The Labyrinth of Multiple Testing: How to avoid the pitfall of false positives

FWER control

12th SISMEC National Congress 2023

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Outline

1. FamilyWise Error Rate (FWER)

- 2. Bonferroni (single-step)
- 3. Holm (step-wise)
- 4. Closed Testing
- 5. Gatekeeping strategies
- 6. Summary

FamilyWise Error Rate (FWER)

		Null hypothesis False True		
		False	True	Tot
Test	Rejected	5	V	R
	Rejected Not rejected	T	U	m-R
	Tot	m_1	m_0	m

$$\mathsf{FWER} = \mathbb{P}(\mathsf{at\ least\ one\ type\ I\ error}) = \mathbb{P}({\color{red} \textcolor{red} \textcolor{black}{V}} > 0)$$

A procedure **controls** it if FWER $\leq \alpha$.

Šidàk correction

If I want to check the **FWER** at the α level, at which individual $\widetilde{\alpha}$ level should I reject the individual tests?

$$\begin{split} \mathrm{FWER} &= \mathbb{P} \big(p_i \leq \widetilde{\alpha} \text{ for at least one } i \text{ true null hypothesis} \big) \\ &= \mathbb{P} \Big(\bigcup_{i \in \{ \text{true null hypotheses} \}} \{ p_i \leq \widetilde{\alpha} \} \Big) \\ &= 1 - \mathbb{P} \Big(\bigcap_{i \in \{ \text{true null hypotheses} \}} \{ p_i > \widetilde{\alpha} \} \Big) = \\ &\qquad (deMorgan) \\ &= 1 - (1 - \widetilde{\alpha})^{m_0} = (m_0 : \#\{ \text{true null hypothesis} \}) \\ &\qquad (\text{we don't know } m_0, \text{ we know that though } m_0 \leq m) \\ &\leq 1 - (1 - \widetilde{\alpha})^m \end{split}$$

Šidàk correction

From this, we get:

$$\alpha = 1 - (1 - \widetilde{\alpha})^m$$

$$1 - \alpha = (1 - \widetilde{\alpha})^m$$

$$(1 - \alpha)^{1/m} = (1 - \widetilde{\alpha})$$

$$\widetilde{\alpha} = 1 - (1 - \alpha)^{1/m}$$

Then, it is enough to reject every single hypothesis at the level

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(i.e., I reject the p-values for which $p \leq \widetilde{\alpha}$)

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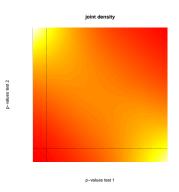
$$\widetilde{\alpha} = 1 - (1 - \alpha)^{1/m}$$

(i.e., I reject the p-values for which $p \leq \tilde{\alpha}$)

PROBLEM: it is valid only when the p-values are **INDEPENDENT**. In most cases, the tests have dependence-induced dependence between the original variables.

Dependent P-values

It may happen that $\mathbb{P}(\text{at least one false rejection of } H_0) > (!)1 - (1 - \alpha)^2$



Remark: Remember, however, that the marginal distributions are uniform because the two tests are under H_0 .

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Boole

Boolean inequality

Let two events A e B:

$$\mathbb{P}(A \cup B) = \mathbb{P}(A) + \mathbb{P}(B) - \mathbb{P}(A \cap B)$$

SO

$$\mathbb{P}(A \cup B) \leq \mathbb{P}(A) + \mathbb{P}(B)$$

Generalizing A_1, \ldots, A_m :

$$\mathbb{P}(\bigcup_{i=1}^m A_i) \leq \sum_{i=1}^m \mathbb{P}(A_i)$$

Equality

Equality occurs when events are disjointed

FamilyWise Error Rate (FWER)

Bonferroni inequality

Reduce α Reject H_i if $p_i \leq \tilde{\alpha} = \alpha/m$ (m = number of hypotheses)

FWER control

$$\begin{split} \mathrm{FWER} &= & \mathbb{P} \big(p_i \leq \alpha/m \; \; \text{for at least one } i \; \text{true null hypothesis} \big) \\ &= & \mathbb{P} \Big(\bigcup_{i \in \{ \text{true null hypothesis} \}} \{ p_i \leq \alpha/m \} \Big) \\ &\leq & \sum_{i \in \{ \text{true null hypothesis} \}} \mathbb{P} \big(p_i \leq \alpha/m \big) \\ &\leq & m_0 \frac{\alpha}{m} \leq m \frac{\alpha}{m} = \alpha \end{split}$$

Bonferroni Procedure

Multiplicity adjusted p-value

$$|\widetilde{p}_i = mp_i|$$
 for $i = 1, \ldots, m$ and reject if $\widetilde{p}_i \leq lpha$

Advantages

- Very simple
- Controls the FWER under **any** dependency

Disadvantages

■ Conservative (adjusted p-values are often high, leading to few rejections)

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- **1.** First step: adjusted p-value: $p \cdot m$; reject if $\leq \alpha$
- **2.** After r rejections, adjusted p-value: $p \cdot (m-r)$
- 3. Stop as soon as nothing is rejected

Adj. p-value:
$$p_A 5$$
 $p_B 5$ $p_C 5$ $p_D 5$ $p_E 5 \le ?\alpha$

$$\mathcal{H}\setminus\mathcal{R}$$
:









Bonferroni

 \mathcal{R} :

¹Holm S. (1979) A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics*; 6(2):65–70.

- **1.** First step: adjusted p-value: $p \cdot m$; reject if $\leq \alpha$
- **2.** After *r* rejections, adjusted p-value: $p \cdot (m-r)$
- 3. Stop as soon as nothing is rejected

Suppose p_A and p_C are significant

Adj. p-value: $p_A 5$ $p_B 5$ $p_C 5$ $p_D 5$ $p_E 5$ $\leq ?\alpha$

 $\mathcal{H} \setminus \mathcal{R}$:











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- **1.** First step: adjusted p-value: $p \cdot m$; reject if $\leq \alpha$
- **2.** After r rejections, adjusted p-value: $p \cdot (m-r)$
- 3. Stop as soon as nothing is rejected

Adjusted p-value:
$$p \cdot 3$$

Adj. p-value: - p_B3 - p_D3 p_E3 $\leq ?\alpha$

 $\mathcal{H} \setminus \mathcal{R}$:

В

D

Е

 \mathcal{R} :

Α

C

¹Holm S. (1979) A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics*; 6(2):65–70.

- **1.** First step: adjusted p-value: $p \cdot m$; reject if $\leq \alpha$
- **2.** After r rejections, adjusted p-value: $p \cdot (m-r)$
- 3. Stop as soon as nothing is rejected

Suppose p_D is significant

Adj. p-value: $-p_B3 - p_D3 p_E3 \le ?\alpha$

 $\mathcal{H} \setminus \mathcal{R}$:







 \mathcal{R} :

Α



¹Holm S. (1979) A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics*; 6(2):65–70.

- **1.** First step: adjusted p-value: $p \cdot m$; reject if $\leq \alpha$
- **2.** After r rejections, adjusted p-value: $p \cdot (m-r)$
- 3. Stop as soon as nothing is rejected

Adjusted p-value:
$$p \cdot 2$$

Adj. p-value:
$$-p_B2$$
 - $-p_E2 \le ?\alpha$

$$\mathcal{H} \setminus \mathcal{R}$$
:

$$\mathcal{R}: A C$$

¹Holm S. (1979) A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics*; 6(2):65–70.

- **1.** First step: adjusted p-value: $p \cdot m$; reject if $\leq \alpha$
- **2.** After r rejections, adjusted p-value: $p \cdot (m-r)$
- 3. Stop as soon as nothing is rejected

No rejections. Stop

Adj. p-value: -
$$p_B 2$$
 - - $p_E 2 \le ?\alpha$

$$\mathcal{H} \setminus \mathcal{R}$$
:

$$\mathcal{R}$$
: A C

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Closed Testing²

Closed Set of Hypotheses (all possible intersections)

Initial Hypotheses



²R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. Biometrika 63: 655-660.

Closed Testing²

Top Node Test (e.g., MANOVA)

Closed Set **ABC** AC BC

²R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. Biometrika 63: 655-660.

Closed Testing⁴

- lacktriangle Test each hypothesis at level lpha
- Reject an individual hypothesis A if you reject all hypotheses where A is component.

Example: Reject H_A if $p_A \leq \alpha$, $p_{AB} \leq \alpha$, $p_{AC} \leq \alpha$ and $p_{ABC} \leq \alpha$

Relevance: **ANY** multiple testing procedure can be written as Closed Testing procedure. ³ This makes easy to prove the control of the Type I error for new procedures.

Disadvantage: The tested hypotheses often become too many: $= 2^{\text{hypotheses}} - 1$ (i.e., research focuses on shortcuts. see next...)

³Goeman, Hemerik, and Solari (2021) Only closed testing procedures are admissible for controlling false discovery proportions. Ann. Statist. 49(2): 1218-1238

 $^{^4}$ R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. Biometrika 63: 655-660.

Holm as a Closed Testing procedure

$$\begin{array}{c|c} & & & & \\ & 3 \min(p_A, p_B, p_C) \\ & & & \\ 2 \min(p_A, p_B) & 2 \min(p_A, p_C) & 2 \min(p_B, p_C) \\ & & & \\ \hline A & & B & C \\ & p_A & p_B & p_C \end{array}$$

Assume w.l.o.g. $p_A \le p_B \le p_C$:

- $3 \min(p_A, p_B, p_C) \le \alpha$ implies $2 \min(p_A, p_B) \le \alpha$, $2 \min(p_A, p_C) \le \alpha$ and $p_A \le \alpha$, that is Reject H_A
- $2 \min(p_B, p_C) \le \alpha$ implies $p_B \le \alpha$ (already $3 \min(p_A, p_B, p_C) \le \alpha$ and $2 \min(p_A, p_B) \le \alpha$), that is Reject H_B .

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Union-intersection hypothesis

Reject the global hypothesis of no effect if there is evidence of an effect with respect to **AT LEAST ONE** individual objective:

- the trial's outcome is declared positive if at least one analysis produces a significant result,
- Each analysis is independently clinically relevant
- Each endpoint, dose, or population analysis independently provides proof of efficacy

Let denote the hypotheses H_1, \ldots, H_m corresponding to the multiple objectives tested against the alternative hypotheses K_1, \ldots, K_m :

$$H_I: \cap_{i=1}^m H_i$$
 versus $H_U: \cup_{i=1}^m K_i$

→ adjust for multiplicity!

Gatekeeping strategies

Multiple objectives pursued in clinical trials typically exhibit a **hierarchical** structure \rightarrow Primary and secondary objectives.

To construct a **gatekeeping procedure**, one first needs to define two or more families of analyses, for example:

- Primary and secondary endpoints: Primary endpoints determine the trial's outcome, and key secondary endpoints provide useful supportive information about efficacy and safety
- **Primary and secondary populations**: General population versus **subgroups** of patients who are more likely to benefit from treatment
- Primary and secondary tests: Noninferiority assessment as the primary analysis followed by a superiority assessment

Gatekeeping strategies

Family 1: $F_1 = \{H_1, \dots, H_{k_1}\}$, null hypotheses

Family m: $F_m = \{H_{k_{m-1}+1}, \dots, H_{k_m}\}$, null hypotheses

Each family (except for the last one) serves as a **gatekeeper** for the next one, in the sense that one must pass it to perform analyses in the next family

 \rightarrow increase power by accounting for hierarchical structure of multiple families.

- α allocation: Initial distribution of the error rate α across the hypotheses.
- α **propagation**: "Use it or lose it" principle: After a hypothesis is rejected, the significance level used can be applied to remaining non-rejected hypotheses. \rightarrow follows from the closure principle and does not result in EWER inflation.
 - Sequential Testing: Families of hypotheses are tested sequentially starting with Family $1 \to \text{Error}$ rate is transferred along the sequence
 - Sequential testing with re-testing: Families of hypotheses are tested sequentially starting with Family 1 with a re-testing loop \rightarrow Error rate is transferred along the sequence and then back to Family 1
 - **Simultaneous testing**: Families of hypotheses are tested simultaneously → Error rate is transferred among families

Sequential Testing

(three ordered endpoints: high, medium, low doses versus placebo)

A primary endpoint

B secondary endpoint

C tertiary endpoint

Sequential Testing

(three ordered endpoints: high, medium, low doses versus placebo) Start test A at α

B secondary endpoint

tertiary endpoint

Sequential Testing

(three ordered endpoints: high, medium, low doses versus placebo) Suppose $p_A < \alpha$

> A primary endpoint

B secondary endpoint

C tertiary endpoint

Sequential Testing (three ordered endpoints: high, medium, low doses versus placebo) Go on to test B at α

Sequential Testing (three ordered endpoints: high, medium, low doses versus placebo) Suppose $p_B > \alpha$. Stop

A
primary
endpoint

B
secondary
endpoint

α

C tertiary endpoint

Sequential procedure as a Closed Testing procedure

Hypotheses are pre-ordered, and individual tests are also used for intersection hypotheses:

$$ABC$$

$$p_{ABC} = p_{A}$$

$$AB$$

$$AC$$

$$p_{AB} = p_{A}$$

$$p_{AC} = p_{A}$$

$$p_{BC} = p_{B}$$

$$A$$

$$B$$

$$D_{B}$$

$$D_{C}$$

- $p_A \le \alpha$ implies $p_{AB} = p_{AC} = p_{ABC} = p_A \le \alpha$
- $p_B \le \alpha$ implies $p_{BC} = p_B \le \alpha$ (and $p_{AB} = p_{ABC} \le \alpha$ already).

Parallel Gatekeeping ⁵

Family 1 is a **parallel gatekeeper** for Family 2, i.e., **at least one** hypothesis must be rejected in Family 1 to proceed to Family 2.

Example: Schizophrenia trial

Objective: Evaluate the efficacy of a treatment in patients diagnosed with

schizophrenia

Design: Two doses of treatment (Doses L and H) versus placebo.

Treatment effect on at least one dose must be significant.

Primary endpoint: Positive and Negative Symptoms Scale (PANSS) total

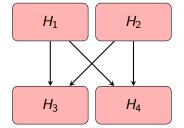
score

Two patient populations: General population and subpopulation (based on a genotypic classifier)

 $^{^5}$ Dmitrienko, A., Offen, W. W., and Westfall, P. H. (2003). Gatekeeping strategies for clinical trials that do not require all primary effects to be significant. Statistics in medicine, 22(15), 2387-2400.

Parallel Gatekeeping

Family 1



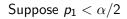
Family 2

Family 1: $\{H_1, H_2\}$ Doses L and H versus Placebo in overall population **Family 2**: $\{H_3, H_4\}$ Doses L and H versus Placebo in subpopulation

Start test H_1 and H_2 at $\alpha/2$

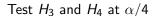
 H_1 Dose L overall population H_2 Dose H overall $\frac{\alpha}{2}$

 H_3 Dose L sub-population H_4 Dose H sub-population

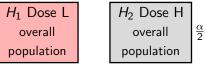


 H_1 Dose L overall population H_2 Dose H overall $\frac{\alpha}{2}$

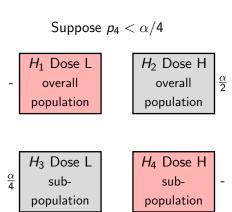
 H_3 Dose L sub-population H_4 Dose H sub-population

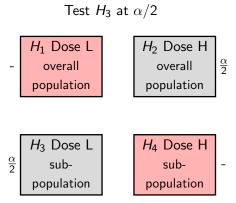


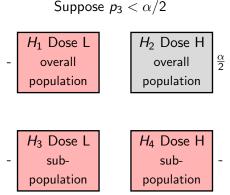


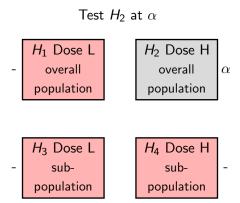




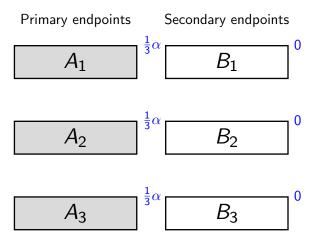




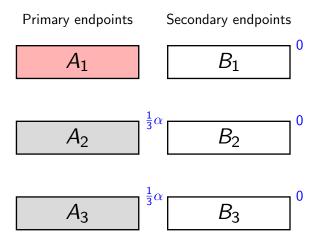




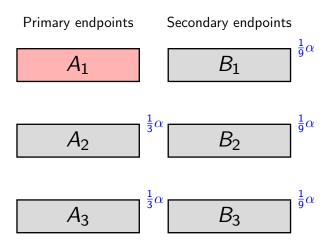
Test all primary endpoints at $\alpha/3$



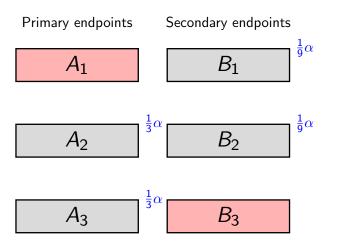
If we reject a few...



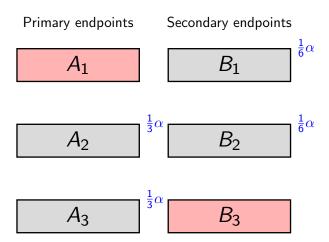
Go on with the secondary endpoints with the available α



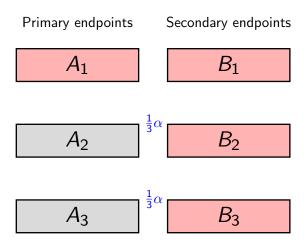
Suppose we are able to reject some of the secondary endpoints. . .



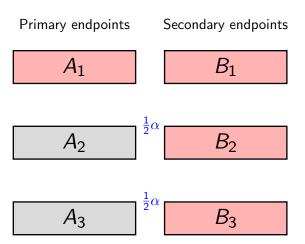
Go on doing Holm for the secondary endpoints



And if we reject all secondary ones...



Go on doing Holm for the primary endpoints



Intersection-Union test

Intersection-Union testing arises naturally in studies when a significant outcome with respect to two or more objectives is required in order to declare the study successful.

- All analyses must show benefit
- The trial's outcome is positive if all analyses produce a significant outcome

$$H_I: \cup_{i=1}^m H_i$$
 versus $H_U: \cap_{i=1}^m K_i$

→ no multiplicity adjustment!

Serial Gatekeeping ⁶

Family 1 is a **serial gatekeeper** for Family $2 \rightarrow All$ hypotheses must be rejected in Family 1 to proceed to Family 2.

Example: Alzheimer's diseases trial

Objective: Evaluate the effects of a treatment on cognition and global

changes in patients with mild to moderate Alzheimer's disease

Design: Treatment versus placebo

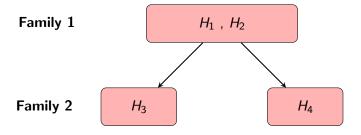
Primary endpoints: Endpoint 1: Cognition endpoint (ADAS-Cog),

Endpoint 2: Clinical global scale (CIBIC plus)

Treatment effect on both endpoints must be significant

Secondary endpoints; Endpoint 3: Biochemical marker, Endpoint 4: Imaging marker

⁶Westfall, P. H., Krishen, A. (2001). Optimally weighted, fixed sequence and gatekeeper multiple testing procedures. Journal of Statistical Planning and Inference, 99(1), 25-40.

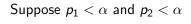


Family 1: $\{H_1, H_2\}$ Treatment versus Placebo on cognition and clinical global scale

Family 2: $\{H_3, H_4\}$ Treatment versus Placebo on biochemical and imaging marker

Start test H_1 and H_2 at α

 H_1 Treatment cognition H_2 Treatment clinical global scale H_3 Treatment biochemical marker H_4 Treatment imaging marker

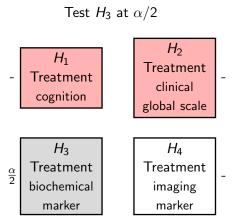


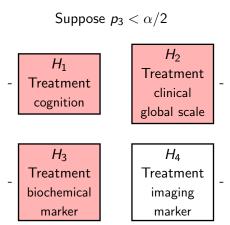
 H_1 Treatment cognition

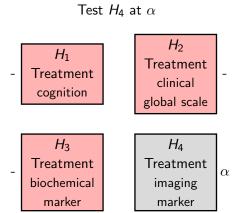
 H_2 Treatment
clinical
global scale

H₃
Treatment
biochemical
marker

H₄
Treatment imaging marker







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Family-Wise Error

■ Generalizes Type I errors to the case of multiple hypotheses

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- Controls the probability of at least one false rejection among all rejections

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- Adjusts p-values (adjusted p-values are always equal to or worse than the unadjusted p-values)

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Family-Wise Error

- Generalizes Type I errors to the case of **multiple hypotheses**
- Controls the probability of at least one false rejection among all rejections
- Adjusts p-values (adjusted p-values are always equal to or worse than the unadjusted p-values)
- Understand the **hierarchical/sequential structure** of hypotheses testing → increase power

R Software

- Bonferroni and Holm: library(stats); p.adjust()
- Closed Testing: library(cherry); closed()
- Post-hoc and more: library(multcomp); glht()