# Answers to exercises in Handout 1

**Remember:** make sure you have the carnivora data set loaded into your workspace (using *read.csv*) and named *carni*.

## Q1. Tabulate the number of species in each Family of the superfamily *Caniformia*.

```
temp1 <- subset(carni, SuperFamily == "Caniformia")
temp1 <- droplevels(temp1)
table(temp1$Family)
```

```
>
>   Ailuridae     Canidae Mustelidae Procyonidae     Ursidae
>           1          18         30           4           4
```

## Q2. Using the carnivore data set, produce a box plot featuring female weight (FW) for the *Canidae*, *Felidae* and *Ursidae* together on the same plot.

```
temp1 <- subset(carni, Family %in% c("Canidae", "Felidae", "Ursidae"))
temp1 <- droplevels(temp1)
plot(temp1$Family, temp1$FW)
```

## Q3. Using the carnivore data set, make a table showing the average (mean) birth weight (BW) for Families in Superfamily *Feliformia*.

```
temp1 <- subset(carni, SuperFamily == "Feliformia")
temp1 <- droplevels(temp1)
tapply(temp1$BW, temp1$Family, FUN = mean, na.rm = TRUE)
```

```
>    Felidae  Hyaenidae Viverridae
>      418.1     1096.5       96.6
```

## Q4. Plot the relationship between log female weight (FW) and litter size (LS) in the *Mustelidae*.

```
temp1 <- subset(carni, Family == "Mustelidae")
plot(log(temp1$FW), temp1$LS)
```
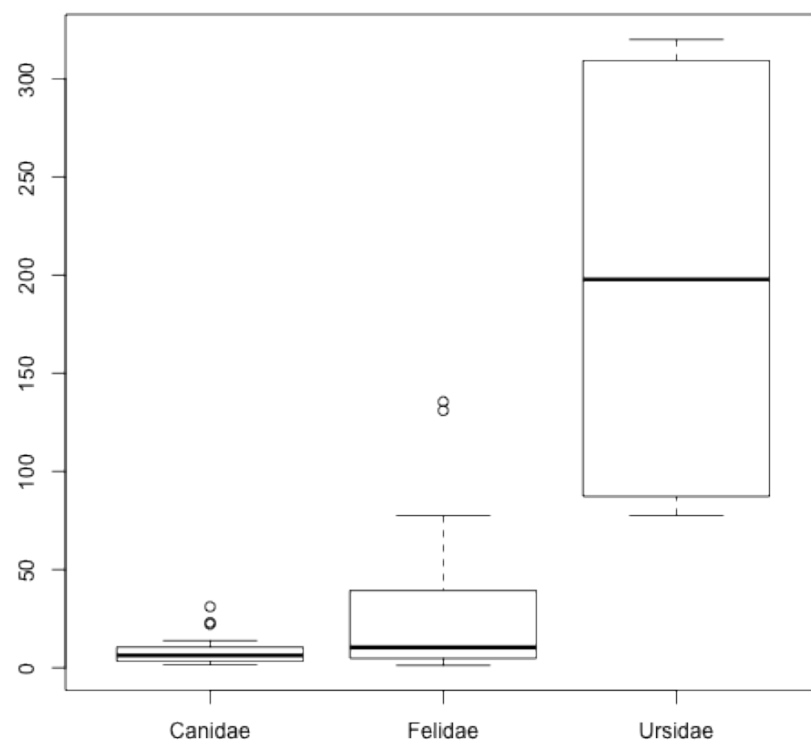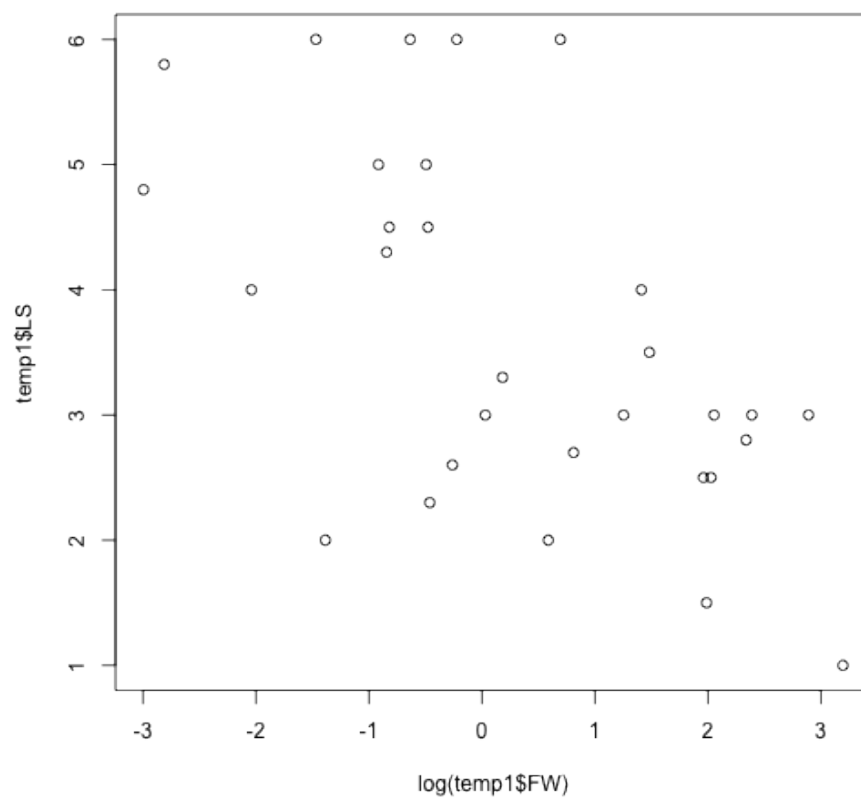
Figure 1: A box plot for Q2

Figure 2: The plot for Q4

**Q5.  Identify the largest and smallest (by female weight (FW)) species in the *Viverridae* family.  What are their brain sizes (FB)?**

```
temp1 <- subset(carni, Family == "Viverridae")
which.min(temp1$FW)
```

```
> [1] 27
```

```
which.max(temp1$FW)
```

```
> [1] 12
```

```
temp1[c(27, 12), ]   #You can read off the brain sizes in the FB column
```

```
>          Order SuperFamily     Family     Genus                Species    FW
> 84 Carnivora  Feliformia Viverridae   Helogale     Helogale parvula  0.27
> 69 Carnivora  Feliformia Viverridae Acrctictis Arctictis binturong 13.00
>       SW FB    SB   LS   GL   BW WA AI  LY  AM IB
> 84  0.27  5  4.75  3.6 51.0  NA NA NA  NA 450  4
> 69 13.00 38 40.80  3.0 90.3 319 56 NA 216
```

You could also do it like this:

```
temp1 <- subset(carni, Family == "Viverridae")
x <- c(which.min(temp1$FW), which.max(temp1$FW))
temp1[x, ]
```

```
>          Order SuperFamily     Family     Genus                Species    FW
> 84 Carnivora  Feliformia Viverridae   Helogale     Helogale parvula  0.27
> 69 Carnivora  Feliformia Viverridae Acrctictis Arctictis binturong 13.00
>       SW FB    SB   LS   GL   BW WA AI  LY  AM IB
> 84  0.27  5  4.75  3.6 51.0  NA NA NA  NA 450  4
> 69 13.00 38 40.80  3.0 90.3 319 56 NA 216
```

You can simply look at the output to see that the smallest species (by female weight) is *Helogale parvula* with a brain size of 5g.  The largest species is *Arctictis binturong* with a brain size of 38g.