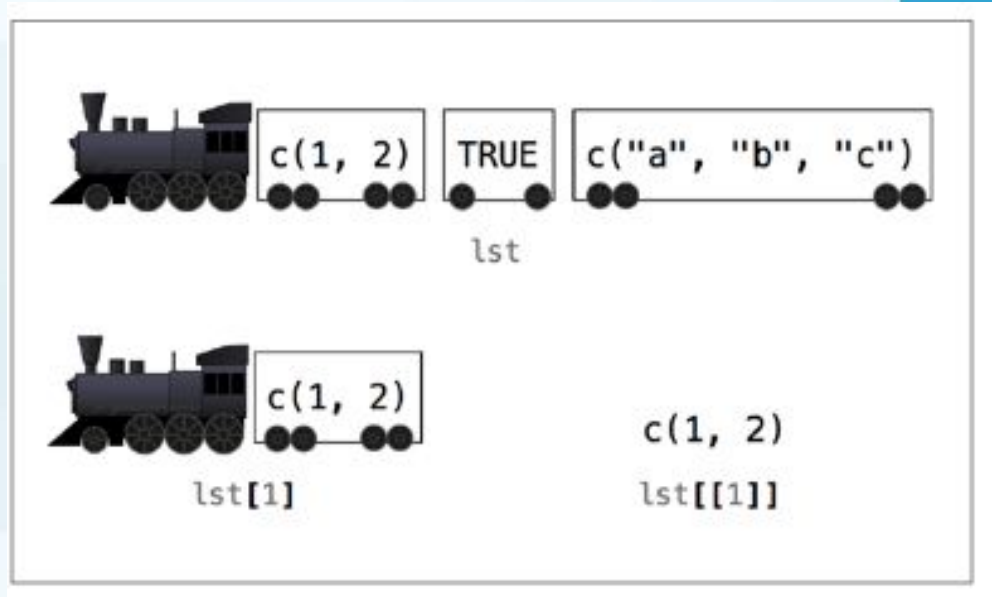
Using [] operator

`a[1]`

`a['A']`

Using \$ operator

`a$A`



Modifying List Element

```
list1[[1]] = c("d","e","f")
```

```
list1$'letters' = c("aa","bb","cc")
```



Merging Lists

```
list1 <- list(1,2,3)
```

```
list2 <- list("Sun","Mon","Tue")
```

```
merged.list <- c(list1,list2)
```



Converting List to Vector

```
v1 <- unlist(list1)
```



Date



Create a Date

```
xd <-as.Date("2016-03-13")
```

```
xd <-as.Date("5 Aug 2016",format="%d %b %Y")
```

%Y : Year with century

%y : Year without century

%m : Month in decimal

%B : Full month name

%b : Abbreviated month name

%d : Day in decimal

Working with Date



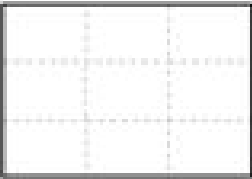
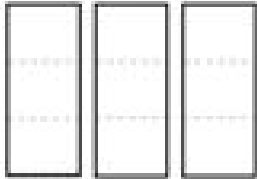
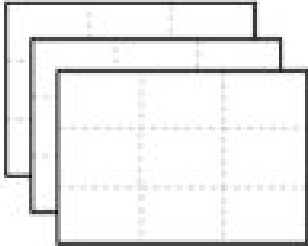
`weekdays(xd)`

`months(xd)`

`xd+7`



Data Types Summary

	single type	multiple types
1D	Vector 	List 
2D	Matrix 	Data frame 
nD	Array 	

Module 3

Packages & Data Sets



Packages



R Packages

<https://cran.r-project.org/web/views/>

CRAN Task Views

Bayesian	Bayesian Inference
ChemPhys	Chemometrics and Computational Physics
ClinicalTrials	Clinical Trial Design, Monitoring, and Analysis
Cluster	Cluster Analysis & Finite Mixture Models
DifferentialEquations	Differential Equations
Distributions	Probability Distributions
Econometrics	Econometrics
Environmetrics	Analysis of Ecological and Environmental Data
ExperimentalDesign	Design of Experiments (DoE) & Analysis of Experimental Data
Finance	Empirical Finance
Genetics	Statistical Genetics
Graphics	Graphic Displays & Dynamic Graphics & Graphic Devices & Visualization
HighPerformanceComputing	High-Performance and Parallel Computing with R
MachineLearning	Machine Learning & Statistical Learning
MedicalImaging	Medical Image Analysis
MetaAnalysis	Meta-Analysis
Multivariate	Multivariate Statistics
NaturalLanguageProcessing	Natural Language Processing
NumericalMathematics	Numerical Mathematics
OfficialStatistics	Official Statistics & Survey Methodology
Optimization	Optimization and Mathematical Programming
Pharmacokinetics	Analysis of Pharmacokinetic Data
Phylogenetics	Phylogenetics, Especially Comparative Methods
Psychometrics	Psychometric Models and Methods
ReproducibleResearch	Reproducible Research
Robust	Robust Statistical Methods
SocialSciences	Statistics for the Social Sciences
Spatial	Analysis of Spatial Data
SpatioTemporal	Handling and Analyzing Spatio-Temporal Data
Survival	Survival Analysis
TimeSeries	Time Series Analysis

Install and Load a Package

1. Install package

```
install.packages("ggplot2")
```

2. Load a package

```
library("ggplot2")
```



Update Packages

```
update.packages()
```



Unload and Remove Package

```
detach("package:ggplot2", unload = TRUE)
```

```
remove.packages("ggplot2")
```



RStudio Package Management

install and load package in RStudio

unload and remove a package in RStudio

The screenshot displays the RStudio interface with a red circle highlighting the 'Packages' tab in the top right pane. The 'Console' pane shows the 'Install' and 'Update' buttons. The 'Files' pane shows the 'Name' and 'Description' columns. The 'Environment' pane shows the 'Global Environment' with variables H, labels, and M. The 'Values' pane shows the values for these variables.

Packages in library '/Library/Frameworks/R.framework/Versions/3.2/Resources/library':

DBI	R Database Interface
KernSmooth	Functions for Kernel Smoothing Supporting Wand & Jones (1995)
MASS	Support Functions and Datasets for Venables and Ripley's MASS
Matrix	Sparse and Dense Matrix Classes and Methods
NMF	Algorithms and Framework for Nonnegative Matrix Factorization (NMF)
R.methodsS3	S3 Methods Simplified
R.oo	R Object-Oriented Programming with or without References
R2HTML	HTML exportation for R objects
RColorBrewer	ColorBrewer Palettes

Environment History

Global Environment

Values

H	num [1:5] 7 12 28 3 41
labels	chr [1:4] "A" "B" "C" "D"
M	chr [1:5] "Mar" "Apr" "May" "Jun" ...

Console

Files Packages Help Viewer

Install Update

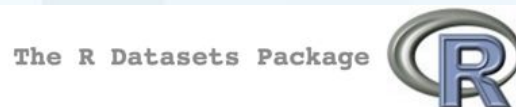
Name	Description	Version
System Library		
<input type="checkbox"/> bitops	Bitwise Operations	1.0-6
<input type="checkbox"/> boot	Bootstrap Functions (Originally by Angelo Canty for S)	1.3-18
<input type="checkbox"/> caTools	Tools: moving window statistics, GIF, Base64, ROC AUC, etc.	1.17.1
<input type="checkbox"/> chron	Chronological Objects which can Handle Dates and Times	2.3-47
<input type="checkbox"/> class	Functions for Classification	7.3-14
<input type="checkbox"/> cluster	"Finding Groups in Data": Cluster Analysis Extended Rousseeuw et al.	2.0.3
<input type="checkbox"/> codetools	Code Analysis Tools for R	0.2-14
<input type="checkbox"/> coin	Conditional Inference Procedures in a Permutation Test Framework	1.1-2
<input type="checkbox"/> colorspace	Color Space Manipulation	1.2-6
<input type="checkbox"/> combinat	combinatorics utilities	0.0-8
<input type="checkbox"/> compiler	The R Compiler Package	3.2.4
<input checked="" type="checkbox"/> datasets	The R Datasets Package	3.2.4
<input type="checkbox"/> DBI	R Database Interface	0.3.1
<input type="checkbox"/> dichromat	Color Schemes for Dichromats	2.0-0
<input type="checkbox"/> digest	Create Compact Hash Digests of R Objects	0.6.9
<input type="checkbox"/> doParallel	Foreach Parallel Adaptor for the 'parallel' Package	1.0.10
<input type="checkbox"/> e1071	Misc Functions of the Department of Statistics, Probability Theory Group (Formerly: E1071), TU Wien	1.6-7
<input type="checkbox"/> evaluate	Parsing and Evaluation Tools that Provide More Details than the Default	0.9
<input type="checkbox"/> foreach	Provides Foreach Looping Construct for R	1.4.3
<input type="checkbox"/> foreign	Read Data Stored by Minitab, S, SAS, SPSS, Stata, Systat, Weka, dBase, ...	0.8-66

Data Sets



R Dataset Packages

<http://stat.ethz.ch/R-manual/R-devel/library/datasets/html/00Index.html>



Documentation for package 'datasets' version 3.3.0

- [DESCRIPTION file.](#)

Help Pages

[A](#) [B](#) [C](#) [D](#) [E](#) [F](#) [G](#) [H](#) [I](#) [J](#) [K](#) [L](#) [M](#) [N](#) [O](#) [P](#) [Q](#) [R](#) [S](#) [T](#) [U](#) [V](#) [W](#)

[datasets-package](#)

The R Datasets Package

-- A --

[ability.cov](#)
[airmiles](#)
[AirPassengers](#)
[airquality](#)
[anscombe](#)
[attenu](#)
[attitude](#)
[austres](#)

Ability and Intelligence Tests
Passenger Miles on Commercial US Airlines, 1937-1960
Monthly Airline Passenger Numbers 1949-1960
New York Air Quality Measurements
Anscombe's Quartet of 'Identical' Simple Linear Regressions
The Joyner-Boore Attenuation Data
The Chatterjee-Price Attitude Data
Quarterly Time Series of the Number of Australian Residents

-- B --

[beaver1](#)
[beaver2](#)
[beavers](#)
[RIsales](#)

Body Temperature Series of Two Beavers
Body Temperature Series of Two Beavers
Body Temperature Series of Two Beavers
Sales Data with Leading Indicator

Load Data Set

```
data(sleep)
```

```
# Check the structure of dataase  
str(sleep)
```



RStudio Import Dataset

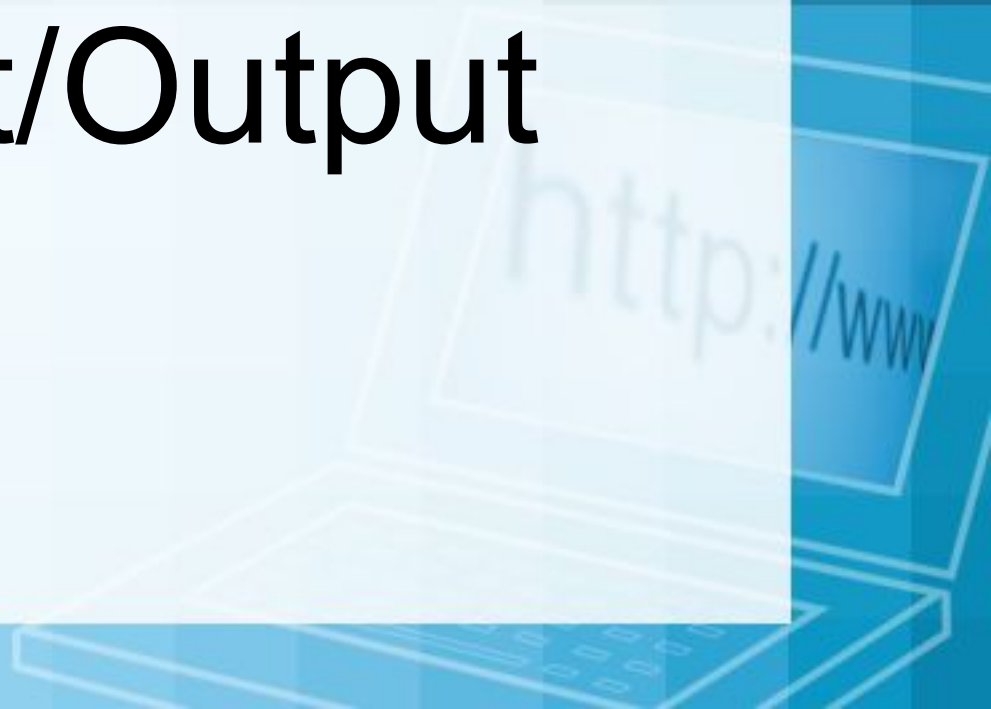
Upload from local file

Upload from Web URL



Module 4

File Input/Output



Working Directory

1. Get current working directory

`getwd()`

2. Set current working directory

`setwd("...")`

3. Add function

`source("...")`



CSV File



Read CSV File

```
a <- read.csv("input.csv", header = TRUE)
```

```
View(a)
```

Ex:csvimport.R



Import Dataset in RStudio

Import Dataset

Name

test

Encoding

Automatic

Heading

☒ Yes ☐ No

Row names

Automatic

Separator

Comma

Decimal

Period

Quote

Double quote (")

Comment

None

na.strings

NA

☒ Strings as factors

Input File

gender,height,weight,age
Female,152,81,42
Female,171,92,38
Male,165,78,26

Data Frame

gender	height	weight	age
Female	152	81	42
Female	171	92	38
Male	165	78	26

Import

Cancel

Write CSV File

```
write.csv(a,"output.csv")
```



Ex: CSV Read/Write

1. Read a data set from a csv file
2. Add one more row of data
3. Write the data back to a csv file

Time: 5 min



Text File



Read Text File

```
a <- read.table("file.txt", header = TRUE, sep  
= "\t")
```

Ex:readwritetext.R



Write Text File

```
write.table(a1, "file.txt", sep="\t")
```

Ex:readwritetext.R



Module 5

Charts



Bar Chart



Bar Chart Syntax

```
barplot(H,xlab,ylab,main, names.arg,col)
```

H - a vector or matrix

xlab - label for x axis.

ylab - label for y axis.

main - title of the bar chart.

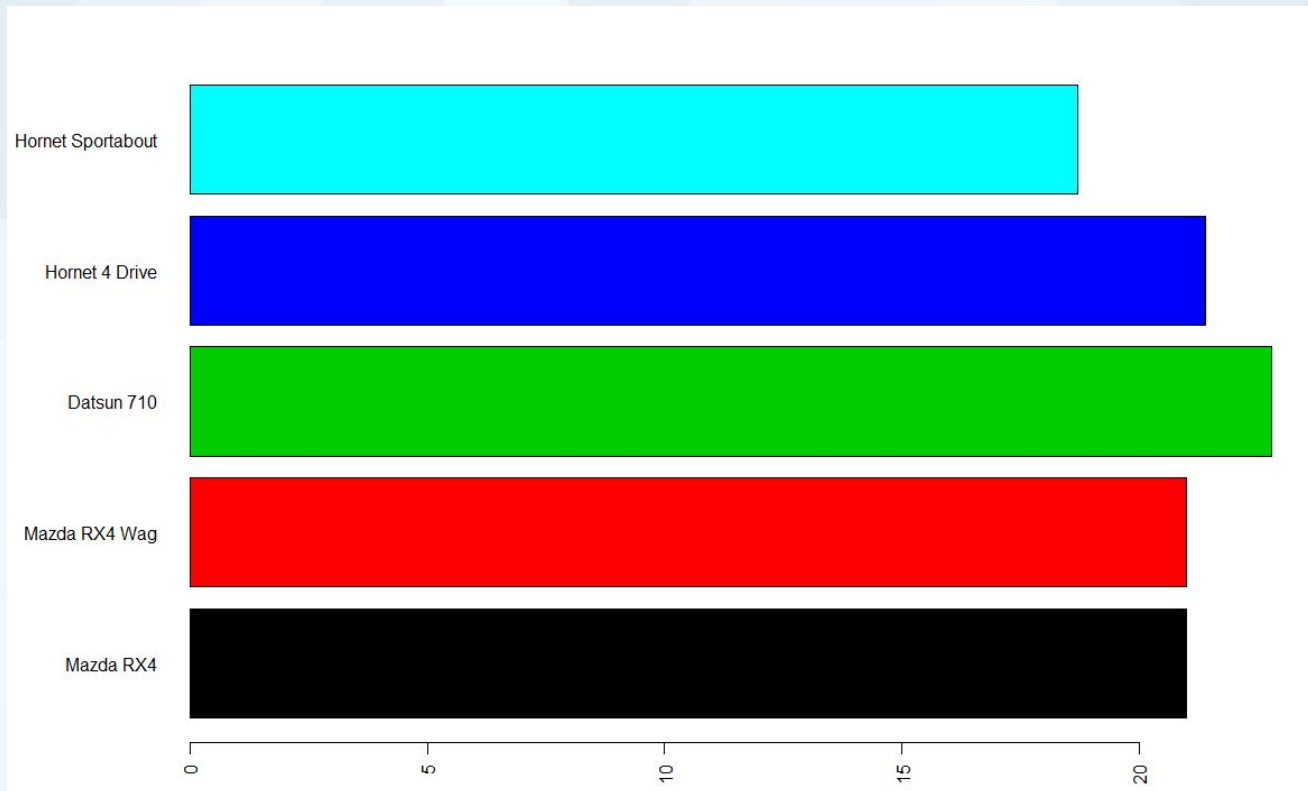
names.arg - vector of names appearing under each bar.

col - colors to the bars in the graph.

Bar Chart Example

```
par(mar = c(2.5, 8, 2.5, 2.5))
```

```
barplot(mtcars$mpg[1:5], names.arg = row.names(mtcars)[1:5],  
col = 1:5, las = 2, horiz = FALSE)
```



Color List

colors()



Box Plot



Boxplot Syntax

```
boxplot(x,data,notch,varwidth,names,main)
```

x - formula.

data - data frame.

notch - Set as TRUE to draw a notch.

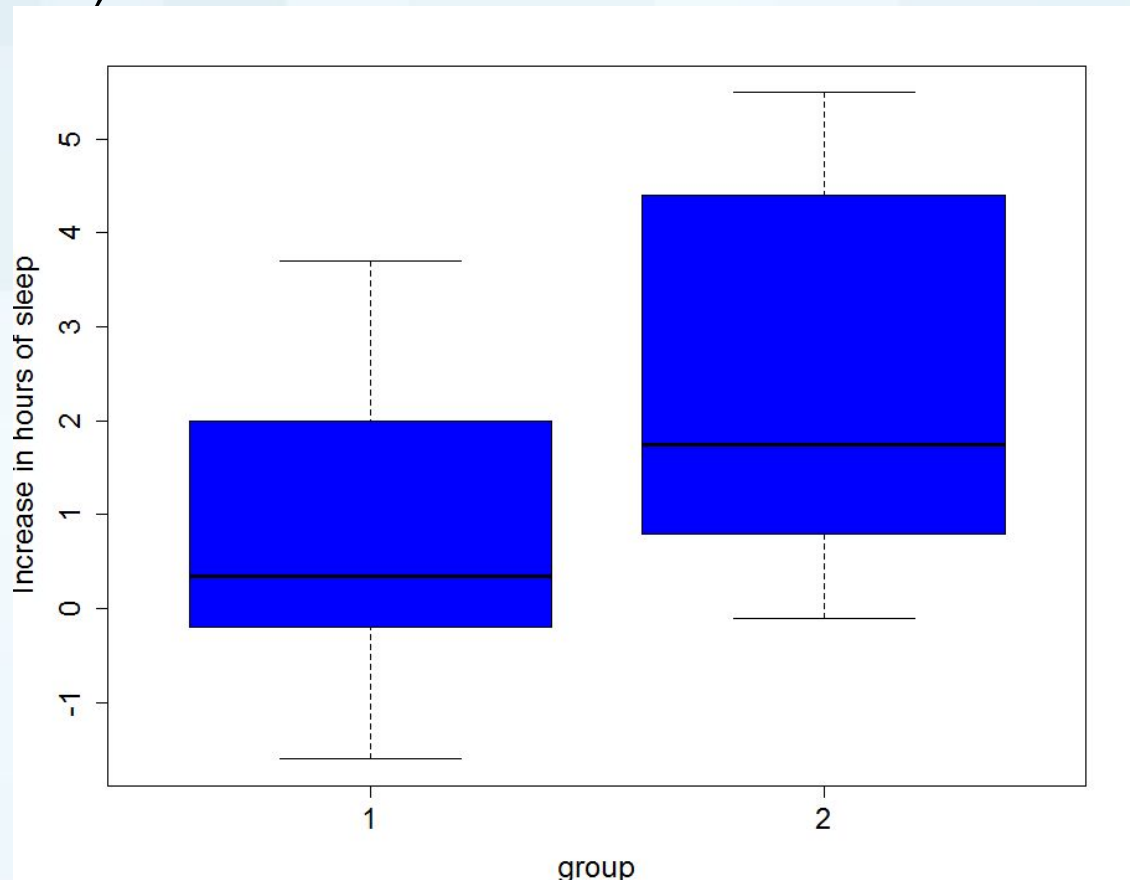
varwidth - Set as true to draw width of the box proportionate to the sample size.

names - group labels

main - title to the graph.

Boxplot Example

```
boxplot(extra ~ group, data = sleep, col = "blue",  
ylab = "Increase in hours of sleep", xlab = "group", cex.lab = 1.5,  
cex.axis = 1.5)
```



Pie Chart



Pie Chart Syntax

`pie(x, labels, radius, main, col, clockwise)`

`x` - vector

`labels` - description to the slices.

`radius` - radius (value between -1 and +1).

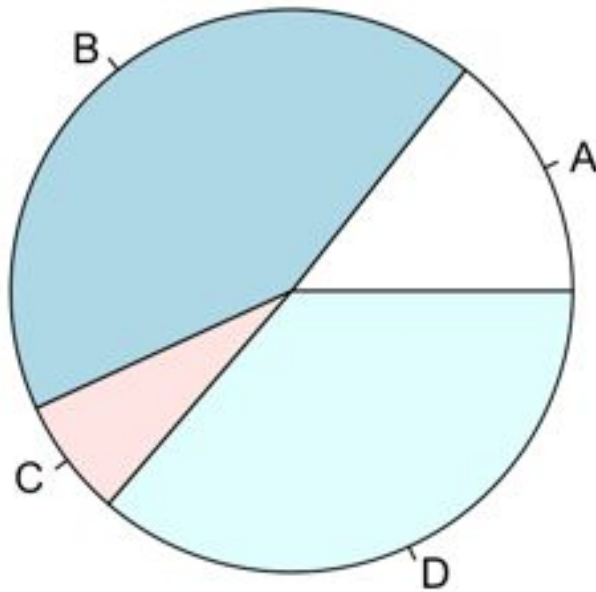
`main` - title of the chart.

`col` - color palette.

`clockwise` - drawn clockwise or anti clockwise.

Pie Chart

```
x <- c(21, 62, 10, 53)  
labels <- c("A", "B", "C", "D")  
pie(x, labels)
```



Histogram



Histogram Syntax

```
hist(v,main,xlab,xlim,ylim,breaks,col,border)
```

`v` - a vector

`main` - title of the chart.

`col` - set color of the bars.

`border` - set border color of each bar.

`xlab` - description of x-axis.

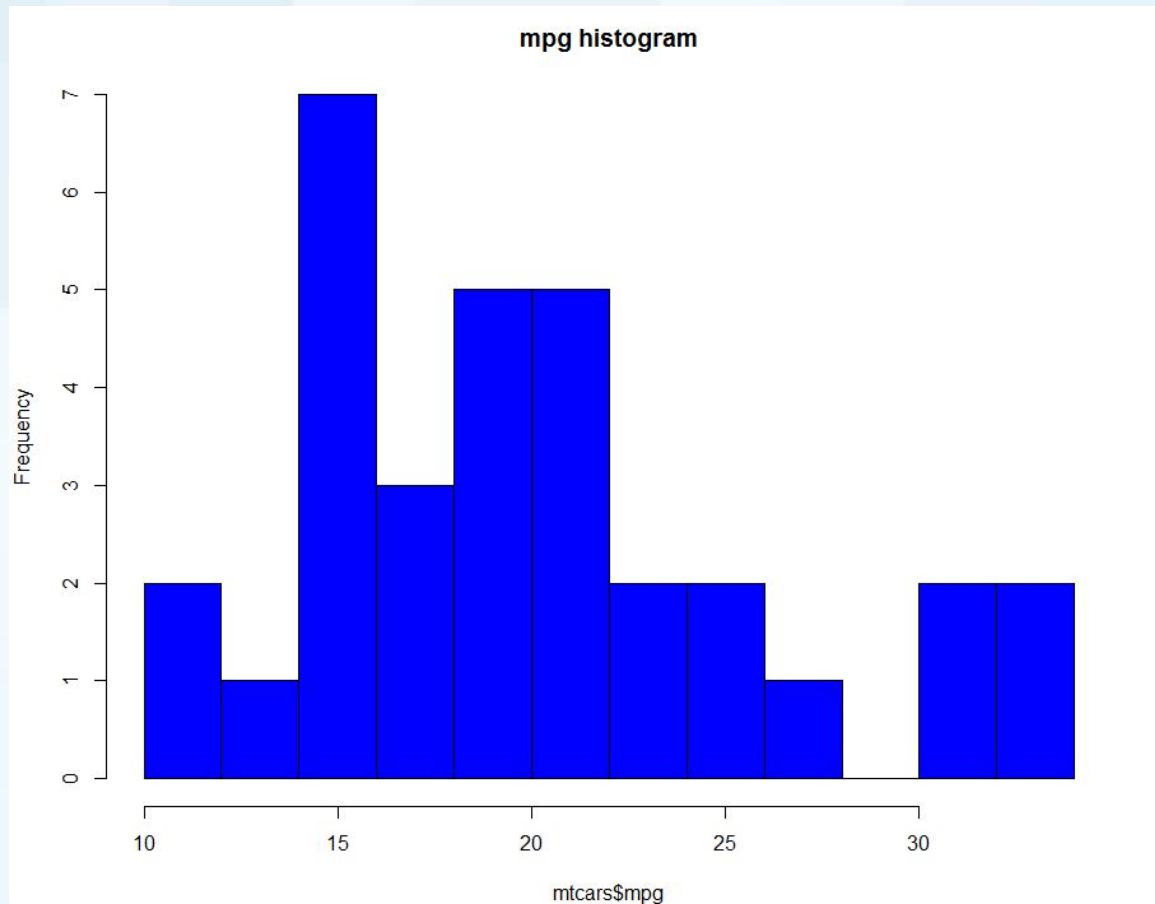
`xlim` - range of values on the x-axis.

`ylim` - range of values on the y-axis.

`breaks` - the width of each bar.

Histogram

```
hist(mtcars$mpg, breaks = 10, col="blue", main = "mpg  
histogram")
```



Line Plot



Line Plot Syntax

```
plot(v,type,col,xlab,ylab)
```

v - a vector

type - "p" to draw only the points, "l" to draw only the lines and "o" to draw both points and lines.

xlab - label for x axis.

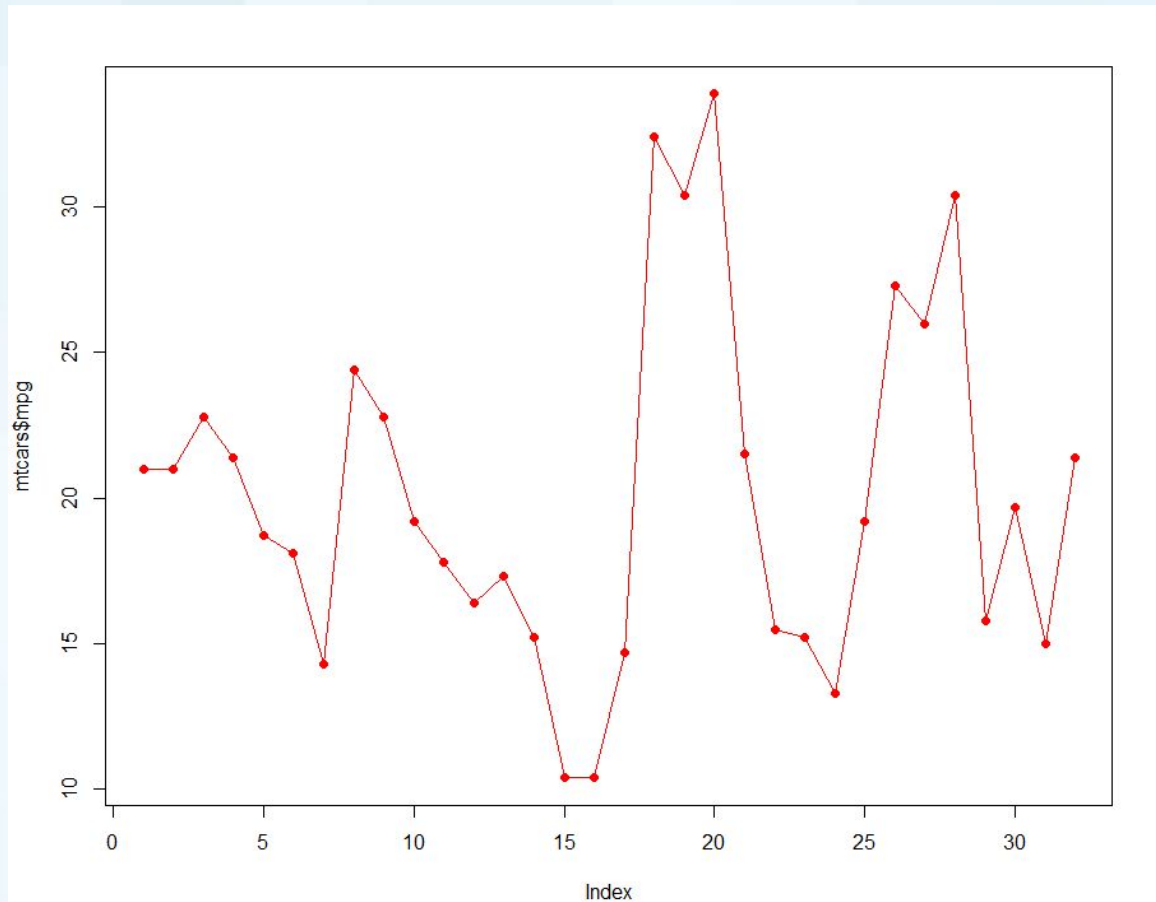
ylab - label for y axis.

main - Title of the chart.

col - colors to both the points and lines.

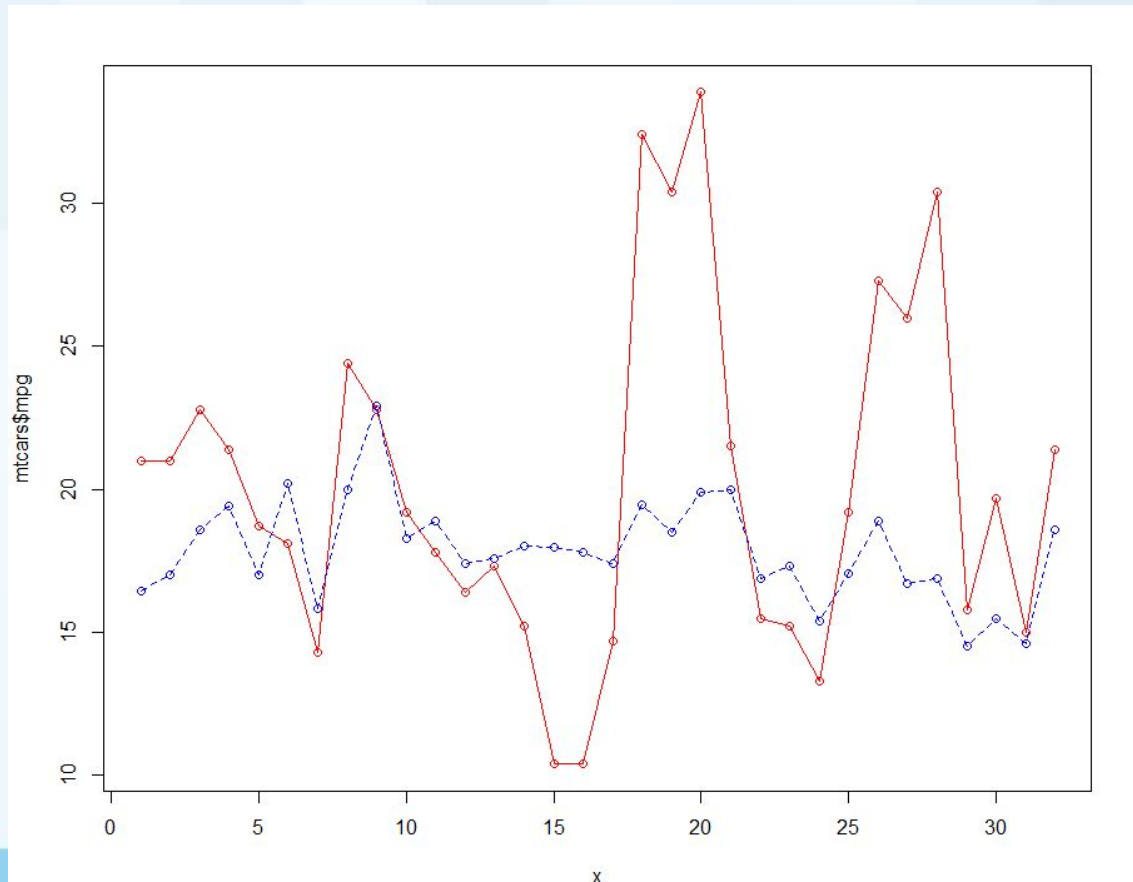
Plot

```
plot(mtcars$mpg, type = "p", col = "red", xlab = "Index", pch = 19)
```



Multiple Lines in a Line Chart

```
plot(mtcars$mpg, type = "o", col = "red", xlab = "x")  
lines(mtcars$qsec, type = "o", col = "blue", lty = 2)
```



Scatter Plot



X-Y Scatter Plot Syntax

`plot(x, y, main, xlab, ylab, xlim, ylim, axes)`

`x` - x data set

`y` - y data set

`main` - Title of the chart.

`type` - type of points

`xlab` - label for x axis.

`ylab` - label for y axis

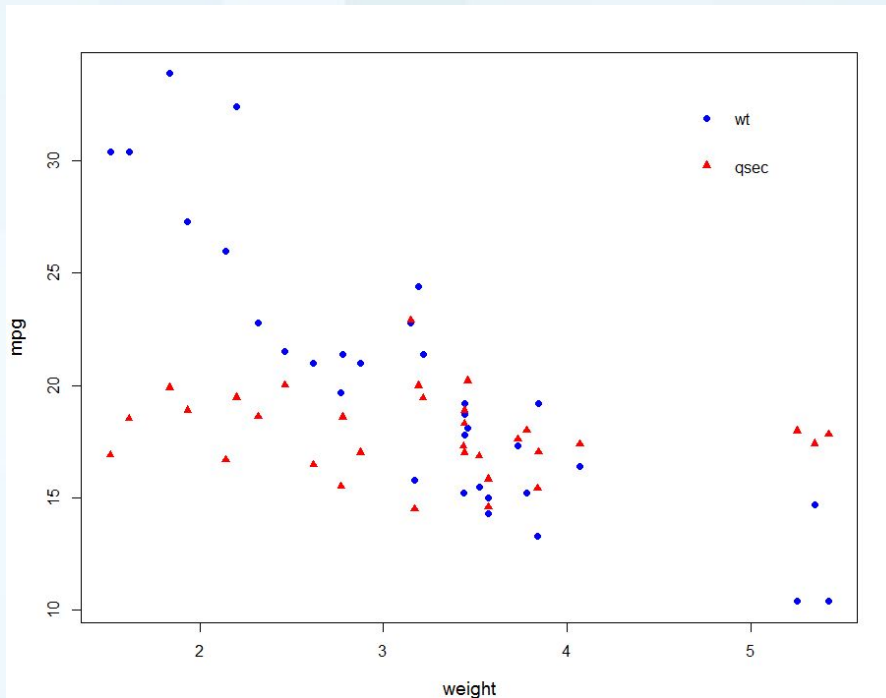
`xlim` - x limits

`ylim` - y limits

`axes` - axes should be drawn on the plot.

X-Y Scatter Plot Example

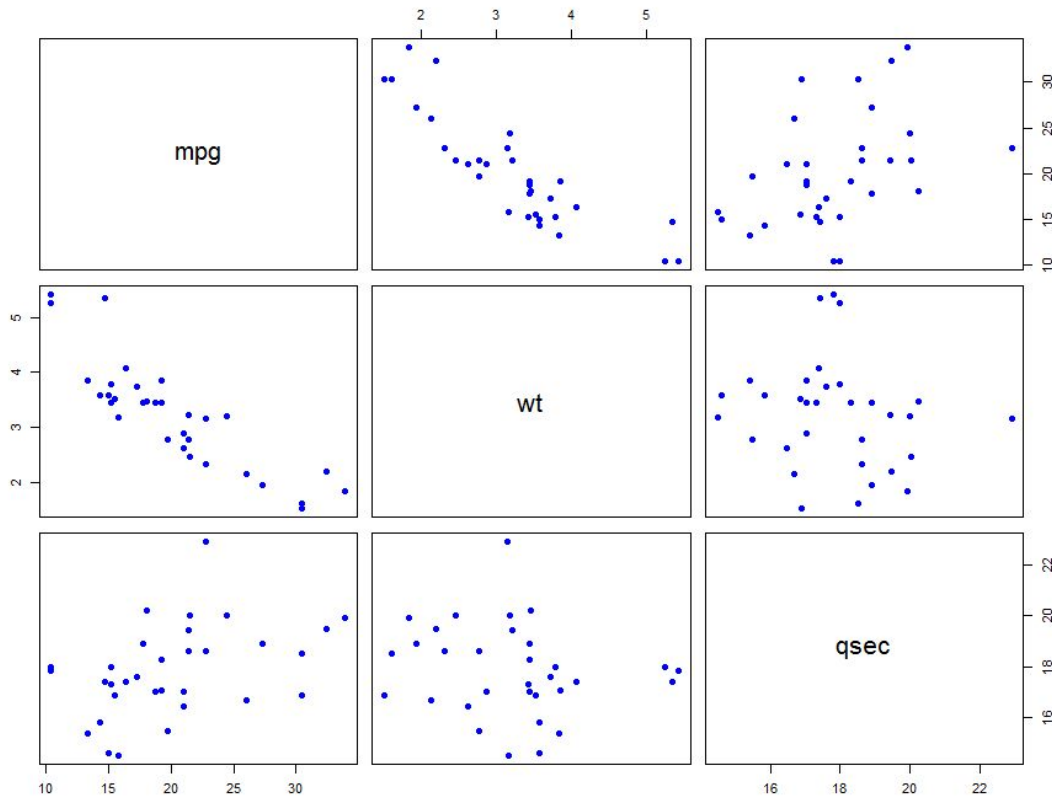
```
plot(mtcars$wt, mtcars$mpg, col = "blue", pch=19, xlab="weight", ylab="mpg",  
     cex.lab=1.2)  
points(mtcars$wt, mtcars$qsec, col = "red", pch = 17)  
legend(x=4.6,y=34, legend=c("wt", "qsec"), pch = c(19,17), col = c('blue', 'red'),  
      bty="n")
```



scatterplot.R

Multiple Scatter Plot

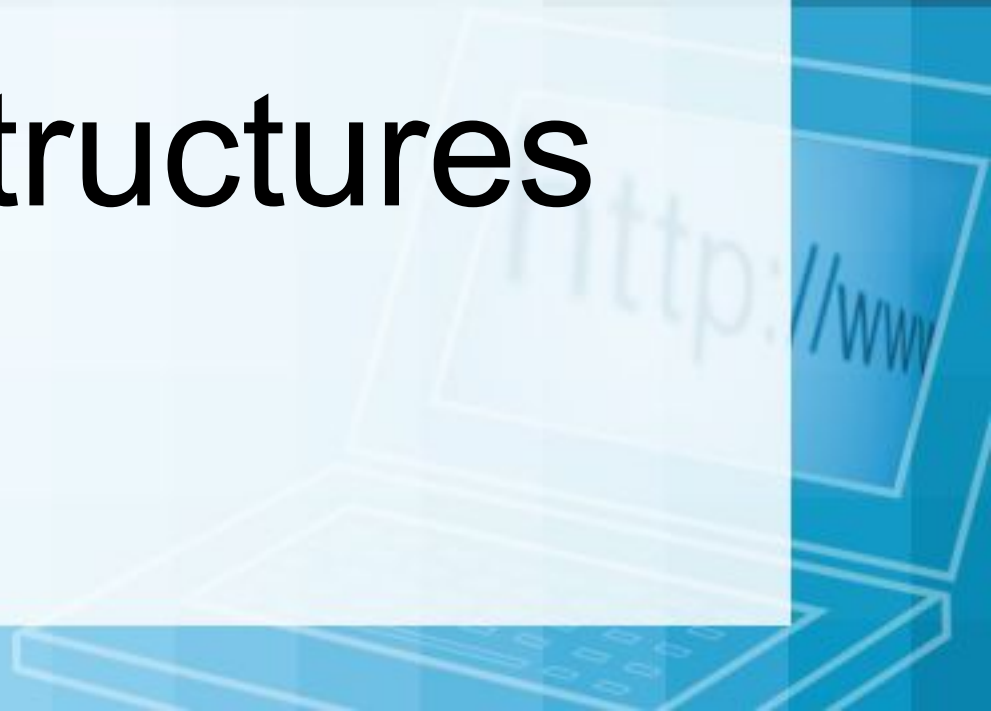
```
plot(mtcars[,c(1,6,7)], col = "blue", pch=19)
```



erplot.R

Module 6

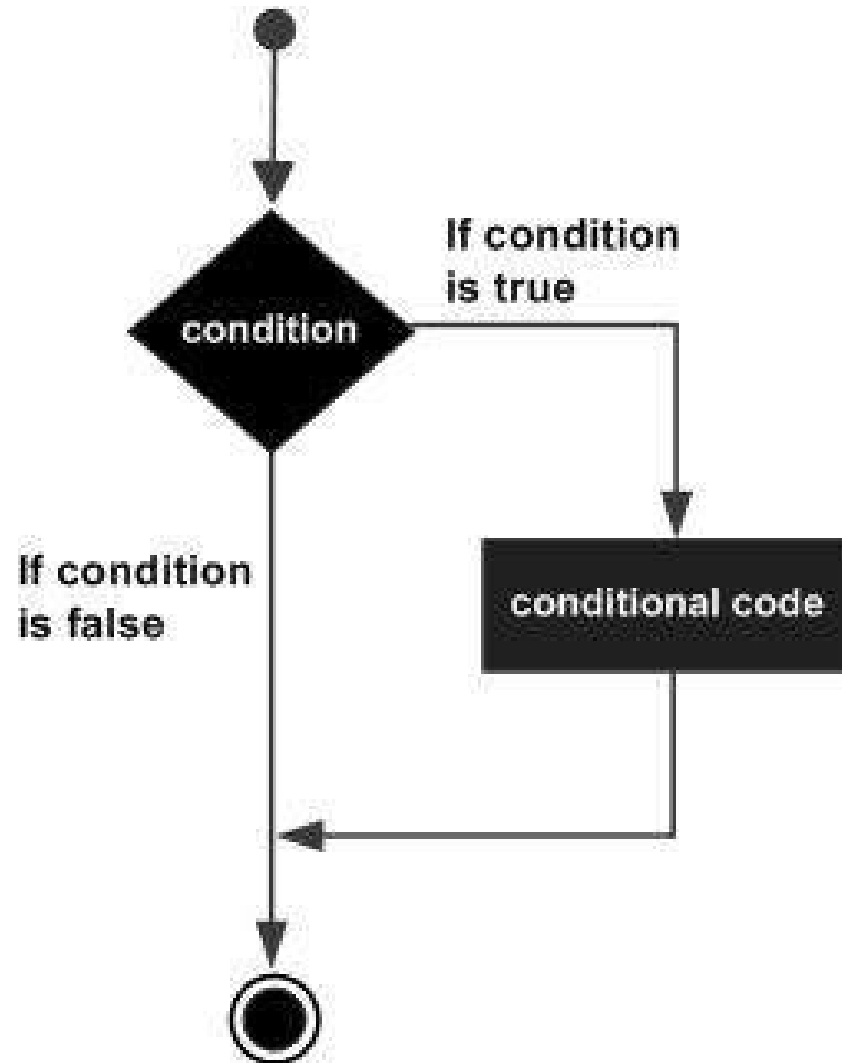
Control Structures



Conditional



if Statement



if Syntax

```
if (condition) {  
    do Something  
}
```



if Statement Example

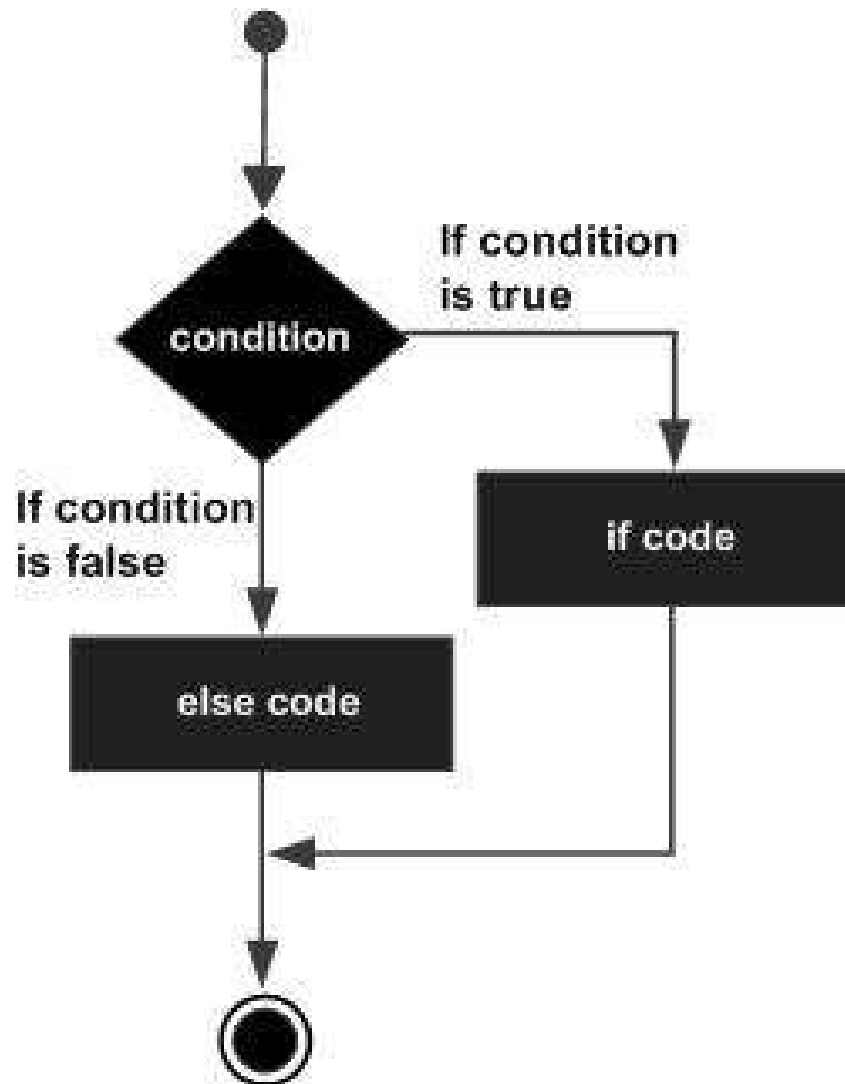
```
x <- 3
```

```
y <- 4
```

```
if (x<y) {  
  print("x is smaller than y")  
}
```

Ex file: ifelse.R

if-else Statement



if-else Syntax

```
if (condition) {  
    do Something}  
else {  
    do Something Else}
```



If-else Statements

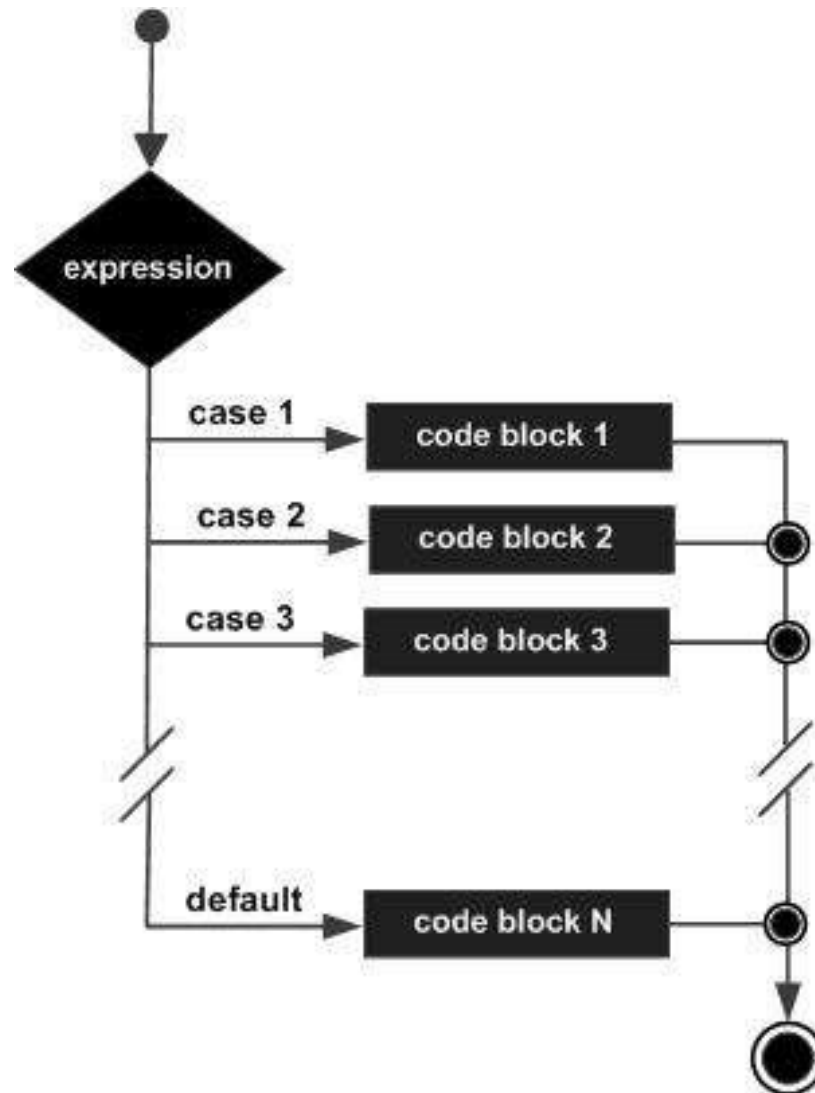
```
x <- 5
```

```
y <- 4
```

```
if (x<y) {  
  print("x is smaller than y")  
} else {  
  print("x is larger than y")  
}
```

Ex file: ifelse.R

Switch Statement



Switch Syntax

```
switch(expression, case1, case2, case3....)
```



Switch Statements

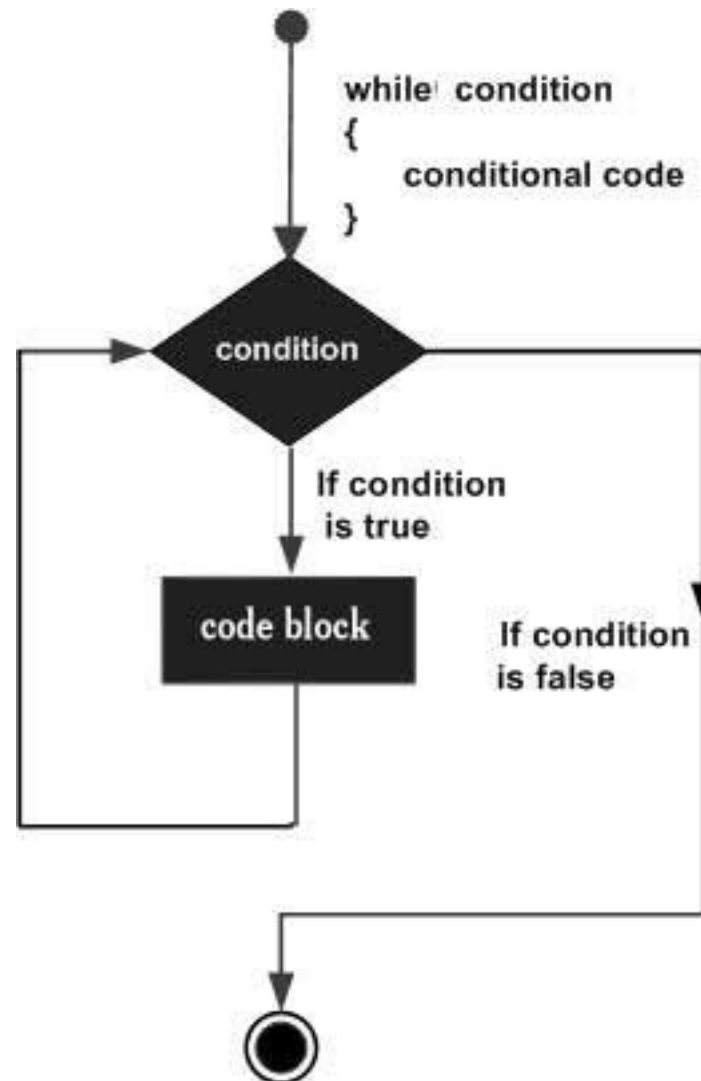
```
x <- "three"  
switch(x,  
  zero = print(0),  
  one =  print(1),  
  two =  print(2),  
  three = print(3),  
  print("i understand only upto three :("))
```

Ex file: ifelse.R

Loop



While Loop Statement



While Loops Syntax

```
while (condition) {  
    do Something  
}
```



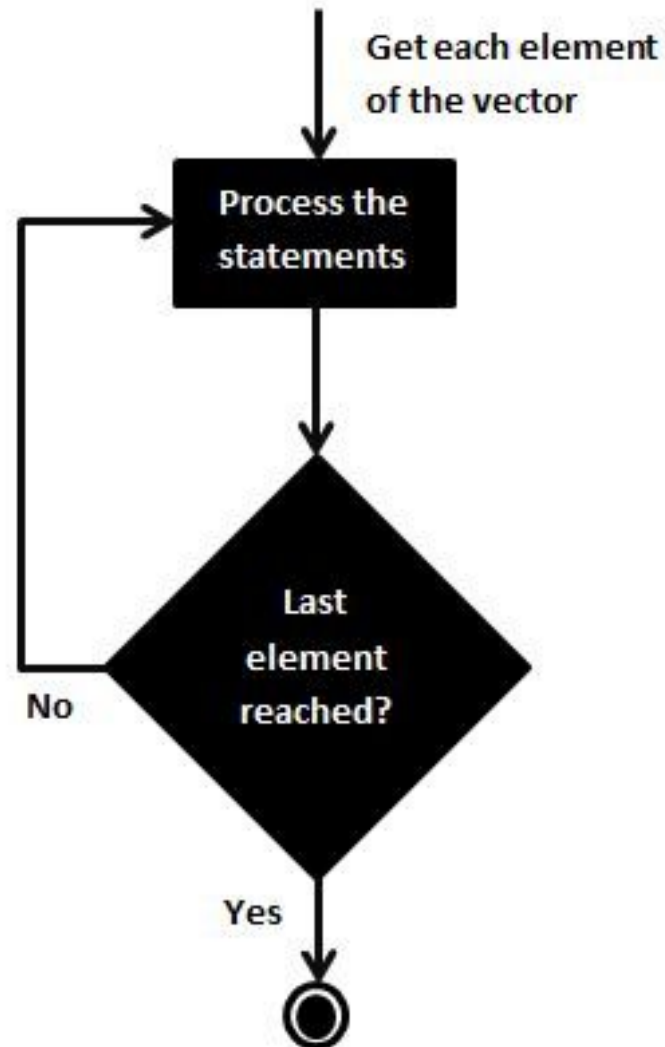
While Loops Examples

```
x <- 0  
while (x<10) {  
  print(x)  
  x = x+1  
}
```

While loop can potentially be infinite loop,
be careful!

Ex file: whileloop.R

For Loop Statement



For Loops Syntax

```
for (value in vector) {  
    statements  
}
```



For Loops Example

```
v <- c(1,2,3,4,5)
for ( i in v) {
  print(i)
}
```

Ex file: forloop.R



Next

```
for ( i in 1:10) {  
  if (i == 7) {next}  
  print(i)  
}
```

Ex file: next.R



Break

```
for ( i in 1:10) {  
  if (i == 7) {break}  
  print(i)  
}
```

Ex file: Break.R



Challenge


1. Read data1.csv
2. Do a subset of month of May and June
3. Count the number of days where temp is more than 65

Time: 10 mins



Hint to Challenge

```
data <- read.csv('data1.csv',header=TRUE)
data.month <- subset(data, Month<7)
data.month.temp <- data.month$Temp
a = 0
for (i in data.month.temp) {
  if (i >65) { a = a +1}
}
print(a)
```



Operators



Arithmetic Operators

Addition	+
Substraction	-
Multiplication	*
Division	/
Modulus	%%



Logical Operators

and &&

or ||

not !

elementwise

and &

or |



Module 7

Function



Function syntax

```
variable_name <- function(arg_1, arg_2, ...) {  
  Function body  
}
```

The last expression is the return value



Built In Functions in R

`factorial(3)`

`mean(1:6)`



Function Examples

```
f <- function(x,y) {  
  x*x+y*y*y  
}
```

```
filter <- function(x) {  
  x[x>0]  
}
```

Ex file: function.R



Function with Default Args

```
above10 <- function(x,n=10) {  
  x[x>n]  
}
```

```
f <- function(a, b = 1, c = 2, d = NULL) {  
}
```

Ex file: function.R

Named Args

```
f <- function(x,y) {  
  x*x+y*y*y  
}
```

```
f(x=3,y=2)
```

```
f(x=2,y=3)
```



Argument Matching

The order of argument matching is

1. Check for exact match for a named argument
2. Check for a partial match
3. Check for a positional match



... Argument

The ... argument indicate a variable number of arguments that are usually passed on to other functions.

```
f <- function(x,y,...) {  
  plot(x,y,...)  
}
```

Eg

```
f(x,y,col="red",main="sine")
```

Nested Function

```
make.power <- function(n) {  
  pow <- function(x) {  
    x^n  
  }  
  pow  
}
```

```
cube = make.power(3)  
cube(4)
```



Challenge: Function

Write a function to roll 2 dices, return the sum of the 2 dices

1 dice : 1, 2,3,4,5,6



Advanced Functions



Apply

Applies a function to sections of an array and returns the results in an array.

Syntax

```
apply(array, margin, function, ...)
```

margin: 1 (row), 2 (column)

Eg

```
apply(mtcars, 2, max)
```

```
apply(mtcars, 2, mean)
```



Lapply

Applies a function to elements in a list or a vector and returns the results in a list.

Syntax

```
lapply(list, function, ...)
```

Eg

```
lapply(mtcars, max)
```

```
lapply(mtcars, mean)
```



Module 8

Statistical Application of R



Basic Statistics



Mean Syntax

```
mean(x, trim = 0, na.rm = FALSE, ...)
```

trim is used to drop some observations from both end of the sorted vector

na.rm is used to remove the missing values from the input vector.

Eg:

```
mean(x)
```

```
mean(x,trim=0.3)
```

Ex:selectingdata.R

Median Syntax

```
median(x, na.rm = FALSE)
```

x is the input vector.

na.rm is used to remove the missing values from the input vector.

Ex: `selectingdata.R`

Summary

`summary(x)`

Min, 1st Q, Median, Mean, 3rd Q, Max

Ex: `selectingdata.R`



Sample

```
sample(1:6,size=2)
```

```
sample(1:6,size=2, replace=TRUE)
```

```
sample(c('head','tail'),size=1,prob=c(0.2,0.8))
```



Challenge : Sample

Create a function to return the sum of two dices rolling



Hint to Challenge

```
roll <- function() {  
  ...  
  dice <- sample(1:6,size=2,replace=TRUE)  
  ....  
}
```



Correlation



Correlation

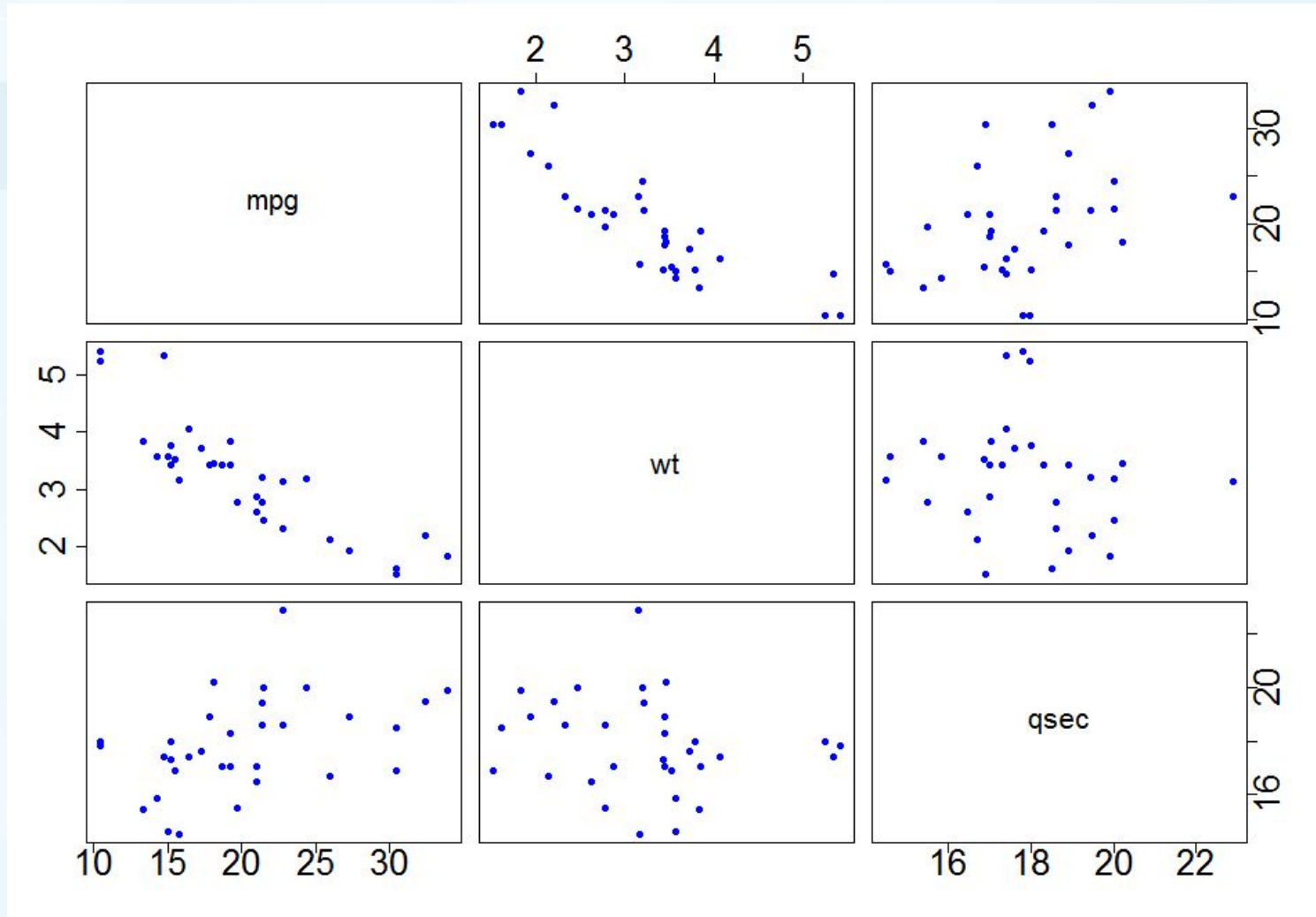
It provides a measure of strength and direction of linear relationship between two variables

```
> corMat <- cor(mtcars[,c(1,3,6)])  
> round(corMat,2)
```

	mpg	disp	wt
mpg	1.00	-0.85	-0.87
disp	-0.85	1.00	0.89
wt	-0.87	0.89	1.00

Ex:correlation.R

Relationship among selected variables of mtcars dataset

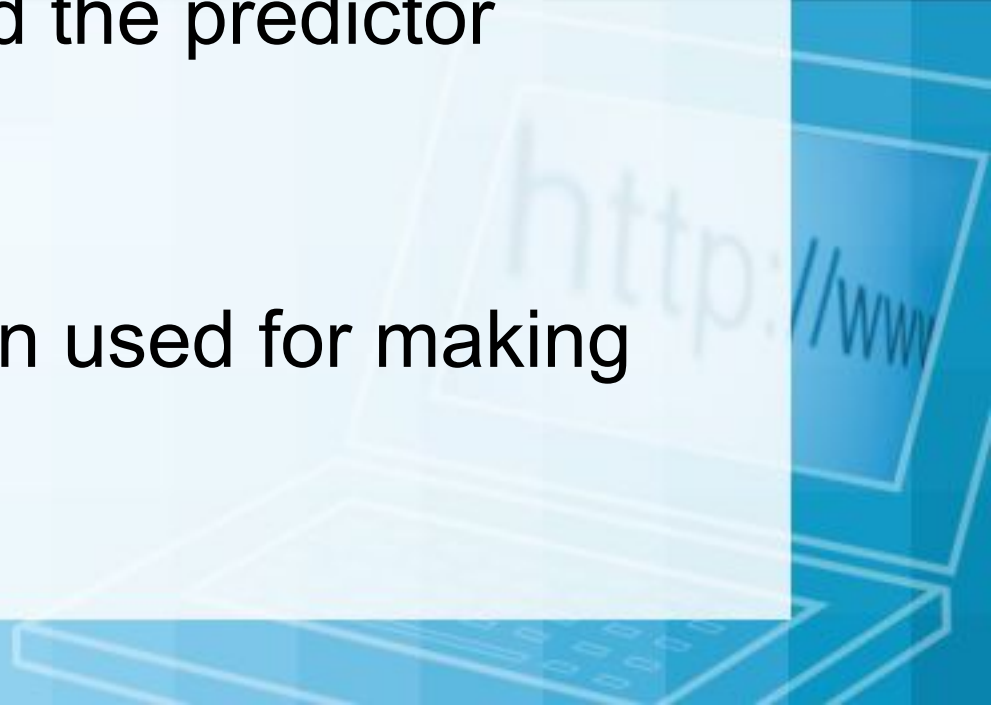


Linear Regression

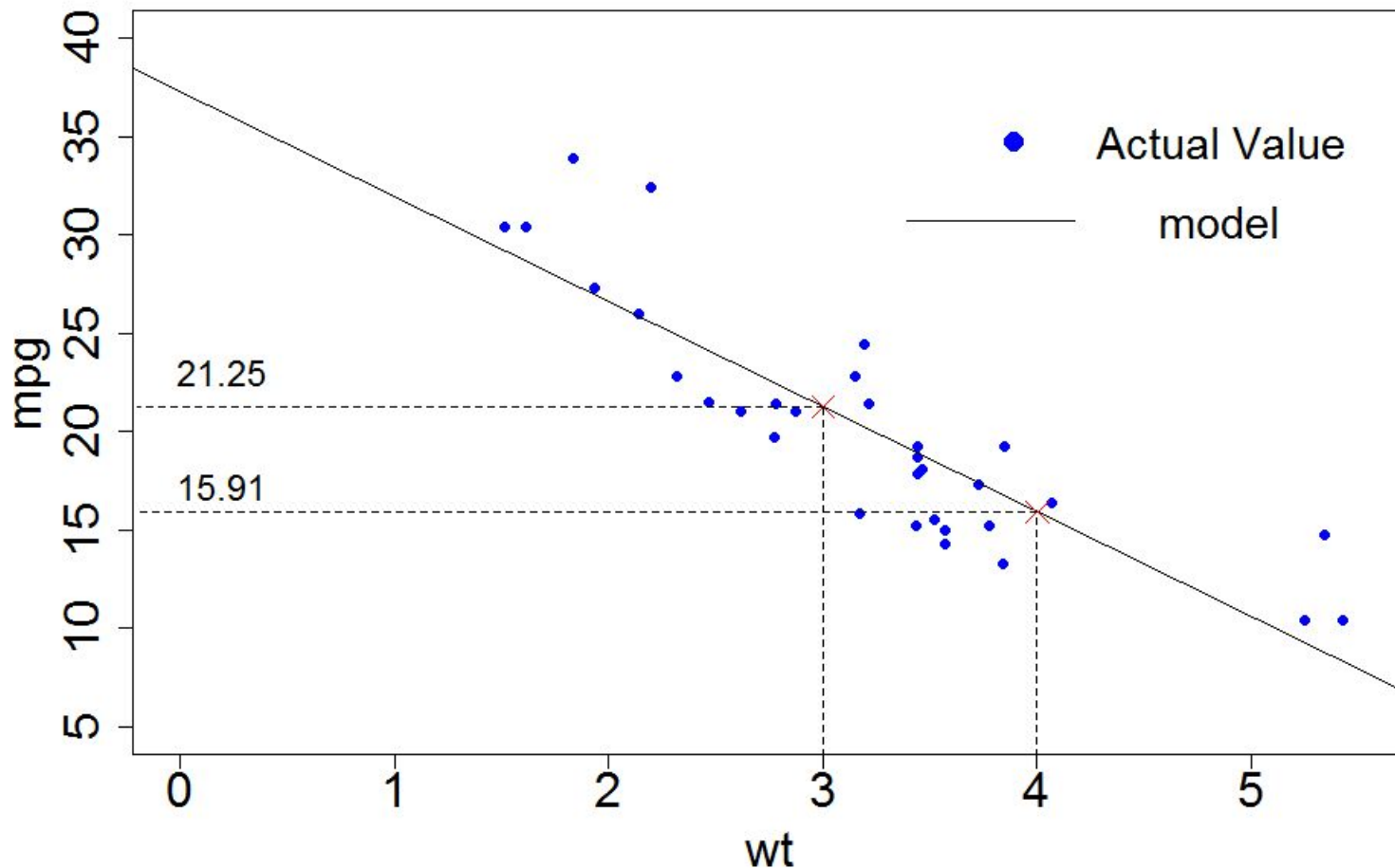


Linear Regression

- Used for modeling quantitative response
- Involves finding a straight line that best describes the relationship between the response variable and the predictor variables
- The best fit line is then used for making prediction



Linear Regression Example: mtcars dataset



Linear Regression Code

```
> lmModel <- lm(mpg ~ wt, data = mtcars)
> predValue <- predict(lmModel, data.frame
(wt = 3))
```

```
> coef(lmModel)
```

```
> sumModel <- summary(lmModel)
```

```
> sumModel$r.squared
```

```
> lmModel <- lm(mpg ~ wt + qsec, data =
mtcars)
```

Distributions

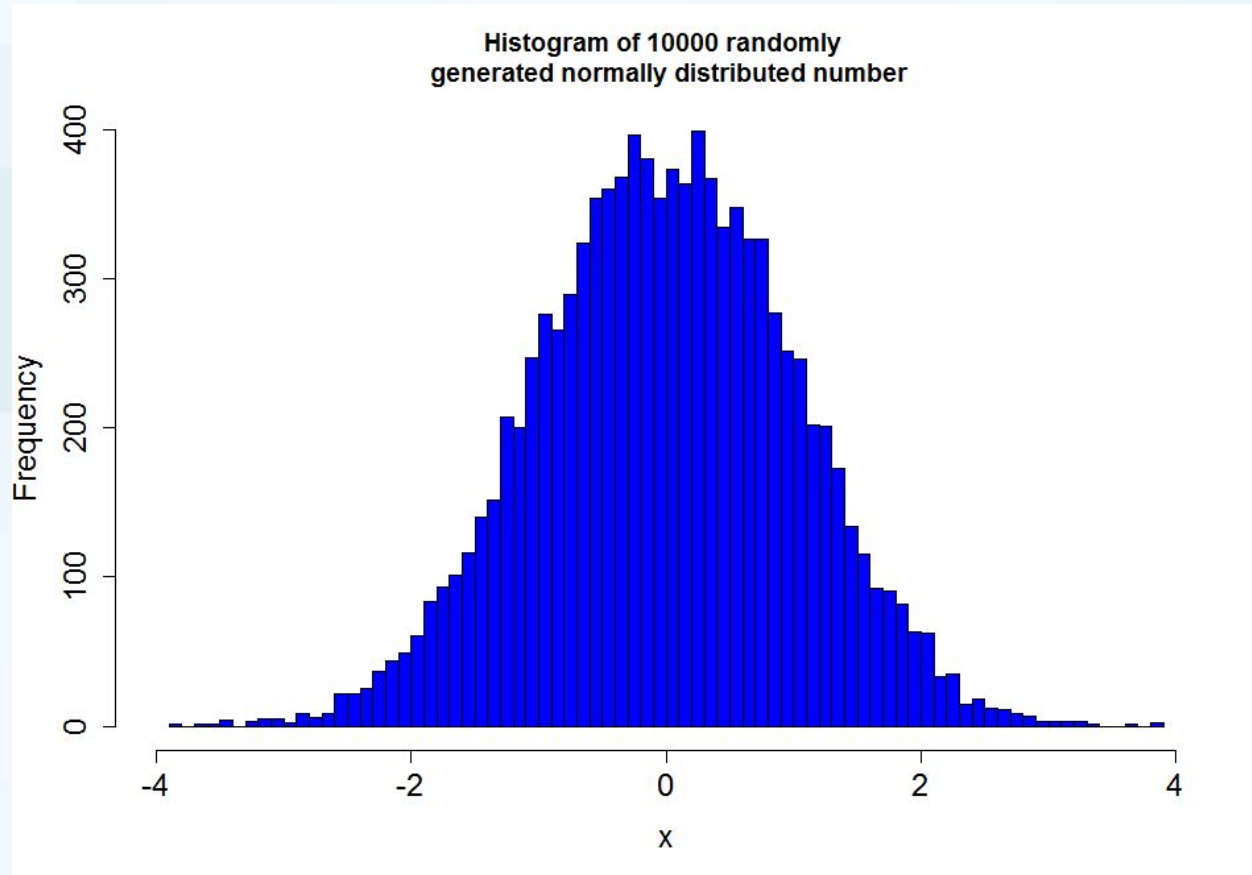


Probability Distribution

It is a function that gives the theoretical probability of observing a random variable to have a particular value when the variable is discrete or to fall within a certain range.

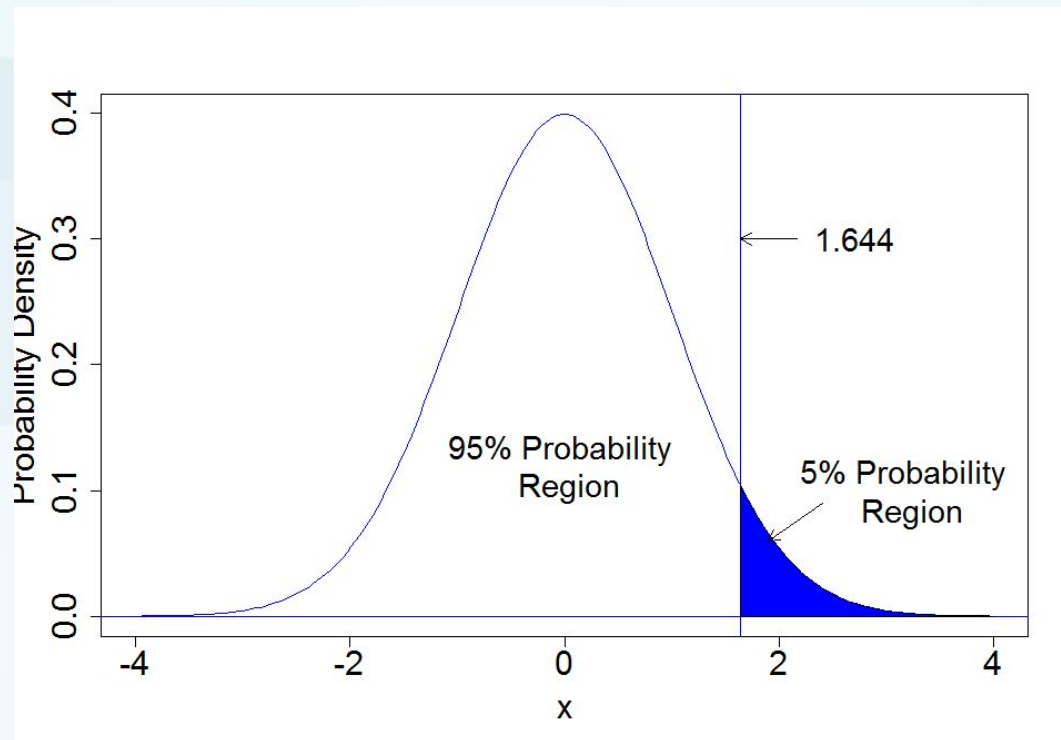
The most famous probability distribution is the **normal (Gaussian) distribution**

Histogram of 10000 Normally Distributed numbers



```
> rnorm(n, mean = 0, sd = 1) # generates n normally distributed numbers
```

Normal Distribution: probability density and related quantities



```
> x <- seq(from = -4, to = 4, length.out = 200)
```

```
> dnorm(x, mean = 0, sd = 1) # generates probability density
```

```
> qnorm(p=0.95, mean = 0, sd = 1) # gives the quantile associated with p
```

```
> pnorm(q=1.644, mean = 0, sd = 1) # gives the probability associated with q
```

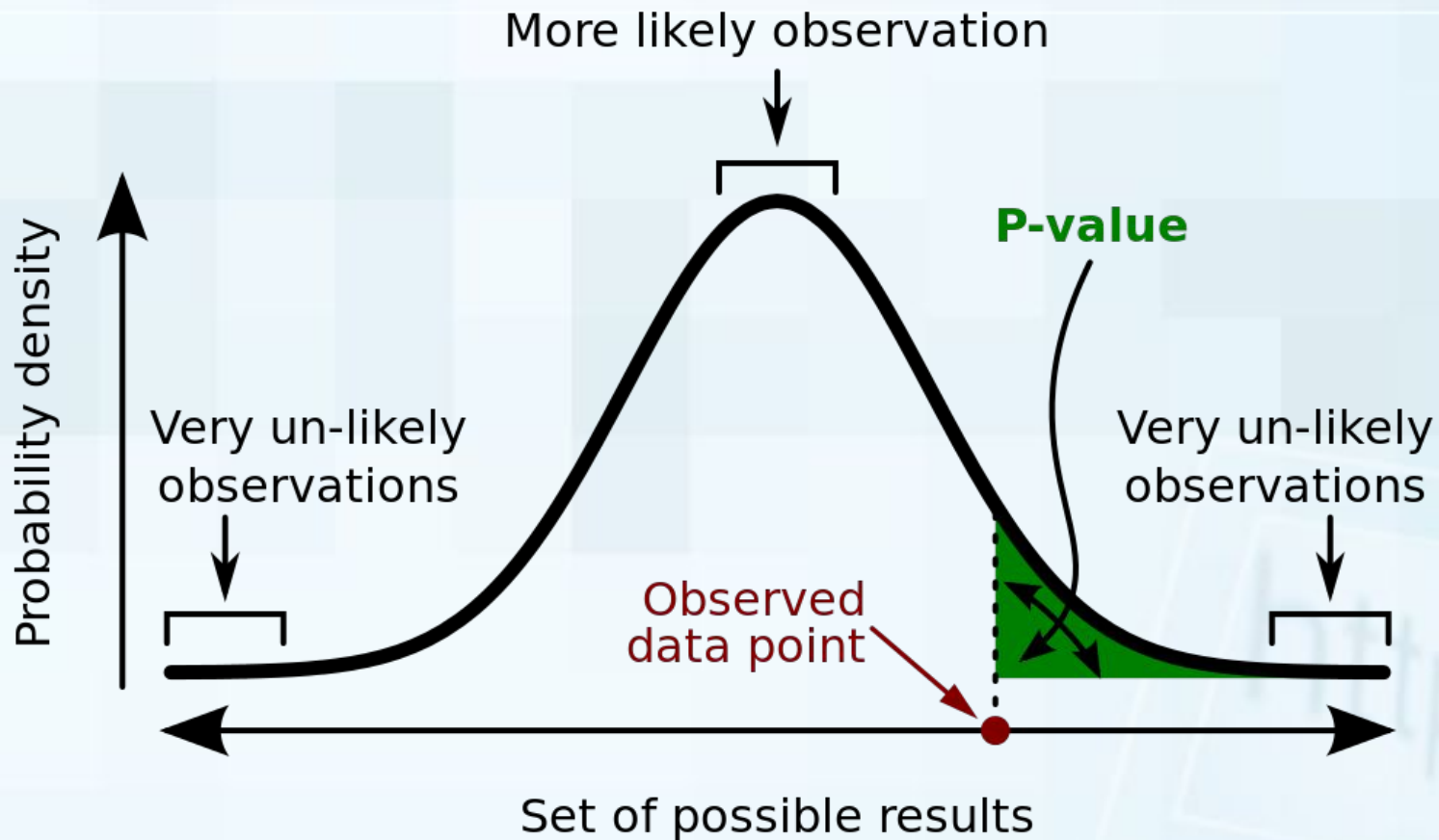
Hypothesis Testing



Hypothesis Testing

- Used to determine if different sets of observations come from the same underlying distribution
- Under NULL HYPOTHESIS assumption it is assumed that they come from the same distribution
- If the p-value assuming that the NULL HYPOTHESIS is true is less than 0.05 then NULL HYPOTHESIS is rejected

P-Value



A **p-value** (shaded green area) is the probability of an observed (or more extreme) result assuming that the null hypothesis is true.

Guideline for p-value

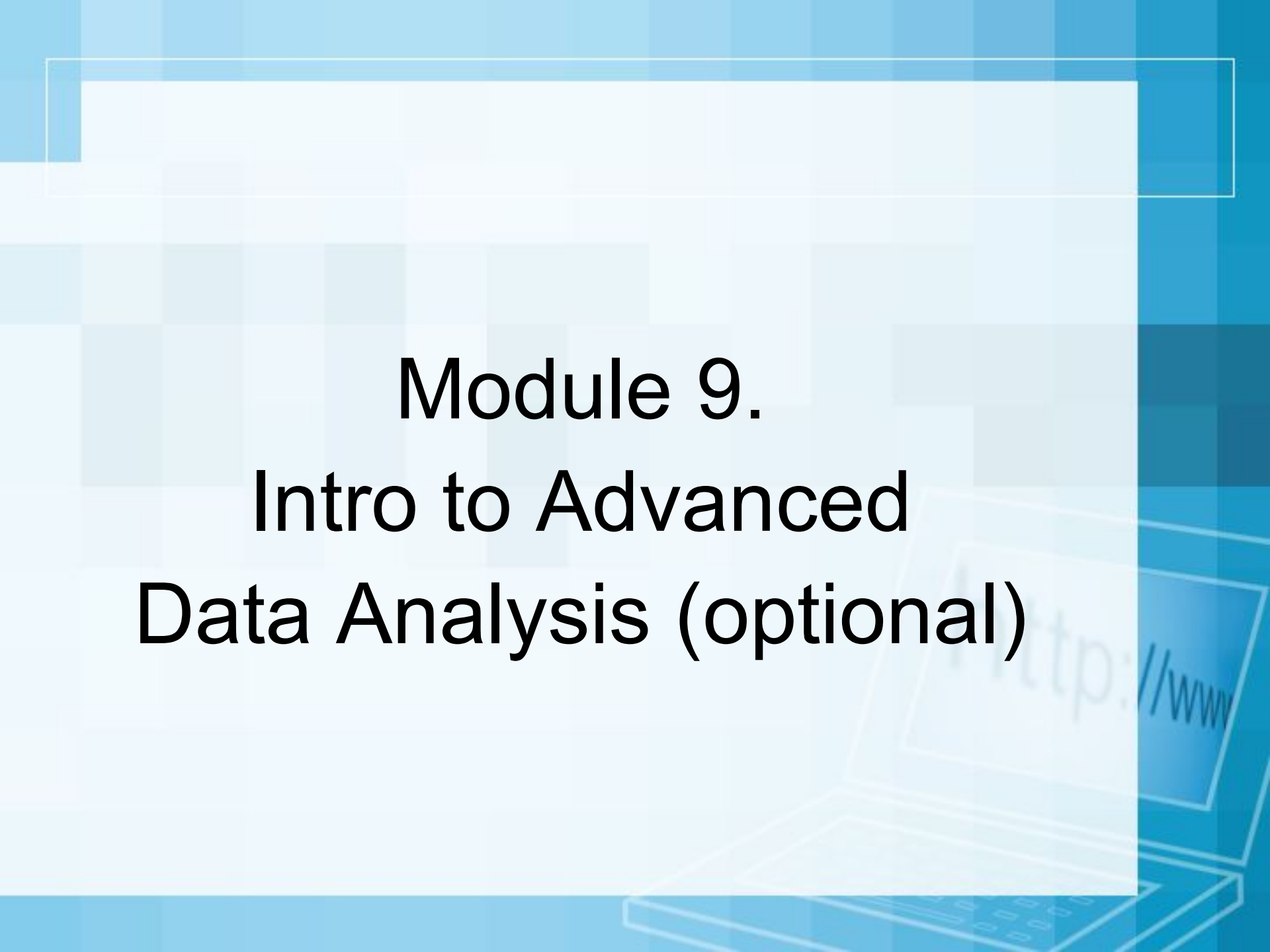
If p value $> .10 \rightarrow$ “not significant”

If p value $\leq .10 \rightarrow$ “marginally significant”

If p value $\leq .05 \rightarrow$ “significant”

If p value $\leq .01 \rightarrow$ “highly significant.”





Module 9.

Intro to Advanced Data Analysis (optional)

T-Test



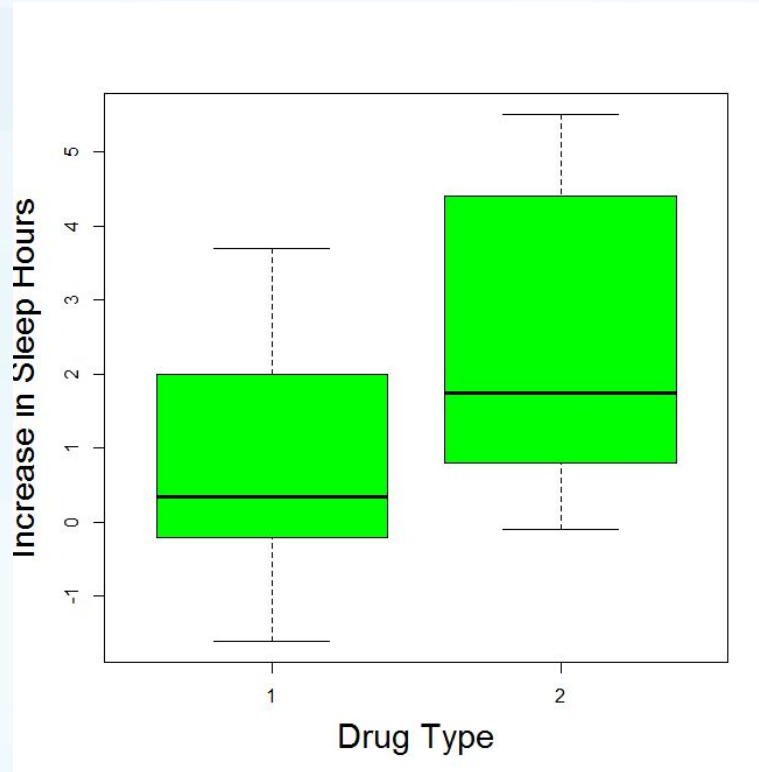
T-Test Application

To test if the mean of two different groups of observations differ, when the observations were carried out

- 1) on two different sets of participants
(independent group)
- 2) the same set of participants at different time
(paired)

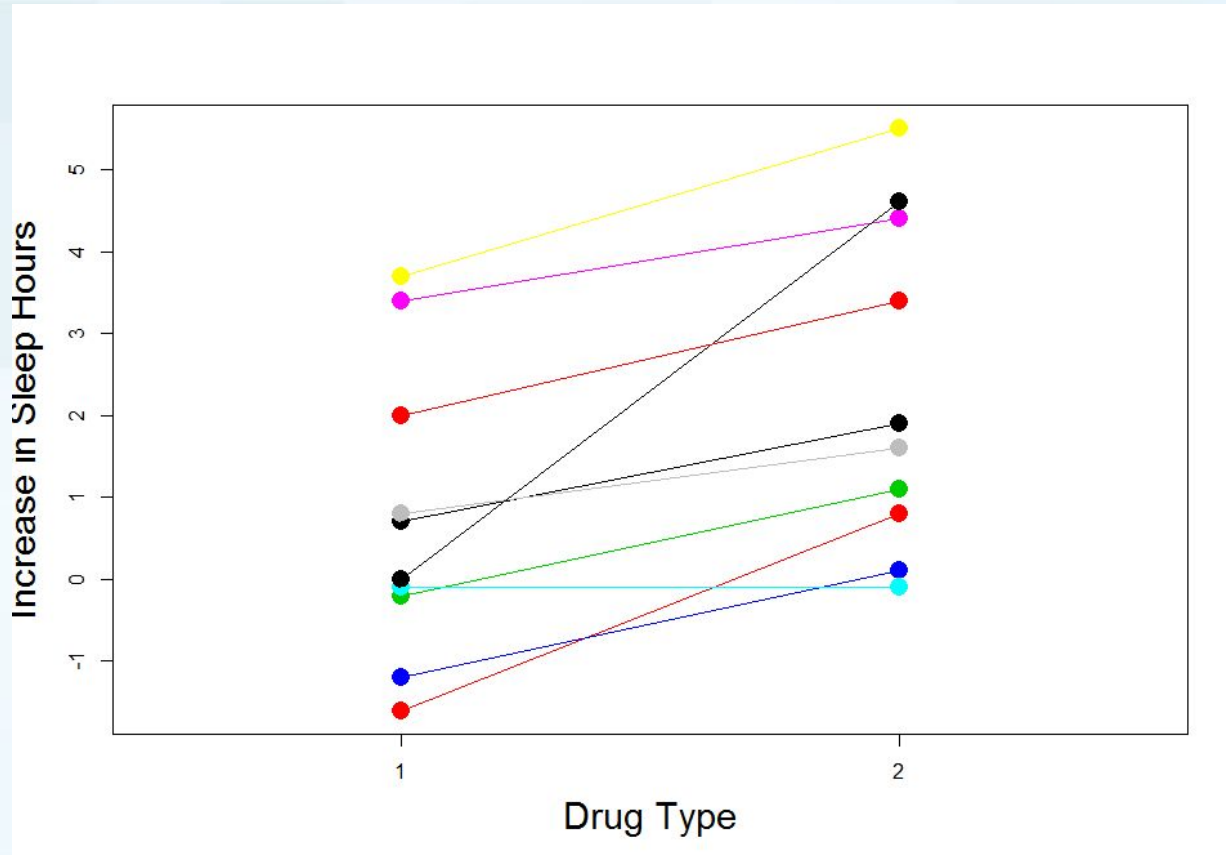


Are the mean increase in sleep hours different for the two drug types: 1



```
> t.test(extra~group,data = sleep)
```

Are the mean increase in sleep hours different for the two drug type: 2



```
> t.test(extra ~ group, sleep, paired=TRUE)
```

ANOVA

When there are more than 2 groups then we use ANOVA to test if there are statistically significant difference between the means.

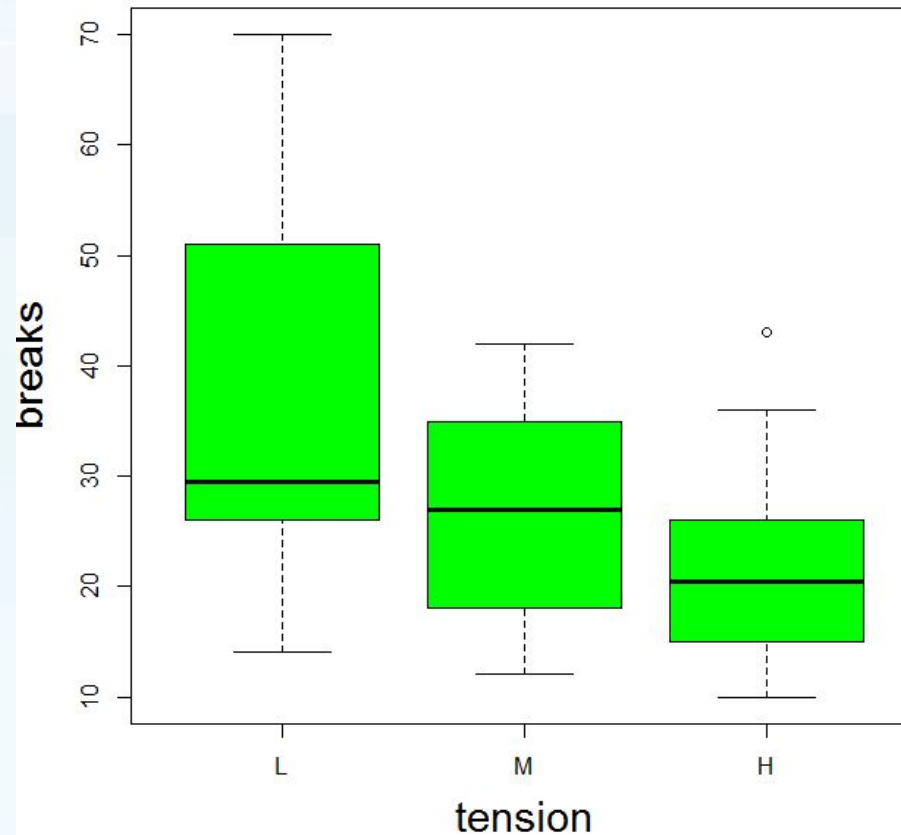
Anova does this by analysing the variance in the data set.



One Way ANOVA



Are there differences in the mean number of breaks when different tensions are applied

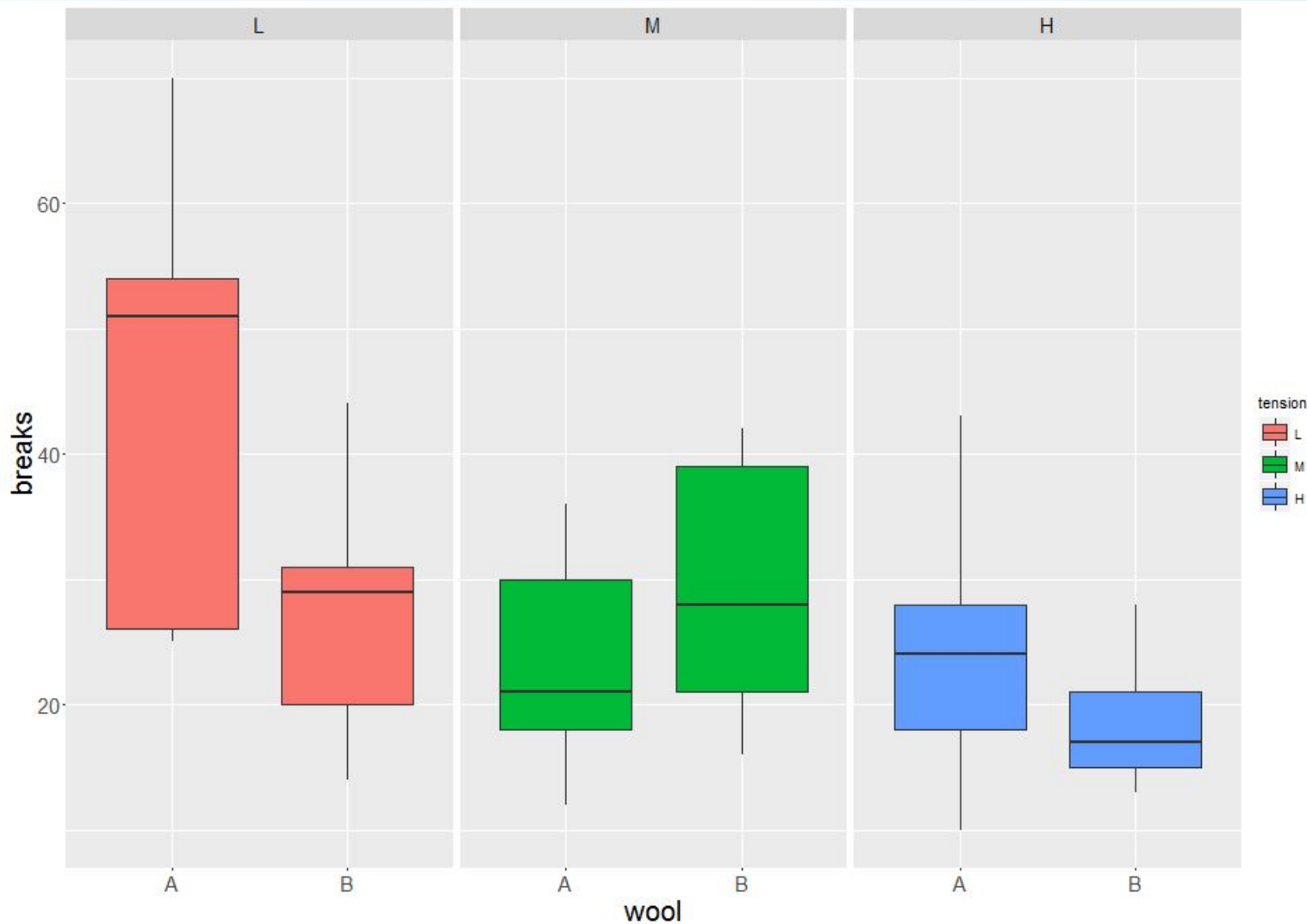


```
> aov1 <- aov(breaks ~ tension, data = warpbreaks)
> summary(aov1)
> TukeyHSD(aov1))
```

Two-Way ANOVA



Does the type of wool affects the number of breaks when different tension is applied?



Two -way ANOVA testing on warpbreaks data

```
> aov2 <- aov(breaks ~ wool + tension + wool:tension, data = warpbreaks)
```

```
> summary(aov2)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
wool	1	451	450.7	3.765	0.058213 .
tension	2	2034	1017.1	8.498	0.000693 ***
wool:tension	2	1003	501.4	4.189	0.021044 *
Residuals	48	5745	119.7		

```
> TukeyHSD(aov2)
```

```
> tapply(warpbreaks$breaks, list(warpbreaks$tension, warpbreaks$wool),  
mean)
```

Chi Square Test

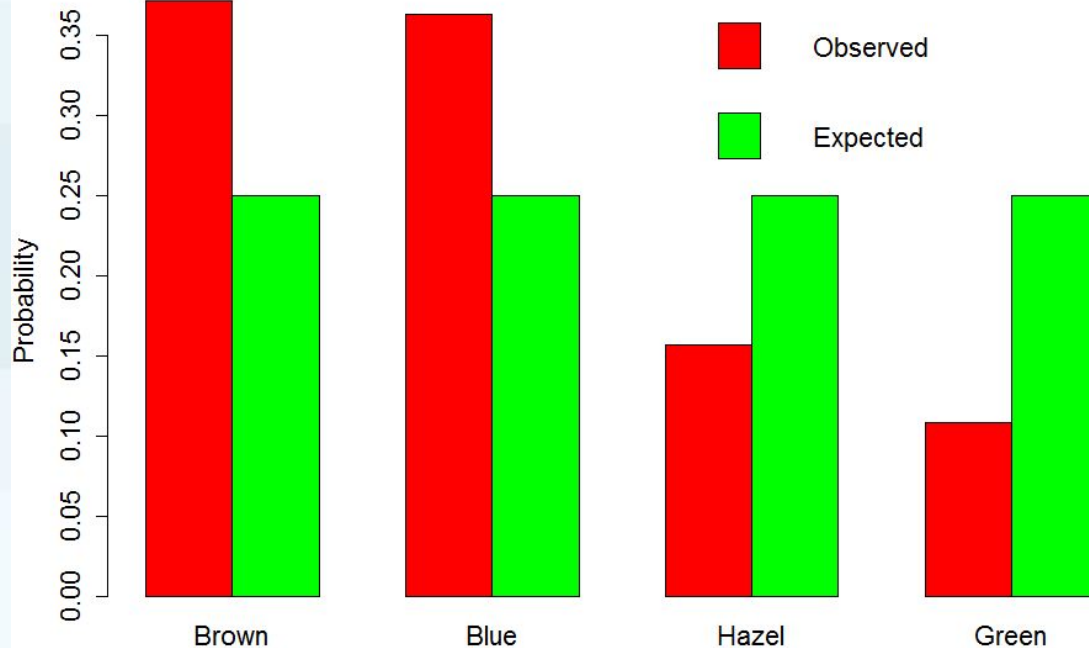


Chi Square Test Application

A chi-squared test, also referred to as χ^2 test (or chi-square test), is used to compare observed frequencies with the frequencies expected under some null hypothesis



Chi Square Test



```
> eyeCol <- apply(HairEyeColor, 2, sum)
> chisq.test(eyeCol, p = c(0.25, 0.25, 0.25, 0.25))
```

Cluster Analysis



Cluster Analysis

- Cluster analysis or clustering is the task of grouping a set of objects in such a way that objects in the same group (called a cluster) are more similar to each other than to those in other groups (clusters)
- Cluster analysis is used in data mining, machine learning, pattern recognition, image analysis, information retrieval, and bioinformatics.

Clustering Algorithm

- Hierarchical clustering (connectivity model)
- K Means clustering (centroid model)



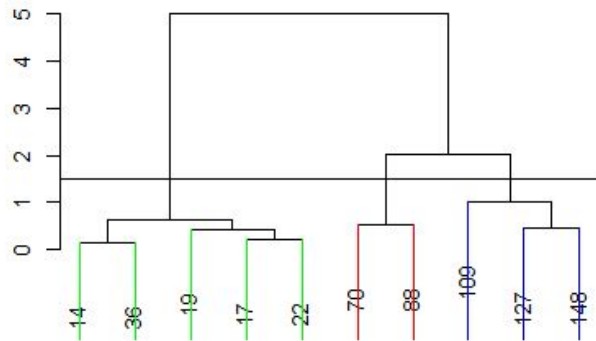
Hierarchical Clustering

- Hierarchical clustering connects "objects" to form "clusters" based on their distance.
- At different distances, different clusters will form, which can be represented using a dendrogram

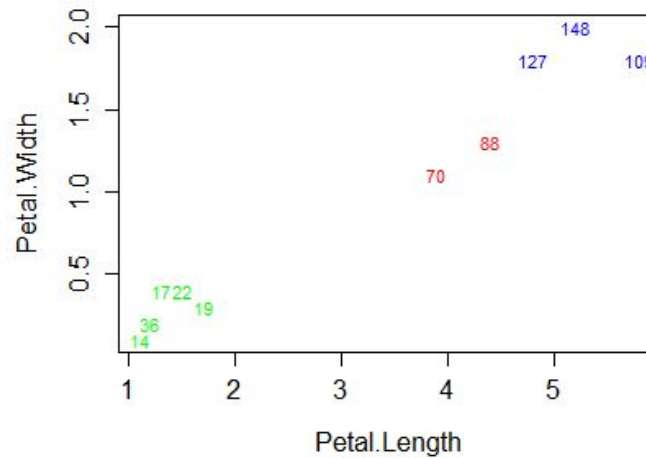


Hierarchical Clustering illustration on a subset of Iris data

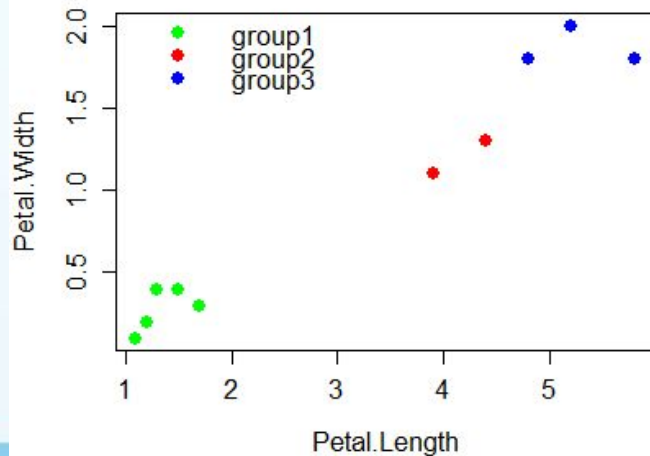
Dendrogram



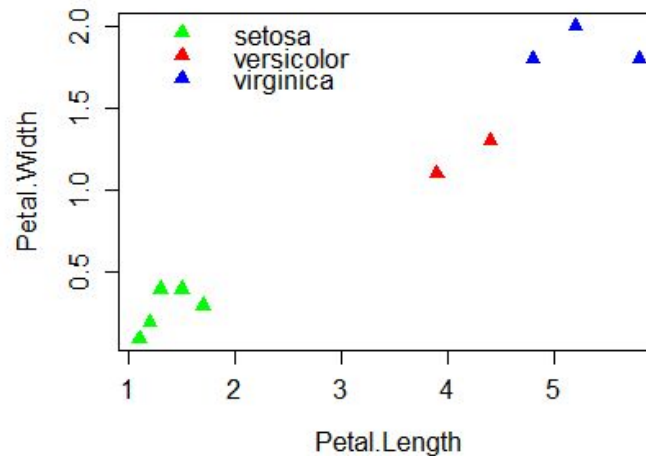
hclust (*, "complete")



Identified Groups



Actual Species



Hierarchical Clustering on a subset of iris dataset

```
### data preprocessing for hierarchical clustering.
```

```
> set.seed(4) # For reproducibility in subsetting
```

```
> index <- sample(c(TRUE, FALSE), nrow(iris), p = c(0.05, 0.95),  
replace = TRUE)
```

```
> myIris <- iris[index,3:4] # Choose only 5% of observations
```

```
### Clustering done on a subset of iris data which is named myIris
```

```
> disM <- dist(myIris) # calculate distance Matrix
```

```
> irisClust <- hclust(disM) # do hierarchical clustering
```

```
> clusters <- cutree(irisClust, k = 3) # make three clusters
```

```
> clusters # output the cluster associated with each observation
```

K- Means Clustering

- Place K points into the space represented by the objects that are being clustered. These points represent initial group centroids.
- Assign each object to the group that has the closest centroid.
- When all objects have been assigned, recalculate the positions of the K centroids.
- Repeat Steps 2 and 3 until the centroids no longer move. This produces a separation of the objects into groups from which the metric to be minimized can be calculated.

The diagram shows the objective function formula for K-Means clustering: $J = \sum_{j=1}^k \sum_{i=1}^n \|x_i^{(j)} - c_j\|^2$. Annotations include: 'number of clusters' pointing to k , 'number of cases' pointing to n , 'case i ' pointing to $x_i^{(j)}$, 'centroid for cluster j ' pointing to c_j , and 'Distance function' pointing to the norm $\|x_i^{(j)} - c_j\|^2$. The label 'objective function' is followed by an arrow pointing to J .

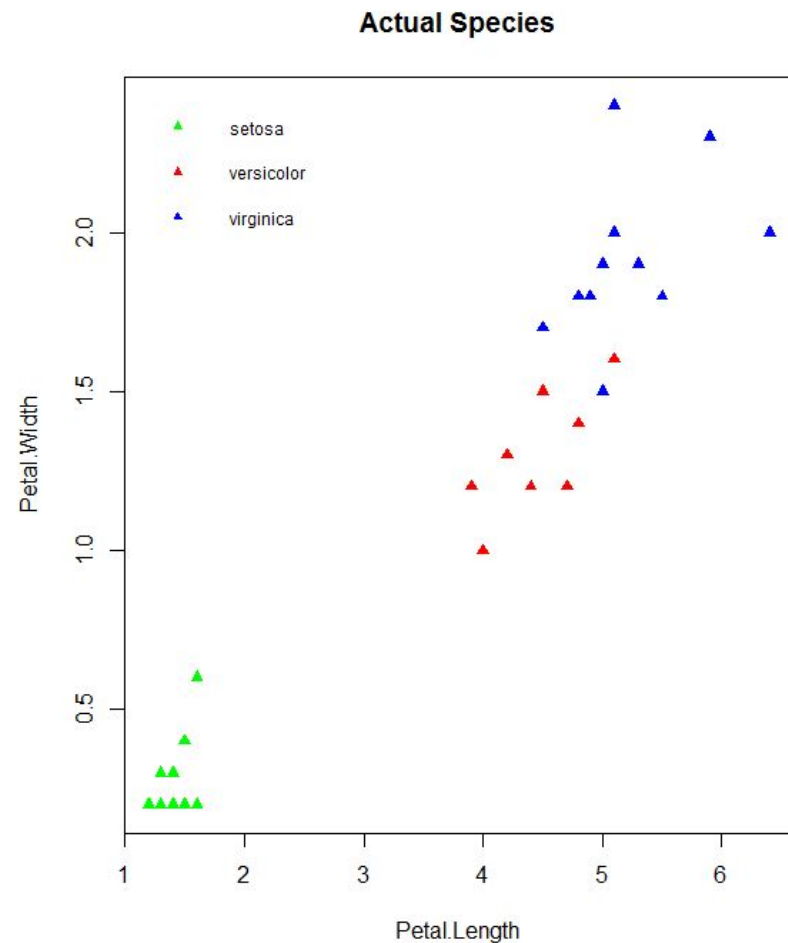
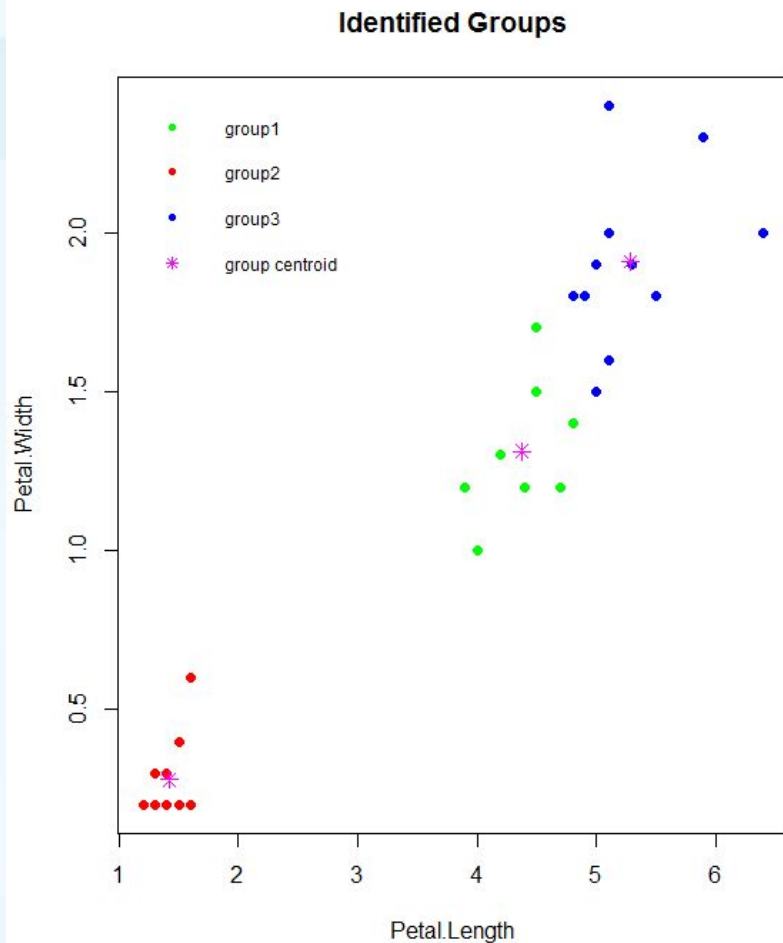
number of clusters number of cases centroid for cluster j

case i

objective function $\leftarrow J = \sum_{j=1}^k \sum_{i=1}^n \|x_i^{(j)} - c_j\|^2$

Distance function

K- Means Clustering illustration on subset of iris data set



K- Means Clustering on a subset of iris dataset

#Data Preprocessing

```
> set.seed(100)
> index <- sample(c(TRUE, FALSE), nrow(iris), p = c(0.2, 0.8), replace = TRUE)
> myIris <- iris[index,3:4]
> group <- iris$Species[index]
```

kmeans clustering on a subset of iris data set called myIris

```
> set.seed(100)
> predGroup <- kmeans(myIris, centers = 3, nstart = 10)
> predGroupC <- ifelse(predGroup$cluster==1, "setosa", ifelse(
  predGroup$cluster==2, "versicolor", "virginica"))
> predGroupC <- factor(predGroupC)
> table(predGroupC, group)
```

Resources

- R Packages : <https://cran.r-project.org/web/views/>
- R Packages http://cran.stat.ucla.edu/web/packages/available_packages_by_name.html
- R Packages <http://crantastic.org/>





Thank
You

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