Advanced R programming: solutions 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 21:18:10 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.

```
methods("mean")

## [1] mean.Date     mean.default  mean.difftime
## [4] mean.POSIXct  mean.POSIXlt
```

   - Examine the source code of `mean`.

```
body("mean")
```

   - What are the arguments of `mean`?

```
args("mean")

## function (x, ...)
## NULL
```

   - Create a function called `mean.cohort` that returns a vector containing the mean weight and mean height.[1]

```
mean.cohort = function(x, ...) {
    m1 = mean(x$details[, 1], ...)
    m2 = mean(x$details[, 2], ...)
    return(c(m1, m2))
}
```

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]

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

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

- Create a default `sd` function. Look at `cor.default` in the notes for a hint.

  ```
  sd = function(x, ...) UseMethod("sd")
  sd.default = function(x, ...) stats::sd(x, ...)
  sd.cohort = function(x, ...) {
      s1 = sd(x$details[, 1], ...)
      s2 = sd(x$details[, 2], ...)
      return(c(s1, s2))
  }
  ```

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.

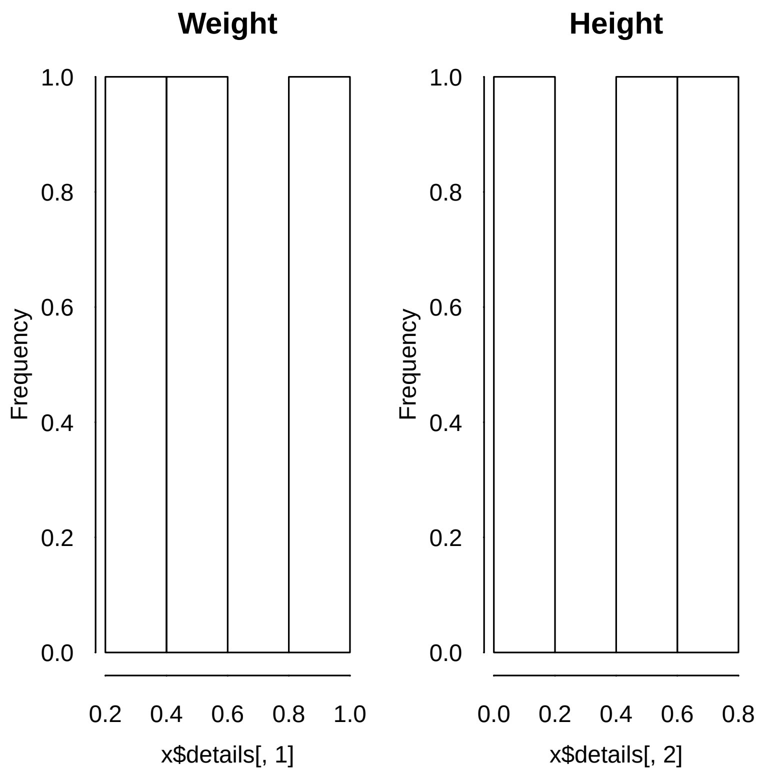
```
## hist is already a generic
body(hist)

## UseMethod("hist")

## Match the args
args(hist)

## function (x, ...)
## NULL

## Function
hist.cohort = function(x, ...) {
    op = par(mfrow = c(1, 2))
    hist(x$details[, 1], main = "Weight")
    hist(x$details[, 2], main = "Height")
    par(op)
}
hist(cc)
```



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 ç was a cohort object,

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

would return the first three rows of the data frame.

```
## Lots of methods available.
methods("[")

##  [1] [.acf*            [.AsIs
##  [3] [.bibentry*       [.data.frame
##  [5] [.Date            [.difftime
##  [7] [.factor          [.formula*
##  [9] [.getAnywhere*    [.hexmode
## [11] [.listof          [.noquote
## [13] [.numeric_version [.octmode
## [15] [.pdf_doc*        [.person*
## [17] [.POSIXct         [.POSIXlt
## [19] [.raster*         [.roman*
## [21] [.simple.list     [.terms*
## [23] [.ts*             [.tskernel*
## [25] [.warnings
##
##    Non-visible functions are asterisked

## Examine [.data.frame
```

```
args("[.data.frame")

## function (x, i, j, drop = if (missing(i)) TRUE else length(cols) ==
##     1)
## NULL

"[.cohort" = function(x, ...) {
    x$details = x$details[...]
    x
}
```

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

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

```
## Lots of methods available.
methods("[<-")

## [1] [<-.data.frame [<-.Date       [<-.factor
## [4] [<-.POSIXct    [<-.POSIXlt    [<-.raster*
## [7] [<-.ts*
##
##    Non-visible functions are asterisked

## Examine [.data.frame
args("[<-.data.frame")

## function (x, i, j, value)
## NULL

"[<-.cohort" = function(x, i, j, value) {
    x$details[i, j] = value
    x
}
cc[1:3, ] = 55
```

3 S4 objects

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

1. 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.

    ```
    isGeneric("mean")

    ## [1] FALSE
    ```

```
setGeneric("mean")

## [1] "mean"
```

- Using `setMethod`, create a `mean` method for the `Cohort` class.[3]

[3] Be careful to match the arguments.

```
setMethod("mean", signature = c("Cohort"), definition = function(x,
    ...) {
    m1 = mean(x@details[, 1], ...)
    m2 = mean(x@details[, 2], ...)
    return(c(m1, m2))
})

## [1] "mean"
```

2. Repeat the above steps for the `sd` function.

```
isGeneric("sd")

## [1] FALSE

setGeneric("sd")

## [1] "sd"

setMethod("sd", signature = c("Cohort"), definition = function(x,
    na.rm = FALSE) {
    m1 = sd(x@details[, 1], na.rm = na.rm)
    m2 = sd(x@details[, 2], na.rm = na.rm)
    return(c(m1, m2))
})

## [1] "sd"
```

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.

```
isGeneric("hist")

## [1] FALSE

setGeneric("hist")

## [1] "hist"

setMethod("hist", signature = c("Cohort"), definition = function(x) {
    op = par(mfrow = c(1, 2))
    hist(x@details[, 1], main = "Weight")
    hist(x@details[, 2], main = "Height")
    par(op)
})
```

```
## [1] "hist"
```

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 ç was a cohort object,

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

would return the first three rows of the data frame.

```
isGeneric("[")

## [1] TRUE

getGeneric("[")

## standardGeneric for "[" defined from package "base"
##
## function (x, i, j, ..., drop = TRUE)
## standardGeneric("[", .Primitive("["))
## <bytecode: 0x18e9870>
## <environment: 0x16aec10>
## Methods may be defined for arguments: x, i, j, drop
## Use  showMethods("[")  for currently available ones.

## Can you determine what drop does?
setMethod("[", signature = c("Cohort"), definition = function(x,
    i, j, ..., drop = TRUE) {
    x@details = x@details[i, j, ..., drop = drop]
    x
})

## [1] "["
```

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

```
isGeneric("[<-")

## [1] FALSE

setGeneric("[<-")

## [1] "[<-"

setMethod("[<-", signature = c("Cohort"), definition = function(x,
    i, j, value) {
    x@details[i, j] = value
    x
})
```

```
## [1] "[<-"

coh_s4[1, ] = 5
```

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.

[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.

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

## [1] 0.0003052

r$get_state()

## [1] 655390

r$get_seed()

## [1] 10
```

```
## Solutions - see below
```

- 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
```

«P2, echo=echo» @

Solutions

Solutions are contained within the course package

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