Lecture 30: Multiple testing considerations

Motivation: differential gene expression

Suppose a biologist is interested in identifying genes which are *differentially expressed* under different biological treatments. The biologist observes 10 subjects under treatment A, and 10 subjects under treatment B. Gene expression measurements $X_{i,j}$ (treatment A) and $Y_{i,j}$ (treatment B) are recorded for 1000 different genes ($i=1,\ldots,1000, j=1,\ldots,10$).

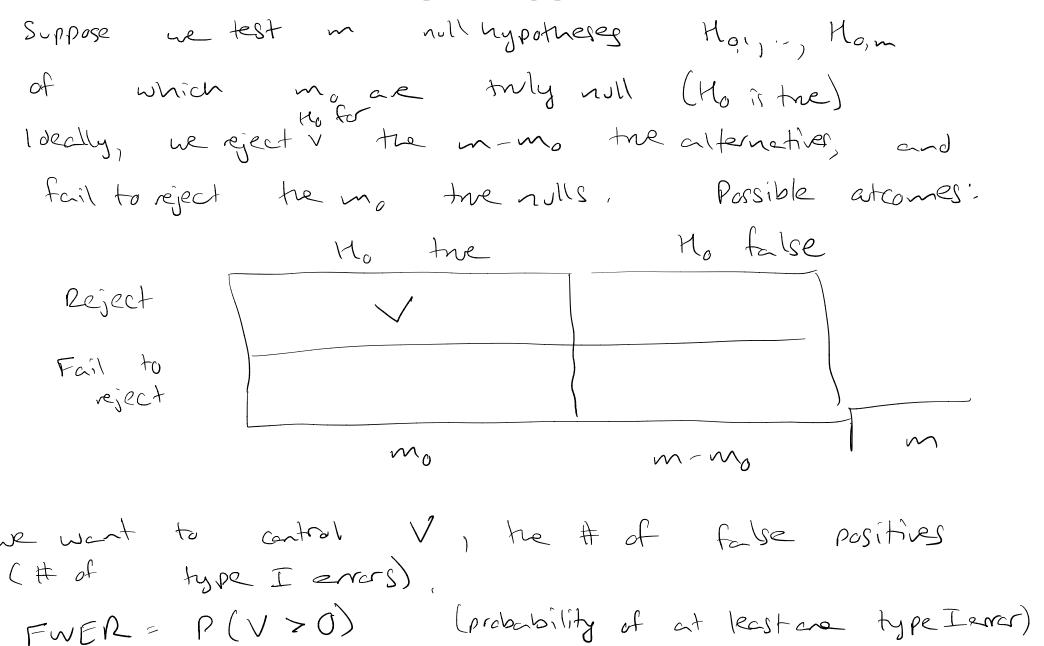
For each gene i, the biologist tests $H_0: \mu_{i,A} = \mu_{i,B}$, rejecting when the p-value is below a threshold α .

If H_0 is actually true for all 1000 genes, how many false positives do we expect?

Motivation: multiple testing

In what other settings might we test many hypotheses?

Outcomes for multiple hypothesis tests



Family-wise error rate

Definition: Suppose we test m null hypotheses $H_{0,1}, \ldots, H_{0,m}$. The family-wise error rate is the probability of making at least one type I error:

$$FWER = P\left(\bigcup_{i:H_{0,i} \text{ is true}} \{\text{reject } H_{0,i}\}\right)$$

Suppose all m tests are independent, and $H_{0,i}$ is true for all tests. For each test, we reject if the corresponding p-value

$$p_i < \alpha$$
. What is the FWER?

FWER = $P(\bigcup_{i:\text{Mo,i me}} \text{ supect Mo,i}) = P(\bigcup_{i=1}^{\infty} \text{ reject Ho,i})$

= $1 - P(\text{Fail to reject all Mo,i})$
 $1 - (1 - \alpha)^m$ (independence)

The Sidak correction

$$FWER = P\left(\bigcup_{i:H_{0,i} \text{ is true}} \{\text{reject } H_{0,i}\}\right)$$

If all m hypotheses are independent, at what threshold α^* should we reject each test, such FWER $\leq \alpha$?

FWER
$$= 1 - (1 - \alpha^*)^m$$
 (= exactly when all max thily null)

=> $1 - (1 - \alpha^*)^m = \alpha$ => $\alpha^* = 1 - (1 - \alpha)^{\frac{1}{m}}$

Example: $n=100$, $\alpha = 0.05$ $\alpha^* = 0.00051$

Sidual correction: Reject the, if $\beta = 1 - (1 - \alpha)^{\frac{1}{m}}$

The Bonferroni correction

$$FWER = P\left(\bigcup_{i:H_{0,i} \text{ is true}} \{\text{reject } H_{0,i}\}\right)$$

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P(U réject Ho,i) L L P(réject Ho,i) L L m d*

i:Ho,i istne

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Bonferani correction: Reject when $P_i \perp \frac{d}{m}$ \Rightarrow FWER \leq $m(\frac{d}{m}) = d$ (in fact, FWER \leq $m_0(\frac{d}{m})$ but don't usually know m_0) $\frac{d}{d} \perp 1 - (1 - d)^{\frac{1}{m}}$ So Bonferrani is made conservative than Sidak

Holm's procedure

Suppose we test 5 hypotheses, and observe p-values 0.4, 0.01, 0, 0, 0. Does it still seem reasonable to use the Bonferroni cutoff $\alpha/5$ for each test?

Holm's procedure

FWER = P(min Pil) (K)

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Suppose we test m null hypotheses $H_{0,1}, \ldots, H_{0,m}$. Let p_i be the corresponding p-value for test i.

- Order the p-values $p_{(1)} \leq p_{(2)} \leq \cdots \leq p_{(m)}$
- Let $i^* = \min \{i : p_{(i)} > \frac{\alpha}{m-i+1} \}$
- Reject $H_{0,(i)}$ for all $i < i^*$

Claim: Holm's procedure controls FWER at level α Proof; let Io = {i; Hoir is the} let mo = | Io | (# of the let j= min (Io) (ViL), Mo(i) is false) Holm's procedure compares P(i) to $\frac{d}{mj+1}$. If $P(j) > \frac{d}{mj+1}$. fail to reject all the nulls. And since $i = \min(I_0)$ and there are more elements in I_0 , $m - j + 1 \ge m_0$ and fail to reject all the nulls if $p(j) > m_0$