

Section 5.7 Multiple Comparisons and Fisher's Least Significant Difference

Loaded needed packages.

```
library(Stat2Data)
library(mosaic)
```

EXAMPLE 5.24 Fisher's LSD for the fruit flies

Create a dataframe for **FruitFlies** and look at the structure of the data.

```
data("FruitFlies")
str(FruitFlies)

## 'data.frame':   125 obs. of  7 variables:
## $ ID          : int  1 2 3 4 5 6 7 8 9 10 ...
## $ Partners    : int  8 8 8 8 8 8 8 8 8 8 ...
## $ Type        : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Longevity   : int  35 37 49 46 63 39 46 56 63 65 ...
## $ Thorax      : num  0.64 0.68 0.68 0.72 0.72 0.76 0.76 0.76 0.76 ...
## $ Sleep       : int  22 9 49 1 23 83 23 15 9 81 ...
## $ Treatment   : Factor w/ 5 levels "1 pregnant","1 virgin",...: 3 3 3 3 3 3 3 3 3 3 ...
```

Compute summary statistics for the groups.

```
FFStats=favstats(Longevity~Treatment,data=FruitFlies)[c("Treatment","n","mean","sd")]
FFStats
```

```
##   Treatment  n  mean      sd
## 1 1 pregnant 25 64.80 15.65248
## 2 1 virgin  25 56.76 14.92838
## 3 8 pregnant 25 63.36 14.53983
## 4 8 virgin  25 38.72 12.10207
## 5      none 25 63.56 16.45215
```

One-way ANOVA model and table for fruit flies

```
FFAnova=aov(Longevity~Treatment,data=FruitFlies)
summary(FFAnova)
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Treatment    4  11939   2984.8    13.61 3.52e-09 ***
## Residuals   120   26314     219.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Extract the MSE and compute LSD

```
tstar=qt(0.975,FFAnova$df.residual)
MSE=summary(FFAnova)[[1]]$"Mean Sq"[2]    #gets the MSE from aov summary
ni=FFStats$n[1]
LSD=tstar*sqrt(MSE)*sqrt(1/ni+1/ni)
round(LSD,2)
```

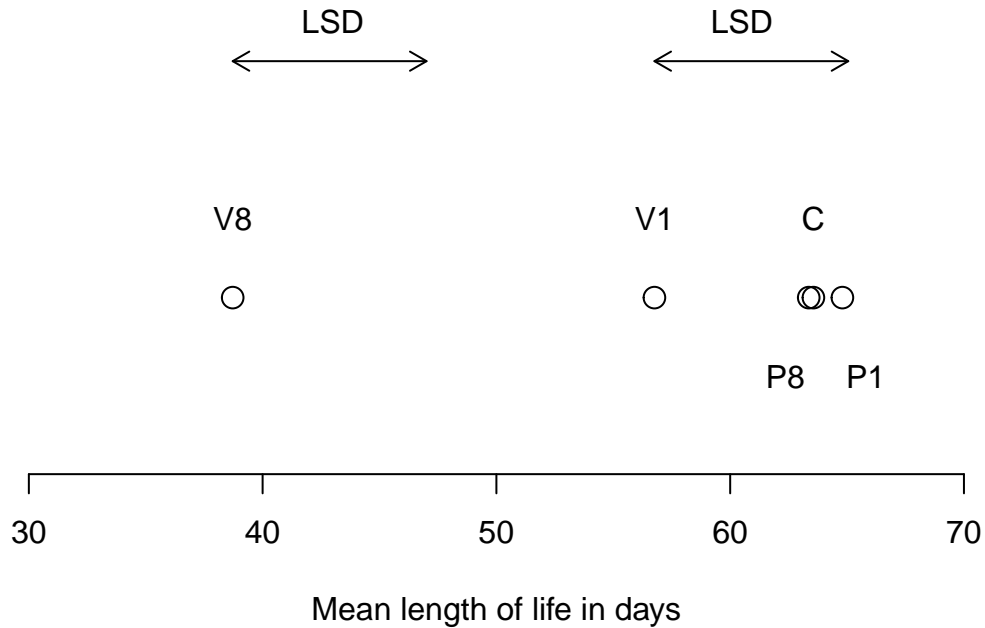
```
## [1] 8.29
```

FIGURE 5.27 Differences among the means of the five groups of fruit flies

```
y=rep(2,5)
plot(FFStats$mean,y, xlim=c(30,70), ylim=c(1,4), yaxt="n",ylab="", bty = "n", xlab="Mean length of life

#rest below is labelling the ponts and showing LSD
FFMean=FFStats$mean
text(FFMean[1]+1, 1.5, "P1")
text(FFMean[2], 2.5, "V1")
text(FFMean[3]-1, 1.5, "P8")
text(FFMean[4], 2.5, "V8")
text(FFMean[5],2.5,"C")

arrows(FFMean[4], 3.5, FFMean[4]+LSD, 3.5, length=0.1,code=3)
arrows(FFMean[2], 3.5, FFMean[2]+LSD, 3.5, length=0.1,code=3)
text(43, 3.75, "LSD")
text(60.5, 3.75, "LSD")
```



We see that the 8 virgins group (mean=38.72) is well below (more than 8.29) the next smallest group mean (1 virgin=56.76). The other three groups are all within 8.29 of the point for 1 virgin.

Alternative Solutions to Example 5.24

First, using pairwise t test.

Note: The command `p.adjust.method="none"` does Fisher's LSD. See Section 8.2 for a discussion of other methods for adjusting for multiple comparisons.

```
pairwise.t.test(FruitFlies$Longevity,FruitFlies$Treatment,p.adjust.method="none")
```

```
##
## Pairwise comparisons using t tests with pooled SD
##
## data: FruitFlies$Longevity and FruitFlies$Treatment
##
##      1 pregnant 1 virgin 8 pregnant 8 virgin
## 1 virgin  0.057    -        -          -
## 8 pregnant 0.732    0.118    -          -
## 8 virgin  7.3e-09   3.4e-05  3.7e-08    -
## none      0.768    0.107    0.962     3.0e-08
##
## P value adjustment method: none
```

Now, using the asbio package.

```
library(asbio)
```

```
pairw.anova(FruitFlies$Longevity,FruitFlies$Treatment,method="lsd")
```

```
##
## 95% LSD confidence intervals
##
##               LSD   Diff   Lower   Upper   Decision
## mu1 pregnant-mu1 virgin 8.29266 8.04 -0.25266 16.33266 FTR H0
## mu1 pregnant-mu8 pregnant 8.29266 1.44 -6.85266 9.73266 FTR H0
## mu1 virgin-mu8 pregnant 8.29266 -6.6 -14.89266 1.69266 FTR H0
## mu1 pregnant-mu8 virgin 8.29266 26.08 17.78734 34.37266 Reject H0
## mu1 virgin-mu8 virgin 8.29266 18.04 9.74734 26.33266 Reject H0
## mu8 pregnant-mu8 virgin 8.29266 24.64 16.34734 32.93266 Reject H0
## mu1 pregnant-munone 8.29266 1.24 -7.05266 9.53266 FTR H0
## mu1 virgin-munone 8.29266 -6.8 -15.09266 1.49266 FTR H0
## mu8 pregnant-munone 8.29266 -0.2 -8.49266 8.09266 FTR H0
## mu8 virgin-munone 8.29266 -24.84 -33.13266 -16.54734 Reject H0
##               Adj. p-value
## mu1 pregnant-mu1 virgin 0.05728
## mu1 pregnant-mu8 pregnant 0.73159
## mu1 virgin-mu8 pregnant 0.11771
## mu1 pregnant-mu8 virgin 0
## mu1 virgin-mu8 virgin 3e-05
## mu8 pregnant-mu8 virgin 0
## mu1 pregnant-munone 0.7677
## mu1 virgin-munone 0.1071
## mu8 pregnant-munone 0.96199
## mu8 virgin-munone 0
```