Statistics I The multiple problems of multiple testing

Einar Andreas Rødland

7 September 2009

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Multiple testing

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Multiple hypothesis testing

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Multiple comparisons

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Example: Is the coin *fair*, or is either head or tail more likely?



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Example: Is the coin *fair*, or is either head or tail more likely?

1. Toss coin N times.



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Example: Is the coin *fair*, or is either head or tail more likely?

- 1. Toss coin N times.
- 2. Count the number of heads and tails.



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comparisons

Example: Is the coin *fair*, or is either head or tail more likely?

- 1. Toss coin N times.
- 2. Count the number of heads and tails.
- 3. Compare to what would be expected from a fair coin.



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Example: Is the coin *fair*, or is either head or tail more likely?

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Example:

If we toss a fair coin 20 times, we can compute the probability of getting x heads (x = 0, ..., 20).



Number of heads

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Example:

If we toss a fair coin 20 times, we can compute the probability of getting x heads (x = 0, ..., 20).

The probability of getting at most 5 heads is appr. 2%; that of 15 more is also appr. 2%.



Number of heads

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Example:

If we toss a fair coin 20 times, we can compute the probability of getting x heads (x = 0, ..., 20).

The probability of getting at most 5 heads is appr. 2%; that of 15 more is also appr. 2%.



Our test: The number of heads should be between 6 and 14, otherwise we should reject the null-hypothesis (i.e. that the coin is fair).

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Type I and Type II errors

Null-hypothesis:

The coin is fair.

Our test: Toss 20 times. Reject null-hypothesis if number of heads in not between 6 and 14.



Number of heads

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Type I and Type II errors

Null-hypothesis:

The coin is fair.

Our test: Toss 20 times. Reject null-hypothesis if number of heads in not between 6 and 14.

0.01 Type I error: 0.00 False positive. Even if the coin is fair, we have 4% likelihood of rejecting the null-hypothesis.



Number of head

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Type I and Type II errors

Null-hypothesis:

The coin is fair.

Our test: Toss 20 times. Reject null-hypothesis if number of heads in not between 6 and 14.

 Type I error:
 Image: Construction of the coin is fair, we have

 4% likelihood of rejecting the null-hypothesis.

Type II error: False negative. Even if the coin is biased, we may end up retaining the null-hypothesis.



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Significance level: The risk of Type I error (false positive) of a given test.

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Significance level: The risk of Type I error (false positive) of a given test.

It is very common to make tests at the 5% significance level: i.e. so that false positive risk is *at most* 5%.

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It is very common to make tests at the 5% significance level: i.e. so that false positive risk is *at most* 5%.

If the false positive risk is less than the selected significance level, the test is *conservative*.

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Significance level: The risk of Type I error (false positive) of a given test.

It is very common to make tests at the 5% significance level: i.e. so that false positive risk is *at most* 5%.

If the false positive risk is less than the selected significance level, the test is *conservative*.

If the false positive risk is larger than the selected significance level, the test is **wrong**!

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Our experiment:

We toss the coin 20 times and get 7 heads.



Number of heads

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Our experiment:

We toss the coin 20 times and get 7 heads.

P-value:

The likelihood of getting this outcome or one that deviates even more from what is expected under the null-hypothesis.



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P-value correction

Our experiment:

We toss the coin 20 times and get 7 heads.

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 $P = Pr[X \le 7 \text{ or } X \ge 13 \mid \text{null-hyp.}] = 0.263 \text{ (or 26.3\%)}.$

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Our experiment:

We toss the coin 20 times and get 7 heads.

P-value:

The likelihood of getting this outcome or one that deviates even more from what is expected under the null-hypothesis.



 $P = Pr[X \le 7 \text{ or } X \ge 13 \mid \text{null-hyp.}] = 0.263 \text{ (or } 26.3\%).$

The deviation from the null-hypothesis is *statistically significant* at the 5% *significance level* if $P \le 0.05$.

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The P-values give a measure of the statistical strength of the evidence against the null-hypothesis.



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The P-values give a measure of the statistical strength of the evidence against the null-hypothesis.

P>0.05 At the 5% significance level, this is considered to be what you could expect if the null-hypothesis is true.

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P from 0.01 to 0.05 Considered statistically significant, but not strong evidence.

P<0.01 Fairly strong evidence.

P<0.001 Strong evidence.

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The P-values give a measure of the statistical strength of the evidence against the null-hypothesis.

- P>0.05 At the 5% significance level, this is considered to be what you could expect if the null-hypothesis is true.
- P from 0.01 to 0.05 Considered statistically significant, but not strong evidence.
 - P<0.01 Fairly strong evidence.
 - P<0.001 Strong evidence.

The P-value does not tell if the deviation from the null-hypothesis is small or large, important or unimportant.

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What if we don't assume that the coin is fair?

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What if we don't assume that the coin is fair?

Hypothesis *p*: Assume the coin has probability *p* of head in each toss for some probability $p \in [0, 1]$.

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What if we don't assume that the coin is fair?

Hypothesis *p*: Assume the coin has probability *p* of head in each toss for some probability $p \in [0, 1]$.

Test which values of p may be rejected, and which must be retained as possible values. If tests are at the 5% significance level, the retained values of p form the 95% confidence interval.

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What if we don't assume that the coin is fair?

Hypothesis *p*: Assume the coin has probability *p* of head in each toss for some probability $p \in [0, 1]$.

Test which values of p may be rejected, and which must be retained as possible values. If tests are at the 5% significance level, the retained values of p form the 95% confidence interval.

The null-hypothesis that the coin is fair (p = 1/2) is retained if p = 1/2 is contained in the confidence interval.

For 7 heads in 20 tosses, the 95% confidence interval for the probability of heads is [0.15, 0.59], which contains 1/2.

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Example:

Let's test five coins to see if they are fair.



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Example:

Let's test five coins to see if they are fair.

Toss each coin 20 times, and use our test.



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Example:

Let's test five coins to see if they are fair.

Toss each coin 20 times, and use our test.

If the coins are fair, for each we have 4% likelihood of a Type I error.



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Example:

Let's test five coins to see if they are fair.

Toss each coin 20 times, and use our test.

If the coins are fair, for each we have 4% likelihood of a Type I error.

There is appr. 20% risk of making at least one Type I error.



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The problem of multiple hypothesis testing

When performing several tests, the chance of getting one or more false positives increases.

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The problem of multiple hypothesis testing

When performing several tests, the chance of getting one or more false positives increases.

Multiple testing problem: Need to controll the risk of false positives (Type I error) when performing a large number of tests.

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Bad solution to the multiple testing problem

The big DON'T: It is **not** permissible to perform several tests and only present those that gave the desired outcome.





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Bad solution to the multiple testing problem

The big DON'T: It is **not** permissible to perform several tests and only present those that gave the desired outcome.





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P-value correction

All-against-all correlations

Pearson correlation P-value	sign_ germB	sign_ lymph	sign_ prolif	BHP6	MHC
sign_germB	1.00000	0.16336	-0.05530	-0.08362	0.17837
Germinal center B cell sign.		0.0113	0.3938	0.1967	0.0056
sign_lymph	0.16336	1.00000	-0.31586	-0.02660	0.15082
Lymph node signature	0.0113		<.0001	0.6818	0.0194
sign_prolif	-0.05530	-0.31586	1.00000	0.14079	-0.13411
Proliferation signature	0.3938	<.0001		0.0292	0.0379
BHP6	-0.08362	-0.02660	0.14079	1.00000	0.08650
BMP6	0.1967	0.6818	0.0292		0.1817
MHC	0.17837	0.15082	-0.13411	0.08650	1.00000
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Computing all pairwise correlations and then presenting only those that are statistically significant, is not acceptable!

Example data: Expression from 100 genes, outcome is survival. Perform T-test for each gene.



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Example data: Expression from 100 genes, outcome is survival. Perform T-test for each gene.

Rank	Gene	P-value	Rank	Gene	P-value	
1	GENE84X	0.00037	13	GENE6X	0.02083	
2	GENE73X	0.00431	14	GENE71X	0.02401	
3	GENE48X	0.00544	15	GENE49X	0.02463	
4	GENE1X	0.00725	16	GENE38X	0.02751	
5	GENE81X	0.00769	17	GENE46X	0.02804	
6	GENE91X	0.00793	18	GENE75X	0.02892	
7	GENE96X	0.00803	19	GENE36X	0.04072	
8	GENE22X	0.00907	20	GENE83X	0.04519	
9	GENE95X	0.00977	21	GENE8X	0.04608	
10	GENE58X	0.01734	22	GENE21X	0.05213	
11	GENE77X	0.01911	23	GENE78X	0.06940	
12	GENE33X	0.01974	24	GENE16X	0.07046	

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Example data: Expression from 100 genes, outcome is survival. Perform T-test for each gene.

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5	GENE81X	0.00769	17	GENE46X	0.02804	
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7	GENE96X	0.00803	19	GENE36X	0.04072	
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11	GENE77X	0.01911	23	GENE78X	0.06940	
12	GENE33X	0.01974	24	GENE16X	0.07046	

Presenting only those with small P-value is inappropriate when we have done 100 tests!

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Other cases where multiple testing occurs

Example: A researcher wants to compare incidence of disease between rural and urban populations. He finds a difference for two out of ten common diseases (P=0.02 and 0.03 resp.).

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Other cases where multiple testing occurs

Example: A researcher wants to compare incidence of disease between rural and urban populations. He finds a difference for two out of ten common diseases (P=0.02 and 0.03 resp.).

Example: A researcher wants to check if health depends on social status. Both health and social status can be measured in many different, although similar, ways. He checks all combinations.

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Other cases where multiple testing occurs

Example: A researcher wants to compare incidence of disease between rural and urban populations. He finds a difference for two out of ten common diseases (P=0.02 and 0.03 resp.).

Example: A researcher wants to check if health depends on social status. Both health and social status can be measured in many different, although similar, ways. He checks all combinations.

Example: A researcher cannot decide which is more appropriate to use: Pearson correlation or Spearman. He picks the one that gives the lowest P-value.

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Result: If you perform *N* tests at a significance level α , then the probability of having at least one false positive is at most $N \times \alpha$.

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Result: If you perform *N* tests at a significance level α , then the probability of having at least one false positive is at most $N \times \alpha$.

In many cases, the risk will be less, but this result is true even in the worst of cases.

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It is also correct if some of the null-hypotheses are actually wrong.

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Result: If you perform *N* tests at a significance level α , then the probability of having at least one false positive is at most $N \times \alpha$.

In many cases, the risk will be less, but this result is true even in the worst of cases.

It is also correct if some of the null-hypotheses are actually wrong.

May use this to formulate a *multiple test* that controls the over-all risk of having a false positive.

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Bonferroni: If you perform *N* tests at a significance level α/N , then the probability of having at least one false positive is at most α .

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Bonferroni: If you perform *N* tests at a significance level α/N , then the probability of having at least one false positive is at most α .

Bonferroni P-value: If you run *N* tests, multiply all the P-values by *N* to get the Bonferroni corrected P-values.

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Bonferroni: If you perform *N* tests at a significance level α/N , then the probability of having at least one false positive is at most α .

Bonferroni P-value: If you run *N* tests, multiply all the P-values by *N* to get the Bonferroni corrected P-values.

Result: The likelihood of getting a Bonferroni corrected P-value less than α for a true null-hypothesis is at most α .

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Outline Hypothesis testing Multiple testing P-value correction

Pearson correlation / P-value

sign_germB
Germinal center B cell sign.

Lymph node signature 0.0113 sign_prolif -0.05530 -0.31586 - Proliferation signature 0.3938 <.0001 - BHP6 -0.08362 -0.02660 0.14079 DMP6 0.1967 0.6818 0.0292 MHC 0.17837 0.15082 -0.13411 0.0864 MHC class II signature 0.0056 0.0194 0.0379 0.18	sign_lymph	0.16336	-		
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Multiply each P-value by 10 to get the Bonferroni corrected P-value.

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Pearson correlation / P-value

sign_germB
Germinal center B cell sign.

sign_lymph	0.16336	-		
Lymph node signature	0.0113			
sign_prolif	-0.05530	-0.31586	-	
Proliferation signature	0.3938	<.0001		
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BMP6	0.1967	0.6818	0.0292	
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T-tests done for 100 genes. Bonferroni correction requires us to multiply all P-values with 100.

Rank	Gene	P-value	Rank	Gene	P-value
1	GENE84X	0.00037	13	GENE6X	0.02083
2	GENE73X	0.00431	14	GENE71X	0.02401
3	GENE48X	0.00544	15	GENE49X	0.02463
4	GENE1X	0.00725	16	GENE38X	0.02751
5	GENE81X	0.00769	17	GENE46X	0.02804
6	GENE91X	0.00793	18	GENE75X	0.02892
7	GENE96X	0.00803	19	GENE36X	0.04072
8	GENE22X	0.00907	20	GENE83X	0.04519
9	GENE95X	0.00977	21	GENE8X	0.04608
10	GENE58X	0.01734	22	GENE21X	0.05213
11	GENE77X	0.01911	23	GENE78X	0.06940
12	GENE33X	0.01974	24	GENE16X	0.07046

Multiple testing

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P-value correction

Multiple comparisons

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Only the smallest P-value survives Bonferroni correction.

Most micro arrays now contains more than 40.000 probes: too many to test them one by one and hope that they can survive Bonferroni correction.

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Bonferroni correction is the most common multiple testing correction:

It is very simple.

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Bonferroni correction is the most common multiple testing correction:

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P-value correction

Multiple comparisons

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P-value correction

Multiple comparisons

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Multiple testing

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Multiple comparisons

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P-value correction

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However, Bonferroni-correction is often conservative!

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P-value correction

Pearson correlation / P-value

sign_germB
Germinal center B cell sign.

sign_lymph	0.16336	-		
Lymph node signature	0.0113			
sign_prolif	-0.05530	-0.31586	-	
Proliferation signature	0.3938	<.0001		
BHP6	-0.08362	-0.02660	0.14079	-
BMP6	0.1967	0.6818	0.0292	
MHC	0.17837	0.15082	-0.13411	0.08650
MHC class II signature	0.0056	0.0194	0.0379	0.1817

Only one P-value would survive Bonferroni correction.

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Pearson correlation / P-value

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However, getting P<0.05 for 5 of the remaining 9 correlations seems unlikely to happen by chance.

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Pearson correlation / P-value

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Only one P-value would survive Bonferroni correction.

However, getting P<0.05 for 5 of the remaining 9 correlations seems unlikely to happen by chance.

In this case, Bonferroni correction is very conservative.

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Exists less conservative methods.



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P-value correction

Exists less conservative methods.

Bonferroni–Holm Like Bonferroni, but correct the *k*-th smallest P-value with a factor N + 1 - k.

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P-value correction

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P-value correction
Alternative P-value corrections

Exists less conservative methods.

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Simes' procedure If there are *k* P-values less than *q*, the *over-all* P-value is at most $q \times N/k$.

False discovery rate Relaxes the criteria by allowing *some* false positives.

Some procedures (e.g. Simes') require caution: test the *over-all* hypothesis that *all* the null-hypotheses are true. Need not tell you which of the null-hypotheses are rejected, only that they cannot all be retained.

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Multiple testing

P-value correction

Over-all tests of multiple hypotheses

Example: We compute all pairwise correlations for 10 variables (that's 45 pairs). The smalles P-values we get are 0.0014, 0.0021, 0.0025 and 0.0031. None of these would survive the Bonferroni correction.

Simes' procedure would give an over-all P-value of $0.0031 \times 45/4 = 0.035$. However, it would be wrong to conclude that all four of these correlations are non-zero at the 5% significance level.

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Simes' procedure would give an over-all P-value of $0.0031 \times 45/4 = 0.035$. However, it would be wrong to conclude that all four of these correlations are non-zero at the 5% significance level.

Over-all tests are often more powerful than e.g. Bonferroni, but lead to conclusions that are harder to interpret and explain. Multiple testing

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P-value correction

How to interpret and present P-values in a multiple testing setting:

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How to interpret and present P-values in a multiple testing setting:

P-value survives Bonferroni correction: Corrected P-value is reliable. Multiple testing

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How to interpret and present P-values in a multiple testing setting:

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P-value survives Bonferroni correction: Corrected P-value is reliable.

Over-all test is not statistically significant: No reason to believe there are any statistically significant P-values.

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How to interpret and present P-values in a multiple testing setting:

P-value survives Bonferroni correction: Corrected P-value is reliable.

Over-all test is not statistically significant: No reason to believe there are any statistically significant P-values.

Conflict: If the uncorrected P-value is statistically significant, but Bonferroni corrected is not, proceed with caution! This may indicate a possible, but unreliable, finding.

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P-value correction

Ideally, one should perform one test only, and decide on the test prior to analysing the data. Multiple testing

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P-value correction

Ideally, one should perform one test only, and decide on the test prior to analysing the data.

In reality, data is scarce, and one wants to performe more analyses, get more results and test more hypotheses.

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One compromise is to divide analyses into two parts:

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In reality, data is scarce, and one wants to performe more analyses, get more results and test more hypotheses.

One compromise is to divide analyses into two parts:

Hypothesis testing: As rigorous as can be done! Want reliable conclusions.

Hypothesis generating: Less rigorous, allowing data mining, multiple testing, etc. Conclusions are not expected to be reliable in themselves, but give good ideas/candidates for further research. Multiple testing E. A. Rødland Outline

Multiple testing P-value correction

Outline

Hypothesis testing

Multiple hypothesis testing

P-value correction

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One special case of multiple testing is pairwise comparisons of groups.

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One special case of multiple testing is pairwise comparisons of groups.

Example: A doctor is comparing 6 different treatments to find which reduces blood pressure the most by giving each treatment to 10 different patients.

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One special case of multiple testing is pairwise comparisons of groups.

Example: A doctor is comparing 6 different treatments to find which reduces blood pressure the most by giving each treatment to 10 different patients.

Can use ANOVA (Analysis of Variance) to check if there is any variation between the treatments, and T-tests to compare each pair of treatments. There are 15 pairs, so P-values need to correct for multiple testing. Multiple testing

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Group	x LSME	CAN	95% Con:	fidence	Limits		
1	1.8647	23	1.1949	959	2.534487		
2	0.6066	15	-0.063	L49	1.276378		
3	2.6211	.82	1.9514	118	3.290945		
4	0.7891	.82	0.1194	118	1.458946		
5	1.1964	42	0.526	578	1.866206		
6	3.3970	56	2.727	292	4.066820		
Source	DF	Туре	III SS	Mean	Square	F Value	Pr > F
Group	5	60.2	1737137	12.0	4347427	10.79	<.0001

ANOVA shows that there is variation between the treatments (P<0.0001), but this does not tell us which treatments differ.

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All-against-all comparisons

Tukey: Adjustment of P-values for all-against-all T-tests.

Tukey	1	2	3	4	5	6
1		0.0999	0.6014	0.2215	0.7182	0.0236
2	0.0999		0.0011	0.9988	0.8109	<.0001
3	0.6014	0.0011		0.0037	0.0429	0.5749
4	0.2215	0.9988	0.0037		0.9538	<.0001
5	0.7182	0.8109	0.0429	0.9538		0.0003
6	0.0236	<.0001	0.5749	<.0001	0.0003	
Tukey	Me	an N	gr			
	2 2	071 10				

	А		3.3971	10	6
В	Α		2.6212	10	3
В		С	1.8647	10	1
		С	1.1964	10	5
		С	0.7892	10	4
		С	0 6066	10	2

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One-against-all comparisons

Dunnet: Adjustment of P-values for one-against-all T-tests.

Group	x LSMEAN	Pr > t
1	1.86472306	
2	0.60661459	0.0419
3	2.62118151	0.3680
4	0.78918174	0.1028
5	1.19644178	0.4854
6	3.39705568	0.0090

E.g. if group 1 is placebo or the standard treatment against which the others should be compared.

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Some links

StatSoft textbook Good overview of methods and concepts: http://statsoft.com/textbook/stathome.html SAS manuals Thorough with overview of analysis

procedures found in SAS: http://support.sas.com/onlinedoc/913/

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