

# SCS 2211 - Laboratory II

#### Importing Data

- We can import data into R using several formats
- o TXT → name=read.table("filename.txt",header=TRUE)
- CSV → name=read.csv("filename.csv",header=TRUE)

### Reading Data into R

- read.table, read.csv, for reading tabular data
- readLines, for reading lines of a text file
- source, for reading in R code files (inverse of dump)
- dget, for reading in R code files (inverse of dput)
- load, for reading in saved workspaces
- o unserialize, for reading single R objects in binary form

#### Importing Data

```
> #Reading a csv file
> iris data=read.csv("/Users/Piyumi/Downloads/Iris.csv")
> head(iris data)
 i..sepal.length sepal.width petal.length petal.width variety
          5.1
                                      0.2 Setosa
                   3.5
                             1.4
          4.9
                   3.0
                          1.4
                                     0.2 Setosa
                3.2 1.3
          4.7
                                     0.2 Setosa
                         1.5
          4.6 3.1
                                     0.2 Setosa
                         1.4
                3.6
          5.0
                                     0.2 Setosa
                          1.7
          5.4
                   3.9
                                     0.4 Setosa
```

#### Paths And Directory Names

In windows system:

```
"\Users\Piyumi\Downloads\Iris.csv"
```

But in previous slide (slide No: 04) we have used

```
"/Users/Piyumi/Downloads/Iris.csv"
```

 In R, we use forward slashes for the directories because backslashes are actually used for escape characters.

```
> double_quote <- "\"" # or '"'
> single_quote <- '\'' # or "'"
> double_quote
[1] "\""
> writeLines(double_quote)
"
> |
```

#### dput() and dump()

```
> y <- data.frame(a = 1, b = "a")</pre>
> dput(y)
structure(list(a = 1, b = "a"), class = "data.frame", row.names = c(NA,
-1L))
> ## Send 'dput' output to a file
> dput(y, file = "y.R")
> ## Read in 'dput' output from a file
> new.y <- dget("y.R")
> new.y
 a b
1 1 a
                                     > x <- "foo"
                                     > y <- data.frame(a = 1L, b = "a")</pre>
                                     > dump(c("x", "y"), file = "data.R")
                                     > rm(x, y)
                                     > source("data.R")
                                     > str(y)
                                     'data.frame': 1 obs. of 2 variables:
                                      $ a: int 1
                                      $ b: chr "a"
```

```
> matHap
   DYS19 DXYS156Y DYS389m DYS389n DYS389p DYS389q DYS390m DYS390n DYS390p
      14
               12
                                12
H1
                                                 10
                                                                  10
      15
               13
                                13
                                                   9
                                                                  10
H3
      15
               11
                                                 10
H4
                                                                  10
H5
      17
               13
                                11
                                                 10
                                                                  10
H7
      13
               12
                                12
                                                 11
                                                                  11
      16
               11
                                12
                                                 10
                                                                  10
H8
H9
      16
               11
                                11
                                                                  10
                                                 10
   DYS390q DYS392 DYS393 YAPbcbc SRY1532bb 92R7bb
               15
                       13
H1
H3
               13
                       12
H4
               11
                       14
                       12
H5
               14
                       14
H7
               14
H8
               11
                       15
H9
               11
                       14
> #save as a R object
> save(matHap,file="matHap.RData")
> #save as a txt file
> save(matHap,file="matHap.RData")
> #read the saved txt file
> file.show("matHap.txt")
```

## Working with data - Names

- R objects can have names.
- Matrices and data frames can have both column and row names.

Object	Set column names	Set row names
data frame	names()	row.names()
matrix	colnames()	rownames()

#### Working with data - Missing Values

- NA
- NAN
- NA values have a class also, so there are integer NA, character NA, etc.
- We can use complete.cases(), na.omit (), na.rm() to clean missing values.

#### Working with data – Replacing Missing Values

- NA
- NAN
- NA values have a class also, so there are integer NA, character NA, etc.
- We can use complete.cases(), na.omit (), na.rm() to clean missing values.

#### Working with data – Replacing Missing Values

#### MICE

```
> #data imputation
> install.packages("mice")
Installing package into 'C:/Users/Piyumi/Documents/R/win-library/4.1'
(as 'lib' is unspecified)
--- Please select a CRAN mirror for use in this session ---
trying URL 'https://cloud.r-project.org/bin/windows/contrib/4.1/mice 3.13.0.zip'
Content type 'application/zip' length 2041441 bytes (1.9 MB)
downloaded 1.9 MB
package 'mice' successfully unpacked and MD5 sums checked
The downloaded binary packages are in
        C:\Users\Piyumi\AppData\Local\Temp\RtmpcTgLSj\downloaded packages
> library(mice)
```

### Working with data – Replacing Missing Values

```
> data(mammalsleep)
> dim(mammalsleep)
[1] 62 11
> md.pattern(mammalsleep)
   species bw brw pi sei odi ts mls gt ps sws
42
 ?mammalsleep
starting httpd help server ... done
> imputed Data <- mice(mammalsleep, m=5, maxit = 50, method = 'pmm', seed = 500)
```

### Working with data – Assignment 1

- Download the resource file given in Ims.
- 2. Read all the data in births into "birth\_new" and save it as "birth\_new.Rdata".
- 3. Select the births that happen only on Saturday into sat1 and display 5 rows of the resulting data.
- 4. Use the "dplyr" package to follow next steps.
- 5. Filter the births happen on "day\_of\_week == 6" into sat2.
- 6. Try using "Sat2 <- birthn %>% filter(day\_of\_week == 6)". What did you get?
- 7. Format your data output received in step 3 using "as\_tibble()".
- 8. Group the births\_new by the day\_of\_week.
- 9. Get the group means.
- 10. Sort the result of step 9.
- 11. Get the summary.
- 12. Repeat step 8,9,10 in a nested operation.

#### Working with data

- x % f(y) is equivalent to just executing f(x,y)
- o If we need to execute a sequence of functions: h(g(f(x,y),z),m)
- $\circ$  We can use x %>% f(y) %>% g(z) %>% h(m) that gives the same answer.
- To find out the average of Friday 13th births:

```
> birthn %>%
+ filter(day_of_week == 5) %>%
+ filter(date_of_month == 13) %>%
+ summarise(mean(births))
   mean(births)
1     11949.96
> |
```