

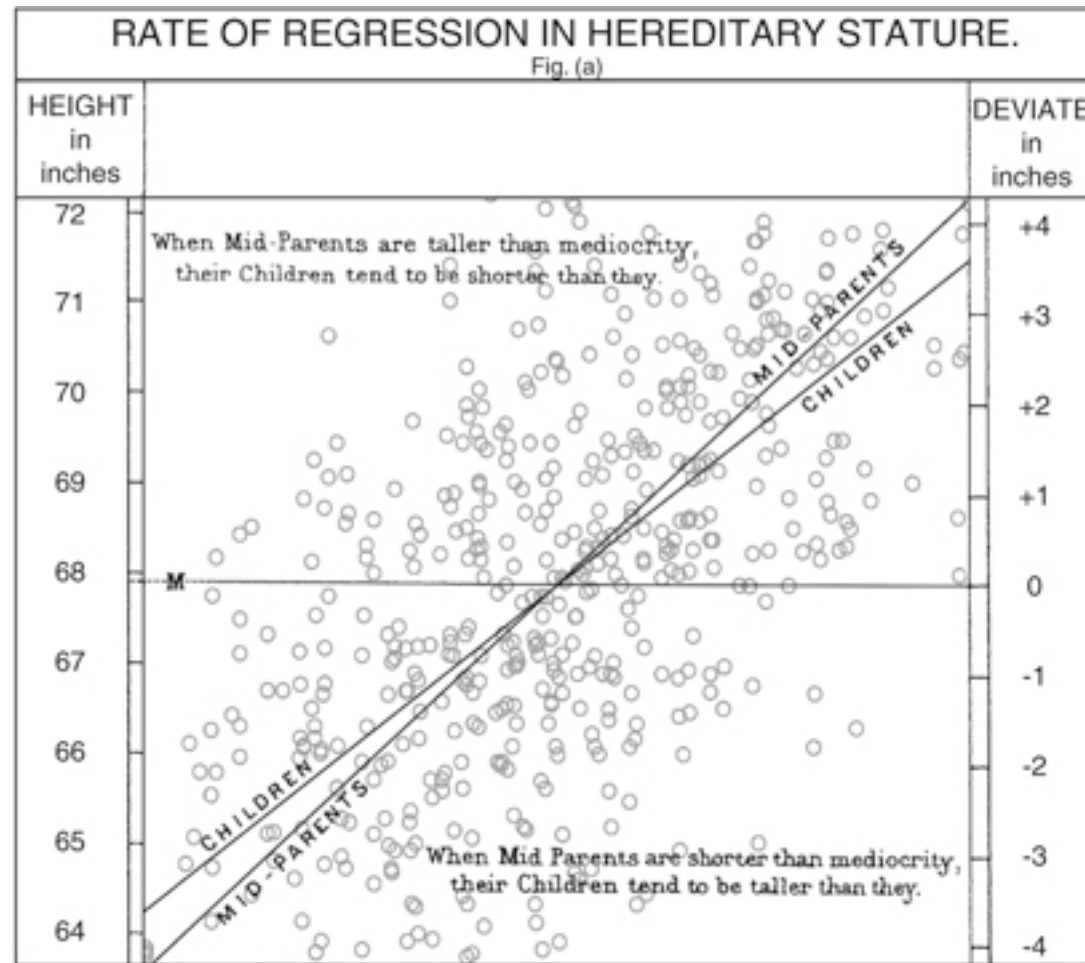
Basic least squares

Jeffrey Leek, Assistant Professor of Biostatistics
Johns Hopkins Bloomberg School of Public Health

Goals of statistical modeling

- Describe the distribution of variables
- Describe the relationship between variables
- Make inferences about distributions or relationships

Example: Average parent and child heights



<http://www.nature.com/ejhg/journal/v17/n8/full/ejhg20095a.html>

Still relevant

Article

European Journal of Human Genetics (2009) **17**, 1070–1075; doi:10.1038/ejhg.2009.5; published online 18 February 2009

Predicting human height by Victorian and genomic methods

Yurii S Aulchenko^{1,2,7}, Maksim V Struchalin^{1,3,7}, Nadezhda M Belonogova^{2,4}, Tatiana I Axenovich², Michael N Weedon⁵, Albert Hofman¹, Andre G Uitterlinden⁶, Manfred Kayser³, Ben A Oostra¹, Cornelia M van Duijn¹, A Cecile J W Janssens¹ and Pavel M Borodin^{2,4}

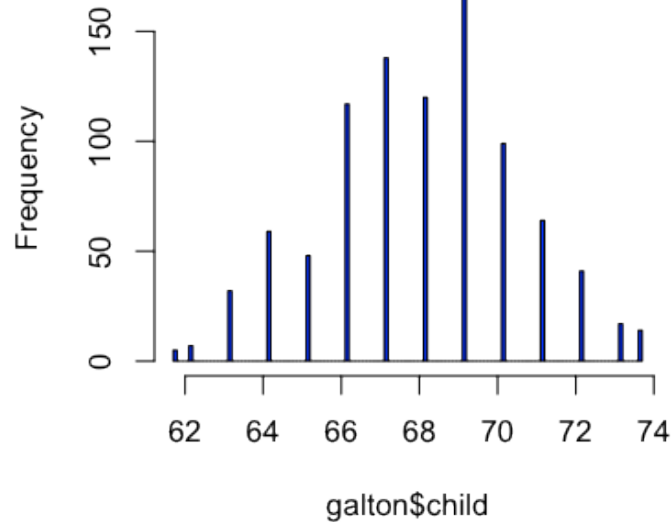
<http://www.nature.com/ejhg/journal/v17/n8/full/ejhg20095a.html>

[Predicting height: the Victorian approach beats modern genomics](#)

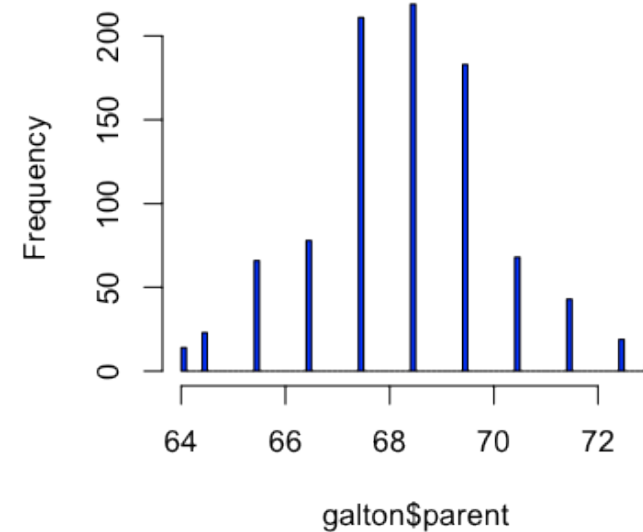
Load Galton Data

```
library(UsingR); data(galton)
par(mfrow=c(1,2))
hist(galton$child,col="blue",breaks=100)
hist(galton$parent,col="blue",breaks=100)
```

Histogram of galton\$child

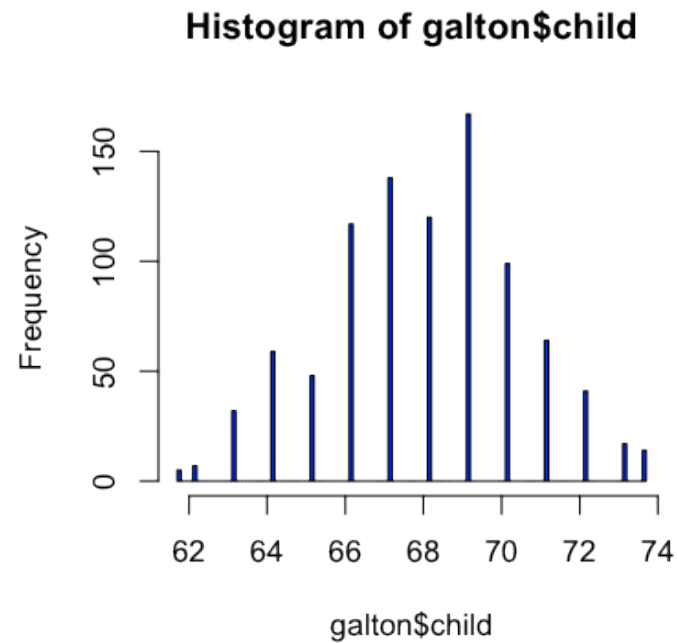


Histogram of galton\$parent



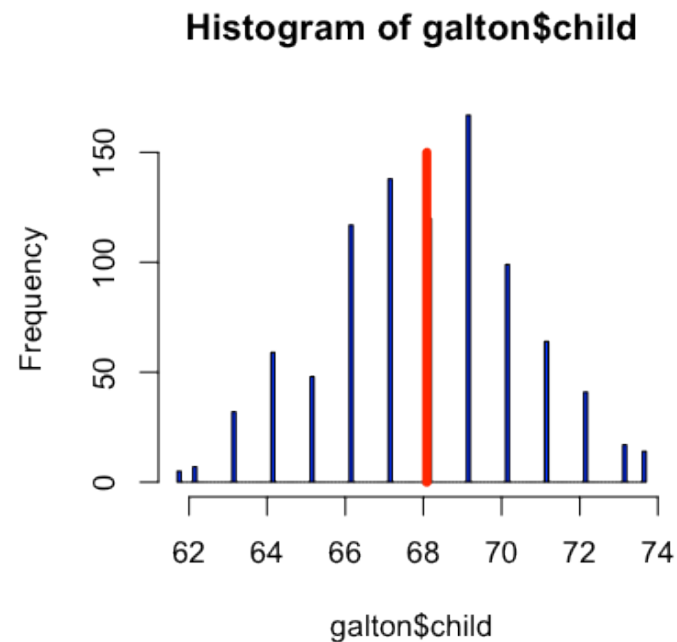
The distribution of child heights

```
hist(galton$child,col="blue",breaks=100)
```



Only know the child - average height

```
hist(galton$child,col="blue",breaks=100)  
meanChild <- mean(galton$child)  
lines(rep(meanChild,100),seq(0,150,length=100),col="red",lwd=5)
```



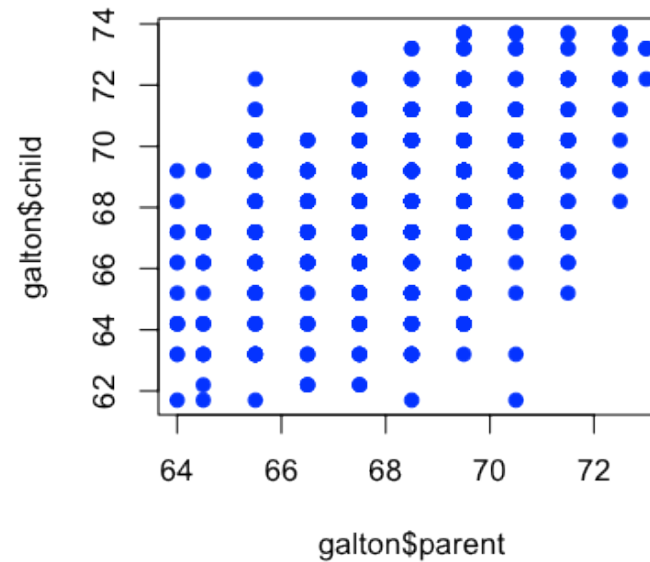
Only know the child - why average?

If C_i is the height of child i then the average is the value of μ that minimizes:

$$\sum_{i=1}^{928} (C_i - \mu)^2$$

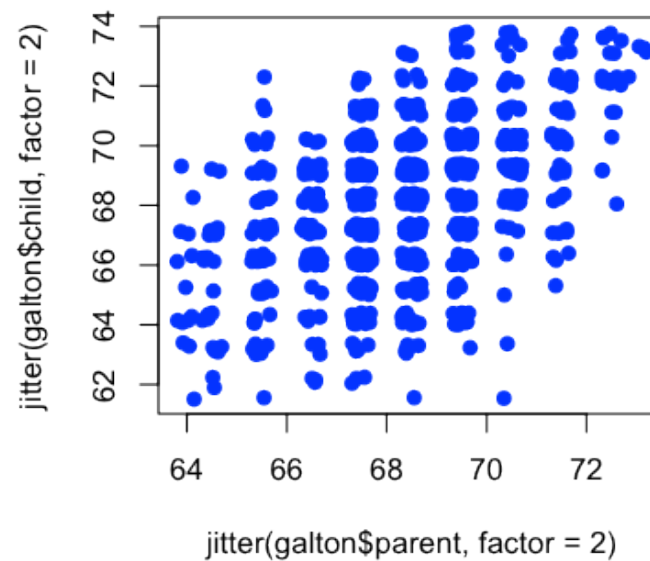
What if we plot child versus average parent

```
plot(galton$parent,galton$child,pch=19,col="blue")
```



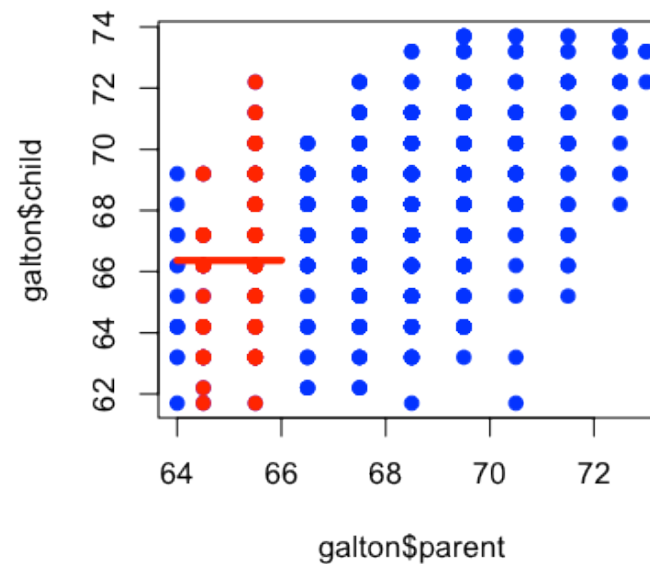
Jittered plot

```
set.seed(1234)  
plot(jitter(galton$parent, factor=2), jitter(galton$child, factor=2), pch=19, col="blue")
```



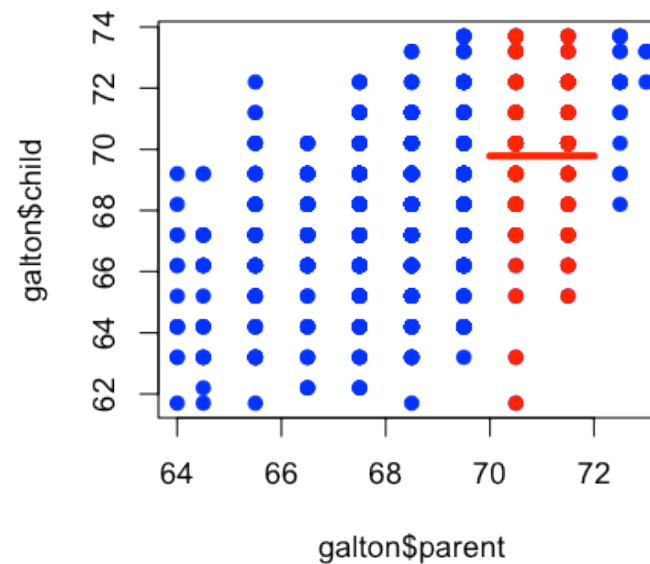
Average parent = 65 inches tall

```
plot(galton$parent,galton$child,pch=19,col="blue")  
near65 <- galton[abs(galton$parent - 65)<1, ]  
points(near65$parent,near65$child,pch=19,col="red")  
lines(seq(64,66,length=100),rep(mean(near65$child),100),col="red",lwd=4)
```



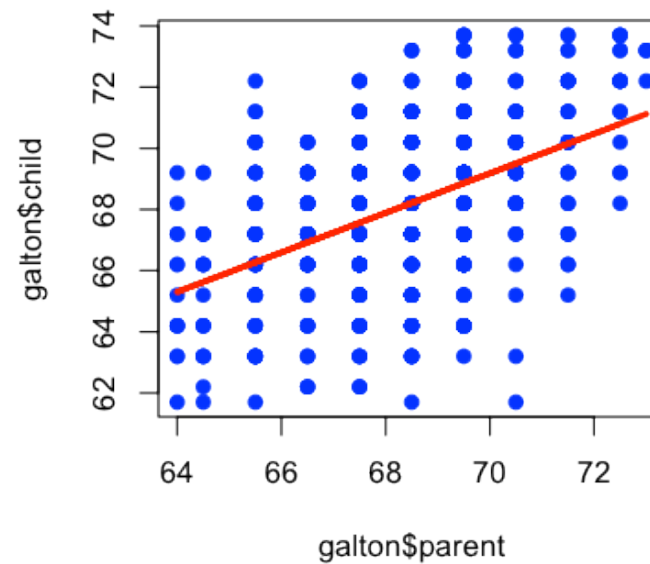
Average parent = 71 inches tall

```
plot(galton$parent,galton$child,pch=19,col="blue")  
near71 <- galton[abs(galton$parent - 71)<1, ]  
points(near71$parent,near71$child,pch=19,col="red")  
lines(seq(70,72,length=100),rep(mean(near71$child),100),col="red",lwd=4)
```



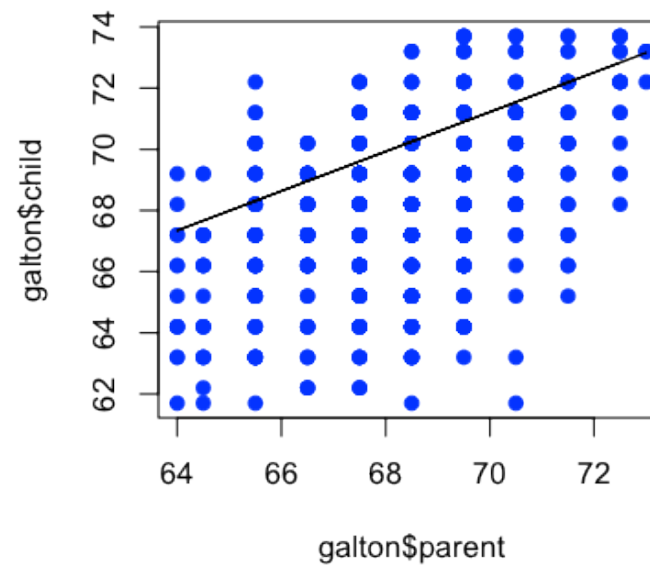
Fitting a line

```
plot(galton$parent,galton$child,pch=19,col="blue")  
lm1 <- lm(galton$child ~ galton$parent)  
lines(galton$parent,lm1$fitted,col="red",lwd=3)
```



Why not this line?

```
plot(galton$parent,galton$child,pch=19,col="blue")  
lines(galton$parent, 26 + 0.646*galton$parent)
```



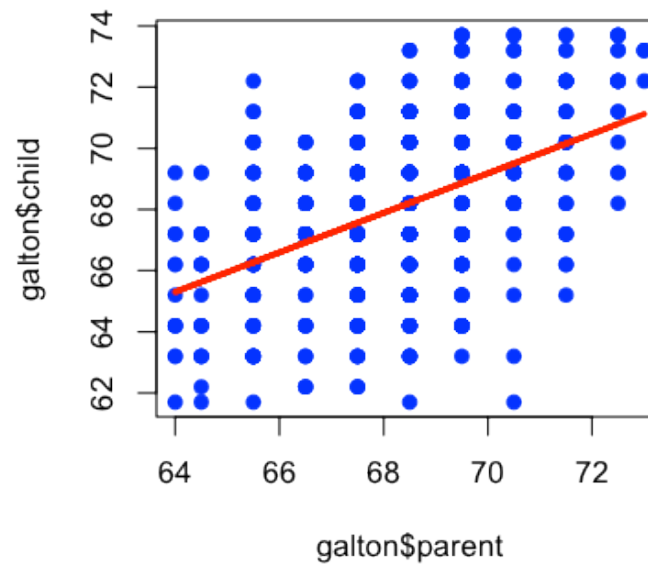
The equation for a line

If C_i is the height of child i and P_i is the height of the average parent, then we can imagine writing the equation for a line

$$C_i = b_0 + b_1 P_i$$

Not all points are on the line

```
plot(galton$parent,galton$child,pch=19,col="blue")  
lines(galton$parent,lm1$fitted,col="red",lwd=3)
```



Allowing for variation

If C_i is the height of child i and P_i is the height of the average parent, then we can imagine writing the equation for a line

$$C_i = b_0 + b_1 P_i + e_i$$

e_i is everything we didn't measure (how much they eat, where they live, do they stretch in the morning...)

How do we pick best?

If C_i is the height of child i and P_i is the height of the average parent, pick the line that makes the child values C_i and our guesses

$$\sum_{i=1}^{928} (C_i - \{b_0 + b_1 P_i\})^2$$

Plot what is leftover

```
par(mfrow=c(1,2))  
plot(galton$parent,galton$child,pch=19,col="blue")  
lines(galton$parent,lm1$fitted,col="red",lwd=3)  
plot(galton$parent,lm1$residuals,col="blue",pch=19)  
abline(c(0,0),col="red",lwd=3)
```

