# Multiple testing

#### **Session 4**

MATH 80667A: Experimental Design and Statistical Methods for Quantitative Research in Management HEC Montréal

### Outline

### **Multiple testing**

Statistical fallacies and the reproducibility crisis

# Multiple testing

# Scientifist, investigate!

Having found a significant difference between group means, you proceed to look at all pairwise differences:  $\binom{K}{2}$  tests for K groups.

- ullet 3 tests if K=3 groups
- ullet 10 tests if K=5 groups
- 45 tests if K=10

Many tests!

### Family-wise error rate

If you do a single hypothesis test — and your testing procedure is well calibrated (model assumptions met), there is a probability  $\alpha$  of making a type I error if the null is true.

Why lpha=5%? Essentially **arbitrary**...

If one in twenty does not seem high enough odds, we may, if we prefer it, draw the line at one in fifty or one in a hundred. Personally, the writer prefers to set a low standard of significance at the 5 per cent point, and ignore entirely all results which fails to reach this level.

Fisher, R.A. (1926). The arrangement of field experiments. Journal of the Ministry of Agriculture of Great Britain, 33:503-513.

### How many tests?

Dr. Yoav Benjamini looked at the number of inference / tests performed in the Psychology replication project

Open Science Collaboration. (2015). Estimating the reproducibility of psychological science. Science, 349(6251), aac4716.

The number of tests performed ranged from 4 to 700, with an average of 72.

Most studies did not account for selection.

### Motivation

• If we do m independent comparisons, each one at the level  $\alpha$ , the probability of making at least one type I error, say  $\alpha^*$ , is

$$lpha^{\star} = 1 ext{-probability of making no type I error} \ = 1 - (1 - lpha)^m$$

With  $\alpha=5\%$ 

- m=4 tests,  $lpha^\star pprox 0.185$ .
- m=72 tests,  $lpha^\star pprox 0.975$ .

Tests need not be independent... but can show  $\alpha^{\star} \leq m\alpha$ .

# Family of hypothesis

Consider a family of m null hypothesis  $\mathscr{H}_{01},\ldots,\mathscr{H}_{0m}$  tested.

• The family may depend on the context, but all hypothesis that are scientifically relevant and could be reported.

#### Should be chosen a priori and pre-registered

**Keep it small**: the number of planned comparisons for a one-way ANOVA should be less than the number of groups K.

### Notation

Define

$$R_i = egin{cases} 1 & ext{if we reject } \mathscr{H}_{0i} \ 0 & ext{if we fail to reject } \mathscr{H}_{0i} \end{cases}$$

with  $R=R_1+\cdots+R_m$  the total number of rejections (  $0\leq R\leq m$  ).

$$V_i = \left\{egin{array}{ll} 1 & ext{type I error for } \mathscr{H}_{0i} & (R_i = 1 ext{ and } \mathscr{H}_{0i} ext{ is true}) \ 0 & ext{otherwise} \end{array}
ight.$$

Thus  $V=V_1+\cdots+V_m$  is the number of null hypothesis rejected by mistake.

### Familywise error rate

The familywise error rate is the probability of making at least one type I error per family

$$\mathsf{FWER} = \Pr(V \geq 1)$$

If we use a procedure that controls for the family-wise error rate, we talk about simultaneous inference (or simultaneous coverage for confidence intervals).

### Bonferroni's procedure

Consider a family of m hypothesis tests and perform each test at level lpha/m.

- reject  $H_{i0}$  if the associated p-value  $p_i \leq lpha/m$ .
- ullet build confidence intervals similarly with 1-lpha/m quantiles.

If the (raw) p-values are reported, reject  $\mathscr{H}_{0i}$  if  $m \times p_i \geq \alpha$  (i.e., multiply reported p-values by m)

# Holm's sequential method

Order the p-values of the family of m tests from smallest to largest

$$p_{(1)} \leq \cdots \leq p_{(m)}$$

associated to null hypothesis  $\mathscr{H}_{0(1)},\ldots,\mathscr{H}_{0(m)}$ .

**Idea** use a different level for each test, more stringent for smaller p-values.

Coupling Holm's method with Bonferroni's procedure: compare  $p_{\left(1\right)}$  to

$$lpha_{(1)}=lpha/m$$
 ,  $p_{(2)}$  to  $lpha_{(2)}=lpha/(m-1)$  , etc.

### Holm-Bonferroni procedure

#### **Sequential testing**

- ullet start with the smallest p-value
- check significance one test at a time
- stop when the first nonsignificant p-value is found or no more test in store.

#### **Conclusion**

If 
$$p_{(j)} \geq lpha_{(j)}$$
 but  $p_{(i)} \leq lpha_{(i)}$  for  $i=1,\ldots,j-1$  (all smaller  $p$ -values)

- ullet reject  $\mathscr{H}_{0(1)},\ldots,\mathscr{H}_{0(j-1)}$
- fail to reject  $\mathscr{H}_{0(j)},\ldots,\mathscr{H}_{0(m)}$

If 
$$p_{(i)} \leq lpha_{(i)}$$
 for all test  $i=1,\ldots,m$ 

• reject 
$$\mathscr{H}_{0(1)},\ldots,\mathscr{H}_{0(m)}$$

### Numerical example

Consider m=3 tests with raw p-values 0.01, 0.04, 0.02.

$i$ $p_{(i)}$	Bonferroni	Holm-Bonferroni
1 0.01	3  imes 0.01 = 0.03	3 imes 0.01 = 0.03
2 0.02	$3\times0.02=0.06$	$2\times0.02=0.04$
$3\ 0.05$	$3\times0.05=0.12$	1 imes0.05=0.04

Reminder of Holm–Bonferroni: multiply by (m-j+1) the jth smallest p-value  $p_{(j)}$  and compare to  $\alpha$ .

### Why choose Bonferroni's procedure?

- simple
- generally applicable (any design)
- but dominated by sequential procedures (Holm-Bonferroni uniformly more powerful)
- ullet low power when the number of test m is large
- *m* must be prespecified

### Alternative measures

The FWER does not make a distinction between one or multiple type I errors.

We can also look at the more stringent criterion **per-family error rate**, PFER = E(V), the expected (theoretical average) number of false positive.

One can show that

$$\mathsf{FWER} = \Pr(V \ge 1) \le \mathsf{E}(V),$$

Any procedure that controls the per-family error rate thus also controls the familywise error rate: Bonferroni does.

### Methods dedicated for one-way ANOVA

Described in Dean, Voss and Draguljić (2017) in more details.

Specialized to the one-way ANOVA setting

All methods assume (require) equal variance and independent observations.

- **Tukey**'s honestly significant difference (HSD) method: best choice to compare all pairwise differences, based on the largest possible pairwise mean differences, with extensions for unbalanced samples.
- **Scheffé**'s method: applies to any contrast (properties depends on n and K, not the number of test). Better than Bonferroni if m is large. Can be used for any design, but not powerful.
- Dunnett's method: only for all pairwise contrasts relative to a specific baseline (control).

# Adjustment for one-way ANOVA

Similar ideas but different critical coefficients. All derived using software.

Proceed only if there is a significant difference between groups, i.e. if we reject global null.

With K=5 groups and n=9 individuals per group (arithmetic example), critical value for two-sided test of zero difference with standardized t-test statistic and  $\alpha=5\%$  are

- Scheffé's (all contrasts): 3.229 (agricolae::scheffe.test)
- Tukey's (all pairwise differences): 2.856 (TukeyHSD, agricolae::HSD.test)
- Dunnett's (difference to baseline): 2.543 (DescTools::DunnettTest)
- ullet unadjusted Student's t-distribution: 2.021

# False discovery rate

Suppose that  $m_0$  out of m hypothesis are true null (so  $\mathscr{H}_0$  holds  $m_0$  times).

The **false discovery rate** is the proportion of false discovery among rejected nulls,

$$\mathsf{FDR} = egin{cases} rac{V}{R} & R > 0, \ 0 & R = 0. \end{cases}$$

False discovery rate offers weak-FWER control

the property is only guaranteed under the scenario where all null hypotheses are true.

# False discovery rate vs FWER

A simultaneous procedure that controls family-wise error rate (FWER) ensure any selected test has type I error  $\alpha$ .

The false discovery rate (FDR) is less stringent: it's a guarantee for the proportion **among selected** discoveries.

But false discovery rate is scalable:

- 2 type I errors out of 4 tests is unacceptable.
- 2 type I errors out of 100 tests is probably okay.

# Controlling false discovery rate

#### The Benjamini-Hochberg (1995) procedure

1. Order the p-values from the m tests from smallest to largest:

$$p_{(1)} \leq \cdots \leq p_{(m)}$$

2. For level q, set

$$k = \max\left\{i: p_{(i)} \leq rac{i}{m}q
ight\}$$

3. Reject  $\mathscr{H}_{0(1)},\ldots,\mathscr{H}_{0(m)}$ .

# Picture of Benjamini-Hochberg

Plot the *m p*-values against their rank.

To ensure FDR  $\leq q$ , reject null hypotheses corresponding to p-value that fall below the line of slope q/m.

### Exercice

Table S3

Planned Comparisons in Study 2

	Other (immersed & distanced) vs. Self-immersed	Self-distanced vs. Self-immersed	Other-distanced vs. Other-immersed	Other (immersed & distanced) vs. Self-distanced
Variables	t (p-value)	t (p-value)	t (p-value)	t (p-value)
LIMITS	1.74 (.09)	2.16 (.03)	0.06 (.96)	0.81 (.42)
COMPR	2.02 (.046)	1.95 (.05)	0.05 (.96)	0.31 (.76)
PERSP	4.82 (< .001)	2.83 (.005)	0.74 (.46)	1.28 (.20)
CHANGE	1.80 (.08)	0.06 (.96)	0.15 (.88)	1.63 (.11)

*Note*. LIMITS - Recognition of limits of knowledge; COMPR - Search for a compromise; PERSP - Consideration of others' perspectives; CHANGE - Recognition of change; Planned comparisons include information from all four cells in the denominator.

Grossman, I. and E. Kross (2014). Exploring "Solomon's paradox": Self-distancing eliminates the self-other asymmetry in wise reasoning about close relations in younger and older adults, *Psychological Science*, 25(8) 1571-1580

### Rant about *p*-values

The American Statistical Association (ASA) published a list of principles guiding (mis)interpretation of p-values.

- (2) *P*-values do not measure the probability that the studied hypothesis is true
- (3) Scientific conclusions and business or policy decisions should not be based only on whether a p-value passes a specific threshold.
- (4) P-values and related analyses should not be reported selectively
- (5) *p*-value, or statistical significance, does not measure the size of an effect or the importance of a result