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- In this setting, we need to be careful to avoid incorrectly rejecting too many null hypotheses, i.e. having too many false positives.

## A Quick Review of Hypothesis Testing

Hypothesis tests allow us to answer simple “yes-or-no” questions, such as:

- Is the true coefficient  $\beta_j$  in a linear regression equal to zero?
- Does the expected blood pressure among mice in the treatment group equal the expected blood pressure among mice in the control group?

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2. Construct the test statistic
3. Compute the  $p$ -value
4. Decide whether to reject the null hypothesis

# 1. Define the Null and Alternative Hypotheses

- We divide the world into *null* and *alternative* hypotheses.
- The null hypothesis,  $H_0$ , is the default state of belief about the world. For instance:
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  2. There is no difference in the expected blood pressures.
- The alternative hypothesis,  $H_a$ , represents something different and unexpected. For instance:
  1. The true coefficient  $\beta_j$  is non-zero.
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- Let  $\hat{\mu}_t / \hat{\mu}_c$  respectively denote the average blood pressure for the  $n_t / n_c$  mice in the treatment and control groups.
- To test  $H_0 : \mu_t = \mu_c$ , we use a two-sample  $t$ -statistic

$$T = \frac{\hat{\mu}_t - \hat{\mu}_c}{s \sqrt{\frac{1}{n_t} + \frac{1}{n_c}}}$$

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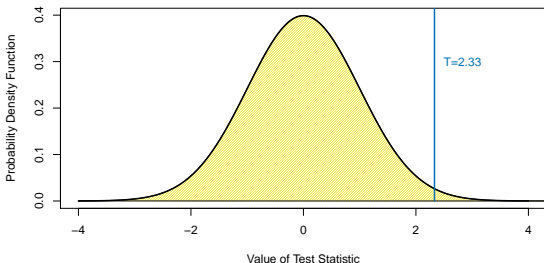


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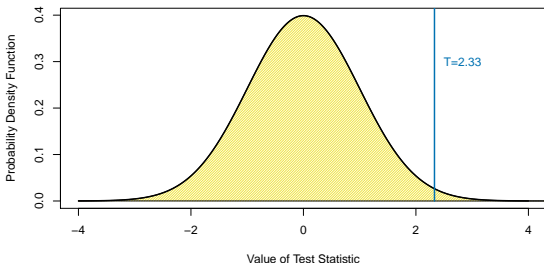
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- The  $p$ -value is 0.02 because, if  $H_0$  is true, we would only see  $|T|$  this large 2% of the time.

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- If the  $p$ -value is sufficiently small, then we will want to *reject*  $H_0$  (and, therefore, make a potential “discovery”).
- *But how small is small enough?* To answer this, we need to understand the *Type I error*.

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		<b>Truth</b>	
		$H_0$	$H_a$
<b>Decision</b>	Reject $H_0$	Type I Error	Correct
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- If we only reject  $H_0$  when the p-value is less than  $\alpha$ , then the Type I error rate will be at most  $\alpha$ .
- So, *we reject  $H_0$  when the p-value falls below some  $\alpha$* : often we choose  $\alpha$  to equal 0.05 or 0.01 or 0.001.

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- If we reject all null hypotheses for which the  $p$ -value falls below 0.01, then how many Type I errors will we make?

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  - We'd expect one coin (on average) to come up all tails.
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  - The p-value for the null hypothesis that this particular coin is fair is less than 0.002!
  - So we would conclude it is not fair, i.e. we *reject*  $H_0$ , even though it's a fair coin.
- If we test a lot of hypotheses, we are almost certain to get one very small p-value by chance!





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- If  $m = 10,000$ , then we expect to falsely reject 100 null hypotheses by chance!
- *That's a lot of Type I errors, i.e. false positives!*

## The Family-Wise Error Rate

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- $\text{FWER} = \Pr(V \geq 1)$

	$H_0$ is True	$H_0$ is False	Total
Reject $H_0$	$V$	$S$	$R$
Do Not Reject $H_0$	$U$	$W$	$m - R$
Total	$m_0$	$m - m_0$	$m$

## Challenges in Controlling the Family-Wise Error Rate

$$\begin{aligned}\text{FWER} &= 1 - \Pr(\text{do not falsely reject any null hypotheses}) \\ &= 1 - \Pr\left(\bigcap_{j=1}^m \{\text{do not falsely reject } H_{0j}\}\right).\end{aligned}$$



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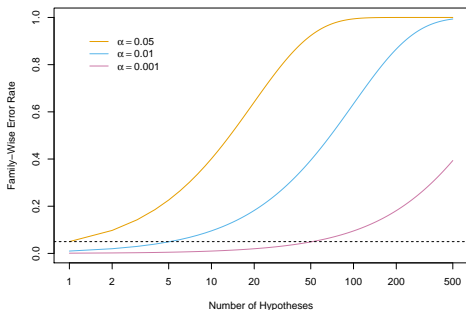
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## The Bonferroni Correction

$$\begin{aligned}\text{FWER} &= \Pr(\text{falsely reject at least one null hypothesis}) \\ &= \Pr(\cup_{j=1}^m A_j) \\ &\leq \sum_{j=1}^m \Pr(A_j)\end{aligned}$$

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- If we only reject hypotheses when the p-value is less than  $\alpha/m$ , then

$$\text{FWER} \leq \sum_{j=1}^m \Pr(A_j) \leq \sum_{j=1}^m \frac{\alpha}{m} = m \times \frac{\alpha}{m} = \alpha,$$

because  $\Pr(A_j) \leq \alpha/m$ .

- This is the *Bonferroni Correction*: to control FWER at level  $\alpha$ , reject any null hypothesis with p-value below  $\alpha/m$ .

## Fund Manager Data

Manager	Mean, $\bar{x}$	$s$	$t$ -statistic	$p$ -value
One	3.0	7.4	2.86	0.006
Two	-0.1	6.9	-0.10	0.918
Three	2.8	7.5	2.62	0.012
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- $H_{0j}$ : the  $j$ th manager's expected excess return equals zero.
- If we reject  $H_{0j}$  if the  $p$ -value is less than  $\alpha = 0.05$ , then we will conclude that the *first* and *third* managers have significantly non-zero excess returns.

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- However, we have tested multiple hypotheses, so the FWER is *greater* than 0.05.

## Fund Manager Data with Bonferroni Correction

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- Now the FWER is at most 0.05.

# Holm's Method for Controlling the FWER

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- Holm's method controls the FWER at level  $\alpha$ .



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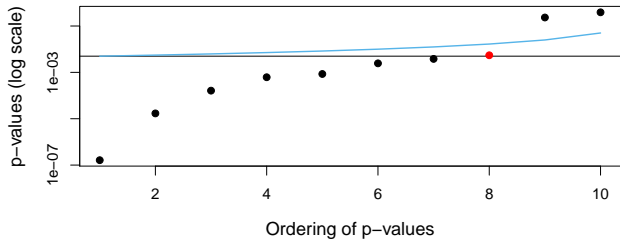
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- The Holm procedure rejects the first two null hypotheses, because
  - $p_{(1)} = 0.006 < 0.05/(5 + 1 - 1) = 0.0100$
  - $p_{(2)} = 0.012 < 0.05/(5 + 1 - 2) = 0.0125$ ,
  - $p_{(3)} = 0.601 > 0.05/(5 + 1 - 3) = 0.0167$ .

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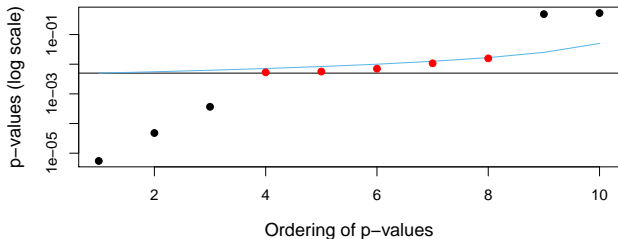
- The ordered  $p$ -values are  $p_{(1)} = 0.006$ ,  $p_{(2)} = 0.012$ ,  $p_{(3)} = 0.601$ ,  $p_{(4)} = 0.756$  and  $p_{(5)} = 0.918$ .
- The Holm procedure rejects the first two null hypotheses, because
  - $p_{(1)} = 0.006 < 0.05/(5 + 1 - 1) = 0.0100$
  - $p_{(2)} = 0.012 < 0.05/(5 + 1 - 2) = 0.0125$ ,
  - $p_{(3)} = 0.601 > 0.05/(5 + 1 - 3) = 0.0167$ .
- Holm rejects  $H_0$  for the *first* and *third* managers, but Bonferroni only rejects  $H_0$  for the *first* manager.

## A Comparison with $m = 10$ p-values



- Aim to control FWER at 0.05.
- p-values below the black horizontal line are rejected by Bonferroni.
- p-values below the blue line are rejected by Holm.
- Holm and Bonferroni make the same conclusion on the black points, but only Holm rejects for the red point.

## A More Extreme Example



- Now five hypotheses are rejected by Holm but not by Bonferroni ....
- .... even though both control FWER at 0.05.

## Holm or Bonferroni?

- Bonferroni is simple ... reject any null hypothesis with a p-value below  $\alpha/m$ .
- Holm is slightly more complicated, but it will lead to more rejections while controlling FWER!!
- So, *Holm is a better choice!*

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- Bonferroni and Holm are general procedures that will work in most settings. However, in certain special cases, methods such as Tukey and Scheffé can give better results: *i.e. more rejections while maintaining FWER control.*

# The False Discovery Rate

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Reject $H_0$	$V$	$S$	$R$
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- This is a tough ask when  $m$  is large! It will cause us to be super conservative (i.e. to very rarely reject).
- Instead, we can control the *false discovery rate*:

$$\text{FDR} = E(V/R).$$

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$$\text{FDR} = \text{E} \left( \frac{V}{R} \right) = \text{E} \left( \frac{\text{number of false rejections}}{\text{total number of rejections}} \right)$$



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- FWER controls  $\text{Pr}(\text{at least one false rejection})$ .
- FDR controls the fraction of candidates in the smaller set that are really false rejections. This is what she needs!

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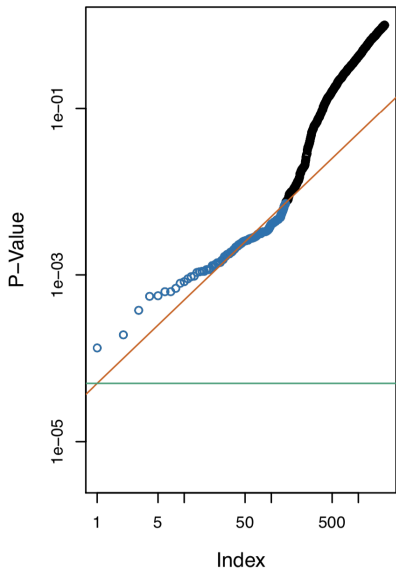
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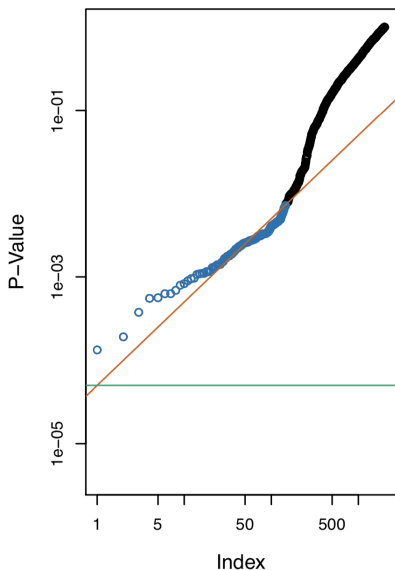
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Then,  $\text{FDR} \leq q$ .

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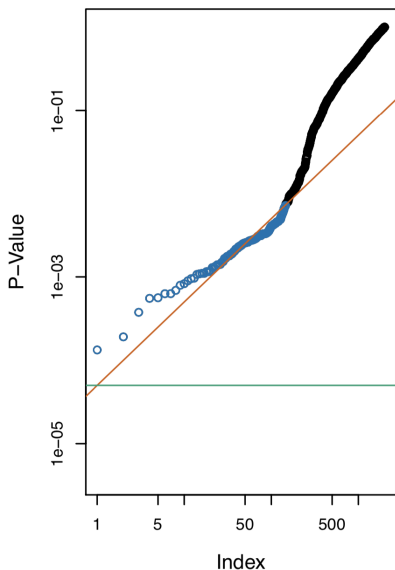


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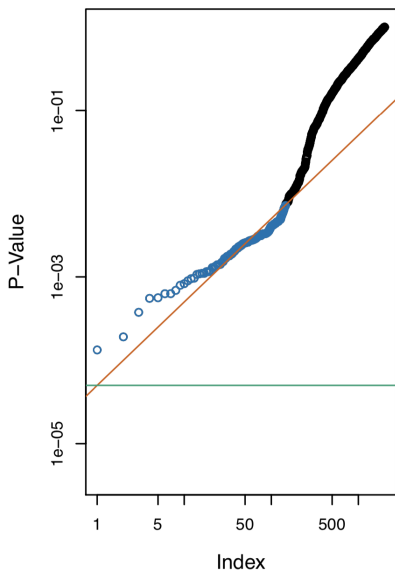
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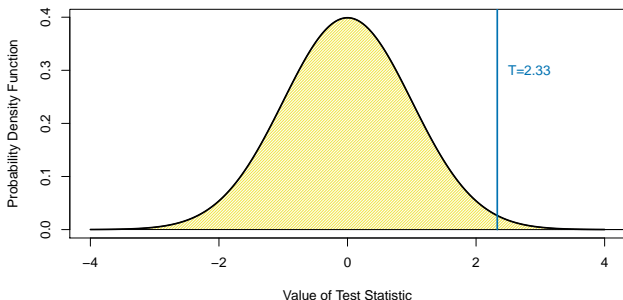
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- To control FWER at level  $\alpha = 0.05$  using Bonferroni:
  - We reject any null hypothesis for which the  $p$ -value is less than  $0.05/5$ .
  - So, we reject only  $H_{01}$ .

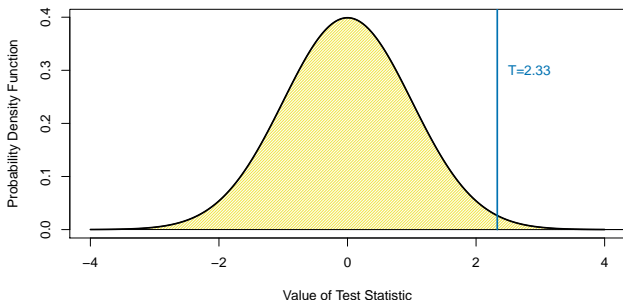
## Re-Sampling Approaches

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- What if this *theoretical null distribution* is unknown?

# A Re-Sampling Approach for a Two-Sample t-Test, Part 1

- Suppose we want to test  $H_0 : E(X) = E(Y)$  versus  $H_a : E(X) \neq E(Y)$ , using  $n_X$  independent observations from  $X$  and  $n_Y$  independent observations from  $Y$ .
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- Let's take a *permutation* or *re-sampling* approach....

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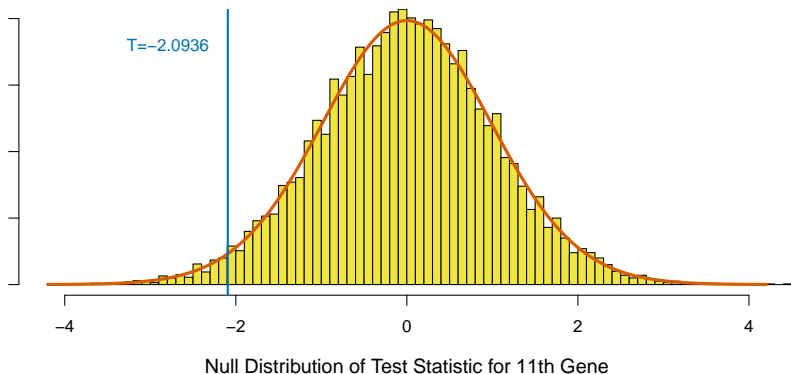
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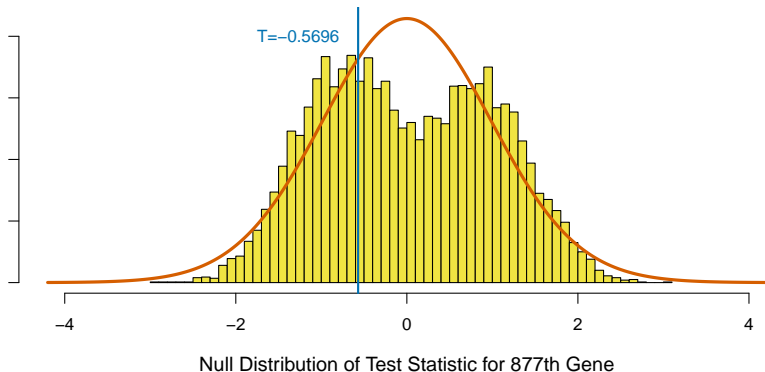
$$\frac{\sum_{b=1}^B \mathbf{1}_{(|T^{*b}| \geq |T|)}}{B}.$$

## Application to Gene Expression Data, Part 1



Theoretical  $p$ -value is 0.041. Re-sampling  $p$ -value is 0.042.

## Application to Gene Expression Data, Part 2



Theoretical  $p$ -value is 0.571. Re-sampling  $p$ -value is 0.673.

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- Re-sampling approaches are useful if the theoretical null distribution is unavailable, or requires stringent assumptions. *(So, they're always useful!)*
- An extension of the re-sampling approach to compute a  $p$ -value can be used to control FDR.
- This example involved a two-sample  $t$ -test, but similar approaches can be developed for other test statistics.