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] 15.36 11.04 12.49 13.57 15.39 16.68 11.71 10.86 12.33 14.94 14.34
> [12] 18.25 14.70 16.31 18.65 10.37 19.13 19.19 15.87 15.46 17.83 14.66
> [23] 15.00 11.02 13.32
```

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] "Tails"
```

(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!")}
```

```
> Heads - you win!
```

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"))
```

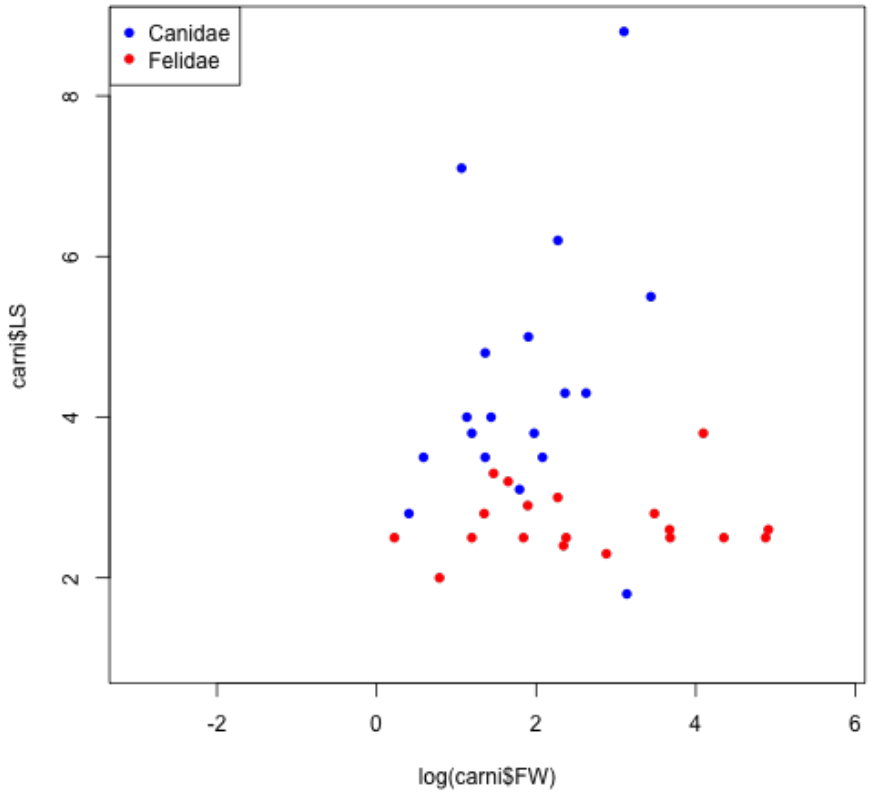

Figure 1: Relationship between log female weight and litter size in the Canidae and Felidae

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)")
```

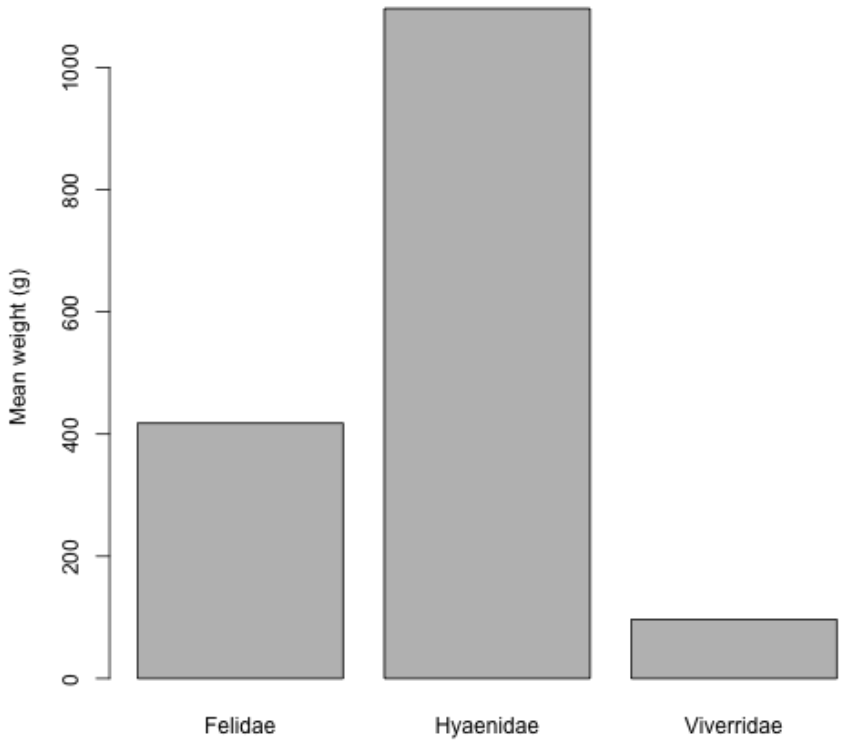

Figure 2: Bar plot showing mean birth weight for the familes in *Feliformia*