

# Permutation-based multiple testing with R - theory 1/2

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# Outline

## 1 Introduction

Some examples

Some remarks

## 2 FamilyWise Error Rate (FWER)

Definition + Bonferroni

Holm (step-wise)

Closed Testing

## 3 FWER control by Permutations tests

Permutation Bonferroni

Westfall & Young: permutation Holm<sup>1</sup>

Closed Testing

## 4 Conclusion

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<sup>1</sup>Westfall PH, Young SS (1993) Resampling-Based Multiple Testing: Examples and Methods for p-Value Adjustment. Wiley



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# 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?

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

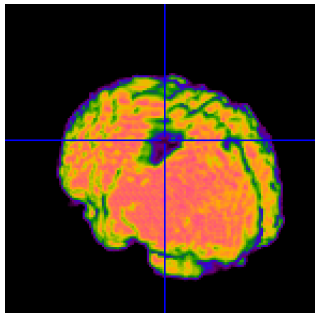
e.g. self report inventory (web), psychological tests or social surveys

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?



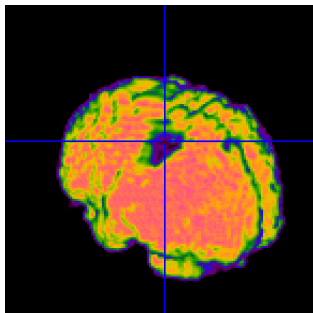
## A further example: fMRI studies



A map of brain activity for each subject



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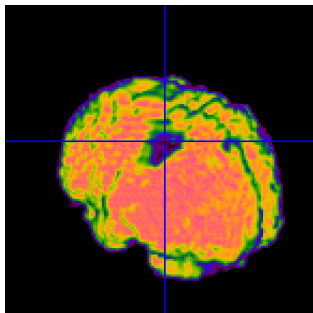
A map of brain activity for each subject

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





# A further example: fMRI studies



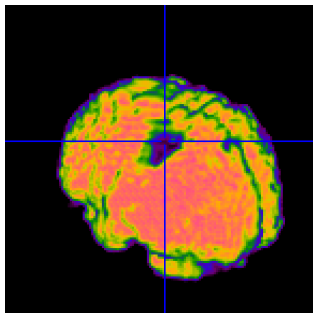
A map of brain activity for each subject

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

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



# A further example: fMRI studies



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!



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# Hypothesis testing, a single test

## compare the two hypos:

- $H_0$ : 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  $p \leq .05$  ( $\alpha = .05$ ) reject  $H_0$  (and incline to  $H_1$ )**



# Errors

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

**Power:**

$$\begin{aligned} P(p \leq .05 | H_1) &= 1 - P(p > .05 | H_1) \\ &= 1 - P(\text{Type II error}) \end{aligned}$$

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

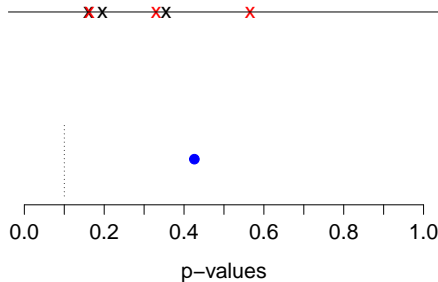
We control the  $P(\text{type I Error})$  (ie  $\leq .05$ )  
and (try) to maximize the power (i.e. minimize *type II error*)



# Type I Error:

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

$t = -0.886$  ,  $p = 0.426$

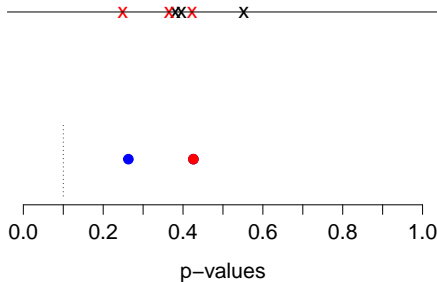




# Type I Error:

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

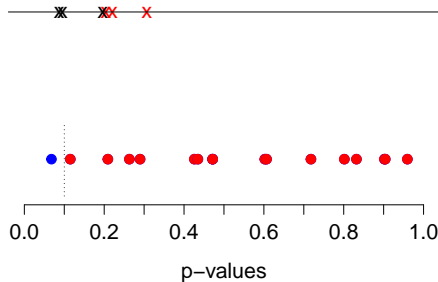
$t = 1.301$  ,  $p = 0.263$



# Type I Error:

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

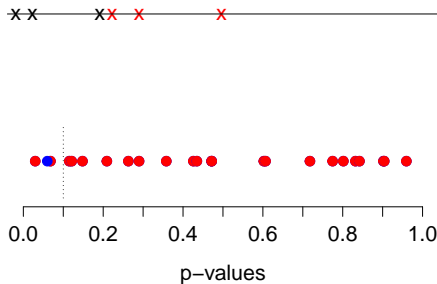
$t = -2.484$  ,  $p = 0.068$



# Type I Error:

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

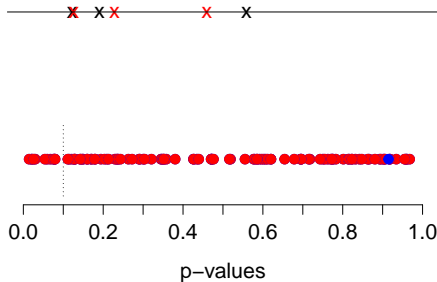
$t = -2.602$  ,  $p = 0.06$



# Type I Error:

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

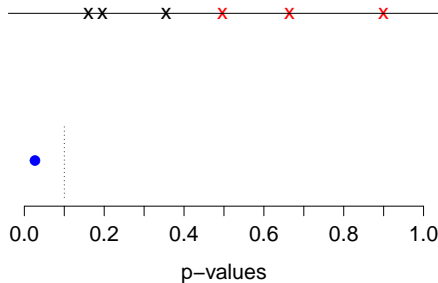
$t = 0.114$  ,  $p = 0.915$



# Power:

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

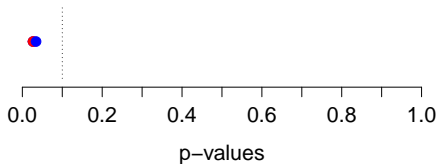
$t = -3.426$ ,  $p = 0.027$



# Power:

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

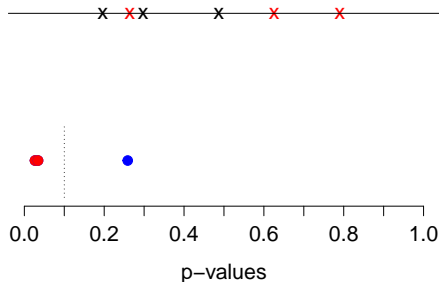
$t = -3.154$  ,  $p = 0.034$



# Power:

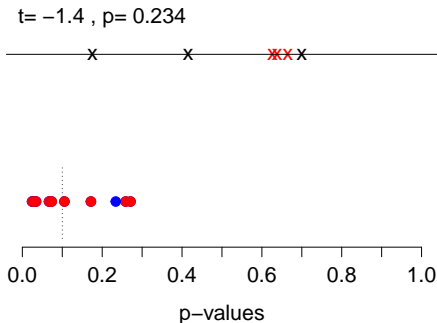
$P(p \leq .05 | H_1 = \text{groups are NOT equal})$

$t = -1.315$ ,  $p = 0.259$



# Power:

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

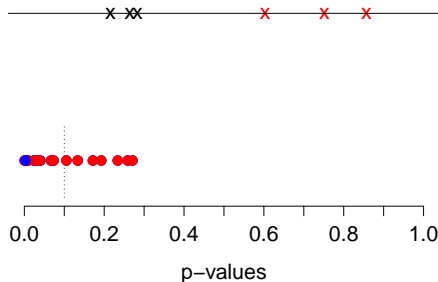




# Power:

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

$t = -6.331$ ,  $p = 0.003$

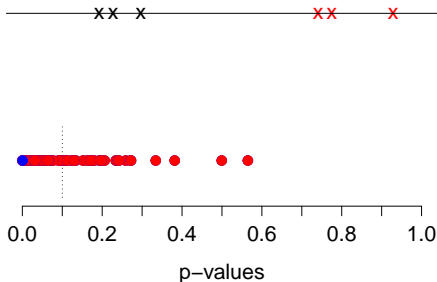


# Power:

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

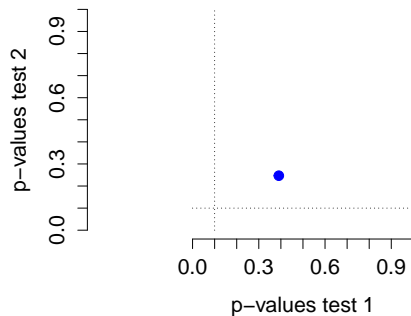
e.g.: Power :  $P(p \leq 0.05 | H_1) = 0.75$

$t = -8.81$  ,  $p = 0.001$



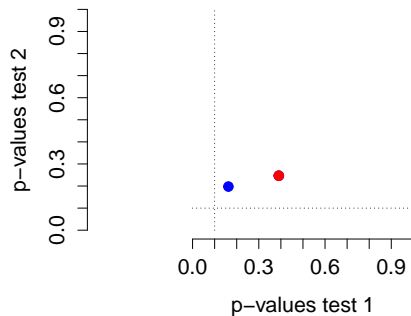
# Type I Error, Two Tests

Probability of at LEAST one (false) rejection?



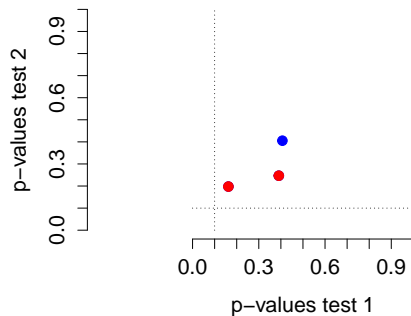
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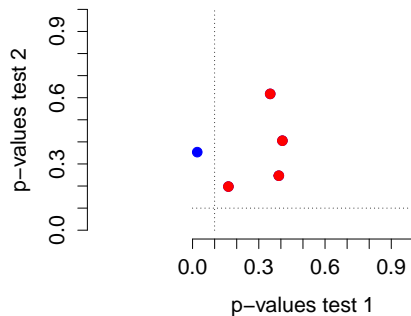
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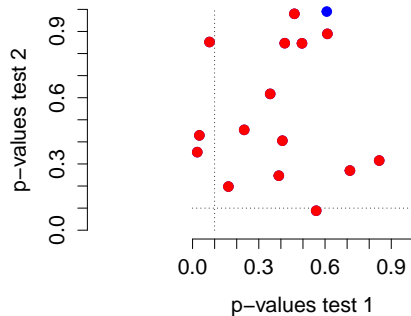
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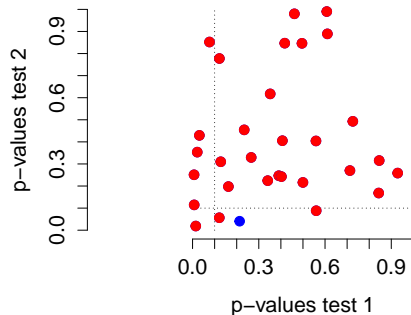
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# Type I Error, Two Tests

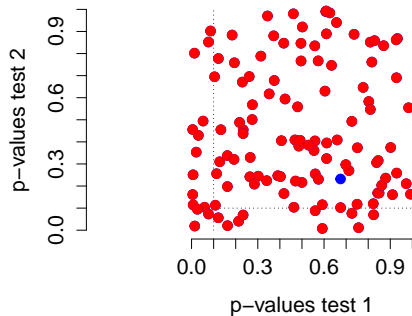
Probability of at LEAST one (false) rejection?





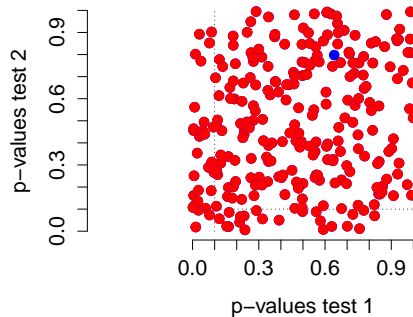
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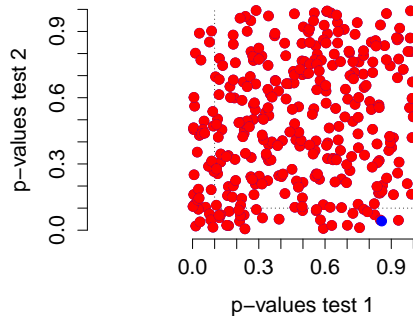
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Probability of at LEAST one (false) rejection?



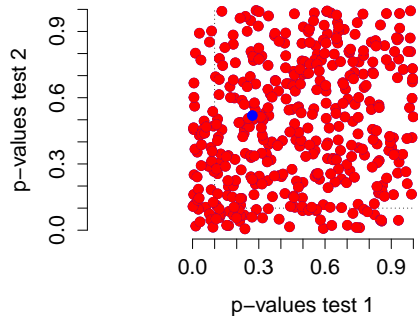
# Type I Error, Two Tests

Probability of at LEAST one (false) rejection?



# Type I Error, Two Tests

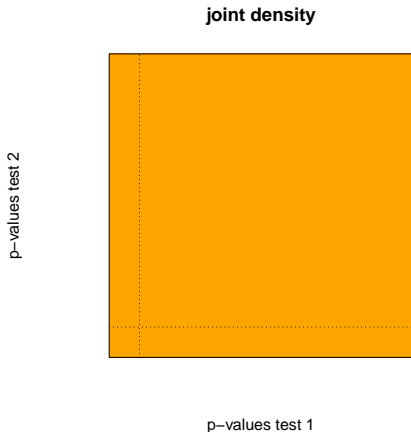
Probability of at LEAST one (false) rejection?



# Type I Error, Two Tests

Probability of at LEAST one (false) rejection?

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



# Probability of false rejections

*m* independent tests (p-values)

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

**Probability of AT LEAST a rejection**

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



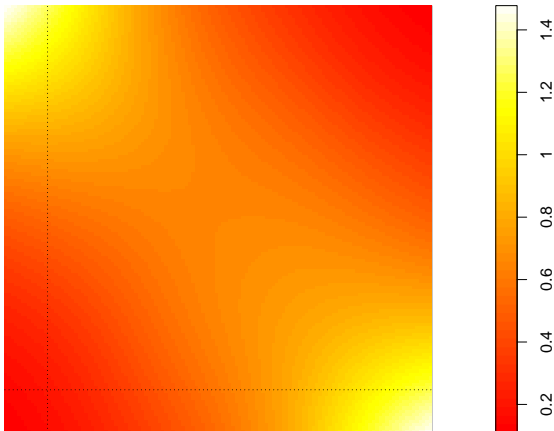
# Probability of AT LEAST one Type I error as a function of number of tests



# Dependent tests

In most of the real cases:

joint density



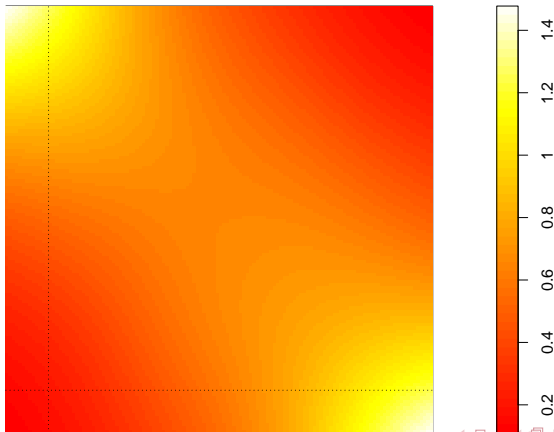


# Dependent tests

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?



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# 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**

$$\begin{aligned}\text{FWER} &= P(p_i \leq \alpha/m \text{ for at least one True null hypo}) \\ &= P\left(\bigcup_{i \in \{\text{true null hypotheses}\}} \{p_i \leq \alpha/m\}\right) \\ &\leq \sum_{i \in \{\text{true null hypotheses}\}} P(p_i \leq \alpha/m) \\ &\leq \#\{\text{true null hypotheses}\} \frac{\alpha}{m} \leq \alpha\end{aligned}$$



# 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)



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# Holm's procedures <sup>7</sup>

- 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:  $p_A^5$   $p_B^5$   $p_C^5$   $p_D^5$   $p_E^5$   $\leq ? \alpha$

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

$\mathcal{R}$  :

---

<sup>7</sup>Holm S. (1979) A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics*; 6 (2): 65-70.





# Holm's procedures <sup>7</sup>

- 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:  $p_A/5$   $p_B/5$   $p_C/5$   $p_D/5$   $p_E/5 \leq ?\alpha$

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

$\mathcal{R}$  :

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- 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:      -       $p_B 3$       -       $p_D 3$        $p_E 3 \leq ? \alpha$

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



$\mathcal{R}$  :



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# Holm's procedures <sup>7</sup>

- ❶ First step: adjusted p-value:  $p \cdot m$ ; reject if  $\leq \alpha$
- ❷ After  $r$  rejections, adjusted p-value:  $p \cdot (m - r)$
- ❸ just do not reject anything, Stop.

**Suppose  $p_D$  significant**

Adj. p-value:      -       $p_B/3$       -       $p_D/3$        $p_E/3 \leq ?\alpha$

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



$\mathcal{R}$  :



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- ❸ just do not reject anything, Stop.

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

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

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



$\mathcal{R}$  :



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- ❷ After  $r$  rejections, adjusted p-value:  $p \cdot (m - r)$
- ❸ just do not reject anything, Stop.

**No rejections: Stop**

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

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



$\mathcal{R}$  :



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# Closed Testing<sup>9</sup>

Closure of hypos (all possible intersections)

**hypos to test**

A

B

C

---

<sup>9</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. *Biometrika* 63: 655-660.



# Closed Testing<sup>9</sup>

Test the overall null hypo (eg MANOVA)

## Closure

ABC

AB

AC

BC

A

B

C

---

<sup>9</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. *Biometrika* 63: 655-660.





# Closed Testing<sup>9</sup>

test at level  $\alpha$

ABC  $\alpha$

AB

AC

BC

A

B

C

---

<sup>9</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. *Biometrika* 63: 655-660.



# Closed Testing<sup>9</sup>

Suppose significant

ABC -

AB

AC

BC

A

B

C

---

<sup>9</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. *Biometrika* 63: 655-660.



# Closed Testing<sup>9</sup>

Go on

ABC -

AB  $\alpha$  AC  $\alpha$  BC  $\alpha$

A

B

C

---

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# Closed Testing<sup>9</sup>

Test at level  $\alpha$

ABC -

AB - AC - BC  $\alpha$

A

B

C

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# Closed Testing<sup>9</sup>

Go on

ABC -

AB - AC - BC  $\alpha$

A  $\alpha$  B C

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# Closed Testing<sup>9</sup>

**A is signif. if all above are signif.**

ABC -

AB - AC - BC  $\alpha$

A - B C

---

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# Closed Testing<sup>9</sup>

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

A is signif. if all above are signif.

ABC -

AB - AC - BC  $\alpha$

A - B C

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# Bonferroni is conservative

## Bonferroni bound

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

## By Boole's inequality

Guaranteed:  $\text{FWER} \leq \alpha$ , but often  $\text{FWER} < \alpha$

## 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?

$$\begin{aligned}\text{FWER} &= P(p_i \leq \tilde{\alpha} \text{ for at least one } i \text{ with } H_i \text{ true}) \\ &= P\left(\bigcup_{i \in T} \{p_i \leq \tilde{\alpha}\}\right) \\ &= P\left(\min_{i \in T} p_i \leq \tilde{\alpha}\right) \leq \alpha\end{aligned}$$

## 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

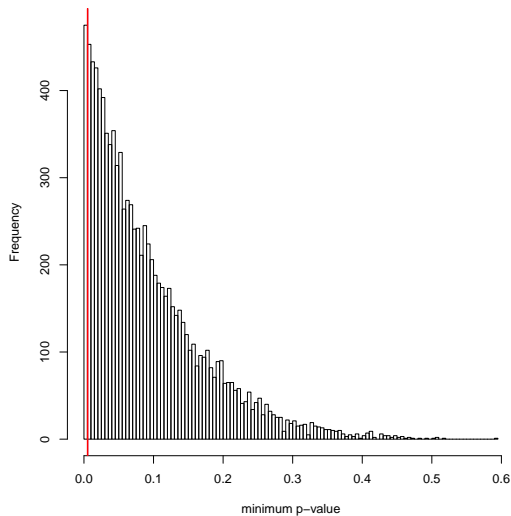
- 1 Calculate the smallest p-value  $m$  for the real data
- 2 Randomly permute the data
- 3 Calculate new p-values for all tests based on permuted data
- 4 Calculate the smallest p-value  $m^\pi$  for permuted data
- 5 Repeat permutation many (say  $k=1000$ ) times:  $m_1^\pi, \dots, m_k^\pi$
- 6 Calculate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

## Multiple testing result

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



# 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

- 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



# Outline

## 1 Introduction

Some examples

Some remarks

## 2 FamilyWise Error Rate (FWER)

Definition + Bonferroni

Holm (step-wise)

Closed Testing

## 3 FWER control by Permutations tests

Permutation Bonferroni

Westfall & Young: permutation Holm<sup>12</sup>

Closed Testing

## 4 Conclusion

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<sup>12</sup>Westfall PH, Young SS (1993) Resampling-Based Multiple Testing: Examples and Methods for p-Value Adjustment. Wiley





# 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
  - Do single step min-P to calculate  $\tilde{\alpha}$
  - 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  $p_A \leq p_B \leq p_C$

- 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
- 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
- Test  $H_C$ :  $p_C$ 
  - 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  $t_{ABC} \geq t_\alpha$



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# Closed Testing<sup>14</sup>

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

## Closure Set

ABC

AB

AC

BC

A

B

C

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

<sup>14</sup>R Marcus, E Peritz, KR Gabriel (1976). On closed testing procedures with special reference to ordered analysis of variance. *Biometrika* 63: 655-660.



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# 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 ...





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



# Summary

## Error FamilyWise

- Generalize the Type I error to the case of multiple hypotheses



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- corrects the p-value (adjusted p-value always equal to or greater than the unadjusted p-value)



# Summary

## Error FamilyWise

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- Control the probability of at LEAST a false rejection
- corrects the p-value (adjusted p-value always equal to or greater 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()`

