# Toward multilevel variance decomposition of interactions in non-linear structural equation models

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## Acknowledgment



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## Second order linear differential equation

$$\ddot{x}(t) = \eta x(t) + \zeta \dot{x}(t) \tag{1}$$

- ► x a position (1 dimensional)
- ▶ t time
- ightharpoonup x(t) position as a function of time
- ▶  $\eta$ ,  $\zeta$  parameters to estimate





#### An oscillator

$$\ddot{x}(t) = \eta x(t) + \zeta \dot{x}(t) \tag{2}$$

- ▶ When  $x(t) = \dot{x}(t) = 0$  then the system is at equilibrium
- ▶ When  $\eta < 0$  and  $\eta + \zeta^2/4 < 0$ , x will oscillate
- ▶ Otherwise,  $x \to \pm \inf$  as  $t \to \inf$





## Resilience: Physical and psychological



- ▶ variable thermostats
- ▶ recovery from negative (or positive) emotional shocks





#### As a statistical model

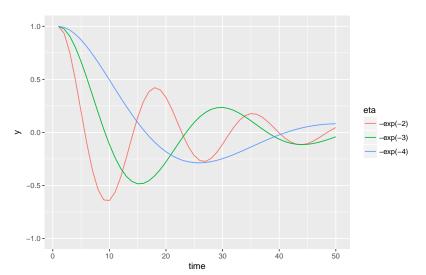
$$\ddot{x}(t) = \eta x(t) + \zeta \dot{x}(t) \tag{3}$$

- ▶ x measured with some noise
- ▶ t known
- $\triangleright \eta, \zeta$  parameters to estimate





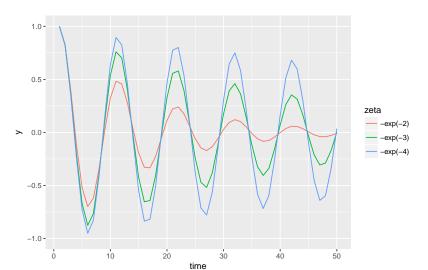
## $\eta$ , frequency







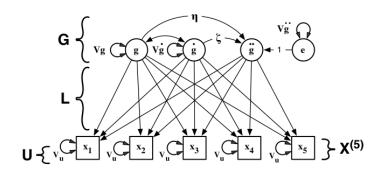
## $\zeta$ , damping







## Path diagram







## Time delay embedding





## Potential multilevel applications

arousal amplitude variance by age decile

- $\eta$ |age decile
- $\blacktriangleright \eta | \text{person}$
- ▶ time

stressor resonance duration by group

- $\zeta|\text{group}$
- $ightharpoonup \zeta|person$
- ▶ time

heredity of frequency and damping





#### What model?

Which model do we need?

Nice if we can stay in a maximum likelihood SEM framework: asymptotically unbiased and minimum variance





## Random slopes

$$Y_{ij} = (\beta_0 + \beta_0 j) + (\beta_1 + \beta_1 j) x_{ij}$$
 (5)

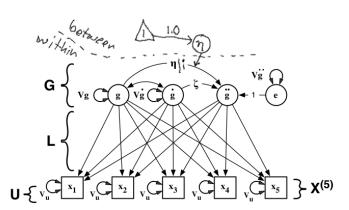
- ightharpoonup i enumerates within groups
- $\triangleright$  j is the group
- ightharpoonup Y is the response
- $\triangleright \beta$  are parameters
- $\blacktriangleright$  x is given (e.g. measurement time)

Product is between a parameter and a given value (x)





## Path diagram



Product is between two latent variables





## Variance of a regression coefficient

$$Var(\eta) \equiv Var \left[ \frac{Cov(\ddot{x}, x)}{Var(x)} \right]$$

$$Var(\zeta) \equiv Var \left[ \frac{Cov(\dot{x}, x)}{Var(x)} \right]$$
(6)

$$Var(\zeta) \equiv Var \left[ \frac{Cov(\dot{x}, x)}{Var(x)} \right]$$
 (7)





#### Mean structure

In SEM, variables are assumed to be centered (mean deviation form).<sup>1</sup>

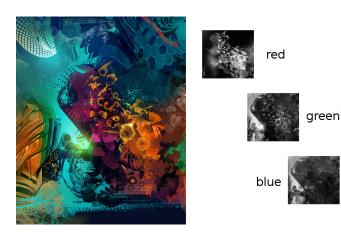
$$E(\xi_1) = E(\xi_2) = 0 \tag{8}$$

$$E(\xi_1 \xi_2) = E(\xi_1) E(\xi_2) + \text{Cov}(\xi_1, \xi_2) = \text{Cov}(\xi_1, \xi_2)$$
 (9)

 $Cov(\xi_1, \xi_2)$  of Equation 9 is non-Normal



## What does a latent interaction look like through a Normal lens?





## Mixture approaches

#### General approach<sup>2</sup>

- ▶ Components represent different outcomes of  $Cov(\xi_1, \xi_2)$
- ▶ Per-row component weights determined by per-row likelihood

Cannot extend to multileve





<sup>&</sup>lt;sup>2</sup>Klein and Moosbrugger (2000); Jedidi, Jagpal, and DeSarbo (1997)

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 $<sup>^2</sup>$ Klein and Moosbrugger (2000); Jedidi et al. (1997)  $\square$  >  $\checkmark \square$  >  $\checkmark$   $\blacksquare$  >  $\checkmark$   $\blacksquare$  >  $\checkmark$ 

## Modeling frameworks

Two-stage maximum likelihood

Bayesian using Monte Carlo sampling





## Two-stage parameter recovery simulation

#### Fully crossed design:

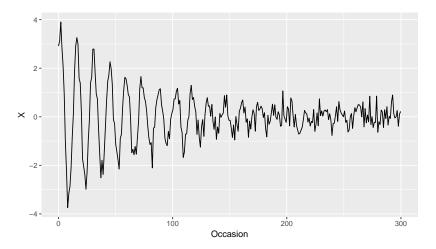
- ightharpoonup number of twins = 100, 200, 400, 800
- ightharpoonup additive genetic variance = 0, 0.25, 0.5, 0.75
- ▶ 300 time points
- ▶ 200 Monte Carlo replications

$$\log(-\eta) \sim \mathcal{N}(-1.6, 0.6) \tag{10}$$

$$\log(-\zeta) \sim \mathcal{N}(-3.0, 0.6) \tag{11}$$

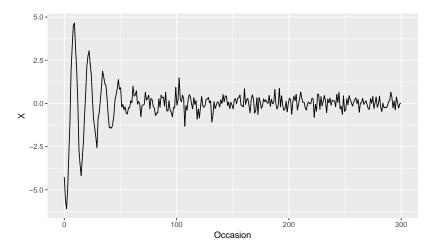






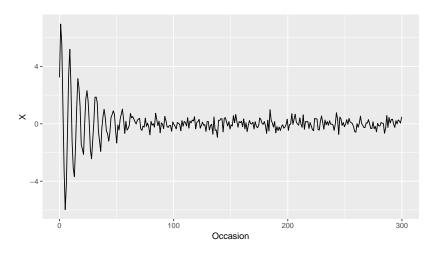






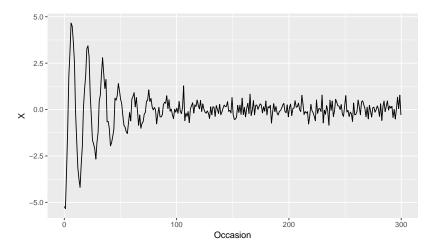








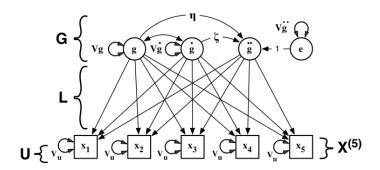








## Path diagram







## Variance decomposition

$$U = \begin{pmatrix} \eta_1 & \eta \zeta_1 & 0 & 0\\ \eta \zeta_1 & \zeta_1 & 0 & 0\\ 0 & 0 & \eta_2 & \eta \zeta_2\\ 0 & 0 & \eta \zeta_2 & \zeta_2 \end{pmatrix}$$
 (12)

$$AE = \begin{pmatrix} A+E & kA \\ kA & A+E \end{pmatrix} \tag{13}$$

$$\Sigma = U + AE \tag{14}$$

- ightharpoonup U is populated with the inverse Hessian
- $\blacktriangleright$  A and E are 2-by-2 covariance matrices
- $\blacktriangleright$  k is 1.0 for MZ and 0.5 for DZ
- means are freely estimated





## 95% interval coverage

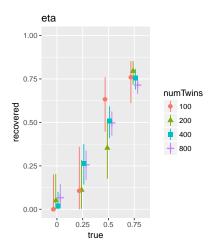
numTwins	agv	$_{ m eta}$	zeta
100	0.00	0.97	0.96
100	0.25	0.97	0.99
100	0.50	0.94	0.97
100	0.75	0.98	0.99
200	0.00	0.98	0.97
200	0.25	0.96	0.98
200	0.50	0.96	1.00
200	0.75	0.96	0.99
400	0.00	0.96	0.98
400	0.25	0.96	0.99
400	0.50	0.94	0.99
400	0.75	0.95	1.00
800	0.00	0.92	0.94
800	0.25	0.91	0.97
800	0.50	0.92	1.00
800	0.75	0.94	1.00

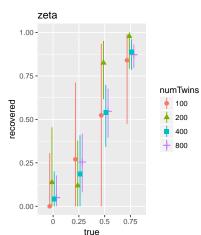






## One replication

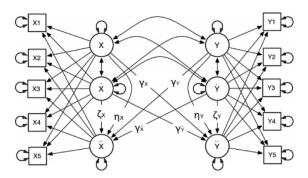








#### Future Directions



 $\label{eq:Figure 3.} Figure \ 3. \quad \hbox{Coupled latent differential equation model (coupled LDE)}.$ 

Accounting for a common environment?  $\!\!^3$ 



<sup>&</sup>lt;sup>3</sup>Hu, Boker, Neale, and Klump (2014)

### **Future Directions**



Full Bayesian





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