# Permutation-based multiple testing with $\mbox{\it R}$ - theory 2/2

Livio Finos livio.finos@unipd.it

University of Padua

Ribno (Bled), Slovenia, 23/09/18



#### **Outline**

#### Introduction

Some examples
Some remarks

#### FamilyWise Error Rate (FWER)

Definition + Bonferroni Holm (step-wise) Closed Testing

#### **FWER control by Permutations tests**

Permutation Bonferroni Westfall & Young: permutation Holm<sup>1</sup> Closed Testing

#### Conclusion

#### Microarray study

Compare 20,000 genes activity between disease and control group:

#### Top 5 genes out of 20,000

Gene	p-value
OCIAD2	5.5e-6
NEK3	6.7e-6
TAF5	7.1e-6
FOXD4L6	7.5e-6
ADIG	8.8e-6
:	:
	•

#### Small p-value?

- $\circ$  a p=5.5e-6: very unlikely (evidende in favour of  $H_1$ )
- o it is unlikely also on the light of 20,000 tested hypotheses?
- is OCIAD2 really differentially expressed?
- o what about NEK3?

#### Surveys

e.g. self report inventory (web), psychological tests or social surveys

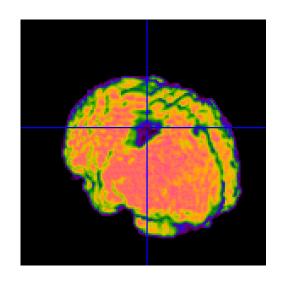
For each question we can get one or more tests (e.g. comparing the opinions of two groups of people)

#### Surveys

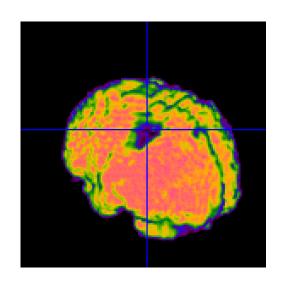
e.g. self report inventory (web), psychological tests or social surveys

For each question we can get one or more tests (e.g. comparing the opinions of two groups of people)

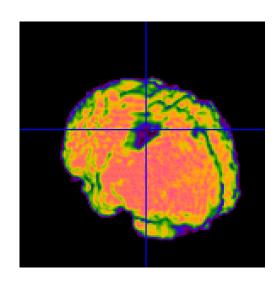
**Question**: Do we need to control for multiple type I errors?



A map of brain activity for each subject



A map of brain activity for each subject
A p-value for each voxel (=pixel, point)

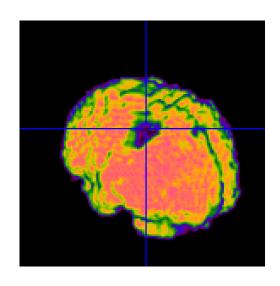


A map of brain activity for each subject

A p-value for each voxel (=pixel, point)

The output is a list of most significant

The output is a list of most significant voxels (among the thousands tested)



A map of brain activity for each subject

A p-value for each voxel (=pixel, point)

The output is a list of most significant voxels (among the thousands tested)

**Question**: Do we need to control for multiple type I errors?

#### **Further examples**

#### **Kinematics of human movements**

a test for each aspect of the movement

#### Regression models (e.g. LM e GLM)

a t-test for each parameter of the model

#### **Anova**

All pairs comparisons (post-hoc)

Every times we get more than one p-value ...

**Question**: Do we need to control for multiple type I errors?



#### **Further examples**

#### **Kinematics of human movements**

a test for each aspect of the movement

#### Regression models (e.g. LM e GLM)

a t-test for each parameter of the model

#### **Anova**

All pairs comparisons (post-hoc)

#### Every times we get more than one p-value ...

**Question**: Do we need to control for multiple type I errors?

**Answer**: Yes, of course!

#### Hypotesis testing, a single test

#### compare the two hypos:

- $\circ$   $H_0$ : two groups are Equal, Y doesn't depend on X, nothing to publish :(
- $H_1$ : two groups are Different, Y does depend on X, publish it! :)

Each test produces a p-value p, if  $p \le .05$  ( $\alpha = .05$ ) reject  $H_0$  (and incline to  $H_1$ )

#### **Errors**

- **Type I** (false positive): Reject  $H_0$  when it is TRUE  $P(Type\ I\ error) = P(p \le .05|H_0) = .05$
- Type II (false negative): Don't reject  $H_0$  when it is FALSE  $P(Type\ II\ error) = P(p > .05|H_1)$

Power:

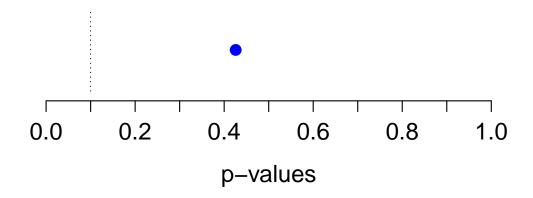
$$P(p \le .05|H_1) = 1 - P(p > .05|H_1)$$
$$= 1 - P(Type\ II\ error)$$

## Power is nothing without control (Asymmetric relevance of errors)

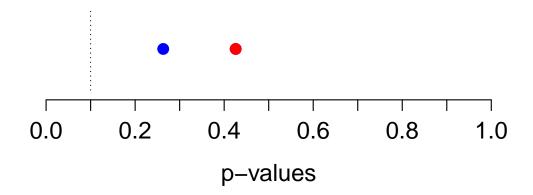
We control the  $P(type\ I\ Error)$  (ie  $\leq .05$ ) and (try) to maximize the power (i.e. minimize  $type\ II\ error$ )



$$P(p \le .05|H_0 = \text{groups are equal}) = ?$$



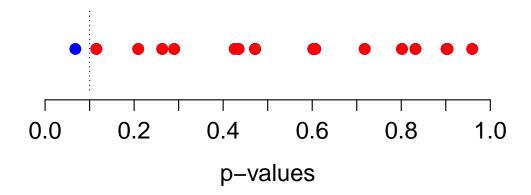
$$P(p \le .05|H_0 = \text{groups are equal}) = ?$$



$$P(p \le .05|H_0 = \text{groups are equal}) = ?$$

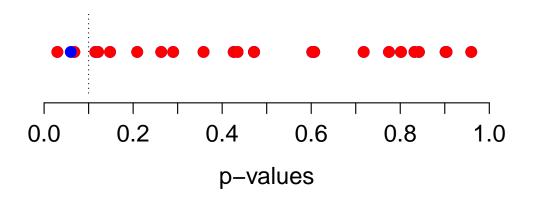
$$t = -2.484$$
,  $p = 0.068$ 



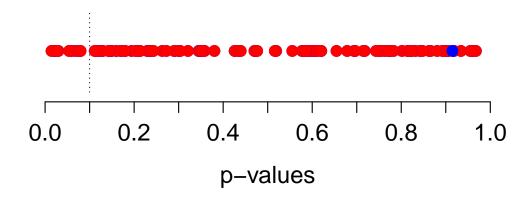


$$P(p \le .05|H_0 = \text{groups are equal}) = ?$$

$$t = -2.602$$
,  $p = 0.06$ 

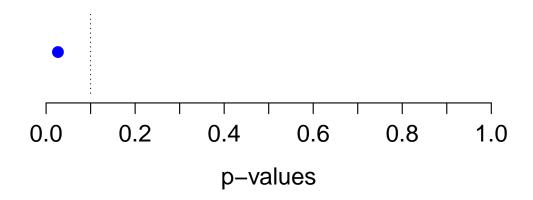


$$P(p \le .05|H_0 = \text{ groups are equal}) = 0.05$$



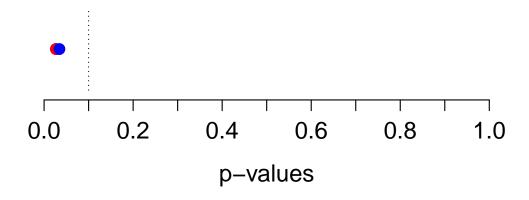
$$P(p \le .05|H_1 = \text{ groups are NOT equal})$$

$$t = -3.426$$
,  $p = 0.027$ 

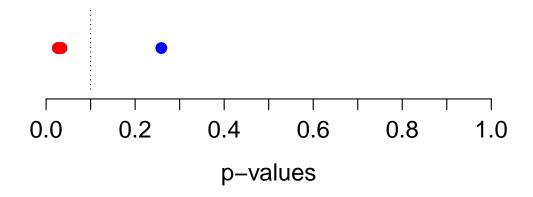


$$P(p \le .05|H_1 = \text{ groups are NOT equal})$$

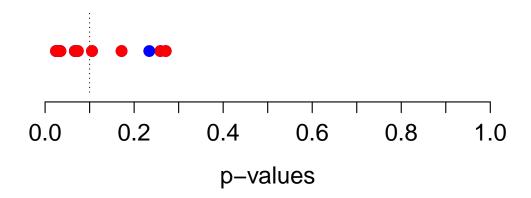
$$t = -3.154$$
,  $p = 0.034$ 



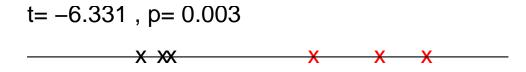
$$P(p \le .05|H_1 = \text{ groups are NOT equal})$$

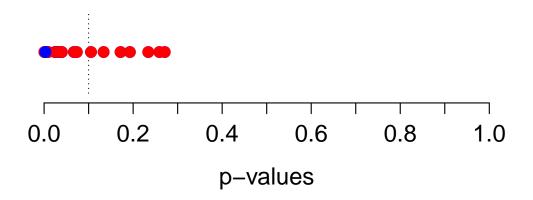


$$P(p \le .05|H_1 = \text{ groups are NOT equal})$$

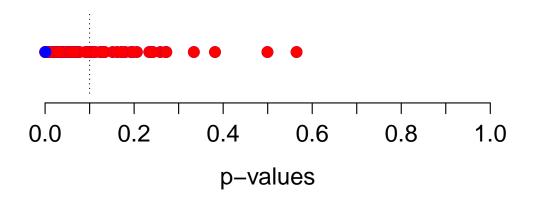


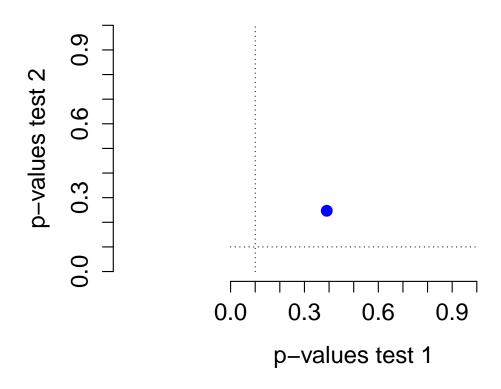
$$P(p \le .05|H_1 = \text{ groups are NOT equal})$$

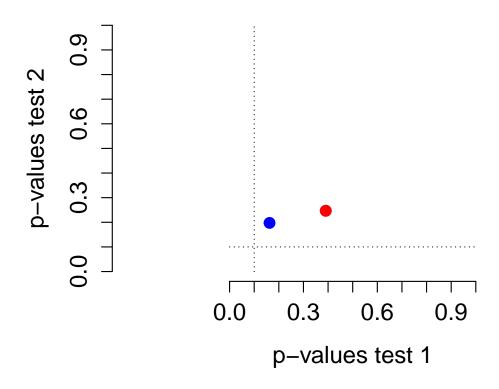


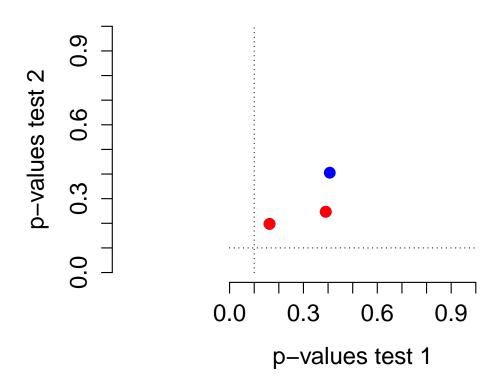


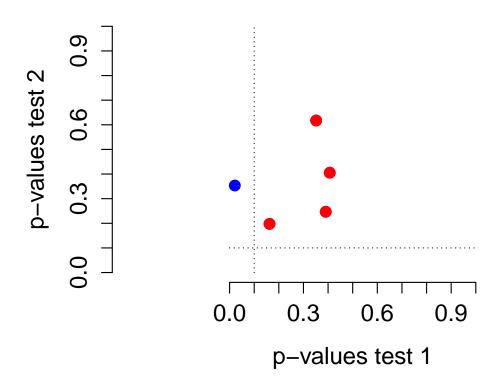
$$\mathbf{P}(\mathbf{p} \leq .05 | \mathbf{H_1} = \text{ groups are NOT equal})$$
  
e.g.:  $Power: P(p \leq 0.05 | H_1) = 0.75$ 

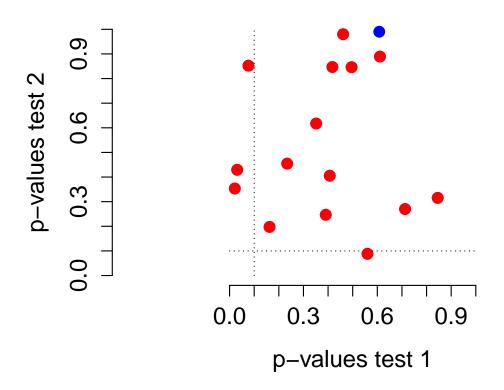


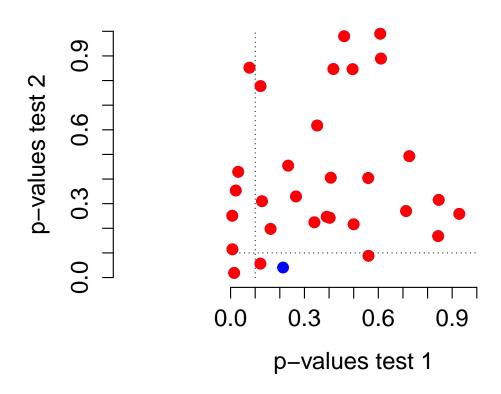


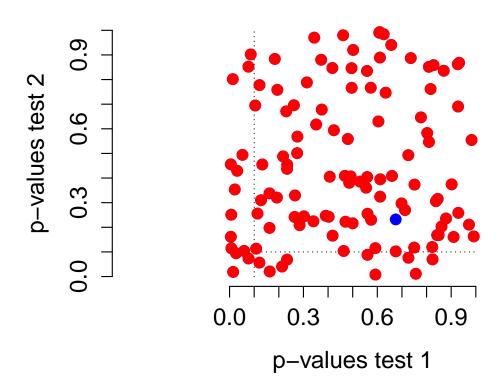


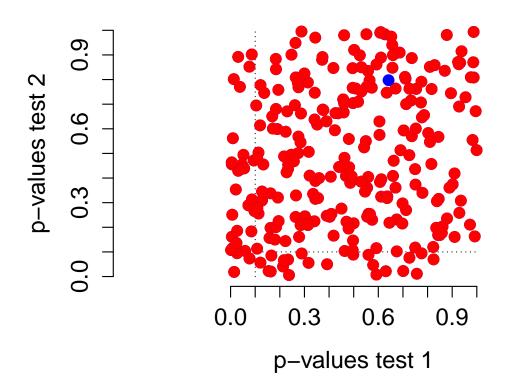


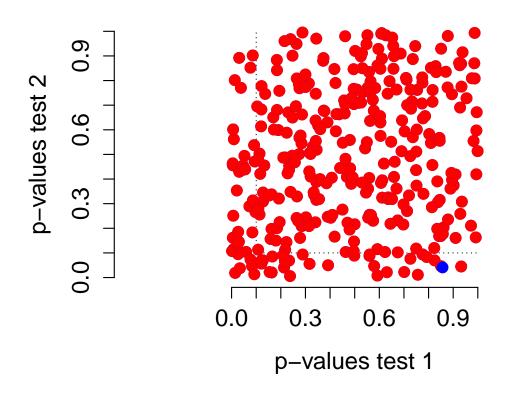


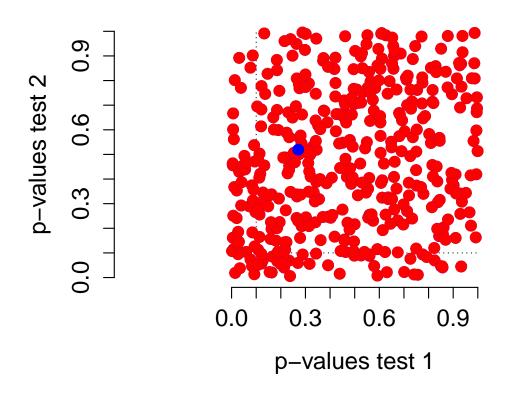










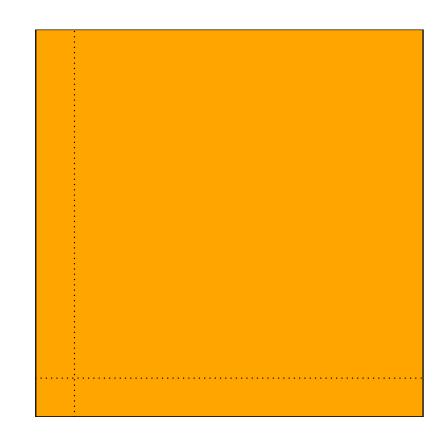


Probability of at LEAST one (false) rejection?

$$= .05 + .05 - (.05 * .05) = 1 - (1 - .05)^{2} = .0975 = 1 - (1 - \alpha)^{2}$$

#### joint density

p-values test 2



#### Probability of false rejections

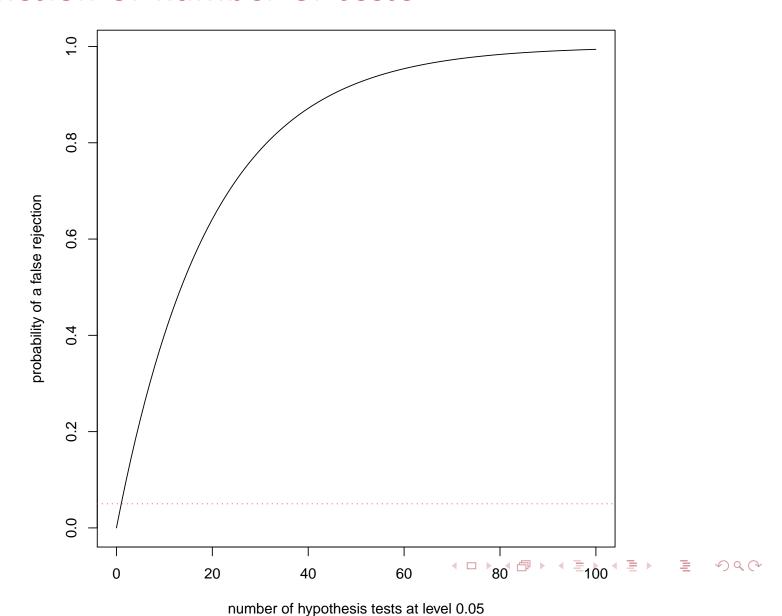
m independent tests (p-values)

Reject 
$$H_0$$
 if  $p \leq \alpha$ 

Probability of AT LEAST a rejection

$$P = 1 - (1 - \alpha)^m$$

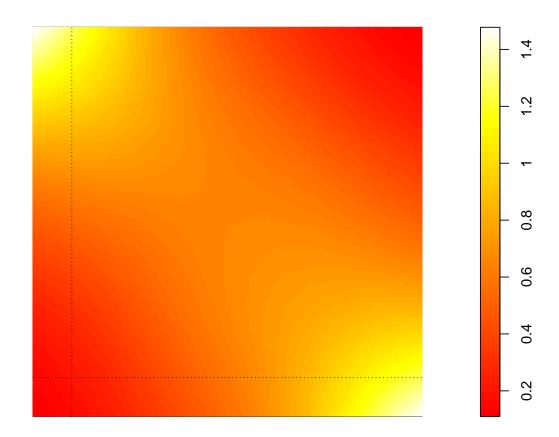
# Probability of AT LEAST one Type I error as a function of number of tests



# **Dependent tests**

In most of the real cases:

joint density

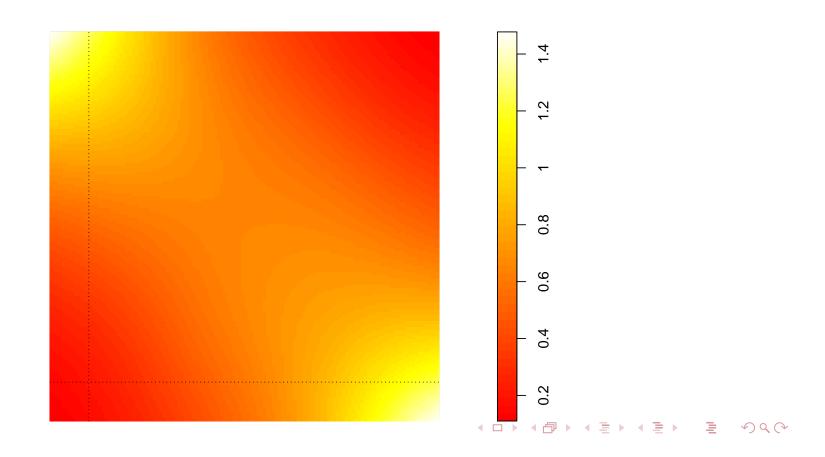


# **Dependent tests**

In most of the real cases:

$$P(\text{At least one false rejection}) > (!)1 - (1 - \alpha)^2$$

#### joint density



# Type I errors

How to define the type I error when there are many hypotheses?

Which procedures control this error?

## **Outline**

#### Introduction

Some examples
Some remarks

## FamilyWise Error Rate (FWER)

Definition + Bonferroni Holm (step-wise) Closed Testing

## **FWER control by Permutations tests**

Permutation Bonferroni Westfall & Young: permutation Holm<sup>2</sup> Closed Testing

#### Conclusion

# FamilyWise Error Rate (FWER)

## Probability of AT LEAST one false rejection

## **Bonferroni Inequality**

Reject  $H_i$  if  $p_i \leq \alpha/m$  (m = number of hypotheses)

#### control FWER

FWER = 
$$P(p_i \le \alpha/m \text{ for at least one True null hypo})$$
  
=  $P(\bigcup_{i \in \{\text{true null hypotheses}\}} \{p_i \le \alpha/m\})$   
 $\le \sum_{i \in \{\text{true null hypotheses}\}} P(p_i \le \alpha/m)$   
 $\le \#\{\text{true null hypotheses}\}\frac{\alpha}{m} \le \alpha$ 

## Bonferroni procedure

## Multiplicity-adjusted p-value

$$\tilde{p}_i = mp_i \ i = 1, \dots, m$$
 and rejects it if  $\leq \alpha$ 

#### **Pros**

- Very easy
- Control the FWER under any dependence

#### **Cons**

Conservative (Adj. P-values very high, few rejections)

- **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.** just do not reject anything, Stop.

#### Bonferroni

Adj. p-value:  $p_A5$   $p_B5$   $p_C5$   $p_D5$   $p_E5$   $\leq ?\alpha$ 

 $\mathcal{H} \setminus \mathcal{R}$ : A B C D

 $\mathcal{R}$ :

- **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.** just do not reject anything, Stop.

## Suppose $p_A$ and $p_C$ significant

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

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











 $\mathcal{R}$ :

<sup>&</sup>lt;sup>3</sup>Holm 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.** just do not reject anything, Stop.

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

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

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











<sup>&</sup>lt;sup>3</sup>Holm 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.** just do not reject anything, Stop.

## Suppose $p_D$ significant

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

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











<sup>&</sup>lt;sup>3</sup>Holm 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.** just do not reject anything, Stop.

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

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

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





 $\mathcal{R}: A$ 







<sup>&</sup>lt;sup>3</sup>Holm 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. just do not reject anything, Stop.

### No rejections: Stop

Adj. p-value:  $-p_B2$  -  $-p_E2 \leq ?\alpha$   $\mathcal{H} \setminus \mathcal{R}:$   $\mathcal{B}$ 

Closure of hypos (all possible intersections)

hypos to test

Α

В

С

<sup>&</sup>lt;sup>4</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. Biometrika 63: 655+660.

Test the overall null hypo (eg MANOVA)

Closure

ABC

AB

AC

ВС

А

В

C

<sup>&</sup>lt;sup>4</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. Biometrika 63: 655-660.

test at level  $\alpha$ 

ABC

AB AC BC

A B C

<sup>&</sup>lt;sup>4</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. Biometrika 63: 655-660.

## **Suppose significant**

ABC

AB

AC

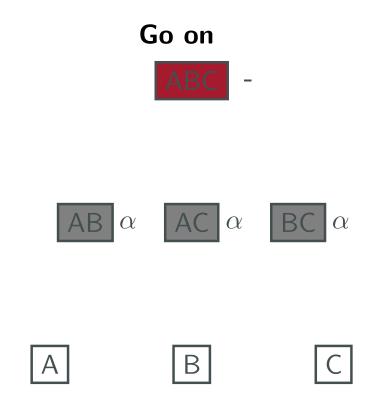
BC

Α

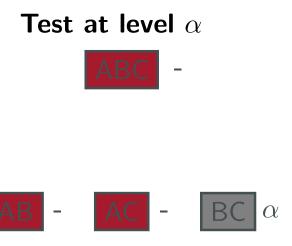
В

C

<sup>&</sup>lt;sup>4</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. Biometrika 63: 655-660.



<sup>&</sup>lt;sup>4</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. Biometrika 63: 655-660.

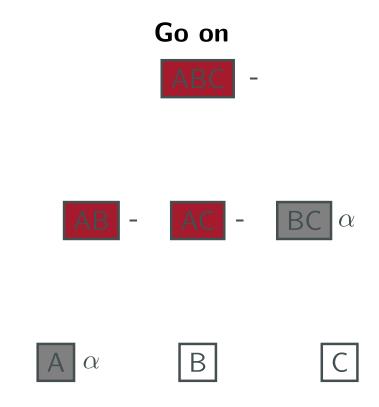




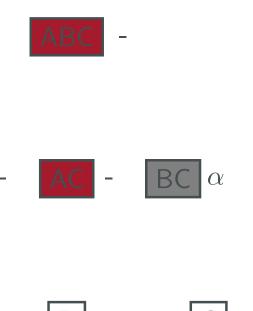
В

С

<sup>&</sup>lt;sup>4</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. Biometrika 63: 655+660.



A is signif. if all above are signif.



<sup>&</sup>lt;sup>4</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. Biometrika 63: 655+660.

Cons: too much tests very quickly:  $=2^{\#hypos}-1$ 

A is signif. if all above are signif.



$$oxed{\mathsf{AB}}$$
 -  $oxed{\mathsf{AC}}$  -  $oxed{\mathsf{BC}}$   $lpha$ 



<sup>&</sup>lt;sup>4</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. Biometrika 63: 655-660.

## **Outline**

#### Introduction

Some examples
Some remarks

## FamilyWise Error Rate (FWER)

Definition + Bonferroni Holm (step-wise) Closed Testing

## **FWER** control by Permutations tests

Permutation Bonferroni Westfall & Young: permutation Holm<sup>5</sup> Closed Testing

#### Conclusion

## Bonferroni is conservative

#### **Bonferroni** bound

Reject for p-values at most  $\alpha/m$ 

## By Boole's inequality

Guaranteed: FWER  $\leq \alpha$ , but often FWER  $< \alpha$ 

## Can we improve?

Reject for p-values at most  $\tilde{\alpha} > \alpha/m$ , while keeping FWER control

#### Yes we can

By permutations

# Improved Bonferroni

#### Reduced $\alpha$

Reject  $H_i$  if  $p_i \leq \tilde{\alpha}$ 

#### **Control of FWER?**

FWER = 
$$P(p_i \le \tilde{\alpha} \text{ for at least one } i \text{ with } H_i \text{ true})$$
  
=  $P(\bigcup_{i \in T} \{p_i \le \tilde{\alpha}\})$   
=  $P(\min_{i \in T} p_i \le \tilde{\alpha}) \le \alpha$ 

#### How can we determine the value of $\tilde{\alpha}$ ?

Using permutations to find the distribution of the minimum p-value

# Multiple testing using permutations

## The single step min-P method

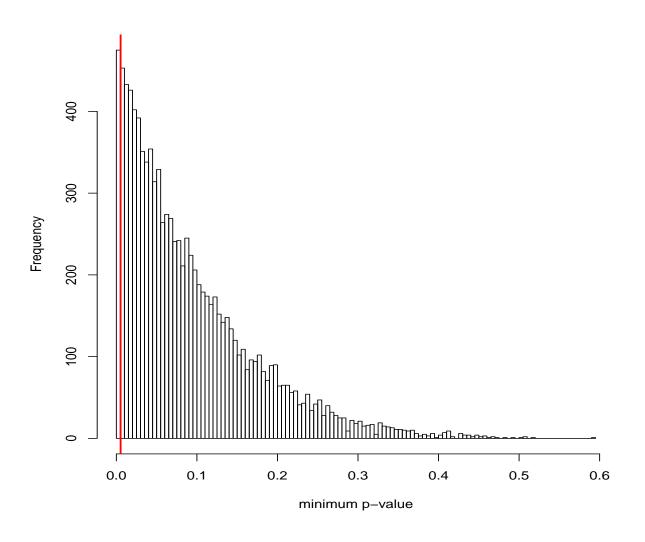
- **1.** Calculate the smallest p-value m for the real data
- 2. Randomly permute the data
- 3. Calculate new p-values for all tests based on permuted data
- **4.** Calculate the smallest p-value  $m^{\pi}$  for permuted data
- **5.** Repeat permutation many (say k=1000) times:  $m_1^{\pi}, \ldots, m_k^{\pi}$
- **6.** Calculate  $\tilde{\alpha}$  as the  $\alpha$ -quantile of  $m_1^{\pi}, \ldots, m_k^{\pi}$

## Multiple testing result

Reject all hypotheses with (non-permuted) p-values at most  $\tilde{lpha}$ 



# Histogram of the smallest p-value of 10 independent tests



## **Correlation structure of p-values**

#### **Permutation**

- Destroys correlation between covariates and response
- Retains correlation among covariates

## Consequence

- o P-values of correlated genes remain correlated in permutations
- Distribution of minimum p-value correctly takes correlations into account

## Gain relative to Bonferroni

### Min-P permutation critical value

In the example data:  $\tilde{\alpha}=0.00527$  vs  $\alpha/m=0.005$ 

## When is the gain large?

Negatively correlated p-values: typically no gain

Independent p-values: minimal gain

Positively correlated p-values: gain can be large

#### Genomic data

Genes typically strongly positively correlated

# Sequential permutation multiple testing

## Single step

Single step min-P is permutation equivalent of Bonferroni

#### What about Holm?

Permutation equivalent of Holm's method: Westfall & Young

# Westfall & Young min-P

## The min-P algorithm

- Start with all hypotheses
- Repeat
  - $\circ$  Do single step min-P to calculate  $ilde{lpha}$
  - $\circ$  Reject hypotheses with p-value  $\leq \tilde{\alpha}$
  - Remove rejected hypotheses
- Until no new rejections occur

# Westfall & Young min-p (and max-t)

Westfall & Young min-p: shortcut using min-p combining function (m tests).

# Westfall & Young min-p (and max-t)

Westfall & Young min-p: shortcut using min-p combining function (m tests).

Suppose three hypotheses tested and  $p_A \leq p_B \leq p_C$ 

- $\circ$  Test  $H_A$ ,  $H_B$  and  $H_C$  using min-p:  $p_{ABC}$ 
  - if  $p_{ABC} \leq \alpha$  reject  $H_A$  and go on
  - if  $p_{ABC} > \alpha$  STOP
- $\circ$  Test  $H_B$  and  $H_C$  using min-p:  $p_{BC}$ 
  - if  $p_{BC} \leq \alpha$  reject  $H_B$  and go on
  - if  $p_{BC} > \alpha$  STOP
- $\circ$  Test  $H_C$ :  $p_C$ 
  - $\circ$  if  $p_C \leq \alpha$  reject  $H_C$  and STOP
  - if  $p_C > \alpha$  STOP

For max-t procedure substitute  $p_{ABC} \leq \alpha$  with  $t_{ABC} \geq t_{\alpha}$ 



Test in each node: any multivariate permutation test (eg alternative to Manova)

Adjusted  $\tilde{p}_A = \max(p_A, p_{AB}, p_{AC}, p_{ABC})$ 

<sup>&</sup>lt;sup>6</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. Biometrika 63: 655-660. ▶ ■ ✓

## **Outline**

#### Introduction

Some examples
Some remarks

## FamilyWise Error Rate (FWER)

Definition + Bonferroni Holm (step-wise) Closed Testing

## **FWER control by Permutations tests**

Permutation Bonferroni Westfall & Young: permutation Holm<sup>7</sup> Closed Testing

#### **Conclusion**

# Accounting for dependences: adjusted p-value lower (i.e. more rejections)

#### When?

Negative correlation: generally no gain p-value Independents: little or no gain Positive correlation: big gain, usually (NB: a test with bi-directional alternative and with negative correlation produce p-value positively correlated)

#### How?

```
in R: library(flip); flip(); flip.adjust()
```

#### Real data

The variables of real datasets are often correlated then . . .

# Accounting for dependences: adjusted p-value lower (i.e. more rejections)

#### When?

Negative correlation: generally no gain p-value Independents: little or no gain Positive correlation: big gain, usually (NB: a test with bi-directional alternative and with negative correlation produce p-value positively correlated)

#### How?

```
in R: library(flip); flip(); flip.adjust()
```

#### Real data

The variables of real datasets are often correlated then ... permutations are (often) convenient



## **Error FamilyWise**

Generalize the Type I error to the case of multiple hypotheses

## **Error FamilyWise**

- Generalize the Type I error to the case of multiple hypotheses
- Control the probability of at LEAST a false rejections

## **Error FamilyWise**

- Generalize the Type I error to the case of multiple hypotheses
- Control the probability of at LEAST a false rejections
- o corrects the p-value (adjusted p-value always equal to or greather than the unadjusted p-value)

## **Error FamilyWise**

- Generalize the Type I error to the case of multiple hypotheses
- Control the probability of at LEAST a false rejections
- corrects the p-value (adjusted p-value always equal to or greather than the unadjusted p-value)

#### **R Software**

- Bonferroni and Holm library(stats); p.adjust()
- Testing Closed library(cherry); closed()
- Permutations Westfall & Young library(flip); flip.adjust()