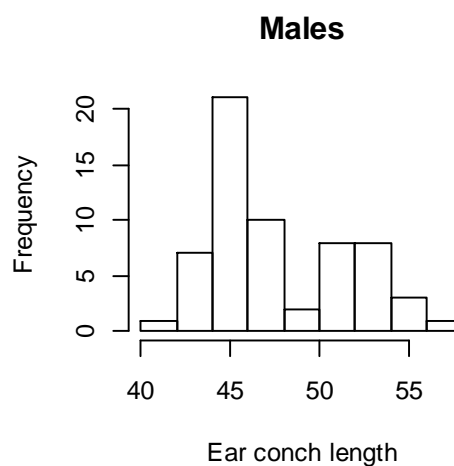
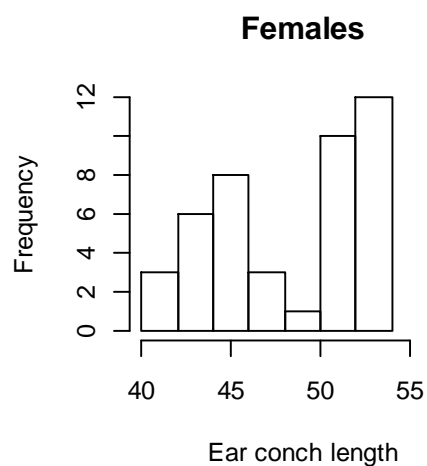
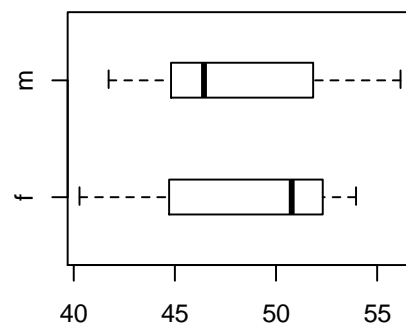
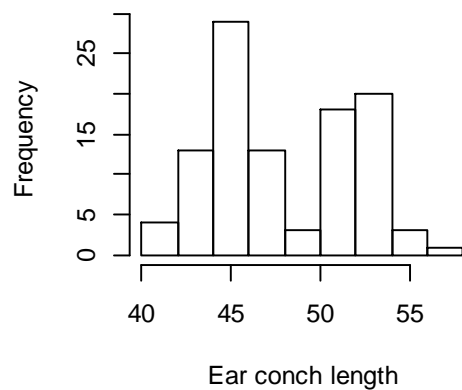


Stat 462: Lab 3 solutions

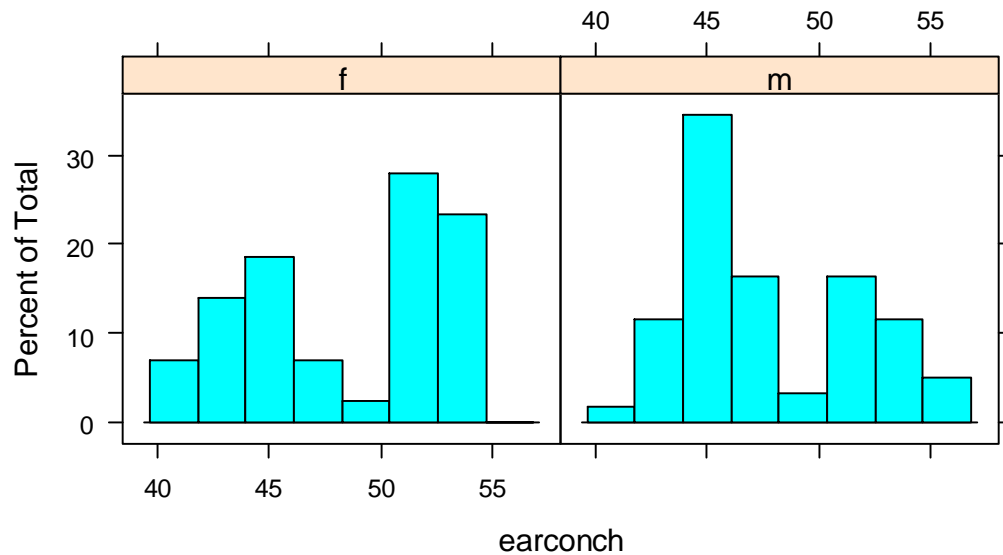
```
# 2.3
library( DAAG )
par(mfrow=c(2,2))
firstHist <- hist(possum$earconch, main="", xlab="Ear conch length")
boxplot(earconch ~ sex, data=possum, boxwex=0.3, horizontal=TRUE)

hist(possum$earconch[possum$sex == "f"], main="Females"
      , xlab="Ear conch length", xlim = range(firstHist$breaks) )
hist(possum$earconch[possum$sex == "m"], main="Males"
      , xlab="Ear conch length", xlim = range(firstHist$breaks) )
```

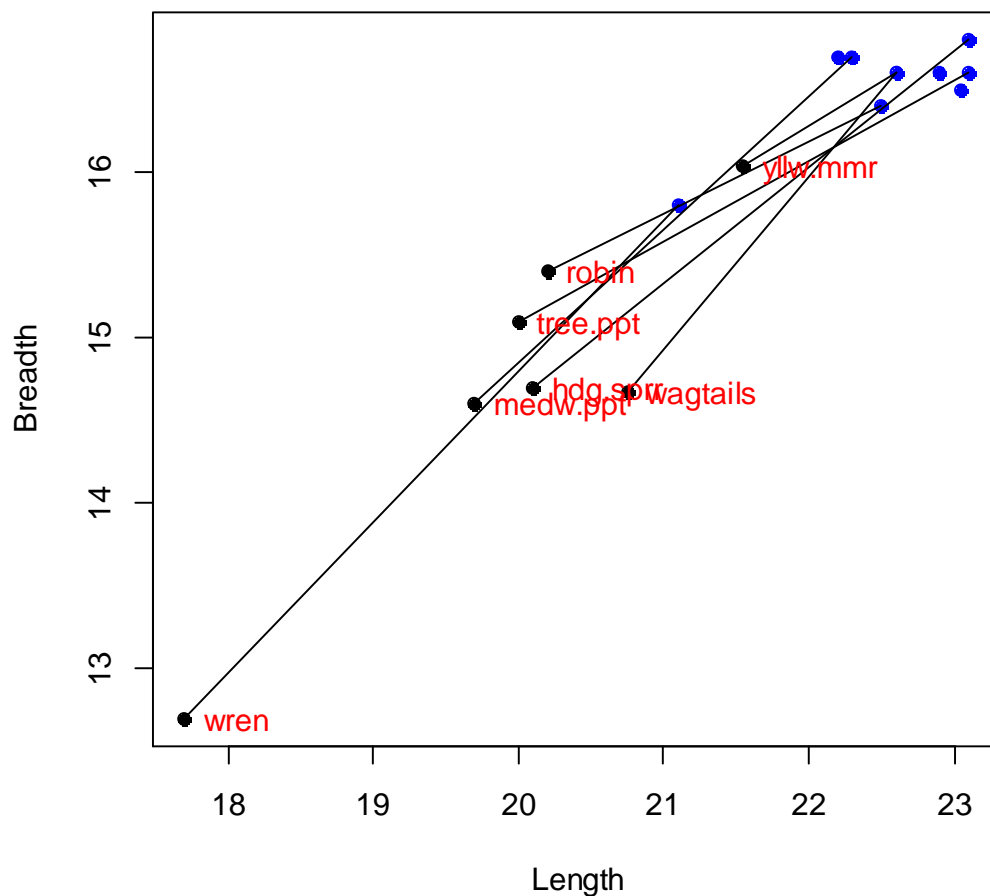


It seems that sex differences are not the whole story here.

```
# Nicer side-by-side boxplots
library(lattice)
histogram(~ earconch | sex, data=possum)
```

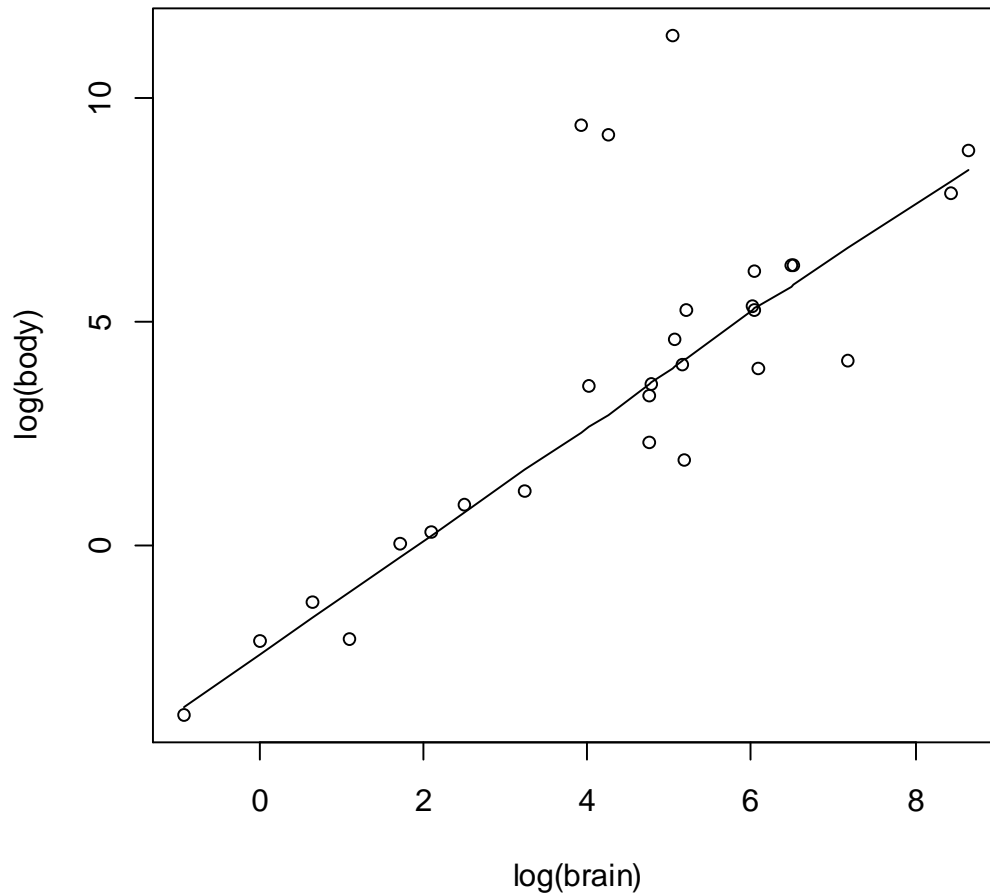


```
# 2.5
# There were a couple of errors due to there being 10 rows
# in the original cuckoohosts data.frame rather than 12.
# I also modified the colours and plotting characters and
# moved the labels to the right of the points.
attach(cuckoohosts)
plot(c(clength, hlength), c(cbreadth, hbreadth)
     , col=c("blue","black")[rep(1:2,c(10,10))], pch=19
     , xlab = "Length", ylab = "Breadth" )
for(i in 1:10) lines(c(clength[i], hlength[i]), c(cbreadth[i],
hbreadth[i]))
text(hlength, hbreadth, abbreviate(rownames(cuckoohosts),8),
col="red", pos=4)
detach(cuckoohosts)
```



The longer the line, the larger the difference in size between the cuckoo eggs and the host eggs.

```
# 2.10
> with(Animals, cor(brain, body))
[1] -0.005341163
> with(Animals, cor(log(brain), log(body)))
[1] 0.7794935
> with(Animals, cor(log(brain), log(body), method="spearman"))
[1] 0.7162994
# Check linearity of relationship
> with(Animals, plot(log(brain), log(body)))
> with(Animals, lines(lowess((log(body)~log(brain))))))
```

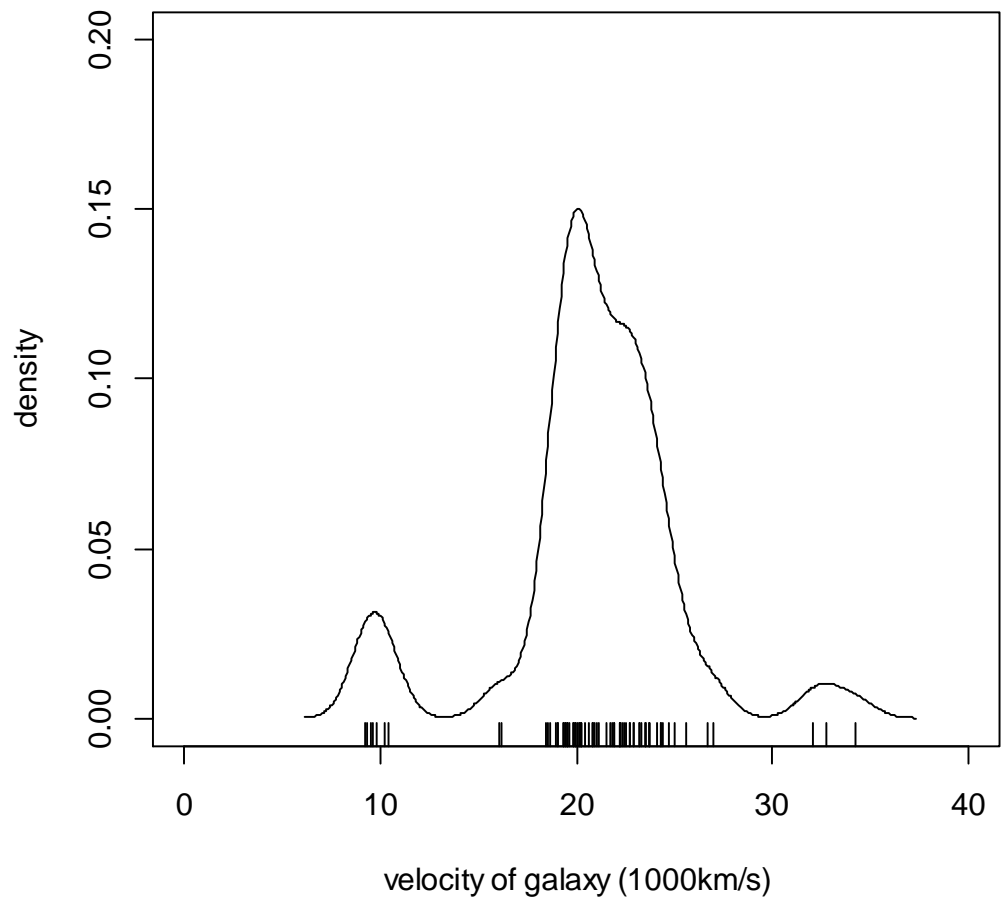


The relationship looks quite linear except for a few positive outliers. The pearson correlation is probably OK here, despite the outliers, but the spearman correlation is OK too. Recall that since the spearman correlation is based only on ranks, the log-log transformation is unnecessary:

```
> with(Animals, cor(brain, body, method="spearman"))
[1] 0.7162994
```

#2.13

```
gal <- galaxies/1000
plot(x = c(0, 40), y = c(0, 0.2), type = "n"
     , xlab = "velocity of galaxy (1000km/s)", ylab = "density")
rug(gal)
lines(density(gal), lty = 1)
```



There does appear to be at least two clusters. There is also a long right tail to the larger (central) cluster, possibly with a third small cluster of three galaxies at high velocity.