



# Multiple testing

Statistical Inference

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```
## Error: object 'opts_chunk' not found
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## Error: object 'knit_hooks' not found
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# Key ideas

- Hypothesis testing/significance analysis is commonly overused
- Correcting for multiple testing avoids false positives or discoveries
- Two key components
  - Error measure
  - Correction

# Three eras of statistics

**The age of Quetelet and his successors**, in which huge census-level data sets were brought to bear on simple but important questions: Are there more male than female births? Is the rate of insanity rising?

The classical period of Pearson, Fisher, Neyman, Hotelling, and their successors, intellectual giants who **developed a theory of optimal inference capable of wringing every drop of information out of a scientific experiment**. The questions dealt with still tended to be simple Is treatment A better than treatment B?

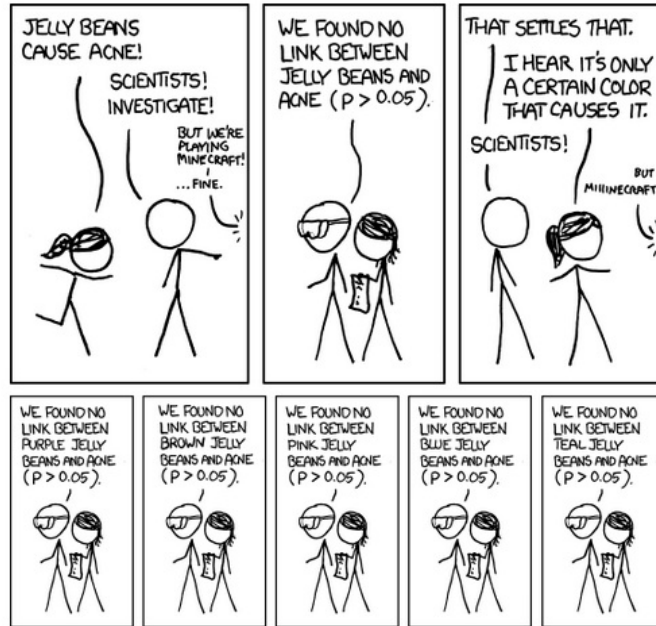
**The era of scientific mass production**, in which new technologies typified by the microarray allow a single team of scientists to produce data sets of a size Quetelet would envy. But now the flood of data is accompanied by a deluge of questions, perhaps thousands of estimates or hypothesis tests that the statistician is charged with answering together; not at all what the classical masters had in mind. Which variables matter among the thousands measured? How do you relate unrelated information?

<http://www-stat.stanford.edu/~ckirby/brad/papers/2010LSlexcerpt.pdf>

# Reasons for multiple testing

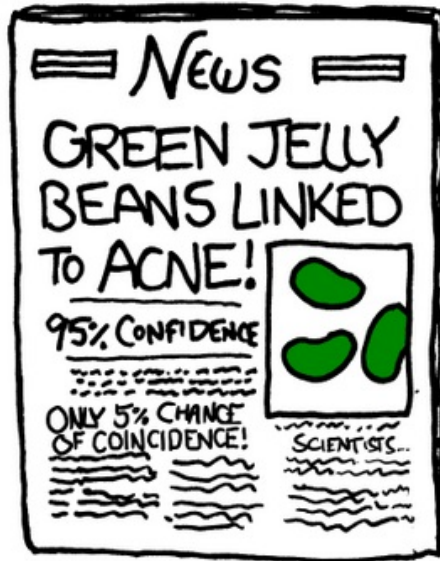


# Why correct for multiple tests?



<http://xkcd.com/882/>

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# Types of errors

Suppose you are testing a hypothesis that a parameter  $\beta$  equals zero versus the alternative that it does not equal zero. These are the possible outcomes.

	$\beta=0$	$\beta \neq 0$	HYPOTHESES
Claim $\beta=0$	U	T	m-R
Claim $\beta \neq 0$	V	S	R
Claims	$m_0$	$m-m_0$	m

**Type I error or false positive (V)** Say that the parameter does not equal zero when it does

**Type II error or false negative (T)** Say that the parameter equals zero when it doesn't

# Error rates

**False positive rate** - The rate at which false results ( $\beta = 0$ ) are called significant:  $E\left[\frac{V}{m_0}\right]^*$

**Family wise error rate (FWER)** - The probability of at least one false positive  $\{\rm Pr\}(V \geq 1)$

**False discovery rate (FDR)** - The rate at which claims of significance are false  $E\left[\frac{V}{R}\right]$

- The false positive rate is closely related to the type I error rate  
[http://en.wikipedia.org/wiki/False\\_positive\\_rate](http://en.wikipedia.org/wiki/False_positive_rate)



# Controlling the false positive rate

If P-values are correctly calculated calling all  $P < \alpha$  significant will control the false positive rate at level  $\alpha$  on average.

**Problem:** Suppose that you perform 10,000 tests and  $\beta = 0$  for all of them.

Suppose that you call all  $P < 0.05$  significant.

The expected number of false positives is:  $10,000 \times 0.05 = 500$  false positives.

**How do we avoid so many false positives?**

# Controlling family-wise error rate (FWER)

The [Bonferroni correction](#) is the oldest multiple testing correction.

## Basic idea:

- Suppose you do  $m$  tests
- You want to control FWER at level  $\alpha$  so  $\Pr(V \geq 1) < \alpha$
- Calculate P-values normally
- Set  $\alpha_{\text{fwer}} = \alpha/m$
- Call all P-values less than  $\alpha_{\text{fwer}}$  significant

**Pros:** Easy to calculate, conservative **Cons:** May be very conservative

# Controlling false discovery rate (FDR)

This is the most popular correction when performing *lots* of tests say in genomics, imaging, astronomy, or other signal-processing disciplines.

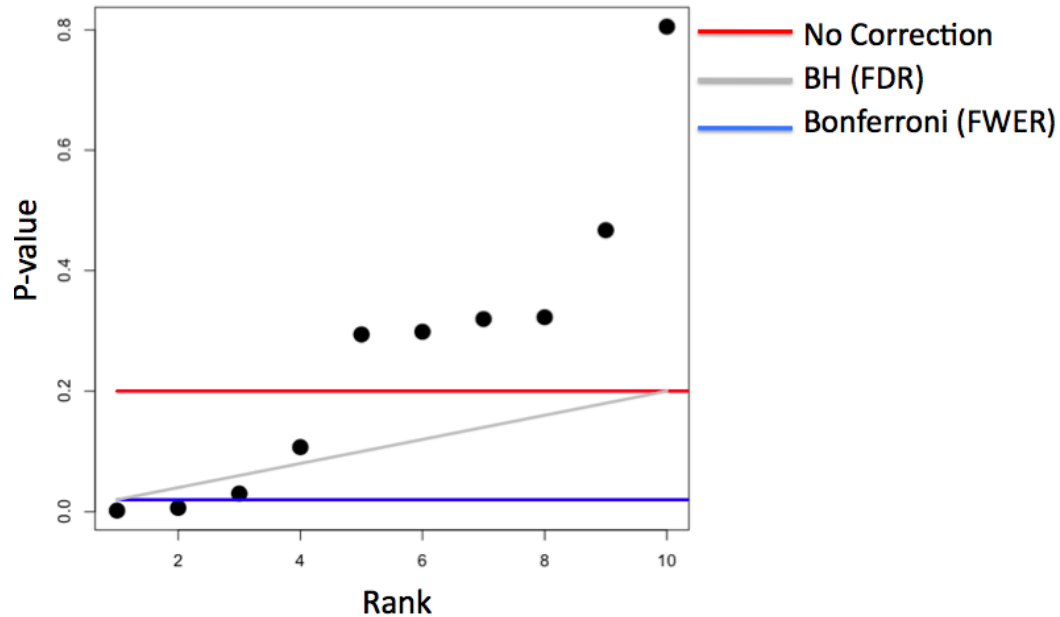
## Basic idea:

- Suppose you do  $m$  tests
- You want to control FDR at level  $\alpha$  so  $E\left[\frac{V}{R}\right]$
- Calculate P-values normally
- Order the P-values from smallest to largest  $P_{(1)}, \dots, P_{(m)}$
- Call any  $P_{(i)} \leq \alpha \times \frac{i}{m}$  significant

**Pros:** Still pretty easy to calculate, less conservative (maybe much less)

**Cons:** Allows for more false positives, may behave strangely under dependence

# Example with 10 P-values



Controlling all error rates at  $\alpha = 0.20$

# Adjusted P-values

- One approach is to adjust the threshold  $\alpha$
- A different approach is to calculate "adjusted p-values"
- They *are not p-values* anymore
- But they can be used directly without adjusting  $\alpha$

## Example:

- Suppose P-values are  $P_1, \dots, P_m$
- You could adjust them by taking  $P_i^{\text{fwer}} = \max\{m \times P_i, 1\}$  for each P-value.
- Then if you call all  $P_i^{\text{fwer}} < \alpha$  significant you will control the FWER.

# Case study I: no true positives

```
set.seed(1010093)
pValues <- rep(NA, 1000)
for (i in 1:1000) {
  y <- rnorm(20)
  x <- rnorm(20)
  pValues[i] <- summary(lm(y ~ x))$coeff[2, 4]
}

# Controls false positive rate
sum(pValues < 0.05)
```

```
## [1] 51
```

# Case study I: no true positives

```
# Controls FWER  
sum(p.adjust(pValues, method = "bonferroni") < 0.05)
```

```
## [1] 0
```

```
# Controls FDR  
sum(p.adjust(pValues, method = "BH") < 0.05)
```

```
## [1] 0
```

# Case study II: 50% true positives

```
set.seed(1010093)
pValues <- rep(NA, 1000)
for (i in 1:1000) {
  x <- rnorm(20)
  # First 500 beta=0, last 500 beta=2
  if (i <= 500) {
    y <- rnorm(20)
  } else {
    y <- rnorm(20, mean = 2 * x)
  }
  pValues[i] <- summary(lm(y ~ x))$coeff[2, 4]
}
trueStatus <- rep(c("zero", "not zero"), each = 500)
table(pValues < 0.05, trueStatus)
```

```
##      trueStatus
##      not zero zero
## FALSE      0  476
## TRUE      500   24
```



# Case study II: 50% true positives

```
# Controls FWER
table(p.adjust(pValues, method = "bonferroni") < 0.05, trueStatus)
```

```
##      trueStatus
##      not zero zero
## FALSE      23  500
## TRUE      477    0
```

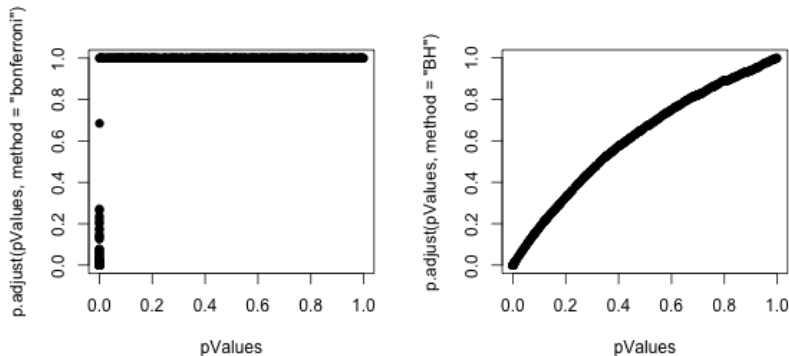
```
# Controls FDR
table(p.adjust(pValues, method = "BH") < 0.05, trueStatus)
```

```
##      trueStatus
##      not zero zero
## FALSE      0  487
## TRUE     500   13
```

# Case study II: 50% true positives

## P-values versus adjusted P-values

```
par(mfrow = c(1, 2))  
plot(pValues, p.adjust(pValues, method = "bonferroni"), pch = 19)  
plot(pValues, p.adjust(pValues, method = "BH"), pch = 19)
```



# Notes and resources

## Notes:

- Multiple testing is an entire subfield
- A basic Bonferroni/BH correction is usually enough
- If there is strong dependence between tests there may be problems
  - Consider method="BY"

## Further resources:

- [Multiple testing procedures with applications to genomics](#)
- [Statistical significance for genome-wide studies](#)
- [Introduction to multiple testing](#)