Practical 2

Jumping Rivers

S3 objects

1. Following the cohort example in the notes, suppose we want to create a `mean` method.
2. List all S3 methods associated with the `mean` function.
3. Examine the source code of `mean`.
4. What are the arguments of `mean`?
5. Create a function called `mean.cohort` that returns a vector containing the mean weight and mean height. Ensure that you can pass in the standard `mean` arguments, i.e.`na.rm`.‘
6. Let's now make a similar function for the standard deviation
7. Look at the arguments of the `sd` function.
8. Create an function call `sd.cohort` that returns a vector containing the weight and height standard deviation. Ensure that you can pass in the standard `sd` arguments, i.e.`na.rm`.‘
9. Create a default `sd` function. Look at `cor.default` in the notes for a hint.
10. 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.
11. Use the `body` function to check if the function is already a generic function.
12. Use the `args` function to determine the arguments.
13. Create a `summary.cohort` function
14. 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. You can either use base or **ggplot2**, again we'll be using **ggplot2**. To get both plots onto one plotting window, try using the `grid.arrange()` function from **gridExtra** package.
15. 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.

16. 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
```

Solutions

Solutions are contained within the course package

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