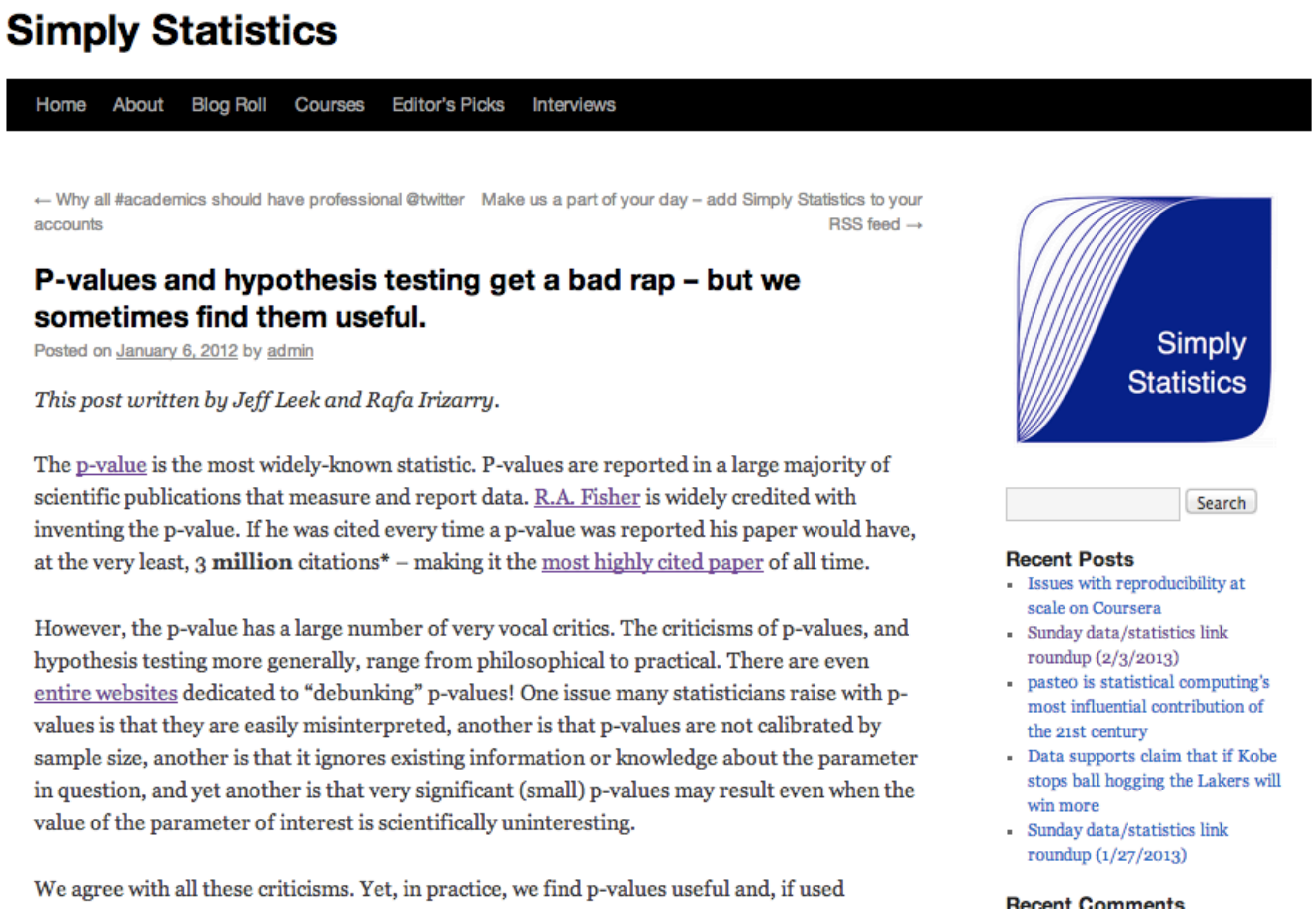
P-values

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

P-values

- Most common measure of "statistical significance"
- Commonly reported in papers
- Used for decision making (e.g. FDA)
- Controversial among statisticians
  - http://warnercnr.colostate.edu/~anderson/thompson1.html

Not everyone thinks P-values are awful



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P-values and hypothesis testing get a bad rap – but we sometimes find them useful.

Posted on January 6, 2012 by admin

This post written by Jeff Leek and Rafa Irizarry.

The p-value is the most widely-known statistic. P-values are reported in a large majority of scientific publications that measure and report data. R.A. Fisher is widely credited with inventing the p-value. If he was cited every time a p-value was reported his paper would have, at the very least, 3 **million** citations* – making it the most highly cited paper of all time.

However, the p-value has a large number of very vocal critics. The criticisms of p-values, and hypothesis testing more generally, range from philosophical to practical. There are even entire websites dedicated to "debunking" p-values! One issue many statisticians raise with p-values is that they are easily misinterpreted, another is that p-values are not calibrated by sample size, another is that it ignores existing information or knowledge about the parameter in question, and yet another is that very significant (small) p-values may result even when the value of the parameter of interest is scientifically uninteresting.

We agree with all these criticisms. Yet, in practice, we find p-values useful and, if used

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What is a P-value?

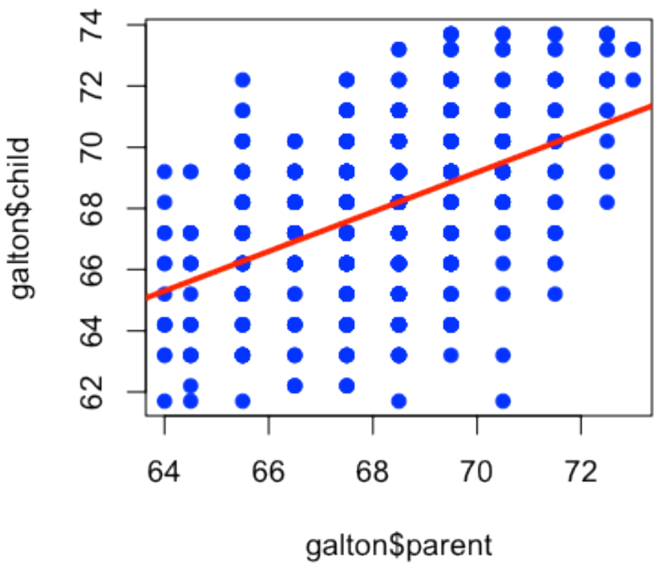
Idea: Suppose nothing is going on - how unusual is it to see the estimate we got?

Approach:

1. Define the hypothetical distribution of a data summary (statistic) when "nothing is going on" (*null hypothesis*)
2. Calculate the summary/statistic with the data we have (*test statistic*)
3. Compare what we calculated to our hypothetical distribution and see if the value is "extreme" (*p-value*)

Galton data

```
library(UsingR); data(galton)
plot(galton$parent,galton$child,pch=19,col="blue")
lm1 <- lm(galton$child ~ galton$parent)
abline(lm1,col="red",lwd=3)
```



If there was no relation between mid-parent/child height would we be surprised to see a line that

Null hypothesis/distribution

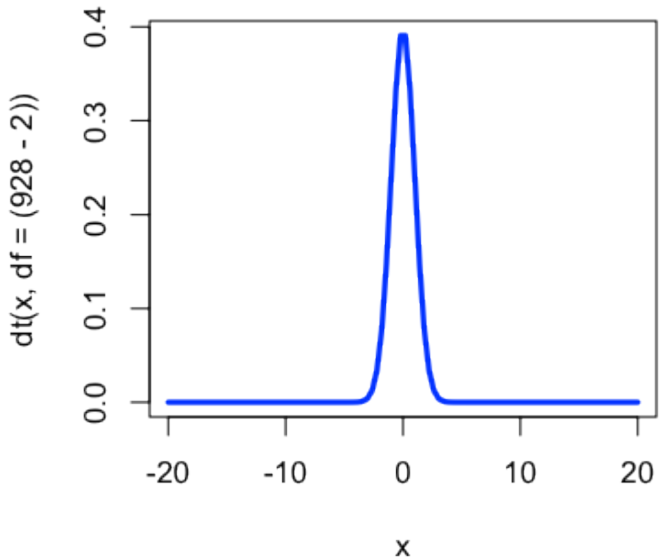
$$\frac{\hat{b}_1 - b_1}{S.E.(\hat{b}_1)} \sim t_{n-2}$$

H_0: That there is no relationship between parent and child height ($b_1 = 0$). Under the null hypothesis the distribution is:

$$\frac{\hat{b}_1}{S.E.(\hat{b}_1)} \sim t_{n-2}$$

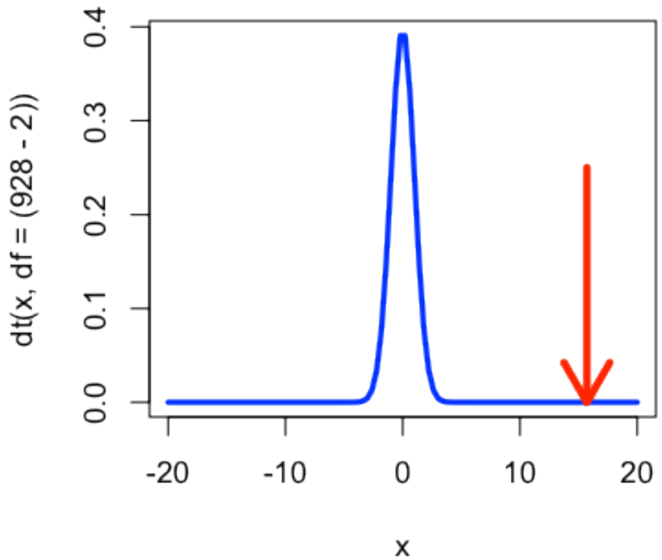
Null distribution

```
x <- seq(-20,20,length=100)
plot(x,dt(x,df=(928-2)),col="blue",lwd=3,type="l")
```



Null distribution + observed statistic

```
x <- seq(-20,20,length=100)
plot(x,dt(x,df=(928-2)),col="blue",lwd=3,type="l")
arrows(summary(lm1)$coeff[2,3],0.25,summary(lm1)$coeff[2,3],0,col="red",lwd=4)
```



Calculating p-values

```
summary(lm1)
```

```

Call:
lm(formula = galton$child ~ galton$parent)

Residuals:
   Min     1Q Median     3Q    Max
-7.805 -1.366  0.049  1.634  5.926

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   23.9415     2.8109    8.52   <2e-16 ***
galton$parent   0.6463     0.0411   15.71   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.24 on 926 degrees of freedom
Multiple R-squared: 0.21,   Adjusted R-squared: 0.21
F-statistic:  247 on 1 and 926 DF,  p-value: <2e-16
```

A quick simulated example

```
set.seed(9898324)
yValues <- rnorm(10); xValues <- rnorm(10)
lm2 <- lm(yValues ~ xValues)
summary(lm2)
```

```

Call:
lm(formula = yValues ~ xValues)

Residuals:
   Min     1Q Median     3Q    Max 
-1.546 -0.570  0.136  0.771  1.052 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    0.310      0.351    0.88     0.40
xValues        0.289      0.389    0.74     0.48

Residual standard error: 0.989 on 8 degrees of freedom
Multiple R-squared: 0.0644, Adjusted R-squared: -0.0525
```

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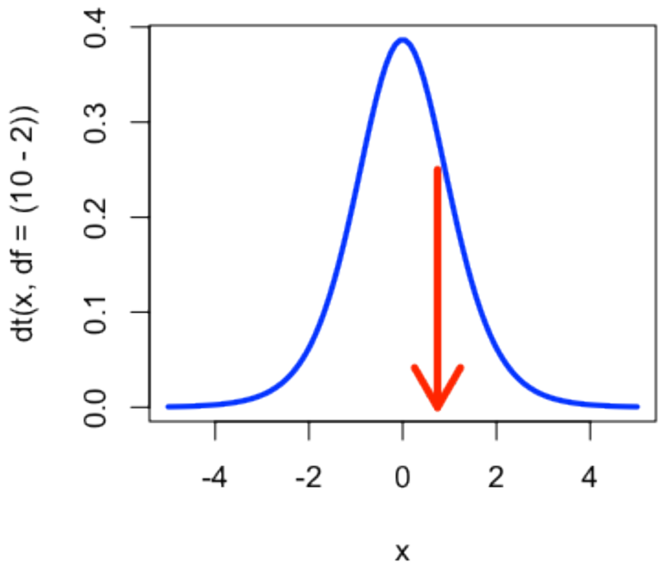
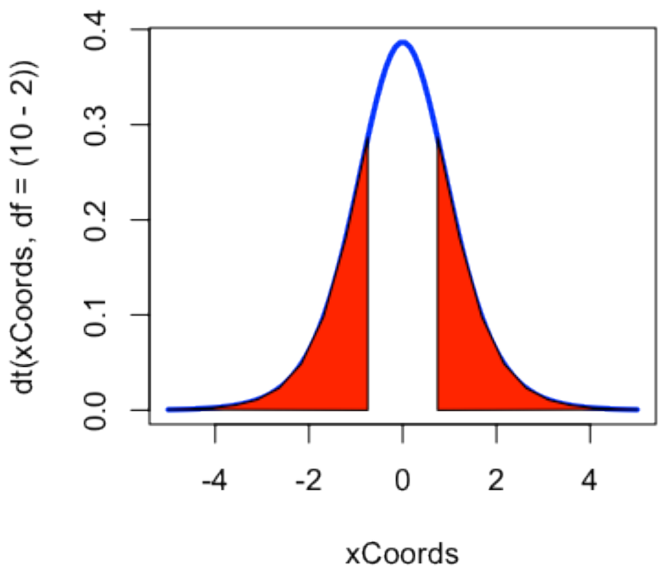
A quick simulated example

```
x <- seq(-5,5,length=100)
plot(x,dt(x,df=(10-2)),col="blue",lwd=3,type="l")
arrows(summary(lm2)$coeff[2,3],0.25,summary(lm2)$coeff[2,3],0,col="red",lwd=4)
```



A quick simulated example

```
xCoords <- seq(-5,5,length=100)
plot(xCoords,dt(xCoords,df=(10-2)),col="blue",lwd=3,type="l")
xSequence <- c(seq(summary(lm2)$coeff[2,3],5,length=10),summary(lm2)$coeff[2,3])
ySequence <- c(dt(seq(summary(lm2)$coeff[2,3],5,length=10),df=8),0)
polygon(xSequence,ySequence,col="red"); polygon(-xSequence,ySequence,col="red")
```



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Simulate a ton of data sets with no signal

```
set.seed(8323); pValues <- rep(NA,100)
for(i in 1:100){
  xValues <- rnorm(20);yValues <- rnorm(20)
  pValues[i] <- summary(lm(yValues ~ xValues))$coeff[2,4]
}
hist(pValues,col="blue",main="",freq=F)
abline(h=1,col="red",lwd=3)
```

Simulate a ton of data sets with signal

```
set.seed(8323); pValues <- rep(NA,100)
for(i in 1:100){
  xValues <- rnorm(20);yValues <- 0.2 * xValues + rnorm(20)
  pValues[i] <- summary(lm(yValues ~ xValues))$coeff[2,4]
}
hist(pValues,col="blue",main="",freq=F,xlim=c(0,1)); abline(h=1,col="red",lwd=3)
```

Simulate a ton of data sets with signal

```
set.seed(8323); pValues <- rep(NA,100)
for(i in 1:100){
  xValues <- rnorm(100);yValues <- 0.2* xValues + rnorm(100)
  pValues[i] <- summary(lm(yValues ~ xValues))$coeff[2,4]
}
hist(pValues,col="blue",main="",freq=F,xlim=c(0,1)); abline(h=1,col="red",lwd=3)
```

Some typical values (single test)

- $P < 0.05$ (significant)
- $P < 0.01$ (strongly significant)
- $P < 0.001$ (very significant)

In modern analyses, people generally report both the confidence interval and P-value. This is less true if many many hypotheses are tested.

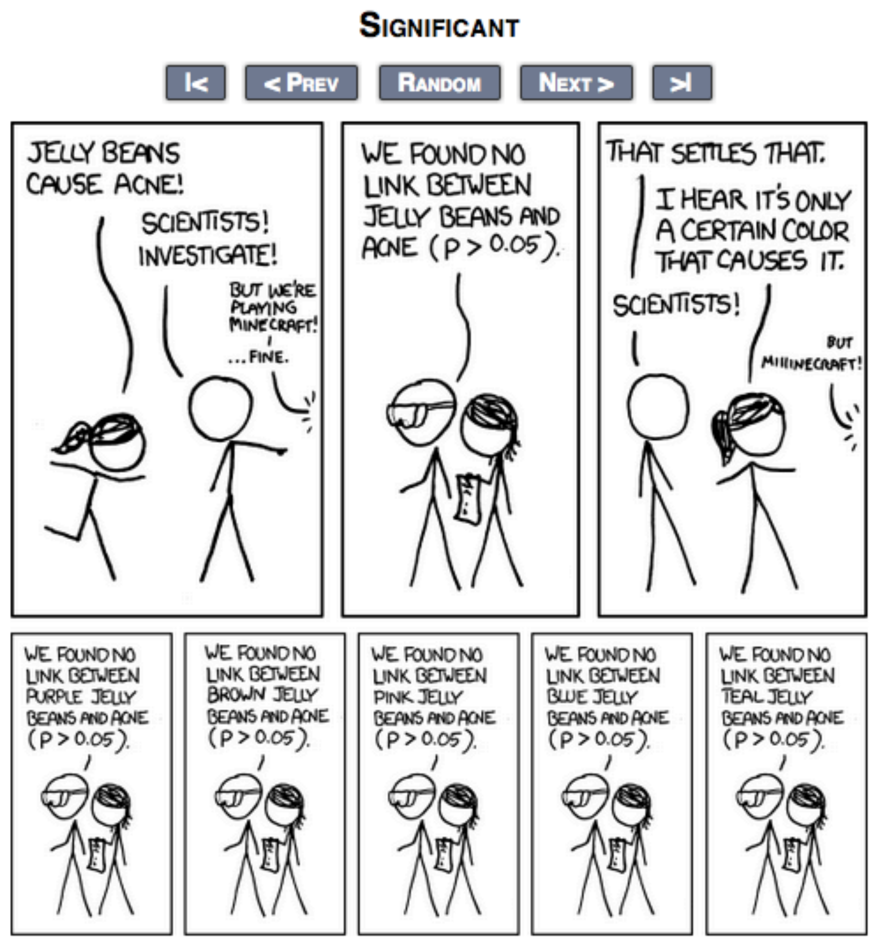
How you interpret the results

```
summary(lm(galton$child ~ galton$parent))$coeff
```

```
              Estimate Std. Error t value  Pr(>|t|)
(Intercept)    23.9415    2.81088   8.517 6.537e-17
galton$parent   0.6463    0.04114  15.711 1.733e-49
```

A one inch increase in parental height is associated with a 0.77 inch increase in child's height (95% CI: 0.42-1.12 inches). This difference was statistically significant ($P < 0.001$).

Be careful!



http://xkcd.com/882/

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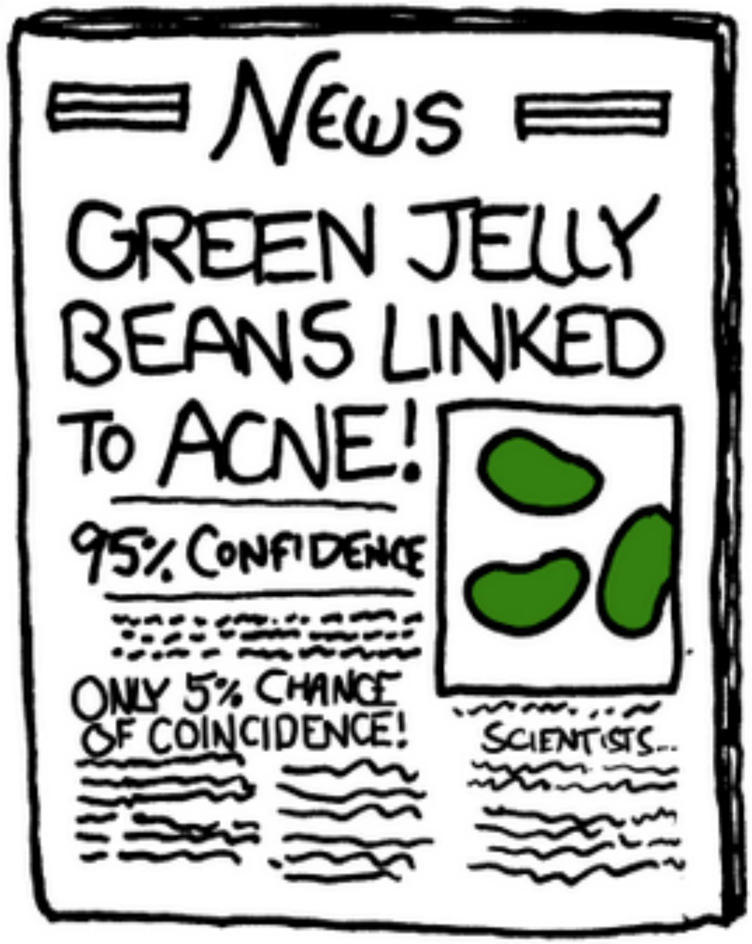
Be careful!



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