

Advanced R programming: solutions 2

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August 18, 2016

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.

```
methods("mean")  
  
## [1] mean,ANY-method      mean,Cohort-method  
## [3] mean.Date              mean.POSIXct  
## [5] mean.POSIXlt            mean.cohort  
## [7] mean.default            mean.difftime  
## see '?methods' for accessing help and source code
```

- 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))  
}
```

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.

```
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], ...)
```

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

```

    return(c(s1, s2))
}

```

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

```

## summary is already a generic
body(summary)

## standardGeneric("summary")

## Match the args
args(summary)

## function (object, ...)
## NULL

## Function
summary.cohort = function(object, ...) summary(object$details, ...)

```

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.

```

## hist is already a generic
body(hist)

## standardGeneric("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)
}

```

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.

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

## [1] [,Cohort-method      [,nonStructure-method
## [3] [.AsIs                [.Date
## [5] [.Dlist                [.POSIXct
## [7] [.POSIXlt              [.acf*
## [9] [.bibentry*           [.cohort
## [11] [.data.frame           [.difftime
## [13] [.factor               [.formula*
## [15] [.fseq*               [.getAnywhere*
## [17] [.hexmode              [.listof
## [19] [.noquote              [.numeric_version
## [21] [.octmode              [.pdf_doc*
## [23] [.person*             [.raster*
## [25] [.roman*              [.simple.list
## [27] [.table                [.terms*
## [29] [.ts*                 [.tskernel*
## [31] [.warnings
## see '?methods' for accessing help and source code

## 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
}
```

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
```

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

```
## [1] [<- ,Cohort-method      [<- ,data.frame-method
## [3] [<- .Date                 [<- .POSIXct
## [5] [<- .POSIXlt              [<- .cohort
## [7] [<- .data.frame          [<- .factor
## [9] [<- .numeric_version     [<- .raster*
## [11] [<- .ts*
## see '?methods' for accessing help and source code

## 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
```

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.

```
isGeneric("mean")
## [1] TRUE
setGeneric("mean")
## [1] "mean"
```

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

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

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

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

³ Be careful to match the arguments.

```

isGeneric("sd")

## [1] TRUE

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 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.

```

isGeneric("summary")

## [1] TRUE

setGeneric("summary")

## [1] "summary"

setMethod("summary", signature=c("Cohort"),
          definition=function(object, ...) {
            summary(object@details)
          }
)

## [1] "summary"

```

4. 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] TRUE

```

```

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"

```

5. Create a `[` method for the cohort class. This method should return a cohort object, but with the relevant rows sub setted.

```

isGeneric("[")

## [1] TRUE

getGeneric('[')

## standardGeneric for "[" defined from package "base"
##
## function (x, i, j, ..., drop = TRUE)
## standardGeneric("[", .Primitive("["))
## <bytecode: 0x24800a8>
## <environment: 0x2477918>
## 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] "["

```

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

```

isGeneric("<-")

## [1] TRUE

```

```

setGeneric('[<-')

## [1] "[<-"

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

## [1] "[<-"

coh_s4[1,]= 5

```

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

```

##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

```

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$r()

## [1] 0.0003051898

r$r()

## [1] 0.001831097

r$get_num_calls()

## [1] 2
```

```
## Solutions ##
randu = setRefClass("randu",
  fields = list(calls = "numeric",
               seed="numeric",
               state="numeric"))
randu$methods(get_state = function() state)
randu$methods(set_state = function(initial) state <<- initial)
randu$methods(get_seed = function() seed)
randu$methods(get_num_calls = function() calls)
randu$methods(r = function() {
  calls <<- calls + 1
  state <<- (65539*state) %% 2^31
  return(state/2^31)
})
```

Solutions

Solutions are contained within the course package

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