Research Analysis

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Last time

- What is a statistical test?
- Chi-square
- t-test
- Paired t-test



Today

- ANOVA
- Posthoc tests
- Two-way ANOVA
- Repeated measures ANOVA



Recall: hypothesis testing

Anatomy of a statistical test If your change had no effect, what would the world look like?

No difference in means

• This is known as the null hypothesis

No slope in relationship



Anatomy of a statistical test Given the difference you observed, how likely is it to have

occurred by chance?



Probability of seeing a mean difference at least this large, by chance, is 0.012



Probability of seeing a slope at least this large, by chance, is 0.012





Errors

Difference detected?

True positive

Υ

Ν

Y

Type 2 error get more data?

Difference exists? N







Type I error (false positive)





p-value

- The probability of seeing the observed difference by chance
 - In other words, P(Type I error)
- Typically accepted levels: 0.05, 0.01, 0.001

t-test: compare two means "Do people fix more bugs with our IDE bug suggestion

"Do people fix more bugs w callouts?"

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ANOVA: compare N means • "Do people fix more bugs with our IDE bug suggestion callouts, with warnings, or with nothing?"

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Rough intuition for ANOVA test How much of the total variation can be accounted for by looking at the means of each condition?

total deviation from grand mean deviation of factor mean from grand mean

deviation of response from factor mean

 Y_{2} .

ANalysis Of VAriance (ANOVA) Degrees of freedom: how many values can vary?

(Using n and r)

Degrees of freedom in individual data points: n - I Degrees of freedom in factor level averages: r - I Combined: n - r

Finaly: run the test! How large is the value we constructed from the F distribution? • Test if $F^* > F(1 - \alpha; r - 1, n)$ > aov <- aov(value ~ group, data)</pre> > summary(aov) Df Sum Sq Mean Sq F value Pr(>F) 2 22.75 11.38 12.1 0.00032 factor group Residuals 21 19.75 0.94 error ("what's left")

F(2,21)3 factor levels hopefully p < .0024 observations top >> bottom

$$p - \gamma$$

Reporting an ANOVA

news feed source on number of likes (F(2, 21)=12.1, p<.001)."

> aov	<-	aov(va	lue	~ (group	, da	ato	ג)			
<pre>> summary(aov)</pre>											
		Df	Sum	Sq	Mean	Sq	F	value			
group		2	22.	.75	11.	. 38		12.1	(
Resid	uals	s 21	19.	. 75	0	.94					

"A one-way ANOVA revealed a significant difference in the effect of

Pr(>F)0.00032 ***

Posthoc tests

ANOVA! Are we done no

- Significant means "One of the μ_i are different."
- That's not very helpful: "There is some difference between populating the Facebook news feed with friends vs. strangers vs. only Michael's status updates"

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Estimating pairwise differences • Which pairs of factor levels are different from each other? 90.0 67.5 Mean likes 45.0 22.5 0.0 Friend feed

Stranger feed

Michael feed

Roughly: we do pairwise t-tests

Stranger feed

Michael feed

But...familywise error! • $\alpha = .05$ implies a .95 probability of being correct If we do m tests, the actual probability of being correct is now: $\alpha^m = .95 \cdot .95 \cdot .95 \cdot ...$

< .95

Bonferroni correction

- Avoid familywise error by adjusting lpha to be more conservative • Divide α by the number of comparisons you make • 4 tests at $\alpha = .05$ implies using $\alpha = .0125$
- Conservative but accurate method of compensating for multiple tests

Bonferroni correction

> pairwise.t.test(value, group, p.adj='bonferroni')

Pairwise comparisons using t tests with pooled SD

data: value and group

Α B B 0.02971 -C 0.00023 0.15530

P value adjustment method: bonferroni

lukey test

- Less conservative than Bonferroni
- Compares all pairs of factor level means

> TukeyHSD(aov) Tukey multiple comparisons of means 95% family-wise confidence level

Fit: aov(formula = value ~ group, data = data)

\$group diff lwr upr B-A 1.375 0.1527988 2.597201 0.0257122 C-A 2.375 1.1527988 3.597201 0.0002167 C-B 1.000 -0.2222012 2.222201 0.1222307

p adj

Reporting

 "Posthoc tests using Bonferroni correction revealed that friend feed and Michael feed were significantly better than a stranger feed (p<.05), but the two were not significantly different from each other (p=.32)."

Crossed study designs

- total likes on Facebook:
 - Strong ties vs. weak ties in your news feed
- (e.g., "You last liked a story from John Hennessy in January") • This is a 2 x 2 study: two factor levels for each factor {tie strength, reminder}

Suppose you wanted to measure the impact of two factors on

Presence of a reminder of the last time you liked each friend's content

Interaction effects

- Sometimes the basic model of between factors
 - Data: People who see strong tie active
 - Result: Grand mean 8, strong tion
 in this cell is 20

Sometimes the basic model doesn't capture subtle interactions

Data: People who see strong ties and have a reminder are especially

• Result: Grand mean 8, strong tie mean 11, reminder mean 7, but mean

Wo-factor ANOVA test

Test for main effects and interaction

> anova(lm(time ~ device * technique)) Analysis of Variance Table

Response: time

Df	Sum Sq	Mean Sq	F
1	981.0	981.02	9
2	3423.8	1711.90	16
2	75.3	37.65	
42	435.9	10.38	
	Df 1 2 2 42	Df Sum Sq 1 981.0 2 3423.8 2 75.3 42 435.9	<pre>Df Sum Sq Mean Sq 1 981.0 981.02 2 3423.8 1711.90 2 75.3 37.65 42 435.9 10.38</pre>

factor or interaction SS MS

Main effects are significant, but interaction effect is also significant

F

Pr(>F) value 4.5291 2.581e-12 *** 4.9547 < 2.2e - 16 ***3.6275 0.03522 *

P

Significant interaction?

- effects the story is more complicated
- Inspect to figure it out:

Significant interactions mean that you can't just report the main

Repeated measures

Within-subjects studies

- Control for individual variation using the mean response for each participant
- Before: we found the mean effect of each treatment
- Now: we find the mean effect of each participant

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Repeated measures in R

repeated measures error term

effect of subtracting out the participant means

remaining main effects

- > summary(aov)

Error: factor(participant) Residuals 7 5.167 0.7381

```
> aov <- aov(value ~ factor(group) +</pre>
+ Error(factor(participant)/factor(group)), repeatframe)
```

```
Df Sum Sq Mean Sq F value Pr(>F)
Error: factor(participant):factor(group)
```

```
Df Sum Sq Mean Sq F value Pr(>F)
factor(group) 2 22.75 11.375 10.92 0.00139 **
Residuals 14 14.58 1.042
```


All together now

Always follow every step!

- I. Visualize the data
- 2. Compute descriptive statistics (e.g., mean) 3. Remove outliers >2 standard deviations from the mean 4. Check for heteroskedasticity and
- non-normal data
 - Try log, square root, or reciprocal transform
 - ANOVA is robust against non-normal data, but not against heteroskedasticity
- 5. Run statistical test
- 6. Run any posthoc tests if necessary

