

Advanced R programming: practical 2

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1 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 summary method for the cohort class. When the summary function is called on a cohort object it should call the base summary on the `details` element.

- Use the `body` function to check if the function is already a generic function.
- Use the `args` function to determine the arguments.
- Create a `summary.cohort` function

4. Create a `hist` method for the cohort class. When the `hist` function is called on a cohort object, it should produce a single plot showing two histograms - one for height and another for weight.

5. Create a `[` method for the cohort class. This method should return a cohort object, but with the relevant rows sub setted. For example, if `cc` was a cohort object, then

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

would return the first three rows of the data frame.

6. 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
```

2 *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 summary method for the cohort class
 - Use `isGeneric` to determine if an S4 generic exists.
 - Use `setGeneric` to set the generic method (if necessary).
 - Create an S4 summary method.
- 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.
- Create a `<-` method for the cohort class. This method should allow us to replace values in the `details` data frame.

I've intentionally mirrored the functions from section 1 of this practical to highlight the differences.

³ Be careful to match the arguments.

3 *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] 0.0003051898

r$get_state()

## [1] 655390

r$get_seed()

## [1] 10
```

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] 0.0003051898

r$r()

## [1] 0.001831097

r$get_num_calls()

## [1] 2
```

Solutions

Solutions are contained within the course package

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