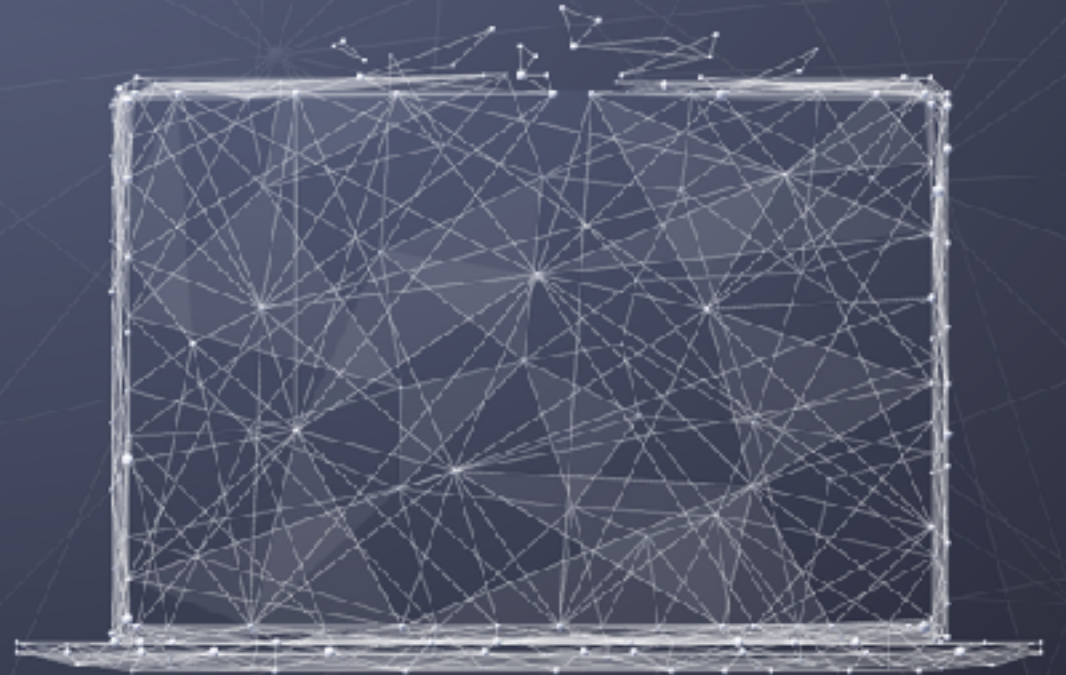


Data Science Foundations of Decision Making

Multiple hypothesis testing



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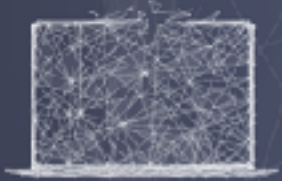
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Recall: hypothesis testing errors

	H_0 true	H_1 true
Accept H_0	Correct $1-\alpha$	Type II error β
Reject H_0	Type I error α	Correct $1-\beta$

- α = Type I error; β = Type II error



Testing more than one hypothesis



Testing more than one hypothesis

- If we perform one hypothesis tests, what is the probability of a false positive?
(i.e., reject the null when it is true)
 - $P(\text{Making an error}) = \alpha$ *(typically 0.05)*
 - $P(\text{Not making an error}) = 1 - \alpha$ *(1-0.05 = 0.95)*

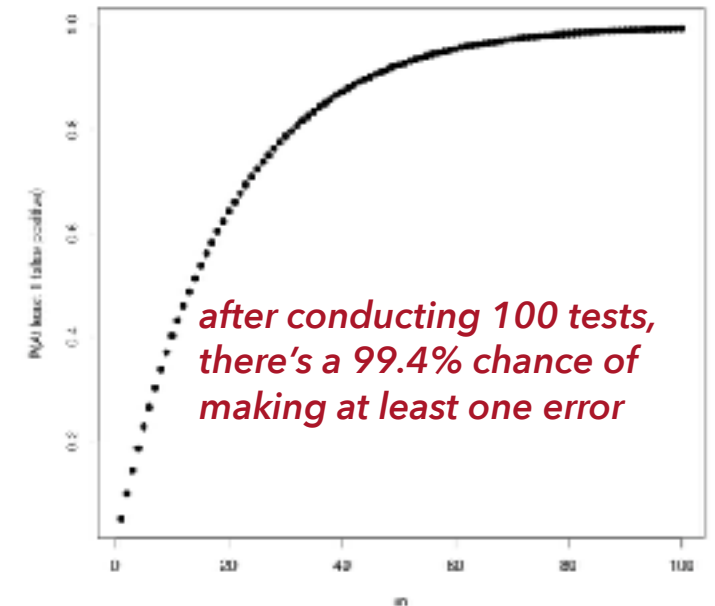


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- In general, if we perform m hypothesis tests, what is the probability of at least one false positive?
 - $P(\text{Not making an error in } m \text{ tests}) = (1 - \alpha)^m$
when $m=2$, $0.95^2=0.90$
 - $P(\text{Making at least one error in } m \text{ tests}) = 1 - (1 - \alpha)^m$
1-0.95²=0.10

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The # of test conducted increase , the chance to make error↑



What happens when you test multiple hypotheses?

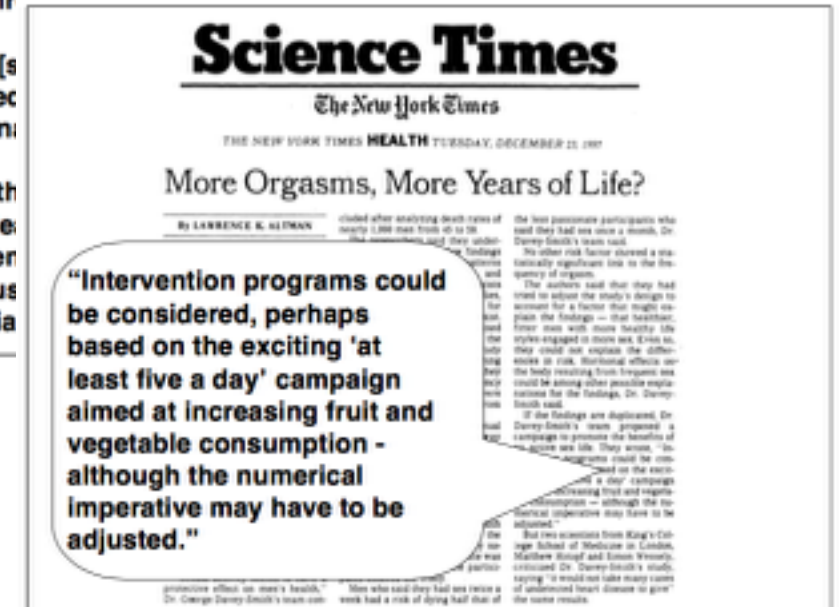


Things identified as cancer risks (Altman and Simon 1992)

- Electric razors
- Fluorescent lights
- Allergies
- Being a waiter
- Owning a pet bird
- Eating hot dogs
- Being short
- Being tall
- Having a refrigerator
- ...

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Multiple comparisons

- Investigators often test dozens of hypotheses, and don't always decide on those hypotheses before they have looked at their data
- Hypothesis tests and p-values are much harder to interpret when multiple comparisons have been made



Adjusting for multiple hypotheses

- When people say “adjusting p-values for the number of hypothesis tests performed” what they mean is controlling the Type I error rate α
- This is a very active area of statistics - many different methods have been developed
- Simple corrections adjust the level of significance to ensure that experiment-wide Type I error rates are controlled



Bonferonni correction

- Very simple method for ensuring that the overall Type I error rate of α is maintained when performing m independent hypothesis tests
- Approach: reject any hypothesis with $p\text{-value} \leq \alpha/m$
- For example, to ensure an experiment-wide Type I error rate of $\alpha=0.05$ when 10,000 hypothesis tests are performed, Bonferroni correction uses a p-value threshold of $\alpha^* = 0.05/10000 = 5 \times 10^{-6}$ to declare significance



Example

- A study published in the New England Journal of Medicine investigated whether vitamin intake affected the risk of breast cancer
- The study carried out hypothesis tests concerning:
 - vitamin C, vitamin E, and vitamin A
- And reported three separate p-values:
 - 0.67 for vitamin C, 0.07 for vitamin E, and 0.001 for vitamin A



Example

- Interpreting each p-value is straightforward, but what do they mean together?
- Suppose we set the type I error rate at $\alpha = 0.05$ for each test; what is the probability of committing at least one type I error?
- $P(\text{At least one error} \mid \text{All three } H_0 \text{ are true}) = 1 - 0.953 = 14.3\%$



Example

- Instead of testing each individual hypothesis at $\alpha = 0.05$, we use a Bonferroni corrected $\alpha^* = 0.05/m$
- For the vitamin study, $m = 3$ so $\alpha^* = 0.017$
- Thus, the vitamin A finding is still significant even in light of the multiple comparisons that were made (recall that its p-value was 0.001)

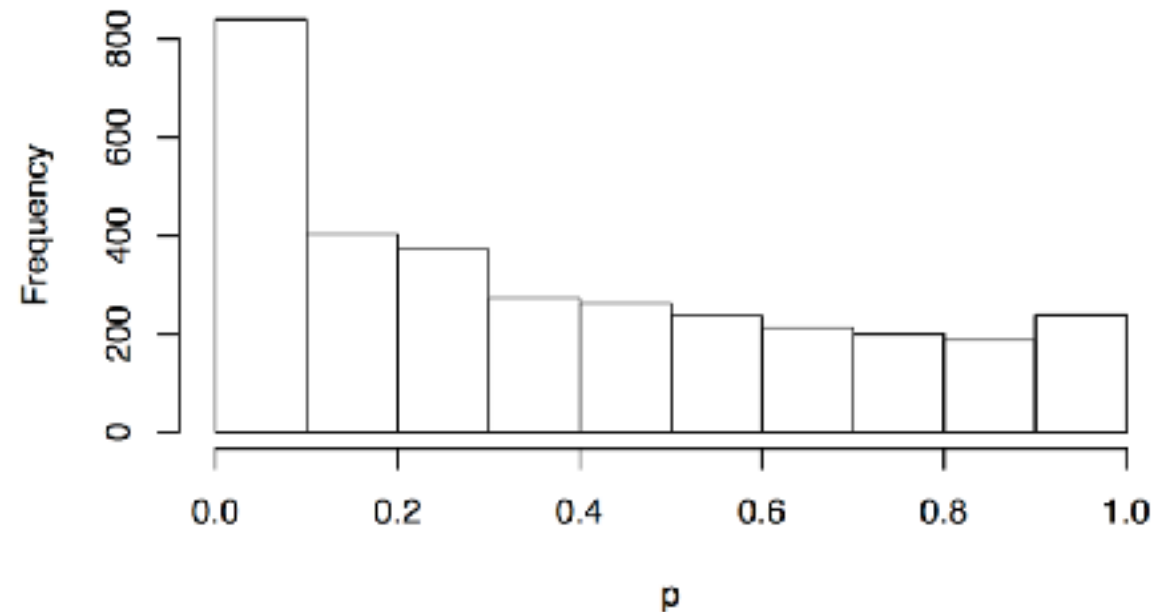


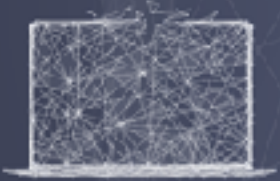
Bonferroni limitations

- The Bonferroni approach works well when the number of hypotheses is fairly small and making a single type I error is costly
- However, studies often test large numbers of hypotheses, expecting to find dozens of significant results, and if 3 or 4 type I errors were introduced, no great harm would be done
- Examples: AB testing, genome-wide studies

Breast cancer gene study

- For example, a landmark study by researchers at the National Institutes of Health tried to find genes associated with breast cancer
- They looked at 3,226 genes and found 207 genes with a pvalue less than $\alpha = 0.01$





False discovery rate



False discovery rate

- If they had used the Bonferroni correction, they would have had to test each gene using a significance level of $\alpha^* = 1.0 \times 10^{-5}$
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- If they had used the Bonferroni correction, they would have had to test each gene using a significance level of $\alpha^* = 1.0 \times 10^{-5}$
 - This is quite strict, only four of pvalues are below this threshold
- An alternative to the Bonferroni correction that is as strict is controlling the false discovery rate (FDR)
- Instead of trying to control the overall probability of a type I error, the FDR controls the proportion of significant findings that are type I errors
 - If a cutoff of α for the individual hypothesis tests results in s significant findings among m tests, then the false discovery rate is:

$$FDR = \frac{m\alpha}{s}$$



FDR for breast cancer gene study



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- In the breast cancer study, there were 207 p-values below $\alpha = 0.01$ so

$$FDR = \frac{m\alpha}{s} = \frac{3226 \cdot 0.01}{207} = 0.156$$



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$$FDR = \frac{3226 \cdot 0.0038}{122} = 0.10$$

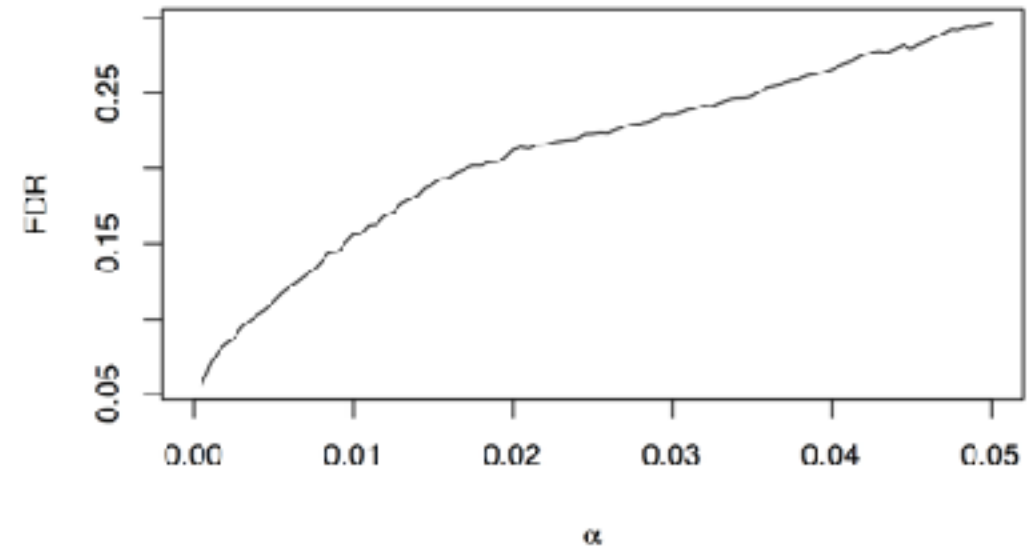
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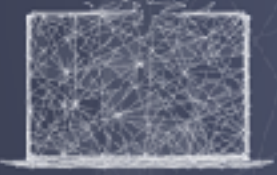
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- If we choose an FDR of 0.10, then we'd set the pvalue threshold to $\alpha^* = 0.0038$ because there are 122 genes with p-val's less than 0.0038

$$FDR = \frac{3226 \cdot 0.0038}{122} = 0.10$$





Takeaways

- When you're the investigator, you can account for multiple comparisons because you can keep track of all the comparisons/tests that are made
- Beware of other investigators that make many comparisons but only publish the few that were significant
 - Exploratory analyses can easily generate hundreds of p-values, many of which will be significant
- The FDA regulates this for clinical trials by requiring investigators to:
 - Plan all analyses before the data are collected
 - Complete and report all planned analyses