STAT3401: Lab exercises concerning Hotelling's T^2 test

Paul Hewson

16th November 2007

1 Two sampling Hotelling's T^2 test

We are going to consider an example using data from Flea Beetles reported by Lubischew (1962) and used in Flury (1997). We are going to use **R** as a sophisticated calculator and work through a lot of the calculations long hand first.

```
> library(Flury)
> ?flea.beetles
> data(flea.beetles)
```

It can be seen that there is a factor "Species" denoting whether the beetles are from 'oleracea' or 'carduorum'. There are four numeric variables as follows: 'TG'; Distange of the Transverse Groove to the posterior border of the prothorax (microns), 'Elytra'; Length of the Elytra (in units of 0.01mm), 'Second.Antenna'; Length of the second antennal joint (microns) and 'Third.Antenna'; Length of the third antennal joint (microns). We need to estimate the mean for each sample, and calculate the difference between the two vectors:

```
> mu <- by(flea.beetles[,-1], flea.beetles$Species, colMeans)
> mudiff <- mu[[1]] - mu[[2]]
> p <- dim(flea.beetles)[2] - 1 ## how many variables are we using
```

The next step is to extract the two covariance matrices:

```
> covmats <- by(flea.beetles[,-1], flea.beetles$Species, cov)
> covmats
```

```
flea.beetles$Species: oleracea
                     TG    Elytra Second.Antenna Third.Antenna
TG             187.59649 176.86257       48.37135     113.58187
```

```
Elytra          176.86257 345.38596       75.97953     118.78070
Second.Antenna   48.37135  75.97953       66.35673      16.24269
Third.Antenna   113.58187 118.78070       16.24269     239.94152
------------------------------------------------------------
flea.beetles$Species: carduorum
                      TG    Elytra Second.Antenna Third.Antenna
TG             101.83947 128.06316       36.98947      32.59211
Elytra         128.06316 389.01053      165.35789      94.36842
Second.Antenna  36.98947 165.35789      167.53684      66.52632
Third.Antenna   32.59211  94.36842       66.52632     177.88158
```

and then to estimate the pooled covariance matrix $\boldsymbol{S}$ for the flea beetle data (where N[1] gives n_1, N[2] gives n_2), can be calculated as:

```
> N <- xtabs(~flea.beetles[,1])
> pooledS <- ((N[1]-1) * covmats[[1]] + (N[2]-1) * covmats[[2]]) / (N[1] + N[2] -2)
> pooledS
```

```
                      TG   Elytra Second.Antenna Third.Antenna
TG             143.55910 151.8034       42.52660      71.99253
Elytra         151.80341 367.7878      121.87653     106.24467
Second.Antenna  42.52660 121.8765      118.31408      42.06401
Third.Antenna   71.99253 106.2447       42.06401     208.07290
```

```
> Sinv <- solve(pooledS)
> Sinv
```

```
                         TG        Elytra Second.Antenna Third.Antenna
TG              0.013257964 -0.0053492256   0.0015134494 -0.0021617878
Elytra         -0.005349226  0.0066679441  -0.0047337699 -0.0005969439
Second.Antenna  0.001513449 -0.0047337699   0.0130490933 -0.0007445297
Third.Antenna  -0.002161788 -0.0005969439  -0.0007445297  0.0060093005
```

Having calculated the inverse of the pooled correlation matrix we also need the scaling factor $\frac{n_1 n_2}{n_1+n_2}$. Hotellings T^2 is then quite straightforward to calculate:

```
> scaleFact <- (N[1]*N[2]) / (N[1]+N[2])
> Hotellings <-  t(mudiff) %*% Sinv %*% mudiff * scaleFact
> Hotellings
```

```
         [,1]
[1,] 133.4873
```

which is the value of the T^2 statistic. We could work with this value directly, but it is more convenient to transform it into something we can compare with the F distribution.

```
       [,1]
[1,] 30.666
```

and we compare this with an F distribution having p and $(n_1 + n_2 - p - 1)$ d.f.

And we can check this as follows:

```
> pf(test, p, N[1]+N[2]-p-1,lower.tail = FALSE )
```

which gives us the area under the curve from our test statistic (30.666) to ∞. Clearly in this case, we have reject H_0, i.e. there is evidence that the mean vectors, $\bar{\boldsymbol{x}}_{oleracea} = (194.4737, 267.0526, 137.3684, 185.9474)$, $\bar{\boldsymbol{x}}_{carduorum} = (179.55, 290.80, 157.20, 209.25)$, for the two species differ. This is perhaps no surprise if you consider the data - do look at the scatterplot suggested by the helpfile.

- How would you modify the code to carry out a one sample T^2 test?
- You may wish to repeat this exercise with the `turtles` data.

You also should note that in practice this calculation is done my means of the QR decomposition, details are given in Seber (1984). There is no in-built **R** function for doing these calculations - a nice little project for someone. The `manova()` function can be persuaded to carry out a two sample Hotelling's T^2 test as follows:

```
> hotel.test <- manova(as.matrix(flea.beetles[,-1]) ~ flea.beetles[,1])
> summary(hotel.test, test = "Hotelling")
```

2 Drawing the ellipses

This illustration is based on, but differs from code provided by Marco Bee to accompany Flury (1997). Firstly, we need a function to draw ellipses:

```
> ellipse <- function(covmat, centroid, csquare, resolution, plot = TRUE) {
+ angles <- seq(0, by = (2 * pi)/resolution, length = resolution)
+   sd <- covmat[1,2] / sqrt(covmat[1,1] * covmat[2,2])
+     projmat <- matrix(0,2,2)
+     projmat[1,1] <- sqrt(covmat[1,1] %*% (1+sd)/2)
+     projmat[1,2] <- -sqrt(covmat[1,1] %*% (1-sd)/2)
```

```
+     projmat[2,1] <- sqrt(covmat[2,2] %*% (1+sd)/2)
+     projmat[2,2] <- sqrt(covmat[2,2] %*% (1-sd)/2)
+ circle <- cbind(cos(angles), sin(angles))
+ ellipse <- t(centroid + sqrt(csquare) * projmat %*% t(circle))
+ if (plot == TRUE) {lines(ellipse)}
+ return(ellipse)
+ }
```

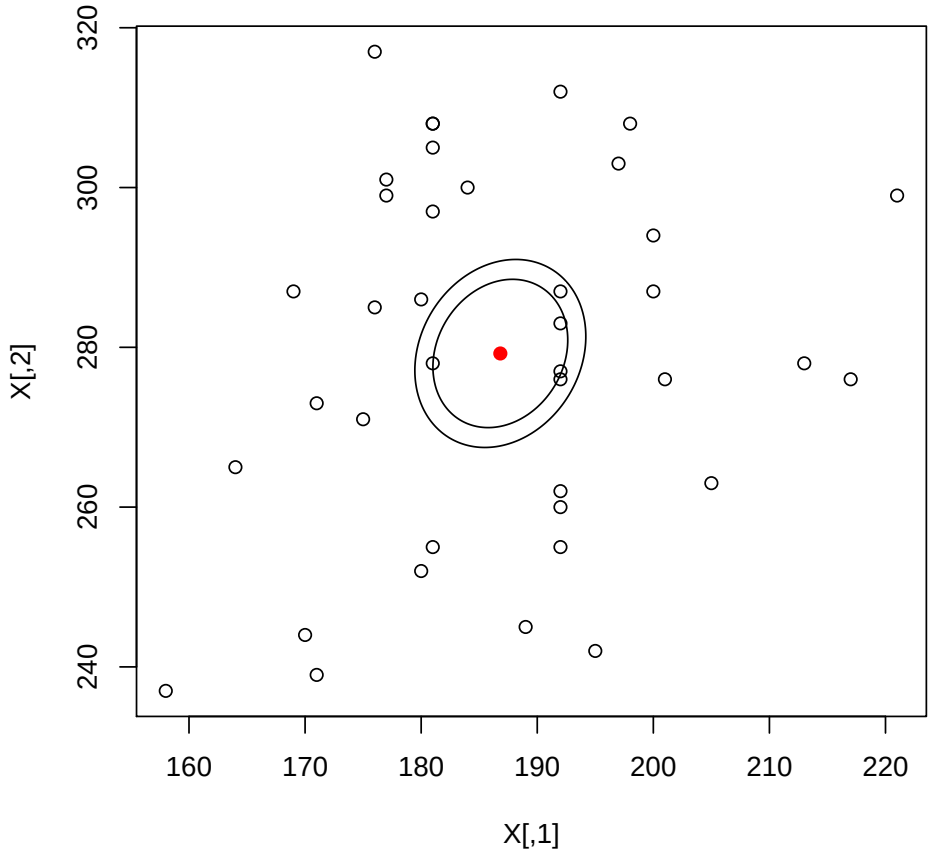
It is possible to define a function which calculates c^2 and calls the ellipse routine (I'm not completely convinced this is doing the calculation correctly yet, in particular I'm not sure I'm using the correct tail).

```
> mean.ellipse <- function (data, alpha=0.05, resolution=500)
+ {
+ xbar <- colMeans(data)
+ n <- dim(data)[1]
+ p <- dim(data)[2]
+ f <- qf(1-alpha, p, n-p)
+ csquare <- ((n-1)/n) * (p / (n-p)) * f
+ cat(csquare)
+ ellipse <- ellipse(cov(data), xbar, csquare, resolution)
+ }
```

For illustrative purposes, we'll create a $n \times 2$ data object from our flea beetles. Do note here that we are *only* using two variables!

Given the above functions, it is quite straightforward to plot the centroids and constant density ellipses:

```
> X <- cbind(flea.beetles[,2], flea.beetles[,3])
> plot(X)
> points(t(colMeans(X)), pch = 16, col = "red")
> mean.ellipse(X, alpha = 0.01)
> mean.ellipse(X, alpha = 0.05)
```



- Can you estimate the elongation of the ellipse? (Well, yes you can, but how?)

You may be interested in contrasting these with the univariate confidence intervals. As an aide memoire, some code for doing this is given below:

```
> abline(v = confint(lm(X[,1]~1)))
> abline(h = confint(lm(X[,2]~1)))
```

In this case you shouldn't see much difference. But repeat this exercise withthe turtles data and you should see a very different picture.

- Can you plot the simultaneous confidence ellipses (see Johnson and Wichern for details)?