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# **Permutation and Exact Tests**

## **&**

# **False Detection Rate**

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## **Exact and Permutation Tests**

- Computer-intensive methods for hypothesis testing
- Permutation Test (randomization test):  
Used when distribution of the test statistic (under the null hypothesis) is unknown
- Exact Test:  
Used when sample sizes are small, so standard asymptotic (large sample) procedures do not work well
- All permutation tests are exact tests but not vice-versa. Exact test maintains the Type I error level without any large sample approximations/assumptions

## **Example - HPV vaccine trial**

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- 200 uninfected women are randomly assigned 1:1 to HPV vaccine or placebo (i.e., 100 to each group)
- After 1 year subjects are tested for HPV infection (yes/no)
- Does the probability of infection differ between the two groups?

What is a useful model for these data?

## Example - HPV vaccine trial

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**Vaccine group: Binomial(100,  $p_v$ )**

**Placebo group: Binomial(100,  $p_p$ )**

Scientific Question:

*Is the risk of infection the same or different in the two groups?*

Restate in terms of the model:

$H_0: p_v = p_p$  ("null hypothesis")

vs.  $H_a: p_v < p_p$

## **Example - HPV vaccine trial**

Results:

	<u>Vaccine</u>	<u>Placebo</u>	<u>Total</u>
HPV+	20	40	60
HPV-	80	60	140
	100	100	200

The overall infection rate is 30%, but we observe 20% and 40% for vaccine and placebo, respectively. What if we repeated the experiment ... would we see similar results? We know that sample results are variable. Could the difference go the other way? Could a difference this large be due to chance alone?

## Example - HPV vaccine trial

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We first need a way of summarizing the difference in the infection probabilities between vaccine and placebo groups. A useful summary has these features:

- Summarize the differences between the groups in a single number.

Example  $\Rightarrow p_v - p_p$

- One particular value (say, 0) of the summary corresponds to the null hypothesis being exactly true.

Example  $\Rightarrow p_v - p_p = 0$

- We expect values near 0 if the null hypothesis is true; we expect values far from 0 if the null hypothesis is false.
- But how near is near? How far is far?

## Example - HPV vaccine trial

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We need to figure out what sort of distribution of values we would see for our summary statistic if the experiment were repeated many times and the null hypothesis were true.

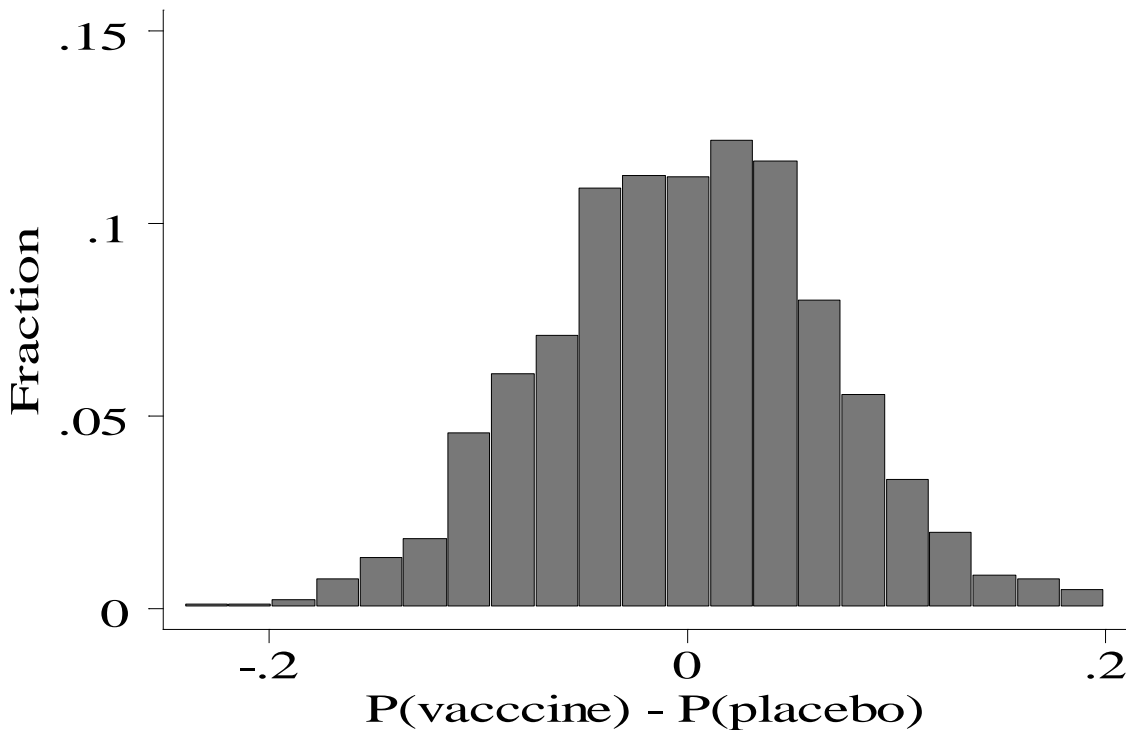
Imagine the following experiment:

- make up a deck of 200 cards
- mark the word “HPV+” on 60 of them
- shuffle and deal two groups of 100
- form a 2 x 2 table from the results
- calculate your summary statistic
- repeat many times
- plot the results

This experiment should give us an idea of what we expect to see **if the null hypothesis is true.**

## Example - HPV vaccine trial

Here is the distribution of differences  $p_v - p_p$  that we might expect to see if the null hypothesis is true:



Summarize the results by reporting what proportion of the simulated results are as “extreme” or more so than the observed result (p value).

**$\Rightarrow$  only 3/2000 simulated differences were more extreme than the observed difference of -0.2**

**$\Rightarrow p = .0015$**



## Example - HPV vaccine trial

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### Summary:

We have constructed a valid test of the hypothesis,  $H_0: p_V = p_P$ , using a **randomization test**. There are four steps involved:

1. Pick a model for the data and restate the scientific question in terms of the model (null hypothesis)
2. Choose (any) reasonable summary statistic that quantifies deviations from the null hypothesis
3. Resample data assuming the null hypothesis is true and compute the summary statistic for each resampled data set.
4. Compare the observed value of the summary statistic to the null distribution generated in Step 3.

## Permutation Test for Correlation

Assume data are pairs  $(X_{1i}, X_{2i})$ ,  $i = 1, 2, \dots, n$

1.  $H_0: \rho = 0$
2. Compute  $r_{\text{obs}} = \text{corr}(X_1, X_2)$
3. Mix up the  $X_{1i}$  and  $X_{2i}$ ; i.e., for each  $X_{1i}$  randomly choose  $X_{2i}'$  from all the  $X_2$ 's.  
Compute  $r_{\text{perm}} = \text{corr}(X_1, X_2')$
4. Repeat Step 3 many times and compare  $r_{\text{obs}}$  to the distribution of  $r_{\text{perm}}$

Note: There are  $n!$  possible pairings. If  $n$  is small, you can enumerate all possible pairings.

## Permutation Tests - Summary

- Useful when we can do resampling under the null hypothesis
- Permutation samples are drawn without replacement
- If the sample size is small, you can enumerate all possible permutations, otherwise generate many permutations.
- Fewer assumptions than e.g. t-test (i.e., no assumption about skewness or normality of underlying distribution)
- Many standard nonparametric methods (e.g., Wilcoxon Rank Sum Test) are permutation tests based on ranks.
- Good Reference:  
Manly (2007). *Randomization, Bootstrap and Monte Carlo Methods in Biology*.  
Chapman & Hall/CRC.

## Fisher's Exact Test

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**Motivation:** When a  $2 \times 2$  table contains cells that have fewer than 5 expected observations, the  $\chi^2$  approximation to the distribution of  $X^2$  is known to be poor. This can lead to incorrect inference since the p-values based on this approximation are not valid.

**Solution:** Use Fisher's Exact Test

	D+	D-	Total
E+	$a$	$b$	$n_1$
E-	$c$	$d$	$n_2$
Total	$m_1$	$m_2$	$N$

## Fisher's Exact Test

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**Example:** A retrospective study is done among men aged 50-54 who died over a 1-month period. The investigators tried to include equal numbers of men who died from cardiovascular disease (CVD) and those that did not. Then, asking a close relative, the dietary habits were ascertained.

	High Salt	Low Salt	Total
CVD	5	30	35
Non-CVD	2	23	25
Total	7	53	60

A calculation of the odds ratio yields:

$$OR = \frac{5 \times 23}{2 \times 30} = 1.92$$

## Fisher's Exact Test

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	D+	D-	Total
E+			$n_1$
E-			$n_2$
Total	$m_1$	$m_2$	$N$

If we **fix all of the margins** then any one cell of the table will allow the remaining cells to be filled. Note that  $a$  must be greater than 0, less than both  $n_1$  and  $m_1$ , and an integer. Thus there are only a relatively few number of possible table configurations if either  $n_1$  or  $m_1$  is small (with  $n_1, n_2, m_1, m_2$  fixed).

Under the null hypothesis,

$$H_0 : OR = 1$$

we can use the hypergeometric distribution (a probability distribution for discrete rv's) to compute the probability of any given configuration. Since we have the distribution of a statistic ( $a$ ) under the null, we can use this to compute p-values. You will *never* do this by hand ....

## Fisher's Exact Test

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**Example:** (Rosner, p. 370) Cardiovascular disease.

	High Salt	Low Salt	Total
CVD	5	30	35
Non-CVD	2	23	25
Total	7	53	60

Possible Tables:

0		35
		25
7	53	60

1		35
		25
7	53	60

2		35
		25
7	53	60

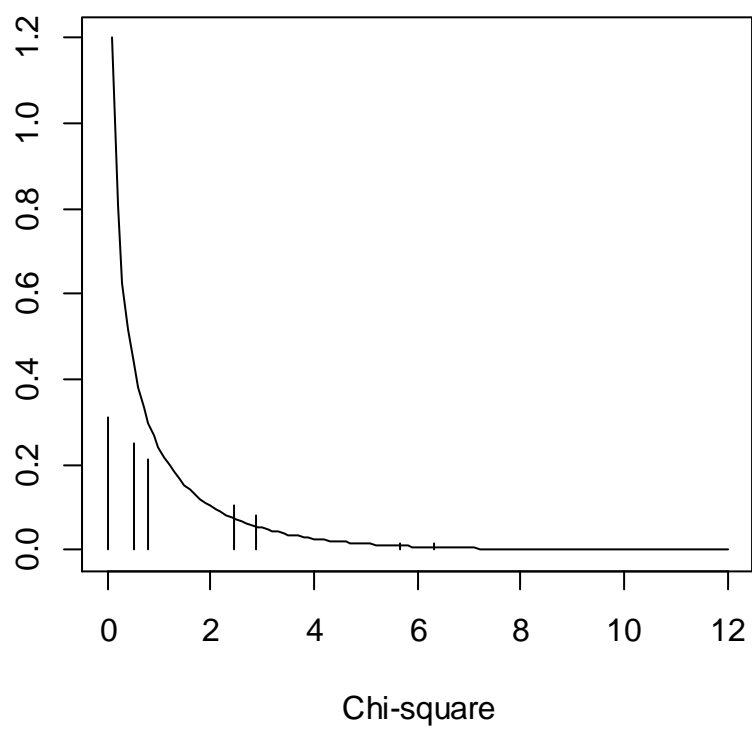
3		35
		25
7	53	60

4		35
		25
7	53	60

5		35
		25
7	53	60

6		35
		25
7	53	60

7		35
		25
7	53	60





# Fisher Exact Test Using Stata

Fisher's exact  
test.

```
. cci 5 30 2 23,exact
```

	Exposed	Unexposed	Total	Proportion Exposed
Cases	5	30	35	0.1429
Controls	2	23	25	0.0800
Total	7	53	60	0.1167

	Point estimate	[95% Conf. Interval]
Odds ratio	1.916667	.2789585 21.62382 (exact)
Attr. frac. ex.	.4782609	-2.584763 .9537547 (exact)
Attr. frac. pop	.068323	

```
1-sided Fisher's exact P = 0.3747
2-sided Fisher's exact P = 0.6882
```

# Fisher Exact Test Using Stata

The usual chi-squared test, for comparison.

```
. cci 5 30 2 23

-----+-----+-----+-----+-----+-----+-----+-----+-----+
|      Exposed      |      Unexposed      |      Total      |      Proportion      |
|-----+-----+-----+-----+-----+-----+-----+-----+-----+
|      Exposed      |      Unexposed      |      Total      |      Exposed      |
|-----+-----+-----+-----+-----+-----+-----+-----+-----+
Cases |          5          |          30          |          35          |          0.1429          |
Controls |          2          |          23          |          25          |          0.0800          |
-----+-----+-----+-----+-----+-----+-----+-----+-----+
Total |          7          |          53          |          60          |          0.1167          |
|-----+-----+-----+-----+-----+-----+-----+-----+-----+
|      Point estimate      |      [95% Conf. Interval]      |
|-----+-----+-----+-----+-----+-----+-----+-----+-----+
Odds ratio |          1.916667          |          .2789585          |          21.62382          |          (exact)          |
Attr. frac. ex. |          .4782609          |          -2.584763          |          .9537547          |          (exact)          |
Attr. frac. pop |          .068323          |          |          |          |          |
|-----+-----+-----+-----+-----+-----+-----+-----+-----+
chi2(1) =          0.56   Pr>chi2 = 0.4546
```

## **False Discovery Rate**

For some studies, answering the scientific question of interest may require testing hundred, thousands, or millions of hypotheses. This is especially true of genetics.

E.g. Hedenfalk et al (2001) screened 3226 genes using microarrays to find differential expression between BRCA-1 and BRCA-2 mutation positive tumors.

Issue: If a traditional hypothesis testing approach is taken and we conduct 3226 tests at the 0.05 level, then we expect (up to) 161 false positive findings. Unfortunately, they are not labeled as such!

Traditional Solution (Bonferroni correction): If we conduct each test at an  $\alpha = .05/3226 = .000015$  level then the probability of 1 or more false positive findings will be  $\sim 0.05$ . But, ... with such a stringent  $\alpha$  level we are likely to miss many true positive results.

New Solution: Don't try to eliminate false positives ... control them

## False Discovery Rate

	Reject null	Fail to reject	
Null true	F	$m_0 - F$	$m_0$
Alternative true	T	$m_1 - T$	$m_1$
	S	$m - S$	m

- false positive rate =  $F / m_0$
- false discovery rate =  $F / S$

Idea: Control the false discovery rate (q-value) instead of the false positive rate (p-value)

## **False Discovery Rate**

E.g. Hedenfalk data

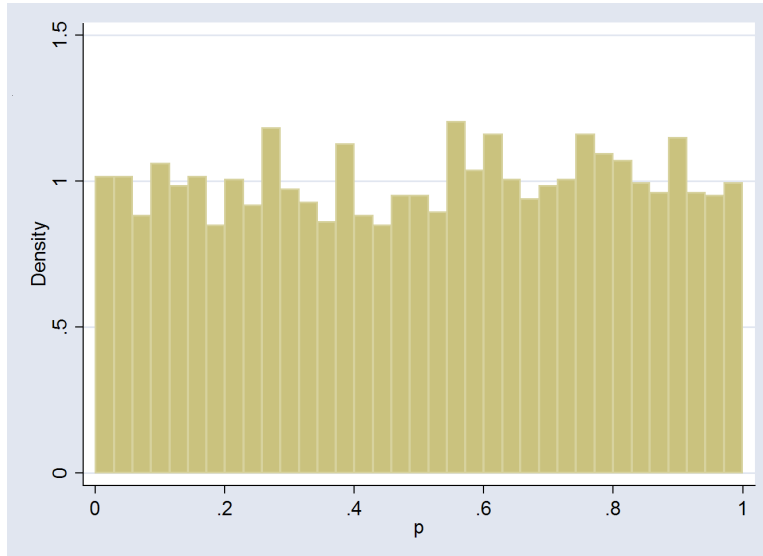
- Order the 3170 p-values (56 genes were excluded from this analysis):  $p_i$ ,  $i = 1 \dots 3170$
- Pick a p-value cutoff, say  $\alpha$ ; reject  $H_0$  for all  $p_i < \alpha$ .

Q: What is the FDR associated with this choice of  $\alpha$ ?

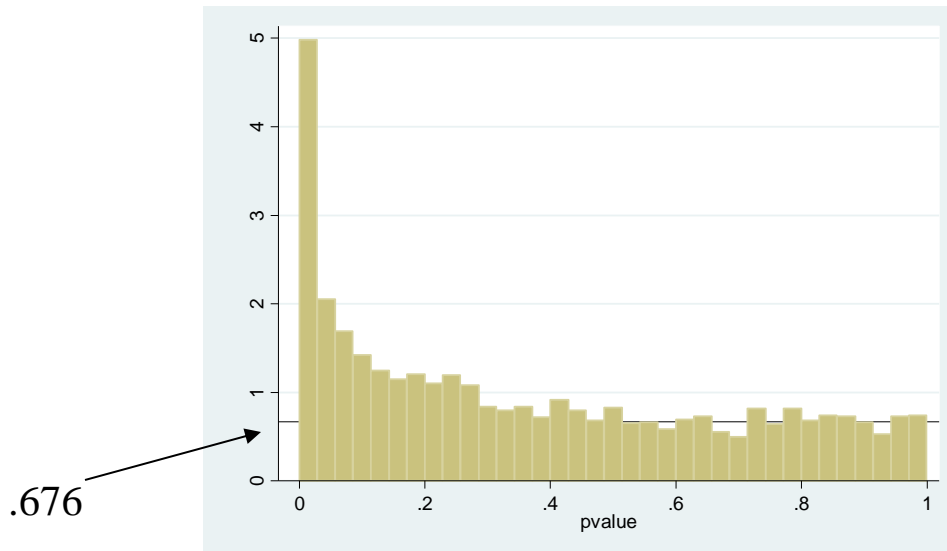
- $FDR = F/S$
- $S = \#\{p_i < \alpha\}$
- $F = \alpha * m_0$
- $FDR = q\text{-value} = \alpha * m_0 / \#\{p_i < \alpha\}$
- I know  $S$ , I know  $\alpha$ , what is  $m_0$ ?

## False Discovery Rate

Distribution of 3170 p-values when all null hypotheses are true



Distribution of 3170 p-values from Hedenfalk et al. Height of the line gives estimated proportion of true null hypotheses.



$$m_0(\lambda) = \frac{\#\{p_i > \lambda; i = 1 \dots m\}}{(1 - \lambda)}$$

## False Discovery Rate

- $q(\alpha) = \alpha * m_0(\lambda) / \#\{p_i < \alpha\}$   
(technically  $q(\alpha) = \min_{t \geq \alpha} q(t)$  )
- Program QVALUE (<http://genomine.org/qvalue/>) or `p.adjust()` in R
- Eg. Hedenfalk et al. ( $m_0(.5) = 2143$ )

		No. differentially expressed	
<u>q</u>	<u><math>\alpha</math></u>	<u><math>\#\{p_i &lt; \alpha\}</math></u>	<u>expected false pos</u>
.01	.0000126	5	0
.05	.00373	160	8
.10	.0148	317	32

- Using traditional methods Hedenfalk et al. concluded 9-11 genes were differentially expressed.