Introducing the R statistical language

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R Programming

R is a high-level **statistical programming language**.

R is very efficient at

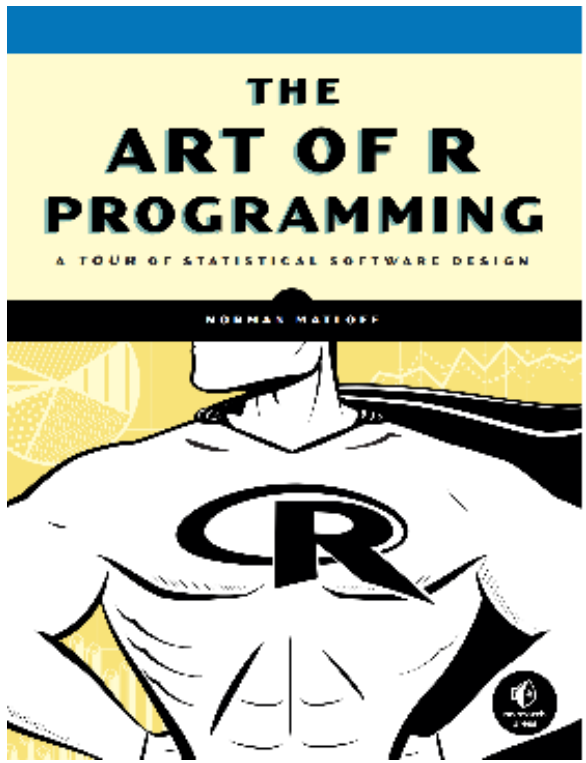
- vectors and matrices operations
- large datasets processing
- data visualization
- statistical/machine-learning modelling

One of the most popular statistical programming languages:

- you can find online solutions to your programming questions.
- Stackoverflow
- CrossValidated

Literature

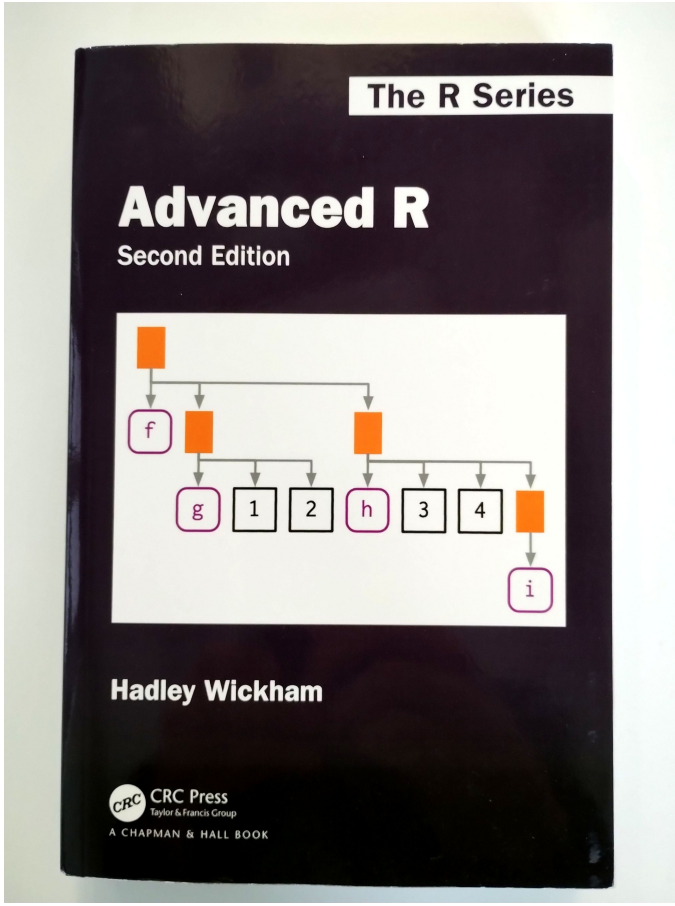
The Art of R Programming: a tour of statistical software design.



Ebook available via the University library.

If you want something more in depth on the language itself:

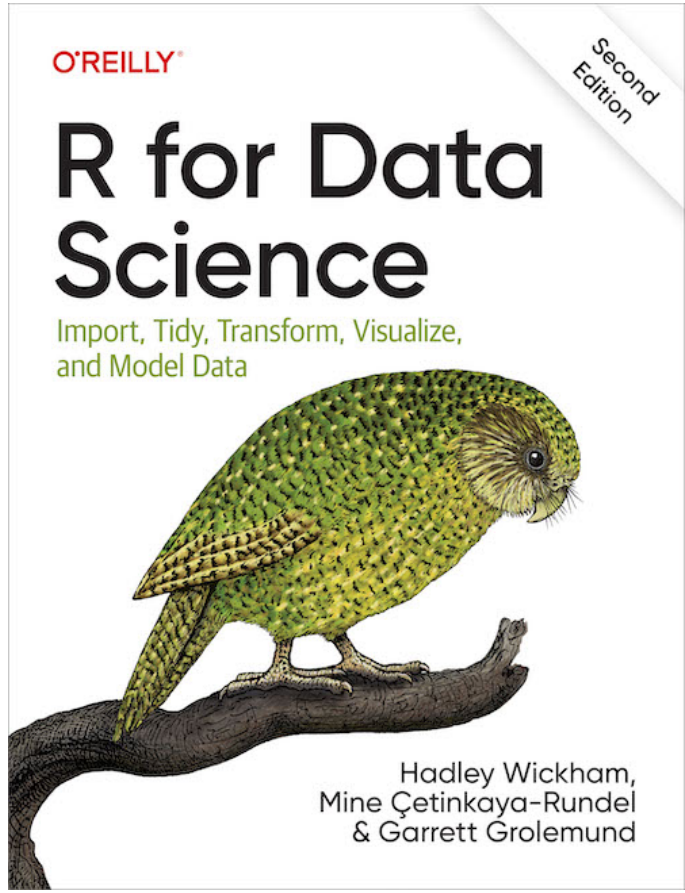
Advanced R (second edition)



Ebook freely available here. There is also a book with solutions to the exercises.

For something more focussed on data analysis in R:

R for Data Science (second edition)



Ebook freely available here.

Note that this relies on a set of R packages (the Tidyverse) that we will not use.

Course objectives

Understand essential features of R programming.

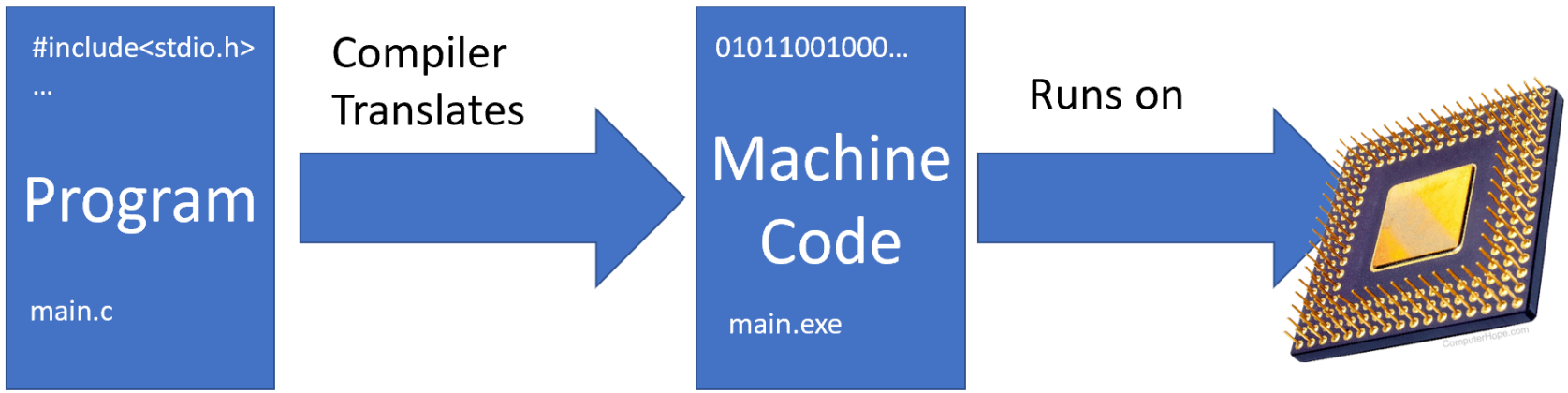
Be able to write and test basic **statistical algorithms** in R, with appropriate coding paradigms.

Understand the **differences between C and R**, and be able to decide which one to use when facing a task.

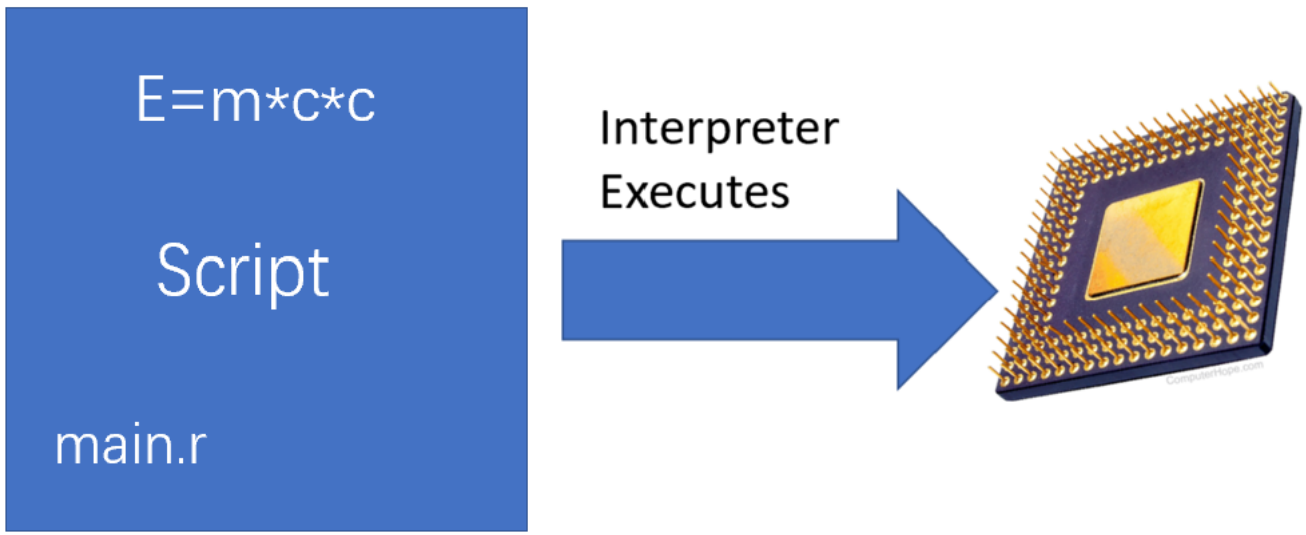
Be able to code a basic data science project using R by calling existing statistics/data science libraries.

R is an Interpreted Language

Compiled programming language (e.g., C/C++)



Interpreted programming language (e.g., R/Python)



Interpreted Languages

Interpreted languages do **not** need compilation.

The script is sent to a software called "interpreter" and is executed by it.

No executable file is produced (there is no app!).

The interpreter executes your code file **line by line**, and **you can even stop your program and make changes**.

It is impossible to do so in compiled languages. Once your program has been compiled and started running, you cannot stop it and modify the code.

Examples of Interpreted Languages

Most websites are written by interpreted languages:

- HTML and Javascript are both interpreted languages.
- Your browsers (e.g. Edge/Chrome) are interpreters.
- They download, interpret the program (webpage source code) and render the outcome to the screen.

Most data science languages are interpreted languages:

- MATLAB/Python/R.
- Interpreted language allows users to stop the execution, inspect intermediate outcomes and make necessary changes.

Pros

- No compilation step needed. Runs immediately.
- Flexible coding. No need to write the whole program in one go. You can delay the programming until you see the earlier execution results.

Cons

- Slower than compiled language, code requires interpretation.
- No executable is produced. To run your code, your users must have **your code** and **install the interpreter**.
- Some interpreters, like MATLAB, are not free.

Pro or Con:

- The source code is visible to the user.

Languages such as Julia have a JIT compiler and might offer the best of both worlds.

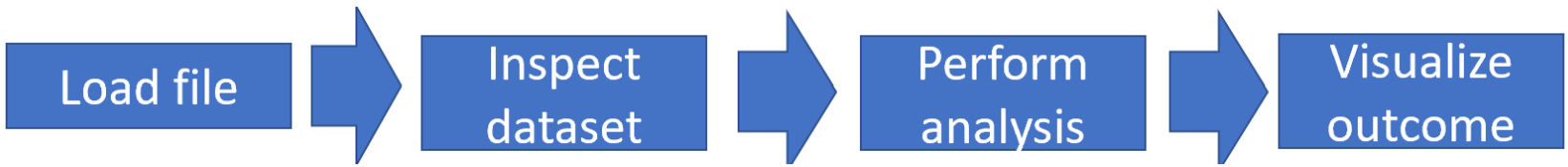
Interpreted Languages are Ideal for Data Science Projects

Common data science project workflow:

1. Parse/Load the dataset from file.
2. Inspect the dataset **interactively**:
   - visualize some basic facts about your dataset.
   - determine what analysis you would like to run.
3. Code the algorithm
   - inspect the outcome of the algorithm
   - determine how to visualize the outcome.
4. Code the visualization part

Key point: often we do not know what we want to do in advance.

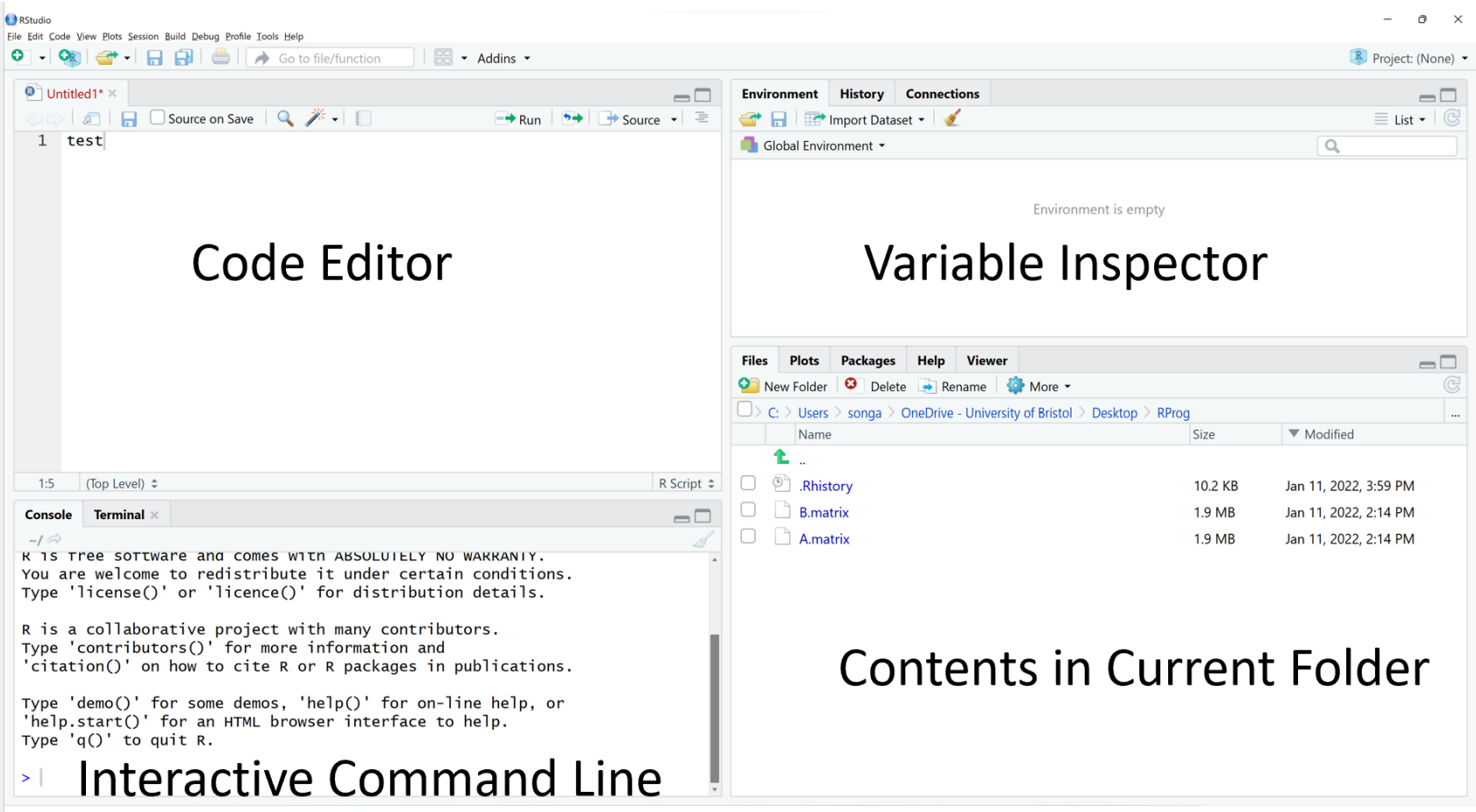
Interpreted Language allows you to cut your workflow into pieces, and program them adaptively, not in one go.



R allows your code to be adaptive, based on previous execution results.

RStudio: An R Development Environment

Instead of using VSCode, we will use RStudio as the development environment for R programming.



NOTE Rstudio != R in same way as VSCode != C++.

Note that R comes with a set of **recommended packages**.

You can install many more packages from the Comprehensive R Archive Network (CRAN).

On the 1st of March 2024, there were 20503 packages on CRAN.

Tutorial on RStudio.

Scalar Variables in R

To create a scalar variable in R:

```
a <- 10
# Now a is a scalar variable stores the value 10.
# Comments in R starts with #
```

Unlike C, you do not to specify the variable type. **R will guess the variable type**.

The assignment operator in R is <-.

`a = 10` also works, but we recommend you use <-.

You can inspect a's value by typing `a` in the command line.

```
a
```

```
[1] 10
```

Data Types in R

R has 5 basic data types: numerical (double), integer, character, logical and complex.

```
> a <- 10
> typeof(a) # what is the type of a?
[1] "double"
```

```
> a <- 10L # Appending "L" indicates an integer
> typeof(a)
[1] "integer"
```

```
> a <- TRUE # TRUE or FALSE
> typeof(a)
[1] "logical"
```

```
a <- "hello world!"
> typeof(a)
[1] "character"
```

Arithmetic and Logical/Relational operators are mostly the same as in C (see Sec 7.2 in ART). There are a few differences:

%% modular arithmetic

```
10%%3
[1] 1
```

%/% integer division

```
10%/%3
[1] 3
```

Standard division

```
10/3
[1] 3.333333
```

^ Exponentiation

```
2^10 # 2 to the 10th power
[1] 1024
```

Vectors in R

There is no "array" in R.

However, you can create and manipulate a vector easily.

Note: R **uses 1-based index**, different from C and python.

```
v <- c(1,2,3,4)
v[1]
```

```
[1] 1
```

Here c stands for "combine" or "concatenate". Example:

```
v2 <- c(5,6,7,8)
c(v, v2)
```

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

c works also with R `lists`.

Flow Control in R

If and If-Else in R is exactly the same as in C (See ART Sec 7.1).

```
a <- 1
if (a == 1){
  print("a is one!")
}
[1] "a is one!"
```

```
a <- 2
if (a == 1){
  print("a is one!")
} else {
  print("a is NOT one!")
}
[1] "a is NOT one!"
```

If-Else Ladder

```
a <- 3
if (a == 1) {
  print("a is one!");
} else if (a == 2) {
  print("a is two!");
} else if (a == 3) {
  print("a is three!");
} else {
  print("I do not know!");
}
[1] "a is three!"
```

Same as in C but `printf -> print`.

While Loop

While loop is exactly the same as in C (See ART Sec 7.1).

```
a <- 10
while(a>0){
  if(a<5){
    break
  }
  a <- a - 1 # a-- will not work!
}
a
[1] 4
```

`break` works in the same way too.

To skip an iteration in R loop, use `next`.

There is no do-while loop in R.

For Loop

For loop in R is slightly different from C (See ART Sec 7.1):

```
for (i in 1:10){
    # i takes 1 in the first iteration,
    # i takes 2 in the second iteration ...
    print(i)
}
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
[1] 6
[1] 7
[1] 8
[1] 9
[1] 10
```

Step by step:

```
a <- 1:10
a
```

```
 [1]  1  2  3  4  5  6  7  8  9 10
```

Then in `for (i in a)` will take each value in `a`.

Another example:

```
letters[1:3]
```

```
[1] "a" "b" "c"
```

```
for (i in letters[1:3]){
    cat(i)
}
```

```
abc
```

You can get nice output by using paste:

```
paste("a", "b")
```

```
[1] "a b"
```

```
paste(letters[1], letters[2])
```

```
[1] "a b"
```

So

```
for (i in letters[1:3]){
    cat(paste(i, "\n"))
}
```

```
a
b
c
```

Built-in Functions

There are many built-in statistical/mathematical functions in R.

We can call them directly, without loading any library.

For example, to find the absolute value of a, we can

```
> a <- -10
> abs(a)
[1] 10
```

If you want help on the usage of abs, you can simply type

```
> ?abs
```

Help should show up on the right pane.

Write Your Own Functions

You can write your own function using the following syntax:

```
smaller_than_10 <- function(n){
  if(n<10){
    return(TRUE)
  }else{
    return(FALSE)
  }
}
```

Function name followed by `<- function(argument list)`.

You can call a function in the same way as in C:

```
> smaller_than_10(12)
[1] FALSE
> smaller_than_10(0)
[1] TRUE
```

Functions behave as if inputs are **passed by value**

```
a <- c(1,2,3,4)
dosomething <- function(v){
  v[1] <- -10
  return(v)
}
dosomething(a)
[1] -10   2   3   4
a
[1] 1 2 3 4
v
# Error: object 'v' not found
# v is a local variable, not visible outside of function
```

Truth is that R uses copy-on-modify: A copy is made only when objects are modified.

Example:

```
x <- c(1, 2)
y <- x
```

Is y a copy of x?

```
tracemem(x)
```

```
[1] "<0x564e596e29b8>"
```

```
tracemem(y)
```

```
[1] "<0x564e596e29b8>"
```

No, but it becomes a copy as soon as you modify it:

```
y[1] <- 3
```

```
tracemem[0x564e596e29b8 -> 0x564e59c4ee78]: eval eval eval
```

The same happens with functions:

```
a <- c(1,2,3,4)
tracemem(a)
```

```
[1] "<0x564e59d19a08>"
```

```
dosomething <- function(v){
  tracemem(v)
  v[1] <- -10
  return(v)
}
z <- dosomething(a)
```

```
tracemem[0x564e59d19a08 -> 0x564e58a2ba08]: dosomething eva
```

You can work routinely in R without knowing about this.

But for an example where this matters, see the bonus slides at the end.

Conclusion

1. R is a interpreted, high-level, statistical language.
   - Pros and Cons
2. Interpreted language does not need compilation and your code can be modified when your program is running.
3. R's **scalar syntax** is very similar to C.
   - Assignment uses <-.
   - No need to declare a variable before assignment.
   - Comments start with #.
   - No need to add ; at the end of each statement.

However, as we will see in the next week, vector programming in R can be very different from what we have seen in C.

Homework (Pre-sessional work)

If you are on university PCs, you can skip the first two steps.

1. Download R
   - https://www.stats.bris.ac.uk/R/
2. Install and Launch RStudio
   - https://www.rstudio.com/products/rstudio/download/#download
3. Try code blocks in the slides
   - Write code in the code editor and press ctrl+enter to execute the code line by line.
   - Create R scripts and save them.

Homework (Submit)

Write a program that determines the number of primes smaller or equal than a natural number `n, n>=2`.

Recall:

- A factor is an integer that divides exactly into a whole number without a remainder. E.g., 3 is a factor of 12.
- A prime has only 2 factors, 1 and itself.

Pseudo Code, suppose that `n` is the number of interest:

Loop over i going from 2 to n (1 is not a prime!)

1. Loop over j going from 1 to i
   - If j is factor of i add it to the count of factors of i
2. If i has only two factors, it is a prime and it should be added to the number of primes $<=$ n

Homework (Submit)

You should:

1. Translate above pseudo code into R code
   - Use only for() loops.
   - Write your code in the code editor and test it.
   - After the execution, check the "environment pane" on the top right corner of Rstudio:
     - What are the variables?
     - Why do they have the value they hold?
2. What is the computational complexity of our code?
   - Hint: count how many loop iterations will be executed when the program runs.

Homework

3. Time the execution of your code using `Sys.time()`

```
start_time <- Sys.time()
#your code here
end_time <- Sys.time()
end_time - start_time

# Time difference of 0.0009999275 secs
```

Set `n <- 5000` and time the execution (select all and ctrl + enter).

How long does it take?

Predict how long it will take when setting `n <- 10000` before running the code.

Validate your prediction by actually running the code.

Homework (Challenge)

4. Are you able to wrap your R code into a function?
5. Try to make your code faster using a smarter algorithm:
   - Hint: in loop over j, if i already has 3 factors then you already know that it's not a prime.
   - Hint: prime numbers are all odd (except for 2).
   - Compare the smart algorithm with the original version in terms of correctness and speed.
6. Write the same prime number counting program in C, compile and run it:
   - When setting `n = 5000`, which programming language is faster? faster by how much?

- Use the skeleton C code in `Lab_Primes_template.c`.

BONUS SLIDES

Here we are creating a vector with 10 million elements and we are setting the `ii`-th element to 1 at each iteration:

```
x <- 1:1e7
n <- 500

tic <- Sys.time()
for(ii in 1:n){
  x[ii] <- 1
}
( Sys.time() - tic ) # 0.1 seconds on my computer
```

```
Time difference of 0.151659 secs
```

the function `Sys.time` returns the current time.

Here we do the same but using a function

```
dosomething <- function(v, ii){
  v[ii] <- 1
  return(v)
}

tic <- Sys.time()
for(ii in 1:n){
  x <- dosomething(v = x, ii)
}
( Sys.time() - tic ) # 30 seconds on my computer,
                     # 300 times slower
```

Here the whole vector `x` gets copied each time we run `v[ii] <- 1`.