

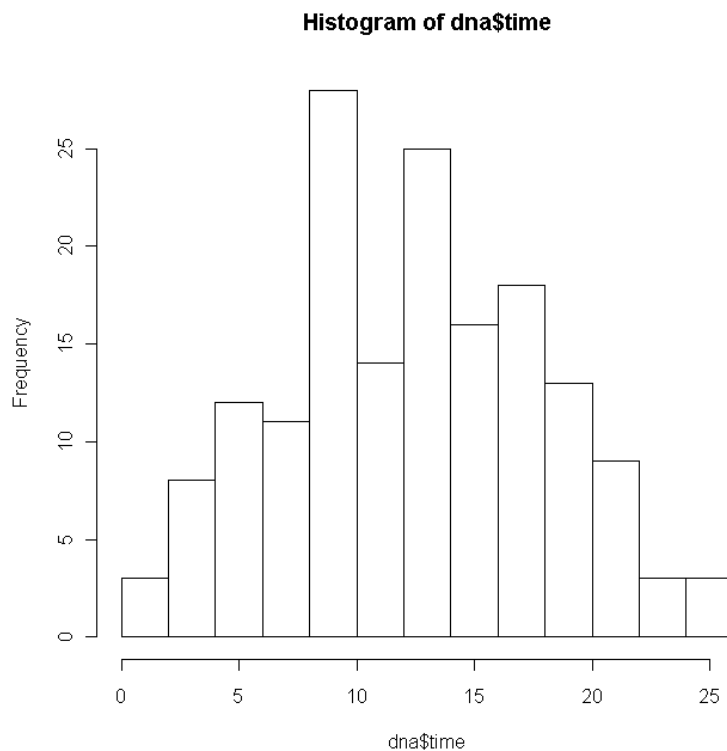
The following reads the data from the webpage. One of the variables is called time.

```
dna <- read.table("http://www.fiu.edu/~dwright/steps/dna.dat", header=TRUE)
```

To make the basic histogram, do (we could attach the data, but for these examples we will not):

```
hist(dna$time)
```

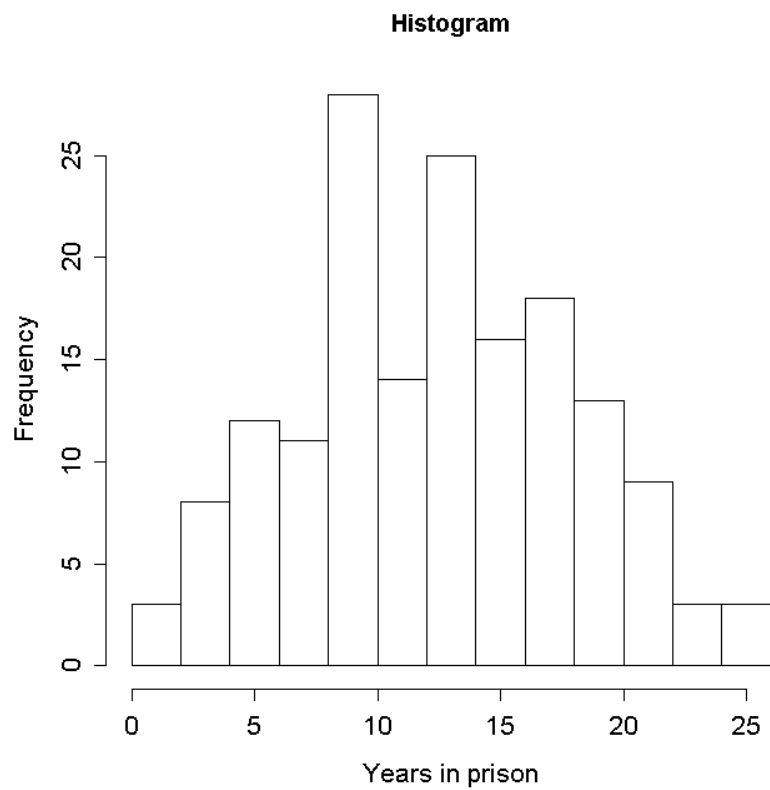
and you get:



You can change the labels and character sizes with the following command:

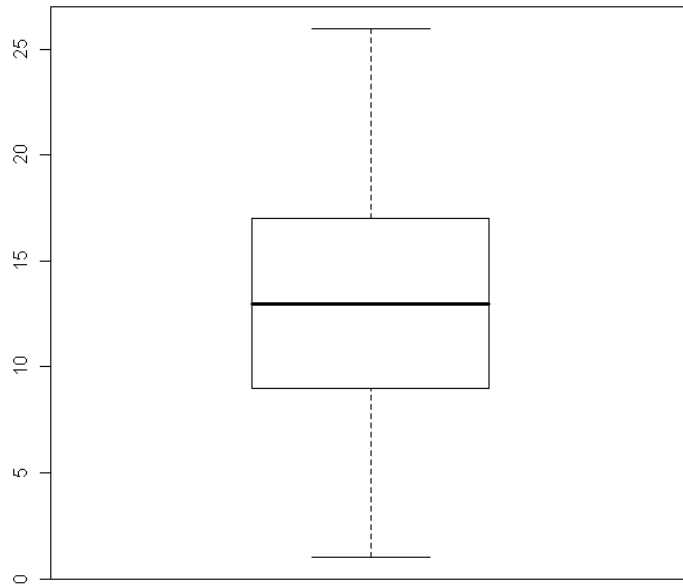
```
hist(dna$time,xlab="Years in prison", main="Histogram", cex.axis=1.3,  
cex.lab=1.3)
```

You get:



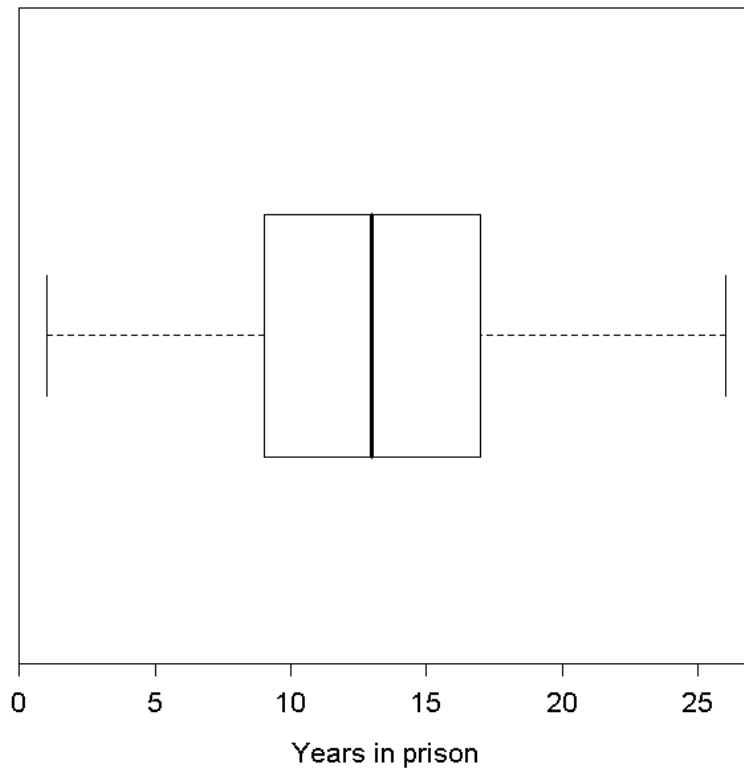
Similarly, the default boxplot is simple to do:

```
boxplot(dna$time)
```



but more things can be done like:

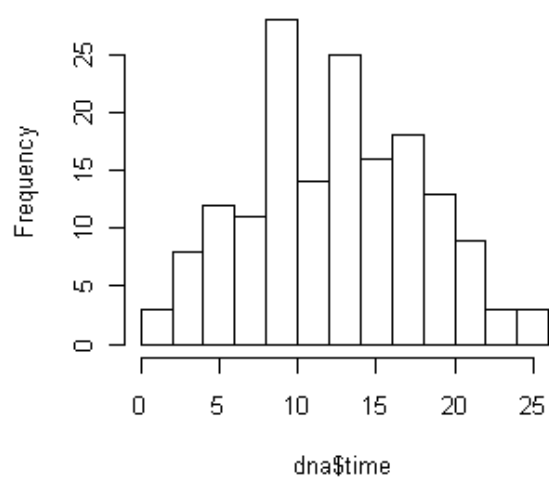
```
boxplot(dna$time, horizontal=TRUE, cex.lab=1.3, xlab="Years in prison",  
cex.axis=1.3)
```



If you want to produce a plot with all four of these graphs you can use the **par** command:

```
par(mfrow=c(2,2))
hist(dna$time)
hist(dna$time,xlab="Years in prison", main="Histogram", cex.axis=1.3,
     cex.lab=1.3)
boxplot(dna$time)
boxplot(dna$time,horizontal=TRUE,cex.lab=1.3,xlab="Years in prison",
       cex.axis=1.3)
par(mfrow=c(1,1))
```

**Histogram of dna\$time**



**Histogram**

