

Programming concepts

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PDF

Note This Unit will be posted in phases as I get the material ready. 2022-09-09: Currently only Sections 1-6 are available.

References:

- Books on R listed on the syllabus: Adler, Chambers, Wickham
- [R intro manual](#) and [R language manual](#) (R-lang), both on CRAN.
- Murrell, Introduction to Data Technologies

(Optional) Videos

There are various videos from 2020 in the bCourses Media Gallery that you can use for reference if you want to. Note that I’ve reorganized the material in this Unit relative to 2020, so the section numbers and ordering in the videos may differ from that in the current Unit, but you should be able to match things up fairly easily.

1. Strings and regular expressions
2. Type/class coercion
3. Object-oriented programming - S3 classes
4. Object-oriented programming - R6 classes

Overview

This unit covers a variety of programming concepts, illustrated in the context of R and with comments about and connections to other languages. It also serves as a way to teach some advanced features of R. In general the concepts are relevant in other languages, though other languages may implement things differently. One of my goals for the unit is for us to think about why things are the way they are in R. I.e., what principles were used in creating the language and what choices were made? While other languages use different principles and made different choices, understanding what one language does in detail will be helpful when you are learning another language or choosing a language for a project.

I’ll likely refer to R syntax as *statements* or *expressions*, meaning any code that is a valid, complete R expression. But note that the term *expression* also means a specific type of object within the R language, as seen late in this Unit when we discuss computing on the language.

1. Text manipulation, string processing and regular expressions (regex)

Text manipulations in R have a number of things in common with Python, Perl, and UNIX, as many of these evolved from UNIX. When I use the term *string* here, I'll be referring to any sequence of characters that may include numbers, white space, and special characters, rather than to the character class of R objects. The string or strings will generally be stored as an R character vector.

String processing and regular expressions in R

For details of string processing in R, including use of regular expressions, see the [string processing tutorial](#). (You can ignore the sections on Python if you wish.) That tutorial then refers to the [bash shell tutorial](#) for details on regular expressions.

In class we'll work through some problems in the string processing tutorial, focusing in particular on the use of regular expressions with the *stringr* package. This will augment our consideration of regular expressions in the shell, in particular by seeing how we can replace patterns in addition to finding them.

Regex/string processing challenges

We'll work on these challenges (and perhaps one or two others) in class in the process of working through the string processing tutorial.

1. What regex would I use to find any number with or without a decimal place.
2. Suppose a text string has dates in the form "Aug-3", "May-9", etc. and I want them in the form "3 Aug", "9 May", etc. How would I do this search and replace operation? (Alternatively, how could I do this without using regular expressions at all?)

Side notes on special characters in R

Recall that when characters are used for special purposes, we need to 'escape' them if we want them interpreted as the actual character. In what follows, I show this in R, but similar manipulations are sometimes needed in the shell and in Python.

This can get particularly confusing in R as the backslash is also used to input special characters such as newline (`\n`) or tab (`\t`).

Here are some examples of using special characters.

Note It is hard to compile the Rmd file correctly for these R chunks, so I am just pasting in the output from running in R 'manually' in some cases.)

```
tmp <- "Harry said, \"Hi\""
## cat(tmp) # prints out without a newline -- this is hard to show in the pdf
tmp <- "Harry said, \"Hi\".\n"
cat(tmp) # prints out with the newline
```

Harry said, "Hi".

```
tmp <- c("azar", "foo", "hello\tthere\n")
cat(tmp)
```

azar foo hello there

```
print(tmp)
```

```
[1] "azar"          "foo"          "hello\tthere\n"
```

```
grep("[\tz]", tmp)  ## search for a tab or a 'z'
```

```
[1] 1 3
```

As a result, in R we often need two backslashes when working with regular expressions. In the next examples, the first backslash says to interpret the next backslash literally, with the second backslash being used to indicate that the caret (^) should be interpreted literally and not as a special character in the regular expression syntax.

```
## Search for characters that are not 'z'
## (using ^ as regular expression syntax)
grep("[^z]", c("a^2", "93", "zzz", "zit", "azar"))
```

```
[1] 1 2 4 5
```

```
## Search for either a '^' (as a regular character) or a 'z':
grep("[\\^z]", c("a^2", "93", "zzz", "zit", "azar"))
```

```
[1] 1 3 4 5
```

```
## This fails (and the Rmd won't compile) because
## '\\^' is not an escape sequence (i.e., a special character):
## grep("[\\^z]", c("a^2", "93", "zit", "azar", "zzz"))
## Error: '\\^' is an unrecognized escape in character string starting ""[\\^"
```

```
## Search for exactly three characters
## (using . as regular expression syntax)
grep("^.{3}$", c("abc", "1234", "def"))
```

```
[1] 1 3
```

```
## Search for a period (as a regular character)
grep("\\.", c("3.9", "27", "4.2"))
```

```
[1] 1 3
```

```
## This fails (and the Rmd won't compile) because
## '\.' is not an escape sequence (i.e., a special character):
## grep("\.", c("3.9", "27"))
## Error: '\.' is an unrecognized escape in character string starting "\".
```

Challenge Explain why we use a single backslash to get a newline and double backslash to write out a Windows path in the examples here:

```
## Suppose we want to use a \ in our string:
cat("hello\nagain")
```

```
hello
again
```

```
cat("hello\\nagain")
```

```
hello\nagain
```

```
cat("My Windows path is: C:\\Users\\My Documents.")
```

```
My Windows path is: C:\Users\My Documents.
```

For more information, see `?Quotes` in R and the subsections of the string processing tutorial that discuss backslashes and escaping.

Advanced note: Searching for an actual backslash gets even more complicated, because we need to pass two backslashes as the regular expression, so that a literal backslash is searched for. However, to pass two backslashes, we need to escape each of them with a backslash so R doesn't treat each backslash as part of a special character. So that's four backslashes to search for a single backslash! Yikes. One rule of thumb is just to keep entering backslashes until things work!

```
## Search for an actual backslash
tmp <- "something \\ other\n"
cat(tmp)
```

```
something \ other
```

```
grep("\\\\", tmp)
```

```
[1] 1
```

```
try(grep("\\", tmp))
```

```
Warning in grep("\\", tmp): TRE pattern compilation error 'Trailing backslash'
```

```
Error in grep("\\", tmp) :  
  invalid regular expression '\\', reason 'Trailing backslash'
```

Warning Be careful when cutting and pasting from documents that are not text files as you may paste in something that looks like a single or double quote, but which R cannot interpret as a quote because it's some other ASCII quote character. If you paste in a " from PDF, it will not be interpreted as a standard R double quote mark.

Similar things come up in the shell and in Python, but in the shell you often don't need two backslashes. E.g. you could do this to look for a literal ^ character.

```
grep '\^' file.txt
```

2. Interacting with the operating system and external code and configuring R

Interacting with the operating system

Scripting languages allow one to interact with the operating system in various ways. Most allow you to call out to the shell to run arbitrary shell code and save results within your session.

I'll assume everyone knows about the following functions/functionality for interacting with the filesystem and file in R: *getwd*, *setwd*, *source*, *pdf*, *save*, *save.image*, *load*.

- To run UNIX commands from within R, use `system()`, as follows, noting that we can save the result of a system call to an R object:

```
system("ls -al")    ## results apparently not shown when compiled...  
files <- system("ls", intern = TRUE)  
files[1:5]
```

```
[1] "0-bash-shell.sh" "badCode.R"      "cache"          "calc_mean.py"  
[5] "convert.sh"
```

- There are also a bunch of functions that will do specific queries of the filesystem, including

```
file.exists("unit2-dataTech.Rmd")
```

```
[1] TRUE
```

```
list.files("../data")
```

```
[1] "airline.csv"      "coop.txt.gz"      "cpds.csv"  
[4] "hivSequ.csv"      "IPs.RData"        "precip.txt"  
[7] "precipData.txt"   "RTADDataSub.csv"  "stackoverflow-2016.db"
```

- There are some tools for dealing with differences between operating systems. *file.path* is a nice example:

```
list.files(file.path("../", "data"))

[1] "airline.csv"          "coop.txt.gz"          "cpds.csv"
[4] "hivSequ.csv"          "IPs.RData"            "precip.txt"
[7] "precipData.txt"       "RTADDataSub.csv"      "stackoverflow-2016.db"
```

It's best if you can to write your code in a way that is *agnostic* to the underlying operating system.

- To get some info on the system you're running on:

```
Sys.info()

      sysname
      "Linux"
     release
"5.4.0-120-generic"
     version
"#136-Ubuntu SMP Fri Jun 10 13:40:48 UTC 2022"
     nodename
     "smeagol"
     machine
     "x86_64"
      login
     "paciorek"
       user
     "paciorek"
effective_user
     "paciorek"
```

Controlling the behavior of R

Scripting languages generally allow you to control/customize their behavior in various ways by setting options.

- To see some of the options that control how R behaves, try the *options* function. The *width* option changes the number of characters of width printed to the screen, while *max.print* prevents too much of a large object from being printed to the screen.

```
## options() # this would print out a long list of options
options()[1:4]

$add.smooth
[1] TRUE
```

```
$bitmapType  
[1] "cairo"
```

```
$browser  
[1] "xdg-open"
```

```
$browserNLdisabled  
[1] FALSE
```

```
options()[c('width', 'digits')]
```

```
$width  
[1] 80
```

```
$digits  
[1] 7
```

```
## Often it's nice to have more characters in each line on the screen,  
## but that would cause overly lines in the compiled file.  
## options(width = 120)
```

```
options(max.print = 5000)
```

The *digits* option changes the number of digits of numbers printed to the screen (but be careful as this can be deceptive if you then try to compare two numbers based on what you see on the screen).

```
options(digits = 3)  
a <- 0.123456; b <- 0.1234561  
a; b; a == b
```

```
[1] 0.123
```

```
[1] 0.123
```

```
[1] FALSE
```

More on how to (and how not to) compare real-valued numbers on a computer in Unit 8.

- Use **Ctrl-C** to interrupt execution. This will generally back out gracefully, returning you to a state as if the command had not been started. Note that if R is exceeding the amount of memory available, there can be a long delay. This can be frustrating, particularly since a primary reason you would want to interrupt is when R runs out of memory.
- *sessionInfo* gives information on the current R session and can be very helpful for recording the state of your session (including package versions) to allow for reproducibility.


```
sessionInfo()
```

```
R version 4.2.0 (2022-04-22)
```

```
Platform: x86_64-pc-linux-gnu (64-bit)
```

```
Running under: Ubuntu 20.04.3 LTS
```

```
Matrix products: default
```

```
BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
```

```
LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/liblapack.so.3
```

```
locale:
```

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8       LC_COLLATE=en_US.UTF-8
[5] LC_MONETARY=en_US.UTF-8   LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8      LC_NAME=C
[9] LC_ADDRESS=C              LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

```
attached base packages:
```

```
[1] stats      graphics  grDevices  utils      datasets  methods    base
```

```
other attached packages:
```

```
[1] SCF_4.1.0
```

```
loaded via a namespace (and not attached):
```

```
[1] compiler_4.2.0  magrittr_2.0.3  fastmap_1.1.0   cli_3.3.0
[5] tools_4.2.0     htmltools_0.5.3 yaml_2.3.5       stringi_1.7.8
[9] rmarkdown_2.14  knitr_1.39      stringr_1.4.0   xfun_0.31
[13] digest_0.6.29   jsonlite_1.8.0  rlang_1.0.4     evaluate_0.15
```

- Any code that you wanted executed automatically when starting R can be placed in `~/.Rprofile` (or in individual, project-specific `.Rprofile` files in specific directories). This could include loading packages (see below), sourcing files that contain user-defined functions that you commonly use (you can also put the function code itself in `.Rprofile`), assigning variables, and specifying options via `options()`.
- You can have an R script act as a shell script (like running a bash shell script) as follows. This will probably not work on Linux and Mac.
 1. Write your R code in a text file, say `exampleRscript.R`.
 2. As the first line of the file, include `#!/usr/bin/Rscript` (like `#!/bin/bash` in a bash shell file, as seen in Unit 2) or for more portability across machines, include `#!/usr/bin/env Rscript`.
 3. Make the R code file executable with `chmod`: `chmod ugo+x exampleRscript.R`.
 4. Run the script from the command line: `./exampleRscript.R`

If you want to pass arguments into your script, you can do so as long as you set up the R code to interpret the incoming arguments:

```

args <- commandArgs(TRUE)

## Now args is a character vector containing the arguments.
## Suppose the first argument should be interpreted as a number
## and the second as a character string and the third as a boolean:

numericArg <- as.numeric(args[1])
charArg <- args[2]
logicalArg <- as.logical(args[3])

cat("First arg is: ", numericArg, "; second is: ", charArg,
    "; third is: ", logicalArg, ".\n")

```

Now we can run it as follows in the shell:

```

./exampleRscript.R 53 blah T
./exampleRscript.R blah 22.5 t

```

```

First arg is:  53 ; second is:  blah ; third is:  TRUE .
Warning message:
NAs introduced by coercion
First arg is:  NA ; second is:  22.5 ; third is:  NA .

```

Interacting with external code

Scripting languages such as R, Python, and Julia allow you to call out to “external code”, which often means C or C++ (but also Fortran, Java and other languages).

In fact, the predecessor language to R, which was called ‘S’ was developed specifically (at AT&T’s Bell Labs in the 1970s and 1980s) as an interactive wrapper around Fortran, the numerical programming language most commonly used at the time (and still widely relied on today in various legacy codes).

Calling out to external code is particularly important in languages like R and Python that are often much slower than compiled code and less important in a fast language like Julia (which uses Just-In-Time compilation – more on that later).

In R, one can call directly out to C or C++ code using `.Call` or one can use the [Rcpp package](#). *Rcpp* is specifically designed to be able to write C++ code that feels somewhat like writing R code and where it is very easy to pass data between R and C++.

In Python, one can [directly call out to C or C++ code](#) or one can use *Cython* to interact with C. With Cython, one can: - Have Cython automatically translate Python code to C, if you provide type definitions for your variables. - Define C functions that can be called from your Python code.

3. Packages and namespaces

Scripting languages that become popular generally have an extensive collection of add-on packages available online (the causal relationship of the popularity and the extensive add-on packages goes in both directions). Packages need to be *installed* (once) on your computer and *loaded* (every time you start a new session).

A big part of R's popularity is indeed the extensive collection of add-on packages on [CRAN](#) (and GitHub and elsewhere) that provide much of R's functionality. To make use of a package it needs to be installed on your system (using *install.packages* once only) and loaded into R (using *library* every time you start R).

Some packages are *installed* by default with R and of these, some are *loaded* by default, while others require a call to *library*.

If you want to sound like an R expert, make sure to call them *packages* and not *libraries*. A *library* is the location in the directory structure where the packages are installed/stored.

Loading packages

You can use *library* to either (1) make a package available (loading it), (2) get an overview of the package, or (3) (if called without arguments) to see all the installed packages.

```
library(dplyr)           # load the package
library(help = dplyr)    # get some help info about the package
```

Packages in R (and in Python, Julia, etc.) may be installed in various places on the filesystem, and it sometimes it is helpful (e.g., if you end up with multiple versions of a package installed on your system) to be able to figure out where on the filesystem the package is being loaded from. If you run *library()*, you'll notice that some of the packages are in a system directory and some are in your home directory.

.libPaths() shows where R looks for packages on your system and *searchpaths()* shows where individual packages currently loaded in your session have been loaded from. The help information for *.libPaths* gives some information about how R decides what locations to look in for packages (and how you can modify that).

```
.libPaths()
```

```
[1] "/accounts/vis/paciorek/R/x86_64-pc-linux-gnu-library/4.2"
[2] "/system/linux/lib/R-20.04/4.2.0/x86_64/site-library"
[3] "/usr/lib/R/site-library"
[4] "/usr/lib/R/library"
```

```
searchpaths()
```

```
[1] ".GlobalEnv"
[2] "tools:quarto"
```

```
[3] "/usr/lib/R/library/stats"
[4] "/usr/lib/R/library/graphics"
[5] "/usr/lib/R/library/grDevices"
[6] "/usr/lib/R/library/utils"
[7] "/usr/lib/R/library/datasets"
[8] "/system/linux/lib/R-20.04/4.2.0/x86_64/site-library/SCF"
[9] "/usr/lib/R/library/methods"
[10] "Autoloads"
[11] "/usr/lib/R/library/base"
```

Installing packages

If a package is on CRAN but not on your system, you can install it easily (usually). You don't need root permission on a machine to install a package (though sometimes you run into hassles if you are installing it just as a user, so if you have administrative privileges it may help to use them). Of course in RStudio, you can install via the GUI.

Packages often depend on other packages. In general, if one package depends on another, R will install the dependency automatically, but sometimes you'll need to install a dependency yourself. In general, package dependencies are handled very cleanly in R without you having to worry much about it; this is less the case in Python.

Note that R will generally install the package in a reasonable place by default but you can control where it is installed using the *lib* argument.

```
install.packages('dplyr', lib = '~/Rlibs') # ~/Rlibs needs to exist!
```

You can also download the zipped source file from CRAN and install from the file; see the help page for *install.packages*. This is called “installing from source”. On Windows and Mac, you'll need to do something like this:

```
install.packages('dplyr_VERSION.tar.gz', repos = NULL, type = 'source')
```

This can be handy if you need to install [an older version of a package](#) for reproducibility or because of some dependency incompatibility.

If you've downloaded the binary package (files ending in .tgz for Mac and .zip for Windows) and want to install the package directly from the file, use the syntax above but omit the `type= 'source'` argument.

Source vs. binary packages

The difference between a *source* package and a *binary* package is that the source package has the raw R (and C and Fortran, in some cases) code as text files while the binary package has all the code in a binary/non-text format, including that any C and Fortran code will have already been compiled. To install a source package with C or Fortran code in it, you'll need to have developer/command-line tools (e.g., *XCode* on Mac or *Rtools.exe* on Windows) installed on your system so that you have a compiler.

Managing packages using package managers

For reproducibility, it's important to know the versions of the packages you use (and the version of R). Package managers make it easy to do this. Some useful packages that do package management in R are *checkpoint*, *renv*, and *packrat*. The basic commonality is that they try to make it easy to 'freeze' the versions of the packages you are using, record that information, and restore the versions (potentially on some other machine and by some user other than yourself). The package manager may tell you where the packages are installed, but you can always verify things with `.libPaths()`.

In Python, you can set up and manage isolated environments in which you can control the package versions using `virtualenvs` or `Conda` environments.

Package namespaces

The objects in a package (primarily functions, but also data) are in their own workspaces, and are accessible after you load the package using `library()`, but are not directly visible when you use `ls()`. In other words, each package has its own *namespace*. Namespaces help achieve modularity and avoid having zillions of objects all reside in your workspace. If we want to see the objects in a package's namespace, we can do the following:

```
search()

[1] ".GlobalEnv"      "tools:quarto"    "package:stats"
[4] "package:graphics" "package:grDevices" "package:utils"
[7] "package:datasets" "package:SCF"      "package:methods"
[10] "Autoloads"       "package:base"

## ls(pos = 4) # for the stats package
ls(pos = 4)[1:5] # just show the first few

[1] "abline"      "arrows"      "assocplot" "axis"      "Axis"

ls("package:stats")[1:5] # equivalent

[1] "acf"          "acf2AR"      "add.scope"  "add1"      "addmargins"

ls("package:stats", pattern = "^lm")

[1] "lm"          "lm.fit"      "lm.influence" "lm.wfit"
```

Why have namespaces?

We'll talk more about namespaces when we talk about scope and environments. But as some motivation for why this is useful, consider the following.

The `lm` function calls the `lm.fit` function to calculate the least squares solution in regression.

Suppose we write our own `lm.fit` function that does something else:

```
lm.fit <- function(x)
  print('hi')

x <- 7
lm.fit(x)
```

```
[1] "hi"
```

One might expect that if one now uses `lm()` to fit a regression, that it wouldn't work correctly because we have an `lm.fit` function in our workspace that doesn't calculate the least squares solution. But it works just fine (see below), because `lm` and `lm.fit` are in the `stats` package namespace (see above) and R's scoping rules (more later) ensure that the `lm.fit` that is found when I run `lm` is the `lm.fit` needed to run the regression and not my silly `lm.fit` function in current workspace.

```
n <- 10
x <- runif(n)
y <- runif(n)
mod <- lm(y ~ x)
mod
```

Call:

```
lm(formula = y ~ x)
```

Coefficients:

```
(Intercept)          x
      0.397         0.223
```

Namespaces resolution

Standard practice in R has generally been to load a package and then use any of the items in the package namespace directly, e.g.,

```
library(stringr)
str_detect("hello there", "hello")
```

```
[1] TRUE
```

However, particularly if you're using the package in only a limited way, it can be a nice idea to not load the entire package and instead use the namespace resolution operator in a style that might remind you of Python and some other languages:

```
stringr::str_detect("hello there", "hello")
```

```
[1] TRUE
```

```
import numpy as np
x = np.ndarray([0,3,5])
```

Of course in Python you could also load the entire package (i.e., import the entire namespace), though it's not standard practice:

```
from numpy import *
## OR: from numpy import ndarray
x = ndarray([0,3,5])
```

Loading entire packages often causes 'name collisions' where there are multiple functions (or variables, more genreally) that have the same name. This can be confusing. We'll see how R determines what function to use later in the Unit.

4. Types and data structures

Data structures

Please see the [data structures section of Unit 2](#) for some general discussion of data structures.

We'll also see more complicated data structures when we consider objects in the next section on object-oriented programming.

Types and classes

Overview and static vs. dynamic typing

The term 'type' refers to how a given piece of information is stored and what operations can be done with the information. 'Primitive' types are the most basic types that often relate directly to how data are stored in memory or on disk (e.g., boolean, integer, numeric (real-valued, aka *double* or *floating point*), character, pointer (aka *address*, *reference*)).

In compiled languages like C and C++, one has to define the type of each variable. Such languages are *statically* typed. Interpreted (or scripting) languages such as Python and R have *dynamic* types. One can associate different types of information with a given variable name at different times and without declaring the type of the variable:

```
x <- 'hello'
print(x)
```

```
[1] "hello"
```

```
x <- 7
x*3
```

```
[1] 21
```

In contrast in a language like C, one has to declare a variable based on its type before using it:

```
double y;  
double x = 3.1;  
y = x * 7.1;
```

Dynamic typing can be quite helpful from the perspective of quick implementation and avoiding tedious type definitions and problems from minor inconsistencies between types (e.g., multiplying an integer by a real-valued number). But static typing has some critical advantages from the perspective of software development, including:

- protecting against errors from mismatched values and unexpected user inputs, and
- generally much faster execution because the type of a variable does not need to be checked when the code is run.

More complex types in R (and in Python) often use references (*pointers*, aka *addresses*) to the actual locations of the data. We'll see this in detail later in the Unit.

Types and classes in R

You should be familiar with vectors as the basic data structure in R, with character, integer, numeric, etc. classes. Vectors are either *atomic vectors* or *lists*. Atomic vectors generally contain one of the four following types: *logical*, *integer*, *double* (i.e., *numeric*), and *character*.

Everything in R is an object and all objects have a class. For simple objects class and type are often closely related, but this is not the case for more complicated objects. As we'll see later in the Unit, the class describes what the object contains and standard functions associated with it. In general, you mainly need to know what class an object is rather than its type.

Note You can look at Table 7.1 in the Adler book to see some other types.

Let's look at the type and class of various data structures in R. We'll first see that real-valued are stored as double-precision (8 byte) floating point numbers internally in R (as 'doubles' in C, as the R interpreter is a program written in C).

```
devs <- rnorm(5)  
class(devs)  
[1] "numeric"  
  
typeof(devs)  
[1] "double"  
  
a <- data.frame(x = 1:2)  
class(a)  
[1] "data.frame"
```



```
typeof(a)
[1] "list"

is.data.frame(a)
[1] TRUE

is.matrix(a)
[1] FALSE

is(a, "matrix")
[1] FALSE

m <- matrix(1:4, nrow = 2)
class(m)
[1] "matrix" "array"

typeof(m)
```

```
[1] "integer"
```

In most cases integer-valued numbers are stored as numeric values in R, but there are exceptions such as the result of using the sequence operator, `:`, above. We can force R to store values as integers:

```
vals <- c(1, 2, 3)
class(vals)
[1] "numeric"

vals <- 1:3
class(vals)
[1] "integer"

vals <- c(1L, 2L, 3L)
vals
[1] 1 2 3

class(vals)
```

```
[1] "integer"
```

Attributes

We saw the notion of attributes when looking at HTML and XML, where the information was stored as key-value pairs that in many cases had additional information in the form of attributes.

In R, *attributes* are information about an object attached to an object as something that looks like a named list. Attributes are often copied when operating on an object. This can lead to some weird-looking formatting when in subsequent operations the *names* attribute is carried along:

```
x <- rnorm(10 * 365)
attributes(x)
```

NULL

```
qs <- quantile(x, c(.025, .975))
attributes(qs)
```

\$names

```
[1] "2.5%" "97.5%"
```

```
qs
```

```
2.5% 97.5%
-1.93 1.90
```

```
qs[1] + 3
```

```
2.5%
1.07
```

```
object.size(qs)
```

352 bytes

We can get rid of the attribute:

```
names(qs) <- NULL
qs
```

```
[1] -1.93 1.90
```

```
object.size(qs)
```

64 bytes

A common use of attributes is that rows and columns may be named in matrices and data frames, and elements in vectors:

```
df <- data.frame(x = 1:2, y = 3:4)
attributes(df)

$names
[1] "x" "y"

$class
[1] "data.frame"

$row.names
[1] 1 2

row.names(df) <- c("first", "second")
df

      x y
first 1 3
second 2 4

attributes(df)

$names
[1] "x" "y"

$class
[1] "data.frame"

$row.names
[1] "first" "second"

vec <- c(first = 7, second = 1, third = 5)
vec['first']

first
7

attributes(vec)

$names
[1] "first" "second" "third"
```

Converting between types

This also goes by the term *coercion* and *casting*. Casting often needs to be done explicitly in compiled languages and somewhat less so in interpreted languages like R.

We convert between classes using variants on *as*: e.g.,

```
as.character(c(1,2,3))
```

```
[1] "1" "2" "3"
```

```
as.numeric(c("1", "2.73"))
```

```
[1] 1.00 2.73
```

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

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

```
Levels: a b c
```

Some common conversions are converting numbers that are being interpreted as characters into actual numbers, converting between factors and characters, and converting between logical TRUE/FALSE vectors and numeric 1/0 vectors.

In some cases R will automatically do conversions behind the scenes in a smart way (or occasionally not so smart way). Consider these examples of implicit coercion:

```
x <- rnorm(5)
x[3] <- 'hat' # What do you think is going to happen?
indices <- c(1, 2.73)
myVec <- 1:10
myVec[indices]
```

```
[1] 1 2
```

Be careful of using factors as indices:

```
students <- factor(c("basic", "proficient", "advanced",
                    "basic", "advanced", "minimal"))
score <- c(minimal = 65, basic = 75, proficient = 85, advanced = 95)
score[students]
```

```
advanced
      95
```

```
students[3]
```

```
[1] advanced
Levels: advanced basic minimal proficient
```

```
score[students[3]]
```

```
minimal
65
```

```
score[as.character(students[3])]

```

```
advanced
95
```

What has gone wrong and how does it relate to type coercion?

Here's an example we can work through that will help illustrate how type conversions occur behind the scenes in R.

```
n <- 5
df <- data.frame(label = rep('a', n), val1 = rnorm(n), val2 = rnorm(n))
df
```

```
label val1 val2
1     a 0.437 -0.807
2     a -0.932 -0.133
3     a -0.372  0.655
4     a -1.013 -0.177
5     a  1.171 -1.996
```

```
## Why does the following not work?
try( apply(df, 1, function(x) x[2] + x[3]) )
```

```
Error in x[2] + x[3] : non-numeric argument to binary operator
```

```
## Instead, this will work. Why?
apply(df[, 2:3], 1, function(x) x[1] + x[2])
```

```
[1] -0.370 -1.065  0.283 -1.191 -0.825
```

Data frames and related concepts

Some notes on data frames and operations on data frames

Base R provides a variety of functions for manipulating data frames, but now many researchers use add-on packages (many written by Hadley Wickham as part of a group of packages called the *tidyverse*) to do these manipulations in a more elegant way. [Module 6 of the R bootcamp](#) describes some of these

new tools in more details, but I'll touch on some aspects of this here, without showing much of the tidyverse syntax.

split-apply-combine

Often analyses are done in a stratified fashion - the same operation or analysis is done on subsets of the data set. The subsets might be different time points, different locations, different hospitals, different people, etc.

The split-apply-combine framework is intended to operate in this kind of context: first one splits the dataset by one or more variables, then one does something to each subset, and then one combines the results. The *dplyr* package implements this framework (as does the *pandas* package for Python). One can also do similar operations using various flavors of the *lapply* family of functions such as *by*, *tapply*, and *aggregate*, but the dplyr-based tools are often nicer to use.

split-apply-combine is also closely related to the famous Map-Reduce framework underlying big data tools such as Hadoop and Spark.

It's also very similar to standard SQL queries involving filtering, grouping, and aggregation.

Long and wide formats

Finally, we may want to convert between so-called 'long' and 'wide' formats, which we can motivate in the context of longitudinal data (multiple observations per subject) and panel data (temporal data for each of multiple units such as in econometrics). The wide format has repeated measurements for a subject in separate columns, while the long format has repeated measurements in separate rows, with a column for differentiating the repeated measurements.

```
long <- data.frame(id = c(1, 1, 1, 2, 2, 2),
                  time = c(1980, 1990, 2000, 1980, 1990, 2000),
                  value = c(5, 8, 9, 7, 4, 7))
wide <- data.frame(id = c(1, 2),
                  value_1980 = c(5, 7), value_1990 = c(8, 4), value_2000 = c(9, 7))

long

  id time value
1  1 1980     5
2  1 1990     8
3  1 2000     9
4  2 1980     7
5  2 1990     4
6  2 2000     7

wide

  id value_1980 value_1990 value_2000
1  1          5          8          9
2  2          7          4          7
```

The wide format can be useful in some situations for treating each row as a (multivariate observation), but the long format is often what is needed for analyses such as mixed models, ANOVA, or for plotting, such as with *ggplot2*.

There are a variety of functions for converting between wide and long formats. I recommend *pivot_longer* and *pivot_wider* in the *tidyr* package. There are also older *tidyr* functions called *gather* and *spread*. There are also the *melt* and *cast* in the *reshape2* package. These are easier to use than the functions in base R such as *reshape* or *stack* and *unstack* functions.

Piping

Piping was introduced into R in conjunction with *dplyr* and the *tidyverse*.

The tidyverse pipe is `%>%` while the new base R pipe is `|>`. These are based on the UNIX pipe, which we saw in Unit 3, though they behave somewhat differently in that the output of the previous function is passed in as the *first* argument of the next function. In the shell, the pipe connects *stdout* from the previous command to *stdin* for the next command.

Non-standard evaluation and the tidyverse

Many tidyverse packages use non-standard evaluation to make it easier to code. For example in the following *dplyr* example, you can refer directly to *country* and *unemp*, which are variables in the data frame, without using `data$country` or `data$unemp` and without using quotes around the variable names, as in `"country"` or `"unemp"`. Referring directly to the variables in the data frame is not standard R usage, hence the term “non-standard evaluation”. One reason it is not standard is that *country* and *unemp* are not themselves independent R variables so R can’t find them in the usual way using scoping (discussed later in the Unit).

```
library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

```
filter, lag
```

The following objects are masked from 'package:base':

```
intersect, setdiff, setequal, union
```

```
cpds <- read.csv(file.path('..', 'data', 'cpds.csv'))
```

```
cpds2 <- cpds %>% group_by(country) %>%  
  mutate(mean_unemp = mean(unemp))
```

```
head(cpds2)
```

```
# A tibble: 6 x 7
```

```
# Groups:   country [1]
  year country  vturn outlays realgdpgr unemp mean_unemp
<int> <chr>    <dbl>  <dbl>    <dbl> <dbl>    <dbl>
1  1960 Australia 95.5    NA      NA      1.42    5.52
2  1961 Australia 95.3    NA     -0.07  2.79    5.52
3  1962 Australia 95.3   23.2    5.71  2.63    5.52
4  1963 Australia 95.7   23.0    6.1   2.12    5.52
5  1964 Australia 95.7   22.9    6.28  1.15    5.52
6  1965 Australia 95.7   24.9    4.97  1.15    5.52
```

This ‘magic’ is done by capturing the code expression you write and evaluating it in a special way in the context of the data frame. I believe this uses R’s environment class (discussed later in the Unit), but haven’t looked more deeply.

While this has benefits, this so-called non-standard evaluation makes it harder to program functions in the usual way, as illustrated in the following code chunk, where neither attempt to use the function works.

```
add_mean <- function(data, group_var, summarize_var) {
  data %>% group_by(group_var) %>%
    mutate(mean_of_var = mean(summarize_var))
}

try(cpds2 <- add_mean(cpds, country, unemp))
```

```
Error in group_by(., group_var) :
  Must group by variables found in `.data`.
x Column `group_var` is not found.
```

```
try(cpds2 <- add_mean(cpds, 'country', 'unemp'))
```

```
Error in group_by(., group_var) :
  Must group by variables found in `.data`.
x Column `group_var` is not found.
```

For more details on how to avoid this problem when writing functions that involve tidyverse manipulations, see [this tidyverse programming guide](#).

Note that the tidyverse is not the only place where non-standard evaluation is used. Consider this *lm* call:

```
lm(y ~ x, weights = w, data = mydf)
```

Challenge Where is the non-standard evaluation there?

5. Programming paradigms: object-oriented and functional programming

Object-oriented and functional programming are two important approaches to programming.

Functional programming focuses on writing functions that take inputs and produce outputs. Ideally those functions don't change the state (i.e., the values) of any variables and can be treated as black boxes. Functions can be treated like other variables, such as passing functions as arguments (as one does with *lapply* in R, for example).

Object-oriented programming revolves around objects that belong to classes. The class of an object defines the fields (the data objects) holding information and (often) methods that can be applied to those fields. When one calls a method, it may modify the value of the fields. A statistical analogy is that an object of a class is like the realization (the object) of a random variable (the class).

One can think of functional programming as being focused on actions (or *verbs* to make an analogy with human language). One carries out a computation as a sequence of function calls. One can think of OOP as being focused on the objects (or *nouns*). One carries out a computation as a sequence of operations with the objects, using the class methods.

Many languages are multi-paradigm, containing aspects of both approaches and allowing programmers to use either approach. Both R and Python are like this, though some might consider R to be more functional and Python to be more object-oriented. That said, in R everything is an object and has a class, while there are plenty of function-based operations in Python.

```
import numpy as np
x = np.array([1.2, 3.5, 4.2])
x.shape # field (or attribute) of the numpy array class
x.sum() # method of the class
len(x)  # function
```

Different people have different preferences, but which is better depends on what you are trying to do. If your computation is a data analysis pipeline that involves a series of transformations of some data, a functional approach might make more sense, since the focus is on a series of actions rather than the state of objects. If your computation involves various operations on fixed objects whose state needs to change, OOP might make more sense. For example, if you were writing code to keep track of student information, it would probably make sense to have each student as an object of a Student class with methods such as 'register' and 'assign_grade'.

6. Object-oriented programming (OOP)

Principles

Some of the standard concepts in object-oriented programming include *encapsulation*, *inheritance*, *polymorphism*, and *abstraction*.

Encapsulation involves preventing direct access to internal data in an object from outside the object. Instead the class is designed so that access (reading or writing) happens through the interface set up

by the programmer (e.g., ‘getter’ and ‘setter’ methods). We’ll see this in our R6 class example below.

Inheritance allows one class to be based on another class, adding more specialized features. For example (as in our S3 example), a *glm* class inheriting from an *lm* class.

Polymorphism allows for different behavior of an object or function depending on the context. A polymorphic function behaves differently depending on the input types. A polymorphic object is one that can belong to different classes (e.g., based on inheritance), and a given method name can be used with any of the classes. An example would be having a base or super class called ‘algorithm’ and various specific machine learning algorithms inheriting from that class. All of the classes might have a ‘predict’ method.

Abstraction involves hiding the details of how something is done (e.g., via the method of a class), giving the user an interface to provide inputs and get outputs. By making the actual computation a black box, the programmer can modify the internals without changing how a user uses the system.

Classes generally have *constructors* that initialize objects of the class and *destructors* that remove objects.

Generic function OOP

Much of the object-oriented programming in R uses *generic function OOP*, also known as *functional OOP*. In this style, classes don’t have methods. Instead there are *generic functions* (also known as *generic methods*) that change their behavior based on the type of the input(s). Another way to put it is that the nouns and the verbs are separate, unlike in standard OOP.

Generic function OOP is how the (very) old S3 system in R works. It’s also a key part of the (fairly) new Julia language.

S3 classes in R

S3 classes are widely-used, in particular for statistical models in the *stats* package. S3 classes are very informal in that there’s not a formal definition for an S3 class. Instead, an S3 object is just a primitive R object such as a list or vector with additional attributes including a class name.

Creating our own class

We can create an object with a new class as follows:

```
yog <- list(firstname = 'Yogi', surname = 'the Bear', age = 20)
class(yog) <- 'bear'
```

Actually, if we want to create a new class that we’ll use again, we want to create a *constructor* function that initializes new bears:

```
bear <- function(firstname = NA, surname = NA, age = NA){
  # constructor for 'indiv' class
  obj <- list(firstname = firstname, surname = surname,
```

```

    age = age)
  class(obj) <- 'bear'
  return(obj)
}
smoke <- bear('Smokey', 'Bear')

```

For those of you used to more formal OOP, the following is probably disconcerting:

```

class(smoke) <- "celebrity"

```

Generic methods

The real power of the S3 system comes from defining *class-specific methods*. For example,

```

x <- rnorm(10)
summary(x)

```

```

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-1.443 -0.781  -0.448  -0.357   0.232   0.470

```

```

y <- rnorm(10)
mod <- lm(y ~ x)
summary(mod)

```

Call:

```
lm(formula = y ~ x)
```

Residuals:

```

      Min       1Q   Median       3Q      Max
-1.4644 -0.2216 -0.0485  0.4156  1.1898

```

Coefficients:

```

              Estimate Std. Error t value Pr(>|t|)
(Intercept)   0.4033     0.2909    1.39   0.20
x              0.0384     0.4179    0.09   0.93

```

Residual standard error: 0.79 on 8 degrees of freedom

Multiple R-squared: 0.00105, Adjusted R-squared: -0.124

F-statistic: 0.00843 on 1 and 8 DF, p-value: 0.929

Here *summary* is a generic function (or generic method) that, based on the type of object given to it (the first argument), dispatches a class-specific function (method) that operates on the object.

The above is equivalent to directly calling the class-specific methods:

```
identical(summary(x), summary.default(x))
```

```
[1] TRUE
```

```
identical(summary(mod), summary.lm(mod))
```

```
[1] TRUE
```

This use of generic functions is convenient in that it allows us to work with a variety of kinds of objects using familiar functions. Consider the generic methods *plot*, *print*, *summary*, *[*, and others. We can look at a function and easily see that it is a generic method.

```
summary
```

```
function (object, ...)
  UseMethod("summary")
<bytecode: 0x56006afda8c0>
<environment: namespace:base>
```

The `UseMethod` syntax is what causes the dispatching of the class-specific method associated with `object` and calls that method. In many cases there will be a default method (here, *summary.default*), so if no method is defined for the class, R uses the default. Sidenote: arguments to a generic method are passed along to the selected method by passing along the calling environment.

We can also see what classes have methods for a given generic function.

```
methods(summary)
```

[1] summary,ANY-method	summary,DBIObject-method
[3] summary,diagonalMatrix-method	summary,sparseMatrix-method
[5] summary.aov	summary.aovlist*
[7] summary.aspell*	summary.check_packages_in_dir*
[9] summary.connection	summary.data.frame
[11] summary.Date	summary.default
[13] summary.ecdf*	summary.factor
[15] summary.glm	summary.infl*
[17] summary.lm	summary.loess*
[19] summary.manova	summary.matrix
[21] summary.nlm*	summary.nls*
[23] summary.packageStatus*	summary.pandas.core.frame.DataFrame*
[25] summary.pandas.core.series.Series*	summary.POSIXct
[27] summary.POSIXlt	summary.ppr*
[29] summary.prcomp*	summary.princomp*
[31] summary.proc_time	summary.python.builtin.object*
[33] summary.rlang_error*	summary.rlang_message*
[35] summary.rlang_trace*	summary.rlang_warning*
[37] summary.rlang:::list_of_conditions*	summary.shingle*

```

[39] summary.srcfile           summary.srcref
[41] summary.stepfun          summary.stl*
[43] summary.table            summary.trellis*
[45] summary.tukeysmooth*     summary.vctr_sclr*
[47] summary.vctr_sclr*       summary.warnings
see '?methods' for accessing help and source code

```

We can define a new generic function:

```

summarize <- function(object, ...)
  UseMethod("summarize")

```

Let's try this out on our *bear* class. In reality, we'd write either *summary.bear* or *print.bear* (and of course the generics for *summary* and *print* already exist) but for illustration, I wanted to show how we would write both the generic and the specific method, so I'll write a *summarize* method instead of a *summary* method.

```

summarize.bear <- function(object)
  return(with(object, cat("Bear of age ", age,
    " whose name is ", firstname, " ", surname, ".\n",
    sep = "")))
summarize(yog)

```

Bear of age 20 whose name is Yogi the Bear.

Why use generic functions?

We could have written *summary* as a regular function with a bunch of if statements or if-else clauses (or *switch*) so that it can handle different kinds of input objects.

This has two disadvantages:

1. We need to write the code that does the checking (and all the code for the different cases all lives inside one potentially very long function, unless we create class-specific helper functions).
2. Much more importantly, *summary* will only work for existing classes. And users can't easily extend it for new classes that they create because they don't control the *summary* function. So a user could not add the additional conditions/classes in a big if-else statement. The generic function approach makes the system *extensible* – we can build our own new functionality on what is already in R.

The print method

Like *summary*, *print* is a generic method, with various class-specific methods, such as *print.lm*.

Note that the *print* function is what is called when you simply type the name of the object, so we can have object information printed out in a structured way. Recall that the output when we type the name of an *lm* object is NOT simply a regurgitation of the elements of the list - rather *print.lm* is called.

Similarly, when we used `print(object.size(x))` we are invoking the *object_size*-specific print method which gets the value of the size and then formats it. So there's actually a fair amount going on behind the scenes.

Surprisingly, the *summary* method generally doesn't actually print out information; rather it computes things not stored in the original object and returns it as a new class (e.g., class *summary.lm*), which is then automatically printed, per my comment above (e.g., using *print.summary.lm*), unless one assigns it to a new object. Note that *print.summary.lm* is hidden from user view (it's a private object in the *stats* namespace).

```
out <- summary(mod)
class(out)
```

```
[1] "summary.lm"
```

```
out
```

Call:

```
lm(formula = y ~ x)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-1.4644	-0.2216	-0.0485	0.4156	1.1898

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.4033	0.2909	1.39	0.20
x	0.0384	0.4179	0.09	0.93

Residual standard error: 0.79 on 8 degrees of freedom

Multiple R-squared: 0.00105, Adjusted R-squared: -0.124

F-statistic: 0.00843 on 1 and 8 DF, p-value: 0.929

```
print(out)
```

Call:

```
lm(formula = y ~ x)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-1.4644	-0.2216	-0.0485	0.4156	1.1898

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.4033	0.2909	1.39	0.20
x	0.0384	0.4179	0.09	0.93

```
Residual standard error: 0.79 on 8 degrees of freedom
Multiple R-squared:  0.00105,    Adjusted R-squared:  -0.124
F-statistic: 0.00843 on 1 and 8 DF,  p-value: 0.929
```

```
## One can look at the code for the method (not shown):
## getS3method(f = "print", class = "summary.lm")
```

Inheritance

Let's look at the *lm* class, which builds on lists, and *glm* class, which builds on the *lm* class. Here *mod* is an object (an instance) of class *lm*.

```
library(methods)
ybin <- sample(c(0, 1), 10, replace = TRUE)
ycont <- rnorm(10)
x <- rnorm(10)
mod1 <- lm(ycont ~ x)
mod2 <- glm(ybin ~ x, family = binomial)
class(mod1)
```

```
[1] "lm"
```

```
class(mod2)
```

```
[1] "glm" "lm"
```

```
is.list(mod1)
```

```
[1] TRUE
```

```
names(mod1)
```

```
[1] "coefficients" "residuals"      "effects"         "rank"
[5] "fitted.values" "assign"          "qr"              "df.residual"
[9] "xlevels"      "call"           "terms"           "model"
```

```
is(mod2, "lm")
```

```
[1] TRUE
```

```
methods(class = "lm")
```

```
[1] add1          alias          anova          case.names     coerce
[6] confint       cooks.distance deviance       dfbeta         dfbetas
```

```

[11] drop1          dummy.coef      effects          extractAIC       family
[16] formula        hatvalues       influence         initialize       kappa
[21] labels         logLik          model.frame       model.matrix      nobs
[26] plot           predict         print            proj             qr
[31] residuals      rstandard      rstudent         show             simulate
[36] slotsFromS3    summary        variable.names   vcov
see '?methods' for accessing help and source code

```

Often S3 classes inherit from lists (i.e., are special cases of lists), so you can obtain components of the object using the `$` operator.

As noted with *lm* and *glm* objects, we can assign more than one class to an object. Here *summarize* still works, even though the primary class is *grizzly_bear*.

```

class(yog) <- c('grizzly_bear', 'bear')
summarize(yog)

```

Bear of age 20 whose name is Yogi the Bear.

The classes should nest within one another with the more specific classes to the left, e.g., here a *grizzly_bear* would have some additional fields on top of those of a *bear*, perhaps *number_of_people_killed* (since grizzly bears are much more dangerous than some other kinds of bears), and perhaps additional or modified methods. *grizzly_bear* inherits from *bear*, and R uses methods for the first class before methods for the next class(es).

The above is an example of polymorphism. *yog* is a polymorphic object and the various methods are polymorphic in that *print* can be used with the *bear* class, the *grizzly_bear* class, and other classes beyond that.

Challenge How would you get R to quit immediately, without asking for any more information, when you simply type *k* (no parentheses!) instead of `quit()`? (Hint: you can do this by understanding what happens when you type *k* and how to exploit the S3 system.)

Multiple dispatch OOP

S3 method dispatch involves only the first argument to the function. In contrast, [Julia emphasizes the importance of multiple dispatch](#) as particularly important for mathematical computation. With multiple dispatch, the specific method can be chosen based on more than one argument.

The old (but still used in some contexts) [S4](#) system in R and the (very) new [R7](#) system both provide for multiple dispatch.

As a very simple example unrelated to any specific language, multiple dispatch would allow one to do the following with the addition operator:

```

3 + 7      # 10
3 + 'a'    # '3a'
'hi' + 'there' # 'hi there'

```

The idea of having the behavior of an operator or function adapt to the type of the input(s) is one aspect of *polymorphism*.

Both S4 and R7 are designed to be more formal than the S3 system (recall how we could just ‘create’ an S3 class by giving a class name to an existing list). With S4 and R7, you need to define your classes.

‘Standard’ OOP

What I’m calling ‘standard’ object-oriented programming is the style of OOP used in languages such as Python, C++, and Java. In R, one can use this style via the R6 system (or the older *referenceClass* system).

In this style, objects belong to classes. A class is made up of fields (the data objects) that store information and methods that operate on the fields. Thus, unlike generic function OOP, the verbs are part of the nouns.

We’ll illustrate this style of OOP using an example with an R6 class.

R6 classes

R6 classes are a somewhat new construct in R, with a class-based approach fairly similar to Python and C++. Importantly, they behave like pointers. We’ll discuss pointers in detail later. Let’s work through an example where we set up the fields of the class and class methods, including a constructor.

Example

Our example is to create a class for working with random time series. Each object of the class has specific parameter values that control the stochastic behavior of the time series. With a given object we can simulate one or more time series (realizations).

Here’s the initial definition of the class, with both public (user-facing) and private (internal use only) methods and fields.

```
library(R6)

tsSimClass <- R6Class("tsSimClass",
  ## class for holding time series simulators
  public = list(
    initialize = function(times, mean = 0, corParam = 1) {
      library(fields)
      stopifnot(is.numeric(corParam), length(corParam) == 1)
      stopifnot(is.numeric(times))
      private$times <- times
      private$n <- length(times)
      private$mean <- mean
      private$corParam <- corParam
      private$currentU <- FALSE
      private$calcMats()
    },

    changeTimes = function(newTimes) {
```

```

        private$times <- newTimes
        private$calcMats()
    },

    getTimes = function() {
        return(private$times)
    },

    print = function() { # 'print' method
        cat("R6 Object of class 'tsSimClass' with ",
            private$n, " time points.\n", sep = ' ')
        invisible(self)
    },

    simulate = function() {
        if(!private$currentU)
            private$calcMats()
        ## analogous to mu+sigma*z for generating N(mu, sigma^2)
        return(private$mean + crossprod(private$U, rnorm(private$n)))
    }
),

## private methods and functions not accessible externally
private = list(
    calcMats = function() {
        ## calculates correlation matrix and Cholesky factor
        lagMat <- fields::rdist(private$times) # local variable
        corMat <- exp(-lagMat^2 / private$corParam^2)
        private$U <- chol(corMat) # square root matrix
        cat("Done updating correlation matrix and Cholesky factor.\n")
        private$currentU <- TRUE
        invisible(self)
    },
    n = NULL,
    times = NULL,
    mean = NULL,
    corParam = NULL,
    U = NULL,
    currentU = FALSE
)
)

```

Now let's see how we would use the class.

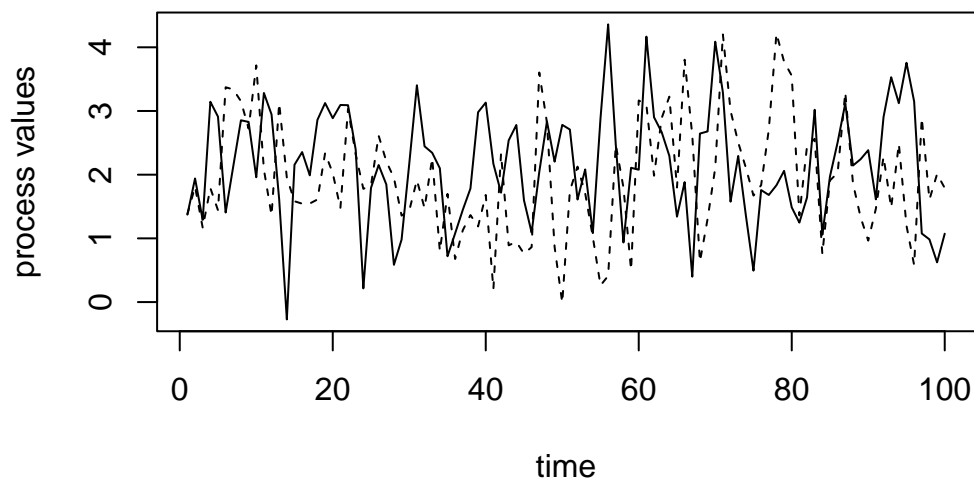
```
myts <- tsSimClass$new(1:100, 2, 1)
```

Done updating correlation matrix and Cholesky factor.

```
myts
```

R6 Object of class 'tsSimClass' with 100 time points.

```
set.seed(1)
## here's a simulated time series
y1 <- myts$simulate()
plot(myts$getTimes(), y1, type = 'l', xlab = 'time',
     ylab = 'process values')
## simulate a second series
y2 <- myts$simulate()
lines(myts$getTimes(), y2, lty = 2)
```



We could set up a different object that has different parameter values. That new simulated time series is less wiggly because the `corParam` value is larger than before.

```
myts2 <- tsSimClass$new(1:100, 2, 4)
```

Done updating correlation matrix and Cholesky factor.

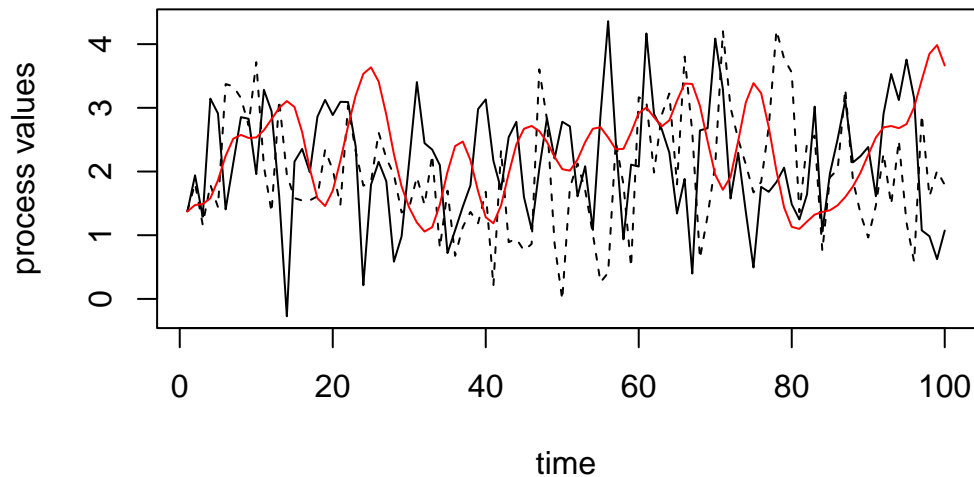
```
set.seed(1)
## here's a simulated time series with a different value of
## the correlation parameter (corParam)
y3 <- myts2$simulate()

plot(myts2$getTimes(), y3, type = 'l', xlab = 'time',
```

```

ylab = 'process values')
lines(myts$getTimes(), y2, lty = 2)
lines(myts2$getTimes(), y3, col = 'red')

```



Copies and references

Next let's think about when copies are made. In the next example `mytsRef` is a copy of `myts` in the sense that both names point to the same underlying object. But no data were copied when the assignment to `mytsRef` was done.

```

mytsRef <- myts
## 'mytsRef' and 'myts' are names for the same underlying object
mytsFullCopy <- myts$clone()

## Now let's change the values of a field
myts$changeTimes(seq(0,1000, length = 100))

```

Done updating correlation matrix and Cholesky factor.

```

myts$getTimes()[1:5]

[1]  0.0 10.1 20.2 30.3 40.4

mytsRef$getTimes()[1:5] # the same as `myts`

[1]  0.0 10.1 20.2 30.3 40.4

mytsFullCopy$getTimes()[1:5] # different from `myts`

```

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

In contrast `mytsFullCopy` is a reference to a different object, and all the data from `myts` had to be copied over to `mytsFullCopy`. This takes additional memory (and time), but is also safer, as it avoids the possibility that the user might modify `myts` and not realize that they were also affecting `mytsRef`.

Encapsulation

Why have private fields (i.e., encapsulation)? The use of private fields shields them from modification by users. In this case, that prevent users from modifying the *times* field. Why is this important? In this example, the correlation matrix and the Cholesky factor *U* are both functions of the vector of times. So we don't want to allow a user to directly modify *times*. If they did, it would leave the fields of the object in inconsistent states. Instead we force them to use *setTimes*, which correctly keeps all the fields in the object internally consistent (by calling *calcMats*). It also allows us to improve efficiency by controlling when computationally expensive operations are carried out.

```
try(myts$times <- 1:10)
```

```
Error in myts$times <- 1:10 : cannot add bindings to a locked environment
```

Final comments

- As we saw above, a copy of an object is just a pointer to the original object, unless we explicitly invoke the *clone* method.
- Classes can inherit from other classes. E.g., if we had a *simClass* and we wanted the *tsSimClass* to inherit from it:

```
R6Class(tsSimClass, inherit = simClass, ...)
```

- If you need to refer to methods and fields you refer to the entire object as either *self* or *private*.

More details on R6 classes can be found in the [Advanced R book](#).