https://intro2r.com/ Chapter 3

CSCI 297b, Spring 2023

April 21, 2023

R basic data types

Numeric	data are numbers that contain a decimal.
Integers	are whole numbers.
Logical data	take on the value of either TRUE or FALSE. There's also another special type of logical called NA to represent missing values.
Character	data are used to represent string values. You can think of character strings as something like a word (or multiple words). A special type of character string is a factor, which is a string but with additional attributes (like levels or an order). We'll cover factors later.

R basic data types

```
num <- 2.2
class(num)
## [1] "numeric"

char <- "hello"
class(char)
## [1] "character"

logi <- TRUE
class(logi)
## [1] "logical"
```

R basic data types

```
is.numeric(num)
## [1] TRUE

is.character(num)
## [1] FALSE

is.character(char)
## [1] TRUE

is.logical(logi)
## [1] TRUE
```

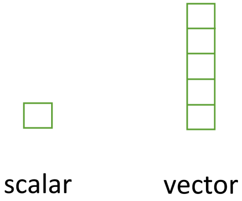
R type conversion

```r
# coerce numeric to character
class(num)
## [1] "numeric"
num_char <-  as.character(num)
num_char
## [1] "2.2"
class(num_char)
## [1] "character"

# coerce character to numeric!
class(char)
## [1] "character"
char_num <- as.numeric(char)
## Warning: NAs introduced by coercion
```

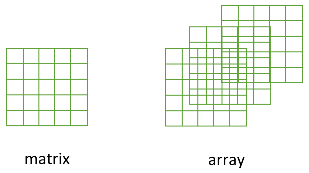
Scalars and Vectors

- A vector with a single element is called a scalar.
- Vectors can contain any single type.
- You can't mix types in a vector.
- NA can mix with any type.



Matrices and arrays

- A matrix is a vector with additional attributes called *dimensions*.
- Arrays are multidimensional matrices.
- Matrices and arrays can contain only a single type.
- They may also contain NAs.



Creating matrices and arrays

```
my_mat <- matrix(1:16, nrow = 4, byrow = TRUE)
my_mat
##      [,1] [,2] [,3] [,4]
## [1,]    1    2    3    4
## [2,]    5    6    7    8
## [3,]    9   10   11   12
## [4,]   13   14   15   16

my_array <- array(1:16, dim = c(2, 4, 2))
my_array
## , , 1
##
##      [,1] [,2] [,3] [,4]
## [1,]    1    3    5    7
## [2,]    2    4    6    8
##
## , , 2
##
##      [,1] [,2] [,3] [,4]
## [1,]    9   11   13   15
## [2,]   10   12   14   16
```

Optional row and column names

```
rownames(my_mat) <- c("A", "B", "C", "D")
colnames(my_mat) <- c("a", "b", "c", "d")
my_mat
##    a  b  c  d
## A  1  2  3  4
## B  5  6  7  8
## C  9 10 11 12
## D 13 14 15 16
```

Transpose a matrix

```
my_mat_t <- t(my_mat)
my_mat_t
##    A B  C  D
## a  1 5  9 13
## b  2 6 10 14
## c  3 7 11 15
## d  4 8 12 16
```

Diagonal elements

```
my_mat_diag <- diag(my_mat)
my_mat_diag
## [1]  1  6 11 16
```

Matrix arithmetic

```
mat.1 <- matrix(c(2, 0, 1, 1), nrow = 2)
                       # notice that the matrix has been filled
                       # column-wise by default
mat.1
##        [,1] [,2]
## [1,]      2    1
## [2,]      0    1

mat.2 <- matrix(c(1, 1, 0, 2), nrow = 2)
mat.2
##        [,1] [,2]
## [1,]      1    0
## [2,]      1    2

mat.1 + mat.2                   # matrix addition
##        [,1] [,2]
## [1,]      3    1
## [2,]      1    3
mat.1 * mat.2                   # element by element products
##        [,1] [,2]
## [1,]      2    0
## [2,]      0    2
```

Matrix multiplication

```
mat.1 <- matrix(c(2, 0, 1, 1), nrow = 2)
mat.1
##      [,1] [,2]
## [1,]    2    1
## [2,]    0    1

mat.2 <- matrix(c(1, 1, 0, 2), nrow = 2)
mat.2
##      [,1] [,2]
## [1,]    1    0
## [2,]    1    2


mat.1 %*% mat.2          # matrix multiplication
##      [,1] [,2]
## [1,]    3    2
## [2,]    1    2
```

Lists

- Notice the double bracket [[ ]] for list items.

```
list_1 <- list(c("black", "yellow", "orange"),
               c(TRUE, TRUE, FALSE, TRUE, FALSE, FALSE),
               matrix(1:6, nrow = 3))
list_1
## [[1]]
## [1] "black"  "yellow" "orange"
##
## [[2]]
## [1]  TRUE  TRUE FALSE  TRUE FALSE FALSE
##
## [[3]]
##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
## [3,]    3    6
```

List elements can be named

```
list_2 <- list(colours = c("black", "yellow", "orange"),
               evaluation = c(TRUE, TRUE ,FALSE,
                              TRUE, FALSE, FALSE),
               time = matrix(1:6, nrow = 3))
list_2
## $colours
## [1] "black"  "yellow" "orange"
##
## $evaluation
## [1]  TRUE  TRUE FALSE  TRUE FALSE FALSE
##
## $time
##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
## [3,]    3    6
```

List elements can be renamed using `names`

```
names(list_1) <- c("colours", "evaluation", "time")
list_1
## $colours
## [1] "black"  "yellow" "orange"
##
## $evaluation
## [1]  TRUE  TRUE FALSE  TRUE FALSE FALSE
##
## $time
##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
## [3,]    3    6
```

Data frames

treat	nitrogen	block	height	weight	leafarea	shootarea	flowers
tip	medium	1	7.5	7.62	11.7	31.9	1
tip	medium	1	10.7	12.14	14.1	46.0	10
tip	medium	1	11.2	12.76	7.1	66.7	10
tip	medium	1	10.4	8.78	11.9	20.3	1
tip	medium	1	10.4	13.58	14.5	26.9	4
tip	medium	1	9.8	10.08	12.2	72.7	9
notip	low	2	3.7	8.10	10.5	60.5	6
notip	low	2	3.2	7.45	14.1	38.1	4
notip	low	2	3.9	9.19	12.4	52.6	9
notip	low	2	3.3	8.92	11.6	55.2	6
notip	low	2	5.5	8.44	13.5	77.6	9
notip	low	2	4.4	10.60	16.2	63.3	6

- Most used data structure for real world data.
- Each row contains an individual **observation**.
- Each column contains a measured **variable**.
- Each column is a vector of a single type.
- Columns can be different types.

Data frames

treat	nitrogen	block	height	weight	leafarea	shootarea	flowers
tip	medium	1	7.5	7.62	11.7	31.9	1
tip	medium	1	10.7	12.14	14.1	46.0	10
tip	medium	1	11.2	12.76	7.1	66.7	10
tip	medium	1	10.4	8.78	11.9	20.3	1
tip	medium	1	10.4	13.58	14.5	26.9	4
tip	medium	1	9.8	10.08	12.2	72.7	9
notip	low	2	3.7	8.10	10.5	60.5	6
notip	low	2	3.2	7.45	14.1	38.1	4
notip	low	2	3.9	9.19	12.4	52.6	9
notip	low	2	3.3	8.92	11.6	55.2	6
notip	low	2	5.5	8.44	13.5	77.6	9
notip	low	2	4.4	10.60	16.2	63.3	6

- Each row is an individual petunia plant.
- treat and nitrogen are **categorical** variables (factors)
- treat has 2 levels, tip and notip
- nitrogen has 3 levels, low, medium, high
- height, weight, leafarea, and shootarea are numeric
- flowers is an integer
- block uses integers, but should be treated as a factor

Data frames

treat	nitrogen	block	height	weight	leafarea	shootarea	flowers
tip	medium	1	7.5	7.62	11.7	31.9	1
tip	medium	1	10.7	12.14	14.1	46.0	10
tip	medium	1	11.2	12.76	7.1	66.7	10
tip	medium	1	10.4	8.78	11.9	20.3	1
tip	medium	1	10.4	13.58	14.5	26.9	4
tip	medium	1	9.8	10.08	12.2	72.7	9
notip	low	2	3.7	8.10	10.5	60.5	6
notip	low	2	3.2	7.45	14.1	38.1	4
notip	low	2	3.9	9.19	12.4	52.6	9
notip	low	2	3.3	8.92	11.6	55.2	6
notip	low	2	5.5	8.44	13.5	77.6	9
notip	low	2	4.4	10.60	16.2	63.3	6

- This type of data is known as **rectangular** or **tidy** data.
- Each column must have the same number of observations.
- Missing data must have NAs in their position.
- Spreadsheets are often NOT tidy.

Constructing data frames

```r
p.height <- c(180, 155, 160, 167, 181)
p.weight <- c(65, 50, 52, 58, 70)
p.names <- c("Joanna", "Charlotte", "Helen", "Karen", "Amy")

dataf <- data.frame(height = p.height,
                    weight = p.weight,
                    names = p.names)
dataf
##   height weight     names
## 1    180     65    Joanna
## 2    155     50 Charlotte
## 3    160     52     Helen
## 4    167     58     Karen
## 5    181     70       Amy
```

- Column names are taken from the constructor.
- Can be changed with `names`.
- Numbers at left are row names automatically produced by R, not another column.
- If the vectors are not the same length R will (quietly) cycle!

Structure of data frames

```
dim(dataf)    # 5 rows and 3 columns
## [1] 5 3

str(dataf)
## 'data.frame':    5 obs. of  3 variables:
##  $ height: num  180 155 160 167 181
##  $ weight: num  65 50 52 58 70
##  $ names : chr  "Joanna" "Charlotte" "Helen" "Karen" ...
```

- Gives type, dimensions, column names, types, a few values.
- Convenient to place this in a comment block in your code when dealing with a data frame, for reference.
- R has automatically made names a character vector, not a factor.

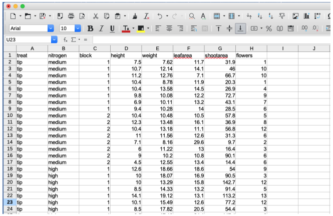
Automatically convert strings to factors

```r
p.height <- c(180, 155, 160, 167, 181)
p.weight <- c(65, 50, 52, 58, 70)
p.names <- c("Joanna", "Charlotte", "Helen", "Karen", "Amy")

dataf <- data.frame(height = p.height,
                    weight = p.weight,
                    names = p.names,
                    stringsAsFactors = TRUE)
str(dataf)
## 'data.frame':    5 obs. of  3 variables:
##  $ height: num  180 155 160 167 181
##  $ weight: num  65 50 52 58 70
##  $ names : Factor w/ 5 levels "Amy","Charlotte",..: 4 2 3
     5 1
```

Preparing data for import

- Easiest way to enter data is use Excel or LibreOffice Calc.
- Save data in tab-delimited or comma-delimited file.
- Keep column headings short.
- No spaces in column headings.
- Avoid special characters, e.g., `mm^2`
- No empty cells! Use NAs.
- Make sure it's tidy!



	A	B	C	D	E	F	G	H	I	J
1	treat	nitrogen	block	height	weight	leafarea	shootarea	flowers		
2	tip	medium	1	7.5	7.62	11.7	31.9	1		
3	tip	medium	1	10.7	12.14	14.1	46	10		
4	tip	medium	1	11.2	12.76	7.1	66.7	10		
5	tip	medium	1	10.4	8.78	11.9	20.3	1		
6	tip	medium	1	10.4	13.58	14.5	26.9	4		
7	tip	medium	1	9.8	10.08	12.2	72.7	9		
8	tip	medium	1	6.9	10.11	13.2	43.1	7		
9	tip	medium	1	9.4	10.28	14	28.5	6		
10	tip	medium	2	10.4	10.48	10.5	57.8	5		
11	tip	medium	2	12.3	13.48	16.1	36.9	8		
12	tip	medium	2	10.4	13.18	11.1	56.8	12		
13	tip	medium	2	11	11.56	12.6	31.3	6		
14	tip	medium	2	7.1	8.16	29.6	9.7	2		
15	tip	medium	2	6	11.22	13	16.4	3		
16	tip	medium	2	9	10.2	10.8	90.1	6		
17	tip	medium	2	4.5	12.55	13.4	14.4	6		
18	tip	high	1	12.6	18.66	18.6	54	9		
19	tip	high	1	10	18.07	16.9	90.5	3		
20	tip	high	1	10	13.29	15.8	142.7	12		
21	tip	high	1	8.5	14.33	13.2	91.4	5		
22	tip	high	1	14.1	19.12	13.1	113.2	13		
23	tip	high	1	10.1	15.49	12.6	77.2	12		
24	tip	high	1	8.5	17.82	20.5	54.4	3		

- **Beware!** `https://genomebiology.biomedcentral.com/articles/10.1186/s13059-016-1044-7`

Importing

```r
flowers <- read.table(file = 'data/flower.txt',
                      header = TRUE, sep = "\t",
                      stringsAsFactors = TRUE)
```

- Forward slash works on ALL systems.
- `header=TRUE` means the first line is variable names.
- `sep="\t"` for tab-delimited files
- `sep=","` for comma-delimited files

Importing

```
> str(flowers)
'data.frame':    96 obs. of  8 variables:
  $ treat     : Factor w/ 2 levels "notip","tip": 2 2 2 2 2 2 2 2 2 2 ...
  $ nitrogen  : Factor w/ 3 levels "high","low","medium": 3 3 3 3 3 3 3 3 3 3 ...
  $ block     : int  1 1 1 1 1 1 1 1 2 2 ...
  $ height    : num  7.5 10.7 11.2 10.4 10.4 9.8 6.9 9.4 10.4 12.3 ...
  $ weight    : num  7.62 12.14 12.76 8.78 13.58 ...
  $ leafarea  : num  11.7 14.1 7.1 11.9 14.5 12.2 13.2 14 10.5 16.1 ...
  $ shootarea: num  31.9 46 66.7 20.3 26.9 72.7 43.1 28.5 57.8 36.9 ...
  $ flowers   : int  1 10 10 1 4 9 7 6 5 8 .
```

- After importing check structure of data frame.
- treat and nitrogen have been converted to factors.
- Usually very helpful to include this as a comment block in your script.

Specialized import functions

```r
# import .csv file with sep = "\t" and header = FALSE
flowers <- read.table(file = 'data/flower.txt')

# import .csv file with sep = ","
# and header = TRUE
flowers <- read.csv(file = 'data/flower.csv')

# import .csv file with dec = "," and sep = ";"
# and header = TRUE
flowers <- read.csv2(file = 'data/flower.csv')

# import tab delim file with sep = "\t" and header = TRUE
flowers <- read.delim(file = 'data/flower.txt')
```

- Avoid importing from spreadsheet files (`.xls` *etc.*).

Import problems

```
Error in file(file, "rt") : cannot open the connection
In addition: Warning message:
In file(file, "rt") :
  cannot open file 'flower.txt': No such file or directory
```

- Spelling mistakes.
- Wrong working directory.
- Forgot the extension (`.txt`, `.csv`, *etc.*).

Forgot `header = TRUE`

```
flowers_bad <- read.table(file = 'data/flower.txt',
                          sep = "\t")
str(flowers_bad)
## 'data.frame':    97 obs. of  8 variables:
##  $ V1: chr  "treat" "tip" "tip" "tip" ...
##  $ V2: chr  "nitrogen" "medium" "medium" "medium" ...
##  $ V3: chr  "block" "1" "1" "1" ...
##  $ V4: chr  "height" "7.5" "10.7" "11.2" ...
##  $ V5: chr  "weight" "7.62" "12.14" "12.76" ...
##  $ V6: chr  "leafarea" "11.7" "14.1" "7.1" ...
##  $ V7: chr  "shootarea" "31.9" "46" "66.7" ...
##  $ V8: chr  "flowers" "1" "10" "10" ...
```

- All of our variables are character (or factor).
- The first value of each variable is the column name.
- R has provided default names, `V1, V2, V3, ...`

Alternative loader functions

```r
library(readr)
# import white space delimited files
all_data <- read_table(file = 'data/flower.txt',
                       col_names = TRUE)

# import comma delimited files
all_data <- read_csv(file = 'data/flower.txt')

# import tab delimited files
all_data <- read_delim(file = 'data/flower.txt',
                       delim = "\t")

# or use
all_data <- read_tsv(file = 'data/flower.txt')
```

- `readr` is from the **tidyverse** collection of packages.
- Many of the arguments are the same as `read.table`
- Returns a `tibble`, which is very similar to a data frame.

Packages for large datasets

- `read.table`
- `ff`
- `bigmemory`

Do exercise 3, part 1

Wrangling data frames

```
flowers <- read.table(file = 'data/flower.txt', header = TRUE, sep = "\t")
str(flowers)
## 'data.frame':    96 obs. of  8 variables:
##  $ treat    : chr  "tip" "tip" "tip" "tip" ...
##  $ nitrogen : chr  "medium" "medium" "medium" "medium" ...
##  $ block    : int  1 1 1 1 1 1 1 1 2 2 ...
##  $ height   : num  7.5 10.7 11.2 10.4 10.4 9.8 6.9 9.4 10.4 12.3 ...
##  $ weight   : num  7.62 12.14 12.76 8.78 13.58 ...
##  $ leafarea : num  11.7 14.1 7.1 11.9 14.5 12.2 13.2 14 10.5 16.1 ...
##  $ shootarea: num  31.9 46 66.7 20.3 26.9 72.7 43.1 28.5 57.8 36.9 ...
##  $ flowers  : int  1 10 10 1 4 9 7 6 5 8 ...
```

The $ notation

```
flowers$height
 [1]  7.5 10.7 11.2 10.4 10.4  9.8  6.9  9.4 10.4 12.3 10.4
[12] 11.0  7.1  6.0  9.0  4.5 12.6 10.0 10.0  8.5 14.1 10.1
[23]  8.5  6.5 11.5  7.7  6.4  8.8  9.2  6.2  6.3 17.2  8.0
[34]  8.0  6.4  7.6  9.7 12.3  9.1  8.9  7.4  3.1  7.9  8.8
[45]  8.5  5.6 11.5  5.8  5.6  5.3  7.5  4.1  3.5  8.5  4.9
[56]  2.5  5.4  3.9  5.8  4.5  8.0  1.8  2.2  3.9  8.5  8.5
[67]  6.4  1.2  2.6 10.9  7.2  2.1  4.7  5.0  6.5  2.6  6.0
[78]  9.3  4.6  5.2  3.9  2.3  5.2  2.2  4.5  1.8  3.0  3.7
[89]  2.4  5.7  3.7  3.2  3.9  3.3  5.5  4.4

f_height <- flowers$height
mean(f_height)
## [1] 6.839583
summary(f_height)
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.200   4.475   6.450   6.840   9.025  17.200

mean(flowers$height)
## [1] 6.839583
summary(flowers$height)
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.200   4.475   6.450   6.840   9.025  17.200
```

Positional indexes

```r
flowers[1, 4]
## [1] 7.5

# this would give you the same
flowers$height[1]
## [1] 7.5
```

Positional indexes

```
flowers[1:10, 1:4]
##    treat nitrogen block height
## 1    tip   medium     1    7.5
## 2    tip   medium     1   10.7
## 3    tip   medium     1   11.2
## 4    tip   medium     1   10.4
## 5    tip   medium     1   10.4
## 6    tip   medium     1    9.8
## 7    tip   medium     1    6.9
## 8    tip   medium     1    9.4
## 9    tip   medium     2   10.4
## 10   tip   medium     2   12.3
```

Positional indexes

```
flowers[c(1, 5, 12, 30), c(1, 3, 6, 8)]
##     treat  block  leafarea  flowers
## 1     tip      1      11.7        1
## 5     tip      1      14.5        4
## 12    tip      2      12.6        6
## 30    tip      2      11.6        5
```

Empty index means "all of them"

```
flowers[1:8, ]
##    treat nitrogen block height weight leafarea shootarea flowers
## 1    tip   medium     1    7.5   7.62     11.7      31.9       1
## 2    tip   medium     1   10.7  12.14     14.1      46.0      10
## 3    tip   medium     1   11.2  12.76      7.1      66.7      10
## 4    tip   medium     1   10.4   8.78     11.9      20.3       1
## 5    tip   medium     1   10.4  13.58     14.5      26.9       4
## 6    tip   medium     1    9.8  10.08     12.2      72.7       9
## 7    tip   medium     1    6.9  10.11     13.2      43.1       7
## 8    tip   medium     1    9.4  10.28     14.0      28.5       6
```

Negative numbers mean "not these"

```
flowers[-(1:85), -c(4, 7, 8)]
##     treat nitrogen block weight leafarea
## 86  notip      low     1   6.01     17.6
## 87  notip      low     1   9.93     12.0
## 88  notip      low     1   7.03      7.9
## 89  notip      low     2   9.10     14.5
## 90  notip      low     2   9.05      9.6
## 91  notip      low     2   8.10     10.5
## 92  notip      low     2   7.45     14.1
## 93  notip      low     2   9.19     12.4
## 94  notip      low     2   8.92     11.6
## 95  notip      low     2   8.44     13.5
## 96  notip      low     2  10.60     16.2
```

Can also use column names

```
flowers[1:5, c("treat", "nitrogen", "leafarea")]
##   treat nitrogen leafarea
## 1   tip   medium     11.7
## 2   tip   medium     14.1
## 3   tip   medium      7.1
## 4   tip   medium     11.9
## 5   tip   medium     14.5
```

- More readable and portable than `flowers[1:5, c(1, 2, 6)]`

Logical indexes

```
big_flowers <- flowers[flowers$height > 12, ]
big_flowers
##    treat nitrogen block height weight leafarea shootarea flowers
## 10   tip   medium     2   12.3  13.48     16.1      36.9       8
## 17   tip     high     1   12.6  18.66     18.6      54.0       9
## 21   tip     high     1   14.1  19.12     13.1     113.2      13
## 32   tip     high     2   17.2  19.20     10.9      89.9      14
## 38   tip      low     1   12.3  11.27     13.7      28.7       5
```

Logical indexes

```
nit_high <- flowers[flowers$nitrogen == "high", ]
nit_high
##     treat nitrogen block height weight leafarea shootarea flowers
## 17    tip     high     1   12.6  18.66     18.6      54.0       9
## 18    tip     high     1   10.0  18.07     16.9      90.5       3
## 19    tip     high     1   10.0  13.29     15.8     142.7      12
## 20    tip     high     1    8.5  14.33     13.2      91.4       5
## 21    tip     high     1   14.1  19.12     13.1     113.2      13
## 22    tip     high     1   10.1  15.49     12.6      77.2      12
....
```

Logical indexes

```
low_notip_high6 <- flowers[flowers$height >= 6 &
                           flowers$nitrogen == "medium" &
                           flowers$treat == "notip", ]
low_notip_high6
##     treat nitrogen block height weight leafarea shootarea flowers
## 51  notip   medium     1    7.5  13.60     13.6     122.2      11
## 54  notip   medium     1    8.5  10.04     12.3     113.6       4
## 61  notip   medium     2    8.0  11.43     12.6      43.2      14
```

Logical indexes using `subset`

```
tip_med_2 <- subset(flowers, treat == "tip" &
                    nitrogen == "medium" &
                    block == 2)
tip_med_2
##    treat nitrogen block height weight leafarea shootarea flowers
## 9    tip   medium     2   10.4  10.48     10.5      57.8       5
## 10   tip   medium     2   12.3  13.48     16.1      36.9       8
## 11   tip   medium     2   10.4  13.18     11.1      56.8      12
## 12   tip   medium     2   11.0  11.56     12.6      31.3       6
## 13   tip   medium     2    7.1   8.16     29.6       9.7       2
## 14   tip   medium     2    6.0  11.22     13.0      16.4       3
## 15   tip   medium     2    9.0  10.20     10.8      90.1       6
## 16   tip   medium     2    4.5  12.55     13.4      14.4       6
```

- We don’t need to use `flowers$treat`

Logical indexes using `subset` and `select`

```
tipplants <- subset(flowers,
                    treat == "tip" &
                    nitrogen == "medium" &
                    block == 2,
                    select = c("treat", "nitrogen", "leafarea"))
tipplants
##    treat nitrogen leafarea
## 9    tip   medium     10.5
## 10   tip   medium     16.1
## 11   tip   medium     11.1
## 12   tip   medium     12.6
## 13   tip   medium     29.6
## 14   tip   medium     13.0
## 15   tip   medium     10.8
## 16   tip   medium     13.4
```

- Selecting both rows and columns.

Ordering data frames

```
height_ord <- flowers[order(flowers$height), ]
height_ord
##    treat nitrogen block height weight leafarea shootarea flowers
## 68 notip     high     1    1.2  18.24     16.6     148.1       7
## 62 notip   medium     2    1.8  10.47     11.8     120.8       9
## 86 notip      low     1    1.8   6.01     17.6      46.2       4
## 72 notip     high     1    2.1  19.15     15.6     176.7       6
## 63 notip   medium     2    2.2  10.70     15.3      97.1       7
## 84 notip      low     1    2.2   9.97      9.6      63.1       2
## 82 notip      low     1    2.3   7.28     13.8      32.8       6
## 89 notip      low     2    2.4   9.10     14.5      78.7       8
## 56 notip   medium     1    2.5  14.85     17.5      77.8      10
## 69 notip     high     1    2.6  16.57     17.1     141.1       3
## 76 notip     high     2    2.6  18.88     16.4     181.5      14
## 87 notip      low     1    3.0   9.93     12.0      56.6       6
## 42   tip      low     2    3.1   8.74     16.1      39.1       3
...
```

Ordering data frames

```
leafarea_ord <- flowers[order(flowers$leafarea, decreasing = TRUE), ]
leafarea_ord
##    treat nitrogen block height weight leafarea shootarea flowers
## 70 notip     high     1   10.9  17.22     49.2     189.6      17
## 13   tip   medium     2    7.1   8.16     29.6       9.7       2
## 24   tip     high     1    6.5  17.13     24.1     147.4       6
## 65 notip     high     1    8.5  22.53     20.8     166.9      16
## 23   tip     high     1    8.5  17.82     20.5      54.4       3
## 66 notip     high     1    8.5  17.33     19.8     184.4      12
## 73 notip     high     2    4.7  13.42     19.8     124.7       5
## 80 notip     high     2    5.2  17.70     19.1     181.1       8
## 17   tip     high     1   12.6  18.66     18.6      54.0       9
## 49 notip   medium     1    5.6  11.03     18.6      49.9       8
## 78 notip     high     2    9.3  18.75     18.4     181.1      16
...
```

Ordering data frames

```
block_height_ord <- flowers[order(flowers$block, flowers$height), ]
block_height_ord
##    treat nitrogen block height weight leafarea shootarea flowers
## 68 notip     high     1    1.2  18.24     16.6     148.1       7
## 86 notip      low     1    1.8   6.01     17.6      46.2       4
## 72 notip     high     1    2.1  19.15     15.6     176.7       6
## 84 notip      low     1    2.2   9.97      9.6      63.1       2
## 82 notip      low     1    2.3   7.28     13.8      32.8       6
## 56 notip   medium     1    2.5  14.85     17.5      77.8      10
## 69 notip     high     1    2.6  16.57     17.1     141.1       3
....
## 38   tip      low     1   12.3  11.27     13.7      28.7       5
## 17   tip     high     1   12.6  18.66     18.6      54.0       9
## 21   tip     high     1   14.1  19.12     13.1     113.2      13
## 62 notip   medium     2    1.8  10.47     11.8     120.8       9
## 63 notip   medium     2    2.2  10.70     15.3      97.1       7
## 89 notip      low     2    2.4   9.10     14.5      78.7       8
## 76 notip     high     2    2.6  18.88     16.4     181.5      14
## 42   tip      low     2    3.1   8.74     16.1      39.1       3
## 92 notip      low     2    3.2   7.45     14.1      38.1       4
....
```

Ordering data frames

```
block_revheight_ord <- flowers[order(flowers$block, -flowers$height), ]
block_revheight_ord
##     treat nitrogen block height weight leafarea shootarea flowers
## 21    tip     high     1   14.1  19.12     13.1     113.2      13
## 17    tip     high     1   12.6  18.66     18.6      54.0       9
## 38    tip      low     1   12.3  11.27     13.7      28.7       5
## 3     tip   medium     1   11.2  12.76      7.1      66.7      10
## 70  notip     high     1   10.9  17.22     49.2     189.6      17
## 2     tip   medium     1   10.7  12.14     14.1      46.0      10
## 4     tip   medium     1   10.4   8.78     11.9      20.3       1
## 5     tip   medium     1   10.4  13.58     14.5      26.9       4
## 22    tip     high     1   10.1  15.49     12.6      77.2      12
....
## 72  notip     high     1    2.1  19.15     15.6     176.7       6
## 86  notip      low     1    1.8   6.01     17.6      46.2       4
## 68  notip     high     1    1.2  18.24     16.6     148.1       7
## 32    tip     high     2   17.2  19.20     10.9      89.9      14
## 10    tip   medium     2   12.3  13.48     16.1      36.9       8
## 25    tip     high     2   11.5  23.89     14.3     101.5      12
## 47    tip      low     2   11.5   8.72     10.2      28.3       6
## 12    tip   medium     2   11.0  11.56     12.6      31.3       6
....
```

Ordering data frames

```
revheight_ord <- flowers[order(-xtfrm(flowers$nitrogen), flowers$height), ]
revheight_ord
##    treat nitrogen block height weight leafarea shootarea flowers
## 62 notip   medium     2    1.8  10.47     11.8     120.8       9
## 63 notip   medium     2    2.2  10.70     15.3      97.1       7
## 56 notip   medium     1    2.5  14.85     17.5      77.8      10
## 53 notip   medium     1    3.5  12.93     16.6     109.3       3
## 58 notip   medium     2    3.9   9.07      9.6      90.4       7
## 64 notip   medium     2    3.9  12.97     17.0      97.5       5
## 52 notip   medium     1    4.1  12.58     13.9     136.6      11
....
## 2    tip   medium     1   10.7  12.14     14.1      46.0      10
## 12   tip   medium     2   11.0  11.56     12.6      31.3       6
## 3    tip   medium     1   11.2  12.76      7.1      66.7      10
## 10   tip   medium     2   12.3  13.48     16.1      36.9       8
## 86 notip      low     1    1.8   6.01     17.6      46.2       4
## 84 notip      low     1    2.2   9.97      9.6      63.1       2
## 82 notip      low     1    2.3   7.28     13.8      32.8       6
## 89 notip      low     2    2.4   9.10     14.5      78.7       8
....
## 39   tip      low     1    9.1   8.96      9.7      23.8       3
## 37   tip      low     1    9.7   6.49      8.1      18.0       3
## 47   tip      low     2   11.5   8.72     10.2      28.3       6
## 38   tip      low     1   12.3  11.27     13.7      28.7       5
## 68 notip     high     1    1.2  18.24     16.6     148.1       7
## 72 notip     high     1    2.1  19.15     15.6     176.7       6
## 69 notip     high     1    2.6  16.57     17.1     141.1       3
....
```

Ordering data frames

```
flowers$nitrogen <- factor(flowers$nitrogen,
                           levels = c("low", "medium", "high"))
nit_ord <- flowers[order(flowers$nitrogen),]
nit_ord
##     treat nitrogen block height weight leafarea shootarea flowers
## 33    tip      low     1    8.0   6.88      9.3      16.1       4
## 34    tip      low     1    8.0  10.23     11.9      88.1       4
## 35    tip      low     1    6.4   5.97      8.7       7.3       2
## 36    tip      low     1    7.6  13.05      7.2      47.2       8
## 37    tip      low     1    9.7   6.49      8.1      18.0       3
## 38    tip      low     1   12.3  11.27     13.7      28.7       5
....
## 93  notip      low     2    3.9   9.19     12.4      52.6       9
## 94  notip      low     2    3.3   8.92     11.6      55.2       6
## 95  notip      low     2    5.5   8.44     13.5      77.6       9
## 96  notip      low     2    4.4  10.60     16.2      63.3       6
## 1     tip   medium     1    7.5   7.62     11.7      31.9       1
## 2     tip   medium     1   10.7  12.14     14.1      46.0      10
## 3     tip   medium     1   11.2  12.76      7.1      66.7      10
....
## 61  notip   medium     2    8.0  11.43     12.6      43.2      14
## 62  notip   medium     2    1.8  10.47     11.8     120.8       9
## 63  notip   medium     2    2.2  10.70     15.3      97.1       7
## 64  notip   medium     2    3.9  12.97     17.0      97.5       5
## 17    tip     high     1   12.6  18.66     18.6      54.0       9
## 18    tip     high     1   10.0  18.07     16.9      90.5       3
## 19    tip     high     1   10.0  13.29     15.8     142.7      12
## 20    tip     high     1    8.5  14.33     13.2      91.4       5
....
```

Adding rows to a data frame

```
# rbind for rows
df1 <- data.frame(id = 1:4, height = c(120, 150, 132, 122),
                            weight = c(44, 56, 49, 45))
df1
##   id height weight
## 1  1    120     44
## 2  2    150     56
## 3  3    132     49
## 4  4    122     45

df2 <- data.frame(id = 5:6, height = c(119, 110),
                            weight = c(39, 35))
df2
##   id height weight
## 1  5    119     39
## 2  6    110     35
```

Adding rows to a data frame

```
df_rcomb <- rbind(df1, df2)
df_rcomb
##   id height weight
## 1  1    120     44
## 2  2    150     56
## 3  3    132     49
## 4  4    122     45
## 5  5    119     39
## 6  6    110     35
```

Adding columns to a data frame

```
df3 <- data.frame(id = 1:4, height = c(120, 150, 132, 122),
                                weight = c(44, 56, 49, 45))
df3
##   id height weight
## 1  1    120     44
## 2  2    150     56
## 3  3    132     49
## 4  4    122     45

df4 <- data.frame(location = c("UK", "CZ", "CZ", "UK"))
df4
##   location
## 1       UK
## 2       CZ
## 3       CZ
## 4       UK
```

Adding columns to a data frame

```
df_ccomb <- cbind(df3, df4)
df_ccomb
##   id height weight location
## 1  1    120     44       UK
## 2  2    150     56       CZ
## 3  3    132     49       CZ
## 4  4    122     45       UK
```

Adding computed columns to a data frame

```
df_rcomb$height_log10 <- log10(df_rcomb$height)
df_rcomb
##   id height weight height_log10
## 1  1    120     44     2.079181
## 2  2    150     56     2.176091
## 3  3    132     49     2.120574
## 4  4    122     45     2.086360
## 5  5    119     39     2.075547
## 6  6    110     35     2.041393
```

Converting type of a column

```
# convert to a factor
df_rcomb$Fid <- factor(df_rcomb$id)
df_rcomb
##   id height weight height_log10 Fid
## 1  1    120     44     2.079181   1
## 2  2    150     56     2.176091   2
## 3  3    132     49     2.120574   3
## 4  4    122     45     2.086360   4
## 5  5    119     39     2.075547   5
## 6  6    110     35     2.041393   6
str(df_rcomb)
## 'data.frame':    6 obs. of  5 variables:
##  $ id          : int  1 2 3 4 5 6
##  $ height      : num  120 150 132 122 119 110
##  $ weight      : num  44 56 49 45 39 35
##  $ height_log10: num  2.08 2.18 2.12 2.09 2.08 ...
##  $ Fid         : Factor w/ 6 levels "1","2","3","4",..: 1 2 3 4 5 6
```

Merging data frames

- Suppose we have one data frame with information about some common rocky shore invertebrates, called `taxa`
- And we have another data frame with infromation about where these invertebrates are usually found, called `zone`
- Can we combine these into one data frame with all information about the invertebrates?

Merging data frames

```
taxa <- data.frame(
         GENUS = c("Patella", "Littorina", "Halichondria", "Semibalanus"),
         species = c("vulgata", "littoria", "panacea", "balanoides"),
         family = c("patellidae", "Littorinidae", "Halichondriidae", "
     Archaeobalanidae"))
taxa
##          GENUS    species          family
## 1      Patella    vulgata      patellidae
## 2    Littorina   littoria    Littorinidae
## 3 Halichondria    panacea Halichondriidae
## 4  Semibalanus balanoides Archaeobalanidae

zone <- data.frame(
    genus = c("Laminaria", "Halichondria", "Xanthoria", "Littorina",
           "Semibalanus", "Fucus"),
    species = c("digitata", "panacea", "parietina", "littoria",
            "balanoides", "serratus"),
    zone = c( "v_low", "low", "v_high", "low_mid", "high", "low_mid"))
zone
##          genus    species    zone
## 1    Laminaria   digitata   v_low
## 2 Halichondria    panacea     low
## 3    Xanthoria  parietina  v_high
## 4    Littorina   littoria low_mid
## 5  Semibalanus balanoides    high
## 6        Fucus   serratus low_mid
```

Merging data frames

```
taxa_zone <- merge(x = taxa, y = zone)
taxa_zone
##       species        GENUS           family        genus     zone
## 1  balanoides  Semibalanus Archaeobalanidae  Semibalanus     high
## 2    littoria    Littorina     Littorinidae    Littorina  low_mid
## 3     panacea Halichondria  Halichondriidae Halichondria      low
```

- Because the two data frames have a column name in common, R assumes you want to join on that column.
- The joined data frame has both `GENUS` and `genus` because they are spelled differently.
- The joined data frame has only those rows with information in BOTH original data frames.

Merging data frames

```
taxa_zone <- merge(x = taxa, y = zone, all = TRUE)
taxa_zone
##      species      GENUS           family       genus    zone
## 1 balanoides Semibalanus Archaeobalanidae Semibalanus    high
## 2   digitata        <NA>             <NA>   Laminaria   v_low
## 3   littoria   Littorina     Littorinidae   Littorina low_mid
## 4    panacea Halichondria  Halichondriidae Halichondria     low
## 5  parietina        <NA>             <NA>  Xanthoria  v_high
## 6   serratus        <NA>             <NA>      Fucus low_mid
## 7    vulgata     Patella      patellidae        <NA>    <NA>
```

- To include ALL data from BOTH frames use `all = TRUE`
- NAs will be substituted for missing data.

Merging data frames

- Use `by.x` and `by.y` if the names are different

```
taxa_zone <- merge(x = taxa, y = zone,
                   by.x = "GENUS",
                   by.y = "genus",
                   all = TRUE)
taxa_zone
##          GENUS    species.x            family  species.y     zone
## 1        Fucus         <NA>              <NA>   serratus  low_mid
## 2  Halichondria     panacea   Halichondriidae    panacea      low
## 3    Laminaria         <NA>              <NA>   digitata    v_low
## 4    Littorina    littoria      Littorinidae   littoria  low_mid
## 5      Patella     vulgata       patellidae       <NA>     <NA>
## 6  Semibalanus  balanoides Archaeobalanidae  balanoides     high
## 7    Xanthoria         <NA>              <NA>  parietina   v_high
```

Merging data frames

- Can use multiple columns

```
taxa_zone <- merge(x = taxa, y = zone,
                   by.x = c("species", "GENUS"),
                   by.y = c("species", "genus"),
                   all = TRUE)
taxa_zone
##      species       GENUS          family    zone
## 1 balanoides  Semibalanus Archaeobalanidae    high
## 2   digitata    Laminaria             <NA>   v_low
## 3   littoria    Littorina      Littorinidae low_mid
## 4    panacea Halichondria  Halichondriidae     low
## 5  parietina    Xanthoria             <NA>  v_high
## 6   serratus        Fucus             <NA> low_mid
## 7    vulgata      Patella       patellidae    <NA>
```

Reshaping data frames

```
long_data <- data.frame(
  subject = rep(c("A", "B", "C", "D"), each = 3),
  sex = rep(c("M", "F", "F", "M"), each =3),
  condition = rep(c("control", "cond1", "cond2"), times = 4),
  measurement = c(12.9, 14.2, 8.7, 5.2, 12.6, 10.1, 8.9,
                              12.1, 14.2, 10.5, 12.9, 11.9))
long_data
##     subject sex condition measurement
## 1         A   M   control        12.9
## 2         A   M     cond1        14.2
## 3         A   M     cond2         8.7
## 4         B   F   control         5.2
## 5         B   F     cond1        12.6
## 6         B   F     cond2        10.1
## 7         C   F   control         8.9
## 8         C   F     cond1        12.1
## 9         C   F     cond2        14.2
## 10        D   M   control        10.5
## 11        D   M     cond1        12.9
## 12        D   M     cond2        11.9
```

Reshaping data frames

```
wide_data <- data.frame(subject = c("A", "B", "C", "D"),
                        sex = c("M", "F", "F", "M"),
                        control = c(12.9, 5.2, 8.9, 10.5),
                        cond1 = c(14.2, 12.6, 12.1, 12.9),
                        cond2 = c(8.7, 10.1, 14.2, 11.9))
wide_data
##   subject sex control cond1 cond2
## 1       A   M    12.9  14.2   8.7
## 2       B   F     5.2  12.6  10.1
## 3       C   F     8.9  12.1  14.2
## 4       D   M    10.5  12.9  11.9
```

Reshaping data frames

```
long_data
##    subject sex condition measurement
## 1        A   M   control        12.9
## 2        A   M     cond1        14.2
## 3        A   M     cond2         8.7
## 4        B   F   control         5.2
## 5        B   F     cond1        12.6
## 6        B   F     cond2        10.1
## 7        C   F   control         8.9
## 8        C   F     cond1        12.1
## 9        C   F     cond2        14.2
## 10       D   M   control        10.5
## 11       D   M     cond1        12.9
## 12       D   M     cond2        11.9
wide_data
##   subject sex control cond1 cond2
## 1       A   M    12.9  14.2   8.7
## 2       B   F     5.2  12.6  10.1
## 3       C   F     8.9  12.1  14.2
## 4       D   M    10.5  12.9  11.9
```

Reshaping data frames

- Long data: each measurement on separate row.
- Wide data: each sample on separate row, multiple measurements per row.

```
long_data
##    subject sex condition measurement
## 1        A   M   control        12.9
## 2        A   M     cond1        14.2
## 3        A   M     cond2         8.7
## 4        B   F   control         5.2
## 5        B   F     cond1        12.6
## 6        B   F     cond2        10.1
## 7        C   F   control         8.9
## 8        C   F     cond1        12.1
## 9        C   F     cond2        14.2
## 10       D   M   control        10.5
## 11       D   M     cond1        12.9
## 12       D   M     cond2        11.9
wide_data
##   subject sex control cond1 cond2
## 1       A   M    12.9  14.2   8.7
## 2       B   F     5.2  12.6  10.1
## 3       C   F     8.9  12.1  14.2
## 4       D   M    10.5  12.9  11.9
```

melt: convert from wide to long

```
library(reshape2)
wide_data    # remind ourselves what the wide format looks like
##   subject sex control cond1 cond2
## 1       A   M    12.9  14.2   8.7
## 2       B   F     5.2  12.6  10.1
## 3       C   F     8.9  12.1  14.2
## 4       D   M    10.5  12.9  11.9

# convert wide to long
my_long_df <- melt(data = wide_data, id.vars = c("subject", "sex"),
                   measured.vars = c("control", "cond1", "cond2"),
                   variable.name = "condition", value.name = "measurement")
my_long_df
##    subject sex condition measurement
## 1        A   M   control        12.9
## 2        B   F   control         5.2
## 3        C   F   control         8.9
## 4        D   M   control        10.5
## 5        A   M     cond1        14.2
## 6        B   F     cond1        12.6
## 7        C   F     cond1        12.1
## 8        D   M     cond1        12.9
## 9        A   M     cond2         8.7
## 10       B   F     cond2        10.1
## 11       C   F     cond2        14.2
## 12       D   M     cond2        11.9
```

Formula notation

- Normally variables refer to the data.

```
> x <- 1:5
> y <- 11:15
> x + y
 [1] 12 14 16 18 20
```

- Occasionally you want to refer to the variables themselves.

```
> ~ x + y
~x + y
> x ~ y
x ~ y
> x ~ y + z
```

- These are used in R to express sets of variables, or relations between sets of variables.

dcast: convert from long to wide

```
long_data   # remind ourselves what the long format look like
##    subject sex condition measurement
## 1        A   M   control        12.9
## 2        A   M     cond1        14.2
## 3        A   M     cond2         8.7
## 4        B   F   control         5.2
## 5        B   F     cond1        12.6
## 6        B   F     cond2        10.1
## 7        C   F   control         8.9
## 8        C   F     cond1        12.1
## 9        C   F     cond2        14.2
## 10       D   M   control        10.5
## 11       D   M     cond1        12.9
## 12       D   M     cond2        11.9

# convert long to wide
my_wide_df <- dcast(data = long_data, subject + sex ~ condition,
                    value.var = "measurement")
my_wide_df
##   subject sex cond1 cond2 control
## 1       A   M  14.2   8.7    12.9
## 2       B   F  12.6  10.1     5.2
## 3       C   F  12.1  14.2     8.9
## 4       D   M  12.9  11.9    10.5
```

Do exercise 3, part 2

Summarizing data frames

```
summary(flowers)
##     treat             nitrogen      block         height           weight     
##  Length:96          low   :32   Min.   :1.0   Min.   : 1.200   Min.   : 5.790  
##  Class :character   medium:32   1st Qu.:1.0   1st Qu.: 4.475   1st Qu.: 9.027  
##  Mode  :character   high  :32   Median :1.5   Median : 6.450   Median :11.395  
##                                 Mean   :1.5   Mean   : 6.840   Mean   :12.155  
##                                 3rd Qu.:2.0   3rd Qu.: 9.025   3rd Qu.:14.537  
##                                 Max.   :2.0   Max.   :17.200   Max.   :23.890  
##     leafarea       shootarea          flowers      
##  Min.   : 5.80   Min.   :  5.80   Min.   : 1.000  
##  1st Qu.:11.07   1st Qu.: 39.05   1st Qu.: 4.000  
##  Median :13.45   Median : 70.05   Median : 6.000  
##  Mean   :14.05   Mean   : 79.78   Mean   : 7.062  
##  3rd Qu.:16.45   3rd Qu.:113.28   3rd Qu.: 9.000  
##  Max.   :49.20   Max.   :189.60   Max.   :17.000  
```

Summarizing data frame subsets

```
summary(flowers[, 4:7])
##       height           weight          leafarea       shootarea
##  Min.   : 1.200   Min.   : 5.790   Min.   : 5.80   Min.   :  5.80
##  1st Qu.: 4.475   1st Qu.: 9.027   1st Qu.:11.07   1st Qu.: 39.05
##  Median : 6.450   Median :11.395   Median :13.45   Median : 70.05
##  Mean   : 6.840   Mean   :12.155   Mean   :14.05   Mean   : 79.78
##  3rd Qu.: 9.025   3rd Qu.:14.537   3rd Qu.:16.45   3rd Qu.:113.28
##  Max.   :17.200   Max.   :23.890   Max.   :49.20   Max.   :189.60

# or equivalently
# summary(flowers[, c("height", "weight", "leafarea", "shootarea")])
```

Summarizing data frames subsets

```
summary(flowers$leafarea)
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    5.80   11.07   13.45   14.05   16.45   49.20

# or equivalently
# summary(flowers[, 6])
```

Summarizing data frames with `table`

```
table(flowers$nitrogen)
##
##    low  medium    high
##     32      32      32
```

Summarizing data frames with 2d `table`

```
table(flowers$nitrogen, flowers$treat)
##
##            notip tip
##   low         16  16
##   medium      16  16
##   high        16  16
```

xtabs: tables with formula notation

```
xtabs(~ nitrogen + treat, data = flowers)
##           treat
## nitrogen  notip tip
##   low        16  16
##   medium     16  16
##   high       16  16
```

- Don't need $ notation

Summarizing data frames

```
xtabs(~ nitrogen + treat + block, data = flowers)
## , , block = 1
##
##           treat
## nitrogen  notip tip
##   low         8   8
##   medium      8   8
##   high        8   8
##
## , , block = 2
##
##           treat
## nitrogen  notip tip
##   low         8   8
##   medium      8   8
##   high        8   8
```

- `xtabs` automatically converted `block` to a factor

Flattening tables with `ftable`

```
ftable(xtabs(~ nitrogen + treat + block, data = flowers))
##                 block 1 2
## nitrogen treat
## low      notip        8 8
##          tip          8 8
## medium   notip        8 8
##          tip          8 8
## high     notip        8 8
##          tip          8 8
```

tapply: table apply

- Separately collect rows for each value of a factor.
- Apply mean to each value of a factor.

```
tapply(flowers$height, flowers$nitrogen, mean)
##      low   medium     high
## 5.853125 7.012500 7.653125
```

Apply `sd` to each value of a factor

```
tapply(flowers$height, flowers$nitrogen, sd)
##      low   medium     high
## 2.828425 3.005345 3.483323
```

Apply summary to each value of a factor

```
tapply(flowers$height, flowers$nitrogen, summary)
## $low
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.800   3.600   5.550   5.853   8.000  12.300
##
## $medium
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.800   4.500   7.000   7.013   9.950  12.300
##
## $high
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.200   5.800   7.450   7.653   9.475  17.200
```

Including na.rm in each value

```
tapply(flowers$height, flowers$nitrogen, mean, na.rm = TRUE)
##      low   medium     high
## 5.853125 7.012500 7.653125
```

- Note that `mean` is the function that needs this information, but it is a parameter to `tapply` that is automatically passed on.

`tapply` with multiple factors

- Make a different group for each combination of values of two factors

```
tapply(flowers$height,
       list(flowers$nitrogen, flowers$treat),
       mean)
##            notip    tip
## low     3.66875 8.0375
## medium  4.83750 9.1875
## high    5.70625 9.6000
```

When you get tired of writing `flowers$` all the time

```
with(flowers, tapply(height, list(nitrogen, treat), mean))
##           notip    tip
## low     3.66875 8.0375
## medium  4.83750 9.1875
## high    5.70625 9.6000
```

aggregate: an alternative to tapply

```
aggregate(flowers[, 4:7],
          by = list(nitrogen = flowers$nitrogen),
          FUN = mean)
##   nitrogen   height    weight leafarea shootarea
## 1      low 5.853125  8.652812 11.14375   45.1000
## 2   medium 7.012500 11.164062 13.83125   67.5625
## 3     high 7.653125 16.646875 17.18125  126.6875
```

aggregate: an alternative to tapply

```
aggregate(flowers[, 4:7],
          by = list(nitrogen = flowers$nitrogen,
                    treat = flowers$treat),
          FUN = mean)
##   nitrogen treat  height    weight leafarea shootarea
## 1      low notip 3.66875  8.289375 12.32500  59.89375
## 2   medium notip 4.83750 11.316875 14.17500  94.53125
## 3     high notip 5.70625 16.604375 18.81875 155.31875
## 4      low   tip 8.03750  9.016250  9.96250  30.30625
## 5   medium   tip 9.18750 11.011250 13.48750  40.59375
## 6     high   tip 9.60000 16.689375 15.54375  98.05625
```

aggregate also accepts formula notation

- How does height depend on nitrogen and treat?

```
aggregate(height ~ nitrogen + treat,
          FUN = mean,
          data = flowers)
##    nitrogen treat   height
## 1       low notip 3.66875
## 2    medium notip 4.83750
## 3      high notip 5.70625
## 4       low   tip 8.03750
## 5    medium   tip 9.18750
## 6      high   tip 9.60000
```

- Also allows `data = flowers` to avoid `flowers$`

aggregate also accepts subset

```
aggregate(height ~ nitrogen + treat,
          FUN = mean,
          subset = flowers < 7,
          data = flowers)
##   nitrogen treat   height
## 1      low notip 3.533333
## 2   medium notip 5.316667
## 3     high notip 3.850000
## 4      low   tip 8.176923
## 5   medium   tip 8.570000
## 6     high   tip 7.900000
```

aggregate also accepts subset

```
aggregate(height ~ nitrogen + treat,
          FUN = mean,
          subset = block == "1",
          data = flowers)
##   nitrogen treat  height
## 1      low notip  3.3250
## 2   medium notip  5.2375
## 3     high notip  5.9250
## 4      low   tip  8.7500
## 5   medium   tip  9.5375
## 6     high   tip 10.0375
```

Change data only with scripts!

- Never edit a data file!
- All data changes, transforms, *etc.* should be in a script.
- This documents all changes.
- Allows undoing changes.
- Your analysis is now transparent and reproducible.
- Gone are the days of making undocumented changes in Excel!
- Data is **read only**!

But if you *really* want a new data file ...

```r
write.table(flowers_df2,
            file = 'data/flowers_04_12.txt',
            col.names = TRUE,
            row.names = FALSE,
            sep = "\t")

write.table(flowers_df2,
            file = 'data/flowers_04_12.csv',
            col.names = TRUE,
            row.names = FALSE,
            sep = ",")

write.csv(flowers_df2,
          file = 'data/flowers_04_12.csv',
          row.names = FALSE)
```

Other export functions: `fwrite`

- `fwrite` is faster for large data frames

```r
library(read.table)
fwrite(flowers_df2,
         file = 'data/flowers_04_12.txt',
         sep = "\t")

fwrite(flowers_df2,
         file = 'data/flowers_04_12.csv')
```

Other export functions from the tidyverse

```
library(readr)
write_tsv(flowers_df2, path = 'data/flowers_04_12.txt')

write_csv(flowers_df2, path = 'data/flowers_04_12.csv')
```

Do exercise 3, part 3