

Making plots in R [things I wish someone told me when I started grad school]

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In honor of “Talk Like a Pirate Day...”

What's a pirates favorite computer language?

In honor of “Talk Like a Pirate Day...”

Rrrrrr!

In honor of “Talk Like a Pirate Day...”

But, why?

In honor of “Talk Like a Pirate Day...”

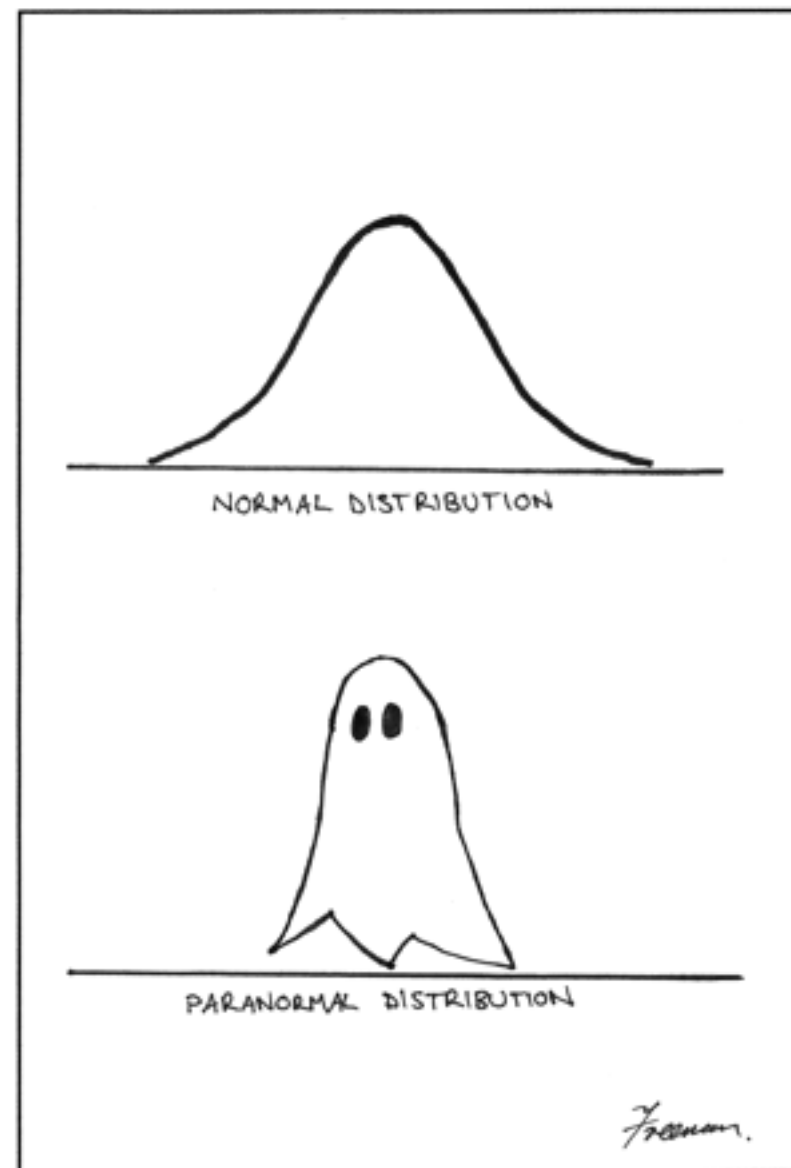
Because they get lost when they go to C

Learning objectives

- Know how to make simple plots:
 - Scatterplot, histogram, density plot, bar plot
- Read “large” datasets into R
- Perform manipulations of large datasets
- Calculate some statistics in R
- Start to become familiar with simulation
- Begin to appreciate and enjoy Kirk’s corny humor

R can simulate data from a probability distribution

Let's look at the normal distribution:



Simulating data from a normal distribution

```
> #first, draw 1000 random values from a standard normal distribution (SD=1):  
> s1<-rnorm(1000,mean=0,sd=1)  
>  
> #now do 1000 drawn from a normal distribution with SD=3.  
> s3<-rnorm(1000,mean=0,sd=3)  
>  
> head(s1)  
[1]  0.26951848 -2.43530911  1.15968499  0.09647798 -0.74425935  0.40504897  
> head(s3)  
[1]  3.6718664  4.8193934 -0.6078601  2.1520862  2.9089759 -3.6002362
```

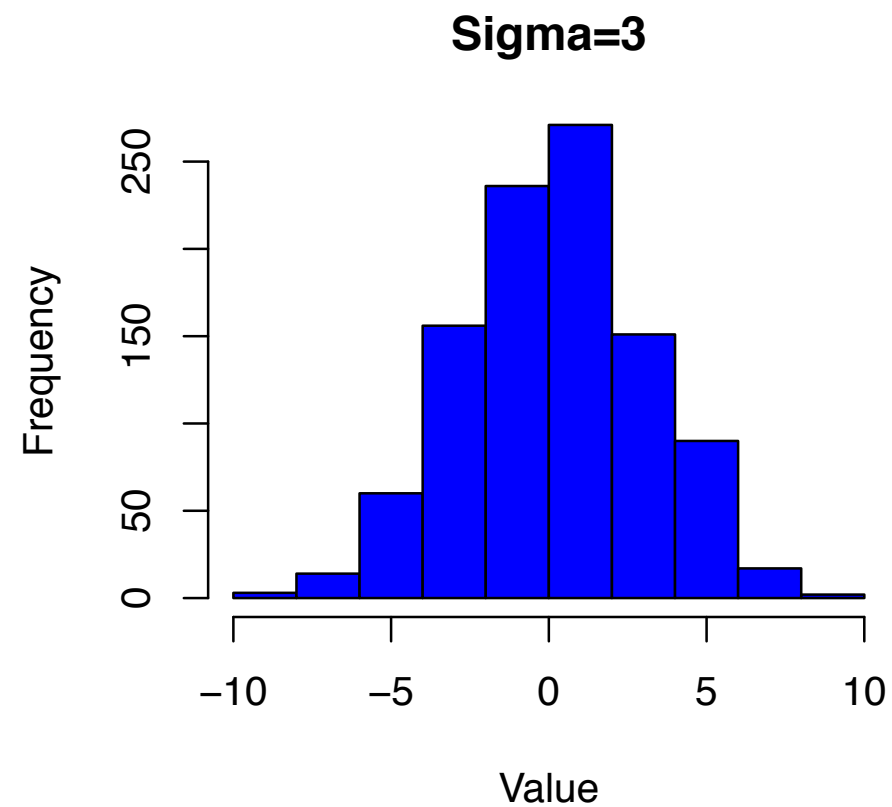
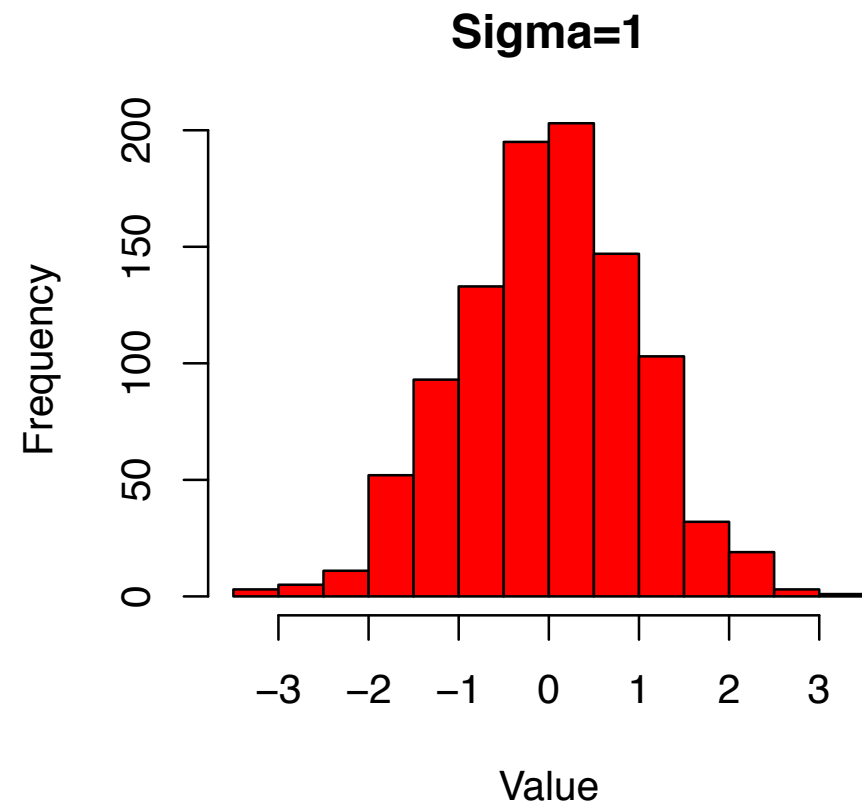

Basic histogram

```
> #plot histograms of both on same panel and save to a file:
> pdf(file="Normal_hist.pdf", width=4,height=7);
> #open the file
>
> par(mfrow=c(2,1), mar=c(4, 4, 3, 2)) #sets plotting area and margins
>
> hist(s1,col=2,xlab="Value",main="Sigma=1") #make first hist
>
> hist(s3,col=4,xlab="Value",main="Sigma=3") #make second hist
>
> dev.off() #shuts off current output device
```

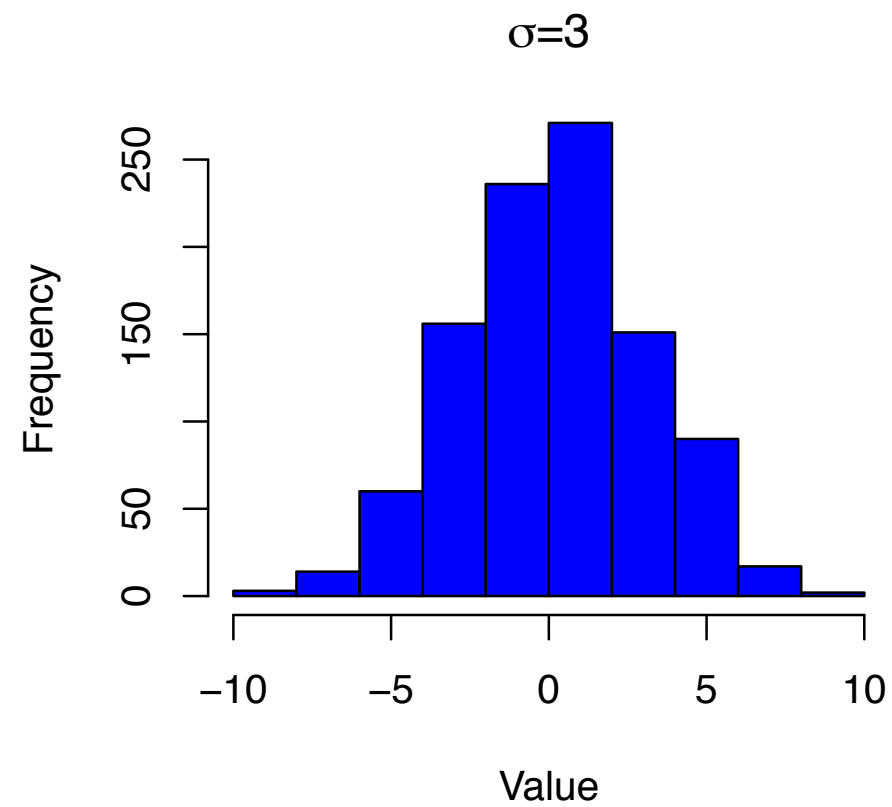
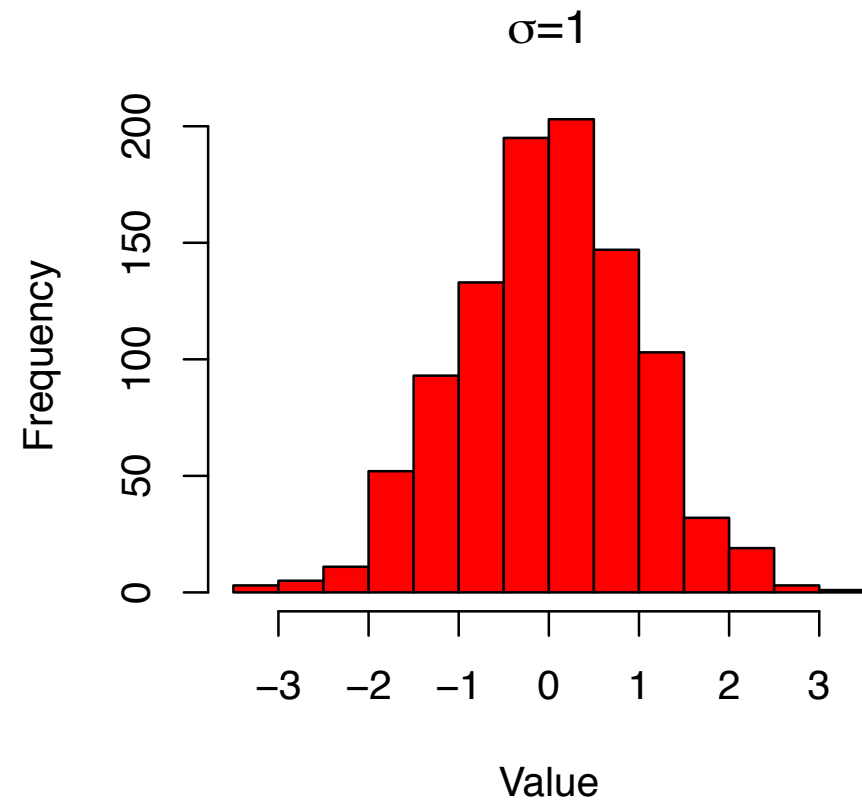
quartz

2

Basic histogram



Getting fancier...



How did I do that?

```
>> #plot histograms of both on same panel and save to a file:
> pdf(file="Normal_hist.fancy.pdf", width=4,height=7);
> #open the file
>
> par(mfrow=c(2,1), mar=c(4, 4, 3, 2)) #sets plotting area and
margins
>
> hist(s1,col=2,xlab="Value",main=expression(paste(sigma,"=1")))
#make first hist
>
> hist(s3,col=4,xlab="Value",main=expression(paste(sigma,"=3")))
#make second hist
>
> dev.off() #shuts off current output device
```

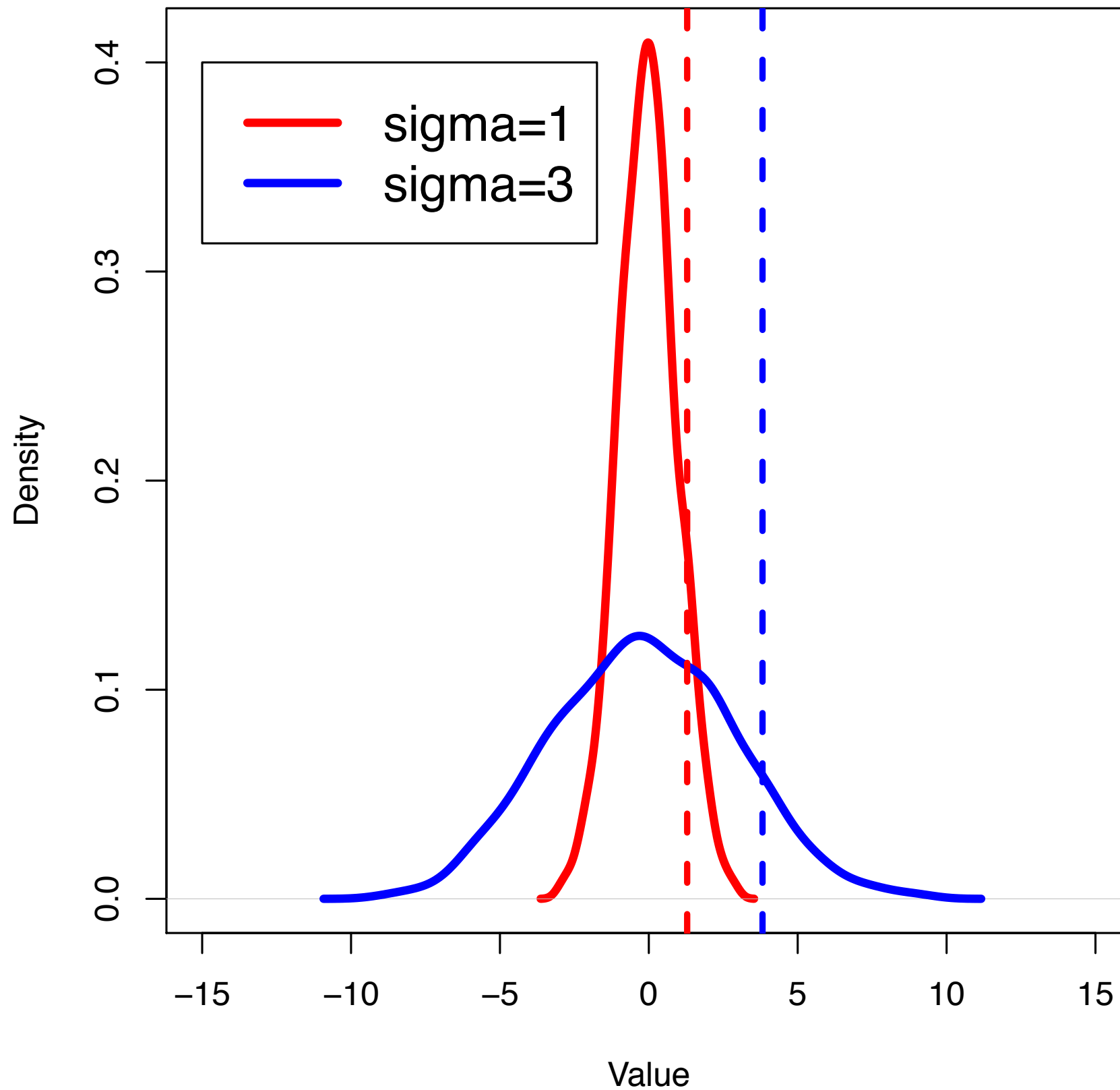
pdf

Smooth density plot

```
> #make smooth density plot:
>
> pdf(file="Normal_density.pdf", width=6,height=6); #open the file
>
> par(mfrow=c(1,1), mar=c(4, 4, 3, 2)) #sets plotting area and margins
>
> plot(density(s1),col=2,lwd=4,xlab="Value",xlim=c(-15,15),main="Normal
distribution")
>
> lines(density(s3),col=4,lwd=4) #add the SD=3 values
>
> legend(-15,0.4,c("sigma=1","sigma=3"),lwd=4,col=c(2,4),cex=1.5) #put a legend on
>
> #we can highlight the upper 10% of each distribution with a vertical line:
> abline(v=quantile(s1,0.9),lty=2,lwd=3,col=2) #puts a vertical line onto the plot
for s1
> abline(v=quantile(s3,0.9),lty=2,lwd=3,col=4) #puts a vertical line onto the plot
for s3
> dev.off()
quartz
2
```

Smooth density plot

Normal distribution



More on “quantile”

> #quantile take a vector of stuff, and returns the value q such that p% of your distribution is less than q.

>

> #for example, find the 75th percentile of the standard normal distribution:

> quantile(s1,0.75)

75%

0.5899364

>

> #quantile with just a vector gives some interesting stuff:

> quantile(s1)

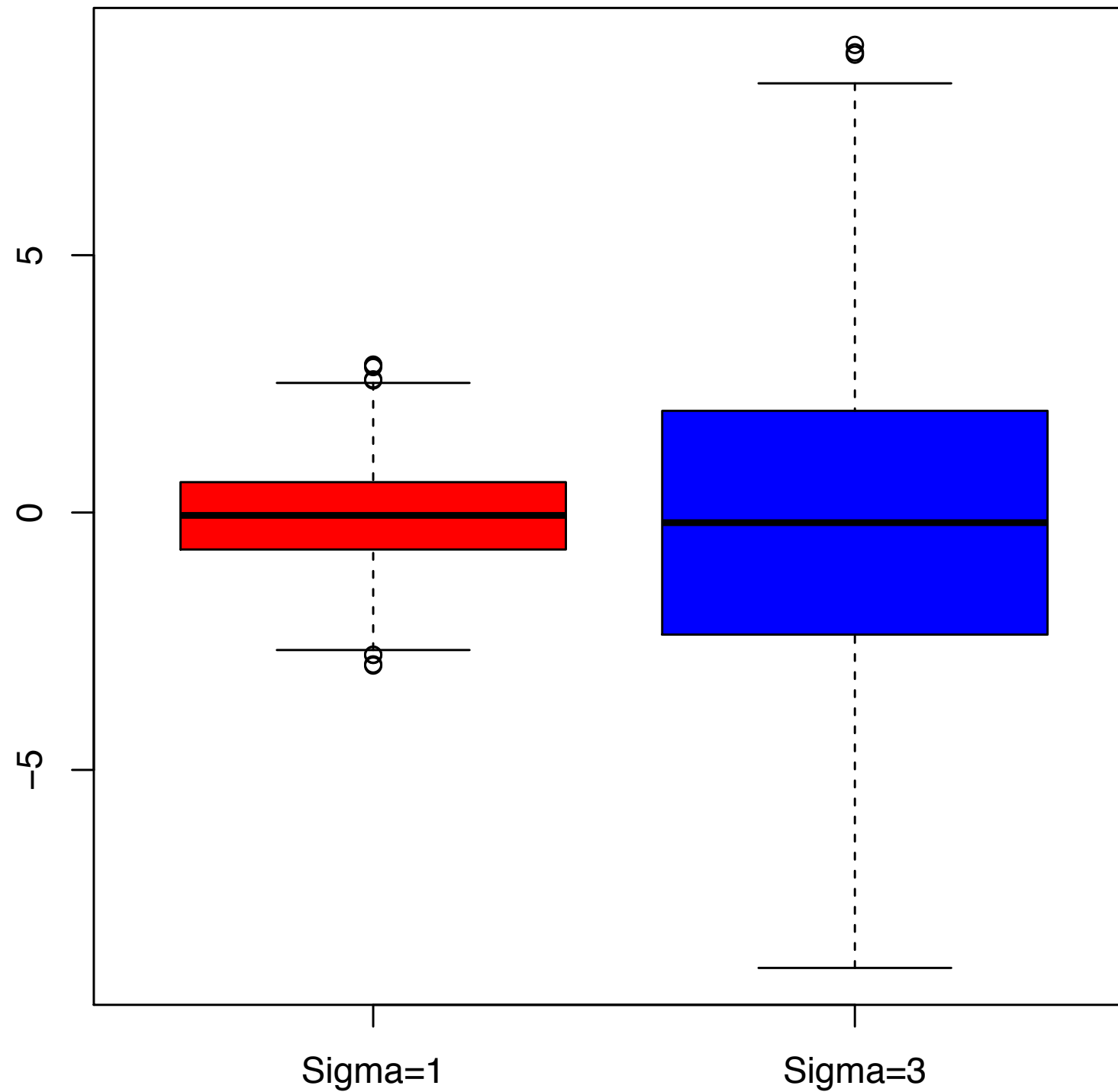
0%	25%	50%	75%	100%
-2.97189479	-0.71435745	-0.05515638	0.58993639	2.87407876

Boxplot

```
> #boxplot:
> pdf(file="Normal_boxplot.pdf", width=6,height=6); #open the file
>
> par(mfrow=c(1,1), mar=c(4, 4, 3, 2)) #sets plotting area and margins
>
> boxplot(cbind(s1,s3),names=c("Sigma=1","Sigma=3"),main="Draws from a
normal distribution",col=c(2,4))
>
> dev.off()
quartz
2
```


Boxplot

Draws from a normal distribution



Histogram with both sets of data on same axes? Can we do it? YES WE CAN!

> #Let's make a histogram of these values, but putting both on the same axes.

> #But, we need to have the same bin widths for both datasets:

>

> bins<-seq(-10,10,by=1)

> hist(s1,breaks=bins)\$breaks

```
[1] -10 -9 -8 -7 -6 -5 -4 -3 -2 -1 0 1 2
3  4  5  6  7  8  9 10
```

>

> hist(s3,breaks=bins)\$breaks

```
[1] -10 -9 -8 -7 -6 -5 -4 -3 -2 -1 0 1 2
3  4  5  6  7  8  9 10
```

>

> #This looks good

>

> counts_s1<-hist(s1,breaks=bins)\$counts

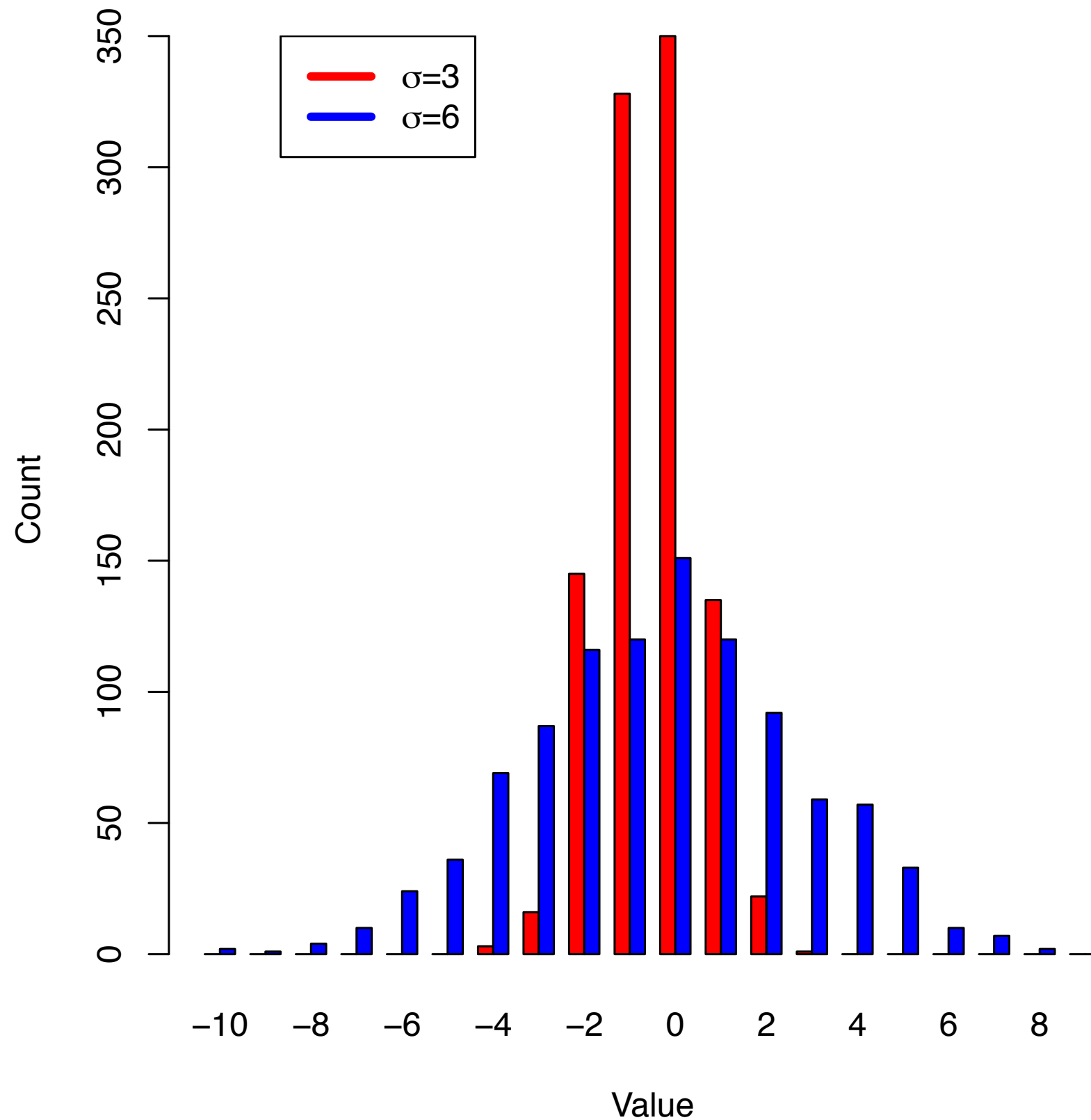
> counts_s3<-hist(s3,breaks=bins)\$counts

Histogram with both sets of data on same axes? Can we do it? YES WE CAN!

```
> #now make the plot:
> pdf(file="normal_barplot.pdf", width=6,height=6); #open the
file
>
> par(mfrow=c(1,1), mar=c(4, 4, 3, 2)) #sets plotting area and
margins
>
>
barplot(rbind(counts_s1,counts_s3),col=c(2,4),beside=T,names.arg=
seq(-10,9.5,by=1),xlab="Value",ylab="Count")
>
>
legend(6,350,c(expression(paste(sigma,"=3")),expression(paste(sig
ma,"=6"))),col=c(2,4),lwd=4)
>
> dev.off()
```

pdf

Histogram with both sets of data on same axes? Can we do it? YES WE CAN!



Finding extreme values

Say we want to find the % of values in a vector that are $>X$...

```
> > #We can find the % of values in s1 that are >3:
```

```
> mean(s1>3)
```

```
[1] 0.001
```

```
> #Only 1 of the 1000 values in s1 is >3
```

```
>
```

```
>
```

```
> mean(s3>3)
```

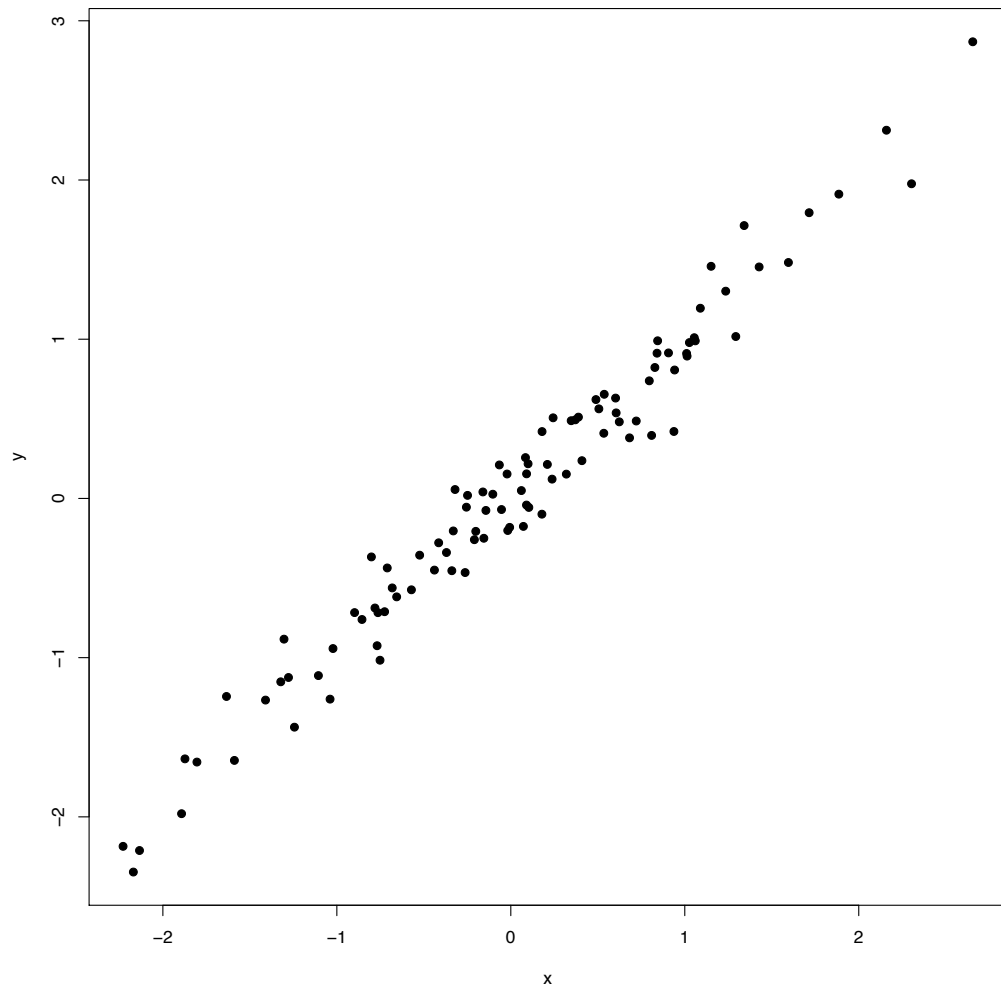
```
[1] 0.168
```

```
> #16.8% of values in s3 are >3
```

Scatterplot pitfalls

```
> #Simple scatterplot:
> pdf(file="/Users/kirk/Dropbox/Kirk_stuff/KEL_bootcamp/scatter_small.pdf",
width=10,height=10); #open the file
>
> par(mfrow=c(1,1), mar=c(4, 4, 3, 2)) #sets plotting area and margins
>
> x<-rnorm(100)
> y<-x+rnorm(100,sd=0.2)
>
> plot(x,y,pch=19)
>
> dev.off()
quartz
2
```

The most annoying thing in R...

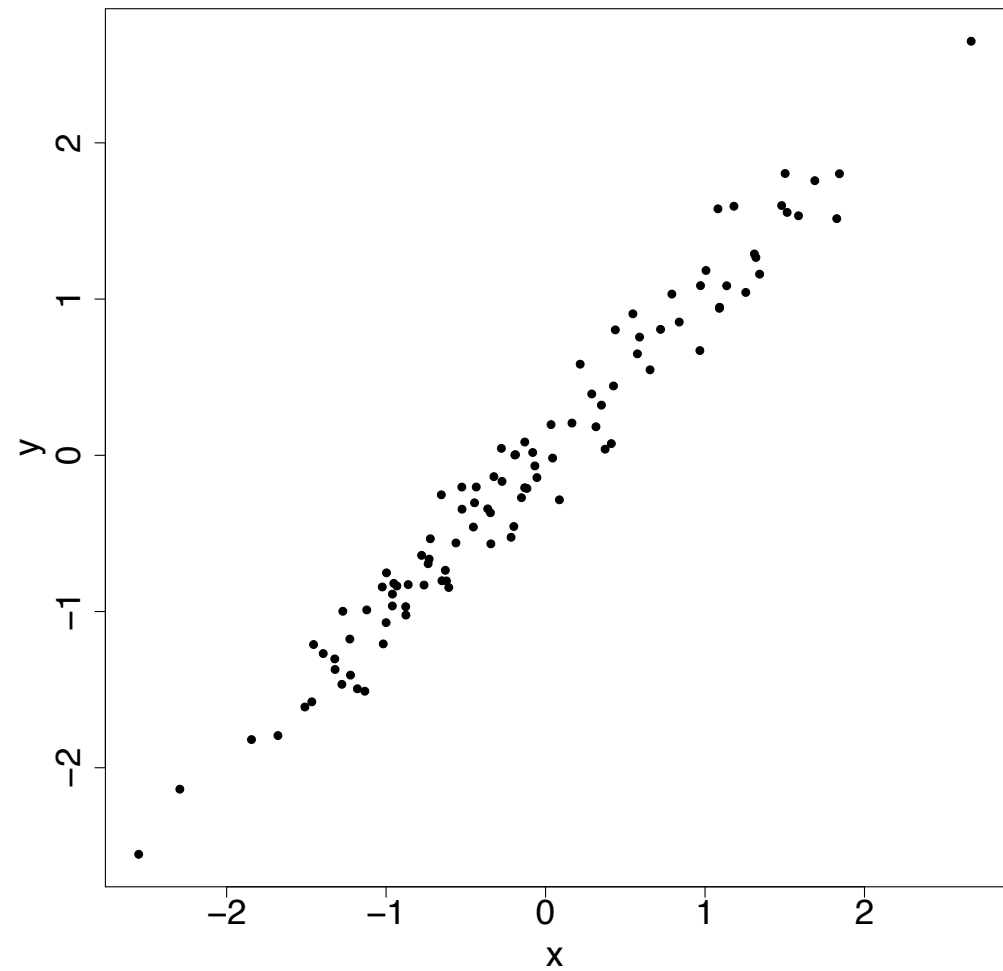
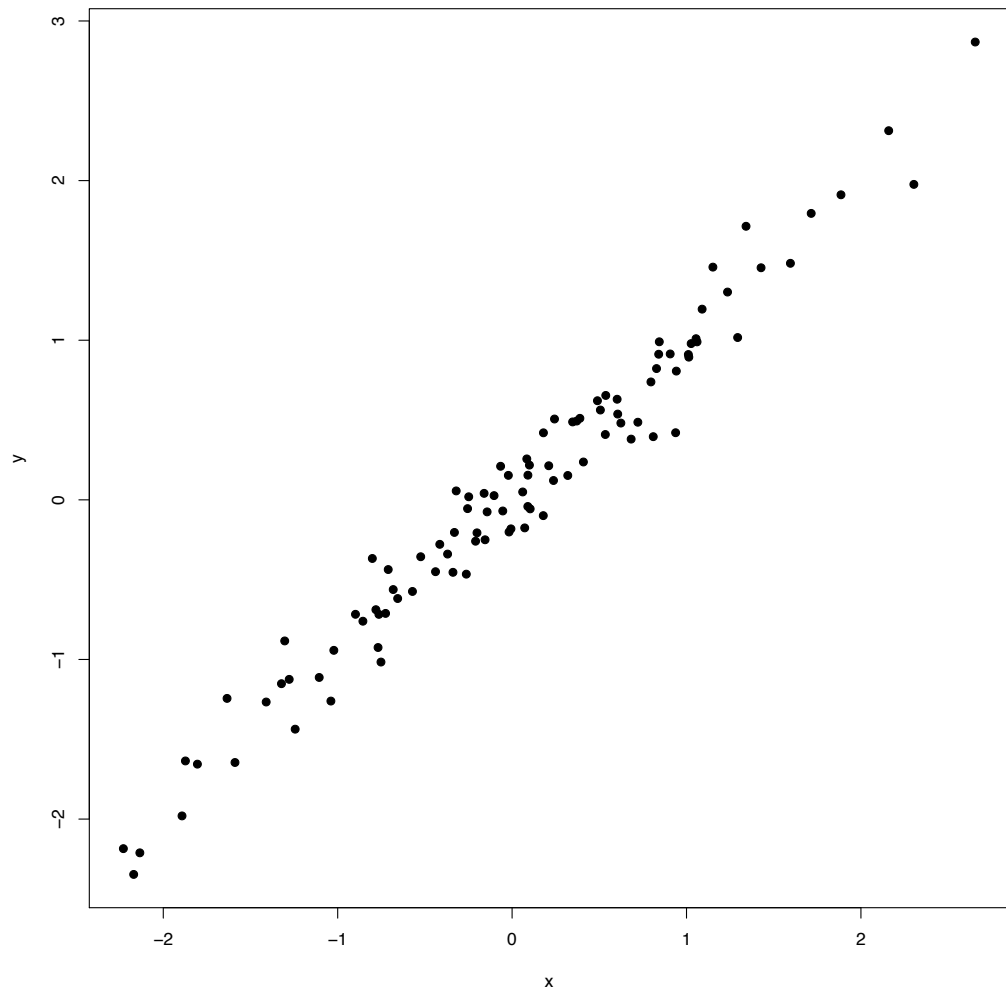


Huh?
What is plotted here?
My tired eyes can't read this....

One way to fix it

```
> #now, try again, make the labels bigger:
> #Simple scatterplot:
> pdf(file="/Users/kirk/Dropbox/Kirk_stuff/KEL_bootcamp/scatter_large.pdf",
width=10,height=10); #open the file
>
> par(mfrow=c(1,1), mar=c(5, 5, 3, 2)) #sets plotting area and margins
>
> x<-rnorm(100)
> y<-x+rnorm(100,sd=0.2)
>
> plot(x,y,pch=19,cex.lab=2,cex.axis=2)
>
> dev.off()
quartz
2
```


One way to fix it



Extended example

Part 1: Hardy-Weinberg in practice

- Read in genotype data from a file (4,014 SNPs in 60 individuals)
- Exploratory plot of heterozygosity vs. allele frequency.
 - Recall that the Hardy-Weinberg expected proportion of heterozygotes H as a function of allele frequency p is: $H = 2p(1 - p)$
- Formal test of Hardy-Weinberg proportions using a χ^2 -test for each SNP

Part 2: Finding a quantitative trait locus via association mapping

- Read in phenotype data from a file (fasting glucose in units of mmol/L)
- Test for each SNP whether genotype is correlated (“associated”) with phenotypic trait value using a linear model framework (and the `lm` function)
- Find which SNP has the association and visualize its effect in a boxplot

Data source

- 2.3 million SNPs genotyped on Hapmap CEU founders (60 individuals). Data downloaded in plink format from plink website.
- SNPs from chromosome 2 and LD pruning undertaken (`--indep-pairwise 50 5 0.2`) to make the data set smaller