

## 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)
```

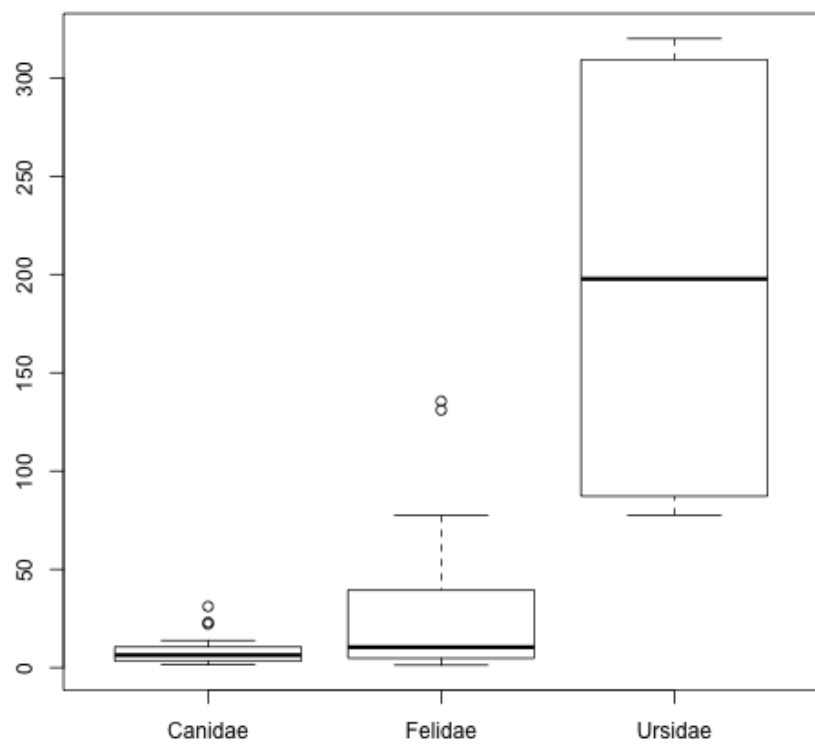


Figure 1: A box plot for Q2

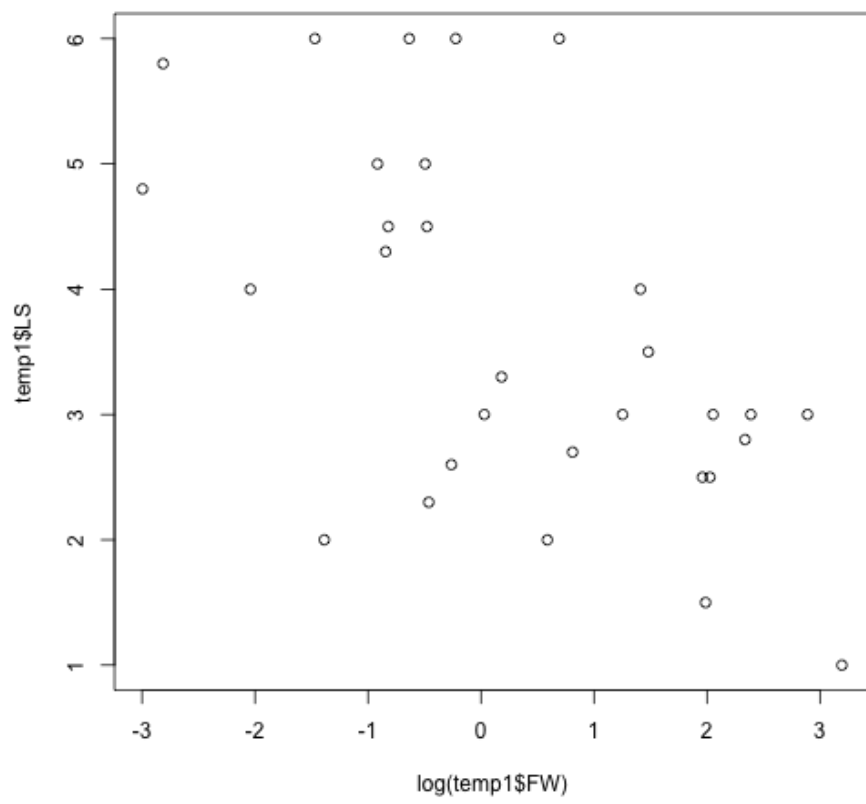


Figure 2: The plot for Q4

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.