

# Data Manipulation

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# Reading Data

## scan()

scan() reads data into a vector or list from the console or from file

- scan is more appropriate when all the data to be read are of the same mode
- Arguments:
  - file: Name of a file. When "", reads from the console
  - what: Type of what gives the type of data to be read. what can also be a list
  - scan calls can be embedded in a call to matrix

```
matrix(scan(), ncol = 3, byrow = TRUE)
```

# Data Frames

## `read.table`

- The `read.table` function is used to read data into R in the form of a data frame, i.e., data with mixed modes
- `read.table` expects each field (variable) to be separated by separators (by default, spaces, tabs, newlines or carriage returns)
  - The `sep` argument can be used to specify an alternative separator
- R provides convenience functions for reading comma- and tab-separated data

`read.csv`

Separated by ,

`read.csv2`

Separated by ; decimal point ,

`read.delim`

Separated by tabs

`read.delim2`

Separated by tabs, decimal point ,

These functions are wrappers for `read.table` with the `sep` argument set appropriately

# Data Frames

## `read.table`: Useful options

---

<code>file</code>	File to be read or a <i>connection</i>
<code>sep</code>	e.g., <code>"\t"</code> , <code>" "</code> , <code>"</code>
<code>dec</code>	Specify decimal point (default is <code>.</code> )
<code>header</code>	TRUE if the the first line are the column names (default to TRUE for <code>read.csv...</code> )
<code>col.names</code>	A vector of column names
<code>stringsAsFactors</code>	Logical. If FALSE, prevent the automatic conversion of character strings into factors
<code>na.strings</code>	By default, NA, NaN, Inf and -Inf are considered as missing values. Change this behaviour using <code>na.strings</code>
<code>skip</code> and <code>nrows</code>	Number of lines to skip and number of lines to read, respectively
<code>fill</code>	If TRUE, observations with fewer variables are filled with NAs or blanks
<code>colClasses</code>	Specify the modes of the columns to be read
<code>fileEncoding</code>	Encoding of the file. Useful for non ASCII characters from other platforms

---

# Data Frames

## Fixed Width Input Files

- Files without delimiters but for which each variable is stored in one column
- Can be read in R using the `read.fwf`
  - `file`: the file to be read
  - `widths`: vector containing the widths of the fields to be read

# readLines

- `readLines` reads some or all text lines from a file or a connection
- Useful, for example, if only some lines of an enormous file need to be read
  - `con`: a connection or file name
  - `n`: The maximal number of lines to read. Negative values indicate that the whole file should be read

# Connections

- Connections provide a flexible way to read data from a variety of sources
- Connections can be used as input for, e.g., `read.table` or `readLines`

Function	Data source
<code>file</code>	Local files
<code>url</code>	Remote read via http or ftp
<code>gzfile</code>	Local gzipped file
<code>unz</code>	Local zip archive
<code>pipe</code>	Output from a command
...	



# Connections

```
myCon <- url("http://taz.de/")
aa <- readLines(myCon, 3)
aa

## [1] "<!DOCTYPE html SYSTEM \"about:legacy-compat\">"
## [2] "<html xmlns=\"http://www.w3.org/1999/xhtml\" xmlns:my=\"mynames\""
## [3] "\t\tContent Management: openNewspaper www.opennewspaper.org based

close(myCon)
```

## Other useful functions

Function	Format
<code>load</code>	Read R data format <code>.rda</code> , <code>.RData</code>
<code>read.dta</code>	Read data saved by Stata ( <b>foreign</b> package)
<code>read.spss</code>	Read data from SPSS ( <b>foreign</b> )
<code>read.ssd</code> , <code>read.xport</code>	Read SAS files

- Read a data from Excel
  - **Export from Excel into a .csv file**
  - On Windows, the **RODBC** package permits to access Excel files
  - **gdata** package — for all platforms. Requires some specific perl modules to be installed
  - **xlsx** package. Requires Java / installation tricky
  - **readxl** package. Not tested (released 15.4.2015)

# The **readr** package

The **readr** package provides alternatives to the base `read.*` functions that are

- 10 times faster (according to <http://blog.rstudio.org/2015/04/09/readr-0-1-0/>)
- more consistent
- more flexible column specification
- ...

`read_csv`

Separated by ,

`read_csv2`

Separated by ; decimal point ,

`read_tsv`

Separated by tabs

`read_delim`

Separated by arbitrary delimiter

# The **readr** package

Three important arguments (similar for all functions)

`file` File name

`col_names` column name; equivalent to header.

- `TRUE`  $\Leftrightarrow$  `header = TRUE` in base R
- `FALSE`
- A character vector to use as column names

`col_types` Override the default column types

Default to `stringsAsFactors = FALSE`!

# Writing Data

- The `save` function can be used to save R objects

```
save(a_data_set, x, y, file = "my_data.rda")
```

- The `write` function
  - Takes an R object and the name of a file or a connection as arguments
  - Writes a ASCII representation of the object
  - The `ncolumns` argument specifies the number of values to write on each line

# Writing Data

- The `write.table` function
  - Requires the name of a data set or matrix (if no file is specified, `write.table()` writes into the console)
  - The `file` argument specifies the destination. `file` can also be a connection
  - `row.names` and `col.names` specify whether to write the rows' and columns' names, respectively
  - `sep` specifies the separator. Default is blank
  - `write.csv` and `write.csv2` available for writing comma-separated files

# Your Turn

- The zip file `data.zip` contains several versions of the same (fake) data set
  - `data1.rda` can be opened using `load()` and will serve as reference
  - `data2` to `data5` are ASCII files
  - `data6.xls` is an Excel file that is rather realistic
- Read all the data sets in R and check whether they compare to the original using, e.g.,

```
all(dd1 == dd2) # dd2 being another data set
```

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# Factors

- Factor are variables in R that take on a limited number of different values
  - Categorical variables
  - Ordinal variables
- Factors are useful for statistical modelling as ordinal variables should be treated differently than continuous variables
- Factors are also useful for statistical report generation. Think SAS labels

# Factors

- Factors are stored internally as numeric values
- A corresponding set of characters is used for displaying

```
aa <- factor(c("cats", "dogs", "apples"))
aa

## [1] cats  dogs  apples
## Levels: apples cats dogs

as.integer(aa)

## [1] 2 3 1
```

# Factor Creation

- Factors are created using the `factor` function
- The `levels` argument permits to control the order
- The `labels` argument is used to change the levels' names
- `ordered = TRUE` creates an ordered factor (ordinal variable)

```
set.seed(21324)
data <- sample(c(1, 2, 3), 10, TRUE)
f0 <- factor(data)
f1 <- factor(data, levels = c(2, 3, 1))
f2 <- factor(data, labels = c("I", "II", "III"))
f3 <- factor(data, levels = c(2, 3, 1),
             labels = c("II", "III", "I"))
```

```
table(f0)
```

```
## f0  
## 1 2 3  
## 4 3 3
```

```
table(f1)
```

```
## f1  
## 2 3 1  
## 3 3 4
```

```
table(f2)
```

```
## f2  
##   I   II  III  
##   4   3   3
```

```
table(f3)
```

```
## f3  
##  II III  I  
##   3   3  4
```

# Factors

- The `levels()` function can be used to change the labels once a factor has been created

```
levels(f0) <- c("I", "II", "III")
f0

## [1] II I III III III I I II I II
## Levels: I II III
```

- The reference level of a factor can be changed using the `relevel` function

```
f0 <- relevel(f0, "II")
f0

## [1] II I III III III I I II I II
## Levels: II I III
```

# Ordered Factors

```
set.seed(433443534)
mon <- sample(month.name, 29, TRUE)
table(factor(mon))
```

```
##
##      April      August  December  February  January      July      June
##          3          2          5          2          3          3          2
##      March      May      November  September
##          1          3          3          2
```

```
mon2 <- factor(mon, levels = month.name,
               ordered = TRUE)
table(mon2)
```

```
## mon2
##      January  February      March      April      May      June      July
##           3          2          1          3          3          2          3
##      August  September  October  November  December
##           2          2          0          3          5
```

Order operator can be used with ordered factors

# When Factors Are a PITA

```
set.seed(423423)
ff <- factor(sample(1:4, 10, TRUE))
```

```
mean(ff)
```

```
## Warning in mean.default(ff): argument is not numeric or logical:
returning NA
```

```
## [1] NA
```

```
ff + 10
```

```
## Warning in Ops.factor(ff, 10): '+' not meaningful for factors
```

```
## [1] NA NA NA NA NA NA NA NA NA
```

```
c(ff, 10) # Not a factor anymore
```

```
## [1] 1 2 1 1 2 1 3 1 2 3 10
```

# When Factors Are a PITA

```
(a <- factor(sample(letters, 10, replace = TRUE)))
```

```
## [1] a u o j i h d g n d  
## Levels: a d g h i j n o u
```

```
(b <- factor(sample(letters, 10, replace = TRUE)))
```

```
## [1] t y k g v k p b d d  
## Levels: b d g k p t v y
```

```
c(a, b)
```

```
## [1] 1 9 8 6 5 4 2 3 7 2 6 8 4 3 7 4 5 1 2 2
```



# When Factors Are a PITA

```
(a <- factor(sample(letters, 10, replace = TRUE)))
```

```
## [1] a u o j i h d g n d  
## Levels: a d g h i j n o u
```

```
(b <- factor(sample(letters, 10, replace = TRUE)))
```

```
## [1] t y k g v k p b d d  
## Levels: b d g k p t v y
```

```
c(a, b)
```

```
## [1] 1 9 8 6 5 4 2 3 7 2 6 8 4 3 7 4 5 1 2 2
```

```
factor(c(as.character(a), as.character(b)))
```

```
## [1] a u o j i h d g n d t y k g v k p b d d  
## Levels: a b d g h i j k n o p t u v y
```

# Factors

- Pros
  - Needed for modelling categorical variable
  - Memory efficient, i.e., factors only need to store values as integer and the unique levels as character strings
  - Nice output

```
table(factor(c(1, 2, 3),  
             labels = c("Healthy", "Diseased", "Dead")))  
  
##  
##   Healthy Diseased      Dead  
##         1         1         1
```

- Cons
  - Require to be cautious for some data manipulation
- I'd recommend reading data using the option `stringsAsFactors=FALSE` and transform variables into factors as needed

# Dates

R provides several options to deal with dates, which is a challenging problem, i.e., time zones, daylight savings, leap second, ...

- `as.Date` handles dates without time
- The **chron** package handles dates and times, but without support for time zones
- The `POSIXct` and `POSIXlt` allow for dates and times with control for time zones
- The **lubridate** packages is supposed to facilitate the use of dates and times in R

**Rule of thumb:** Use the simplest technique possible. If you only have dates, use `as.Date`

# Dates

## as.Date

- `as.Date` accepts a variety of input style through the `format` argument
- Default is `yyyy-mm-dd`

```
as.Date("2014-06-12")
```

```
## [1] "2014-06-12"
```

```
as.Date("12.6.2014", format = "%d.%m.%Y")
```

```
## [1] "2014-06-12"
```

```
as.Date("12 June 14", format = "%d %B %y")
```

```
## [1] "2014-06-12"
```

See `?strptime` for a complete list of format symbols

# Dates

## as.Date

- Internally, dates are stored as the number of days since January 1, 1970
- as.numeric can be used to convert a date to its numeric form

```
as.integer(as.Date("2014-06-12"))
```

```
## [1] 16233
```

- The weekdays and months functions can be used to extract the dates' components
- Calculation on dates: See ?Ops.Date. Addition, subtraction, logical operations (==, <, ...) are available

# Dates

## POSIXct and POSIXlt

- POSIXct is represented as seconds since January 1, 1970 GMT
  - POSIXlt is represented as a list
- Use POSIXct for calculation and POSIXlt for extracting date components

```
(t1 <- as.POSIXct("2014-06-12 10:15:00"))
```

```
## [1] "2014-06-12 10:15:00 CEST"
```

```
(t2 <- as.POSIXlt("2014-06-12 10:15:00"))
```

```
## [1] "2014-06-12 10:15:00 CEST"
```

# Dates

## POSIXct and POSIXlt

```
## Internal representation of t2  
str(unclass(t2))
```

```
## List of 11  
## $ sec : num 0  
## $ min : int 15  
## $ hour : int 10  
## $ mday : int 12  
## $ mon : int 5  
## $ year : int 114  
## $ wday : int 4  
## $ yday : int 162  
## $ isdst : int 1  
## $ zone : chr "CEST"  
## $ gmtoff: int NA
```

# Your Turn

Consider the data set `data7.csv`

- 1 Read the data
- 2 Compute the age of the patients
- 3 `CO_DIABETES` equals 1 if patients have diabetes, otherwise 0
  - Create a factor `Diabetes` with levels `Yes` and `No` with reference value `No`
- 4 `CO_LIVER` equals 1 for mild liver disease, 2 for severe liver disease and 0 for no liver disease
  - Create a factor `Liver_Disease` with levels `Mild`, `Severe`, `No` with reference value `No`
- 5 Create a factor `Gender` with levels `Female` (`sex == 0`) and `Male` (`sex == 1`)



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# Subscripting

- Logical subscripts

```
nums <- c(12, 9, 8, 14, 7, 16, 3, 2, 9)
nums > 10
```

```
## [1] TRUE FALSE FALSE TRUE FALSE TRUE FALSE FALSE FALSE
```

```
nums[nums > 10]
```

```
## [1] 12 14 16
```

```
which(nums > 10)
```

```
## [1] 1 4 6
```

```
nums[which(nums > 10)]
```

```
## [1] 12 14 16
```

```
nums[nums > 10] <- 0
```

```
nums
```

```
## [1] 0 9 8 0 7 0 3 2 9
```

# Subscripting Matrices and Arrays

```
(mat <- matrix(1:12, 4, 3))
```

```
##      [,1] [,2] [,3]
## [1,]    1    5    9
## [2,]    2    6   10
## [3,]    3    7   11
## [4,]    4    8   12
```

```
mat[, c(3, 1)]
```

```
##      [,1] [,2]
## [1,]    9    1
## [2,]   10    2
## [3,]   11    3
## [4,]   12    4
```

# Subscripting Matrices and Arrays

```
mat[, 1]
```

```
## [1] 1 2 3 4
```

```
mat[, 1, drop = FALSE]
```

```
##      [,1]
```

```
## [1,]    1
```

```
## [2,]    2
```

```
## [3,]    3
```

```
## [4,]    4
```

```
mat[mat > 4]
```

```
## [1]  5  6  7  8  9 10 11 12
```

# Lists

Lists are the most general R object.

```
(ll <- list(a = 1:3, b = month.name[1:5], c = c(TRUE, FALSE),
           d = data.frame(y = rnorm(5), x = rbinom(5, 1, .5))))

## $a
## [1] 1 2 3
##
## $b
## [1] "January" "February" "March"    "April"    "May"
##
## $c
## [1] TRUE FALSE
##
## $d
##           y x
## 1 -1.1065764 0
## 2  1.6957258 0
## 3 -1.0641906 1
## 4 -0.0415854 1
## 5  0.8534742 0
```

# Lists

```
class(ll[[4]]); class(ll[["d"]]); class(ll$d)
```

```
## [1] "data.frame"  
## [1] "data.frame"  
## [1] "data.frame"
```

```
class(ll[4])
```

```
## [1] "list"
```

```
ll[c(1, 3)]
```

```
## $a  
## [1] 1 2 3  
##  
## $c  
## [1] TRUE FALSE
```

# Subscripting Data Frames

```
set.seed(4234234)
(df <- data.frame(x = c(rnorm(3), NA, 3),
                     y = c(NA, rexp(2, 0.01), NA, 3)))
```

```
##           x           y
## 1  1.7547348          NA
## 2 -0.3676785 108.34508
## 3 -1.5529115  85.43826
## 4           NA          NA
## 5  3.0000000   3.00000
```

```
df$x
```

```
## [1]  1.7547348 -0.3676785 -1.5529115          NA  3.0000000
```

```
df[, "x", drop = FALSE]
```

```
##           x
## 1  1.7547348
## 2 -0.3676785
## 3 -1.5529115
```

# Subscripting Data Frames

```
df[df$y > 10, ]
```

```
##           x           y
## NA         NA         NA
## 2    -0.3676785 108.34508
## 3    -1.5529115  85.43826
## NA.1         NA         NA
```

```
df[!is.na(df$y) & df$y > 10, ]
```

```
##           x           y
## 2    -0.3676785 108.34508
## 3    -1.5529115  85.43826
```

```
subset(df, y > 10)
```

```
##           x           y
## 2    -0.3676785 108.34508
## 3    -1.5529115  85.43826
```



# Subscripting Data Frames

```
subset(df, y > 10, select = x)
```

```
##           x
## 2 -0.3676785
## 3 -1.5529115
```

```
subset(df, y > 10, select = 1)
```

```
##           x
## 2 -0.3676785
## 3 -1.5529115
```

## Order a data frame

```
df[order(df$x), ]
```

```
##           x           y
## 3 -1.5529115  85.43826
## 2 -0.3676785 108.34508
## 1  1.7547348      NA
## 5  3.0000000   3.00000
## 4           NA      NA
```

# Your Turn

- 1 Compute a variable `hypertension` that equals 1 if `DIAS > 120` **and** `SYS > 80`
- 2 Compute a variable `Hypotension` that equals 1 if `DIAS < 100` **and** `SYS < 65`
- 3 Create a variable that equals 1 if the patient's `CITY` is in New York state (NY)
- 4 Create a data set that contains the patients that have hypotension or hypertension don't live in New York state

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# Data Aggregation

- For simple tabulation and cross-tabulation, the `table`, `fTable` and `xTable` functions are available
- For more complex tasks, the available functions can be classified into two groups
  - Functions that operate on arrays and/or lists (e.g., `*apply`, `sweep`)
  - Functions oriented towards data frames (e.g., `aggregate`, `by`)

# The table function

```
data(iris)
```

```
head(iris)
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	5.1	3.5	1.4	0.2	setosa
## 2	4.9	3.0	1.4	0.2	setosa
## 3	4.7	3.2	1.3	0.2	setosa
## 4	4.6	3.1	1.5	0.2	setosa
## 5	5.0	3.6	1.4	0.2	setosa
## 6	5.4	3.9	1.7	0.4	setosa

# The table function

```
table(iris$Species)
```

```
##  
##      setosa versicolor  virginica  
##      50         50         50
```

```
table(iris$Species, iris$Petal.Length > 6)
```

```
##  
##              FALSE TRUE  
##   setosa         50    0  
##   versicolor     50    0  
##   virginica      41    9
```

```
as.data.frame(table(iris$Species, iris$Petal.Length > 6))
```

```
##      Var1  Var2 Freq  
## 1   setosa FALSE  50  
## 2 versicolor FALSE  50  
## 3  virginica FALSE  41  
## 4   setosa  TRUE   0  
## 5 versicolor  TRUE   0
```

# The table function

```
table(iris$Species, iris$Petal.Length > 6, iris$Sepal.Width > 3.5)
```

```
## , , = FALSE
```

```
##
```

```
##
```

```
##           FALSE TRUE
```

```
##   setosa      34    0
```

```
##   versicolor  50    0
```

```
##   virginica   41    6
```

```
##
```

```
## , , = TRUE
```

```
##
```

```
##
```

```
##           FALSE TRUE
```

```
##   setosa      16    0
```

```
##   versicolor   0    0
```

```
##   virginica    0    3
```

# The table function

```
as.data.frame(table(iris$Species, iris$Petal.Length > 6, iris$Sepal.Width
```

##		Var1	Var2	Var3	Freq
## 1		setosa	FALSE	FALSE	34
## 2		versicolor	FALSE	FALSE	50
## 3		virginica	FALSE	FALSE	41
## 4		setosa	TRUE	FALSE	0
## 5		versicolor	TRUE	FALSE	0
## 6		virginica	TRUE	FALSE	6
## 7		setosa	FALSE	TRUE	16
## 8		versicolor	FALSE	TRUE	0
## 9		virginica	FALSE	TRUE	0
## 10		setosa	TRUE	TRUE	0
## 11		versicolor	TRUE	TRUE	0
## 12		virginica	TRUE	TRUE	3



# The table function

## addmargins

```
tt <- table(iris$Species, iris$Petal.Length > 6)
```

```
addmargins(tt, margin = 1)
```

```
##  
##           FALSE TRUE  
##   setosa      50    0  
##   versicolor  50    0  
##   virginica   41    9  
##   Sum       141    9
```

```
addmargins(tt, margin = c(1, 2))
```

```
##  
##           FALSE TRUE Sum  
##   setosa      50    0  50  
##   versicolor  50    0  50  
##   virginica   41    9  50  
##   Sum       141    9 150
```

# The table function

## prop.table

```
prop.table(tt, margin = 1)
```

```
##  
##           FALSE TRUE  
##   setosa      1.00 0.00  
##   versicolor  1.00 0.00  
##   virginica   0.82 0.18
```

```
prop.table(tt, margin = 2)
```

```
##  
##           FALSE      TRUE  
##   setosa      0.3546099 0.0000000  
##   versicolor  0.3546099 0.0000000  
##   virginica   0.2907801 1.0000000
```

# The ftable function

The ftable function creates **flat** tables

```
ftable(iris$Species, iris$Petal.Length > 6, iris$Sepal.Width > 3.5)
```

```
##                FALSE TRUE
##
## setosa      FALSE    34   16
##             TRUE      0    0
## versicolor FALSE    50    0
##             TRUE      0    0
## virginica   FALSE    41    0
##             TRUE      6    3
```

# The xtabs function

The xtabs function produces similar results as the table function but uses the formula interface

```
iris$sepal_width <- factor(as.integer(iris$Sepal.Width > 3.5),  
                           levels = c(0, 1),  
                           labels = c("<= 3.5", "> 3.5"))
```

```
with(iris, table(Species, sepal_width))
```

```
##           sepal_width  
## Species    <= 3.5 > 3.5  
##   setosa         34   16  
##   versicolor     50    0  
##   virginica      47    3
```

```
xtabs(~ Species + sepal_width, iris)
```

```
##           sepal_width  
## Species    <= 3.5 > 3.5  
##   setosa         34   16  
##   versicolor     50    0  
##   virginica      47    3
```

# Missing values with table

## The useNA and exclude Arguments

```
iris$sepal_widthNA <- iris$sepal_width  
iris$sepal_widthNA[seq(1, 150, 25)] <- NA
```

```
with(iris, table(Species, sepal_widthNA))
```

```
##           sepal_widthNA  
## Species    <= 3.5 > 3.5  
##   setosa      32    16  
##   versicolor  48     0  
##   virginica   45     3
```

```
with(iris, table(Species, sepal_widthNA, useNA = "ifany"))
```

```
##           sepal_widthNA  
## Species    <= 3.5 > 3.5 <NA>  
##   setosa      32    16     2  
##   versicolor  48     0     2  
##   virginica   45     3     2
```

```
## If there is NAs, they will be included
```

# Missing values with `table`

## The `useNA` and `exclude` Arguments

```
with(iris, table(Species, sepal_widthNA, useNA = "always"))
```

```
##              sepal_widthNA
## Species      <= 3.5 > 3.5 <NA>
##   setosa         32    16     2
##   versicolor    48     0     2
##   virginica     45     3     2
##   <NA>           0     0     0
```

```
with(iris, table(Species, sepal_width, useNA = "always"))
```

```
##              sepal_width
## Species      <= 3.5 > 3.5 <NA>
##   setosa         34    16     0
##   versicolor    50     0     0
##   virginica     47     3     0
##   <NA>           0     0     0
```

```
## An NA column is always included, even if there is no missing values
```

## The `useNA` argument is specific to `table`

# Missing values with `table`

## The `useNA` and `exclude` Arguments

### The `exclude` argument

- By default, `exclude = c(NA, NaN)`
- E.g., `exclude = NULL` to include missing values

```
with(iris, table(Species, sepal_widthNA, exclude = NULL))
```

```
##           sepal_widthNA
## Species    <= 3.5 > 3.5 <NA>
##   setosa      32    16     2
##   versicolor  48     0     2
##   virginica   45     3     2
##   <NA>         0     0     0
```

```
## equivalent to useNA = "always"
```

# Missing values with table

## The useNA and exclude Arguments

```
with(iris, table(Species, sepal_widthNA, exclude = "setosa"))
```

```
##           sepal_widthNA
## Species    <= 3.5 > 3.5
## versicolor    48     0
## virginica     45     3
```

```
with(iris, table(Species, sepal_widthNA, exclude = "setosa", useNA = "ifany"))
```

```
##           sepal_widthNA
## Species    <= 3.5 > 3.5 <NA>
## versicolor    48     0     2
## virginica     45     3     2
```

- `exclude = NULL` is equivalent to `useNA="always"`
- `exclude = "somethingElse"` only exclude level "somethingElse" from the factor



# Road Map for Aggregation

Three things to consider

- 1 How are the groups that divide the data defined?
- 2 What is the nature of the data to be operated on?
- 3 What is the desired end result

# Groups Defined as Lists Elements

`sapply` or `lapply` are the appropriate functions

- `lapply` always returns a list
- `sapply` tries to “simplify” the output

# Groups Defined as Lists Elements

`sapply` or `lapply` are the appropriate functions

- `lapply` always returns a list
- `sapply` tries to “simplify” the output

```
myList <- list()
for (i in 1:4) {
  myList[[i]] <- rnorm(n = 3 * i)
}
myList

## [[1]]
## [1]  0.3429579 -0.3193258  0.7808710
##
## [[2]]
## [1]  1.16866312  0.01419804  0.45813283 -0.43180622  0.34224696 -1.30745260
##
## [[3]]
## [1]  1.4005004 -1.7575754 -0.2415508  1.0928182 -1.1926425  1.8645074
## [7] -0.3128976  0.8755070 -1.9690762
##
## [[4]]
## [1]  1.1415283 -1.1269112 -2.2914106  0.9855559 -1.4959317  2.2773178
## [7]  0.5160894 -0.5481570 -0.6098171 -1.4302086  1.2207910 -1.7708338
```

# Groups Defined as Lists Elements

Both for `lapply` and `sapply`, the first argument is a list, the second argument is a function

Third, fourth, ... arguments are further arguments for the function that is applied

```
lapply(myList, length)
```

```
## [[1]]  
## [1] 3  
##  
## [[2]]  
## [1] 6  
##  
## [[3]]  
## [1] 9  
##  
## [[4]]  
## [1] 12
```

```
sapply(myList, length)
```

```
## [1] 3 6 9 12
```

# Groups Defined as Lists Elements

```
myList[[2]][c(3, 5)] <- NA  
sapply(myList, mean)
```

```
## [1] 0.26816768 NA -0.02671217 -0.26099896
```

```
sapply(myList, mean, na.rm = TRUE)
```

```
## [1] 0.26816768 -0.13909942 -0.02671217 -0.26099896
```

```
sapply(myList, quantile, probs = c(0.25, 0.75), na.rm = TRUE)
```

```
##           [,1]           [,2]           [,3]           [,4]  
## 25% 0.0118160 -0.6507178 -1.192642 -1.446639  
## 75% 0.5619144 0.3028143 1.092818 1.024549
```

# Groups Defined as Lists Elements

```
## A user defined function
lapply(myList, function(x) {
  data.frame(
    Mean = mean(x, na.rm = TRUE),
    SD = sd(x, na.rm = TRUE),
    Min = min(x, na.rm = TRUE),
    Max = max(x, na.rm = TRUE))
})

## [[1]]
##      Mean      SD      Min      Max
## 1 0.2681677 0.5538984 -0.3193258 0.780871
##
## [[2]]
##      Mean      SD      Min      Max
## 1 -0.1390994 1.030286 -1.307453 1.168663
##
## [[3]]
##      Mean      SD      Min      Max
## 1 -0.02671217 1.411432 -1.969076 1.864507
##
## [[4]]
##      Mean      SD      Min      Max
## 1 -0.260999 1.446369 -2.291411 2.277318
```

# Groups Defined as Lists Elements

```
## A user defined function
sapply(myList, function(x) {
  data.frame(
    Mean = mean(x, na.rm = TRUE),
    SD = sd(x, na.rm = TRUE),
    Min = min(x, na.rm = TRUE),
    Max = max(x, na.rm = TRUE))
})
```

	[,1]	[,2]	[,3]	[,4]
## Mean	0.2681677	-0.1390994	-0.02671217	-0.260999
## SD	0.5538984	1.030286	1.411432	1.446369
## Min	-0.3193258	-1.307453	-1.969076	-2.291411
## Max	0.780871	1.168663	1.864507	2.277318

# Groups Defined as Lists Elements

```
mySummary <- function(x, na.rm = FALSE) {
  data.frame(
    Mean = mean(x, na.rm = na.rm),
    SD = sd(x, na.rm = na.rm),
    Min = min(x, na.rm = na.rm),
    Max = max(x, na.rm = na.rm))
}
```

```
sapply(myList, mySummary, na.rm = TRUE)
```

##	[,1]	[,2]	[,3]	[,4]
## Mean	0.2681677	-0.1390994	-0.02671217	-0.260999
## SD	0.5538984	1.030286	1.411432	1.446369
## Min	-0.3193258	-1.307453	-1.969076	-2.291411
## Max	0.780871	1.168663	1.864507	2.277318



# Groups Defined as Lists Elements

`sapply` or `lapply` can be used as alternative to loops. This way you don't have to take care too much of the form of the output

```
## check type 1 error of the t-test
check_level <- function(i, n = 100) {
  a <- rnorm(n)
  b <- rnorm(n)
  tt <- t.test(a, b)
  tt$p.value < 0.05
}
```

```
nsimul <- 1000
res <- sapply(1:nsimul, check_level, n = 100)
sum(res) / nsimul

## [1] 0.047
```

# Groups Defined as Lists Elements

For this kind of simple repetitive tasks, the `replicate` function can also be used

```
res2 <- replicate(nsimul, t.test(rnorm(10), rnorm(10))$p.value < 0.05)  
sum(res2) / nsimul  
  
## [1] 0.044
```

- First argument is the number of replication
- Second argument is an *expression*, i.e., a piece of R language and not a function

# Groups Defined by Rows or Columns of a Matrix/Array

In this case, the `apply` function is the logical choice.

The `apply` function requires three arguments

- the array/matrix on which to operate
- An index telling `apply` which dimension to operate on (1 on rows; 2 on columns, c(1, 2) on both)
- The function to use
- Optionally further arguments to be used by the function that we want to apply

```
apply(iris[, 1:4], 2, mean)
```

```
## Sepal.Length  Sepal.Width Petal.Length  Petal.Width  
##      5.843333      3.057333      3.758000      1.199333
```

# Groups Defined by Rows or Columns of a Matrix/Array

```
apply(iris[, 1:4], 2, mySummary)
```

```
## $Sepal.Length
##      Mean      SD Min Max
## 1 5.843333 0.8280661 4.3 7.9
##
## $Sepal.Width
##      Mean      SD Min Max
## 1 3.057333 0.4358663  2 4.4
##
## $Petal.Length
##      Mean      SD Min Max
## 1 3.758 1.765298  1 6.9
##
## $Petal.Width
##      Mean      SD Min Max
## 1 1.199333 0.7622377 0.1 2.5
```

# Groups Defined by Rows or Columns of a Matrix/Array

`rowSums`, `colSums`, `rowMeans`, `colMeans`

These are specialised functions that are potentially way faster than `apply` (which is a general function)

```
colMeans(iris[, 1:4], na.rm = TRUE)
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width  
##      5.843333      3.057333      3.758000      1.199333
```

```
colSums(iris[, 1:4] > 2, na.rm = TRUE)
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width  
##           150           149           100           23
```

# Groups Based on One or More Grouping Variables

A very common operation

A lot of choice in base R + a couple of additional packages that facilitates these operations

- aggregate
- tapply, by
- *split-apply-combine* strategy
  - split, lapply, do.call
  - **plyr**, **dplyr** package
  - ...

# Groups Based on One or More Grouping Variables

## aggregate

A natural choice for data summaries of several variables

- First argument: A formula
  - LHS: Variables to “summarise”
  - RHS: Grouping variables
- Second argument: A data frame
- Third argument: Function to apply
- ...; Further arguments for FUN

```
aggregate(cbind(Sepal.Length, Sepal.Width) ~ Species, iris, mean)
```

```
##      Species Sepal.Length Sepal.Width
## 1      setosa      5.006      3.428
## 2 versicolor      5.936      2.770
## 3  virginica      6.588      2.974
```

# Groups Based on One or More Grouping Variables

## aggregate

```
iris$Petal.Length.f <- factor(iris$Petal.Length > 4.8,  
                             levels = c(FALSE, TRUE),  
                             labels = c("Small petals", "Big petals"))  
aggregate(cbind(Sepal.Length, Sepal.Width) ~ Species + Petal.Length.f,  
          data = iris, FUN = mean)
```

```
##      Species Petal.Length.f Sepal.Length Sepal.Width  
## 1      setosa   Small petals      5.006000      3.428000  
## 2 versicolor   Small petals      5.889130      2.765217  
## 3 virginica    Small petals      5.700000      2.766667  
## 4 versicolor   Big petals      6.475000      2.825000  
## 5 virginica    Big petals      6.644681      2.987234
```



# Groups Based on One or More Grouping Variables

## `tapply`

Returns an array with as many dimensions as there were vectors that defined the groups, but can only process a single vector

```
with(iris, tapply(X = Sepal.Length,  
                  INDEX = list(Species, Petal.Length.f),  
                  FUN = mean))
```

```
##           Small petals Big petals  
## setosa      5.00600      NA  
## versicolor  5.88913    6.475000  
## virginica   5.70000    6.644681
```

# Groups Based on One or More Grouping Variables

## tapply

Also works if FUN does not return a scalar

```
with(iris, tapply(X = Sepal.Length,  
                  INDEX = Species,  
                  FUN = range))
```

```
## $setosa  
## [1] 4.3 5.8  
##  
## $versicolor  
## [1] 4.9 7.0  
##  
## $virginica  
## [1] 4.9 7.9
```

# Groups Based on One or More Grouping Variables

## tapply

```
(tt <- with(iris, tapply(X = Sepal.Length,  
                        INDEX = list(Species, Petal.Length.f),  
                        FUN = range)))
```

```
##           Small petals Big petals  
## setosa      Numeric,2      NULL  
## versicolor Numeric,2      Numeric,2  
## virginica   Numeric,2      Numeric,2
```

In this case, a matrix of lists is returned...

# Groups Based on One or More Grouping Variables

## tapply

But individual elements can still be accessed

```
tt[["setosa", "Small petals"]]
```

```
## [1] 4.3 5.8
```

```
str(tt)
```

```
## List of 6
## $ : num [1:2] 4.3 5.8
## $ : num [1:2] 4.9 7
## $ : num [1:2] 4.9 6.2
## $ : NULL
## $ : num [1:2] 6 6.9
## $ : num [1:2] 5.6 7.9
## - attr(*, "dim")= int [1:2] 3 2
## - attr(*, "dimnames")=List of 2
## ..$ : chr [1:3] "setosa" "versicolor" "virginica"
## ..$ : chr [1:2] "Small petals" "Big petals"
```

# Groups Based on One or More Grouping Variables

by

- `by` is a version of `tapply` oriented towards data frames
- First argument is a data frame, others are as in `tapply`
- `by` returns a list

```
## Don't work, because iris is a data frame
```

```
by(iris[, 1:4], iris$Species, mean)
```

```
## Warning in mean.default(data[x, , drop = FALSE], ...): argument is not numeric or logical:  
returning NA
```

```
## Warning in mean.default(data[x, , drop = FALSE], ...): argument is not numeric or logical:  
returning NA
```

```
## Warning in mean.default(data[x, , drop = FALSE], ...): argument is not numeric or logical:  
returning NA
```

```
## iris$Species: setosa
```

```
## [1] NA
```

```
## -----
```

```
## iris$Species: versicolor
```

```
## [1] NA
```

```
## -----
```

```
## iris$Species: virginica
```

```
## [1] NA
```

# Groups Based on One or More Grouping Variables

## by

```
(ex_by <- by(iris[, 1:4], iris[, "Species"], colMeans))
```

```
## iris[, "Species"]: setosa
## Sepal.Length Sepal.Width Petal.Length Petal.Width
##           5.006           3.428           1.462           0.246
## -----
## iris[, "Species"]: versicolor
## Sepal.Length Sepal.Width Petal.Length Petal.Width
##           5.936           2.770           4.260           1.326
## -----
## iris[, "Species"]: virginica
## Sepal.Length Sepal.Width Petal.Length Petal.Width
##           6.588           2.974           5.552           2.026
```

# Groups Based on One or More Grouping Variables

## by

```
do.call(rbind, ex_by)
```

```
##           Sepal.Length Sepal.Width Petal.Length Petal.Width
## setosa             5.006         3.428         1.462         0.246
## versicolor        5.936         2.770         4.260         1.326
## virginica         6.588         2.974         5.552         2.026
```

- `do.call` takes a *list* of arguments (second argument)
- and prepares a call to a function (first argument), using the list elements as if they had been passed to the function as individual arguments

# Groups Based on One or More Grouping Variables

## Split-Apply-Combine

Term coined by Hadley Wickham (author of the **ggplot2**, **plyr**, **reshape**, **dplyr**, ..., packages)

**Split** Divide the problem into smaller pieces

**Apply** Work on each pieces independently

**Combine** Recombine the pieces

A common problem for both programming and data analysis; many implementations

- In base R: `split()`, `*apply()`, `do.call()`
- R-packages: **plyr**, **doBy**, **dplyr**, **data.table** (to some extent)



# Split-Apply-Combine

## Base R

- Split by species

```
s_iris <- split(iris, iris$Species)

## s_iris is a list with number of items
## equal to the number of levels of iris$Species
length(s_iris) == length(levels(iris$Species))

## [1] TRUE
```

- Apply a function to each item of the list

```
s_means <- lapply(s_iris, function(x) colMeans(x[1:4]))
s_means[[1]]

## Sepal.Length Sepal.Width Petal.Length Petal.Width
##           5.006           3.428           1.462           0.246
```

- Combine

```
(res <- do.call(rbind, s_means))

##           Sepal.Length Sepal.Width Petal.Length Petal.Width
## setosa           5.006           3.428           1.462           0.246
## versicolor       5.936           2.770           4.260           1.326
## virginica        6.588           2.974           5.552           2.026
```

# Split-Apply-Combine

## Base R

```
myLM <- function(x) {  
  temp <- lm(Sepal.Length ~ Petal.Length, x)  
  summary(temp)$coefficients  
}  
  
(res <- lapply(split(iris, iris$Species), myLM))  
  
## $setosa  
##           Estimate Std. Error  t value    Pr(>|t|)  
## (Intercept)  4.2131682   0.4155888 10.137830 1.614927e-13  
## Petal.Length  0.5422926   0.2823153  1.920876 6.069778e-02  
##  
## $versicolor  
##           Estimate Std. Error  t value    Pr(>|t|)  
## (Intercept)  2.407523   0.4462583  5.394909 2.075294e-06  
## Petal.Length  0.828281   0.1041364  7.953806 2.586190e-10  
##  
## $virginica  
##           Estimate Std. Error  t value    Pr(>|t|)  
## (Intercept)  1.0596591  0.46676645  2.270213 2.772289e-02  
## Petal.Length  0.9957386  0.08366764 11.901120 6.297786e-16
```

# Split-ApPLY-Combine

## The **plyr** Package

The `*apply` functions in base R implement the split-apply-combine strategy, but are inconsistent

- `apply()` input arrays; split by row and/or columns; output array
- `lapply()` input list or vector; output list
- `sapply()` input list or vector; simplify to vector
- `tapply()` input data.frame; output depends
- `rapply()`, `vapply()`, `mapply()`

# Split-Apply-Combine

## The **plyr** Package

The `*apply` functions in base R implement the split-apply-combine strategy, but are inconsistent

- `apply()` input arrays; split by row and/or columns; output array
- `lapply()` input list or vector; output list
- `sapply()` input list or vector; simplify to vector
- `tapply()` input data.frame; output depends
- `rapply()`, `vapply()`, `mapply()`

**plyr** brings some consistency: `**ply()`

**first \*** Input type (a array, d data frame, l list)

**second \*** Output type (a array, d data frame, l list, \_ discard)

# plyr

## a\*ply()

```
y <- a*ply(.data, .margins., .fun, ...)
```

**.data** An array

**.margins** Subscripts which the function gets applied over

**.fun** Function to apply to each piece

Returns an array (\*=a), a data.frame (\*=d), a list (\*=l)

# plyr

`l*ply()`

```
y <- l*ply(.data, .fun, ...)
```

`.data` An list

`.fun` Function to apply to each item of the list

Returns an array (`*=a`), a data.frame (`*=d`), a list (`*=l`)

# plyr

## dplyr()

```
y <- dplyr(.data, .variables, .fun, ...)
```

**.data** A data frame

**.variables** Variables defining the groups

**.fun** Function to apply to each group

Returns an array (\*=a), a data.frame (\*=d), a list (\*=l)

# plyr

## d\*ply()

```
(res <- ddply(iris, "Species", myLM))
```

##	Species	Estimate	Std. Error	t value	Pr(> t )
## 1	setosa	4.2131682	0.41558877	10.137830	1.614927e-13
## 2	setosa	0.5422926	0.28231526	1.920876	6.069778e-02
## 3	versicolor	2.4075231	0.44625834	5.394909	2.075294e-06
## 4	versicolor	0.8282810	0.10413643	7.953806	2.586190e-10
## 5	virginica	1.0596591	0.46676645	2.270213	2.772289e-02
## 6	virginica	0.9957386	0.08366764	11.901120	6.297786e-16



# plyr

d\*ply()

```
(res <- ddply(iris, "Species", myLM))
```

##	Species	Estimate	Std. Error	t value	Pr(> t )
## 1	setosa	4.2131682	0.41558877	10.137830	1.614927e-13
## 2	setosa	0.5422926	0.28231526	1.920876	6.069778e-02
## 3	versicolor	2.4075231	0.44625834	5.394909	2.075294e-06
## 4	versicolor	0.8282810	0.10413643	7.953806	2.586190e-10
## 5	virginica	1.0596591	0.46676645	2.270213	2.772289e-02
## 6	virginica	0.9957386	0.08366764	11.901120	6.297786e-16

The only problem with **plyr** is that it is sometimes slow

# The **dplyr** package

The **dplyr** package proposes a “grammar of data manipulation”, i.e., it implements “verbs” useful for data manipulation.

**select** column subset (select variables)

**filter** row subset ( $\Leftrightarrow$  subset in base R)

**mutate** add new/modify rows

**summarise** summary statistics

**arrange** re-order the rows

**do** arbitrary action

- **dplyr** supports data.frames, data.tables (see later) as well as data bases
- Operations can be chained using a pipe operator

# The **dplyr** package

Compute the mean sepal width by species for flower whose petal length is longer than 4.8

```
unloadNamespace("plyr") # conflict with dplyr

## Error in unloadNamespace("plyr"): namespace 'plyr' is imported by
## 'reshape2' so cannot be unloaded

require(dplyr)

iris %>% group_by(Species) %>% filter(Petal.Length > 4.8) %>%
  summarise(mean_width = mean(Petal.Width))

## Source: local data frame [2 x 2]
##
##   Species mean_width
## 1 versicolor    1.575000
## 2 virginica     2.042553
```

# The **dplyr** package

Compute a linear model per species and petal length and summarise the results

```
iris %>% mutate(Petal.Length.f = factor(iris$Petal.Length > 4.8,
  levels = c(FALSE, TRUE),
  labels = c("Small petals", "Big petals"))) %>%
  group_by(Species, Petal.Length.f) %>%
  do(mod = summary(lm(Sepal.Length ~ Petal.Length, data = .))$coefficients) %>%
  do(data.frame(
    Species = .$Species,
    Petal.Length.f = .$Petal.Length.f,
    var = rownames(. $mod),
    coef = .$mod[, 1],
    se = .$mod[, 2],
    p = format.pval(. $mod[, 4], eps = 10^(-3), digits = 2)))

## Warning in rbind_all(out[[1]]): Unequal factor levels: coercing to character
```

```
## Source: local data frame [10 x 6]
```

```
## Groups: <by row>
```

```
##
```

	Species	Petal.Length.f	var	coef	se	p
## 1	setosa	Small petals	(Intercept)	4.2131682	0.41558877	<0.001
## 2	setosa	Small petals	Petal.Length	0.5422926	0.28231526	0.061
## 3	versicolor	Small petals	(Intercept)	2.2844372	0.48523067	<0.001
## 4	versicolor	Small petals	Petal.Length	0.8587048	0.11498472	<0.001
## 5	versicolor	Big petals	(Intercept)	19.5909091	11.55006708	0.23
## 6	versicolor	Big petals	Petal.Length	-2.6363636	2.32129915	0.37
## 7	virginica	Small petals	(Intercept)	-13.1000000	2.71477439	0.130

# The **data.table** package

The **data.table** package enhances the base `data.frame`. The package offers (extremely) fast

- subset
- grouping
- update
- joints (merging)

A `data.table` inherits from `data.frame`, i.e., it is compatible with R functions and packages that only accept `data.frame`.

# The **data.table** package

The general syntax is

```
dt[i, j, by]
```

**i** permits to select rows (A bit like subset)

**j** permits to update/create columns. Extremely flexible (maybe too much?)

**by** permits to “group by”

Additionally, data.tables can be *keyed* by one or more variables, leading to

- ordered data
- faster merging by keyed variables

# The **data.table** package

## Subset rows in `i`

```
require(data.table)
(dt_iris <- data.table(iris, key = "Species"))
```

```
##      Sepal.Length Sepal.Width Petal.Length Petal.Width  Species
##    1:           5.1          3.5          1.4          0.2    setosa
##    2:           4.9          3.0          1.4          0.2    setosa
##    3:           4.7          3.2          1.3          0.2    setosa
##    4:           4.6          3.1          1.5          0.2    setosa
##    5:           5.0          3.6          1.4          0.2    setosa
##  ---
## 146:           6.7          3.0          5.2          2.3 virginica
## 147:           6.3          2.5          5.0          1.9 virginica
## 148:           6.5          3.0          5.2          2.0 virginica
## 149:           6.2          3.4          5.4          2.3 virginica
## 150:           5.9          3.0          5.1          1.8 virginica
##      sepal_width sepal_widthNA Petal.Length.f
##    1:      <= 3.5           NA    Small petals
##    2:      <= 3.5      <= 3.5    Small petals
##    3:      <= 3.5      <= 3.5    Small petals
##    4:      <= 3.5      <= 3.5    Small petals
##    5:      > 3.5       > 3.5    Small petals
```

# The **data.table** package

## Subset rows in `i`

```
dt_iris[Species == "versicolor" & Petal.Length > 4.8]
```

```
##      Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
## 1:           6.9         3.1         4.9         1.5 versicolor
## 2:           6.3         2.5         4.9         1.5 versicolor
## 3:           6.7         3.0         5.0         1.7 versicolor
## 4:           6.0         2.7         5.1         1.6 versicolor
##      sepal_width sepal_widthNA Petal.Length.f
## 1:      <= 3.5      <= 3.5      Big petals
## 2:      <= 3.5      <= 3.5      Big petals
## 3:      <= 3.5      <= 3.5      Big petals
## 4:      <= 3.5      <= 3.5      Big petals
```



# The **data.table** package

## Select columns in j

```
dt_iris[1:3, Species]
```

```
## [1] setosa setosa setosa  
## Levels: setosa versicolor virginica
```

```
dt_iris[1:3, .(Species, Petal.Length)]
```

```
##      Species Petal.Length  
## 1:  setosa           1.4  
## 2:  setosa           1.4  
## 3:  setosa           1.3
```

```
dt_iris[Species == "versicolor" & Petal.Length > 4.8,  
        .(Species, Petal.Length)]
```

```
##      Species Petal.Length  
## 1: versicolor           4.9  
## 2: versicolor           4.9  
## 3: versicolor           5.0  
## 4: versicolor           5.1
```

# The **data.table** package

Compute in `j`: As long as `j-expressions` returns a list, each element of the list will be converted to a column

```
dt_iris[, mean(Petal.Length)]
```

```
## [1] 3.758
```

```
dt_iris[Species == "versicolor", mean(Petal.Length)]
```

```
## [1] 4.26
```

# The **data.table** package

```
dt_iris[Species == "versicolor", .(mean = mean(Petal.Length),  
  sd = sd(Petal.Length))]
```

```
##      mean      sd  
## 1: 4.26 0.469911
```

```
## With a use defined function
```

```
myFun <- function(x) {  
  list(mean = mean(x),  
        sd = sd(x))  
}
```

```
dt_iris[Species == "versicolor", myFun(Petal.Length)]
```

```
##      mean      sd  
## 1: 4.26 0.469911
```

## Special symbol .N

```
dt_iris[Species == "versicolor" & Petal.Length > 4.8,  
  .N]
```

```
## [1] 4
```

# The **data.table** package

## Group by using by

```
dt_iris[, .N, by = .(Species, Petal.Length.f)]
```

```
##      Species Petal.Length.f  N
## 1:      setosa   Small petals 50
## 2: versicolor   Small petals 46
## 3: versicolor    Big petals  4
## 4:  virginica    Big petals 47
## 5:  virginica   Small petals  3
```

```
dt_iris[, myFun(Sepal.Length), by = .(Species, Petal.Length.f)]
```

```
##      Species Petal.Length.f      mean      sd
## 1:      setosa   Small petals 5.006000 0.3524897
## 2: versicolor   Small petals 5.889130 0.5012111
## 3: versicolor    Big petals 6.475000 0.4031129
## 4:  virginica    Big petals 6.644681 0.5955664
## 5:  virginica   Small petals 5.700000 0.7000000
```

# The **data.table** package

Reorder the last output by Species and Petal.Length.f

```
dt_iris[, myFun(Sepal.Length), by = .(Species, Petal.Length.f)]
```

```
##           Species Petal.Length.f      mean      sd
## 1:      setosa    Small petals 5.006000 0.3524897
## 2: versicolor    Small petals 5.889130 0.5012111
## 3: versicolor      Big petals 6.475000 0.4031129
## 4:  virginica      Big petals 6.644681 0.5955664
## 5:  virginica    Small petals 5.700000 0.7000000
```

```
(setkeyv(tmp, c("Species", "Petal.Length.f")))
```

```
##           Species Petal.Length.f      mean      sd
## 1:      setosa    Small petals 5.006000 0.3524897
## 2: versicolor    Small petals 5.889130 0.5012111
## 3: versicolor      Big petals 6.475000 0.4031129
## 4:  virginica    Small petals 5.700000 0.7000000
## 5:  virginica      Big petals 6.644681 0.5955664
```

# The **data.table** package

## Chaining:

```
my_lm <- function(y, x) {
  mod <- summary(lm(y ~ x))$coefficients
  list(var = rownames(mod),
        coef = mod[, 1],
        se = mod[, 2],
        p = format.pval(mod[, 4], eps = 10^(-3), digits = 2))
}
```

```
dt_iris[, Petal.Length.f := factor(Petal.Length > 4.8,
  levels = c(FALSE, TRUE),
  labels = c("Small petals", "Big petals"))
][, my_lm(Sepal.Length, Petal.Length),
  by = .(Species, Petal.Length.f)
][order(Species, Petal.Length.f)]
```

##	Species	Petal.Length.f	var	coef	se	p
## 1:	setosa	Small petals	(Intercept)	4.2131682	0.41558877	<0.001
## 2:	setosa	Small petals	x	0.5422926	0.28231526	0.061
## 3:	versicolor	Small petals	(Intercept)	2.2844372	0.48523067	<0.001
## 4:	versicolor	Small petals	x	0.8587048	0.11498472	<0.001
## 5:	versicolor	Big petals	(Intercept)	19.5909091	11.55006708	0.23
## 6:	versicolor	Big petals	x	-2.6363636	2.32129915	0.37
## 7:	virginica	Small petals	(Intercept)	-13.1000000	2.71477439	0.130
## 8:	virginica	Small petals	x	4.0000000	0.57735027	0.091
## 9:	virginica	Big petals	(Intercept)	1.1908726	0.49934706	0.021
## 10:	virginica	Big petals	x	0.9727855	0.08869172	<0.001

# Your Turn

Other example (see dplyr examples)?

Consider `WM_teams_2014.csv` data set that contains information on each player of the World Cup 2014, e.g., age, club, country, caps (number of plays for the national team)

- 1 Find the three oldest and youngest players for each country
- 2 Create a data set with the mean (with 95% confidence interval), median, 25% and 75% percentile of the players' age stratified on country and position
- 3 Create a data set containing the clubs, number of players in each club that participate in the world cup. The data set should be ordered from highest to lowest