# STA 35C: Statistical Data Science III

**Lecture 18: Multiple Hypotheses Testing** 

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#### **Announcement**

### **Midterm 2** on Fri, May 16 (12:10 pm-1:00 pm in class)

- Arrive early: The exam starts at 12:10 pm and ends at 1:00 pm sharp
- One hand-written cheat sheet: Letter-size (8.5"×11"), double-sided, brief formulas/notes
- Calculator: A simple (non-graphing) scientific calculator is allowed
- No other materials beyond the single cheat sheet (no textbooks, etc.)
- SDC accommodations: Confirm scheduling with AES online ASAP

#### **Preparation tips:**

- Primary coverage: Lectures 12–19 (including next Wed)
- A practice midterm and brief solution key is available on course webpage
- Office hours this week:
  - Instructor: Wed, 4-6pm (extended); no OH on Thu
  - TA: Mon/Thu 1-2pm

# Today's topics

### Multiple hypotheses testing

- Recap: Motivation & challenges
  - Issues arising with multiple tests
  - Real-world concerns: p-hacking & data dredging
- Family-wise error rate (FWER)
  - Definition & intuition
  - Controlling FWER: Bonferroni correction & Holm's step-down
- False discovery rate (FDR)
  - Definition & intuition
  - Controlling FDR: Benjamini-Hochberg procedure

## **Recap: Multiple testing**

#### Single-hypothesis test:

- Typically set up  $H_0$ , and gather data to reject it if there is significant evidence
- Type I error = false positive; Type II error = false negative
- Each test has Type I error at most  $\alpha$  (e.g. 0.05)

#### Modern data analysis: multiple tests simultaneously

- E.g. Testing thousands of predictors or biomarkers to discovery significant ones
- If m is large, false rejections can occur easily by chance
- ullet On average, lpha imes m false positives if each test is at level lpha

**Key challenge:** Address the inflation of false positives as *m* grows

# Related issues: p-hacking and data dredging

Real danger: Searching for "significant" results in many ways until something "works"

- Repeatedly testing different hypotheses/subgroups
- Eventually, some test may yield p < 0.05 by chance

Outcome: Spurious "discoveries"

- Published claims may fail to replicate
- True findings can be overshadowed by noise

**Conclusion:** Systematic multiple-testing corrections are crucial, especially for large m

## Articles warning about misused statistical significance





Figure: Many reproducibility crises trace back to undisclosed multiple testing or selective reporting. Proper adjustments can help mitigate these issues.

# Family-wise error rate (FWER): Definition

**Single test:**  $Pr(Type \mid error) = Pr(reject a true null)$ 

**Multiple tests** (*m* hypotheses):

$$FWER = Pr(reject at least one true H_0),$$

i.e. the probability of any false positive among m tests

**If tests are independent**, and each are at level  $\alpha$ :

$$FWER = 1 - (1 - \alpha)^m,$$

which grows quickly with m

• E.g. m = 20,  $\alpha = 0.05 \implies \text{FWER} \approx 0.64 \gg 0.05$ 

### **Visualization:** FWER grows as *m* increases

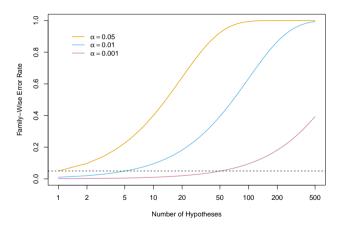


Figure: FWER vs. number of tests m (log scale) for  $\alpha=0.05$  (orange), 0.01 (blue), 0.001 (purple). The dashed line is 0.05. For m=50 and target FWER=0.05, each test must be at  $\alpha=0.001$  [JWHT21, Figure 13.2].

### The Bonferroni correction

#### Key idea:

Observe that

$$\text{FWER} = \Pr\left(\sum_{j=1}^{m} \left\{ \text{Reject } H_j \right\} \right) \leq \sum_{j=1}^{m} \Pr\left(\left\{ \text{Reject } H_j \right\} \right)$$

• Each test is done at level  $\alpha/m \implies \Pr(\{\text{Reject } H_j\}) \leq \alpha/m \implies \text{FWER} \leq \alpha$ 

### The Bonferroni method (Bonferroni correction):

• For each hypothesis  $H_1,\ldots,H_m$ , reject  $H_j$  if only if  $p_j<rac{lpha}{m}$ 

#### **Pros & Cons:**

- Pros: Simple & widely used
- Cons: Often *very conservative*  $\implies$  few rejections (=discoveries) & lower power<sup>1</sup>

 $<sup>^{1}</sup>$ Power = TPR = the fraction of false null hypotheses that are successfully rejected

## **Example: Bonferroni correction**

#### Example

Let m = 6 hypotheses with p-values:

$$p_1 = 0.0018$$
,  $p_2 = 0.009$ ,  $p_3 = 0.021$ ,  $p_4 = 0.034$ ,  $p_5 = 0.045$ ,  $p_6 = 0.070$ .

At  $\alpha=$  0.05, threshold  $=\frac{\alpha}{m}=\frac{0.05}{6}\approx$  0.00833.

Reject 
$$H_j$$
 if  $p_j < 0.00833$ .

Hence:

$$p_1 = 0.0018 < 0.00833 \implies \text{reject } H_1,$$

but  $p_2 = 0.009 > 0.00833$  and the rest are larger. So Bonferroni rejects only  $H_1$ .

**Conclusion:** 1 rejection using Bonferroni, whereas naive p < 0.05 would reject 5 of them  $(p_1, \ldots, p_5)$ .

## Holm's step-down procedure

Holm's method refines Bonferroni to be less conservative:

#### Holm's method

- 1 Specify  $\alpha$ , the level at which to control the FWER
- 2 Compute the *p*-values for the *m* null hypotheses,  $H_{01}, \ldots, H_{0m}$
- 3 Sort p-values so that  $p_{(1)} \leq p_{(2)} \leq \cdots \leq p_{(m)}$
- 4 Define

$$L = \min \left\{ j : p_{(j)} > \frac{\alpha}{m+1-j} \right\}$$

5 Reject all null hypotheses  $H_{0j}$  for which  $p_j < p_{(L)}$ 

#### **Properties:**

- Ensures  $FWER \leq \alpha$
- Rejects at least as many hypotheses as Bonferroni

## **Example: Holm's step-down procedure**

#### Example

- **Step 1:** Set  $\alpha = 0.05$
- **Step 2:**  $p_1 = 0.0018, p_2 = 0.009, p_3 = 0.021, p_4 = 0.034, p_5 = 0.045, p_6 = 0.070.$
- **Step 3:** Sort *p*-values  $p_{(1)} = 0.0018$ ,  $p_{(2)} = 0.009$ ,  $p_{(3)} = 0.021$ ,  $p_{(4)} = 0.034$ ,  $p_{(5)} = 0.045$ ,  $p_{(6)} = 0.070$ .
- **Step 4:** Find L = 3 because

$$p_{(1)} = 0.0018 ? 0.0018 \le \frac{0.05}{6+1-1} = \frac{0.05}{6} \approx 0.00833$$
  $\implies$  reject  $H_{(1)}$ , continue  $p_{(2)} = 0.009 ? 0.009 \le \frac{0.05}{6+1-2} = \frac{0.05}{5} = 0.01$   $\implies$  reject  $H_{(2)}$ , continue  $p_{(3)} = 0.021 ? 0.021 \le \frac{0.05}{6+1-3} = \frac{0.05}{4} = 0.0125?$  No  $\implies$  stop;  $L = 3$ 

**Step 5:** We reject  $H_{(1)}$ ,  $H_{(2)}$  total 2 rejections. The rest are not rejected.

Conclusion: Holm's method rejects 2, whereas Bonferroni rejected only 1.

### Visualization: Bonferroni vs. Holm

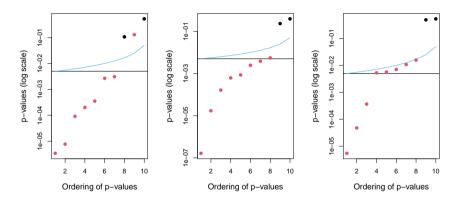


Figure: Each panel shows sorted p-values from a separate simulation of m=10 null hypotheses, with the two true nulls in black and the others in red. Controlling the FWER at 0.05, Bonferroni rejects all points below the **black** line, while Holm rejects all below the **blue** line. The gap between these lines indicates the additional hypotheses Holm rejects but Bonferroni does not. In the middle panel, Holm rejects one more null than Bonferroni; in the right panel, it rejects five more [JWHT21, Figure 13.3].

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# FWER vs. power trade-off

#### **FWER** demands *no* false rejections with probability at least $1 - \alpha$ :

- Very stringent if m is large
- Tends to reduce power (fewer true positives found)

#### In modern "exploratory" studies:

- We may tolerate a small fraction of false positives to discover more true ones
- This leads to the false discovery rate (FDR) approach

## Illustration: power vs. FWER

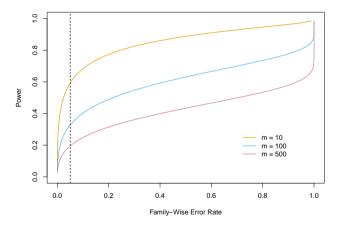


Figure: In a simulation with 90% of m nulls true, the power is displayed against FWER. Colors of the curves: m = 10 (orange), m = 100 (blue), m = 500 (purple). Larger m reduces power. The vertical dashed line marks FWER=0.05 [JWHT21, Figure 13.5].

# False discovery rate (FDR): Definition and motivation

**Motivation:** Controlling FWER can be too conservative for large m

Instead: control the fraction of rejected hypotheses that are false positives

$$FDP = \frac{\# \text{ false positives}}{\# \text{ total rejections}}$$
 ( = 0 if no rejections).

### False discovery rate (FDR) = $\mathbb{E}[\mathsf{FDP}]$

 Among the "discoveries," we want to ensure a fraction up to q may be false positives on average

#### **Properties:**

- Accept a small fraction of false positives, in exchange for more total discoveries
- Typically yields more rejections ("discoveries") than FWER-based methods

# Controlling FDR: Benjamini-Hochberg procedure

### Benamini-Hockberg procedure

- 1 Specify q, the level at which to control the FDR
- 2 Compute the *p*-values for the *m* null hypotheses,  $H_{01}, \ldots, H_{0m}$
- 3 Sort p-values so that  $p_{(1)} \leq p_{(2)} \leq \cdots \leq p_{(m)}$
- 4 Define

$$L = \max\left\{j: p_{(j)} < \frac{qj}{m}\right\}$$

5 Reject all null hypotheses  $H_{0j}$  for which  $p_j \leq p_{(L)}$ 

#### Result:

- Ensures FDR  $\leq q$ , but but not necessarily small FWER
- Typically more powerful, yielding more rejections, than Bonferroni/Holm if m is large

# **Example: Benjamini-Hochberg procedure**

#### Example

**Step 1:** Set q = 0.05

**Step 2:**  $p_1 = 0.0018$ ,  $p_2 = 0.009$ ,  $p_3 = 0.021$ ,  $p_4 = 0.034$ ,  $p_5 = 0.045$ ,  $p_6 = 0.070$ .

**Step 3:** Sort *p*-values  $p_{(1)} = 0.0018$ ,  $p_{(2)} = 0.009$ ,  $p_{(3)} = 0.021$ ,  $p_{(4)} = 0.034$ ,  $p_{(5)} = 0.045$ ,  $p_{(6)} = 0.070$ .

**Step 4:** Find L = 3 because

$$k=1: \quad 0.0018 \le 0.05 \times \frac{1}{6} \approx 0.0083? \checkmark$$
 $k=2: \quad 0.009 \le 0.05 \times \frac{2}{6} \approx 0.0167? \checkmark$ 
 $k=3: \quad 0.021 \le 0.05 \times \frac{3}{6} = 0.025? \checkmark$ 
 $k=4: \quad 0.034 \le 0.05 \times \frac{4}{6} \approx 0.0333? \text{ No } (0.034 > 0.0333)$ 

**Step 5:** Reject  $H_{(1)}, H_{(2)}, H_{(3)}$ .

Conclusion: BH rejects 3, while Holm rejects 2, Bonferroni rejects 1.

# Visual comparison: Bonferroni vs. Benjamini-Hochberg

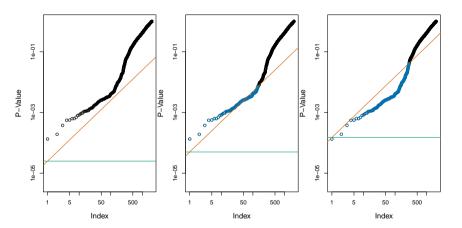


Figure: Panels: same set of m=2000 sorted p-values for the Fund dataset. Green lines: thresholds for FWER control (Bonferroni) at  $\alpha=0.05,\,0.1,\,0.3$  (left to right). Orange lines: thresholds for FDR control (Benjamini-Hochberg) at  $q=0.05,\,0.1,\,0.3$  (left to right). E.g., When the FDR is controlled at  $q=0.1,\,146$  nulls are rejected (center, blue points). At  $q=0.3,\,279$  nulls are rejected (right, blue points) [JWHT21, Figure 13.6].

### Wrap-up

- **FWER** (Bonferroni/Holm):
  - Strictly ensures  $Pr(any false positive) \le \alpha$
  - Conservative for large m, leading to fewer rejections & reduced power
- **FDR** (Benjamini–Hochberg):
  - Controls the expected fraction of false positives among rejections
  - ullet Typically yields more rejections than FWER, especially for large m
- Practical consideration:
  - Use FWER for strict confirmatory analyses needing minimal Type I error
  - Use FDR for exploratory, large-scale studies, tolerating some false positives to gain more discoveries

### References



Gareth James, Daniela Witten, Trevor Hastie, and Robert Tibshirani.

An Introduction to Statistical Learning: with Applications in R, volume 112 of Springer Texts in Statistics.

Springer, New York, NY, 2nd edition, 2021.