Week 11: Linear mixed models & autocorrelation

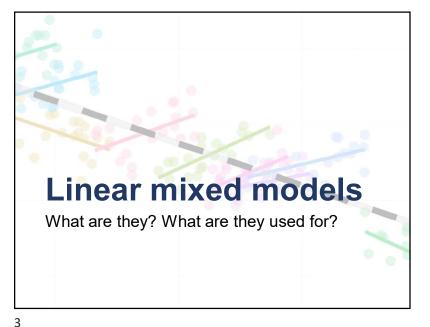
ANTH 674: Research Design & Analysis in Anthropology Professor Andrew Du

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Office Hours: Thursdays, 9:00am-12:00pm In person: GSB 312

Virtual: https://tinyurl.com/F22ANTH674

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Lecture outline

- 1. Linear mixed models
 - 1. What are they? What are they used for?
 - 2. Variance partitioning w/ crossed or nested designs
- 2. Measuring & dealing with autocorrelation
 - 1. Correlograms
 - 2. Association between two variables
 - 1. Cross-correlograms
 - 2. Generalized least squares

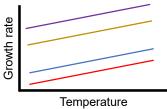
What is a linear mixed model?

- A linear model with **fixed** AND **random** factors/effects
- I've always found the distinction between the two factors confusing, so let's go through them carefully



Fixed factors

- Measured levels are the only ones of interest
- E.g., want to know how intercept of growth rate ~ temperature changes w/ different levels of nitrogen (i.e., ANCOVA)
- Thus far, we have only looked at fixed factors









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Ultimately, depends on research question!

- <u>Fixed factor</u>: estimate how intercept and/or slope changes ~ different N levels (i.e., ANCOVA)
- Random factor: estimate SD of population of intercepts and/or slopes across N levels











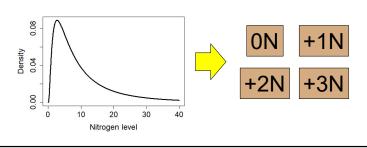






Random factors

- Measured levels are a random, representative sample of some population of levels
- E.g., want to infer something about population of intercepts (i.e., SD of intercepts across levels)



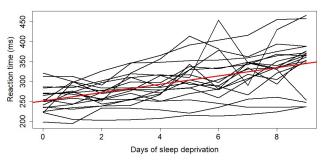
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For example...



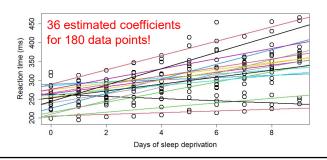
 Study measured reaction times of 18 subjects each day after full night's sleep & then 9 days of sleep deprivation (180 total observations)



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Fixed factor approach

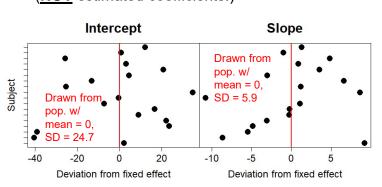
- Estimates intercept & slope of reaction ~ days for each subject (factor level)
- ANCOVA: lm(reaction ~ days * subject)



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Random factor approach

 Can get intercept & slope for each subject (NOT estimated coefficients!)



Random factor approach

 Estimates SD of intercepts & slopes across levels <u>ALONG WITH</u> intercept & slope fixed effects (via maximum likelihood)

Random effects:

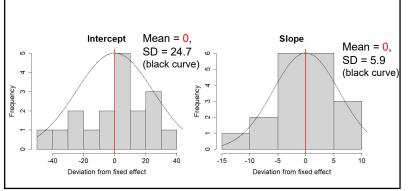
StdDev Corr (Intercept) 24.740241 (Intr) Days 5.922103 0.066 Residual 25.591843

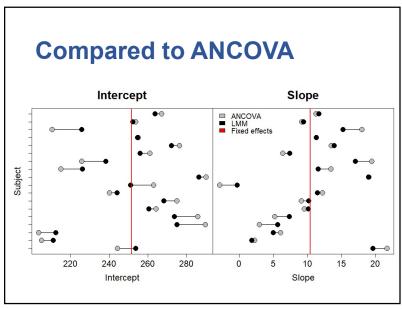
Can only calculate P-values in simple mixed models (e.g., balanced design, no crossed random effects)

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Random factor approach

 Can get intercept & slope for each subject (<u>NOT</u> estimated coefficients!)





Model Complete pooling No pooling Partial pooling

Complete pooling One intercept & slope for all data

No pooling ANCOVA w/ diff. intercepts & slopes

Partial pooling LMM shrinkage

Partial pooling LMM shrinkage

Shrinkage or regularization

 In ANCOVA, each line is fit to data for one factor level only

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- In LMM, levels are drawn from a population, so they are expected to share characteristics (w/ a distribution mean = fixed effect)
 - This is how you can predict for new factor levels w/ LMM (can't do this w/ ANCOVA)
- If a level has few observations, it borrows more information from other levels and is pulled more towards the average (fixed effect)

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Fixed vs. random factors

Fixed factors

- Interested in how intercept and slope changes <u>independently for each subject</u>
- Potentially need to estimate <u>A LOT</u> of coefficients

Random factors

- Interested in the SD of intercepts and slopes across all **possible** subjects
- Estimates fixed effects AND SDs
- Shrinks intercepts & slopes towards means

https://dynamicecology.wordpress.com/2015/11/04/is-it-a-fixed-or-random-effect/

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Questions?



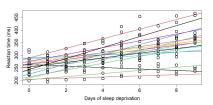
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Reasons for doing LMM

- Factor levels are random sample from larger population → interested in estimating SD of population of intercepts/slopes
- Ratio of data points to # coefficients in ANCOVA too small → overfitting (only need to estimate SDs in LMM)
- 3. Shrink intercepts and slopes towards mean
- 4. Want to account for non-independence in data using a blocking factor (very popular reason)

Reasons for doing LMM

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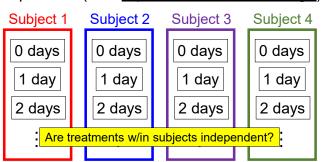
36 estimated coefficients for 180 data points!

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E.g., sleep study



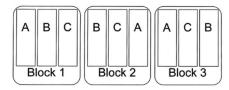
 Each subject is treated as a block, each w/ treatments of different days of sleep deprivation (AKA repeated measures design)



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Analyzing block design

- Can do ANCOVA, but problematic if lots of levels & not enough data
- Also, many times blocks are not of interest (i.e., don't care how intercept/slope change w/ block)
- Can use LMM & include block as a random factor to account for it



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Generalized linear mixed models (GLMMs)

- Mixed model w/ non-normally distributed errors (cf. generalized linear models)
- E.g., presence/absence of lions ~ wildebeest population density w/ plot as blocking factor



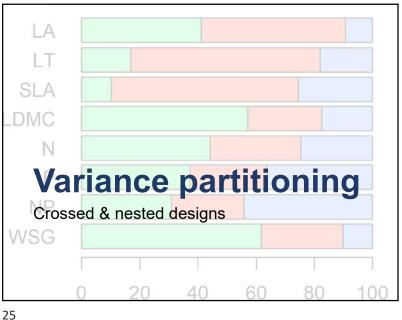
Random factor rules

- Random factor <u>MUST</u> be categorical (i.e., it must be a factor w/ levels)
 - A continuous IV can be entered into model as covariate (only one extra estimated coefficient)
- Need at least five levels (would you calculate SD of a sample w/ < 5 data points?)
 - Otherwise, just make factor a fixed effect

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Questions?





Variance partitioning

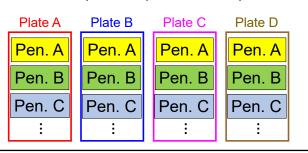
- Can partition DV variance not accounted for by fixed effects among multiple random factors
- Or, can fit an intercept-only model to partition DV variance among random factors



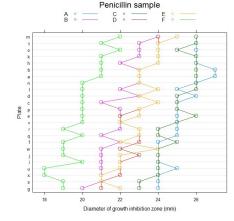
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Multiple random factors

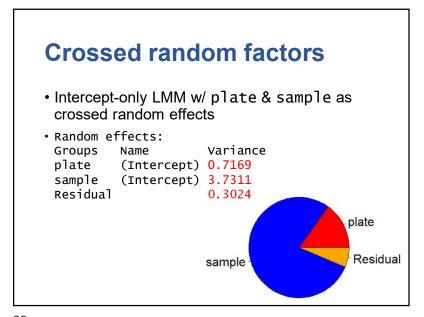
- 1. Crossed random factors: each level from a factor is w/ each level from the other
- E.g., how penicillin inhibiting growth of Bacillus varies across plates & penicillin samples



Crossed random factors

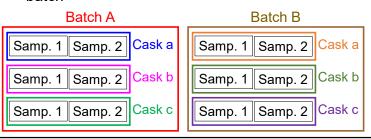


- Fully crossed! Every combination of sample and plate is represented
- Unreplicated and completely balanced (only one observation per sample/plate combo)

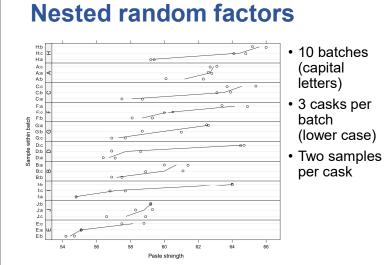


Multiple random factors

- 2. Nested random factors: factors are nested within each other
- E.g., strength of chemical paste, where two samples were taken from each cask from each batch



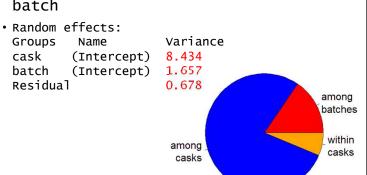
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Nested random factors

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 Intercept-only LMM w/ cask nested within batch





Measuring & dealing w/ autocorrelation

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Non-independent data

- Data across space, time, or a phylogeny will almost always be non-independent
- Data closer in space/time/relatedness will be more similar

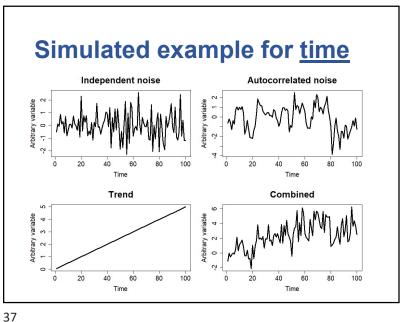


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Three components

- Patterns in space & time (& phylogeny) can be decomposed into three components
- $z(d) = \mu(d) + \eta(d) + \varepsilon$, where (d) means component is a function of distance
 - i.e., pattern = trend + autocorrelated (red) noise + independent (white) noise
 - Temporal data can also include a cyclical component too (e.g., monthly, seasonality, orbital cycles)

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Simulated example for <u>space</u>

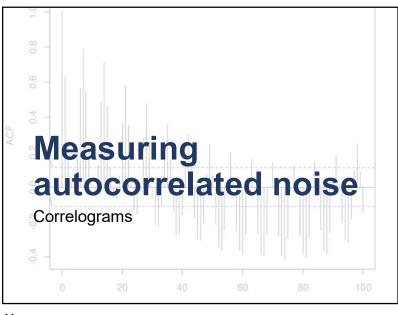
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Autocorrelated noise: nuisance or interesting?

- Nuisance: non-independence violates one of the assumptions of linear models (increases Type I error rate)
 - Must correct for this (e.g., w/ blocking)!
- Interesting: How does strength of autocorrelation vary as a function of distance in space/time/phylogeny?
 - · May tell us something about the underlying process generating autocorrelation!

Questions?

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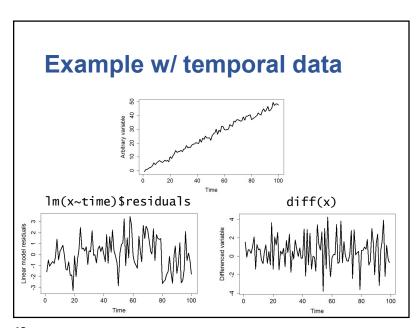


Detrending

- If temporal or spatial data are strongly trended, need to first remove trend (i.e., <u>detrending</u>) to focus on autocorrelated noise
- 1. Can fit a trend to data and take the residuals
- 2. Calculate first differences: $x'_i = x_{i+1} x_i$

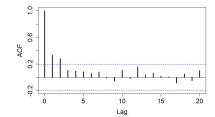
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Autocorrelation function

- Quantifies how time series is correlated with itself at different lags
- E.g., c(1, 2, 3, 4, 5)
 - $\underline{\text{time lag}} = 1$, c(1, 2, 3, 4) vs. c(2, 3, 4, 5)
 - $\underline{\text{time lag}} = 2$, c(1, 2, 3) vs. c(3, 4, 5)

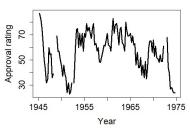


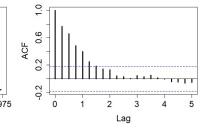
acf(lm(x~time)\$residuals)

- Dashed blue lines delineate null region (assuming white noise)
- Be careful of multiple comparisons!

A real example

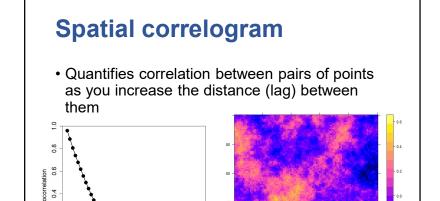
- Quarterly approval rating of US president from 1945 to 1974
- Not strongly trended, so no need to detrend
- Can begin to hypothesize what's generating AC!



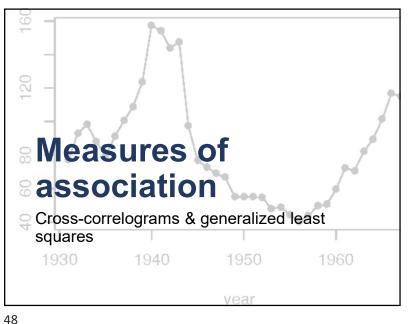


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Questions?



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Comparing two variables

- **1.** <u>Cross-correlograms</u>: looks at how two variables are correlated at different lags
 - Perhaps one variable responds to another only after a certain amount of time/distance
 - As w/ correlation, symmetry between variables
- 2. <u>Generalized least squares</u>: models a DV as a function of one or more IVs, while explicitly modeling errors as non-independent
 - Good if variables are obviously DV or IV, or if you want to do prediction (as w/ linear models)

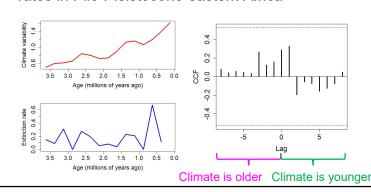
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• E.g., soil organic matter & cadmium level in floodplain of Meuse River, Netherlands • Cross-correlogram • Data binned into distance classes

X coordinates

Cross-correlation function

• E.g., climate variability vs. mammal extinction rates in Plio-Pleistocene eastern Africa



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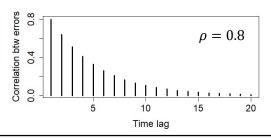
Generalized least squares

- Relaxes GLM assumption of independent errors
- GLS estimates extra parameters to model nonindependent errors
- Parameters estimated using maximum likelihood

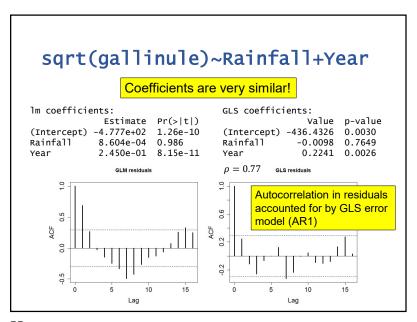
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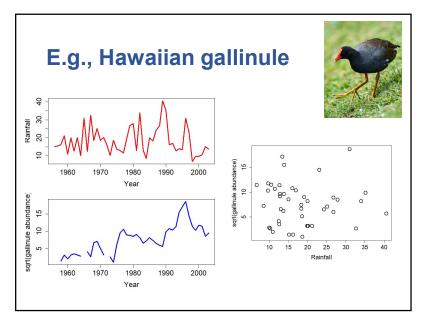
Temporal data

- AR1 autocorrelation error structure is popular
- Correlation between errors one time step apart estimated as ρ (usually positive), two steps apart is ρ^2 , three steps is ρ^3 , etc.



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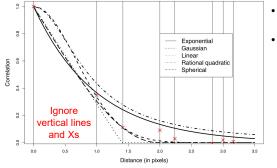




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Spatial data

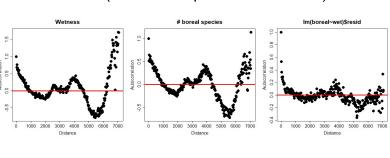
 Non-independence between errors modeled as a function of distance between them



- Five common models
- Different parameterizations will slightly change shape of each model

One last note

 If an IV captures autocorrelation in DV, then there will be no autocorrelation remaining in residuals (GLM assumptions not violated!)



Questions?

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Summary

- Use LMMs (random effects) if:
 - Factor levels are random, representative samples from some larger population and are interested in estimating SD of population of intercepts/slopes
 - 2. Have too few data (prevent overfitting w/ ANCOVA)
 - 3. Want to account for non-independence w/ blocking (and have too few data)
 - 4. Interested in shrinkage of estimates
 - 5. You want to partition variance in DV
- Correlograms quantify autocorrelation structure, which is interesting in itself!
- Cross-correlograms & GLS quantify association btw variables in time/space/phylogeny (but remember, OLS estimates are unbiased!)

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Statistics vignette

Let's play a game...

Rules

- 1. Pick an outcome of three coin flips, e.g., HHH
- 2. I pick my own outcome
- 3. If your outcome appears first in *n* flips, you win

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Why does it work? (an example)

You: HHH

Me: THH

You win only if HHH comes up in first three flips: HHH...

Otherwise, T *must* precede any HHH, and I win:THHH...

https://www.youtube.com/watch?v=Sa9jLWKrX0c

