# Week 6: Statistical inferential goals

ANTH 674: Research Design & Analysis in Anthropology
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Office Hours: Thursdays, 9:00am–12:00pm In person: GSB 312

Virtual: https://tinyurl.com/F22ANTH674

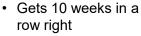
**Statistical vignette** 



- The parable of the Baltimore stockbroker
- Sends out email each week, predicting an increase/decrease for a given stock







 Asks you to invest money w/ him (w/ commission)



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# What's going on behind the scenes

Week 1: Emails 10,240 people



Week 2: Emails 5,120 people



Week 3: Emails 2,560 people

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Week 10: Ten people received ten straight weeks of correct picks

Should you invest or not?

Lecture outline

- Different types of statistical inferential goals:
- 1. Exploratory
- 2. Confirmatory AKA hypothesis testing
  - Problem of multiple comparisons
- 3. Prediction
  - Cross-validation w/ independent data



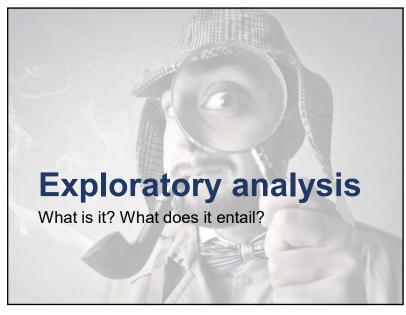
What is statistical inference?

 To understand properties of some larger statistical population by analyzing a smaller sample from said population

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#### Three modes of inference

- 1. Exploratory
- 2. Confirmatory or hypothesis testing
- 3. Prediction
- Each has different, mutually exclusive goals
- Knowing which one is right for your question makes data analysis more straightforward!
- Part of translating research question into statistical question



#### What is exploratory analysis?

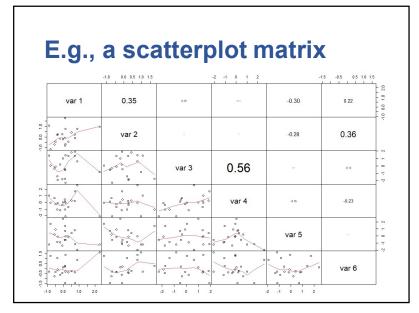
- Analyzing data where patterns and relationships are unknown
- Thus, there is no a priori hypothesis to test!
- E.g., why do people pick their nose?
  - Might collect data on a bunch of IVs & DVs and see if there are any relationships



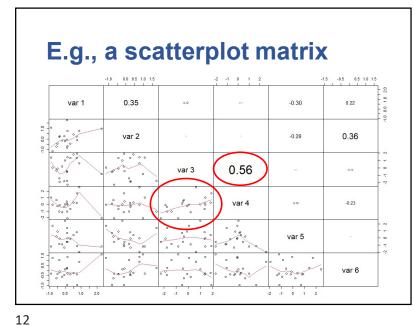
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## **Necessary part of research!**

- Important for a new field, or where we don't know a lot about the variables
- Can lead to the generation of hypotheses after the fact (a posteriori)



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## **Necessary part of research!**

- Important for a new field, or where we don't know a lot about the variables
- Can lead to the generation of hypotheses after the fact (*a posteriori*)
- "Finding the question is often more important than finding the answer."

CANNOT calculate
P-values!

7.

John W. Tukey

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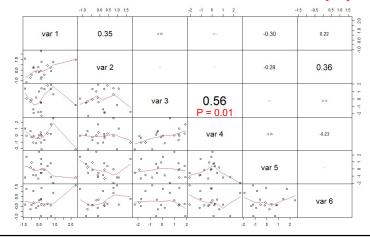
# Why no P-values?

- Type I error: rejecting H<sub>0</sub> when H<sub>0</sub> is true
- Type I error rate = significance level ( $\alpha$ ) = 0.05
- On average, 5% of tests will be P < 0.05 just by chance when H<sub>0</sub> is true
- On average, 5% of tests will also have large statistics just by chance when H<sub>0</sub> is true

	H <sub>o</sub> True	H <sub>0</sub> False
Reject H <sub>0</sub>	Type I Error	Correct Rejection
Fail to Reject H₀	Correct Decision	Type II Error

# Why no P-values?

All rnorm(20)

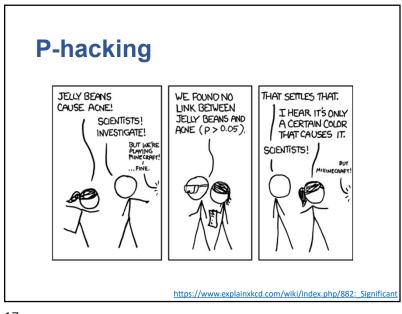


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## cf. Freedman's paradox



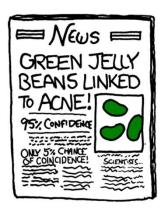
- Even if no relationships exist between variables, can look at many relationships until you get P < 0.05 (or a large statistic)</li>
- But these significant relationships are <u>not</u> real (false positive)! Just got lucky (or in actuality, unlucky)
- Known pejoratively as "P-hacking", "P-fishing", "data dredging", and more



P-hacking WE FOUND NO LINK BETWEEN PURPLE JELLY BEANS AND ACHE (P>0.05) WE FOUND NO LINK BETWEEN BROWN JELLY BEANS AND ACNE (P > 0.05). WE FOUND NO LINK BETWEEN BLUE JELLY BEANS AND ACNE (P>0.05) WE FOUND NO LINK BETWEEN TEAL JELLY BEANS AND ACNE (P > 0.05). DO AM WE FOUND NO LINK BETWEEN GREY JELLY BEANS AND ACNE (P>0.05) WE FOUND NO LINK BETWEEN TAN JELLY BEANS AND ACNE (P > 0.05). WE FOUND A LINK BETWEEN GREEN JELLY BEANS AND ACNE (P < 0.05). WE FOUND NO LINK BETWEEN MAUVE JELLY BEANS AND ACNE (P > 0.05). WE FOUND NO LINK BETWEEN CYAN JELLY BEANS AND ACNE (P>0.05), WE FOUND NO LINK GETWEEN RED JELLY BEANS AND ACHE (P > 0.05). WE FOUND NO LINK BETWEEN SALMON JELLY (P > 0.05) WE FOUND NO LINK BETWEEN LILAC JELLY BEANS AND ACNE (P>0.05), 

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# P-hacking



P-hacking: another way

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- Different subsets of a variable can count as different samples from population; same with collecting more data for a variable
- E.g., "looked at body mass of all primates, but let's now look at great apes only"
- Part of "researcher degrees of freedom" or "garden of forking paths"

"If you don't reveal some insights soon, I'm going to be forced to slice, dice, and drill!"

#### **Garden of forking paths**



- Each (subconscious) decision in data analysis represents a "fork in the road"
  - 1. Choosing among IVs and DVs
  - 2. Collect more data or exclude data
  - 3. Running different tests
  - 4. Not reporting certain tests (file-drawer effect)
  - 5. Reviewers saying you should run a test a different way or more tests
  - 6. And many more

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#### An example

False-Positive Psychology: Undisclosed Flexibility in Data Collection and Analysis Allows Presenting Anything as Significant

Joseph P. Simmons<sup>1</sup>, Leif D. Nelson<sup>2</sup>, and Uri Simonsohn<sup>1</sup>

The Wharton School, University of Pennsylvania, and <sup>2</sup>Haas School of Business, University of California, Berkeley

• "To help illustrate the problem, we conducted two experiments designed to demonstrate something false: that certain songs can change listeners' age. *Everything reported here actually happened*." (italics mine)

# Garden of forking paths On average, 5% will lead to false positives if H<sub>0</sub> is true More forks you explore, more likely to get false positives if H<sub>0</sub> is true 1. 2. 3. Decision number

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#### An example

• Are subjects younger after listening to a song?

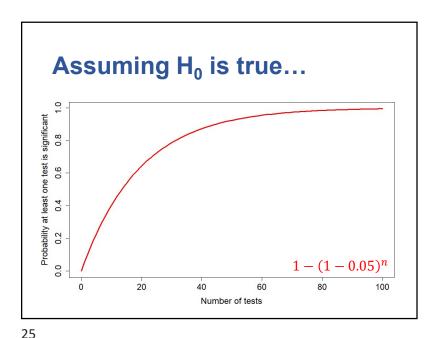




"Kalimba" by Mr. Scruff (control)

"When I'm 64" by The Beatles

- Simulated experiment, data collection, choosing different variables, collecting more data, doing different analyses, etc. (lots of forks!)
- Found subjects were 1.5 years younger after listening to "When I'm Sixty-Four" compared to the control, "Kalimba" (P = 0.04)



**Summary: exploratory** 

- Used when nothing is known about data, and there are no *a priori* hypotheses to test
- Explore what data look like and relationships between variables (i.e., fish to your heart's content! It's okay & even necessary!)
- BUT DO NOT CALCULATE P-VALUES!
- Can generate hypotheses, but emphasize they are a posteriori
- Need to be tested/confirmed with independent dataset

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#### What is confirmatory analysis?

- Testing an *a priori* hypothesis with data using confidence intervals or P-values
- Only time you should calculate P-values!
- Hypotheses can come from intuition, theory, or previous exploratory analyses
- For the third, need an *independent* dataset



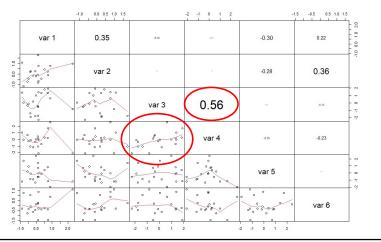
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# **Testing the hypothesis**



- Collect more data for var3 and var4
- E.g., if var3 is time spent nose-picking & var4 is age, collect data from another group of people
- Conduct a test & calculate P-value
- If P < 0.05, H<sub>0</sub> is <u>now</u> falsified (though more replication/confirmation is always good!)
- If P > 0.05, perhaps original exploratory correlation was spurious, or need more testing (e.g., if sample size or effect size too small)

#### **Our scatterplot matrix**



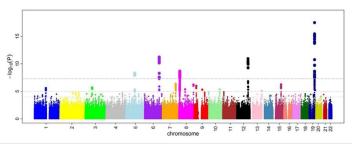
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# Separate exploratory and confirmatory!

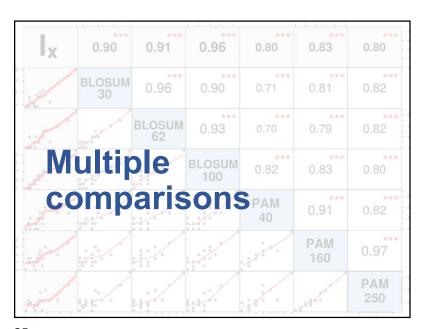
- It is <u>unethical</u> to explore data, calculate P-values, and then present the significant results as *a priori* hypothesis tests (i.e., P-hacking)
- Only get to test one hypothesis for one question for one dataset
- <u>BIG</u> reason why so many results in science are not replicable
- If you do wind up subsetting/collecting more data, doing more tests, etc., should be transparent about it

### **Multiple comparisons**

- But what if research question demands multiple tests and computed P-values?
- Common in genetics (e.g., genome-wide association studies)



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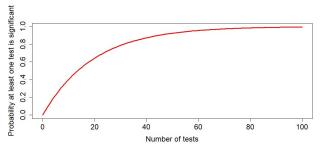




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# **Multiple comparisons**

- If H<sub>0</sub> is true, more tests means more likely to get at least one false positive
- Thus, need to correct P-values if you calculate a lot of them



#### 1. Bonferroni correction

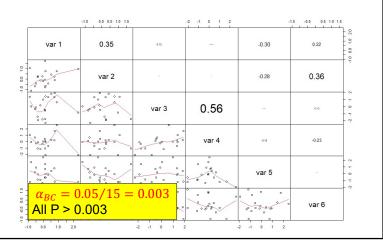
- Adjusts the <u>family-wise error rate</u> (FWER): the probability of ≥ one Type I error in your tests
- Creates a new significance level,  $\alpha_{BC} = \alpha/k$ , where  $\alpha$  is the original significance level (0.05) and k is the number of tests
- E.g., with 20 tests, the probability of at least one false positive is 0.64 at  $\alpha=0.05$
- With 20 tests and  $\alpha_{BC} = 0.05/20 = 0.0025$ , probability of at least one false positive is 0.05

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#### 1. Bonferroni: issues

- Should *k* be the # of tests you publish, the total # tests you ran, total # of tests in the journal?
- Assumes H<sub>0</sub> is true for <u>ALL</u> tests, so it is overly conservative (OK if this is your goal)
- That is, it decreases Type I error but at the expense of increasing Type II error
- Are you really that far off base that <u>NONE</u> of your H<sub>0</sub> are false in reality?!
- A better solution is the Benjamini-Hochberg procedure

#### 1. Bonferroni correction



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#### 2. Benjamini-Hochberg

 Instead of adjusting FWER, adjusts false discovery rate (FDR): proportion of false positives in set of rejected H<sub>0</sub> (i.e., P < 0.05)</li>

	Null	Alternative	
	True	True	Total
Not Called Significant	U	τ	m - R
Called Significant	V	S	R
	$m_0$	<i>m-m</i> <sub>0</sub>	m

$$FDR = \frac{V}{R}$$

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# 2. Benjamini-Hochberg

- 1. Order raw P-values in increasing order
- 2. Find test with highest rank, j, for which corresponding P-value is  $\leq (j/m) \times \delta$ , where  $\delta$  is FDR level (0.05) and m is number of tests
- 3. P-values of rank  $\leq j$  are significant

# 2. Benjamini-Hochberg

Rank (j)	P-value	(j/m)× δ	Reject H <sub>0</sub> ?
1	0.0008	0.005	1
2	0.009	0.010	1
3	0.165	0.015	0
4	0.205	0.020	0
5	0.396	0.025	0
6	0.450	0.030	0
7	0.641	0.035	0
8	0.781	0.040	0
9	0.900	0.045	0
10	0.993	0.050	0

Or just use p.adjust() function in R

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## **Comparing corrections**



- I simulated data and computed 4950 pairwise correlations and P-values (H<sub>0</sub> is false for 1225)
- Using Bonferroni, 94 (8%) were significant
- Using Benjamini-Hochberg, 1165 (95%) were significant
- So BH is **MUCH** better, but still not perfect
- Best solution is to not calculate so many P-values in the first place!

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#### My rules for hypothesis testing

- Distill research question down to as few hypotheses as possible → calculate as few P-values as possible
- Lots of thinking before you collect data and run tests (i.e., go down as few forks as possible)
- Simulate fake data to think and work through your analyses and code
- Communicate/write down your hypothesis & methods before data collection



**Prediction** What is it? What does it entail?

What is prediction?

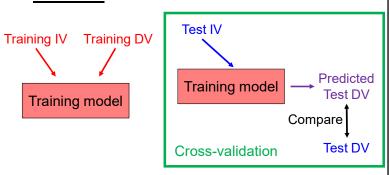
- Fit a model to your data to predict unknown DV values, given **NEW** IV values
- E.g., use lm(body.mass ~ femur.length) to predict body mass using new femoral specimens
- Thus, need to assess how your model does on a **NEW** dataset where DV and IV values are known (i.e., cross-validation)



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#### **Cross-validation**

- Training data: data used to fit model
- Test data: data used to test trained model



#### **Cross-validation**

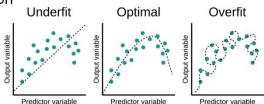
- 1. <u>Holdout method</u>: 80% data reserved for training, 20% for testing (or 75-25, 70-30, etc.)
- <u>k-fold</u>: E.g., 10-fold → use 1<sup>st</sup> 10% of data to test, other 90% to train; 2<sup>nd</sup> 10% to test, other 90% to train; repeat 10x & average model predictions

Performance metrics 1. R<sup>2</sup> btw obs. & pred. DV **Cross-validation** Root-mean-square-error (RMSE): measures difference btw Validation Training obs. & pred. DV Fold Fold 1st Performance 1 K Iterations (K-Folds) Performance a Performance 3  $=\frac{1}{5}\sum$  Performance Performance, Performance 5

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**Overfitting** 

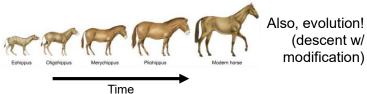
- Cross-validation is done to prevent overfitting (fitting the noise structure specific to one system instead of the signal)
- Therefore, test data (and its noise structure) must be <u>INDEPENDENT</u> from training data
- This is complicated by the presence of autocorrelation



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#### **Autocorrelation**

- How one variable is correlated with itself → correlated errors (noise)
- Specifically, how closer values are more similar
- 1. <u>Temporal autocorrelation</u>: values closer in time are more similar
  - E.g., "tomorrow is likely to be sunny like today"



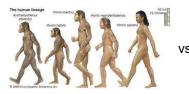
#### **Autocorrelation**

- 1. Temporal autocorrelation
- 2. <u>Spatial autocorrelation</u>: values closer in space are more similar
  - E.g., Tobler's first law of geography



**Autocorrelation** 

- 1. Temporal autocorrelation
- 2. Spatial autocorrelation
- 3. <u>Phylogenetic autocorrelation</u>: values in more closely related taxa are more similar

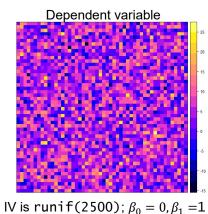


vs.

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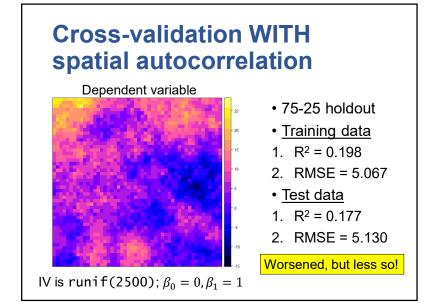
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# **Cross-validation w/ no spatial autocorrelation**



- 75-25 holdout
- Training data
- 1.  $R^2 = 0.278$
- 2. RMSE = 5.054
- Test data
- 1.  $R^2 = 0.238$
- 2. RMSE = 5.172

Both metrics worsened!



### What happened?

#### No spatial autocorrelation

#### **Spatial** autocorrelation

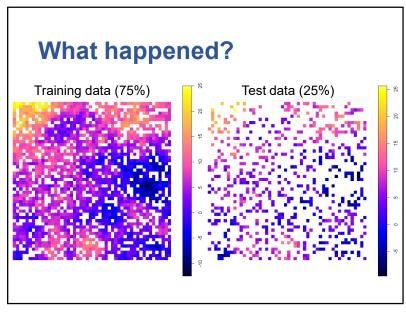
•  $R^2$ : 0.278  $\rightarrow$  0.238

• R<sup>2</sup>: 0.198 → 0.177

• RMSE: 5.054 → 5.172

• RMSE: 5.067 → 5.130

· Same spatial autocorrelation structure is present in both training and test data (not truly independent!)





# **Compare with no spatial** autocorrelation Training data (75%) Test data (25%)

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## What happened?

#### No spatial autocorrelation

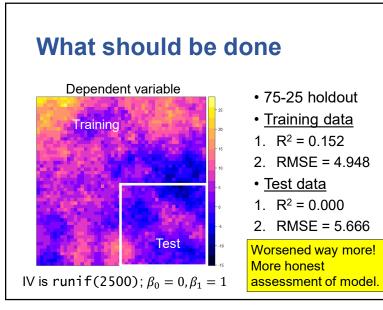
#### **Spatial** autocorrelation

•  $R^2$ : 0.278  $\rightarrow$  0.238

•  $R^2$ : 0.198  $\rightarrow$  0.177

• RMSE:  $5.054 \rightarrow 5.172$  • RMSE:  $5.067 \rightarrow 5.130$ 

- · Same spatial autocorrelation structure is present in both training and test data (not truly independent!)
- Training model is fitting some of the noise structure, which is present in test data
- Thus, overconfident in how model generalizes to new datasets (likely has diff. noise structure)



Questions?

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## **Summary**

- Where does your research fall?
- Which is best for your question?

	Exploratory	Confirmatory	Prediction
Frequentist/ Monte Carlo			
Likelihood			
Bayesian			

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#### **Summary**

- Three main modes of statistical inference:
- 1. Exploratory data analysis
  - Explore patterns and relationships in your data
  - **DO NOT** calculate P-values
- 2. Confirmatory data analysis
  - Tests a priori hypotheses with CIs & P-values
  - · Correct for multiple comparisons if necessary
- 3. Prediction
  - Using fitted model to predict DV in new dataset
  - MUST cross-validate with INDEPENDENT dataset