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Type I and Type II errors Issue Multiple Hypothesis Testing

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Objective + Outline

• Objective

Type I and Type II errors - Issue Multiple Hypothesis Testing

- Outline
- **1. 4 situations - Statistical decision-making**
- **2. Significance level (α)**
- **3. β vs Power (1-β)**
- **4. Relationship α and β**
- **5. Issue with Multiple Testing of hypothesis**

4 situations

Statistical decision-making

Independent-means t-test

In Independent-means t-test:

• Null Hypothesis: no difference between 2 populations' means.

 \checkmark Ho: $\mu_1 = \mu_2$

• Research Hypothesis: difference between 2 populations' means.

 \checkmark H1: $\mu_1 \neq \mu_2$

• Compare p with 0.05:

 p ≤ .05 Reject Null Hypothesis We have **enough evidence** to conclude that the difference between groups is statistically significant.

 \checkmark p > .05 \checkmark Failed to reject Null Hypothesis \checkmark We don't have enough **evidence** to conclude that the difference between groups is statistically significant.

- Ho: $\mu_1 = \mu_2$
- H1: $\mu_1 \neq \mu_2$

 p ≤ .05 Reject Null Hypothesis We have **enough evidence** to conclude that the difference between groups is statistically significant.

 \times **p** $>$ **.05** \triangleright **Failed to reject Null Hypothesis** \triangleright We don't have enough **evidence** to conclude that the difference between groups is statistically significant.

- The probability that the observed difference could have occurred by chance.
	- $\sqrt{\alpha} = 5\%$:
		- 5% probability that observed difference occurred by chance.

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		- 5% risk of **false positive**.

- Predetermined threshold to make a decision about the null hypothesis.
	- \checkmark A cut off point: **p** ≤ **α**
		- \triangleright Reject Null Hypothesis (Ho: $\mu_1 = \mu_2$).
		- \triangleright Accept α risk of false positive.

Note 1: p vs α

Note 2: Strength of evidence

• **α value: 0.05**

- **No sharp distinction between "significant" and "not significant"** results, only increasing the **strength of evidence** against null hypothesis
	- **0.049 ≤ 0.05** vs **0.051 > 0.05**.

Note 2: Strength of evidence

• **α value: 0.05**

- **No sharp distinction between "significant" and "not significant"** results, only increasing the **strength of evidence** against null hypothesis
	- **0.049 ≤ 0.05** vs **0.051 > 0.05**.
	- Observed data not provide **strong enough evidence** to reject the null hypothesis.
	- \checkmark Could still be a real effect or difference, but it might be smaller than the study was able to detect.

Note 2: Strength of evidence

- p-values: continuum and provide a relative measure of strength of evidence:
	- \checkmark p \geq 0.1 insufficient evidence
	- \sqrt{p} < 0.1 weak evidence
	- **p < 0.05 moderate evidence**
	- \sqrt{p} < 0.01 strong evidence
	- \sqrt{p} < 0.001 very strong evidence

• **β**: Probability of making a type II error - failing to reject the null hypothesis when it is actually false.

• **Power: 1 – β:** Probability of observing an effect in the sample.

- \cdot β = 0.2 (20%) \Leftrightarrow Power = 0.8 (80%)
	- \checkmark 20% False Negative.
	- \checkmark If there are true effects to be found in 100 different studies with 80% power, only 80 out of 100 statistical tests will actually detect them.

- Ideally to eliminate false-positive and false-negative results ?
	- \checkmark **a** = **0** \Leftrightarrow **False** positive = **0**
	- \checkmark β = 0 \Leftrightarrow False negative = 0

G*Power: a tool to

- Compute statistical power analyses.
- Compute effect sizes.
- Display graphically the results of power analyses.
- [https://www.psychologie.hhu.de/arbeitsgruppen/allg](https://www.psychologie.hhu.de/arbeitsgruppen/allgemeine-psychologie-und-arbeitspsychologie/gpower) [emeine-psychologie-und-arbeitspsychologie/gpower](https://www.psychologie.hhu.de/arbeitsgruppen/allgemeine-psychologie-und-arbeitspsychologie/gpower)

Statistical power analyses using G Power 3.1: Tests for correlation and regression analyses F Faul, E Erdfelder, A Buchner, AG Lang Behavior research methods, 2009 - Springer

Abstract

G^{*}Power is a free power analysis program for a variety of statistical tests. We present extensions and improvements of the version introduced by Faul, Erdfelder, Lang, and Buchner (2007) in the domain of correlation and regression analyses. In the new version, we have added procedures to analyze the power of tests based on (1) single-sample tetrachoric correlations, (2) comparisons of dependent correlations, (3) bivariate linear regression, (4) multiple linear regression based on the random predictor model, (5) logistic regression, and (6) Poisson regression. We describe these new features and provide a brief introduction to their scope and handling.

Springer

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Statistical test Test family Means: Difference between two independent means (two groups) t tests \checkmark

Type of power analysis

Post hoc: Compute achieved power - given a, sample size, and effect size

100

Sample size group 2

• Ideally to eliminate false-positive and false-negative results ?

```
\checkmark \alpha = 0 \Leftrightarrow False positive = 0.
```
 \checkmark β = 0 \Leftrightarrow False negative = 0.

• **α decrease β increase**.

• Many studies:

 \checkmark α = 0.01 or 0.05

β = 0.1 (Power = 0.9) or 0.20 (Power = 0.80)

Issue of Multiple testing of hypothesis

Multiple testing issue

- \cdot α = 5%: Risk of false positive rate **for 1 test** = 5%.
- Multiple hypothesis tests inflated the risk of type I error **Family-wise / Experiment-wise error rate (FWER).**

Multiple testing issue

Respiratory virus shedding in exhaled breath and efficacy of face masks

Nancy H. L. Leung ¹, Daniel K. W. Chu¹, Eunice Y. C. Shiu¹, Kwok-Hung Chan², James J. McDevitt³, Benien J. P. Hau^{1,4}, Hui-Ling Yen ¹, Yuguo Li⁵, Dennis K. M. Ip¹, J. S. Malik Peiris¹, Wing-Hong Seto^{1,6}, Gabriel M. Leung¹, Donald K. Milton^{7,8} and Benjamin J. Cowling \bullet ^{1,8}

We identified seasonal human coronaviruses, influenza viruses and rhinoviruses in exhaled breath and coughs of children and adults with acute respiratory illness. Surgical face masks significantly reduced detection of influenza virus RNA in respiratory droplets and coronavirus RNA in aerosols, with a trend toward reduced detection of coronavirus RNA in respiratory droplets. Our results indicate that surgical face masks could prevent transmission of human coronaviruses and influenza viruses from symptomatic individuals.

Respiratory virus infections cause a broad and overlapping spectrum of symptoms collectively referred to as acute respiratory virus illnesses (ARIs) or more commonly the 'common cold'. Although mostly mild, these ARIs can sometimes cause severe disease and medically attended ARIs and determining the potential efficacy of surgical face masks to prevent respiratory virus transmission.

Results

We screened 3,363 individuals in two study phases, ultimately enrolling 246 individuals who provided exhaled breath samples (Extended Data Fig. 1). Among these 246 participants, 122 (50%) participants were randomized to not wearing a face mask during the first exhaled breath collection and 124 (50%) participants were randomized to wearing a face mask. Overall, 49 (20%) voluntarily provided a second exhaled breath collection of the alternate type.

Infections by at least one respiratory virus were confirmed by reverse transcription PCR (RT-PCR) in 123 of 246 (50%) partici-

Multiple testing issue

Table 1b | Efficacy of surgical face masks in reducing respiratory virus frequency of detection and viral shedding in respiratory droplets and aerosols of symptomatic individuals with coronavirus, influenza virus or rhinovirus infection

P values for comparing the frequency of respiratory virus detection between the mask intervention were obtained by two-sided Fisher's exact test and (two-sided) P values for mask intervention as predictor of log₁₀ virus copies per sample were obtained by an unadjusted univariate Tobit regression model, which allowed for censoring at the lower limit of detection of the RT-PCR assay, with significant differences in bold. Undetectable values were imputed as 0.3 log₁₀ virus copies per sample. IQR, interquartile range.

Leung NH, Chu DK, Shiu EY, Chan KH, McDevitt JJ, Hau BJ, Yen HL, Li Y, Ip DK, Peiris JS, Seto WH. Respiratory virus shedding in exhaled breath and efficacy of face masks. Nature medicine. 2020 May;26(5):676-80.

Family-wise / Experiment-wise error rate (FWER)

- If perform **m hypothesis independent tests**, **the probability at least 1 false positive** ?
	- \checkmark P (Making Type I error) = α
	- \checkmark P (Not making Type I error) = 1 α
	- \checkmark P (Not making an error in m tests) = $(1 \alpha)^m$
	- \checkmark P (Making at least 1 error in m tests) = 1 (1 α)^m

• Example: m = 100 tests, $\alpha = 0.05 \Rightarrow P = 1 - (1 - 0.05)^{100} = 0.99$

 \triangleright If have 100 hypothesis tests, the probability at least 1 false positive: 99% $\frac{35}{35}$

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P (Making at least 1 error in 12 tests):

$$
1 - (1 - 0.05)^{12} = 0.4596 = 45.96\%
$$

factor(P.value) - 0.001 - 0.01 - 0.05

NguyenVanTuanhttps://www.youtube.com/watch?v=RPjVPHpeu2o&t=2517s

The probability of obtaining at least one false positive result $P(FP \geq 1)$ (own calculation)

 $Life$
 37 Maziarz M, Stencel A. The failure of drug repurposing for COVID-19 as an effect of excessive hypothesis testing and weak mechanistic evidence. History and Philosophy of the Sciences. 2022 Dec;44(4):47.

FWER – Correction

- **Single Step**: equivalent adjustments made to each p-value.
- **Sequential**: adaptive adjustment made to each p-value.

Single Step – Bonferroni Concept

- Simple method to maintain overall Type I error rate (α) when performing m independent hypothesis tests.
- When ?
	- \checkmark Multiple 't' tests / Mann-Whitney
	- Post-hoc test after ANOVA / Kruskal-Wallis test
	- \checkmark Pearson's 'r'
	- \checkmark Chi-square / Contingency table test

Single Step – Bonferroni Concept

- Bonferroni correction: $\alpha^* = \alpha / m$
	- \checkmark α : significance level.
	- \checkmark m : number of hypothesis tests.

Single Step – Bonferroni Concept

- Bonferroni correction: $\alpha^* = \alpha / m$
	- \checkmark α : significance level.
	- \checkmark m : number of hypothesis tests.

• Example: Bonferroni to test 3 hypotheses with p:

H1: p = 0.01

- \checkmark H2: p = 0.02
- \checkmark H3: p = 0.03
	- $\alpha^* = \alpha / m = 0.05 / 3 = 0.0167$

 \Rightarrow We'd need $p \le 0.0167$ to declare significance.

Single Step – Bonferroni Example 1

Table 1b | Efficacy of surgical face masks in reducing respiratory virus frequency of detection and viral shedding in respiratory droplets and aerosols of symptomatic individuals with coronavirus, influenza virus or rhinovirus infection

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 $\alpha^* = \alpha / m = 0.05 / 12 = 0.004$

 \Rightarrow We'd need $p \le 0.004$ to declare significance.

Single Step – Bonferroni Example 2

- Testing **millions of associations** between individual genetic variants and a phenotype of interest
- Multiple-testing threshold to avoid false positives:
	- \checkmark Bonferroni testing threshold: P < 0.05/ 10⁶ = 5 × 10⁻⁸

Overview of steps for conducting GWAS

association studies. Nature Reviews Methods Primers. 2021 Aug₁₃ Uffelmann E, Huang QQ, Munung NS, De Vries J, Okada Y, Martin AR, Martin HC, Lappalainen T, Posthuma D. Genome-wide 26;1(1):59.

Single Step - Controversy over Bonferroni

• **Benefits:**

- \checkmark Controls FWER: \checkmark Type I error risk (False Positive).
- \checkmark Simple + easy to understand.

Single Step - Controversy over Bonferroni

• **Benefits:**

- \checkmark Controls FWER: \checkmark Type I error risk (False Positive).
- \checkmark Simple + easy to understand.

• **Drawbacks:**

- \checkmark \downarrow Type I error (False Positive) \Leftrightarrow \uparrow Type II error (False Negative).
- \checkmark Better for independence: all tests are independent of each other.
- \checkmark Number of tests performed ?
	- All tests in a report or a subset of them.
	- Tests performed but not included in the report.
	- Tests from the same data included in other reports.
- **Treating all tests equally regardless of their importance or relevance**.

Sequential - Holm-Bonferroni

- Holm-Bonferroni correction: $\alpha^* = \alpha / (m i + 1)$
	- \checkmark α : significance level.
	- \checkmark m : number of hypothesis tests.
	- \checkmark i : rank number of pair (by degree of significance).

- Example: Holm-Bonferroni to test 3 hypotheses with p:
	- \checkmark H1: p = 0.01
	- \checkmark H2: p = 0.02
	- \checkmark H3: p = 0.03

Sequential - Holm-Bonferroni

- **Step 1: Order p from smallest to greatest:**
	- \checkmark H1: p = 0.01
	- \checkmark H2: p = 0.02
	- $\sqrt{H3: p} = 0.03$
- **Step 2: α1* for 1 st rank. Compare p-value to α1***:

 $\sqrt{}$ H1: p = 0.01 $\lt \alpha$ α 1^{*} = 0.05 / (3–1+1) = 0.0167 \gt **Reject Null Hypothesis.**

• **Step 3: α2* for 2 nd rank:**

 $\sqrt{ }$ H2: p = 0.02 \approx $\alpha 2^* = 0.05 / (3 - 2 + 1) = 0.025$ \Rightarrow **Reject Null Hypothesis.**

• **Step 4: α3* for 3 rd rank:**

 $\sqrt{}$ H2: p = 0.03 $\lt \alpha3^* = 0.05 / (3 - 3 + 1) = 0.05$ \approx **Reject Null Hypothesis.**

• **Note: The test stops when you reach the first non-rejected hypothesis. All subsequent hypotheses are non-significant.** 47

Bonferroni or Holm-Bonferroni

False Discovery Rate (FDR)

- **FWER** control the probability of falsely rejecting **any** null hypothesis.
- But with **large number of test** α* too low **very low chance reject null hypothesis - super conservative**.
- Instead we can control **False Discovery Rate (FDR).**

False Discovery Rate (FDR)

FDR: The proportion of incorrect rejection of a hypothesis.

 $FDR = FP / (FP + TP) = Number of false rejection / Total number of rejection.$

If I conduct 1,000 hypothesis tests:

• FWER = 5%: Any individual test with a p-value \leq 0.05 / 1,000 would be considered statistically significant.

• FDR = 5%: 100 tests are statistically significant \Rightarrow Expect up to 5 of significant results to be false positives.

FWER vs FDR

Comparison of threshold p values when 50 tests are performed

Verhoeven KJ, Simonsen KL, McIntyre LM. Implementing false discovery rate control: increasing your power. Oikos. 2005 Mar;108(3):643-7.

FWER vs FDR - Example GWAS

- Testing **millions of associations** between individual genetic variants and a phenotype of interest
- Multiple-testing threshold to avoid false positives:
	- \checkmark Bonferroni testing threshold: P < 0.05/ 10⁶ = 5 × 10⁻⁸
	- \checkmark False discovery rate of 0.05/10⁶. .ts in a report of a report of

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Benjamini-Hochberg

- α^* = FDR * (i/m)
	- \checkmark i: rank of p-value.
	- \checkmark m: total number of tests.
	- \checkmark FDR: your chosen false discovery rate.

• Example: FDR = 0.05; H1: $p = 0.01$; H2: $p = 0.03$; H3: $p = 0.04$

• **Note: The test stops when you reach the first non-rejected hypothesis. All subsequent hypotheses are non-significant.**

FWER vs FDR

Take-home messages

- p-values: continuum and provide a relative measure of strength of evidence:
	- \checkmark p \geq 0.1 insufficient evidence
	- \sqrt{p} < 0.1 weak evidence
	- **p < 0.05 moderate evidence**
	- \sqrt{p} < 0.01 strong evidence
	- \sqrt{p} < 0.001 very strong evidence
- **α (False positive) β (False negative) .**
- Multiple hypothesis tests inflated the risk of type I error:
	- FWER: Bonferroni / Holm-Bonferroni
	- \checkmark FDR: Benjamini-Hochberg

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