#### Three Applications of Structural Equation Modeling as a Handy Tool:

A Network Comparison Test, Testing Moderated Mediation, and a Means to Correct for the Effects of Censoring

> Kees-Jan Kan Niels Smits

## Why this title? (Part I)

Sample of questions from consults:

- 'How can I test if a given psychometric network is invariant over males and females?'
- 'Is it correct I need to use a moderated mediation model in order answer my research question?'

- i.e. Can I use SPSS macro PROCESS?

- 'How do I test if the genetic variance in a variabele is different across SES groups?'
  - while the variable was censored (to different extents)

## Why this title? (Part II)

 $\circ_{\circ}$ 

Because I...

- look like a SEM-er
- quack like a SEM-er
- am influenced by Peter Molenaar
  - who translates almost everything to SEM
- ... I often think 'I believe this can be done using SEM!'
- Indeed SEM provided answers to all 3 questions
- In addition, SEM provided 'the best' solutions
  - That is, among the alternatives I encountered
- SEM is such a handy tool!

### Why this title? (Part III)

Based on recent reviewing experience, I expect future questions:

Like: 'How do I test for age changes in comorbidity?'

What pops up? (in the mind of a SEM-er)



### Why this title? (Part III)

What If I told you

- Non-clinical samples are assessed using clinical instruments

#### $\rightarrow$ censored data

ML assumes normality (categorization?)

- The researcher who will pose that question is interested in **psychometric network models** instead of latent variable models

### Why this title? (Part III)

Proposal:

- Implement the psychometric network in SEM
- Fit this model on the raw data so that the 'edges' be moderated by age
- Include correction for censoring effects

### Why this title? (Part IV)

- Integration of the applications
- I thought 'better demonstrate them separately'
  - a network comparison test,
  - testing moderated mediation, and
  - a means to correct for the effects of censoring

# **Application 1**

**A Network Comparison Test** 

#### Psychometric network modeling

BEHAVIORAL AND BRAIN SCIENCES (2010) 33, 137–193 doi:10.1017/S0140525X09991567

#### Comorbidity: A network perspective

#### Network Analysis: An Integrative Approach to the Structure of Psychopathology

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# An alternative to latent variable modeling

BEHAVIORAL AND BRAIN SCIENCES (2010) 33, 137–193 doi:10.1017/S0140525X09991567

Comorbidity: A network perspective



Figure 1. A model of comorbidity between disorders A and B, under the standard assumptions of latent variable modeling. The *circles* represent the disorders (i.e., latent variables) and the *rectangles* represent the observable core symptoms of those disorders (i.e.,  $X_1 - X_5$  for disorder A, and  $Y_1 - Y_5$  for disorder B). In this model, comorbidity is viewed as a correlation between the latent variables, visualized by the *thick bidirectional edge* between disorders A and B.

# An alternative to latent variable modeling

BEHAVIORAL AND BRAIN SCIENCES (2010) 33, 137–193 doi:10.1017/S0140525X09991567

#### Comorbidity: A network perspective



Figure 2. Comorbidity under a network approach. Disorder A consists of bidirectionally related symptoms  $X_1 - X_5$ , and disorder B consists of symptoms  $Y_1 - Y_5$ . Symptoms  $B_1$  and  $B_2$  are *bridge symptoms* that overlap between disorders A and B. In this model, comorbidity arises as a result of direct relations between the bridge symptoms of two disorders.

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# Commonly used analytical techniques



Journal of Statistical Software May 2012, Volume 48, Issue 4. http://www.jstatsoft.org/

qgraph: Network Visualizations of Relationships in Psychometric Data

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Verena D. Schmittmann University of Amsterdam Denny Borsboom University of Amsterdam

#### R package qgraph

Using the qgraph package

Networks based on (partial) correlations Routines to come up with sparse matrices (glassso) Next, these are vizualized

#### A network comparison test (visual comparison?)





#### A network comparison test (correlating network properties?)



#### A network comparison test (permutation tests?)

#### Package 'NetworkComparisonTest'

October 29, 2016

Type Package

Title Statistical Comparison of Two Networks Based on Three Invariance Measures

Version 2.0.1

Date 2016-10-28

Author Claudia D. van Borkulo, with contributions from Sacha Epskamp and Alex Millner

Maintainer Claudia van Borkulo <cvborkulo@gmail.com>

- 1. Invariant network structure
- 2. Invariant edge strength
- 3. Invariant global strength

#### A network comparison test (permutation tests?)

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Van Borkulo et al. "The first invariance hypothesis [ ...] is H0: A1=A2, in which A1 and A2 are the connection strength matrices of graphs (networks) G1 and G2, respectively. To test this hypothesis, we use a distance measure for symmetric n x n matrices: the maximum or  $L^{\infty}$  norm."

#### Why not directly? (but how?) This paper gave me the hint

PSYCHOMETRIKA—VOL. 82, NO. 4, 904–927 DECEMBER 2017 https://doi.org/10.1007/s11336-017-9557-x



#### GENERALIZED NETWORK PSYCHOMETRICS: COMBINING NETWORK AND LATENT VARIABLE MODELS

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- Starting point
- CFA according to SEM-ers:

#### $\widehat{\boldsymbol{\Sigma}} = \boldsymbol{\Lambda} \boldsymbol{\Phi} \boldsymbol{\Lambda}^{\mathrm{T}} + \boldsymbol{\Theta}$

- Implementation:
  - As a system of regression equations
    - Lisrel, Mplus, lavaan, etc.
  - Drawing the model
    - Lisrel, Mplus, Amos, Onyx
  - Matrix algebraic
    - Mx, OpenMx (not) user friendly?

#### $\widehat{\boldsymbol{\Sigma}} = \boldsymbol{\Lambda} \boldsymbol{\Phi} \boldsymbol{\Lambda}^{\mathrm{T}} + \boldsymbol{\Theta}$

- In OpenMx
  - Specify the matrices  $(\Lambda, \Phi, \Theta)$
  - Specify the algebraic expression (equation above)
  - Put them together with the data
  - Solve
  - Multi-group modeling is possible
  - (In)variance: test if the insertion of certain equality constraints (in  $\Lambda$ ,  $\Phi$ , and/or  $\Theta$ ) reduce the model fit significantly

- Alternative expression (RAM model)  $\widehat{\boldsymbol{\Sigma}} = \mathbf{F}(\mathbf{I} - \mathbf{A})^{-1}\mathbf{S}(\mathbf{I} - \mathbf{A})^{-T}\mathbf{F}^{T}$
- In OpenMx (not very different than before)
  - Specify the matrices (now A, S, F, I)
  - Specify the algebraic expression (equation above)
  - Put them together with the data
  - Solve
  - Multi-group modeling is possible
  - (In)variance: test if the insertion of certain equality constraints (in A, and/or S) reduce the model fit significantly

• The network approach (just another alternative)!

 $\widehat{\boldsymbol{\Sigma}} = \boldsymbol{\Delta} (\boldsymbol{I} - \boldsymbol{\Omega})^{-1} \boldsymbol{\Delta}$ 

Ω is a symmetric n×n matrix containing the edges
(partial/semi-partial relations) among the variables
(but with 0's on the diagonal)
I is an n×n identity matrix
Δ is an n×n (diagonal) matrix containing scaling

parameters

• The network approach (just yet another alternative!)

 $\widehat{\boldsymbol{\Sigma}} = \boldsymbol{\Delta} (\boldsymbol{I} - \boldsymbol{\Omega})^{-1} \boldsymbol{\Delta}$ 

In OpenMx (not very different than before)

- Specify the matrices (now  $\Omega$ ,  $\Delta$ , and I,)
- Specify the algebraic expressions (equation above)
- Put them together with the data
- Solve
- Multi-group modeling is possible
- (In)variance: test if the insertion certain equality constraints (in Ω and/or Δ) reduce the model fit significantly



Figure 2. Comorbidity under a network approach. Disorder A consists of bidirectionally related symptoms  $X_1 - X_5$ , and disorder B consists of symptoms  $Y_1 - Y_5$ . Symptoms  $B_1$  and  $B_2$  are *bridge symptoms* that overlap between disorders A and B. In this model, comorbidity arises as a result of direct relations between the bridge symptoms of two disorders.

#### Network modeling in SEM

- Advantage: Confirmatory Network Modeling
  - Testing a priori theoretical networks
  - Replication research

. . . .

- Behavior genetic modelling

$$\begin{split} \widehat{\boldsymbol{\Sigma}} &= \widehat{\boldsymbol{\Sigma}}_{\text{genetic}} + \widehat{\boldsymbol{\Sigma}}_{\text{environmetal}} \\ &= \boldsymbol{\Lambda} (\boldsymbol{\Phi}_{\text{genetic}} + \boldsymbol{\Phi}_{\text{environmental}}) \boldsymbol{\Lambda}^{\text{T}} + \boldsymbol{\Theta}_{\text{genetic}} + \boldsymbol{\Theta}_{\text{environmental}} \\ &= \boldsymbol{\Delta} ((\mathbf{I} - \boldsymbol{\Omega}_{\text{genetic}})^{-1} + ((\mathbf{I} - \boldsymbol{\Omega}_{\text{environmental}})^{-1}) \boldsymbol{\Delta} \end{split}$$

#### Causal Networks

• In causal networks edges are directed paths  $\widehat{\Sigma} = (I - B)^{-1} \Phi (I - B)^{-1}$ 

That's simply path analyses!

# **Application 2**

**Testing Moderated Mediation** 

#### **Mediation:**

A is a cause of B, while B is a cause of C Result: A is a cause of C

More precisely...

#### **Mediation:**

Differences in A give rise to differences in B, while Differences in B give rise tot differences in C. Result: Differences in A give rise to differences in C.

To be even more precise replace 'differences' by:

- individual differences (subject of my talk)
- intraindivual differences (not subject of my talk)
- group differences (.... dunno....yes and no?)

Research question: Does interindividual variable M mediate between interindividual variables X and Y?

Tackle using **the scientific method**:

falsification (rather than verification): + If two competing, falsifiable explanations cannot be rejected parsimony

Basis of model selection!

**Hypothesis** (= stated in the form of a full mediation model)



If true, the model explains there is a relation between IV and DV If true, the indirect effect equals a'\*b'

#### Falsifiable

Model used (partial mediation; weaker hypothesis)



If true, the presence of pathways  $X \rightarrow M$  and  $M \rightarrow Y$  give a partial explain of the relation between X and Y

If true, the indirect effect equals a\*b

Ok, does not run against the original hypothesis But unfalsifiable! (saturated)



**Provided with the unfalsifiable model:** 'Determine if 0 lies inside or outside CI interval of a\*b'

This is not the same as asking 'is my mediation theory (model) (in)correct?' It is not even the same as asking 'Does a\*b lie outside the CI of 0 ( $\alpha\beta = 0$ )'

- **PROVIDED there is mediation**, the result is product a\*b
- The aim of traditional mediation tests is awkward
- Hypothesis test:
  - GIVEN there is mediation
    - Assume there is no mediation(??)
      - But mediaton was the given(!!)
- What I *do* understand:
- a\*b is 0 when a = 0 or b = 0 (or both)
  - implying there would be no mediation
- Why not model these hypotheses explicitly??
- Test WHETHER (we can assume) there is mediation

Fit the saturated model (partial mediation model)
 Drop path(s) and/or specify other falsifiable models
 Compare LL's and select model of preference



Competing (**falsifiable**) model: Is there full mediation? (implying M does mediate)



Competing (**falsifiable**) model Is a 0? (implying M does not mediate)



Competing (**falsifiable**) model Is b 0? (also implying M does not mediate)



Competing (falsifiable) model:

Are both a and b 0? (implying M does not mediate)





Example of another competing (**falsifiable**) model (implying M does not mediate)



If we end up with the saturated model, we cannot conclude there is mediation(!)



If we end up with the saturated model, we cannot conclude there is mediation(!)



#### Testing Moderated Mediation (SPSS macro PROCESS)

What is the substantial interpretation of variable X\*M? Why does X\*M have a direct effect?

#### Saturated (unfalsifiable!)



1) Define the saturated model and explicate which variable moderates which path,

e.g. the independent variable X moderates path b



Works in OpenMx through the use of definition variables

1) Define the saturated model and explicate which variable moderates which path,



Works in OpenMx through the use of definition variables

1) Define the saturated model and explicate which variable moderates which path,



Works in OpenMx through the use of definition variables

Suppose this reflects my hypothesis



1) Fit this saturated model

2) Drop path(s) and/or specify other falsifiable models

3) Compare LL's and select model of preference



Hence the same steps as in normal mediation

Suppose this was the best model (we cannot conclude there is mediation though; model equivalence)

4) Drop the moderation to test if moderation is a necessary assumption



The saturated model wasn't that saturated! With respect to variance-covariance, yes With respect to homo/heteroskedasticity, no

Possible extentions

Moderation in more complex models

- e.g. (causal?) network models



# **Application 3**

a Means to Correct for the Effects of Censoring





highest SES

540

550



https://openmx.ssri.psu.edu/thread/1428

Suggestion by Mike Neale:

 Model a single latent variable which causes, with path=1, two variables

Yc

Yo

- one is ordinal and one is continuous
- For those individuals with censored scores, they are missing (NA) on the continuous variable, and vice-versa
- for those with the continuous variable scored (<[threshold]) - they are marked as missing on the ordinal variable.
- I think this is simplest but the I've never tried it."

# Correction for censoring (Y) $Y_{c}$ $Y_{0}$

Checked performance

- By simulations
  - with and without extra missings
- With results from a FORTRAN tool once developed by prof. Conor Dolan
  - exact same results. i.e. LL, AIC etc.
- Conclusion: Tried and works well!



Extension: Implementation in behavior genetic modeling Simulations told: The method works well!

#### My Research Master student, Maarten Schouten, continued the simulations and just finished his thesis

Eliminating the Biasing Effect of Censoring on Parameter Estimates in Biometrical Structural

Equation Modeling

M. Schouten

11210729

1<sup>st</sup> assessor: dr. K.J. Kan

2<sup>nd</sup> assessor: dr. D. Molenaar

Universiteit van Amsterdam

#### **Background:**

- Standard twin models assume phenotypes are normally distributed.
- Fitting these models on censored data can yield biased parameter estimates
- Data transformation does not eliminate bias
- Categorical modeling reduces power to discriminate among nested models

#### **Objectives:**

- To reassess the biasing effect of censored data on parameter estimates
- To assess the performance of the model that accounts for censoring

In comparison to the aforementioned models



#### **Conclusions:**

The censoring model outperforms both the continuous model, since it diminishes bias, and the categorical model, as it retains power.

# Three applications

Conclusions

#### Conclusion

'How can I test for age changes in comorbidity?'



#### Conclusion

Yves yesterday:

"We may not <u>need</u> SEM after all" (in certain cases) Today:

"SEM is such a handy tool!" (in many cases)

SEM is very flexible

- To a large extent because it provides the opportunity to implement **(in)equality constraints**
- OpenMx provides the opportunity to use matrix algebraic expressions
  - OpenMx is not that user friendly though
  - Implementation of algebraic expressions in lavaan?