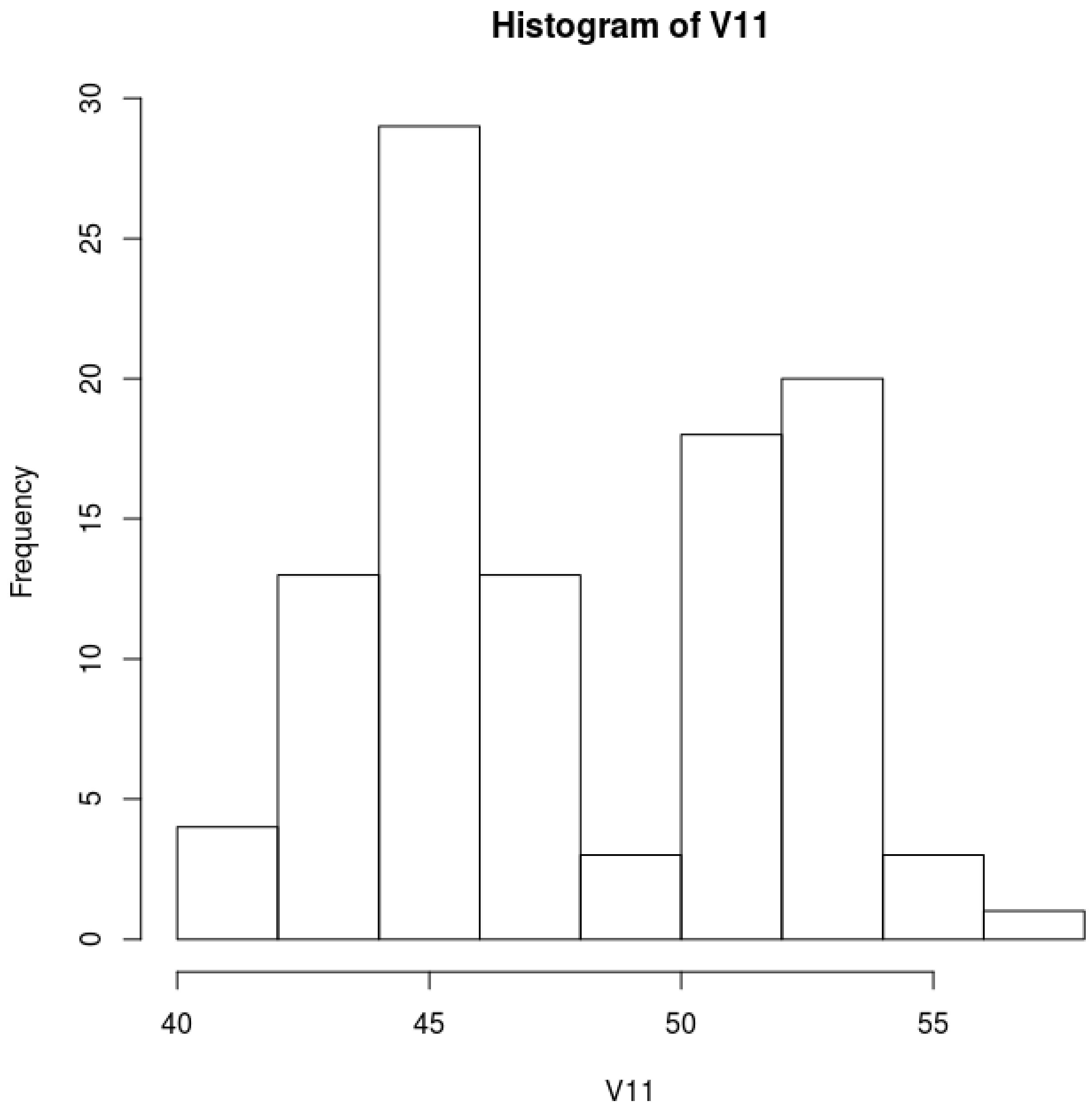
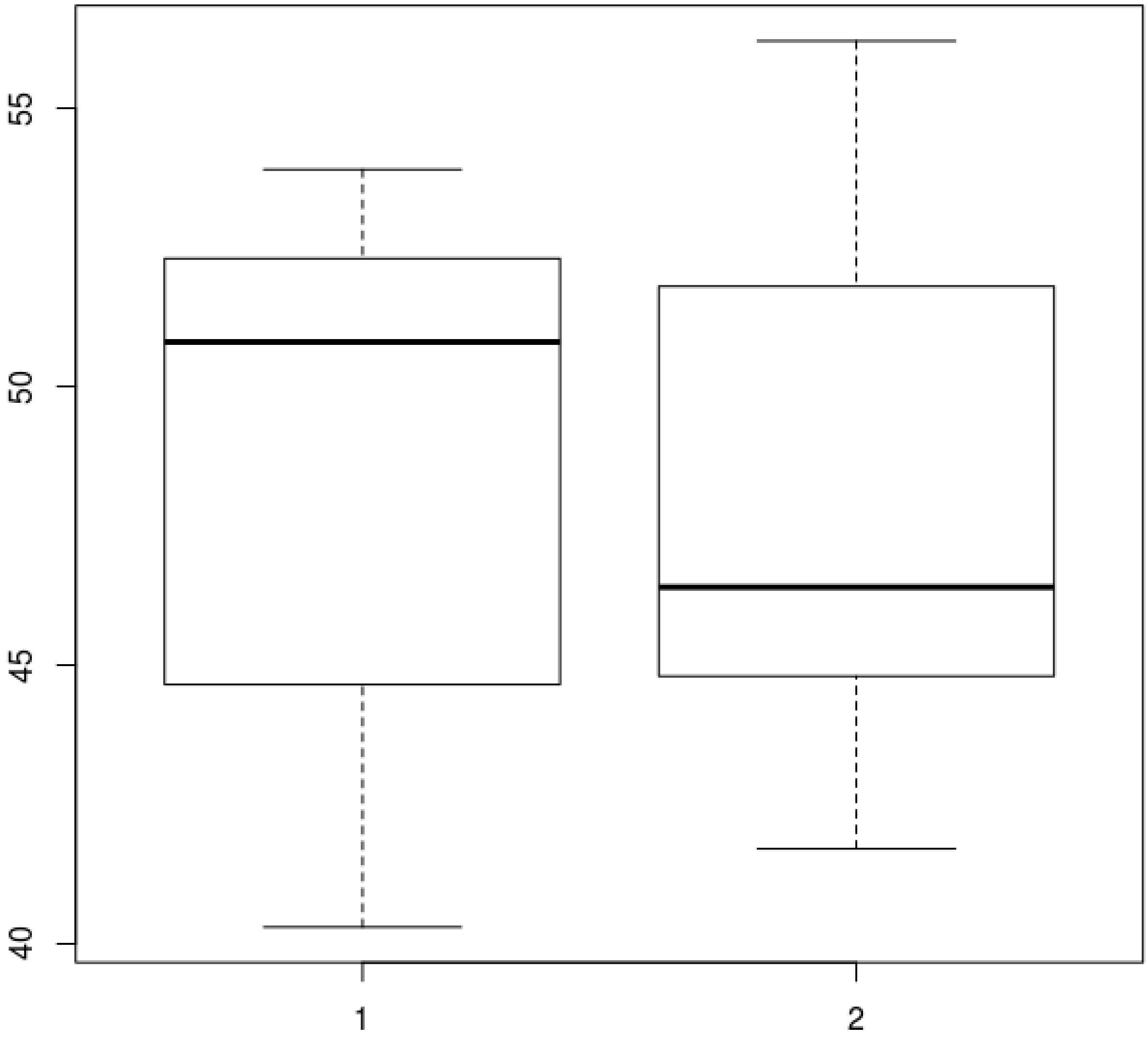
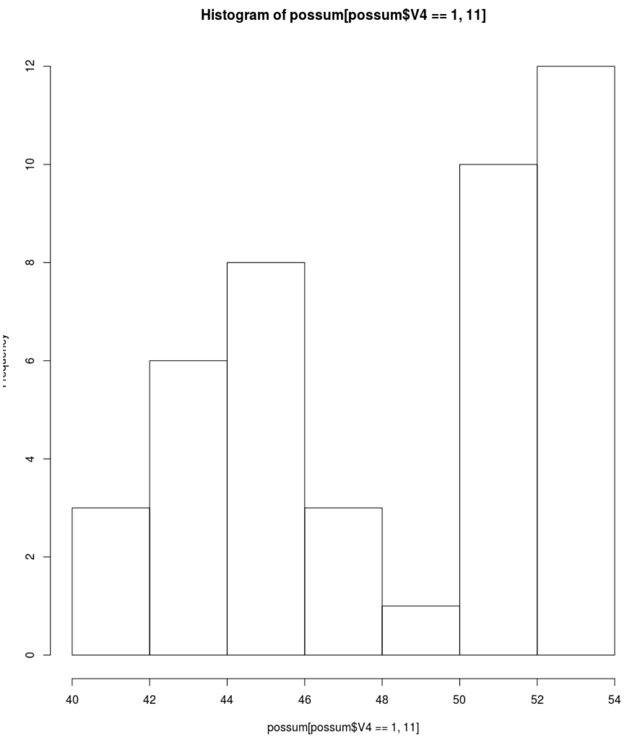
2.3

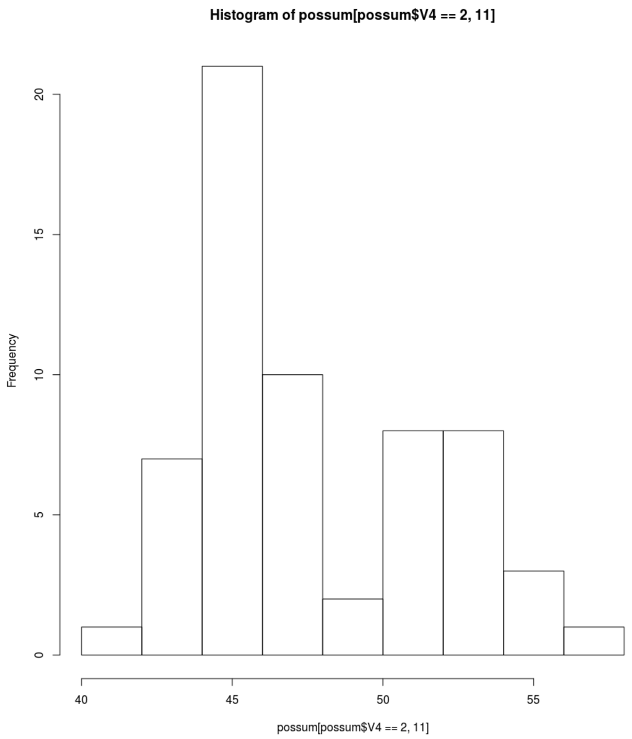
```
> possum <- read.csv("possum.txt", sep=",", header=FALSE)
> head(possum)
  V1 V2 V3 V4 V5   V6   V7   V8   V9  V10  V11  V12  V13 V14
1  1  1  1  2  8 94.1 60.4 89.0 36.0 74.5 54.5 15.2 28.0  36
2  2  1  1  1  6 92.5 57.6 91.5 36.5 72.5 51.2 16.0 28.5  33
3  3  1  1  1  6 94.0 60.0 95.5 39.0 75.4 51.9 15.5 30.0  34
4  4  1  1  1  6 93.2 57.1 92.0 38.0 76.1 52.2 15.2 28.0  34
5  5  1  1  1  2 91.5 56.3 85.5 36.0 71.0 53.2 15.1 28.5  33
6  6  1  1  1  1 93.1 54.8 90.5 35.5 73.2 53.6 14.2 30.0  32
> with(possum, hist(V11)) #earconch is column 11
> with(possum, boxplot(V11~V4)) #sex is column 4
...
> par(mfrow=c(1,2)) #2 histograms
> hist(possum[possum$V4==1,11])
> hist(possum[possum$V4==2,11])
```


Histogram of V11
Frequency
0
5
10
15
20
25
30
40
45
50
55
V11



The measurement distributions have a similar range (with sex 2 having more extreme high values), but with significantly shifted peaks. Sex 1 has its median quite close to the 75th percentile, whereas sex 2 has its peak very close to the 25th percentile. The histogram for 1 would have a tail at the low end, with a peak around 50, and a sharp drop off. The histogram for sex 2 would be similar, but mirrored about x = ~47.



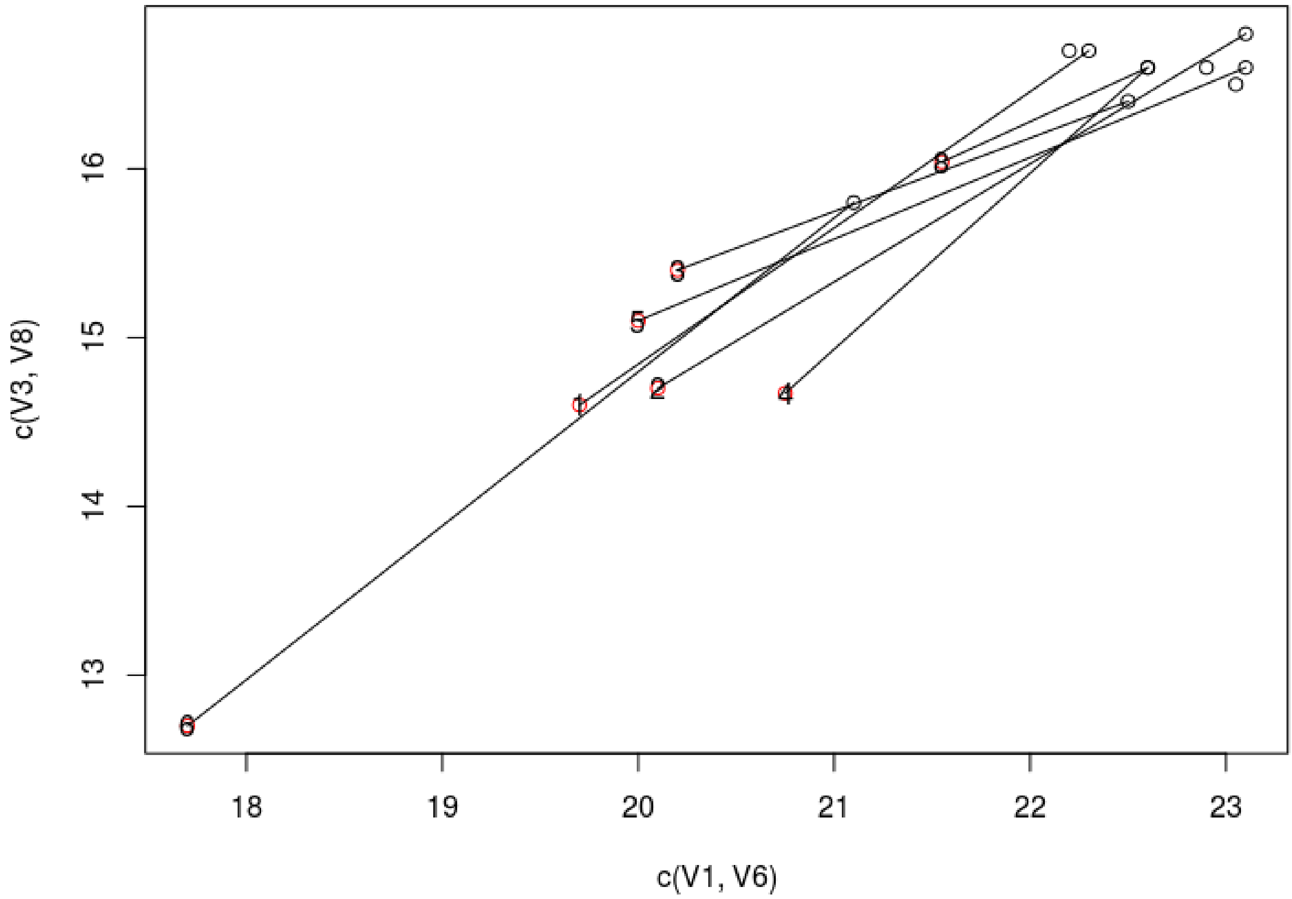


Hmm... I didn't quite guess right. I didn't expect there to be bimodal distributions in the separation by sex based on the box plots. I'm not sure I understand - I would expect that if there were significant numbers of low values for sex 1, then its median would be closer to halfway between the 25th and 75th percentiles. I guess now that I think about it, you wouldn't be able to distinguish the low end distribution accurately just from the box plot.

2.5

File format here.

```
> cuckoo <- read.csv("cuckoohosts.txt",sep = ",", header = FALSE)
> head(cuckoo)
    V1   V2   V3   V4 V5    V6    V7    V8    V9 V10 V11 V12
1 22.3 0.89 16.7 0.38 45 19.70  1.25 14.60  0.56  74  56   6
2 23.1 1.01 16.8 0.52 14 20.10  0.81 14.70 14.70  26   1  19
3 22.5 0.66 16.4 0.53 16 20.20  0.86 15.40 15.40  57   7  11
4 22.6 0.90 16.6 0.45 26 20.75  1.44 14.67  0.37  16  26   3
5 23.1 0.85 16.6 0.44 15 20.00  0.70 15.10  0.48  27  11   4
6 21.1 0.76 15.8 0.30 15 17.70 17.70 12.70  0.37  NA   0  17
> with(cuckoo, plot(c(V1,V6),c(V3, V8),col=c(rep(1,10),rep(2,10))))
> for(i in 1:10)
+   with(cuckoo, lines(c(V1[i],V6[i]),c(V3[i], V8[i])))
> with(cuckoo, text(V6, V8, rownames(cuckoo)))
```



A long line implies that the cuckoo eggs in that particular nest were very different (length and/or breadth-wise) compared to the host eggs. Short lines indicate cuckoo eggs that are quite similar (on average) to the host bird's eggs.

2.10

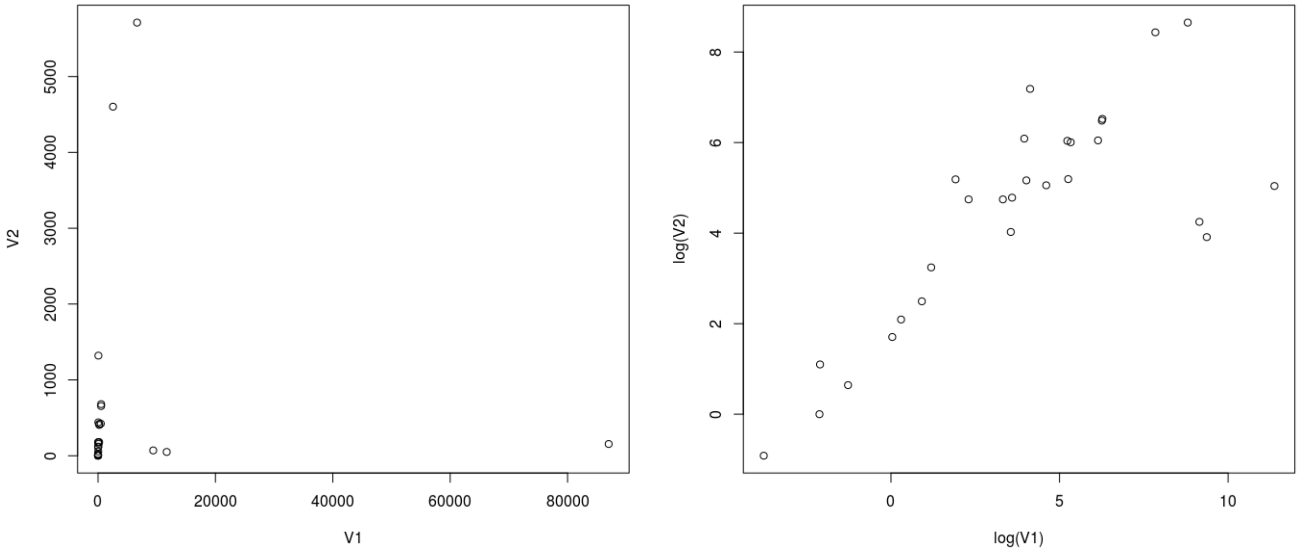
I believe this dataset is described here.

```
> animals <- read.csv("Animals.txt",sep = ",", header = FALSE)
> head(animals)
        V1    V2
1     1.35   8.1
2   465.00 423.0
3    36.33 119.5
4    27.66 115.0
5     1.04   5.5
6 11700.00  50.0
> with(animals, cor(V2, V1))
[1] -0.005341163
> with(animals, cor(log(V2), log(V1)))
[1] 0.7794935
> with(animals, cor(log(V2), log(V1), method="spearman"))
[1] 0.7162994
```

```
> par(mfrow=c(1,2))
> with(animals, plot(V1,V2))
> with(animals, plot(log(V1),log(V2)))
```

From the documentation:

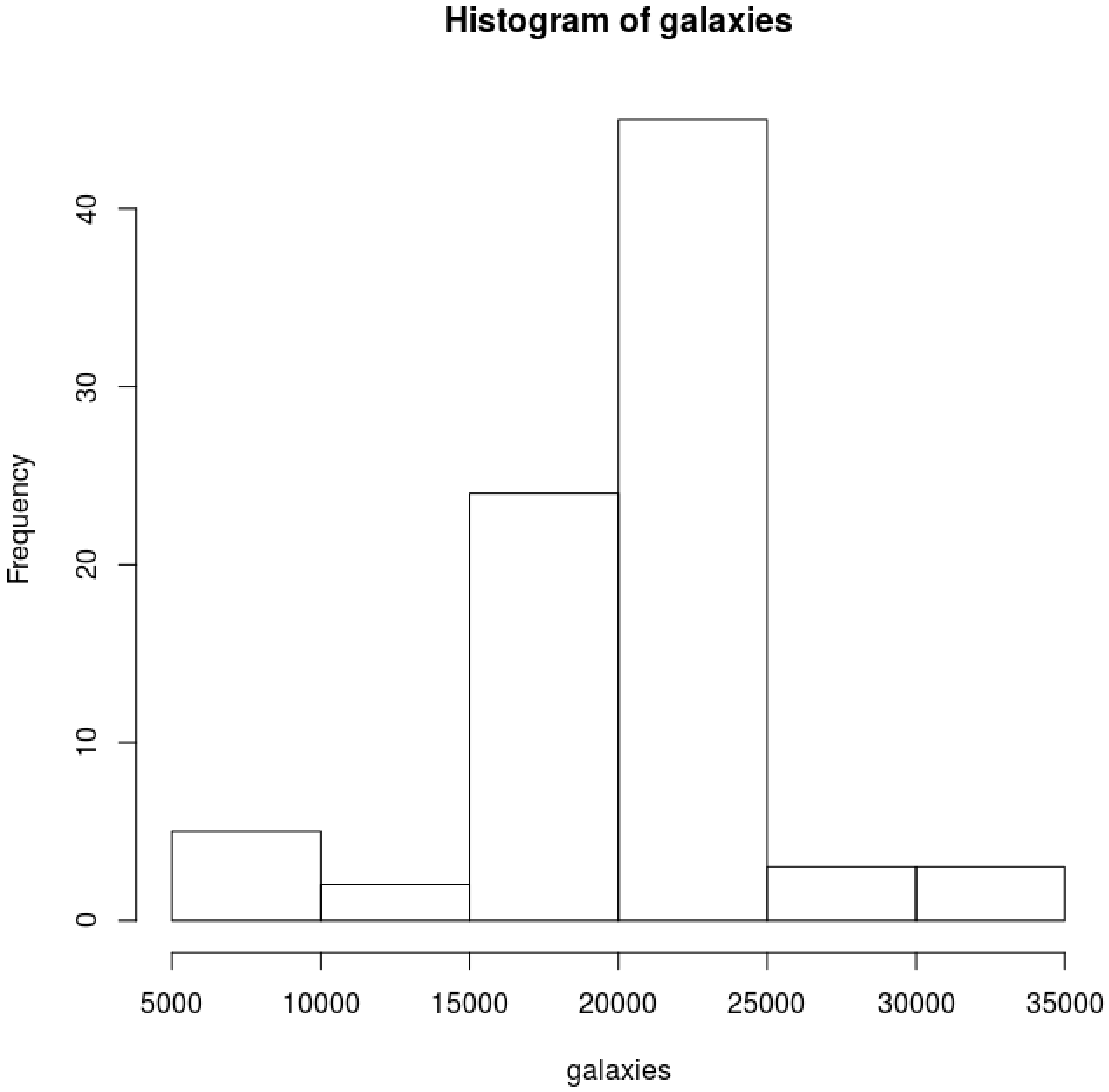
> ‘var’, ‘cov’ and ‘cor’ compute the variance of ‘x’ and the covariance or correlation of ‘x’ and ‘y’ if these are vectors. If ‘x’ and ‘y’ are matrices then the covariances (or correlations) between the columns of ‘x’ and the columns of ‘y’ are computed.
>
> ‘cov2cor’ scales a covariance matrix into the corresponding correlation matrix *efficiently*.
>
> …
>
> For ‘cor()’, if ‘method’ is ‘"kendall"’ or ‘"spearman"’, Kendall's tau or Spearman's rho statistic is used to estimate a rank-based measure of association. These are more robust and have been recommended if the data do not necessarily come from a bivariate normal distribution. For ‘cov()’, a non-Pearson method is unusual but available for the sake of completeness. Note that ‘"spearman"’ basically computes ‘cor(R(x), R(y))’ (or ‘cov(., .)’) where ‘R(u) := rank(u, na.last = "keep")’. In the case of missing values, the ranks are calculated depending on the value of ‘use’, either based on complete observations, or based on pairwise completeness with reranking for each pair.

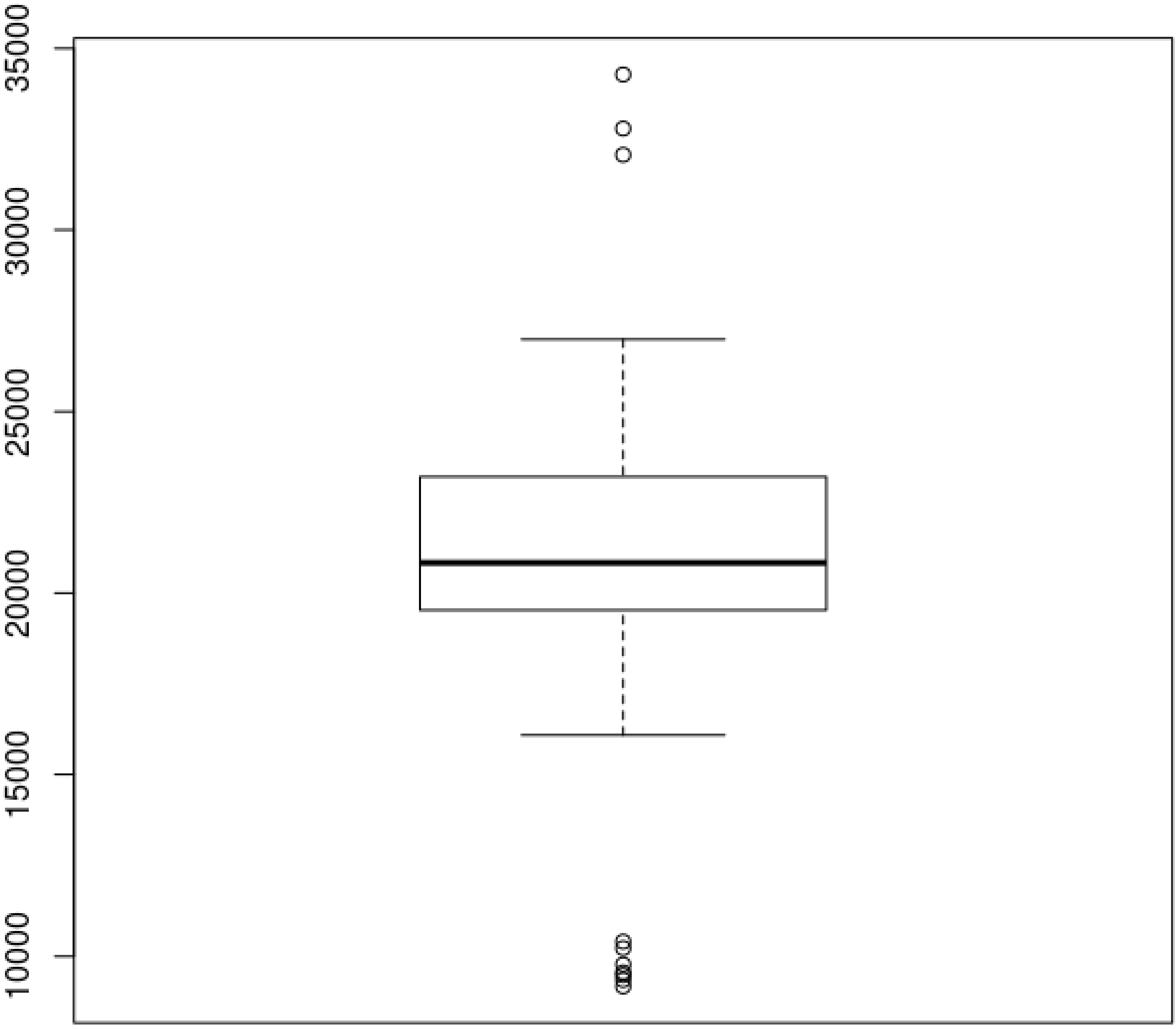


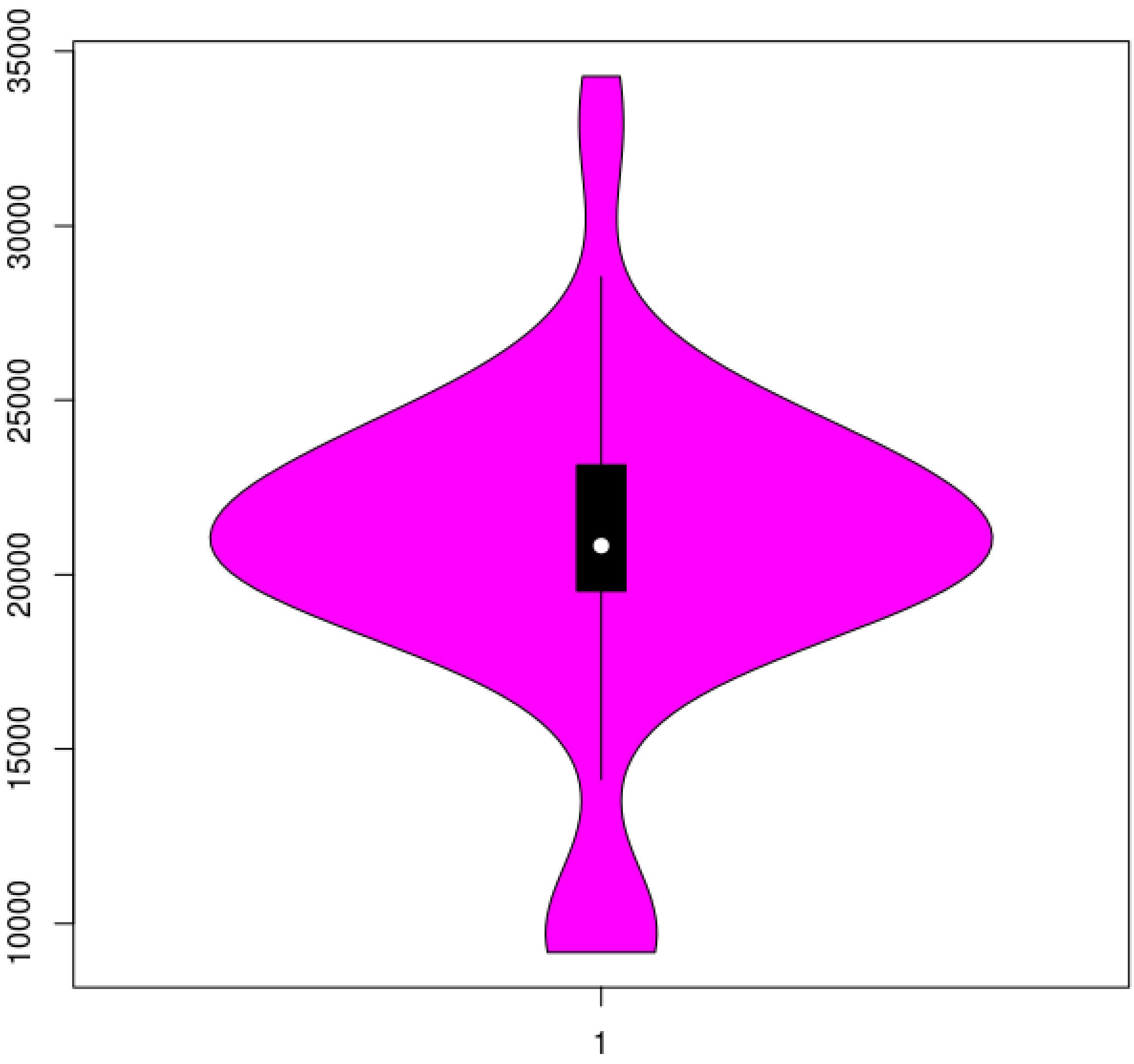
A Bivariate Normal distribution is just something that is normal in 2 dimensions. This data certainly doesn't look normal to me, so I would guess that the Spearman correlation of the log data is the most appropriate here.

2.13

```
> library(MASS)
> library(vioplot)
> head(galaxies)
[1]  9172  9350  9483  9558  9775 10227
> hist(galaxies)
> boxplot(galaxies)
> vioplot(galaxies)
```


Histogram of galaxies
Frequency
0
10
20
30
40
5000
10000
15000
20000
25000
30000
35000
galaxies


35000
30000
25000
20000
15000
10000



The distribution does not look skewed to me. It seems quite clustered around ~22,000. There is something interesting going on around 10,000 - a lot of low end "outliers". This could perhaps be a 2nd population that hasn't been sampled well enough to see smaller distribution below 10,000 (and in fact could b observation bias if it's more difficult to see lower speed galaxies).

Preliminary Exploratory Data Analysis