Answers to exercises in Handout 2

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

Q1. Randomly draw 25 numbers from a uniform distribution from 10 to 20.

```
runif(25, 10, 20)
```

```
>  [1] 10.13 13.29 12.90 14.73 16.74 18.98 11.02 14.46 15.86 16.71 10.34
> [12] 16.53 14.62 16.58 19.07 19.43 18.19 13.38 13.16 20.00 10.87 19.73
> [23] 13.68 19.68 19.56
```

Q2. (a) Write a script to simulate flipping a coin. (b) Add if and else statements to print "Heads - you win!" or "Tails - you lose!" depending on the outcome.

(a) This part is pretty easy:

```
coin <- c("Heads", "Tails")
sample(coin, 1)
```

```
> [1] "Heads"
```

(b) This part was a bit trickier:

```
coin <- c("Heads", "Tails")
if (sample(coin, 1) == "Heads") {
    cat("Heads - you win!")
} else {
    cat("Tails - you lose!")
}
```

```
> Tails - you lose!
```

Q3. Make a scatter plot showing the relationship between log female weight (FW) and litter size (LS) in the *Canidae* and *Felidae* families. Use different colours for the points from each Family.

This is just a case of plotting an empty plot, and using **points** to add in the points, first for the *Canidae* and then for *Felidae*. See Figure 1.

```
plot(log(carni$FW), carni$LS, type = "n")
points(log(carni$FW[carni$Family == "Canidae"]), carni$LS[carni$Family == "Canidae"],
    pch = 16, col = "blue")
points(log(carni$FW[carni$Family == "Felidae"]), carni$LS[carni$Family == "Felidae"],
    pch = 16, col = "red")
legend("topleft", legend = c("Canidae", "Felidae"), pch = 16, col = c("blue",
    "red"))
```

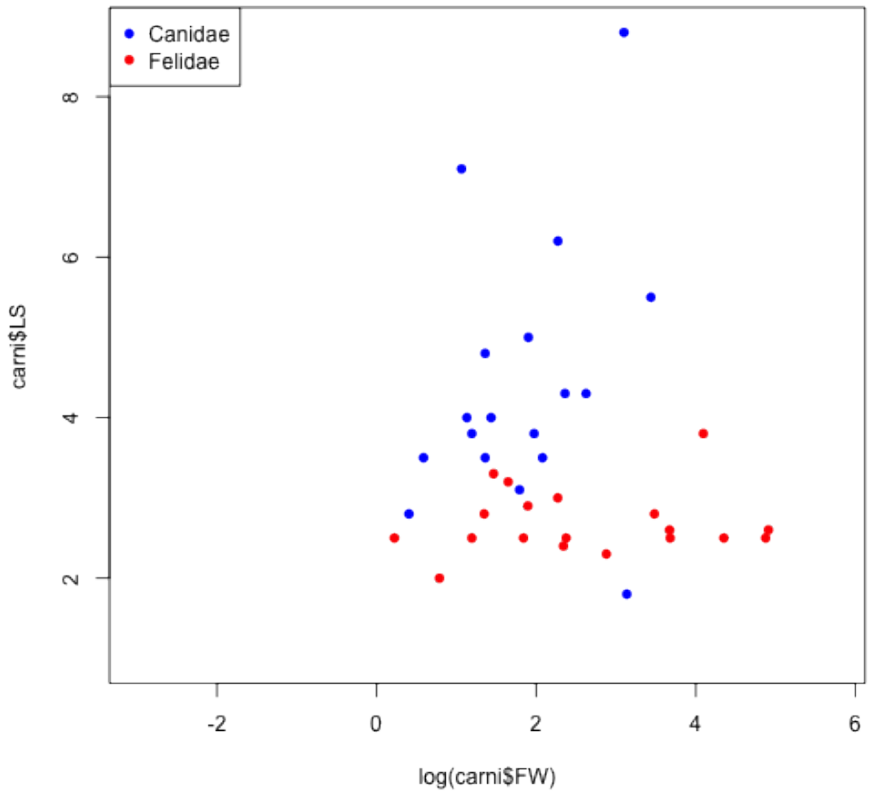

Figure 1: Relationship between log female weight and litter size in the Canidae and Felidae

Q4. Using the carnivore data set, make a barplot showing the mean birth weight (BW) for the Families in Superfamily *Feliformia*.

First we must subset the *carni* data frame, then use **droplevels** to get rid of unnecessary factor levels. Then we can use **tapply** to find the means. Since there are NA values we must use the *na.rm=TRUE* argument to remove them:

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

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

We can pass the results of this **tapply** function to barplot like this:

```
temp <- tapply(Feli$BW, Feli$Family, mean, na.rm = TRUE)
barplot(temp, ylab = "Mean weight (g)")
```

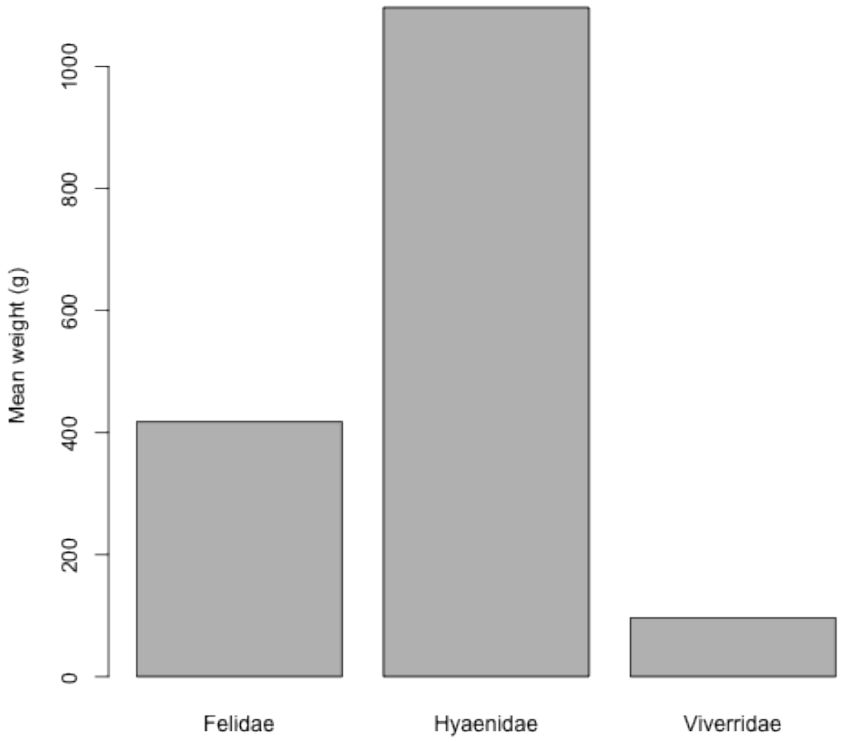

Figure 2: Bar plot showing mean birth weight for the familes in *Feliformia*