

Advanced R programming: practical 2

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1 Rprofile

1. Create an .Rprofile file. Put in the line

```
cat("Successfully loaded .Rprofile at", date(), "\n")

## Successfully loaded .Rprofile at Wed May 7 21:24:21 2014
```

Restart R. Does the welcome message appear.

2. Try adding my suggestions to your .Rprofile

2 S3 objects

1. Following the cohort example in the notes, suppose we want to create a mean method.

- List all S3 methods associated with the mean function.
- Examine the source code of mean.
- What are the arguments of mean?
- Create a function called mean.cohort that returns a vector containing the mean weight and mean height.¹

¹ Ensure that you can pass in the standard mean arguments, i.e. na.rm.

2. Let's now make a similar function for the standard deviation

- Look at the arguments of the sd function.
- Create an function call sd.cohort that returns a vector containing the weight and height standard deviation.²
- Create a default sd function. Look at cor.default in the notes for a hint.

² Ensure that you can pass in the standard sd arguments, i.e. na.rm.

3. Create a hist method for the cohort class. When the hist function is called on a cohort, it should produce a single plot showing two histograms - one for height and another for weight.
4. Create a [method for the cohort class. This method should return a cohort object, but with the relevant rows sub setted. For example, if c was a cohort object,

```
cc[1:3, ]
```

would return the first three rows of the data frame.

5. Create a [<- method for the cohort class. This method should allow us to replace values in the details data frame, i.e.

```
cc[1, 1] = 10
```

3 *S4 objects*

- Following the Cohort example in the notes, suppose we want to make a generic for the mean function.
 - Using the `isGeneric` function, determine if the mean function is an S4 generic. If not, use `setGeneric` to create an S4 generic.
 - Using `setMethod`, create a mean method for the Cohort class.³
- Repeat the above steps for the sd function.
- Create a `hist` method for the cohort class. When the `hist` function is called on a cohort, it should produce a single plot showing two histograms - one for height and another for weight.
- Create a `[]` method for the cohort class. This method should return a cohort object, but with the relevant rows sub setted. For example, if `c` was a cohort object,

```
cc[1:3, ]
```

would return the first three rows of the data frame.

- Create a `<-` method for the cohort class. This method should allow us to replace values in the `details` data frame.

4 *Reference classes*

The example in the notes created a random number generator using a reference class.

- Reproduce the `randu` generator from the notes and make sure that it works as advertised.⁴
- When we initialise the random number generator, the very first state is called the seed. Store this variable and create a new function called `get_seed` that will return the initial seed, i.e.

```
r = randu(calls = 0, seed = 10, state = 10)
r$r()

## [1] 0.0003052

r$get_state()

## [1] 655390

r$get_seed()

## [1] 10
```

I've intentionally mirrored the functions from section 2 of this practical to highlight the differences.

³ Be careful to match the arguments.

⁴ The reference class version, not the function closure generator.

Reference classes also have an initialise method - that way we would only specify the seed and would then initialise the other variables. I'll give you an example in the solutions.

- Create a variable that stores the number of times the generator has been called. You should be able to access this variable with the function `get_num_calls`

```
r = randu(calls = 0, seed = 10, state = 10)
r$get_num_calls()

## [1] 0

r$r()

## [1] 0.0003052

r$r()

## [1] 0.001831

r$get_num_calls()

## [1] 2
```

Solutions

Solutions are contained within the course package

```
library("nclRadvanced")
vignette("solutions2", package = "nclRadvanced")
```