Introduction to Within-Person Analysis and RM ANOVA

- Today's Class:
 - > From between-person to within-person
 - > ANOVAs for longitudinal data
 - \triangleright Variance model comparisons using $-2\Delta LL$

The Two Sides of a (BP) Model

$$y_i = \beta_0 + \beta_1 X_i + \beta_2 Z_i + \beta_3 X_i Z_i + e_i$$

• Model for the Means (Predicted Values):

Our focus today

- Each person's expected (predicted) outcome is a weighted linear function of his/her values on X and Z (and here, their interaction), each measured once per person (i.e., this is a between-person model)
- Estimated parameters are called fixed effects (here, β_0 , β_1 , β_2 , and β_3)
- The number of fixed effects will show up in formulas as k (so k = 4 here)

Model for the Variance ("Piles" of Variance):

- $e_i \sim N(0, \sigma_e^2) \rightarrow$ **ONE** source of residual (unexplained) deviation
- e_i has a mean of 0 with some estimated constant residual variance σ_e^2 , is normally distributed, is unrelated to X and Z, and is unrelated across people (across all observations, just people here)
- Contains residual variance only in above BP model

Review: Variances and Covariances

Variance:

Dispersion of y

Variance
$$(y_t) = \frac{\sum_{i=1}^{N} (y_{ti} - \hat{y}_{ti})^2}{N - k}$$

Covariance:

How y's go together, unstandardized

Covariance
$$(y_1, y_2) = \frac{\sum_{i=1}^{N} (y_{1i} - \hat{y}_{1i})(y_{2i} - \hat{y}_{2i})}{N - k}$$

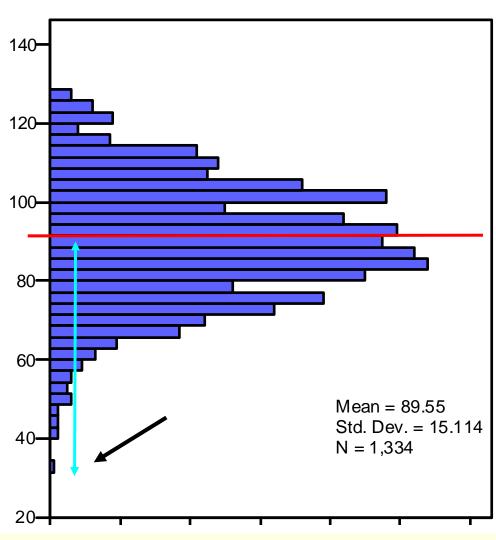
Correlation:

How y's go together, standardized (-1 to 1)

Correlation
$$(y_1, y_2) = \frac{\text{Covariance}(y_1, y_2)}{\sqrt{\text{Variance}(y_1)} * \sqrt{\text{Variance}(y_2)}}$$

N = # people, t = time, i = personk = # fixed effects, $\hat{y}_{ti} = y$ predicted from fixed effects

An Empty Between-Person Model (i.e., Single-Level)



$$y_i = \beta_0 + e_i$$

Filling in values:

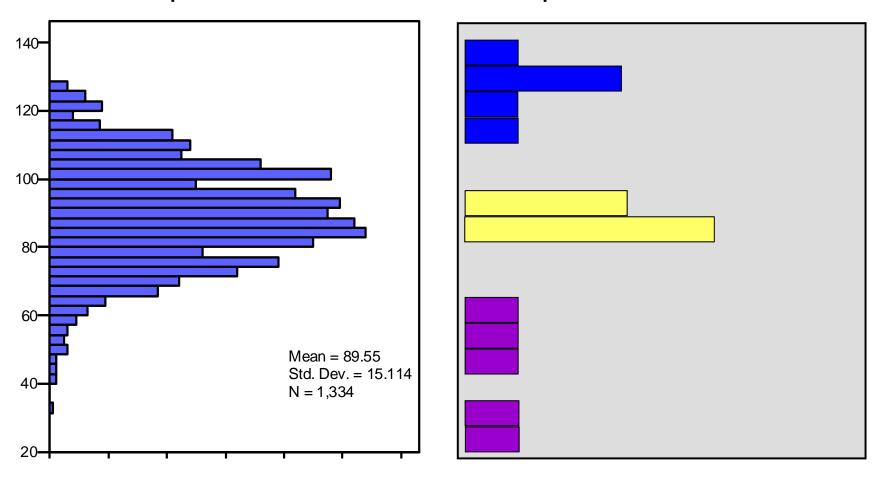
Y Error

Variance:

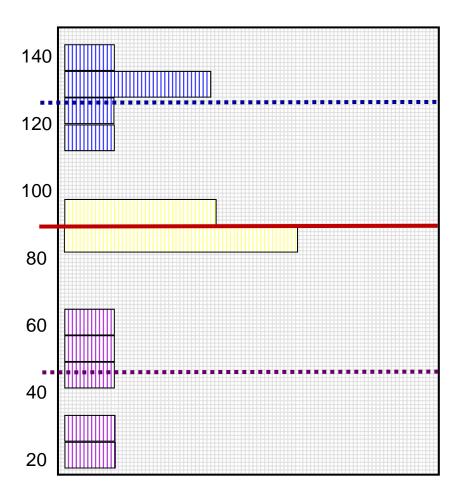
$$\frac{\Sigma (y - y_{\text{pred}})^2}{N - 1}$$

Adding Within-Person Information... (i.e., to become a Multilevel Model)

Full Sample Distribution 3 People, 5 Occasions each



Empty +Within-Person Model



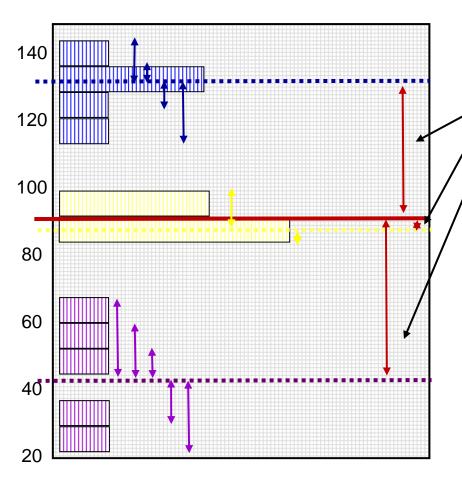
Start off with Mean of Y as "best guess" for any value:

- = Grand Mean
- = Fixed Intercept

Can make better guess by taking advantage of repeated observations:

- = Person Mean
- → Random Intercept

Empty +Within-Person Model



Variance of Y \rightarrow 2 sources:

Between-Person (BP) Variance:

Differences from **GRAND** mean

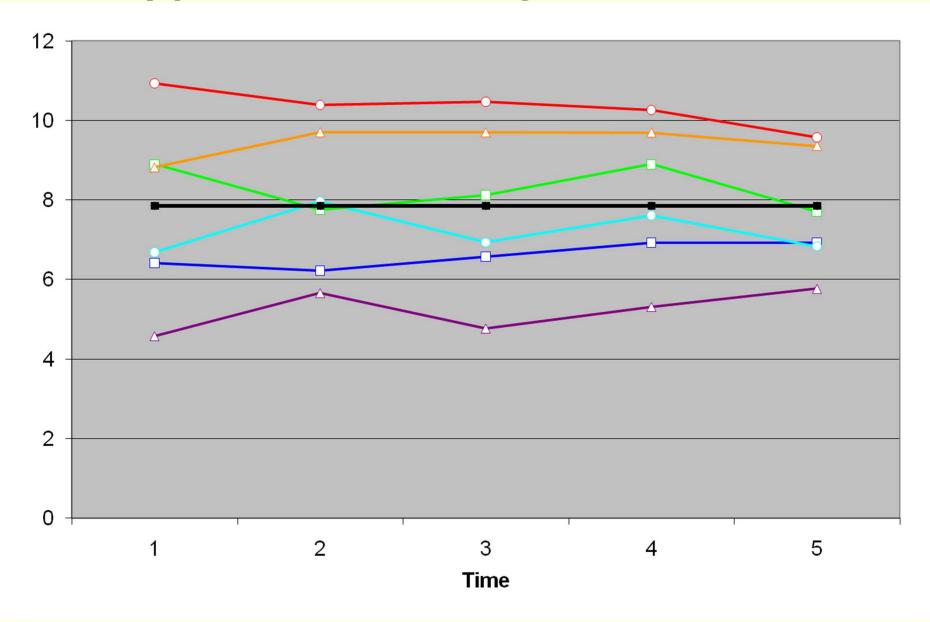
INTER-Individual Differences

Within-Person (WP) Variance:

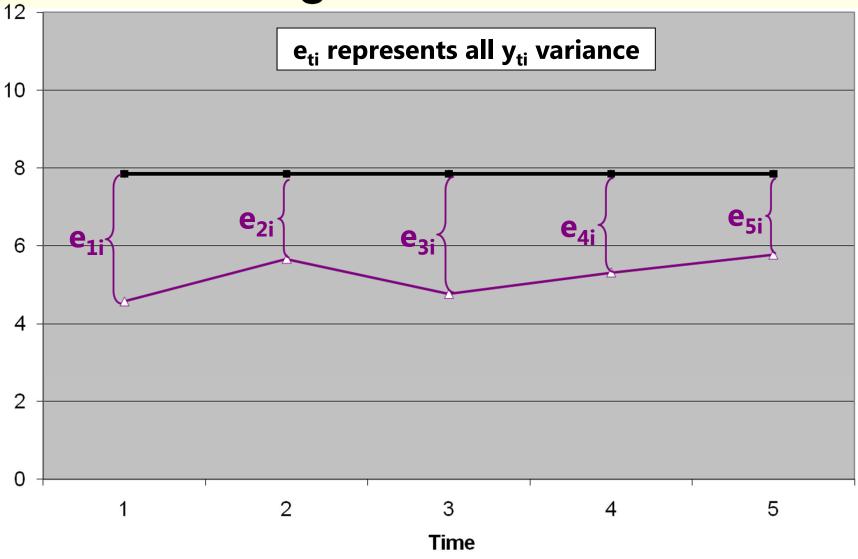
- → Differences from **OWN** mean
- → **INTRA**-Individual Differences
- → This part is only observable through longitudinal data.

Now we have 2 piles of variance in Y to predict.

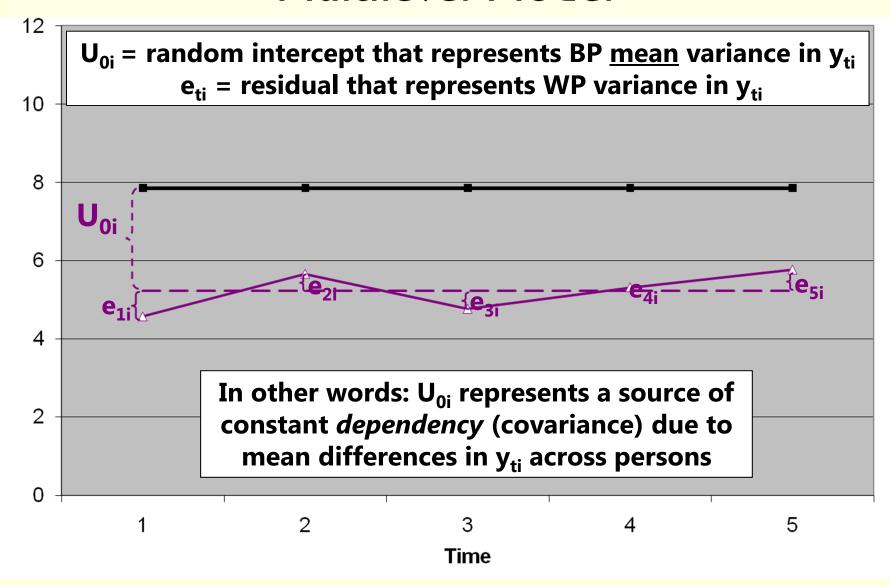
Hypothetical Longitudinal Data



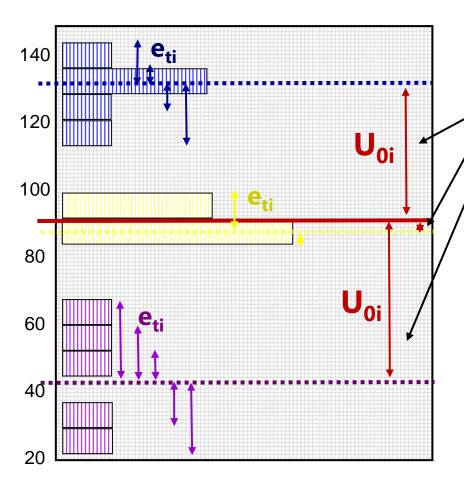
"Error" in a BP Model for the Variance: Single-Level Model



"Error" in a +WP Model for the Variance: Multilevel Model



Empty +Within-Person Model



 y_{ti} variance \rightarrow 2 sources:

Level 2 Random Intercept

<u>Variance</u> (of U_{0i} , as $\tau_{U_0}^2$):

Between-Person Variance

Differences from **GRAND** mean

→ **INTER**-Individual Differences

Level 1 Residual Variance (of e_{ti} , as σ_e^2):

- → Within-Person Variance
- → Differences from **OWN** mean
- → **INTRA**-Individual Differences

BP vs. +WP Empty Models

• Empty Between-Person Model (used for 1 occasion):

$$y_i = \beta_0 + e_i$$

- $> \beta_0$ = fixed intercept = grand mean
- e_i = residual deviation from GRAND mean
- Empty +Within-Person Model (for >1 occasions):

$$y_{ti} = \beta_0 + U_{0i} + e_{ti}$$

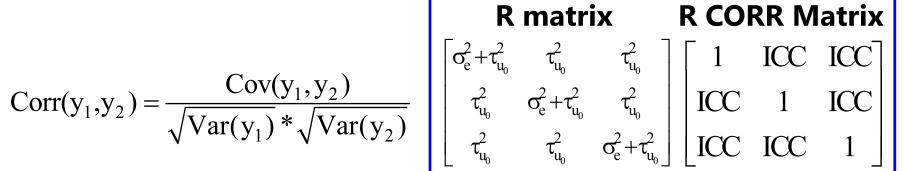
- β_0 = fixed intercept = grand mean
- U_{0i} = random intercept = individual deviation from GRAND mean
- e_{ti} = time-specific residual deviation from OWN mean

Intraclass Correlation (ICC)

Intraclass Correlation (ICC):

$$ICC = \frac{BP}{BP + WP} = \frac{Intercept \, Var.}{Intercept \, Var. + Residual \, Var.} = \frac{\tau_{U_0}^2}{\tau_{U_0}^2 + \sigma_e^2}$$

Corr
$$(y_1, y_2) = \frac{\text{Cov}(y_1, y_2)}{\sqrt{\text{Var}(y_1)} * \sqrt{\text{Var}(y_2)}}$$



- ICC = Proportion of total variance that is between persons
- ICC = Correlation of occasions from same person (in RCORR)
- ICC is a standardized way of expressing how much we need to worry about dependency due to person mean differences (i.e., ICC is an effect size for constant person dependency)

BP and +WP Conditional Models

Multiple Regression, Between-Person ANOVA: 1 PILE

$$y_i = (\beta_0 + \beta_1 X_i + \beta_2 Z_i...) + e_i$$

- e_i → ONE residual, assumed uncorrelated with equal variance across observations (here, just persons) → "BP (all) variation"
- Repeated Measures, Within-Person ANOVA: 2 PILES
 - $y_{ti} = (\beta_0 + \beta_1 X_i + \beta_2 Z_i...) + U_{0i} + e_{ti}$
 - → U_{0i} → A random intercept for differences in person means, assumed uncorrelated with equal variance across persons → "BP (mean) variation" = $\tau_{U_0}^2$ is now "leftover" after predictors
 - $ightharpoonup \mathbf{e_{ti}}
 ightharpoonup A$ residual that represents remaining time-to-time variation, usually assumed uncorrelated with equal variance across observations (now, persons and time) ightharpoonup "**WP variation**" = σ_e^2 is also now "leftover" after predictors

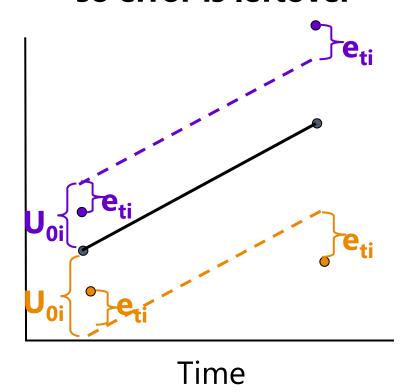
Example Data for BP and WP Models

- 50 kids in a control or treatment group each measured twice
- Hypothesis: Learning outcome should be higher at post-test than pre-test, with a greater difference in the treatment group

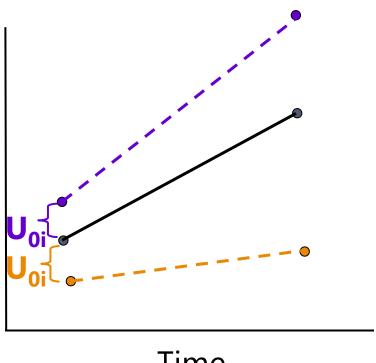
| Means (SE) | Pre-Test | Post-Test | Marginal |
|------------|--------------------------------|---------------------|---------------------|
| Control | 49.08 (1.14) 1.68 2.0 | 54.90 (1.13) | 51.99 <i>(0.89)</i> |
| Treatment | 50.76 (0.91) | | 54.70 (0.87) |
| Marginal | 49.92 <i>(0.73)</i> 6.8 | 56.76 <i>(0.79)</i> | 53.34 (0.64) |

Why error and person*time are the same thing in two-occasion data

Same age slope, so error is leftover



Different age slopes, so no error is leftover



Time

ANOVA for longitudinal data?

- There are 3 possible "kinds" of ANOVAs we could use:
 - Between-Persons/Groups, Univariate RM, and Multivariate RM

NONE OF THEM ALLOW:

- > Missing occasions (do listwise deletion when using least squares)
- > **Time-varying predictors** (covariates are BP predictors only)
- Each includes the same model for the means for time: all possible mean differences (so 4 parameters to get to 4 means)
 - > "Saturated means model": $\beta_0 + \beta_1(T_1) + \beta_2(T_2) + \beta_3(T_3)$
 - > The *Time* variable must be balanced and discrete in ANOVA!
- These ANOVAs differ by what they predict for the correlation across outcomes from the same person in the model for the variance...
 - \rightarrow i.e., **how they "handle dependency"** due to persons, or what they says the variance and covariance of the y_{ti} residuals should look like...

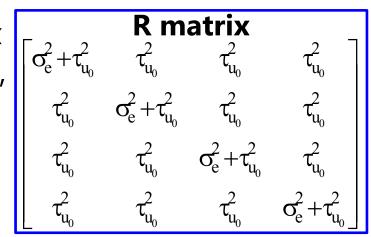
1. Between-Groups ANOVA

- Uses e_{ti} only (total variance = a single variance term of σ_e^2)
- **Assumes no covariance** at all among observations from the same person: *Dependency? What dependency?*
- Will usually be very, very wrong for longitudinal data
 - WP effects tested against wrong residual variance (significance tests will often be way too conservative)
 - Will also tend to be wrong for clustered data, but less so (because the correlation among persons from the same group is not as strong as the correlation among occasions from the same person)
- Predicts a variance-covariance matrix over time (here, 4 occasions) like this, called "Variance Components" (R matrix is TYPE=VC on REPEATED):

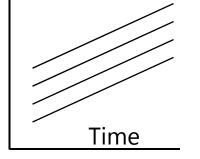
| R matrix | | | | |
|----------|--------------|--------------|--------------|--------------|
| | σ_e^2 | 0 | 0 | 0 |
| | 0 | σ_e^2 | 0 | 0 |
| | 0 | 0 | σ_e^2 | 0 |
| | 0 | 0 | 0 | σ_e^2 |

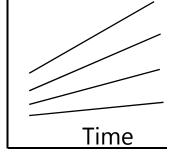
2a. Univariate Repeated Measures

- Separates total variance into two sources:
 - > **Between-Person** (mean differences due to U_{0i} , or $\tau_{U_0}^2$ across persons)
 - ightharpoonup Within-Person (remaining variance due to e_{ti} , or σ_e^2 across time, person)
- Predicts a variance-covariance matrix over time (here, 4 occasions) like this, called "Compound Symmetry" (R matrix is TYPE=CS on REPEATED):
 - Mean differences from U_{0i} are the <u>only</u> reason why occasions are correlated



- Will usually be at least somewhat wrong for longitudinal data
 - If people change at different rates, the variances and covariances over time have to change, too





The Problem with Univariate RM ANOVA

- Univ. RM ANOVA $(\tau_{U_0}^2 + \sigma_e^2)$ predicts **compound symmetry:**
 - > All variances and all covariances are equal across occasions
 - > In other words, the amount of error observed should be the same at any occasion, so a single, pooled residual variance term makes sense
 - > If not, tests of fixed effects may be biased (i.e., sometimes tested against too much or too little error, if error is not really constant over time)
 - > COMPOUND SYMMETRY RARELY FITS FOR LONGITUDINAL DATA
- But to get the correct tests of the fixed effects, the data must only meet a less restrictive assumption of sphericity:
 - ➤ In English → pairwise differences between adjacent occasions have equal variance and covariance (satisfied by default with only 2 occasions)
 - If compound symmetry is satisfied, so is sphericity (but see above)
 - > Significance test provided in ANOVA for where data meet sphericity assumption
 - > Other RM ANOVA approaches are used when sphericity fails...

The Other Repeated Measures ANOVAs...

2b. Univariate RM ANOVA with sphericity corrections

- \triangleright Based on ε \rightarrow how far off sphericity (from 0-1, 1=spherical)
- > Applies an overall correction for model df based on estimated ε, but it doesn't really address the problem that data ≠ model

• 3. Multivariate Repeated Measures ANOVA

All variances and covariances are estimated separately over time (here, n = 4 occasions), called "Unstructured" (R matrix is TYPE=UN on REPEATED)—it's not a model, it IS the data:

| _ R matrix _ | | | |
|-----------------|-----------------|-----------------|-----------------|
| σ_{11}^2 | σ_{12} | σ_{13} | σ_{14} |
| σ_{21} | σ_{22}^2 | σ_{23} | σ_{24} |
| σ_{31} | σ_{32} | σ_{33}^2 | σ_{43} |
| σ_{41} | σ_{42} | σ_{43} | σ_{44}^2 |

- Because it can never be wrong, UN can be useful for complete and balanced longitudinal data with few (e.g., 2-4) occasions (n)
- > Parameters = $\frac{n*(n+1)}{2}$ so it can be hard to estimate with many occasions
- > Unstructured can also be specified to include random intercept variance $\tau_{U_0}^2$
- All other models for the variance are nested under Unstructured, so we can do LRT model comparisons to see if any other model is NOT WORSE

Summary: ANOVA approaches for longitudinal data are "one size fits most"

- Saturated Model for the Means (balanced time required)
 - > All possible mean differences
 - Unparsimonious, but best-fitting (is a description, not a model)
- 3 kinds of Models for the Variance (need complete data in least squares)
 - \rightarrow BP ANOVA (σ_e^2 only) \rightarrow assumes independence and constant variance over time
 - > Univ. RM ANOVA $\left(\tau_{U_0}^2 + \sigma_e^2\right)$ \rightarrow assumes constant variance and covariance
 - ➤ Multiv. RM ANOVA (whatever) → no assumptions; is a description, not a model

there is no structure that shows up in a scalar equation (i.e., the way $U_{0i} + e_{ti}$ does)

MLM will give us more flexibility in both parts of the model:

- > Fixed effects that *predict* the pattern of means (polynomials, pieces)
- Random intercepts and slopes and/or alternative covariance structures that predict intermediate patterns of variance and covariance over time

Comparing Models for the Variance

- Choosing a model for the variance requires assessment of **relative model fit**: how well does the model fit relative to other possible models?
- Relative fit is indexed by overall model log-likelihood (LL):
 - > Log of likelihood for each person's outcomes given model parameters
 - > Sum log-likelihoods across all independent persons = **model LL**
 - Two flavors: Maximum Likelihood (ML) or Restricted ML (REML)
- What you get for this on your output varies by software...
- Given as -2*log likelihood (-2LL) in SAS or SPSS MIXED:
 -2LL gives BADNESS of fit, so smaller value = better model
- Given as just log-likelihood (LL) in STATA MIXED and Mplus:
 LL gives GOODNESS of fit, so bigger value = better model

Comparing Models for the Variance

- Two main questions in choosing a model for the variance:
 - > How does the residual variance differ across occasions?
 - > How are the residuals from the same unit correlated?
- Nested models are compared using a "likelihood ratio test":
 - **-2\DeltaLL test** (aka, " χ^2 test" in SEM; "deviance difference test" in MLM)

```
"fewer" = from model with fewer parameters
"more" = from model with more parameters
```

Results of 1. & 2. must be positive values!

- 1. Calculate **-2\DeltaLL**: if given -2LL, do -2 Δ LL = (-2LL_{fewer}) (-2LL_{more}) if given LL, do -2 Δ LL = -2 *(LL_{fewer} LL_{more})
- 2. Calculate $\Delta df = (\# Parms_{more}) (\# Parms_{fewer})$
- 3. Compare $-2\Delta LL$ to χ^2 distribution with df = Δdf
- 4. Get p-value from CHIDIST in excel or LRTEST option in STATA

Comparing Models for the Variance

- What your p-value for the $-2\Delta LL$ test means:
 - > If you **ADD** parameters, then your model can get **better** (if $-2\Delta LL$ test is significant) or **not better** (not significant)
 - > If you **REMOVE** parameters, then your model can get **worse** (if $-2\Delta LL$ test is significant) or **not worse** (not significant)
- Nested or non-nested models can also be compared by Information Criteria that also reflect model parsimony
 - No significance tests or critical values, just "smaller is better"
 - \rightarrow **AIC** = Akaike IC = -2LL + 2 *(#parameters)
 - > **BIC** = Bayesian IC = -2LL + log(N)*(#parameters)
 - > What "parameters" means depends on flavor (except in stata):
 - ML = ALL parameters; REML = variance model parameters only

Flavors of Maximum Likelihood

Remember that Maximum likelihood comes in 2 flavors:

"Restricted (or residual) maximum likelihood"

- > Only available for general linear models or general linear mixed models (that assume normally distributed residuals)
- > Is same as LS given complete outcomes, but it doesn't require them
- Estimates variances the same way as in LS (accurate) $\rightarrow \frac{\sum (y_i y_{pred})^2}{N k}$

"Maximum likelihood" (ML; also called FIML*)

- Is more general, is available for the above plus for non-normal outcomes and latent variable models (CFA/SEM/IRT)
- > Is NOT the same as LS: it under-estimates variances by $\frac{\sum (y_i y_{pred})^2}{N}$ not accounting for the # of estimated fixed effects \rightarrow
- *FI = Full information \rightarrow it uses all original data (they both do)

Flavors of Full-Information Maximum Likelihood

- Restricted maximum likelihood (REML; used in MIXED)
 - Provides unbiased variances

$$\frac{\sum (y_i - y_{pred})^2}{N - k}$$

- Especially important for small N (< 100 units)</p>
- > -2ΔLL test cannot be used to compare models differing in fixed effects (no biggee; we can do this using univariate or multivariate Wald tests)
- > -2ΔLL test MUST be used to compare different models for the variance
- Maximum likelihood (ML; also used in MIXED)

$$\frac{\sum (y_i - y_{pred})^2}{N}$$

- Variances (and SEs) are too small in small samples
- > Is only option in most software for path models and SEM
- > -2ΔLL test can be used to compare any nested model; must be used to compare different models for the variance

ML vs. REML in a nutshell

Remember "population" vs. "sample" formulas for calculating variance?

"Population"

$$\frac{\sum (y_i - y_{pred})^2}{N}$$

"Sample"

$$\frac{\sum (y_i - y_{pred})^2}{N - k}$$

| All comparisons must have same N!!! | ML | REML |
|---|--|---|
| To select, type | METHOD=ML (-2 log likelihood) | METHOD=REML default (-2 res log likelihood) |
| In estimating variances, it treats fixed effects as | Known (df for having to also estimate fixed effects is not factored in) | Unknown (df for having to estimate fixed effects is factored in) |
| So, in small samples, L2 variances will be | Too small (less difference after N=30-50 or so) | Unbiased (correct) |
| But because it indexes the fit of the | Entire model (means + variances) | Variances model only |
| You can compare models differing in | Fixed and/or random effects (either/both) | Random effects only (same fixed effects) |

Rules for Comparing Models

All observations must be the same across models!

Compare Models Differing In:

| Type of Comparison: | Means Model | Variance Model | Both Means and |
|--|---|---|----------------------------------|
| | (Fixed) | (Random) | Variances Model |
| | Only | Only | (Fixed and Random) |
| Nested? YES, can do significance tests via | Fixed effect p-values from ML or REML OR ML –2ΔLL only (NO REML –2ΔLL) | NO <i>p</i> -values REML –2ΔLL (ML –2ΔLL is ok if big N) | ML –2ΔLL only (NO REML –2ΔLL) |
| Non-Nested? NO signif. tests, instead see | ML AIC, BIC | REML AIC, BIC | ML AIC, BIC only |
| | (NO REML AIC, BIC) | (ML ok if big N) | (NO REML AIC, BIC) |

<u>Nested</u> = one model is a <u>direct subset</u> of the other

Non-Nested = one model is not a direct subset of the other

3 Decision Points for Model Comparisons

1. Are the models **nested** or **non-nested**?

- > Nested: have to add OR subtract effects to go from one to other
 - Can conduct significance tests for improvement in fit
- Non-nested: have to add AND subtract effects
 - No significance tests available for these comparisons

2. Differ in model for the **means**, **variances**, or **both**?

- \rightarrow Means? Can only use $-2\Delta LL$ tests if ML (or p-value of each fixed effect)
- \rightarrow Variances? Can use ML (or preferably REML) $-2\Delta LL$ tests, no p-values
- \triangleright Both sides? Can only use $-2\Delta LL$ tests if ML

3. Models estimated using **ML** or **REML**?

- > ML: All model comparisons are ok
- > REML: Model comparisons are ok for the variance parameters only