

R Basics

I. Calculator

A. Example

2+2

exp (-2)

rnorm (15)

B. Symbolic variables

x <- 2

x +x

1. Variable names

- a. Built from letter, digits, and period
- b. Do not start with period- special case - reserved

C. Data vectors

Weight <- c(60, 72, 57, 90, 95, 72)

c (...) is construct

Weight

sum (Weight)

Calculator functions for calculating the mean:

sum (weight)/length (weight)

mean(weight)

sd(weight)

Height <- c(1.75, 1.80, 1.65, 1.90, 1.74, 1.91)

II. Vocabulary

A. Function Calls

log(x) # log is a function

plot (Height, Weight) # plot is a function

B. Arguments

log(x) # x is an argument

plot (Height, Weight) # height and weight are arguments

plot (Height, Weight, pch=2) # pch=2 - named actual argument

C. Vectors

1. Character vectors

```
Names <- c("Huey", "Dewey", "Louie")
```

```
Names
```

2. Logical vectors

```
State <- c(T,T,F,T)
```

```
State
```

D. Matrix and Arrays

1. Matrix- 2d vector

2. Array- 3d set of vectors

a. I encourage you to import your matrix from excel so we will not be discussing how to construct a matrix in R.

b. In most programming a 2d vector is called an array – confusing

3. Data frame- a data matrix or data set in other programs

a. Data and labels

II. Missing Values

1. NA

III. Help

```
?<Function name>
```

```
? plot
```

```
help (plot)
```

```
help.search (" graph") – when you do not know the function name
```

```
example (plot)
```

IV. Comments

```
# anything after the number sign is skipped – serves as a comment
```

V. Install a package

```
Demonstration
```

VI. Load a package

```
Library (ISwR)
```

VII. Set workspace

A. Make a directory called "Multi" on your drive

```
Example: C:\Working\Multi
```

B. Make a directory in the "Multi" directory called "Lab02"

```
Example: C:\Working\Multi\Lab02
```

VIII. Go to the lab webpage and download the data into the Lab2 directory that you just created

- A. Note the different links
 - 1. Directly to data
 - 2. To a linked webpage
- B. FOR DIRECT LINKS: Right click on the link and save the linked file to C:\Working\Multi\Lab02
- C. FOR LINKED WEBPAGES: Left click on the link to go to the next page and then right click on the data link and save the linked file to C:\Working\Multi\Lab02

IX. Edit data in Excel and export it for R

- A. Open the dataset Men.xlsx using Excel
- B. Inspect the dataset
 - 1. Case in rows, variables in columns
 - 2. First row variables name (remember rule for variable names)
 - a. No spaces
 - b. Names should be descriptive
 - c. Short names are better
 - 3. First column case names
 - 4. Missing values are NA
 - 5. Clean/delete empty space - that MIGHT have had data prior
- C. Export data as a tab- delimited
 - i. File → save as → save as type
 - a. Select text (tab delimited)
 - ii. Close Excel

X. Setting the working directory

- A. Start R
- B. Example
- C. `setwd("C:\\Working\\ Multi \\Lab2\\")`

XI. Importing dataset into R

`Men <- read.table (file=" C:\Working\Multi\Lab02\\Men.txt", header = TRUE)`

XII. Structure function

`str(Men)`

Checkup: Import the Energy.txt dataset into R. Then apply the structure function to confirm proper import. Call the file/dataset in R Energy. Ask for help if you have problems.

XIII. Data Frame and related functions

A. \$ sign

```
Energy$expend
```

B. Unique function

```
unique (Energy$stature)
```

C. Subsetting data

```
ObeseL <- Energy$stature == "obese"
```

```
ObeseL
```

```
Obese <- Energy [ObeseL, ]
```

```
Obese
```

D. Joining data sets

1. Import part 1 name part1

```
part1 <- read.table("C:\\Multi\\part1.txt", header =TRUE)
```

2. Import part 2 name part2

```
part2 <- read.table("C:\\Multi\\part2.txt", header =TRUE)
```

3. Merge the two data sets based on variable "Sample"

```
Whole <- merge (part1, part2, by = "Sample")
```

E. Exporting data (Explain line wrap in this portion)

```
write.table (Whole, file = "C:\\Working\\Multi\\something.txt", sep="," ,  
quote=TRUE, append = FALSE, na = "NA")
```

```
write.table (Whole,  
file = "C:\\Multi\\something.txt",  
sep = "," ,  
quote = TRUE,  
append = FALSE,  
na = "NA")
```

F. Basic function

1. Import file Vegetation.txt in into matrix "Veg"

```
names (Veg)
```

```
str(Veg)
```

```
m <- mean(Veg$R)
```

```
m
```

```
m1 <- mean(Veg$R[Veg$Transect == 1])
```

Show how to backspace to modify

```
m2 <- mean(Veg$R[Veg$Transect == 2])
```

```

m3 <- mean(Veg$R[Veg$Transect == 3])
m4 <- mean(Veg$R[Veg$Transect == 4])
m5 <- mean(Veg$R[Veg$Transect == 5])
m6 <- mean(Veg$R[Veg$Transect == 6])
m7 <- mean(Veg$R[Veg$Transect == 7])
m8 <- mean(Veg$R[Veg$Transect == 8])

```

2. t apply

More efficient

```
tapply(Veg$R, Veg$Transect, mean)
```

can be sd- standard deviation, var- variance, length- length more?

```
Means <- tapply (Veg$R, Veg$Transect, mean)
```

```
SDeviations <- tapply (Veg$R, Veg$Transect, sd)
```

```
SSizes <- tapply (Veg$R, Veg$Transect, length)
```

Means

SDeviations

SSizes

XIV. Bar Graph

```
Color.Table <- table(Men$Color)
```

```

barplot (Color.Table,
beside = TRUE,
legend = FALSE,
ylim = c(0,140), # Length of y axis
ylab = "Frequency", # Y axis label
main = "") # graph title

```

Notice the switch in focus to the graphics window.

```
box()
```

```
barplot (Color.Table, beside = TRUE, legend = FALSE, ylim = c(0,140), ylab =
"Frequency", main = "")
```

? barplot

```
Example(barplot)
```

XV. Histogram

```
hist(Men$Height, main = "", xlab = "Height (cm)", ylim = c(0,80))
```

```
box()
```

? hist
example (hist)

XVI. Box Plot

- A. Also known as a box and whisker plot
- B. Center line represents the median
- C. Upper and lower parts of the box present the upper and lower quartile limits. (IQR)
- D. Lower whisker - The lowest value that is no smaller than 1.5 IQR
- E. Upper whisker - The largest value that is no larger than 1.5 IQR
- F. Region between the whiskers should contain 99% of data if normally distributed

```
boxplot (Class$Height ~ Class$Sex, # Variable by species
data = Class, # Dataset
ylab = " Height (cm)", # y axis label
main = "Class Measurements", # Graph title
boxwex = 0.5) # Width of boxes
```

```
boxplot (Class$Height ~ Class$Sex, data = Class, ylab = "Height (cm)", main =
"Class Measurements", boxwex = 0.5)
```

? boxplot
example (boxplot)

XVII. Scatterplot

```
plot (x = Class$Height, y = Class$Mass,
xlab = "Height (cm)",
ylab = "Mass (kg)",
main = "Class Measurements",
xlim = c(0,200),
ylim = c(0,120),
pch = 16, #controls data symbol on plot (1-25)
cex = 1.25, # controls data symbol size on plot (multiples)
col = Class$Sex) # controls data color on plot (1-8)
```

```
plot (x = Class$Height, y = Class$Mass, xlab = "Height (cm)", ylab = "Mass (kg)",
main = "Class Measurements", xlim = c(0,200), ylim = c(0,120), pch = 16, cex = 1.25,
col = Class$Sex)
```

? plot
example (plot)

XVIII. Line Graph

1. Import the CellBio dataset into R and name it CellBio

```
# Determines the number of treatments = the number of lines in the graph
nTreatment <- max(CellBio$Treatment)
# Determines the range of the data for the X and Y axes
xrange <- range(CellBio$Time)
yrange <- range(CellBio$Weight)

# Establishes the axes for the graph
plot(xrange, yrange, type="n", xlab="Time (mins)", ylab="Percent
Change in Mass")

# Sets the graph parameters (line color and type)
colors <- rainbow(nTreatment)
linetype <- c(1:nTreatment)

# Plots the data and lines in the graph by iterating through the different #
treatments
plotchar <- seq(18, 18+nTreatment, 1)
for (i in 1:nTreatment) {
  treatment <- subset(CellBio, Treatment==i)
  lines(treatment$Time, treatment$Weight,
  type="b",
  lwd=2,
  lty=linetype[i],
  col=colors[i],
  pch=plotchar[i]
  )
}
title("")

# Builds the legend for the graph
legend(xrange[1], yrange[2], unique(CellBio$Solution), cex=0.8,
col=colors,
pch=plotchar,
lty=linetype,
title="Solution"
)
```

XIX. Saving graphics as a file

- A. Right click on the graph
- B. Select save as enhanced metafile (.emf)
- C. Navigate to where you want to save the file.
- D. Give the file a name.
- E. Click save.

XX. Quitting R

q()

XXI. Recording Work

1. A record of commands -> can recreate the workspace later