

Week 8

Multiple testing

key ideas

- hypothesis testing / significance analysis is commonly overused
- correcting for multiple testing avoids false positives or discoveries
- two key components:
 - error measure (what you'd like to control)
 - correction (statistical method used to control error measure)

Types of errors

Suppose you're testing a hypothesis that a parameter $\beta = 0$ vs $\beta \neq 0$

		possible outcomes		hypothesis
		True state $\beta = 0$	$\beta \neq 0$	
claim	$\beta = 0$	U	T	$m - R$
claim	$\beta \neq 0$	V	S	R
claims		m_0	$m - m_0$	m

Type I error (false positive) - V

says that $\beta \neq 0$ but it equals to 0

Type II error (false negative) - T

says that $\beta = 0$ when $\beta \neq 0$

Error rates

- False positive rate

the rate at which false results are called significant

$$E \left[\frac{V}{m_0} \right]$$

- Family wise error rate

the probability of at least one false positive

$$\Pr(V \geq 1)$$

- False Discovery Rate

The rate at which claims of significance are false

$$E \left[\frac{V}{R} \right]$$

Controlling the false positive rate

if P -values are correctly calculated calling all $P < \alpha$ significant will control the false positive rate at level α on average

(all $P < \alpha$ - significant)

but with larger n , the number of false positives is too high!

$$(10000 \cdot 0.05 = 500)$$



- controlling family-wise error rate (FWER)

The Bonferroni correction

the oldest multiple testing correction

basic idea

- suppose you do m tests
- you want to control FWER at level α , so $\Pr(U \geq 1) < \alpha$
- calculate P -values normally
- $\alpha_{\text{fwer}} = \frac{\alpha}{m}$
- call all P -values less than α_{fwer} significant

$$\alpha = 0.05, \quad \alpha_{\text{fwer}} = \frac{0.05}{10000} = (\text{no one FP!})$$

might be too strict
(you would want to allow for FP)

• controlling false discovery rate (FDR)

the most popular ~~test~~ when correlation when performing lots of tests

Basic idea

- you have m tests

- you want to control FDR at level α , so

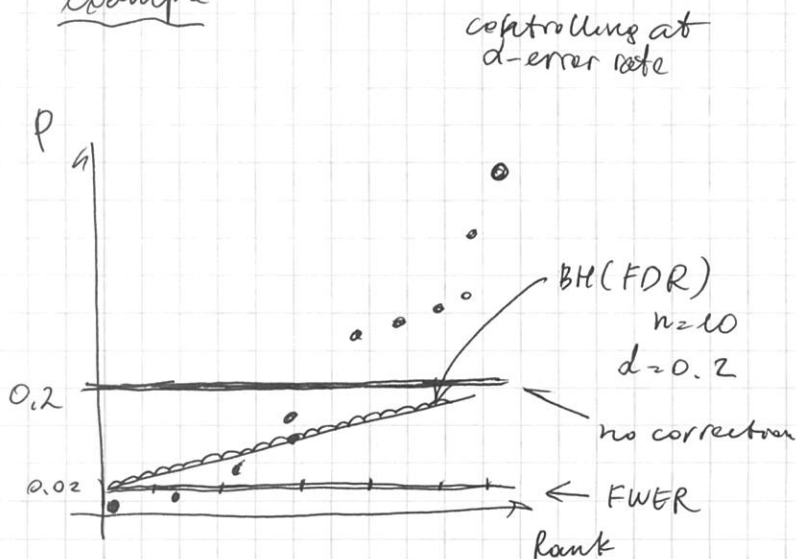
$$E\left[\frac{V}{R}\right]$$

- calculate P -values normally

- order the P -values from smallest to largest

- call any $P_{(i)} \leq \alpha \times \frac{i}{m}$ significant

Example



Adjusted P-value

one approach -

- to adjust the threshold α

- another - to calculate "adjusted p-values"

↓
they are not "p-values"
anymore!

but they can be used directly, without
adjusting α

examples

- suppose we have $p_1 \dots p_m$
- $p_i^{\text{fwer}} = \max(m \times p_i, 1)$ for each p_i
- If $p_i^{\text{fwer}} < \alpha$, it's significant

Example:

Suppose we have no relationship at all

```
set.seed(1010093)
```

```
pvalues = rep(NA, 1000)
```

```
for (i in 1:1000) {
```

```
  x = rnorm(20); y = rnorm(20)
```

```
  pvalues[i] = summary(lm(y ~ x))$coeff[2, 4]
```

```
}
```

```
sum(pvalues < 0.05) = 51!
```

P value
↓

sum

FWER

$$(p.adjust(pValues, method = "bonferroni") < 0.05)$$



0

FDR

$$\text{sum}(p.adjust(pValues, method = "BH") < 0.05)$$



0

Simulation For model checking

regression model

$$Y_i = b_0 + b_1 X_i + e_i$$

for generating:

$$x = \text{rnorm}(50), y = \text{rnorm}(50), b_1 = 1, b_2 = 2$$

$$y = b_0 + b_1 * x + e$$

Monte Carlo error

monte carlo variability - ~~when error term~~
~~is removed~~

when you do more and more simulations,
the accuracy increases

1000 \rightarrow 10000 better

Simulation based on data set

library(UsingR)
data(galton)

lm1 = lm(child ~ parent)

— generating new parent height:

parent0 = rnorm(len, sd = sd(galton\$parent),
mean = mean(galton\$parent))

child0 = lm1\$coeff[1] + lm1\$coeff[2] * parent0 +
+ rnorm(len, sd = summary(lm1)\$sigma)

measuring error
(equal to variability in
residuals)

Notes

- simulation can be applied to missing data problems — simulate what missing data might be
- sensitivity analysis — trying different simulations with different assumptions, and seeing how estimates change