Introduction to Computing for Economics and Management

Midterm Summary

Data vectors

- The fundamental data type in R is the vector
- Data vectors are created with the construct `c`

```
> person.height <- c(1.70, 1.75, 1.62)

> person.height <- c(person.height, 1.81)
```

- Vector elements must all have the same mode
- Available modes: integer, numeric, character, Boolean, complex

Data vectors

- Missing values are denoted with `NA`

- We can assign names to the elements of a data vector to make the vector more readable

```
> person.height <- c(Can=1.70, Cem=1.75, Hande=1.62)

> person.height
  Can   Cem Hande
 1.70  1.75  1.62
```

Data vector indexing

- We can access a single element of a vector by providing the index of the element in square brackets

```
> person.height[1]
Can
1.7
```

- We can select a subvector by providing a Boolean index vector

```
> person.height[c(T,F,T)]
  Can Hande
 1.70  1.62
```

Data vector indexing

- We can specify the element indices directly

```
> person.height[c(1,3)]
  Can Hande
 1.70  1.62
```

- We exclude elements with negative indices

```
> person.height[c(-1, -3)]
 Cem
1.75
```

- We can change the values of the selected elements

```
person.height[1] <- 1.72
```

Data vector filtering

- The idea behind filtering is to apply a Boolean evaluation function to each element of the vector

```
> person.height > 1.65
   Can    Cem Hande
 TRUE   TRUE FALSE
```

- We use the results of the evaluation function for the filtering

```
> person.height[person.height > 1.65]
 Can  Cem
1.72 1.75
```

Data vector sorting

- We use the function `sort` for sorting a vector

```
> sort(person.height)
Hande   Can   Cem
 1.62  1.70  1.75
```

- We can obtain a sorting in descending order

```
> sort(person.height, decreasing = TRUE)
  Cem   Can Hande
 1.75  1.70  1.62
```

- We can sort a vector according to the values of some other vector

```
> person.weight[order(person.height)]
Hande   Can   Cem
   61    65    66
```

Vector recycling

- When applying an operation to two vectors which requires them to be the same length, the shorter one will repeated until it is long enough to match the longer one

```
> c(1, 2, 3) + c(1, 2, 3, 4)
[1] 2 4 6 5

Warning message:
In c(1, 2, 3) + c(1, 2, 3, 4) :
  longer object length is not a multiple of
shorter object length
```

ifelse() function

- `ifelse(test, yes, no)` returns a vector which is created from selected elements from the vectors `yes` and `no`: `yes[i]` is selected if `test[i]` is true and `no[i]` is selected if `test[i]` is false

```
> ifelse(person.height > 1.7, "tall",
"small")
    Can      Cem   Hande
"small"  "tall" "small"
```

Data vector operations

- We can perform calculations with vectors just like ordinary numbers

- Element wise operations

```
> person.height^2
   Can    Cem  Hande
2.9584 3.0625 2.6244
```

- Vector addition, e.g. persons have gained/lost weight

```
> person.weight + c(1.5, 1.75, -0.5)
  Can   Cem Hande
66.50 67.75 60.50
```

Data vector operations

- Operations on multiple vectors

```
> person.weight / person.height^2
     Can      Cem    Hande
21.97134 21.55102 23.24341
```

- The result of a vector calculation can be assigned to a new data vector for further processing

```
> bmi <- person.weight / person.height^2

> bmi
     Can      Cem    Hande
21.97134 21.55102 23.24341
```

Rounding of numbers

- Round to the specified number of decimal places with function `round`

```
> round(bmi, digits=1)
  Can   Cem Hande
 22.0  21.6  23.2
```

- Alternative functions for rounding of numbers are `ceiling`, `floor`, `trunc`, and `signif`

Data vector operations

- Often used functions that operates on vectors are `mean`, `length` and `sd`

```
> bmi <- person.weight / person.height^2

> mean(bmi)
[1] 23.31768

> length(bmi)
[1] 3

> sd(bmi)
[1] 2.294295
```

Creating regular sequences

- The `from:to` syntax is a simple way to generate a sequence from `from` to `to` in steps of 1 or -1

```
> 1:5
[1] 1 2 3 4 5

> 11:15
[1] 11 12 13 14 15

> 3:0
[1] 3 2 1 0

> seq_1_100 <- 1:100
```

Function seq

- `seq` function arguments
  - `from` starting value of the sequence
  - `to` end value of the sequence
  - `by` increment of the sequence
  - `length.out` desired length of the sequence
  - `along.with` take the length from the length of this argument

```
> seq(5, 10)
[1]  5  6  7  8  9 10

> seq(5, 10, 2)
[1]  5  7  9
```

Creating repeated values with function `rep`

- `rep` function arguments and default values
  - `x` vector of factor that is repeated
  - `times = 1` number of times to repeat
  - `length.out = NA` desired length of the result
  - `each = 1` each element of `x` is repeated `each` times

```
> rep(1, 3)
[1] 1 1 1

> rep(1:4, 2)
[1] 1 2 3 4 1 2 3 4

> rep(1:4, each = 2)
[1] 1 1 2 2 3 3 4 4
```

Matrix creation

- In R, a matrix is a vector with two additional attributes, the number of rows and number of columns

- One of the ways to create a matrix is via the `matrix` function to obtain a matrix from a given data vector with `nrow` number of rows and `ncol` number of columns

```
> y <- matrix(c(1,2,3,4),nrow=2,ncol=2)
> y
     [,1] [,2]
[1,]    1    3
[2,]    2    4
```

Matrix column and row notation

```
> y <- matrix(c(1,2,3,4),nrow=2,ncol=2)
> y
     [,1] [,2]
[1,]    1    3
[2,]    2    4
```

Notation for columns: `[,1]` means first column, `[,2]` second column, etc.

Notation for rows: `[1,]` means first row, `[2,]` second row, etc.

Matrix column and row access

- We can access single columns and rows with the respective column/row notation

```
> y <- matrix(c(1,2,3,4),nrow=2,ncol=2)
> y
     [,1] [,2]
[1,]    1    3
[2,]    2    4

> y[,1]
[1] 1 2

> y[2,]
[1] 2 4
```

Matrix single element access

- We can access single elements of the matrix by providing the indices of row and column

```
> y
     [,1] [,2]
[1,]    1    3
[2,]    2    4

> y[1,1]
[1] 1

> y[2,1]
[1] 2
```

Matrix creation order

- Storage of a matrix is in column-major order: first all of column 1 is stored, then all of column 2, etc.

- We can change the column-major order by providing the additional argument `byrow = TRUE` for filling the matrix by rows

```
> y <- matrix(c(1,2,3,4), nrow=2, ncol=2,
byrow=TRUE)

> y
     [,1] [,2]
[1,]    1    2
[2,]    3    4
```

Matrix row names and column names

- We can provide names for the rows and columns of a matrix

```
> y
     [,1] [,2]
[1,]    1    3
[2,]    2    4

> rownames(y) <- c("Row1", "Row2")
> colnames(y) <- c("Col1", "Col2")

> y
     Col1 Col2
Row1    1    3
Row2    2    4
```

Matrix creation with `cbind` and `rbind`

- We can “glue” vectors together, columnwise or rowwise, using the `cbind` and `rbind` functions

```
> cbind(c(1,2), c(3,4))
     [,1] [,2]
[1,]    1    3
[2,]    2    4

> rbind(c(1,2), c(3,4))
     [,1] [,2]
[1,]    1    2
[2,]    3    4
```

Matrix modification with `cbind` and `rbind`

- Add a column to an existing matrix

```
> y <- matrix(c(1,2,3,4),nrow=2)
> y
     [,1] [,2]
[1,]    1    3
[2,]    2    4

> y <- cbind(c(11, 12), y)
> y
     [,1] [,2] [,3]
[1,]   11    1    3
[2,]   12    2    4
```

Matrix recycling

- The automatic lengthening of vectors also works with matrices

```
> z <- matrix(c(1:9),nrow=3)
> z
     [,1] [,2] [,3]
[1,]    1    4    7
[2,]    2    5    8
[3,]    3    6    9

> cbind(10, z)
     [,1] [,2] [,3] [,4]
[1,]   10    1    4    7
[2,]   10    2    5    8
[3,]   10    3    6    9
```

Matrix operations

- Matrix transposition `t(y)`
- Element by element product `y * y`
- Matrix multiplication `y %*% y`
- Matrix scalar multiplication `3 * y`
- Matrix addition `y + y`

Matrix indexing

- We can access more than a single column/row/element at once

```
> z <- matrix(c(1:9),nrow=3)
> z
     [,1] [,2] [,3]
[1,]    1    4    7
[2,]    2    5    8
[3,]    3    6    9
```

- Select columns 2 and 3

```
> z[,c(2,3)]
     [,1] [,2]
[1,]    4    7
[2,]    5    8
[3,]    6    9
```

Matrix indexing

- Select first and second row

```
> z[c(1,2),]
     [,1] [,2] [,3]
[1,]    1    4    7
[2,]    2    5    8
```

- Select third column of first and second row

```
> z[c(1,2),3]
[1] 7 8
```

Matrix indexing

- We use negative subscripts to exclude certain elements, e.g. request all rows except the second

```
> z[,-2]
     [,1] [,2]
[1,]    1    7
[2,]    2    8
[3,]    3    9
```

Matrix indexing

- We can assign new values to submatrices

```
> z
     [,1] [,2] [,3]
[1,]    1    4    7
[2,]    2    5    8
[3,]    3    6    9

> z[c(1:2), c(2:3)] <- matrix(c(20,21,22,23), nrow=2)

> z
     [,1] [,2] [,3]
[1,]    1   20   22
[2,]    2   21   23
[3,]    3    6    9
```

Matrix indexing

- We can delete rows or columns by reassignment, e.g. keep only first two rows and delete third row

```
> z
     [,1] [,2] [,3]
[1,]    1    4    7
[2,]    2    5    8
[3,]    3    6    9

> z <- z[c(1,2),]
> z
     [,1] [,2] [,3]
[1,]    1    4    7
[2,]    2    5    8
```

Matrix filtering

- Similar to data vector filtering, the concept behind is to first apply a Boolean evaluation function

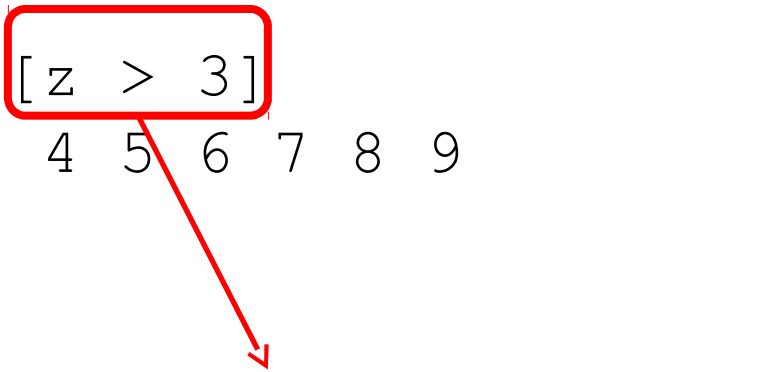
- For each single element, the Boolean evaluation function returns `TRUE` in case of a positive evaluation and `FALSE` in case of a negative evaluation

```
> z > 3
      [,1] [,2] [,3]
[1,] FALSE TRUE TRUE
[2,] FALSE TRUE TRUE
[3,] FALSE TRUE TRUE
```

Matrix filtering

- Similar to data vector filtering, we can perform evaluation and filtering in one line

```
> z[z > 3]
[1] 4 5 6 7 8 9
```



We provide the evaluation function directly in the square brackets for selecting those elements that fulfill the evaluation function

Matrix filtering

- In contrast to data vector filtering, we can perform more complex filtering tasks with matrices, e.g. obtain those rows of matrix `z` having elements in the second column which are at least equal to 5

```
> z
     [,1] [,2] [,3]
[1,]    1    4    7
[2,]    2    5    8
[3,]    3    6    9

> z[z[,2] >= 5,]
     [,1] [,2] [,3]
[1,]    2    5    8
[2,]    3    6    9
```

Matrix function `apply()`

- An often used generic function in R is `apply()`
- `apply()` executes a user-specified function on each of the rows or each of the columns of a matrix
- `apply(m,dimcode,f,fargs)`
  - `m` is the matrix
  - `dimcode` equal to 1 means that the function is applied to rows, `dimcode` equal to 2 means that the function is applied to columns
  - `f` is the function to be applied
  - `fargs` is an optional set of arguments to be supplied to `f`

Writing our own function

- We write a simple function that adds 1 to its input and returns the result

```
> AddOne <- function(x) {x+1}
```

Function name

Function inputs

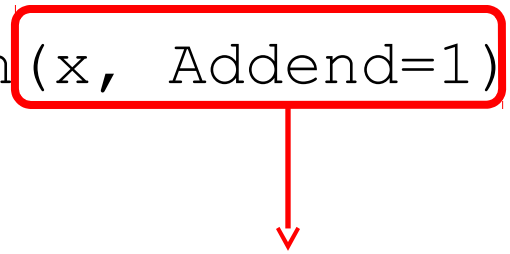
Instructions that take the inputs and use them to compute other values.

The last computed value is returned by default.

Writing our own function

- Let's write another more sophisticated function that adds a user-specified value to its first input

```
> AddValue <- function(x, Addend=1) {x+Addend}
```



In addition to the first input `x` we specify a second input `Addend` with default value 1.

Using our own function with `apply()`

- First we apply `AddValue` to the rows of `z`

```
> z
     [,1] [,2] [,3]
[1,]    1    4    7
[2,]    2    5    8
[3,]    3    6    9

> apply(z,1,AddValue)
     [,1] [,2] [,3]
[1,]    2    3    4
[2,]    5    6    7
[3,]    8    9   10
```

Resulting vector when adding 1 to the first row

Lists

- Lists can combine objects of different types
- We create a list to represent the data from Joe

```
> joe <- list("Joe", 55000, T)
```

- An entire employee database might then be a list of lists

Creating lists

- Let's check our new list `joe`

```
> joe
[[1]]
[1] "Joe"

[[2]]
[1] 55000

[[3]]
[1] TRUE
```

- We observe that the three components name, salary and membership are indexed by `[[1]]`, `[[2]]`, and `[[3]]`

Creating lists

- We better provide name tags for our components when creating a list

```
> joe <- list(name="Joe", salary=55000,
staff=T)

> joe
$name
[1] "Joe"

$salary
[1] 55000

$staff
[1] TRUE
```

List indexing

- We can access list components in several different ways – each of them is useful in different contexts

```
> joe$salary
[1] 55000

> joe[["salary"]]
[1] 55000

> joe[[2]]
[1] 55000
```

Adding list elements

- New components can be added after a list is created
- We can add new components in different ways

```
> joe <- list(name="Joe", salary=55000,
staff=T)

> joe$age <- 39

> joe[[5]] <- 1976

> joe[6:7] <- c(TRUE, TRUE)
```

Deleting list elements

- We can delete a list component by setting it to NULL

```
> joe$salary <- NULL

> joe$staff <- NULL
```

- After deleting, the indices of subsequent elements automatically move up

Vectors as list components

- Beside storing atomic entries like `Joe` or `55000` in a list, we can have vectors as list components

```
> my.list <- list(vec1 = c(1,2), vec2 =
c(3,4), vec3 = 5:7)

> my.list
$vec1
[1] 1 2

$vec2
[1] 3 4

$vec3
[1] 5 6 7
```

Word list

- Let's consider this sentence as our text example:

```
a text consists of a word and another word
and so on and so forth
```

- For each word we need to obtain the location in the text:
  - **a** 1 5
  - **text** 2
  - **consists** 3
  - **of** 4
  - **word** 6 9
  - **and** 7 10 13
  - **another** 8
  - **so** 11 14
  - **on** 12
  - **forth** 15

Word list

- Let's assume that we iterate through our text in a word by word manner: `a, text, consists, of, a, ...`
- Let's further assume that the current word in our iteration is always stored in the variable `word`
- Let's further assume that we have a counter `i` which is increased by 1 for every word: the counter tells the current position in the text

Word list

- Let's start with initializing our word list

```
> word.list <- list()
```

- Our first word `a` is stored in the variable `word`

```
word <- "a"
```

- Since it is our first word, our counter `i` has the value 1

```
> i <- 1
```

- Now we add our current word `a` to our word list

```
> word.list[[word]] <- c(word.list[[word]], i)
```

Word list

- Let's check our word list after the first iteration

```
> word.list
$a
[1] 1
```

- We interpret this intermediate result as word `a` has position `1`

- We go on with a few other words

Word list

- When we check `word.list` again we obtain

```
> word.list
$a
[1] 1 5

$text
[1] 2

$consists
[1] 3

$of
[1] 4
```

Accessing list components

- If the components in a list do have tags, we can obtain them via `names()`

```
> names(joe)
[1] "name"   "salary" "staff"

> names(word.list)
[1] "a"          "text"     "consists" "of"
```

Sort word list alphabetically

- We can write all three steps in one line

```
> word.list[sort(names(word.list))]
$a
[1] 1 5

$consists
[1] 3

$of
[1] 4

$text
[1] 2
```

Accessing list values

- We can obtain list values by using `unlist()`

```
> unlist(joe)
   name  salary   staff
  "Joe" "55000"  "TRUE"

> unlist(word.list)
      a1       a2     text consists       of
       1        5        2        3        4
```

- We observe that in the first case we retrieve a vector of character strings and in the second case a numeric vector

- The reason for the different result modes is that list components are coerced to a common mode during unlist

Applying functions to lists

- `apply()` executes a user-specified function on each of the rows or each of the columns of a matrix, e.g.
  `apply(z,1,mean)` compute the row means of matrix `z`

- The function `lapply()` works like the `apply()` function: the specified function is applied on each component of a list and another list is returned

- `lapply(l, f, fargs)`
  - `l` is the list
  - `f` is the function
  - `fargs` is an optional set of arguments for function `f`

Applying functions to lists

- Example: count number of words from our `word.list`

```
> lapply(word.list, length)
$a
[1] 2

$text
[1] 1

$consists
[1] 1

$of
[1] 1
```

Applying functions to lists

- `sapply()` works like `lapply()` but instead of a list it returns a vector or a matrix

- Previous example with `sapply()`

```
> sapply(word.list, length)
     a   text consists     of
     2      1        1      1
```

Sort word list by word frequency

- We can write all three steps in one line

```
> word.list[order(sapply(word.list, length))]
$text
[1] 2

$consists
[1] 3

$of
[1] 4

$a
[1] 1 5
```

Data frame

- A data frame is like a matrix, with a two-dimensional rows- and columns structure

- Each column may have a different mode, e.g. one column may consist of numbers, and another column might have character strings or Boolean entries

- On a technical level, a data frame is a list: each component of that list consists of equal-length vectors

Creating data frames

- One way to create a data frame is to combine available equal-length vectors

```
> person <- data.frame(height=person.height,
weight=person.weight, member=person.member,
initial=c("C", "C", "H"))

> person
       height weight member initial
Can      1.70     65   TRUE       C
Cem      1.75     66   TRUE       C
Hande    1.62     61  FALSE       H
```

- We observe that the columns retain their original mode and that the vector element names are used to label the rows of the data frame

Accessing data frames

- Since a data frame is technically a list, we can access it via component index values or component names

```
> person[[1]]
[1] 1.70 1.75 1.62

> person[["height"]]
[1] 1.70 1.75 1.62

> person$height
[1] 1.70 1.75 1.62
```

Accessing data frames

- We can access it in a matrix-like fashion as well, e.g. view column 1

```
> person[,1]
[1] 1.70 1.75 1.62
```

- Element in third row, second column

```
> person[3,2]
[1] 61
```

Data frame indexing

- Since data frames can be accessed in a matrix-like fashion, we can select rows and columns in a matrix-like way

- First and second row

```
> person[c(1,2),]
    height weight member
Can   1.70     65   TRUE
Cem   1.75     66   TRUE
```

- Third column of first and second row

```
> person[c(1,2),3]
[1] TRUE TRUE
```

Data frame indexing

- Like for matrices, we can use negative indices to exclude rows or columns

```
> person[-3,]
     height weight member
Can    1.70     65   TRUE
Cem    1.75     66   TRUE

> person[,-3]
       height weight
Can      1.70     65
Cem      1.75     66
Hande    1.62     61
```

Data frame filtering

- Similar to data vector and matrix filtering, the concept behind is to apply a Boolean evaluation function

- Example: retrieve all observations for which person height is at least 1.7

```
> person[person$height >= 1.7,]
    height weight member
Can   1.70     65   TRUE
Cem   1.75     66   TRUE
```

Data frame modifications

- Like for matrices, we can use `rbind()` and `cbind()` to add new rows or columns to a data frame

- Usually, we add a new row in form of a list

```
> person <- rbind(person, Lale=list(1.76, 64, T))

> person
       height weight member
Can      1.70     65   TRUE
Cem      1.75     66   TRUE
Hande    1.62     61   TRUE
Lale     1.76     64   TRUE
```

Data frame modifications

- We use `cbind()` for adding a new column

```
> person <- cbind(person, initial=c("C", "C",
"H", "L"))

> person
       height weight member initial
Can      1.70     65   TRUE       C
Cem      1.75     66   TRUE       C
Hande    1.62     61   TRUE       H
Lale     1.76     64   TRUE       L
```

Data frame modifications

- As an alternative to `cbind()` we can use the $ notation

```
> person$BMI <- person$weight /
person$height^2

> person
      height weight member initial      BMI
Can     1.70     65   TRUE       C 22.49135
Cem     1.75     66   TRUE       C 21.55102
Hande   1.62     61   TRUE       H 23.24341
Lale    1.76     64   TRUE       L 20.66116
```

Data import with `read.table`

The function `read.table` is the most convenient way to read in a rectangular grid of data from a text file

```
> help(read.table)
read.table(file, header = FALSE, sep = "", quote = "\"'",
           dec = ".", row.names, col.names,
           as.is = !stringsAsFactors,
           na.strings = "NA", colClasses = NA, nrows = -1,
           skip = 0, check.names = TRUE,
           fill = !blank.lines.skip,
           strip.white = FALSE, blank.lines.skip = TRUE,
           comment.char = "#",
           allowEscapes = FALSE, flush = FALSE,
           stringsAsFactors = default.stringsAsFactors(),
           fileEncoding = "", encoding = "unknown", text)
```

Data import

- Now, we import the data into the data frame `person.data` by using the function `read.table`

```
> person.data <- read.table(header=TRUE,
"height_weight_data.txt", sep=",")

> person.data
     Name Height Weight
1     Can   1.70     65
2     Cem   1.75     66
3   Hande   1.62     61
4    Lale   1.76     64
5    Arda   1.78     63
6  Bilgin   1.77     84
7     Cem   1.69     75
8   Ozlem   1.75     65
9     Ali   1.73     75
10  Haluk   1.71     81
```

Data modifications

- We add a new column `BMI` like we did before

```
> person.data$BMI <- person.data$Weight /
person.data$Height^2

> person.data
     Name Height Weight      BMI
1     Can   1.70     65 22.49135
2     Cem   1.75     66 21.55102
3   Hande   1.62     61 23.24341
4    Lale   1.76     64 20.66116
5    Arda   1.78     63 19.88385
6  Bilgin   1.77     84 26.81222
7     Cem   1.69     75 26.25958
8   Ozlem   1.75     65 21.22449
9     Ali   1.73     75 25.05931
10  Haluk   1.71     81 27.70083
```

Data modifications

- We can change the values of a column by reassigning the column with the new values, e.g. rounding BMI

```
> person.data$BMI <- round(person.data$BMI, 2)

> person.data
     Name Height Weight   BMI
1     Can   1.70     65 22.49
2     Cem   1.75     66 21.55
3   Hande   1.62     61 23.24
4    Lale   1.76     64 20.66
5    Arda   1.78     63 19.88
6  Bilgin   1.77     84 26.81
7     Cem   1.69     75 26.26
8   Ozlem   1.75     65 21.22
9     Ali   1.73     75 25.06
10  Haluk   1.71     81 27.70
```

Data modifications

- When creating new columns, we can make use of functions to compute the values of a new column

- Let's recapitulate the `ifelse()` function

- `ifelse(test, yes, no)` returns a vector which is created from selected elements from the vectors `yes` and `no`: `yes[i]` is selected if `test[i]` is true and `no[i]` is selected if `test[i]` is false

```
> ifelse(person.height > 1.7, "tall",
"small")
    Can     Cem   Hande
"small"  "tall" "small"
```

Data frame modifications

Let's use `ifelse()` to create a new column which indicates whether BMI is above 22.5

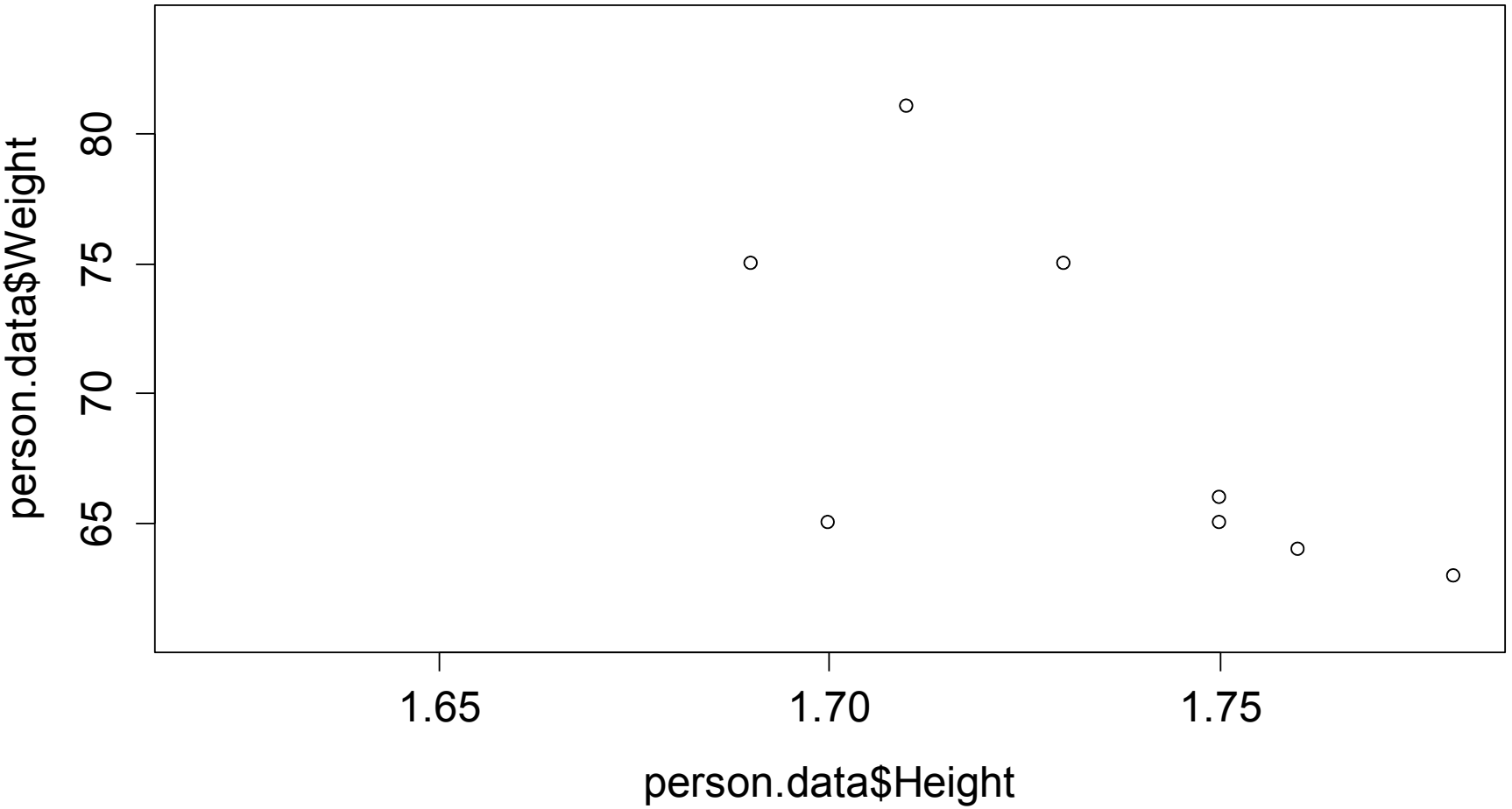
```
> person.data$above22.5 <- ifelse(person.data$BMI>22.5, T ,F)
> person.data
     Name Height Weight   BMI above22.5
1     Can   1.70     65 22.49     FALSE
2     Cem   1.75     66 21.55     FALSE
3   Hande   1.62     61 23.24      TRUE
4    Lale   1.76     64 20.66     FALSE
5    Arda   1.78     63 19.88     FALSE
6  Bilgin   1.77     84 26.81      TRUE
7     Cem   1.69     75 26.26      TRUE
8   Ozlem   1.75     65 21.22     FALSE
9     Ali   1.73     75 25.06      TRUE
10  Haluk   1.71     81 27.70      TRUE
```

Scatter Plot

- Beside numeric summary statistics, a convenient way for data exploration is plotting
- R provides us many powerful tools for plotting
- We will learn more about plotting later
- For now, we create a simple scatter plot by plotting height on the x-axis and weight on the y-axis

```
> plot(person.data$Height, person.data$Weight)
```

Scatter Plot



Merging data frames

- We merge the two data frames using the merge() function

```
> merge(person.data, person.data2)
   Name Height Weight   BMI above22.5 Initial Member
1   Can   1.70     65 22.49     FALSE       C      T
2   Cem   1.69     75 26.26      TRUE       C      T
3   Cem   1.75     66 21.55     FALSE       C      T
4 Hande   1.62     61 23.24      TRUE       H      F
```

Short Summary Vectors

- Integer mode

```
> person.weight <- c(65, 66, 61)
```

- Numeric (floating-point number)

```
> person.height <- c(1.70, 1.75, 1.62)
```

- Character (string)

```
> person.name <- c("Can", "Cem", "Hande")
```

- Logical (Boolean)

```
> person.female <- c(FALSE, FALSE, TRUE)
```

- Complex

```
> complex.numbers <- c(1+2i, -1+0i)
```

Short Summary Vectors

- Assign names to the elements of a data vector

```
> person.height <- c(Can=1.70, Cem=1.75,
Hande=1.62)
```

- Indexing

```
> person.height[c(T,F,T)]
  Can Hande
 1.70  1.62

> person.height[c(1,3)]
  Can Hande
 1.70  1.62

> person.height[-1]
  Cem Hande
 1.75  1.62
```

Short Summary Vectors

- Filtering

```
> person.height[person.height > 1.65]
 Can  Cem
1.72 1.75
```

- Recycling

```
> c(1, 2, 3) + c(1, 2, 3, 4)
[1] 2 4 6 5
```

- Vector operations

```
> person.weight / person.height^2
     Can       Cem    Hande
21.97134 21.55102 23.24341
```

Short Summary Matrices

- Creation

```
> y <- matrix(c(1,2,3,4),nrow=2,ncol=2)

> cbind(c(1,2), c(3,4))
```

- Matrix operations
  - Transposition `t(y)`
  - Element by element product `y * y`
  - Matrix multiplication `y %*% y`
  - Matrix scalar multiplication `3 * y`
  - Matrix addition `y + y`

- Indexing, e.g. select first and second row

```
> z[c(1,2),]
```

Short Summary Matrices

- Assign new values to submatrices

```
> z[c(1:2), c(2:3)] <- matrix(c(20,21,22,23), nrow=2)
```

- Filtering, e.g. obtain those rows of matrix `z` having elements in the second column which are at least equal to 5

```
> z[z[,2] >= 5,]
```

Short Summary Lists

- Creation

```
> joe <- list(name="Joe", salary=55000,
staff=T)
```

- Indexing

```
> joe$salary
> joe[["salary"]]
> joe[[2]]
```

- Vectors as list components

```
> my.list <- list(vec1 = c(1,2), vec2 =
c(3,4), vec3 = 5:7)
```

Short Summary Data frames

- Creation

```
> person <- data.frame(height=person.height,
weight=person.weight)
```

- Indexing

```
> person[[1]]
> person[["height"]]
> person$height
> person[c(1,2),]
> person[-3,]
```

- Filtering

```
> person[person$height >= 1.7,]
```

Short Summary Data frames

- Data import

```
> person.data <- read.table(header=TRUE,
"height_weight_data.txt", sep=",")
```

- Data modifications

```
> person.data$BMI <- person.data$Weight /
person.data$Height^2
```

- Summary

```
> summary(person.data)
```

- Merging

```
> merge(person.data, person.data2)
```