## Object types

Applied Data Science using R, Session 3

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## Goals for today

I. Learn about the use of $R$ packages
II. Understand the main object types in R and their practical relevance
III. Learn how to transform object types into each other
IV. Hear about some useful helper functions and the concept of vectorisation

## Packages

## R packages

- One cool thing about $R$ is that there is a great community of $R$ users that write objects and functions that perform useful purposes and makes them available to all
- This process of 'making available objects to others' is done via the use of $\mathbf{R}$ packages
- You can think of an R package as a collection of assignments and documentations that people pass around
- If you install R, you can use all objects that...
- ...you defined for yourself
- ...are pre-defined in R
- If you want to use objects defined by someone else in her package you need to install this package


## Installing packages

- The official way to distribute packages is via CRAN, the The Comprehensive $R$ Archive Network
- To install a package that was deployed on CRAN you must execute the following command:
install.packages("NAME OF PACKAGE")
- To install the package ineq, for instance, do:

```
install.packages("ineq")
```

- To install packages that were not yet released on CRAN, other functions are available
- After having installed the ineq package, you can use all objects defined by it


## Calling objects defined in packages

- One object defined in ineq is the function Gini()
- Simply calling Gini() does, however, not work
- You need to tell R that $\operatorname{Gini}()$ is defined by the package ineq
- To do use, use : ::
ineq::Gini(c(1,2,3,4))
- You may think of :: as building a bridge between your R session and all objects defined in a package
- A sometimes more convenient way is to use the function library() at the beginning of your script:
library(ineq)
- This makes available all objects of ineq in your current R session


## Packages and masking

- Packages are written by many different people
- It is not unlikely that two packages assign the same name to different objects
- If you then attach both packages, the assignment of the earlier package will be masked
- Try this by attaching the two packages dplyr and plm
- In these cases, you must use : : to access the masked object of the first package
- As a general rule: always use :: whenever masking is a potential problem $\rightarrow$ makes your code much easier to understand for you and others
- Use the function conflicts() to see all names for which conflicts exists


## Recap questions

- What is the main rationale for the use of $R$ packages?
- What is an R package in the most basic sense?
- How can you install R packages from CRAN? Illustrate this using the package "dplyr"
- How can you access objects from a package that you have installed previously? What are the advantages and disadvantages of the different ways you learned about?
- What does it mean to 'attach a package'?
- What do we mean with 'masking' in the context of using $R$ packages?


## Basic object types in R

## Object types in $\mathbf{R}$

To understand computations in R, two slogans are helpful:
Everything that exists is an object.
Everything that happens is a function call.
John Chambers

- We have learned quite a bit about functions, now we turn to objects
- We must distinguish different object types because functions operate differently depending on the type of the object we are processing
- E.g.: 'adding up' numbers is different than 'adding up' words
- Fortunately, there are only a few basic types you must know about
- More complex types are natural modifications of these basic types
- The most general type of object in $R$ is a vector


## Basic object types in R

## Atomic vectors



## Lists ('generic vectors')



- Among the more specific vector types, we will learn about factors and data frames later


## Atomic vectors

- Atomic vectors are composed only of objects of the same type
- We say that an atomic vector is of the same type as are its elements
- We can test for this type using the function typeof()
- There are four main types of atomic vector that are most important:


## Logical values: logical

- Only two* options: TRUE or FALSE
- Often the result of logical operations (e.g. $4>2$ )

> Whole numbers: integer
> A whole number, followed by L: 1L, 2L, 100L, etc. Often the result of counting

## Decimal numbers:

 double- A number with the decimal sign .
- 2.0, 0.8, -7.5, etc.
- The 'standard' number you will use

Letters and words: character

- Might contain all kinds
of tokens and start and
end with "
"2", "Hello!",
"vec_1", etc.


## Creating atomic vectors

- The easiest way to create atomic vectors is the function c() ('concatenate')

```
t_vec <- c(1, 2, 3)
```

- The number of elements that are part of a vector are its length:
- You can test for the length of a vector using length():
length(t_vec)
- c() can also be used to merge atomic vectors or arbitrary length:
t_vec_2 <- c(4, 5, 6)
t_vec_full <- c(t_vec, t_vec_2)


## Coercion

- Sometimes we might want to change the type of an atomic vector
- In this context, the functions as.*() and is.*() are useful
- Substitute the * for the type of vector, and you can test and transform them:
xx <- " 2 "
is.double(xx)
yy <- as.double(xx)
is.double(yy)
- But be beware of some counter-intuitive transformation behaviour:
- as.integer(22.9)
- as.logical(99)


## Intermediate exercises

1. Create a vector containing the numbers $2,5,2.4$ and 11 .
2. What is the type of this vector?
3. Transform this vector into the type integer. What happens?
4. Do you think you can create a vector containing the following elements: "2", "Hallo", 4.0, and TRUE? Why? Why not?

## Helper functions, indexing, and vectorisation

## Some useful helper functions

- There are some types of atomic vectors that you create frequently
- Sequences of numbers, concatenated words, or repetitions
- For case 1 you may use the function seq() with the following arguments:
- from, to: starting and end values of the sequence
- by: increment steps of the sequences (must be numeric)
- length. out: desired length of final sequence
- along.with: creates sequence of same length as object
- Only one of the arguments (ii), (iii), and (iv) can be used, e.g.:
- seq(-5, 5, by=2.5) ; seq(1, 4, length.out=10)


## Some useful helper functions

- There are some types of atomic vectors that you create frequently
- Sequences of numbers, concatenated words, or repetitions
- For case 2 you may use the function paste( ) with the argument sep:
- sep: How should the input vectors be separated?
- This is useful, for instance, if you want to create file names:

```
paste("file_", seq(1,4), ".pdf", sep = "")
```

- Finally, if you want to repeat something, use rep( ):

```
rep("Cool!", 5)
```


## Indexing

- Indexing means referencing a particular position of a vector
- You do this by adding the position in square brackets to the end of the vector
- v_c[3], for instance, returns the third element of the vector v_c
- You can also use this logic to replace these elements:

```
v_c <- c("First", "Second", "Second", "Fourth")
v_c[3] <- "Third!"
```

- But you cannot use this to add new elements to a vector:
v_c[5] <- "Fifth..."
- Add a fifth element to the vector v_c!


## Vectorisation

- One reason why atomic vectors are so popular is that they allow for very fast computations
- For the computer it is much easier to work with sets of objects that all behave the same
- Vectorisation means that an operation is applied to each element of a vector:

```
v_2 <- seq(1, 5)
v_2**2
```

- "To vectorise" a task means to write it in a way that operations are applied to atomic vectors $\rightarrow$ in R, you should do that whenever possible
- A slower alternative are loops, which we learn about later and which are unavoidable in certain situations


## Intermediate exercises

I. Create a vector with the numbers from -2 to 19 (step size: 0.75 )
II. Create an index vector for this first vector (note: an index vector is a vector with all possible indices of the original vector)
III. Compute the log of each element of the first vector using vectorisation. Anything that draws your attention?
IV. What happens if you concatenate vectors of different types using c()? Can you derive a systematization?

- Remember that you can check for the type of an atomic vector using typeof()


## Lists

## Basic object types in $\mathbf{R}$



- Among the more specific vector types, we will learn about factors and data frames later


## Lists

- The second major type of vectors $\rightarrow$ sometimes called generic vectors
- Difference to atomic vectors: lists may contain objects of different types
- Thus, the type of a list is always...

```
l_1 <- list(c(1,2), c("a", "b"), c(TRUE, FALSE, FALSE)); typeof(l_1)
```

- Lists can be complex $\rightarrow$ get an overview using str() :



## Naming and indexing of lists

- The different elements of lists can be named:

```
l_2 <- list("numbers"=c(1,2),
    "letters"=c("a", "b"),
    "logics"=c(TRUE, FALSE, FALSE))
```

- You can retrieve the names using names():
names(1_2)
- You can subset the list using the names:
1_2["letters"]
- And access the elements of the sublists with [ [:
l_2[["letters"]]
- Alternatively use the shortcut $\$$ : $1 \_2 \$$ letters


## Practical differences to atomic vectors

- There are two very important differences to atomic vectors:
- Vectorisation does not work for lists
- Indexing works differently for lists
- To illustrate the first issue compare:

$$
\begin{aligned}
& v_{-}<-c(1,2,3) ; 2 v_{-} \\
& l_{-}<-\operatorname{list}(1,2,3) ; 2 * l_{-}
\end{aligned}
$$

- To illustrate the latter:

```
typeof(l_[1])
typeof(l_[[1]])
```

- Lists are fundamental to more complex data structures we will encounter later


## Final remarks on basic object types

- There are two "strange" data types: NA and NULL
- NA is used to represent absent elements of vectors
- Happens frequently when vectors contain observations
- Many functions behave differently when NAs are present (remember na. rm!):

```
mean(c(1,2,NA)) ; mean(c(1,2,NA), na.rm = TRUE)
```

- You test for NA using is.na():
is.na(c(1, 2, NA))
- To check whether a vector contains missing values, use anyNA(): $\operatorname{anyNA}(c(1,2, N A))$


## Final remarks on basic object types

- There are two "strange" data types: NA and NULL
- NULL is in fact a data type in itself, but in practice its best thought of as a vector of length zero:

```
c()
typeof(NULL)
length(NULL)
is.null(NULL)
```

- You might use NULL mainly in two instances:
- Represent an empty vector of arbitrary type
- Represent and absent vector ( $\neq$ NA, which represents absent elements of vectors)


## Intermediate exercises

- Create a list that has three named elements: "A", "B", and "C"
- The element "A" should contain the square root of the numbers form -2 to 8 (step size: 1)
- The element "B" should contain the log of numbers between 2 and 4 (step size: 0.5)
- The element "C" should contain letters from a1 to g7 (hint: use the predefined vector letters and the function paste())


## Wrap up basic object types

## Atomic vectors

logical

## Vectors

## Lists ('generic vectors')


character

- The central take-aways concern:
- How to test for and transform these types: typeof(), is.*(), as.*()
- How to index them: [, [ [, \$
- How to create typical instances: rep(), paste(), seq()
- We learned about vectorisation and its attractiveness in R
- We also encountered "strange" types such as NA, NULL and NaN


## Summary and outlook

- Next time we will learn about two more advanced object types: factors and data.frames
- We will learn how our knowledge about the basic object types helps us to deal with more advanced types, and how they relate to each other


## Tasks until next session:

1. Fill in the quick feedback survey on Moodle
2. Read the tutorials posted on the course page
3. Do the exercises provided on the course page and discuss problems and difficulties via the Moodle forum
