# Using a Parametric Boostrap Approach for Nested Model Comparisons in Structural Equation Modeling

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#### **Outline**

- Introduction
- Trivial Misspecification
- Research Questions
- Parametric Bootstrap Approach
- Simulation
- Result and Discussion



#### Introduction

- Model evaluation
- Chi-square
- Practical fit Indices
  - Can a single cutoff be applied to any models with any sample sizes and with any types of data?



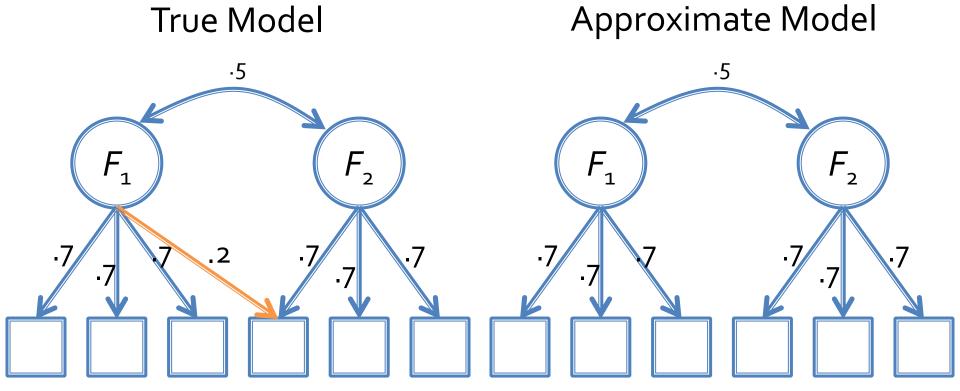
#### Introduction

- Nested Model Comparison
- Chi-square difference test
- Change in fit indices (e.g.,  $\Delta$ CFI)
  - Results of simulation study → Golden rules
  - Creative applications to nongeneralizable situations



# **Trivial Misspecification**

 Hypothesized model approximates the underlying mechanism.

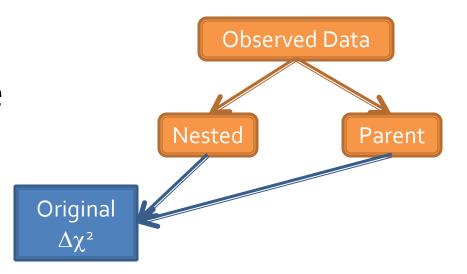


#### Research Questions

- How can the cutoff be tailored for each hypothesized model?
- How can the golden rule be avoided?
- How can the cutoff be accounted for trivial misspecification? → Test of approximate fit

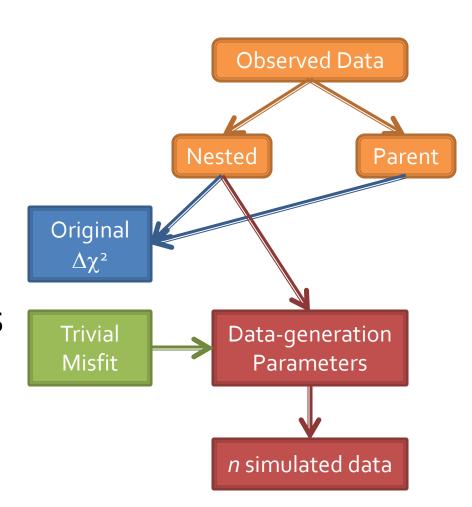


- Fit the nested and parent models to the observed data
- Save the difference in a fit index

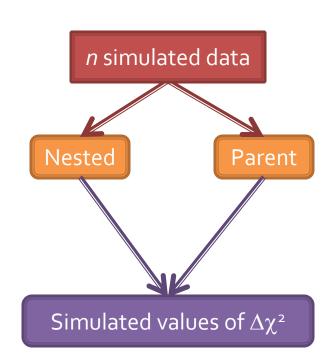




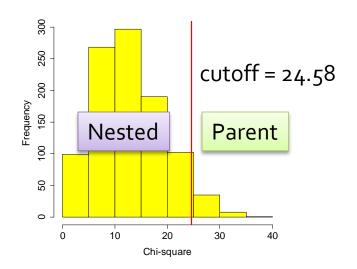
- Use the parameter estimates from the nested model
- Add trivial misspecification
- Generate n datasets (e.g., 1,000)

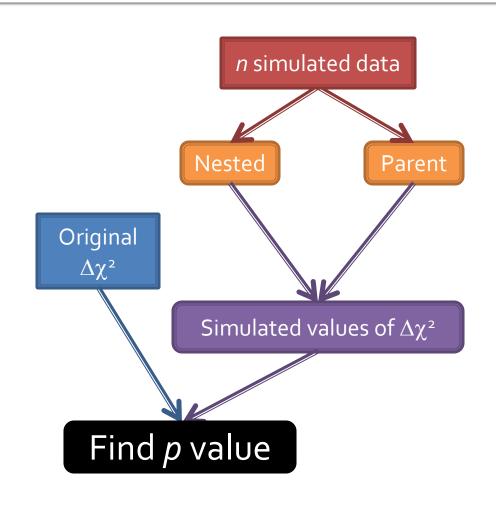


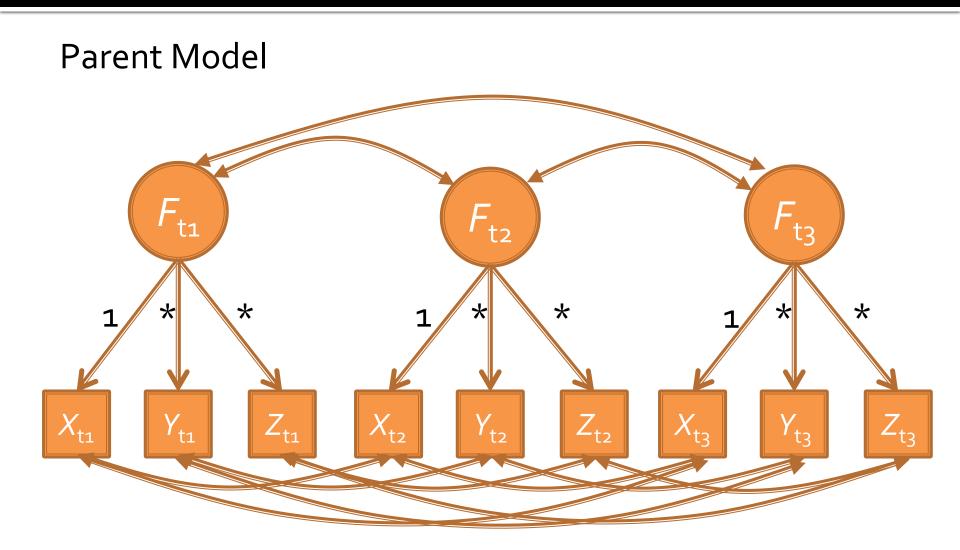
- Fit the nested and parent models to all simulated data
- Save the difference in a fit index for each simulated data
- Plot the distribution of the difference

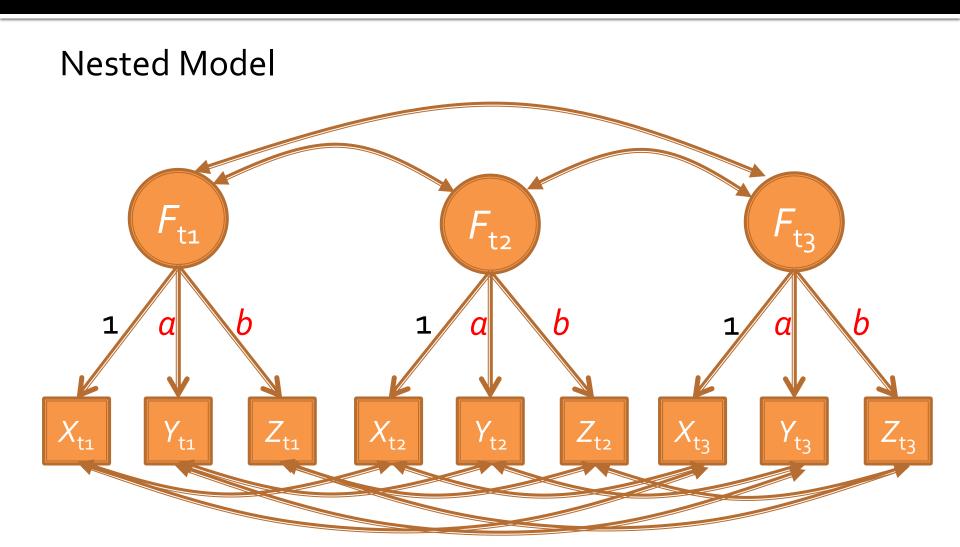


- Find p value
  - $p \le \alpha$  → select the parent model
  - $p > \alpha \rightarrow$  select the nested model





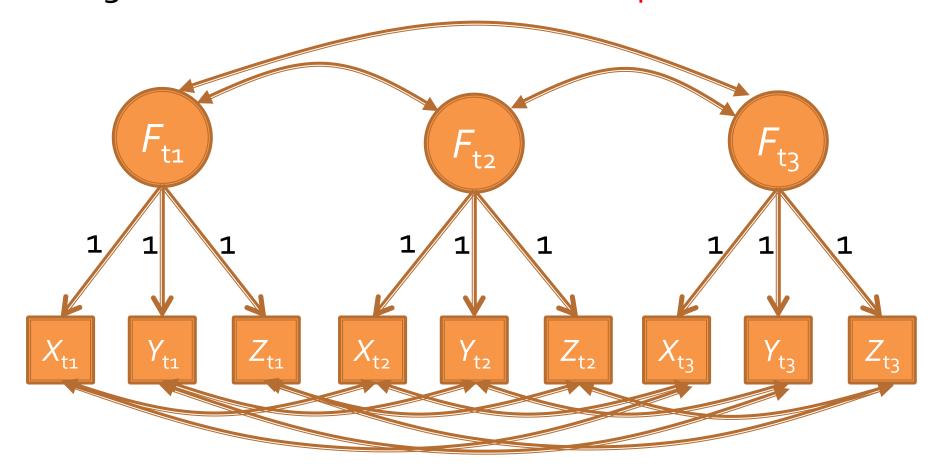




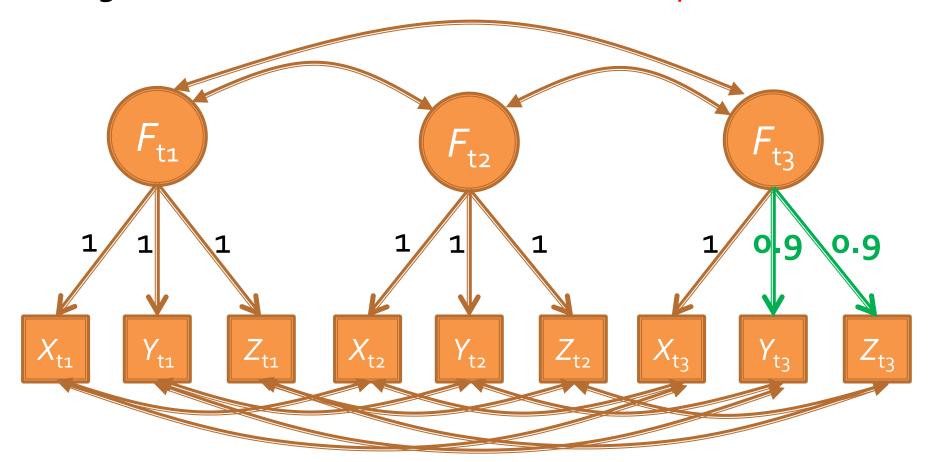
- Sample size: 125, 250, 500, 1000
- Severity of misspecification: None, Trivial,
  Severe



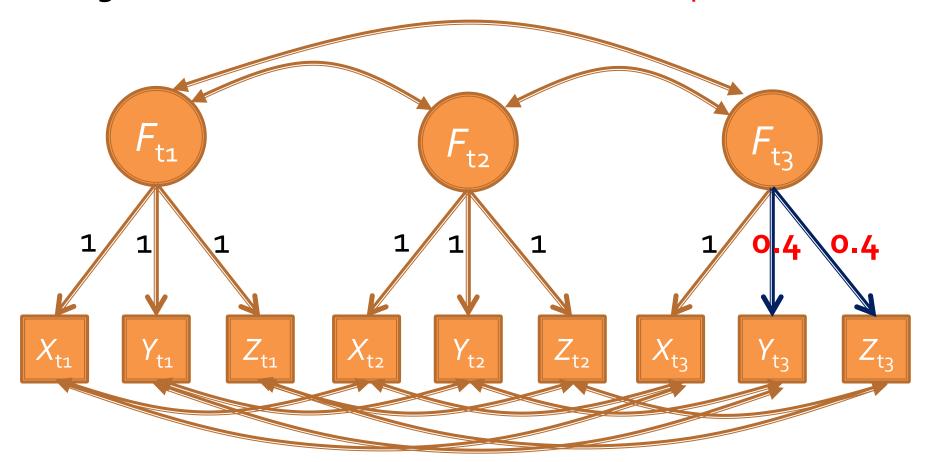
Longitudinal Weak Invariance: No Misspecification



Longitudinal Weak Invariance: Trivial Misspecification



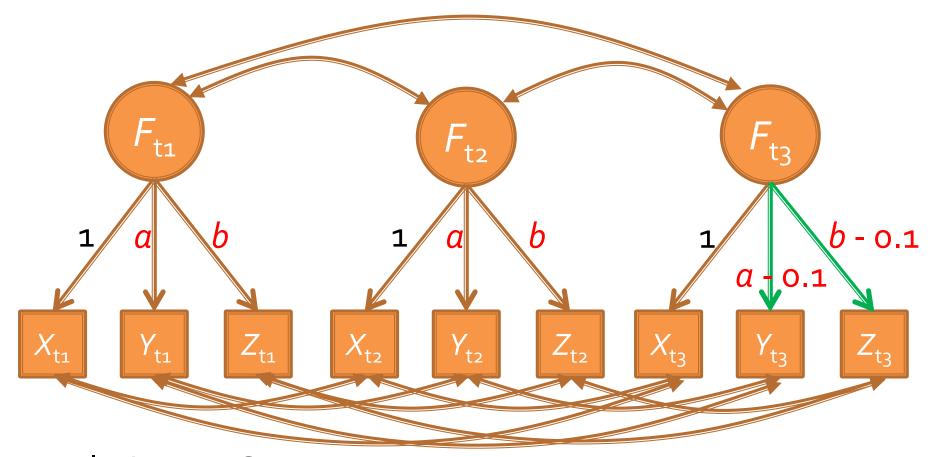
Longitudinal Weak Invariance: Severe Misspecification



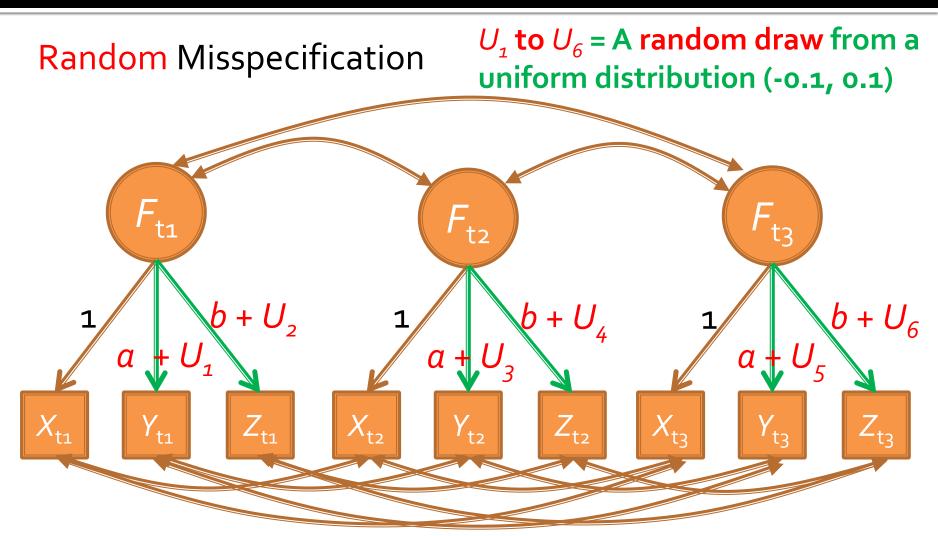
- Sample size: 125, 250, 500, 1000
- Severity of misspecification: None, Trivial,
  Severe
- Three selection methods:
  - Chi-square difference test
  - Change in CFI < .002 (Meade et al., 2008)</li>
  - Parametric Bootstrap
    - No misfit / Fixed / Random / Maximal

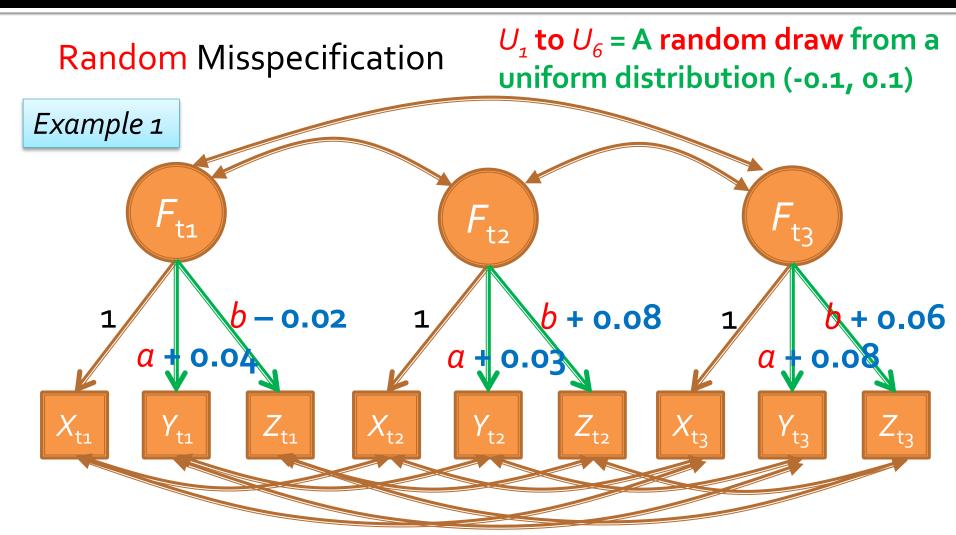


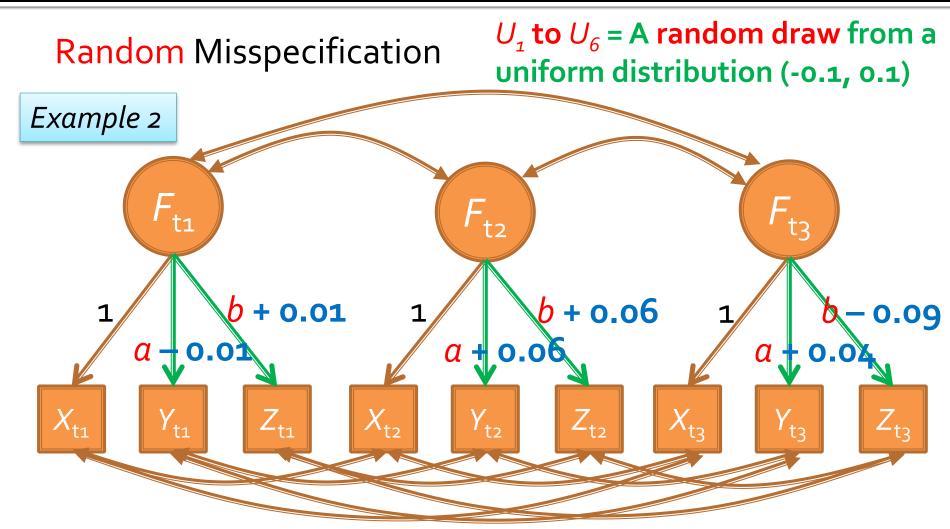
#### **Fixed** Misspecification

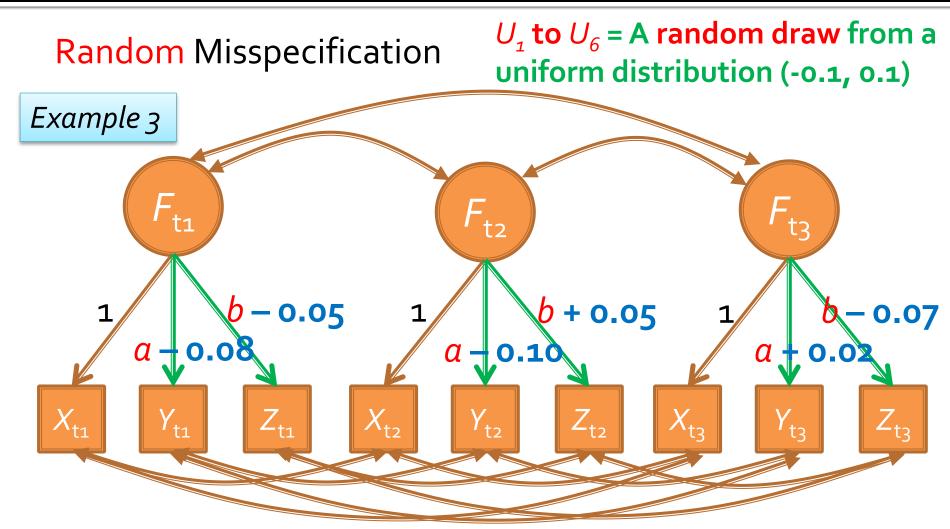


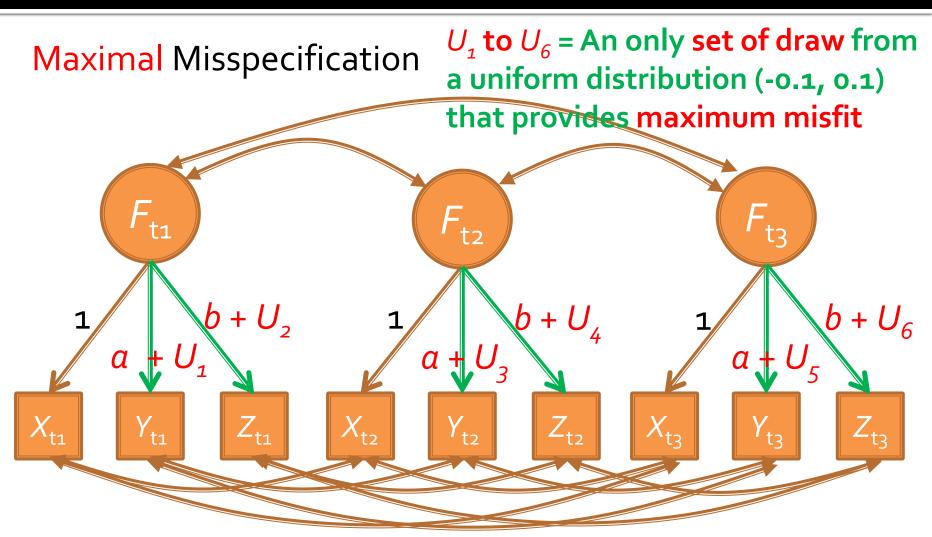
Population RMSEA ≈ .045



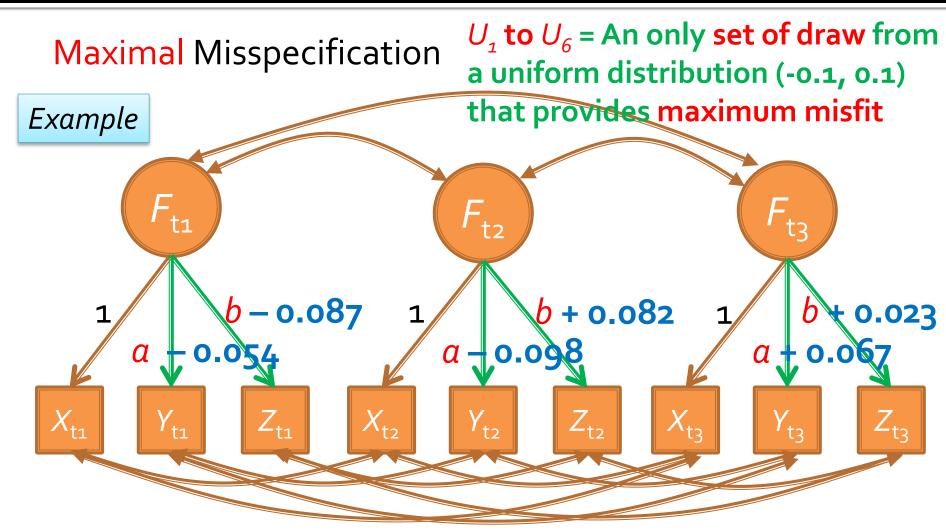






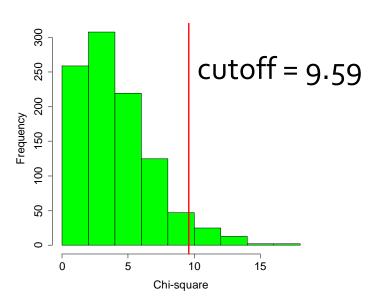


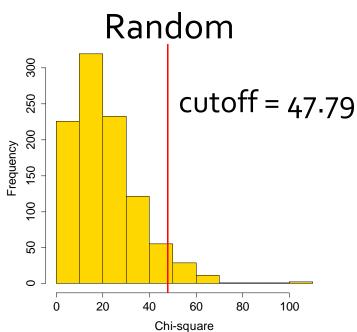
Population RMSEA ≈ .08



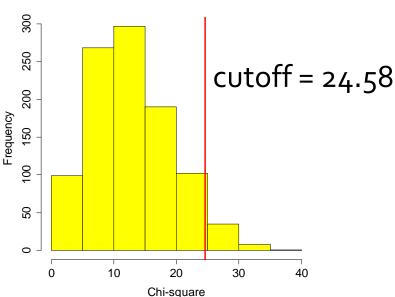
Population RMSEA ≈ .08

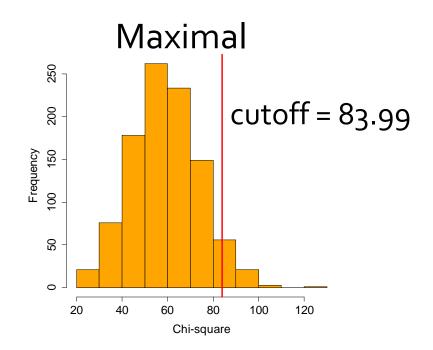
#### No Misspecification







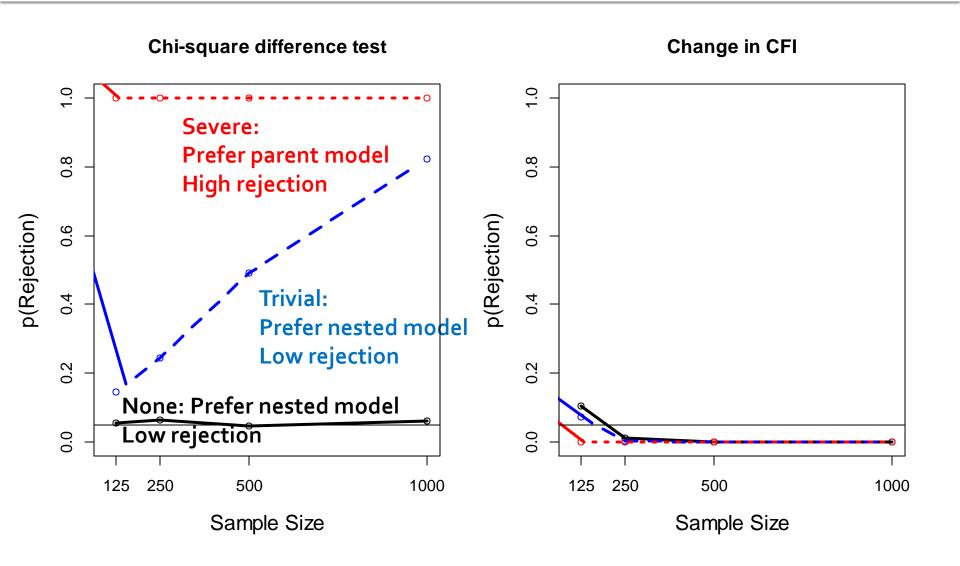




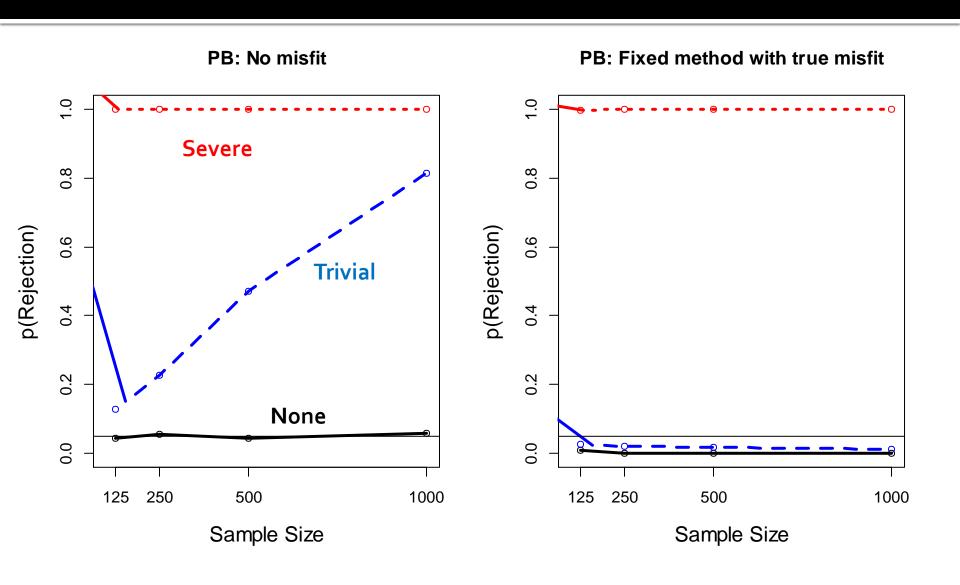
- 1,000 Replications
- Rejection Rate
  - Low when population misfit is none or trivial
  - High when population misfit is severe



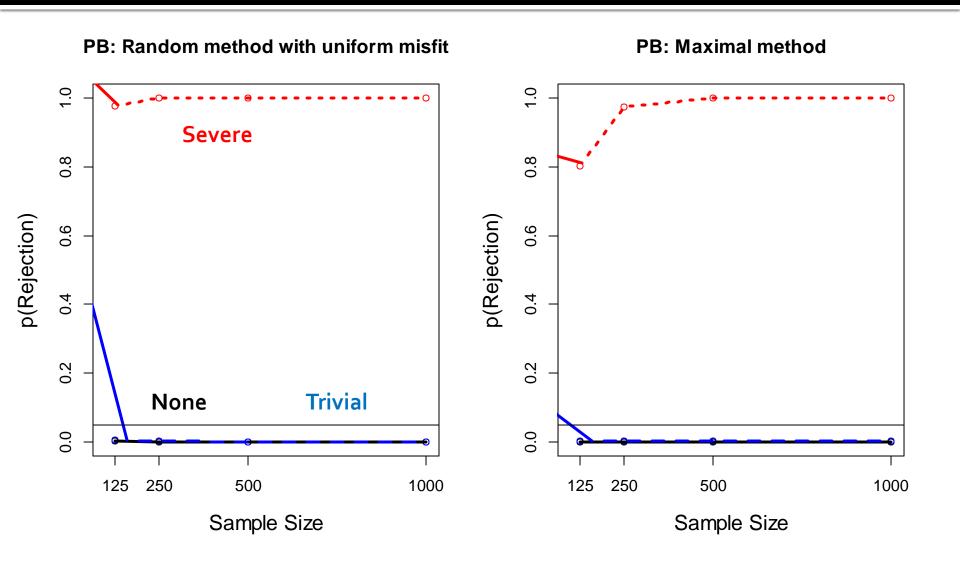
#### Result



# Result



# Result



#### Discussion

- Chi-square test = Parametric bootstrap without trivial misspecification, asymptotically
  - Reject trivial misfit in large sample size
- CFI cutoff of .oo2 (or .o1) has extremely low power
- Parametric bootstrap with defined trivial misspecification is good
  - Avoid universal cutoff criterion
  - Avoid rejection of trivial misspecification
  - Encourage Users to define trivial misspecification

# Discussion

- Can develop your own simulation in R
- Parametric bootstrap approach in absolute fit and nonnested model comparison
- Semi-parametric bootstrap
- This procedure can be implemented in the simsem package in R
  - https://www.simsem.org



# Acknowledgement

- Partial support
  - Grant NSF 1053160 (Wei Wu & Todd D. Little, co-Pls)
  - The Center for Research Methods and Data Analysis at the University of Kansas (Todd D. Little, director)



# Thank you!!

#### Questions, Comments, Concerns

