Programming: practical 2a solutions

In this question, we are going to use a `for` statement to `loop` over a large data set and construct some scatter plots. To generate the data, run the following piece of R code

```
library("nclRprogramming")
```

```
## Loading required package:  nclRintroduction
```

```
data(dummy_data)
dd = dummy_data
```

The data frame `dd` represents an experiment, where we have ten treatments: $A, B, \ldots, J$ and measurements at some time points. We want to create a scatter plot of measurement against time, for each treatment type.

1. First we create a scatter plot of one treatment:

   ```
   plot(dd[dd$treatments=="A",]$time,
        dd[dd$treatments=="A",]$measurement)
   ```

   Since the colnames are a bit long, let's shorten them:

   ```
   colnames(dd) = c("m", "t", "trts")
   ```

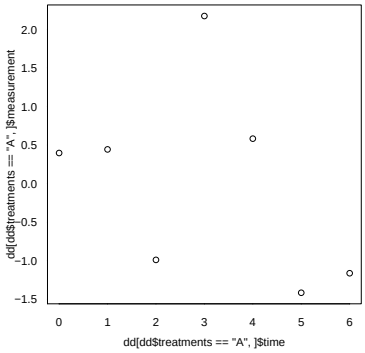

Figure 1: Measurements againts time.

2. To generate a scatter-plot for each treatment, we need to iterate over the different treatment types:

   ```
   for(treat in unique(dd$trts)) {
     plot(dd[dd$trts==treat,]$t,
          dd[dd$trts==treat,]$m)
     readline("Hit return for next plot\n")
   }
   ```

   A few questions:

   - What does `unique(dd$trts)` give?

     ```
     ## It gives all treatments.
     ```

   - In the `for` loop, what variable is changing? What are it's possible values?

     ```
     #The treat variable is changing. It goes through the different treatments.
     ```

   - What does the `readline` function do?

3. The default axis labels aren't great. So we can change the x-axis label using `xlab`:

```
plot(dd[dd$trts==treat,]$t,
     dd[dd$trts==treat,]$m,
     xlab="Time", ylab="Measurement")
```

Use `ylab` to alter the y-axis label.

4. To add a title to a plot we use the `main` argument, viz:

```
plot(dd[dd$trts=="A",]$t,
     dd[dd$trts=="A",]$m,
     main="Treatment",
     xlab="Time", ylab="Measurement")
```

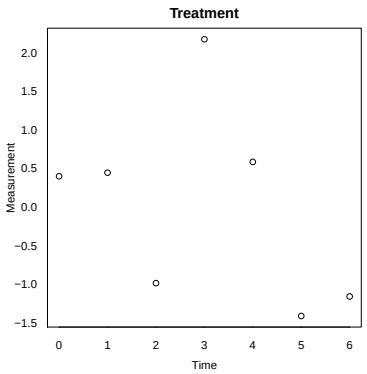

Figure 2: Measurements againts time with a title.

We can combine strings/characters using the `paste` function,

```
paste("Treatment", treat)
```

```
## [1] "Treatment J"
```

Rather than have a static title, make the title of each plot display the treatment type.

```
plot(dd[dd$trts==treat,]$t,
     dd[dd$trts==treat,]$m,
     main=paste("Treament", treat),
     xlab="Time", ylab="Measurement")
```

5. The y-axis range should really be the same in all graphics. Add a `ylim` argument to fix the range.[1]

[1] Hint: Work out the range before the `for` loop.

```
range(dd$m)
```

```
## [1] -1.639  8.113
```

```
plot(dd[dd$trts==treat,]$t,
     dd[dd$trts==treat,]$m,
     main=paste("Treament", treat),
     xlab="Time", ylab="Measurement",
     ylim=c(-2, 10))
```

6. At each iteration, use the `message` function to print the average measurement level across all time points.

```
##Within the for loop have the line
message(mean(dd[dd$trts==treat,]$m))
```

7. On each graph, highlight any observations with a blue point if they are larger than the mean + standard deviations or less than the mean - standard deviations. Use the `points` function to highlight a point. [2] For example, to highlight the points (1,2) and (3, 4) we use the command:

[2] **Hint:** You don't need `if` statements here. Just subset your data frame and pass this new data frame to the points function.

```
  points(c(1, 3), c(2, 4), col=2)


  plot(dd[sel,]$t, dd[sel,]$m,
           ylab=treat, xlab="Time",
           main=paste("Treatment", treat))
  ##Select a particular treament
  sel = (dd$trts == treat)

  ##Calculate the limits
  values = dd[sel,]$m
  message(mean(values))
  upper_lim = mean(values) + sd(values)
  lower_lim = mean(values) - sd(values)

  ##Extract the points
  up_row = dd[sel & dd$m > upper_lim,]
  low_row = dd[sel & dd$m < lower_lim,]

  ##pch=19 gives a solid dot
  ##See ?points
  points(up_row$t, up_row$m, col=4, pch=19)
  points(low_row$t, low_row$m, col=4, pch=19)
```

8. Suppose we wanted to save individual graphs. Add in the `pdf` function to save the resulting graph. To get unique file names, use the paste command:

```
filename = paste("file", treat, ".pdf", sep="")
```

9. Put your code, i.e. the `for` loop and plotting commands, in a function which takes the data frame as an argument.
10. Alter your function to take another argument where you can save the graph in a different directory.

Final piece of code

```
viewgraphs = function(dd, colour=TRUE, save=FALSE) {
  for(treat in unique(dd$trts)) {
    if(save) {
      filename = paste("file", treat, ".pdf", sep="")
      pdf(filename)
    }

    ##Use a different shape in the points
    if(colour) pch = 19
    else pch = 22
```

```
    ##Do selection one
    sel = (dd$trts == treat)
    plot(dd[sel,]$t, dd[sel,]$m,
         ylab=treat, xlab="Time",
         main=paste("Treatment", treat))

    ##Calculate the limits
    values = dd[sel,]$m
    message(mean(values))
    upper_lim = mean(values) + sd(values)
    lower_lim = mean(values) - sd(values)

    ##Extract the points
    up_row = dd[sel & dd$m > upper_lim,]
    low_row = dd[sel & dd$m < lower_lim,]

    ##pch=19 gives a solid dot
    ##See ?points
    points(up_row$t, up_row$m, col=4, pch=19)
    points(low_row$t, low_row$m, col=4, pch=19)
    if(save){
      dev.off()
    } else {
      readline("Hit return for next plot\n")
    }
  }
}
```

Solutions

Solutions are contained within this package:

```
library("nclRprogramming")
vignette("solutions2a", package="nclRprogramming")
```