

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

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# Outline

- Introduction
- Goals
- Trivial Misspecification
- 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?
- Bootstrap approach (Bollen & Stine, 1993; Millsap, 2010, in press)

# Introduction

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

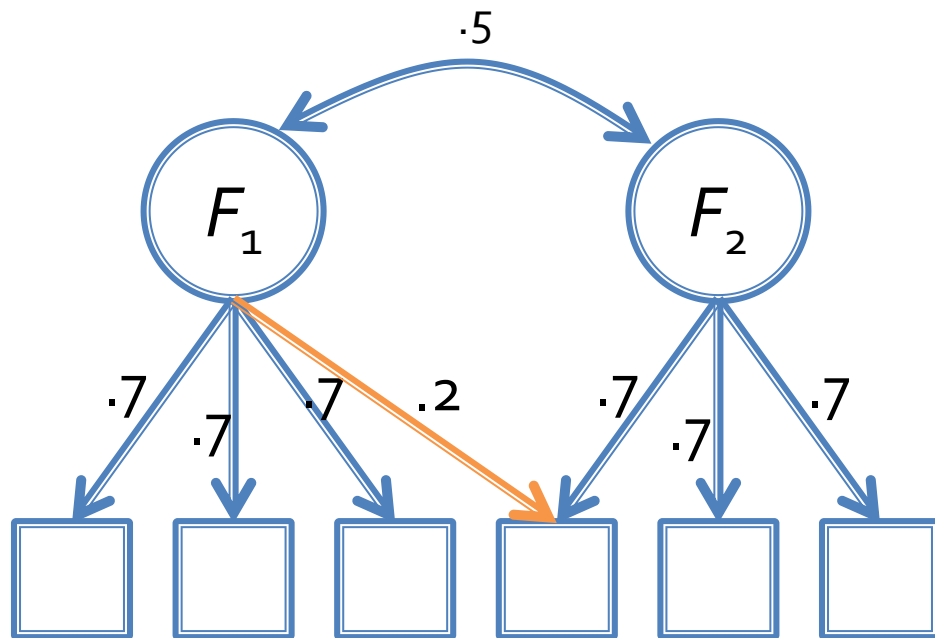
# Goals

- A method to avoid the rule of thumb
- Tailored cutoffs for each hypothesized model
- Test of approximate fit (not exact fit)

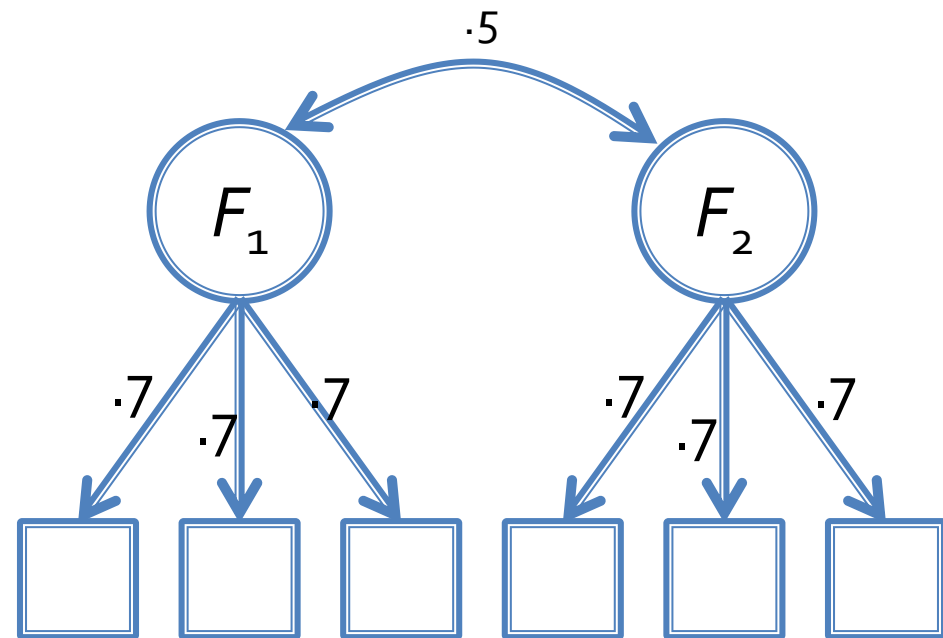
# Trivial Misspecification

- Hypothesized model approximates the underlying mechanism.

True Model

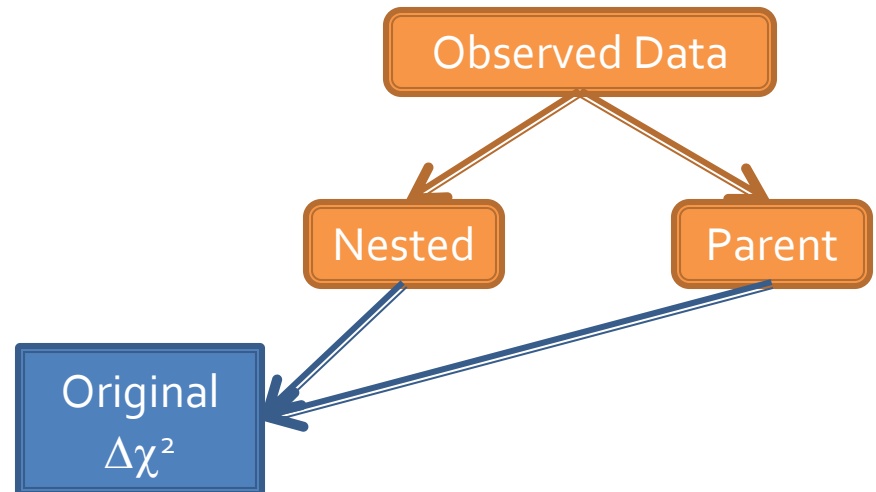


Approximate Model



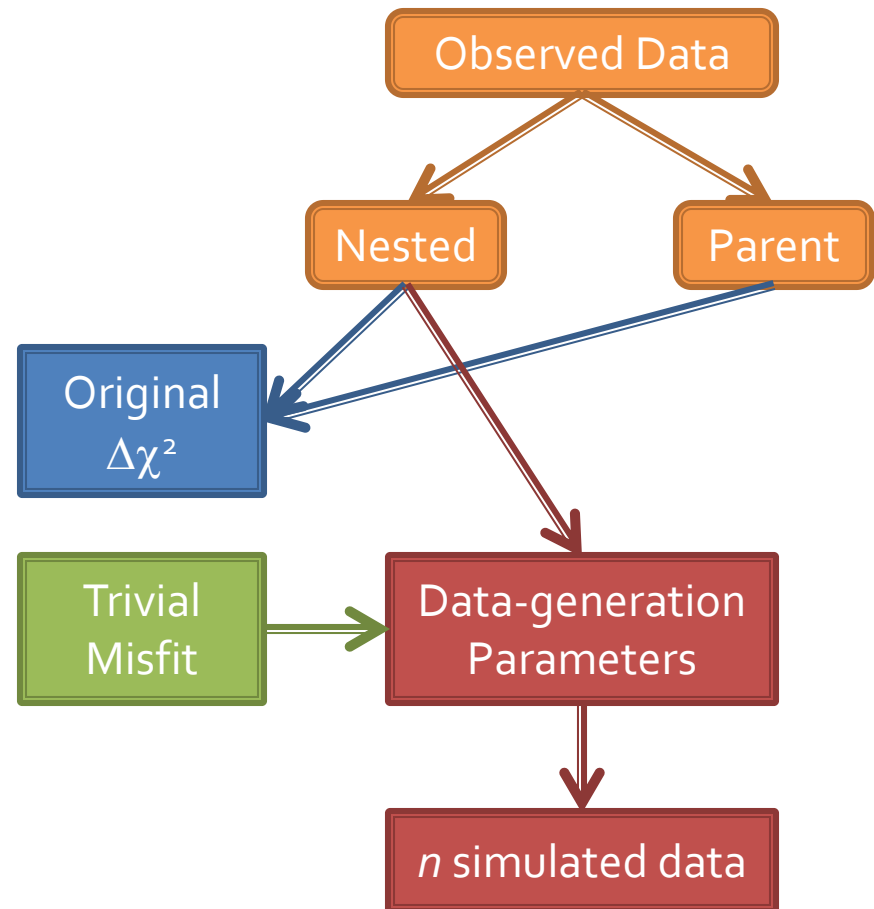
# Parametric Bootstrap

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



# Parametric Bootstrap

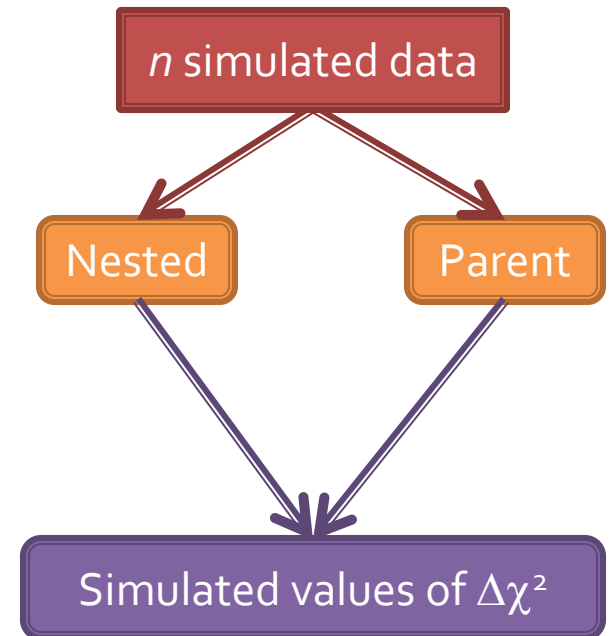
- Use the parameter estimates from the nested model
- Add trivial misspecification
- Generate  $n$  datasets (e.g., 1,000)





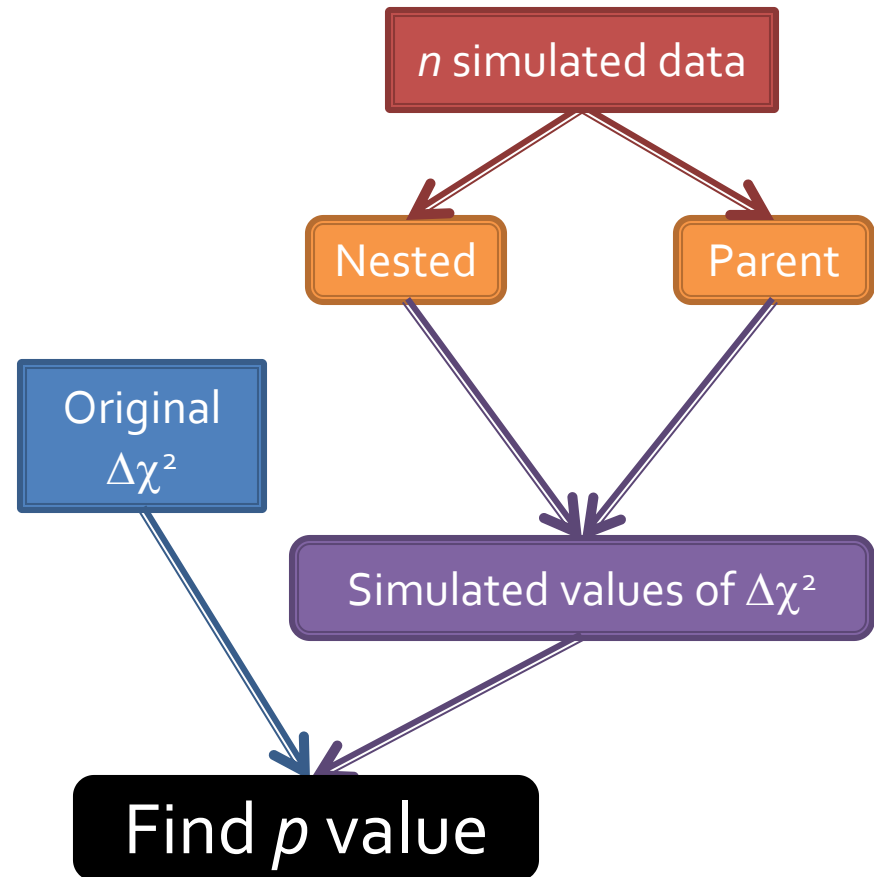
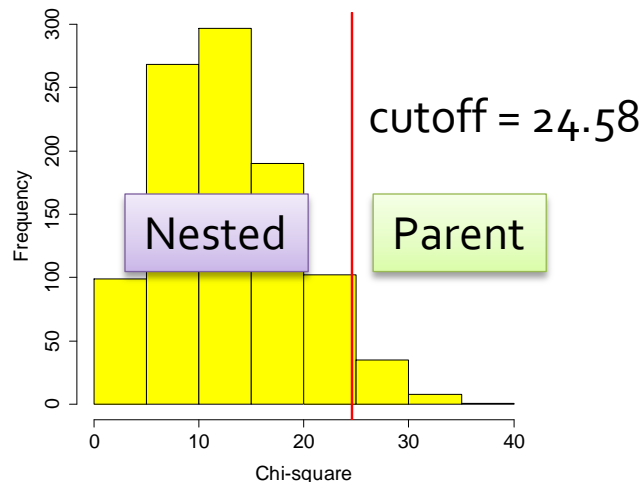
# Parametric Bootstrap

- 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



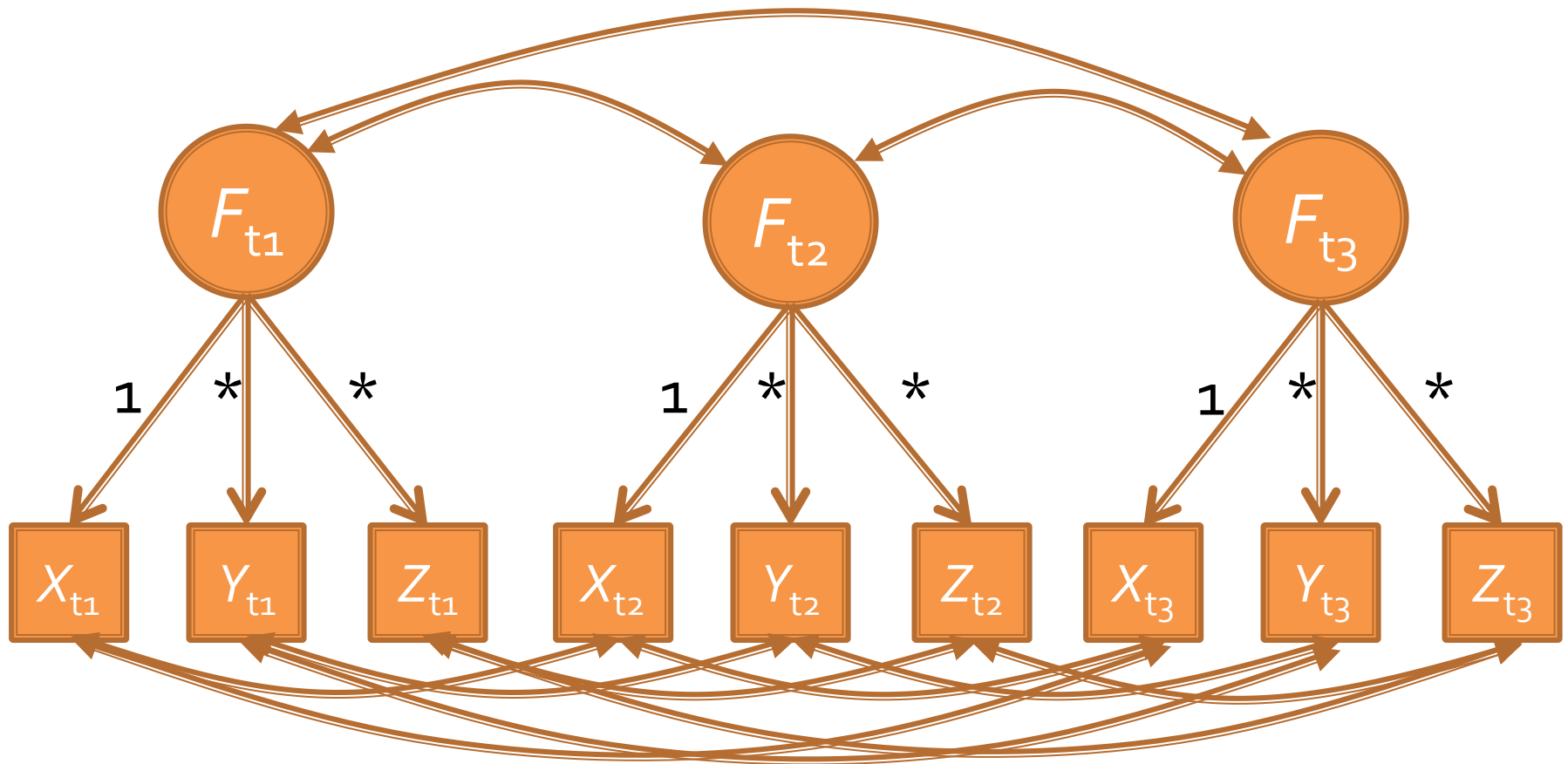
# Parametric Bootstrap

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



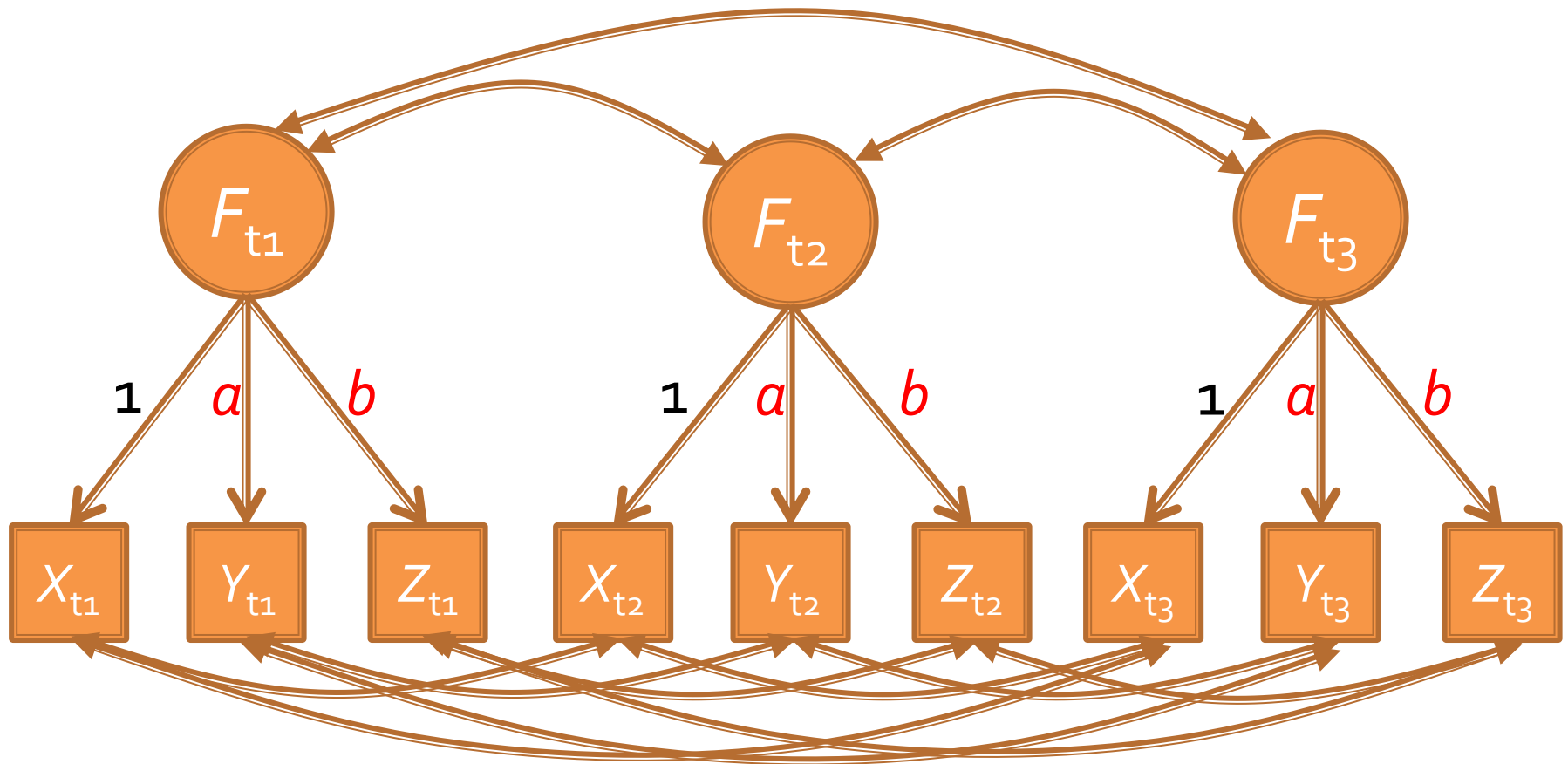
# Simulation

## Parent Model



# Simulation

## Nested Model

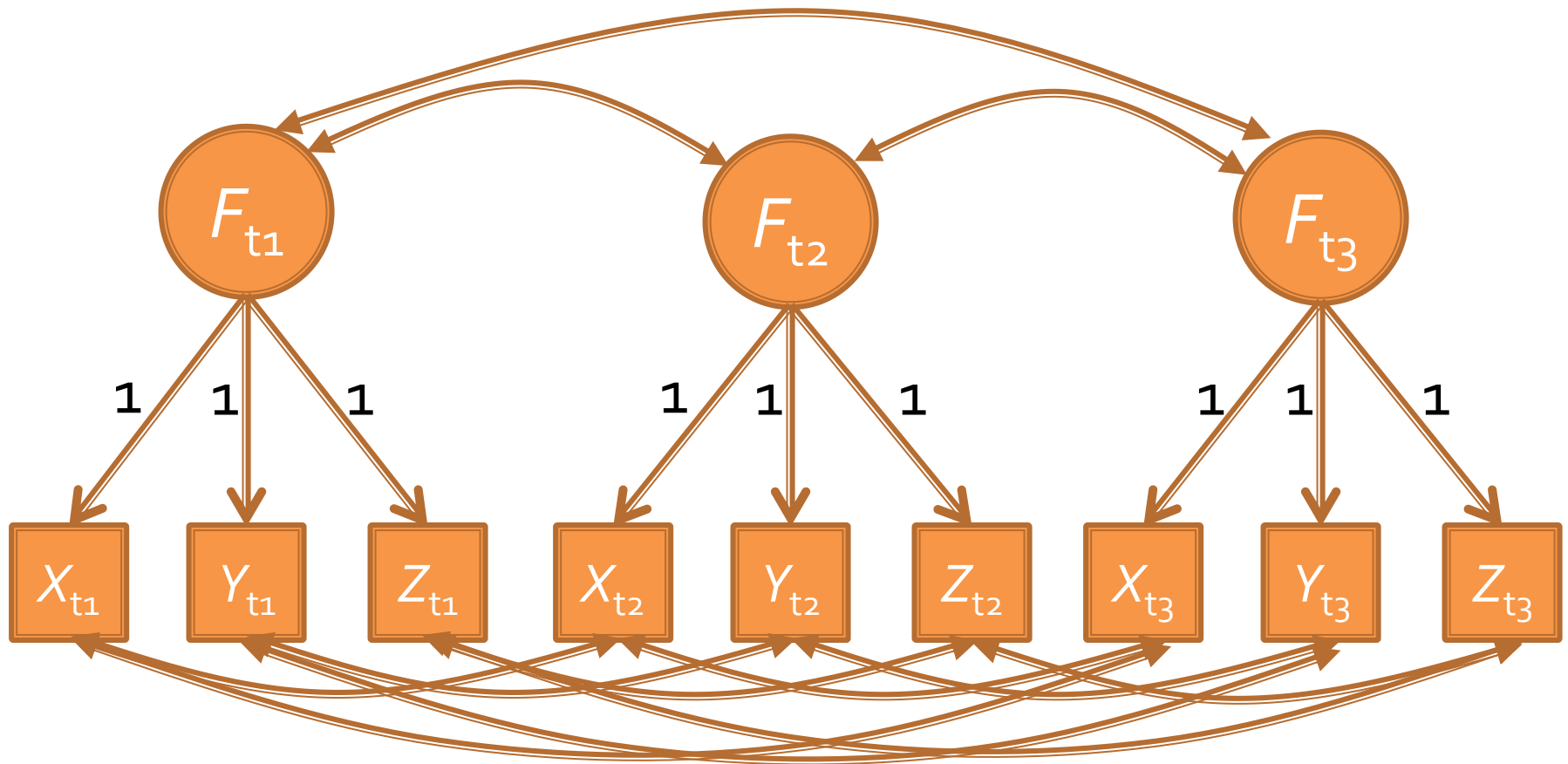


# Simulation

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

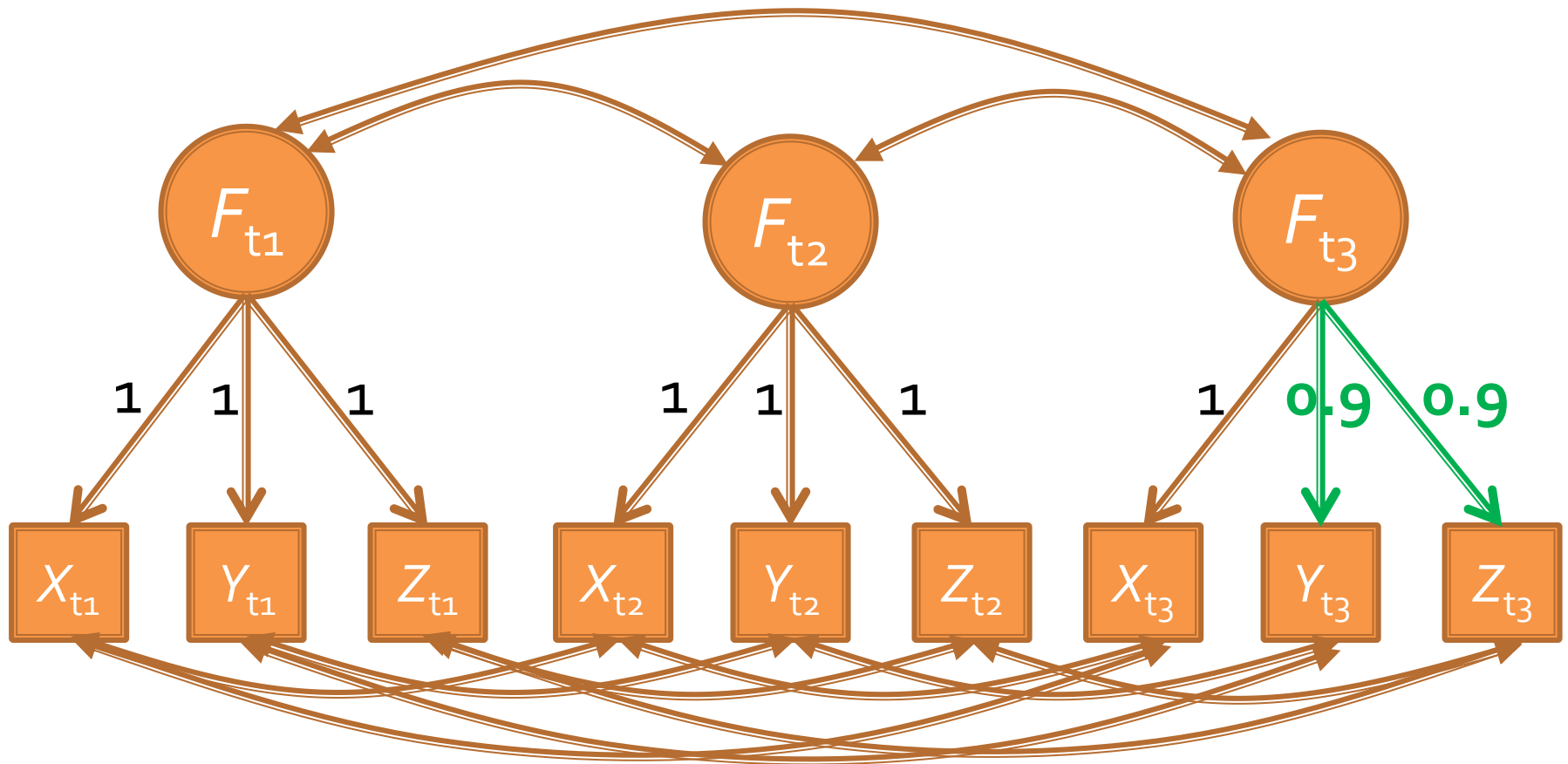
# Simulation

Longitudinal Weak Invariance: **No Misspecification**



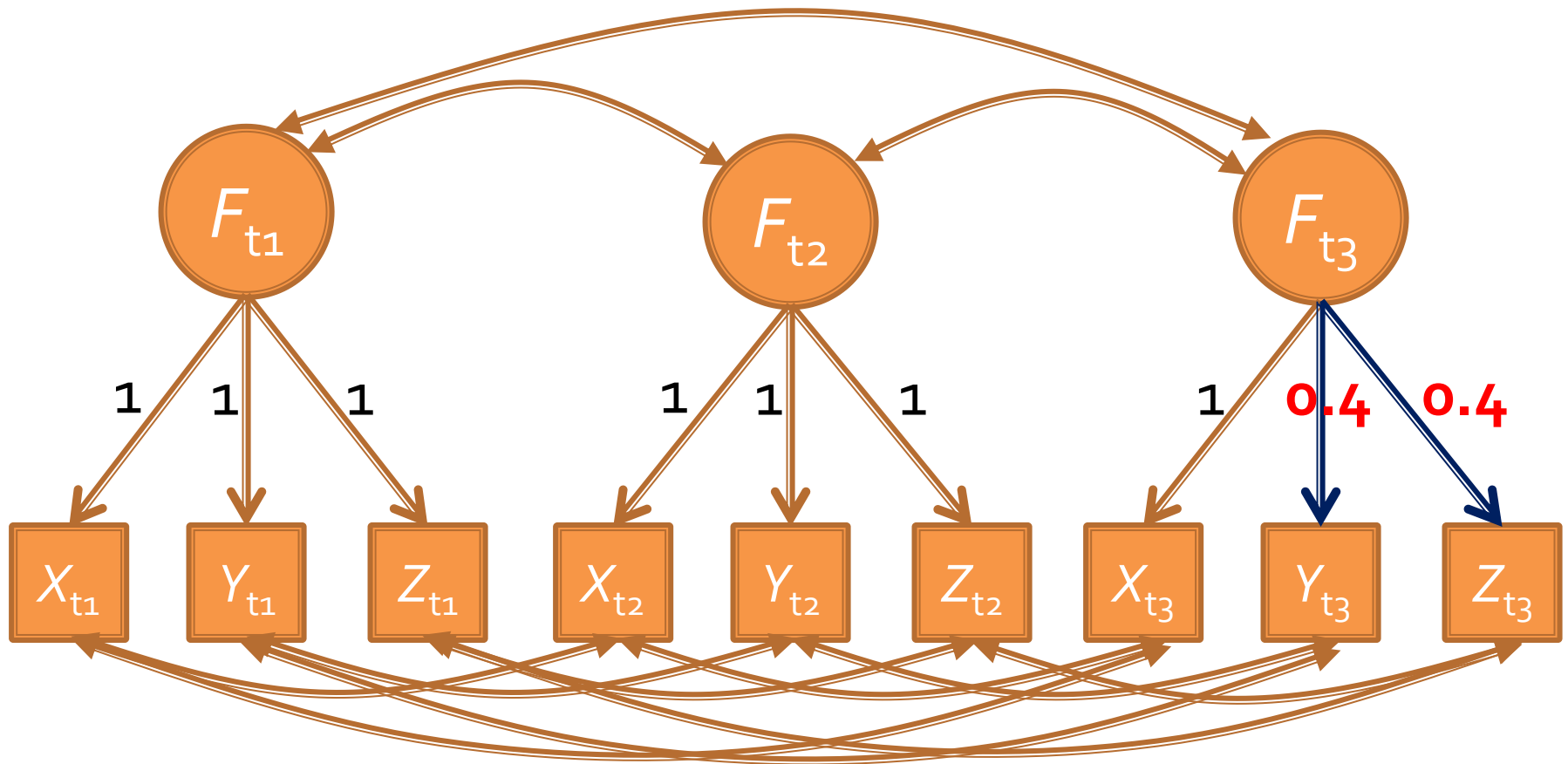
# Simulation

Longitudinal Weak Invariance: **Trivial Misspecification**



# Simulation

Longitudinal Weak Invariance: **Severe Misspecification**



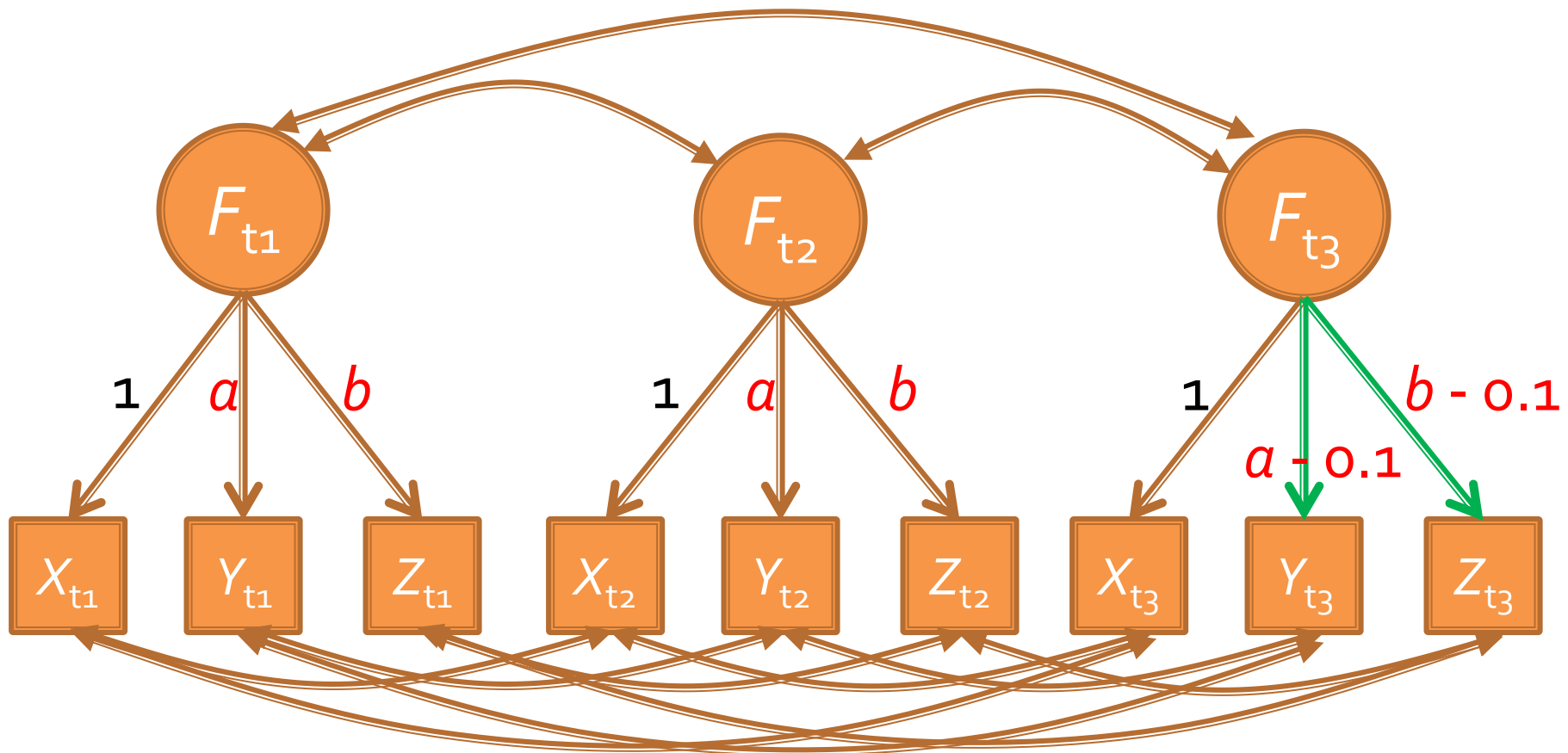


# Simulation

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

# Simulation

Fixed Misspecification

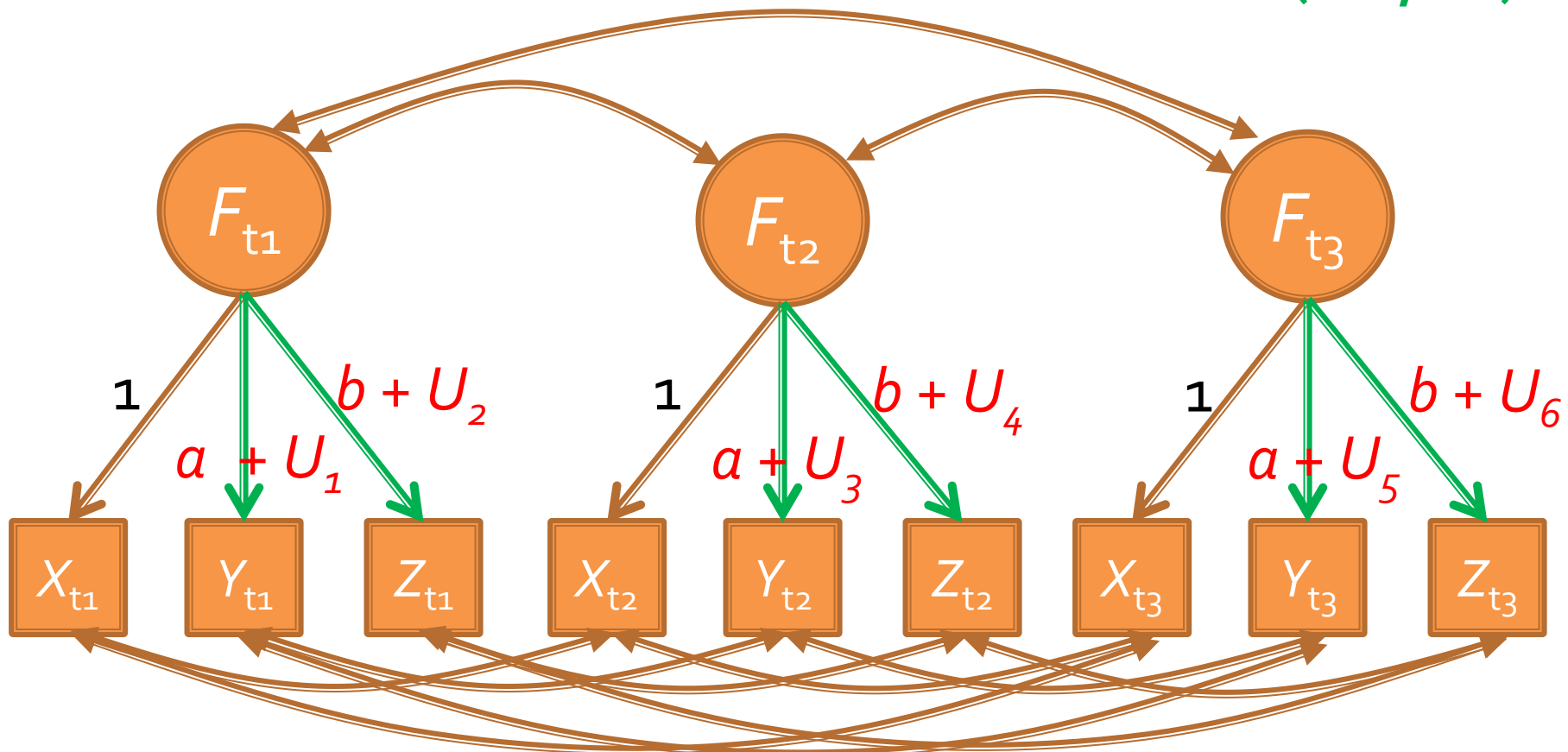


Population RMSEA  $\approx .045$

# Simulation

Random Misspecification

$U_1$  to  $U_6$  = A random draw from a uniform distribution (-0.1, 0.1)



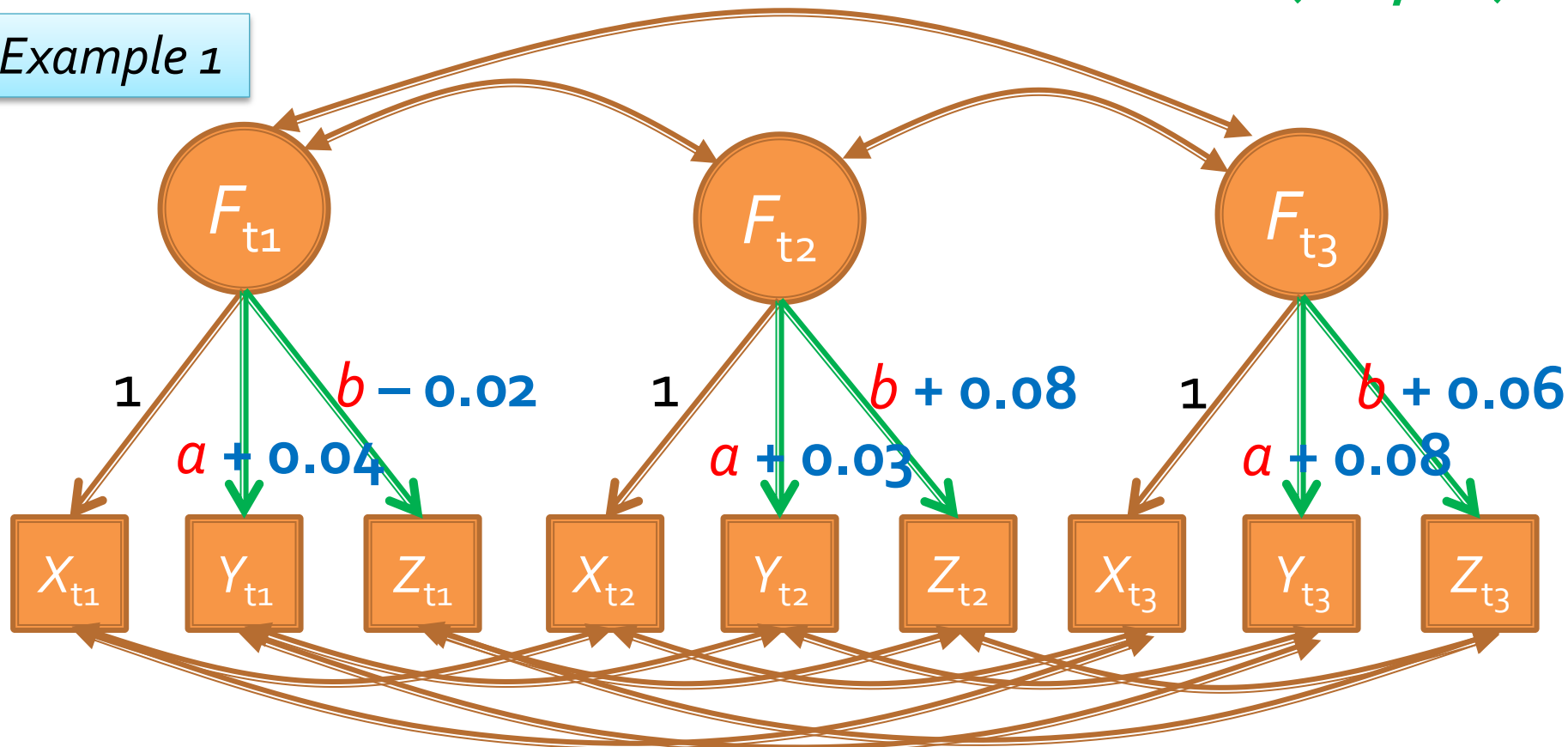
Average Population RMSEA  $\approx .051$

# Simulation

Random Misspecification

$U_1$  to  $U_6$  = A random draw from a uniform distribution (-0.1, 0.1)

Example 1



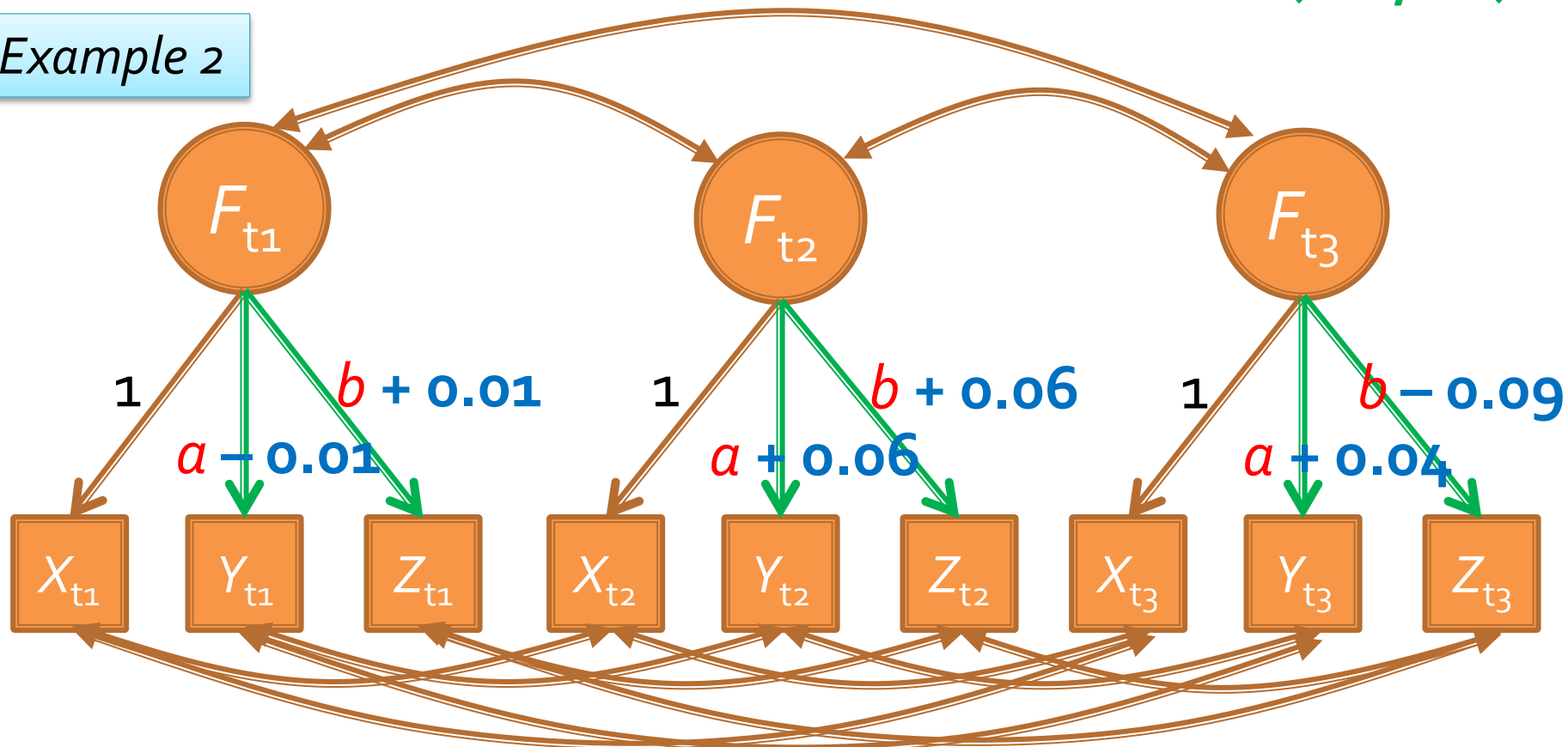
Average Population RMSEA  $\approx .051$

# Simulation

Random Misspecification

$U_1$  to  $U_6$  = A random draw from a uniform distribution (-0.1, 0.1)

Example 2



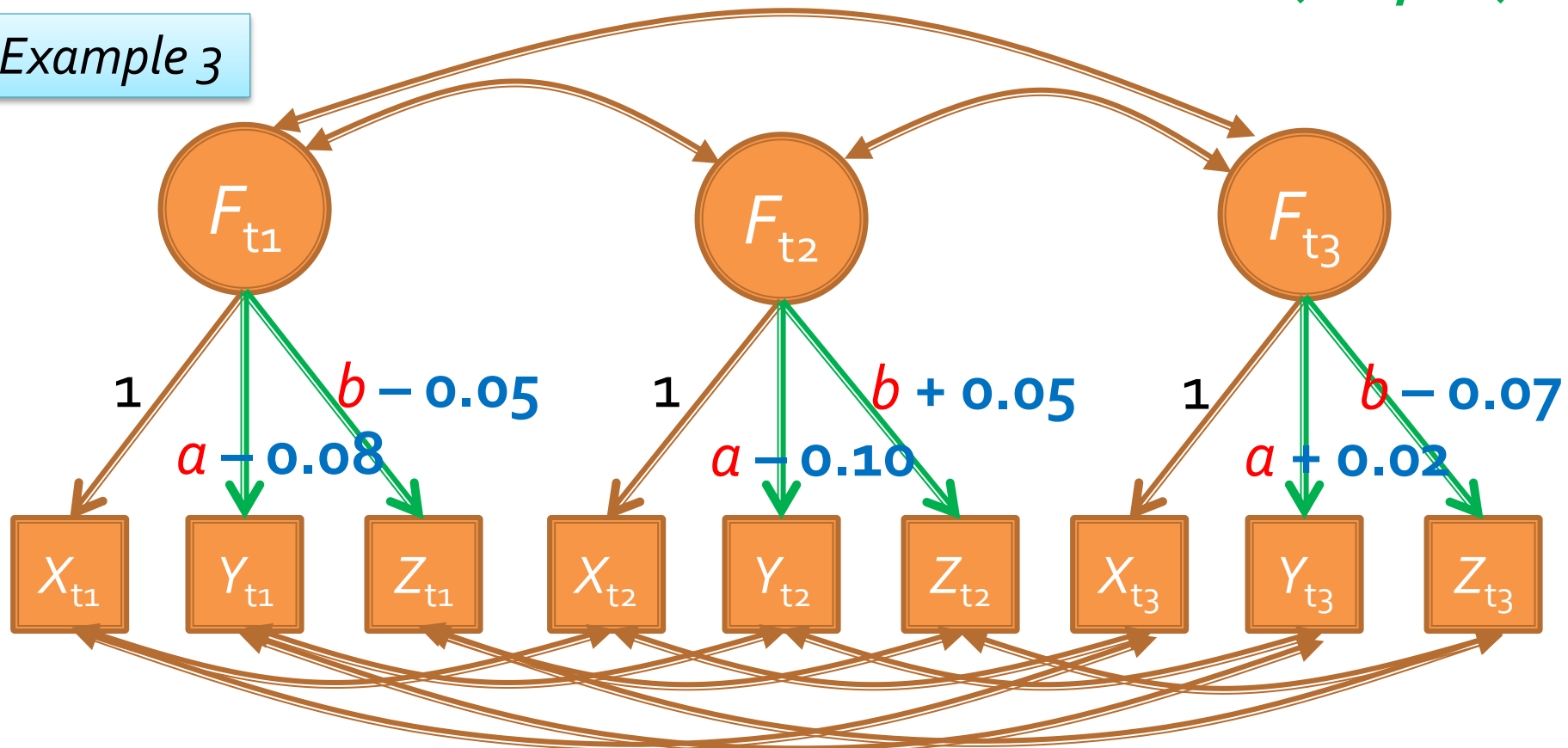
Average Population RMSEA  $\approx .051$

# Simulation

Random Misspecification

$U_1$  to  $U_6$  = A random draw from a uniform distribution  $(-0.1, 0.1)$

Example 3

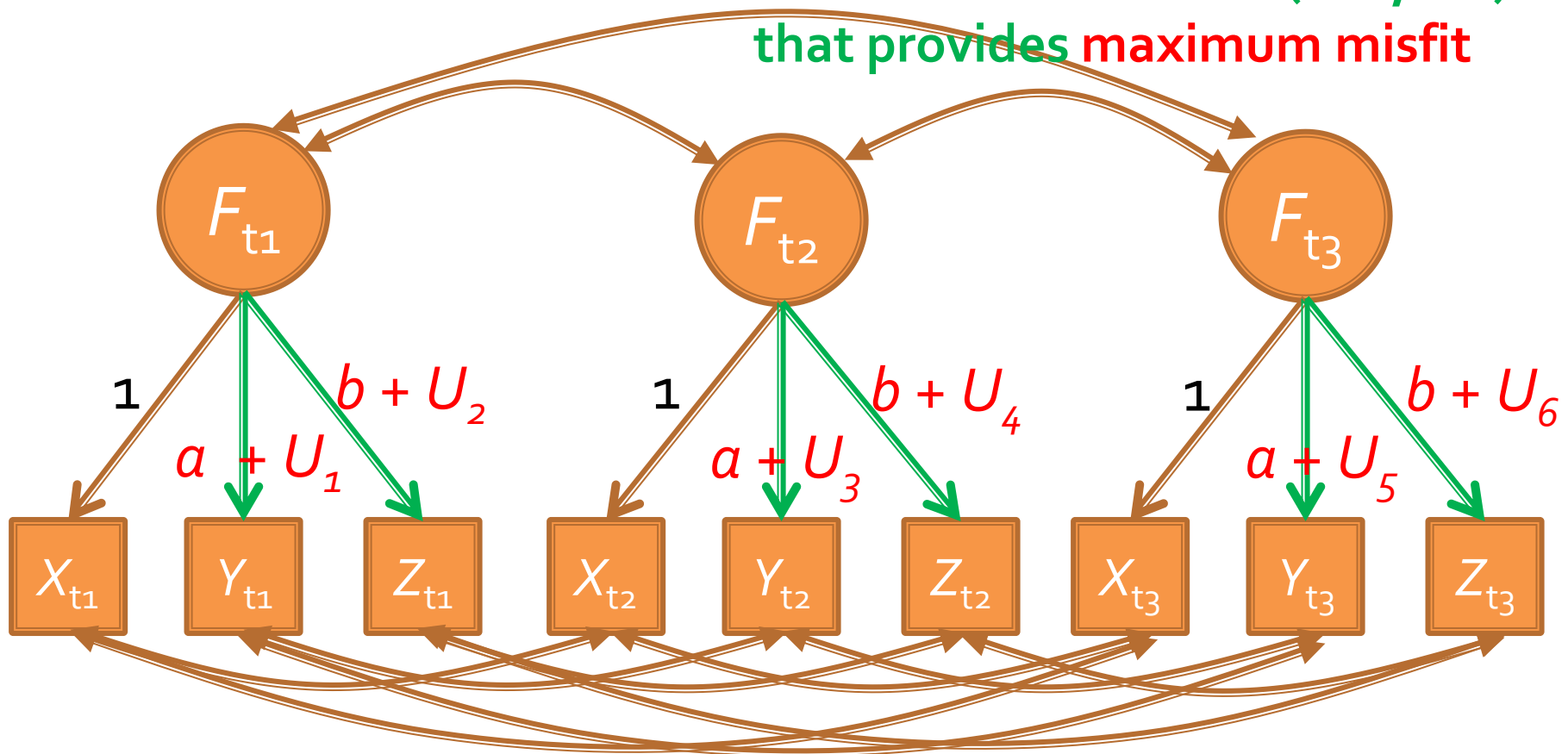


Average Population RMSEA  $\approx .051$

# Simulation

Maximal Misspecification

$U_1$  to  $U_6$  = An only set of draw from a uniform distribution  $(-0.1, 0.1)$  that provides maximum misfit



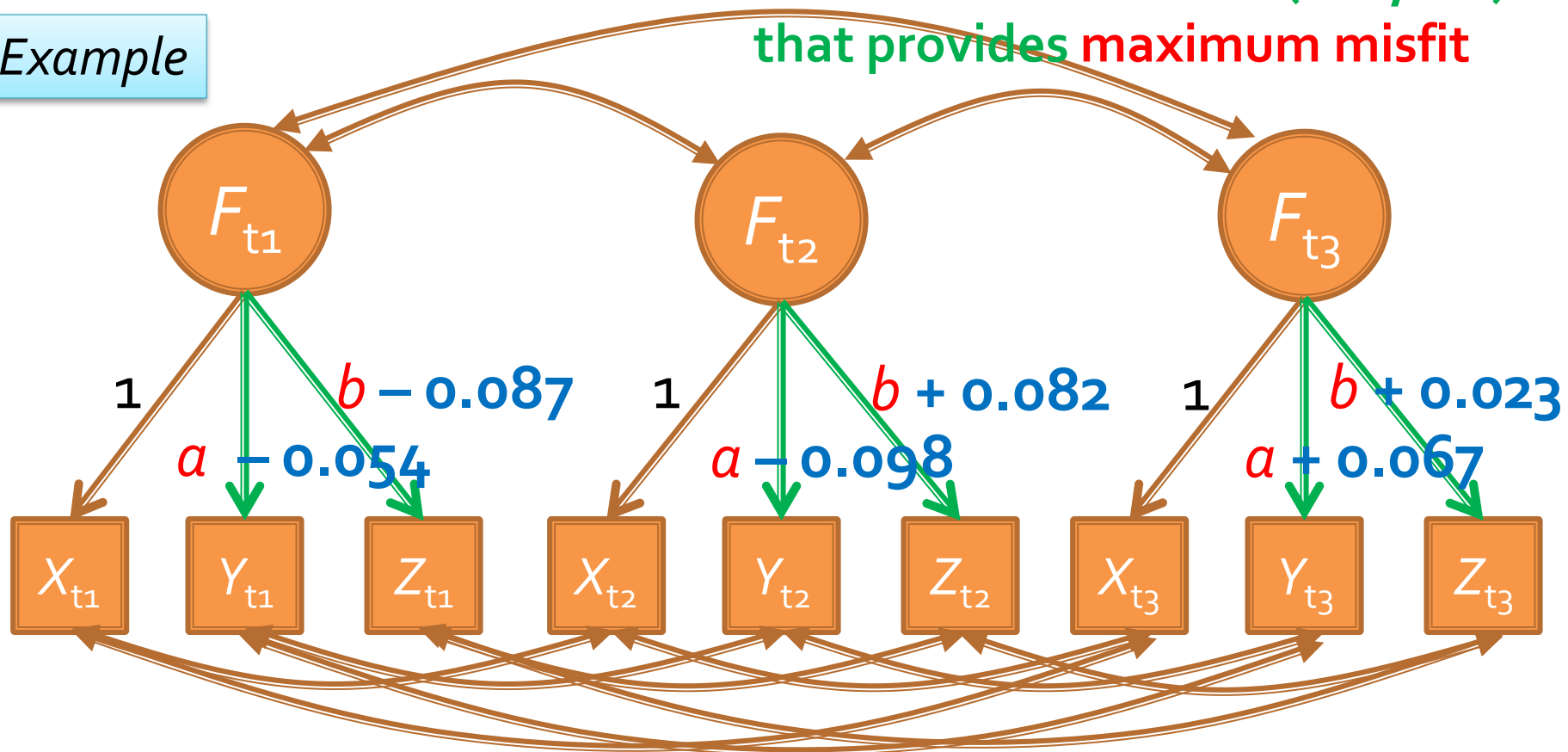
Population RMSEA  $\approx .08$

# Simulation

Maximal Misspecification

Example

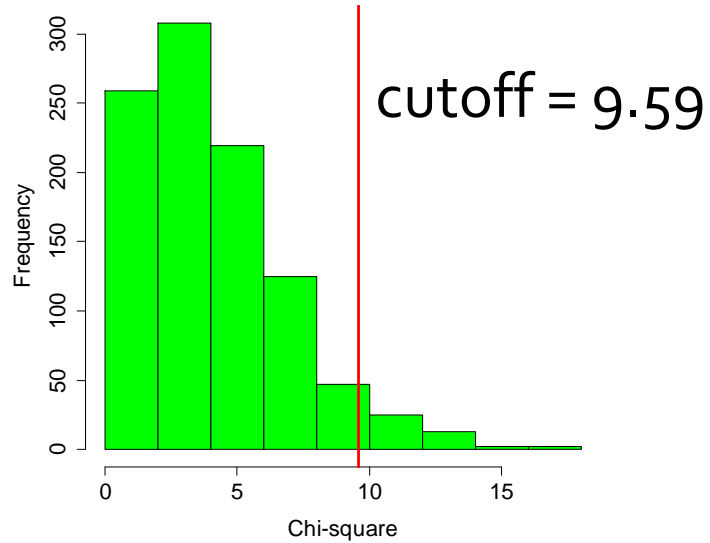
$U_1$  to  $U_6$  = An only set of draw from a uniform distribution  $(-0.1, 0.1)$  that provides maximum misfit



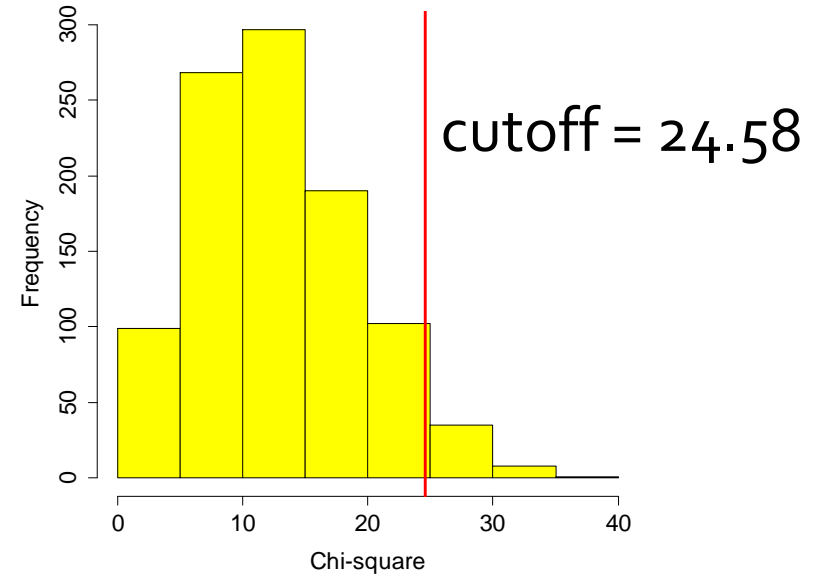
Population RMSEA  $\approx .08$



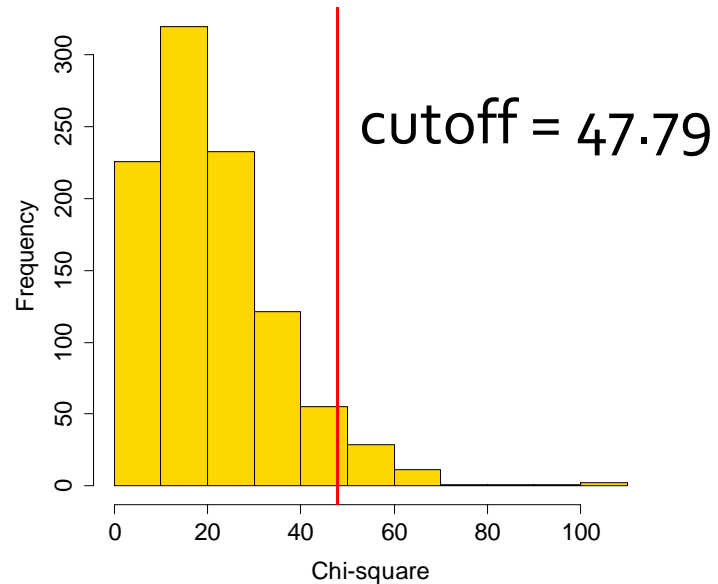
# No Misspecification



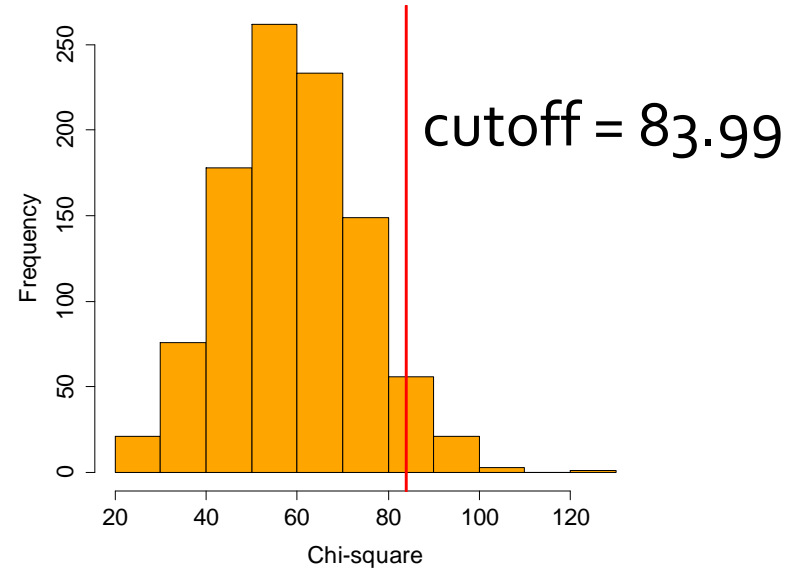
# Fixed



# Random



# Maximal

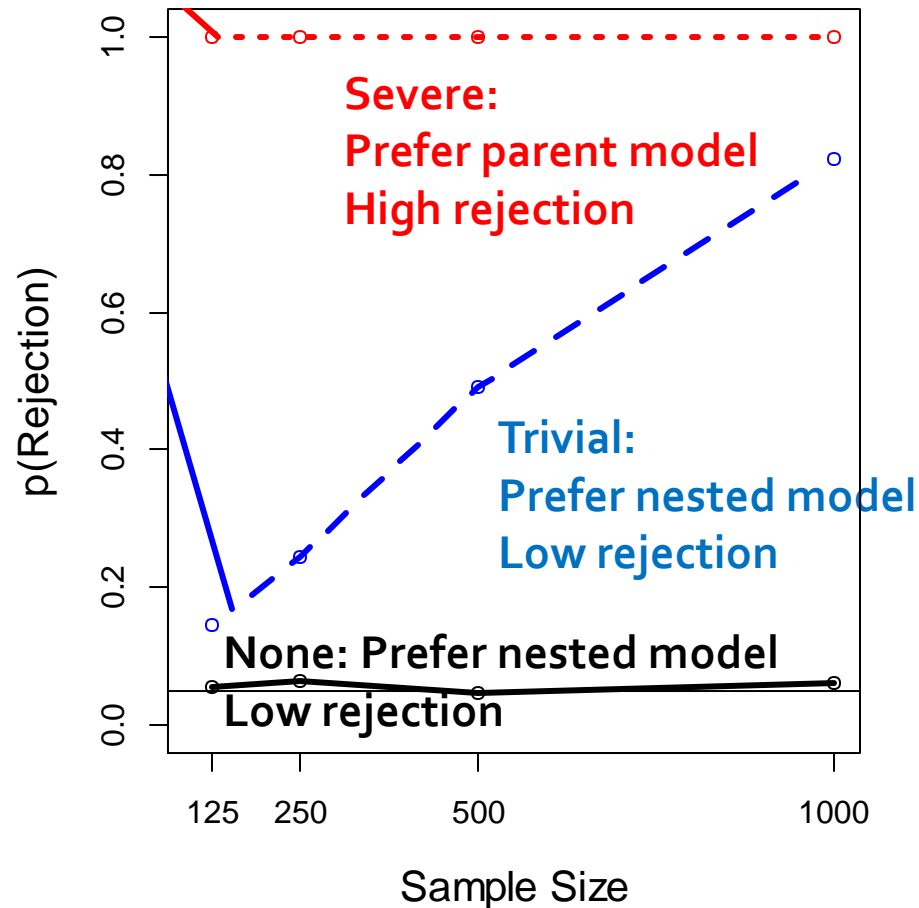


# Simulation

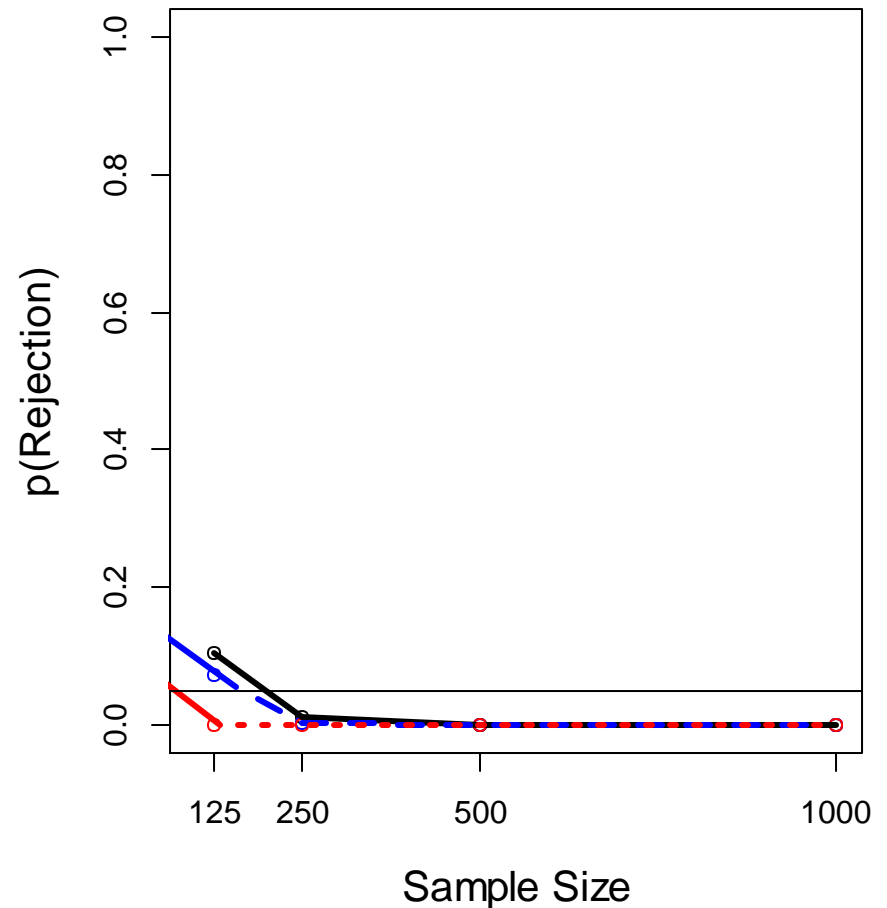
- 1,000 Replications
- Rejection Rate
  - Low when population misfit is none or trivial
  - High when population misfit is severe

# Result

Chi-square difference test

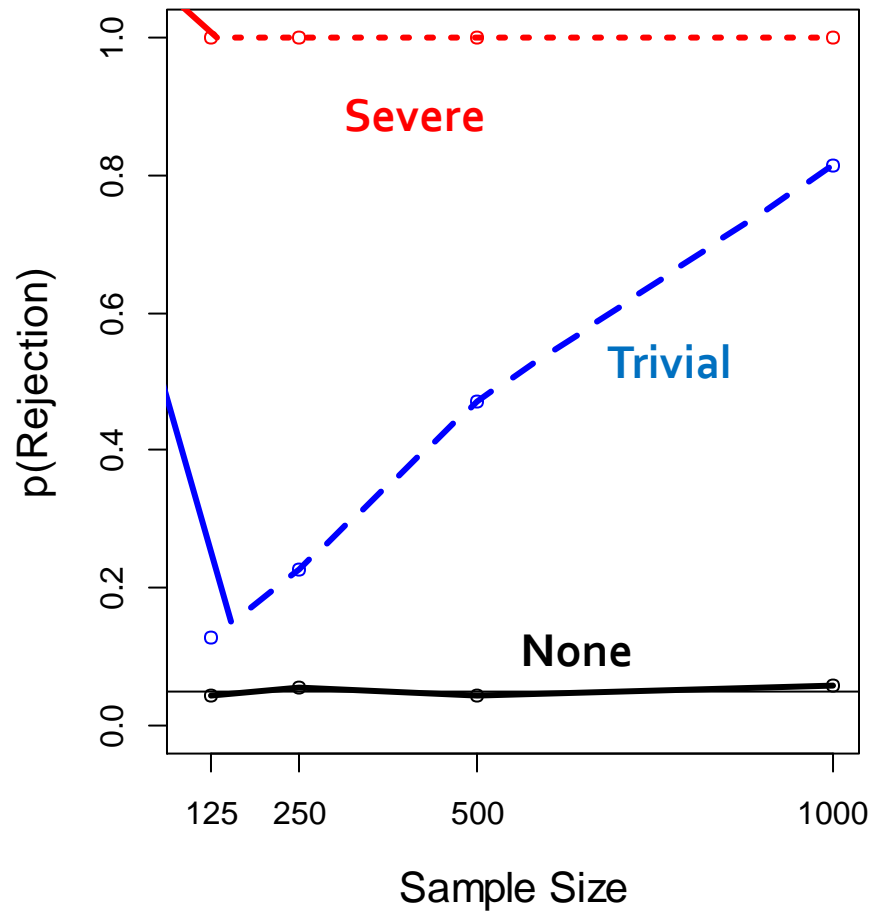


Change in CFI

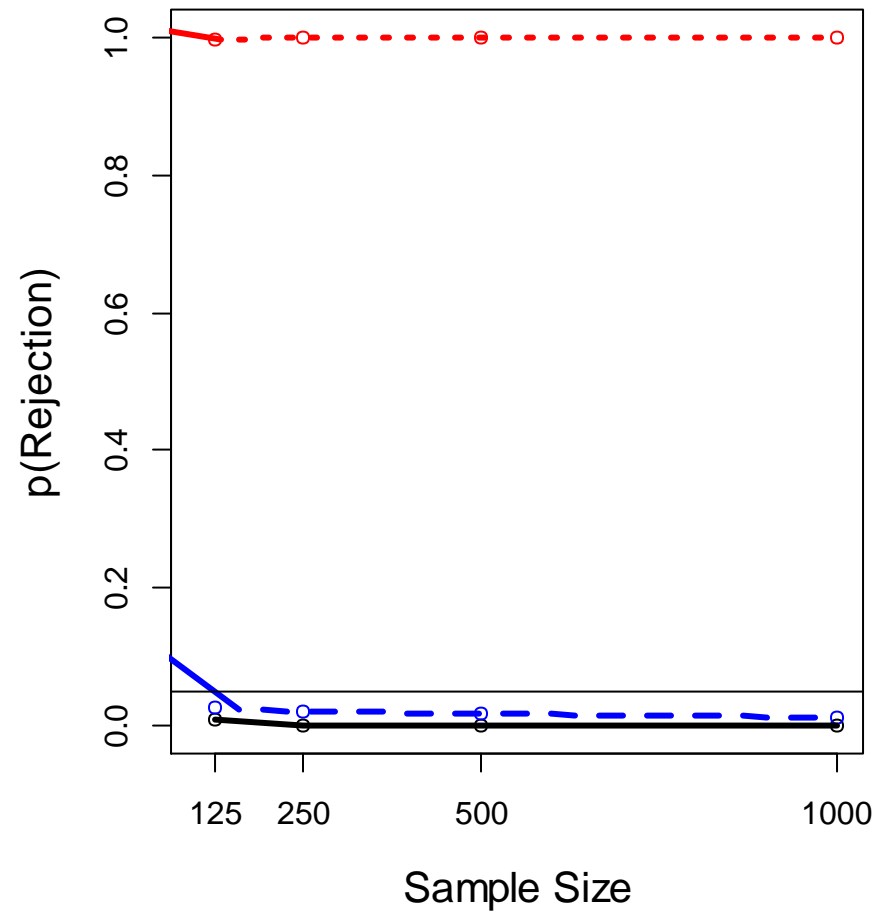


# Result

PB: No misfit

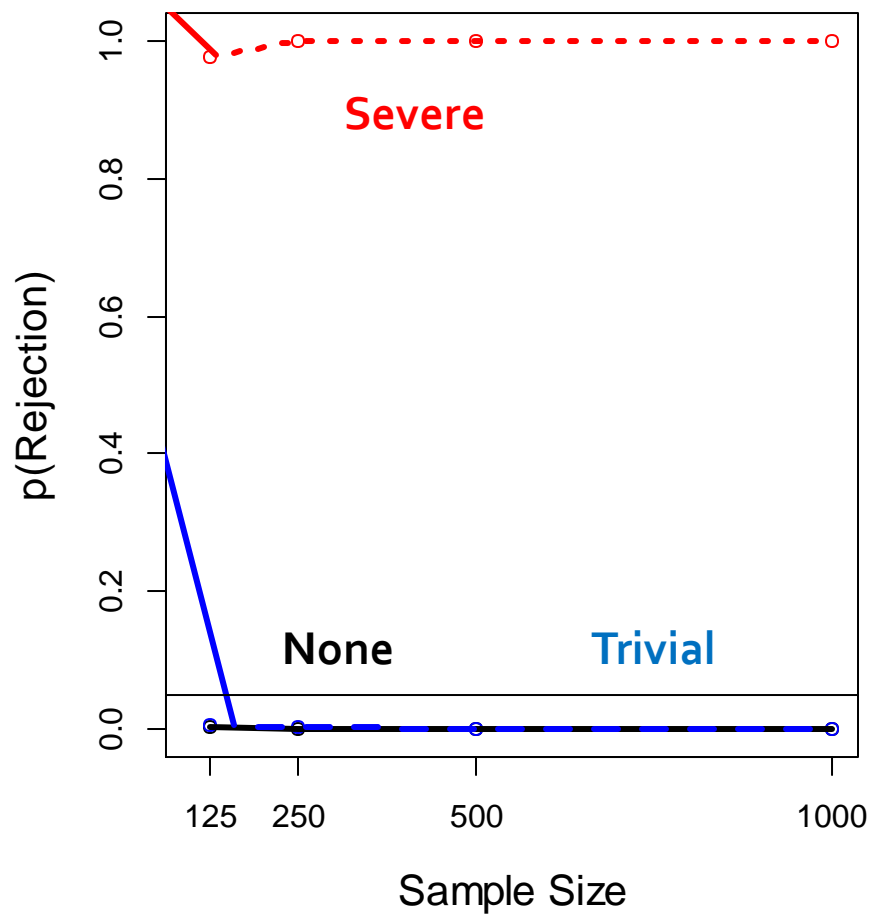


PB: Fixed method with true misfit

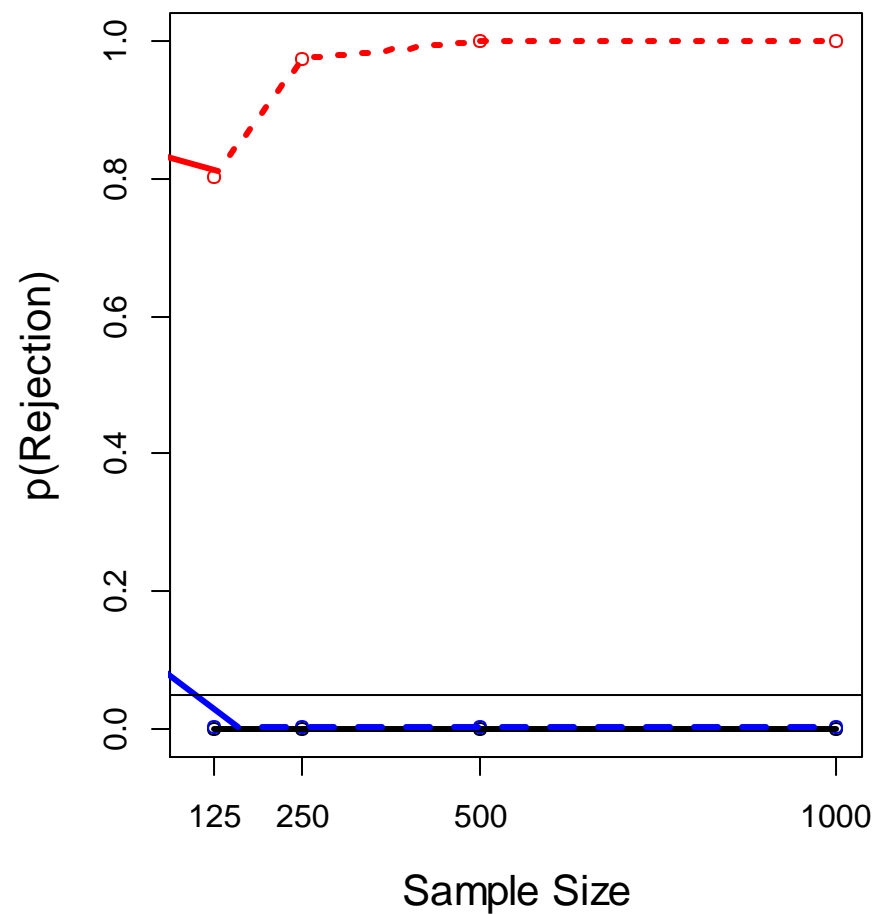


# Result

PB: Random method with uniform misfit



PB: Maximal method



# Discussion

- Chi-square test = Parametric bootstrap without trivial misspecification, asymptotically
  - Reject trivial misfit in large sample size
- CFI cutoff of .002 (or .01) 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
- This procedure can be implemented in the *simsem* package in R: [simsem.org](http://simsem.org)
- Parametric bootstrap approach in absolute fit and nonnested model comparison
- Semi-parametric bootstrap (Bollen & Stine, 1993)
- See the *simsem* package presentation on Thursday 7/12, 9:20, Olive Branch

# Acknowledgement

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



# Thank you!!

## Questions, Comments, Concerns

