Developmental Models

Lindon Eaves, Nathan Gillespie & Brad Verhulst
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Why run longitudinal models?
Why run longitudinal models?

Map changes in the magnitude of genetic & environmental influence across time

ID enduring versus time dependent genetic or environmental risks

Improve power to detect A, C & E
Various models for analysing longitudinal data

1. Cholesky Decomposition
2. Latent growth curve model
3. Auto-regression model
4. Dual Change Score model

Models imply that you look at your variance-covariance matrix & have a theory about the nature of change.
Atheoretical longitudinal model

1. Cholesky Decomposition

Advantages
- Logical: organized such that all factors are constrained to impact later, but not earlier time points
- Requires few assumptions: can predict any pattern of change

Disadvantages
- Atheoretical: no explicit hypothesis of change. Describes patterns of change without accounting for them in terms of one or more simpler and, potentially more informative theoretical possibilities
Theoretical longitudinal models
After inspecting your observed variances-covariances in your repeated measures:

1. **UNFOLDING** Individual genetic and/or environmental differences in inherent growth patterns with age - *Latent growth curve effects*

2. **ACCUMULATION** of individual genetic and/or environmental differences, which are more or less persistent - *Autoregressive effects*

3. Latent growth curve model + Auto-regression model ("**Dual Change Score model:**")

**NB: INSPECT DATA**
1. Latent growth curve model
AKA "random regression", "hierarchial mixed" or "latent growth curve" models

What does the LGC model predict?

1. Variation in latent true scores at each time point is a function of where you begin, or what you begin with, in terms of individual genetic and environmental differences....
2. Variation in latent true scores at each time point is also a function of **UNFOLDING** individual genetic and environmental differences, over time,

Unfolding may involve linear and non-linear rates of change.
Latent growth modelling
Developmental change = **UNFOLDING** of inherent, random genetic & environmental differences in the level & rates of change in behavior over time

Model corresponds to special cases of the **factor model** in which factor loadings from the level (intercept) & change factors are functions of the coefficients of *a priori* contrasts on the levels of age at which the repeated measures were taken
Latent growth modelling
Recap – common pathway

\[
\begin{align*}
A_C &= a_{11} \\
\text{Common Path} &= f_{11} \& f_{21} \\
\text{Phenotype 1} &= a_{s11} \\
\text{Phenotype 2} &= a_{s22} \\
\text{Phenotype 3} &= a_{s33}
\end{align*}
\]
Latent growth modeling
Recap – common pathway

# Algebra for expected variance/covariance

covMZ <- mxAlgebra( expression = rbind( cbind( A+C+E, A+C),
                                       cbind( A+C, A+C+E)), name = "expCovMZ" )

covMZ <- mxAlgebra( expression = rbind( cbind( A+C+E , 0.5%*%A+C),
                                       cbind(0.5%*%A+C , A+C+E)), name = "expCovMZ" )

<table>
<thead>
<tr>
<th></th>
<th>T₁</th>
<th>T₂</th>
</tr>
</thead>
<tbody>
<tr>
<td>MZ</td>
<td>A+C+E</td>
<td>A+C</td>
</tr>
<tr>
<td>T₁</td>
<td>A+C</td>
<td>A+C+E</td>
</tr>
<tr>
<td>T₂</td>
<td>A+C</td>
<td>A+C+E</td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>T₁</th>
<th>T₂</th>
</tr>
</thead>
<tbody>
<tr>
<td>DZ</td>
<td>A+C+E</td>
<td>0.5@A+C</td>
</tr>
<tr>
<td>T₁</td>
<td>0.5@A+C</td>
<td>A+C+E</td>
</tr>
<tr>
<td>T₂</td>
<td>A+C+E</td>
<td>A+C+E</td>
</tr>
</tbody>
</table>
Latent growth modelling
Add another latent factor fix the factor loadings

\[
\begin{pmatrix}
1 & 0 \\
1 & 1 \\
1 & 2
\end{pmatrix}
\begin{pmatrix}
a_{11} \\ a_{21} \\ a_{22}
\end{pmatrix}
\begin{pmatrix}
a_{11} & a_{21} & a_{22}
\end{pmatrix}
+ \begin{pmatrix}
a_{S11} & a_{S21} & a_{S22} \\ a_{S21} & a_{S22} & a_{S32} \\ a_{S22} & a_{S32} & a_{S33}
\end{pmatrix}
= A
\]

# Matrix A to compute additive genetic variance components
\[
\text{covA} <- \text{mxAlgebra( expression=r1 \\ r2 \\ r3, name="A")}
\]

\[
a_{11}^2 + a_{S11}^2 = A_{\text{var time 1}}
\]
\[
a_{11}^2 + 2a_{21}a_{11} + a_{21}^2 + a_{22}^2 + a_{S22}^2 = A_{\text{var time 2}}
\]
\[
a_{11}^2 + 2a_{21}a_{11} + 2a_{21}a_{11} + 2a_{22}^2 + a_{S33}^2 = A_{\text{var time 3}}
\]
Latent growth modelling

\[ \eta_1 \rightarrow \eta_2 \rightarrow \eta_3 \rightarrow \eta_4 \rightarrow \eta_5 \]

\[ \text{Twin Res. 2000 Sep;3(3):165-77.} \]

\textbf{Structured latent growth curves for twin data.}

Neale MC, McArdle JJ.

Figure 7. Resource level of logistic growth model with \( r = 0.1 \) and \( K = 10,000 \).
2. Auto-regression modelling
AKA “simplex modelling” and “Sh%t-St%cks model”

Example means

<table>
<thead>
<tr>
<th>t1_1</th>
<th>t1_2</th>
<th>t1_3</th>
<th>t1_4</th>
<th>t1_5</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.0026</td>
<td>1.3774</td>
<td>3.5220</td>
<td>5.8020</td>
<td>7.7550</td>
</tr>
</tbody>
</table>

Example covariation matrix

<table>
<thead>
<tr>
<th>t1_1</th>
<th>t1_2</th>
<th>t1_3</th>
<th>t1_4</th>
<th>t1_5</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.27</td>
<td>0.78</td>
<td>0.49</td>
<td>0.16</td>
<td>-0.08</td>
</tr>
<tr>
<td>0.78</td>
<td>2.37</td>
<td>2.06</td>
<td>1.52</td>
<td>0.08</td>
</tr>
<tr>
<td>0.49</td>
<td>2.06</td>
<td>3.95</td>
<td>3.59</td>
<td>2.45</td>
</tr>
<tr>
<td>0.16</td>
<td>1.52</td>
<td>3.59</td>
<td>6.52</td>
<td>8.64</td>
</tr>
<tr>
<td>-0.08</td>
<td>0.08</td>
<td>2.45</td>
<td>8.64</td>
<td>21.03</td>
</tr>
</tbody>
</table>

Correlation matrix

<table>
<thead>
<tr>
<th>t1_1</th>
<th>t1_2</th>
<th>t1_3</th>
<th>t1_4</th>
<th>t1_5</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.00</td>
<td>0.45</td>
<td>0.22</td>
<td>0.06</td>
<td>-0.02</td>
</tr>
<tr>
<td>0.45</td>
<td>1.00</td>
<td>0.67</td>
<td>0.39</td>
<td>0.01</td>
</tr>
<tr>
<td>0.22</td>
<td>0.67</td>
<td>1.00</td>
<td>0.71</td>
<td>0.27</td>
</tr>
<tr>
<td>0.06</td>
<td>0.39</td>
<td>0.71</td>
<td>1.00</td>
<td>0.74</td>
</tr>
<tr>
<td>-0.02</td>
<td>0.01</td>
<td>0.27</td>
<td>0.74</td>
<td>1.00</td>
</tr>
</tbody>
</table>

Cross-temporal correlations within subjects arise because time specific sources of individual differences are more or less persistent time, and may, **ACCUMULATE** during development.

Giving rise to a developmental increase in genetic and/or environmental variance, and increased correlations between adjacent measures.
Auto-regression models

\[ \psi_1 \Rightarrow \eta_1 \rightarrow \beta_{21} \eta_2 \rightarrow \beta_{32} \eta_3 \rightarrow \beta_{43} \eta_4 \rightarrow \beta_{54} \eta_5 \]

\[ \epsilon_1 \rightarrow \text{res}_a \rightarrow \epsilon_2 \rightarrow \text{res}_a \rightarrow \epsilon_3 \rightarrow \text{res}_a \rightarrow \epsilon_4 \rightarrow \text{res}_a \rightarrow \epsilon_5 \rightarrow \text{res}_a \]

\[ \Psi \text{ Psi} \quad \text{B Beta} \quad \Lambda \text{ Lambda} \quad \epsilon \text{ Epsilon} \]
Enables partitioning of variation at each time point into:

- Transient genetic & environmental risks unique to each occasion
- Persistent, enduring genetic & environmental risk factors

Examples?

- Snow-ball
- Vocabulary acquisition
- Emotional baggage


matl <- mxMatrix( type="Iden", nrow=nv, ncol=nv, name="I" )

pathAt <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=tFree, values=ValsA, labels=AtLabs, name="at" )

pathAi <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=TRUE, values=iVals, labels=AiLabs, name="ai" )

covA <- mxAlgebra( expression=solve(I - at) %% (ai %% t(ai)), name="A" )
matl <- mxMatrix( type="Iden", nrow=nv, ncol=nv, name="l" )
pathEt <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=tFree, values=tValsE, labels=EtLabs, name="et" )
pathEi <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=TRUE, values=iVals, labels=EiLabs, name="ei" )
pathMe <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=TRUE, labels=c("u","u","u"), values=5, name="me" )
covE <- mxAlgebra( expression=solve( l-et ) \%\% (ei \%\% t(ei))+ (me \%\% t(me)), name="E" )
Auto-regressive model examples
Dual Change Score model
Latent growth curve model + Auto-regression model


A theory of developmental change in quantitative phenotypes applied to cognitive development.
Eaves LJ, Long J, Heath AC.

Fig. 1. Model for longitudinal measures of a continuous trait.
Dual Change Score model
Fig. 3 Structural model of developmental change attributable to auto-regressive and growth curve components. Note: The diagram includes both constant and “change” random effects on growth. The model is easily elaborated to reflect higher order components of growth and can be applied to genetic or environmental components of developmental change or both.
Dual Change Score model
Lisrel model (Jöreskog & Sörbom, 1996) to estimate expectation covariance:

\[ \Lambda \times (I - B) \sim \times (\Gamma \times (\phi) \times \Gamma' + \Psi) \times (I - B) \sim' \times \Lambda' + \epsilon \]
\[ \Lambda x (I-B)^\sim x (\Gamma x \Phi x \Gamma' + \Psi) x (I-B)^\sim' x \Lambda' + \epsilon \]
\[ \Lambda x (I-B) \sim x (\Gamma x \phi x \Gamma' + \Psi) x (I-B)' x \Lambda' + \epsilon \]

gamma <- mxMatrix( type="Full", 
nrow=nFactors, ncol=nGrow, 
free=F, values=c(1,1,1,1,-2,-1,0,1,2,2,-1,-2,-1,2), 
labels=Glabs, name="gamma" )

\[
\begin{array}{ccc}
[1,] & 1 & -2 & 2 \\
[2,] & 1 & -1 & -1 \\
[3,] & 1 & 0 & -2 \\
[4,] & 1 & 1 & -1 \\
[5,] & 1 & 2 & 2 \\
\end{array}
\]
\[ \Lambda x (I-B) \sim x (\Gamma x \phi x \Gamma' + \Psi) x (I-B) \sim' x \Lambda' + \epsilon \]

\[
\psi_2 \quad i_{a_{22}} \quad \eta_1 \quad \text{Time 1} \\
\psi_3 \quad i_{a_{33}} \quad \eta_2 \quad \text{Time 2} \\
\psi_4 \quad i_{a_{44}} \quad \eta_3 \quad \text{Time 3} \\
\psi_5 \quad i_{a_{55}} \quad \eta_4 \quad \text{Time 4} \\
\psi \quad \eta_5 \quad \text{Time 5}
\]

```r
gamma <- mxMatrix(type = "Diag", 
nrow = nFactors, ncol = nFactors, 
free = c(F,T,T,T,T), 
labels = psi_lab_a, 
values = c(0,1,1,1,1)$labels, 
name = "psi_a"
```
\[ \Lambda x (I - B) \sim x (\Gamma x \phi x \Gamma' + \Psi) x (I - B) \sim' x \Lambda' + \epsilon \]

\[ \eta_1 \xrightarrow{\beta_{21}} \eta_2 \xrightarrow{\beta_{32}} \eta_3 \xrightarrow{\beta_{43}} \eta_4 \xrightarrow{\beta_{54}} \eta_5 \]

beta <- mxMatrix(type="Full",
   nrow = nFactors, ncol = nFactors,
   free = betaF, values = betaS,
   ubound = 1, lbound = -1,
   labels = betalab,
   name = "beta")

\[
\begin{array}{cccccc}
[1,] & NA & NA & NA & NA & NA \\
[2,] & "b21" & NA & NA & NA & NA \\
[3,] & NA & "b32" & NA & NA & NA \\
[4,] & NA & NA & "b43" & NA & NA \\
[5,] & NA & NA & NA & "b54" & NA \\
\end{array}
\]
\[ \Lambda \times (I-B) \sim x (\Gamma \times \phi \times \Gamma' + \Psi) \times (I-B)^\prime \times \Lambda' + \epsilon \]

\[\lambda \leftarrow mxMatrix(type="Full", nrow = nVariables, ncol = nFactors, free = loadF, values = loadS, name = "lambda")\]

\[
\begin{pmatrix}
1 & 0 & 0 & 0 & 0 \\
0 & 1 & 0 & 0 & 0 \\
0 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 1
\end{pmatrix}
\]
\[ \Lambda \times (I-B) \sim \times (\Gamma \times \phi \times \Gamma' + \Psi) \times (I-B) \sim' \times \Lambda' + \epsilon \]
\[ \Lambda \times (I-B)^{\sim} \times (\Gamma \times \phi \times \Gamma' + \Psi) \times (I-B)^{\sim'} \times \Lambda' + \epsilon \]
\[(\Lambda \times ( (I-B)^\sim \times \Gamma \times \mu ) )'\]

FacMean <- mxAlgebra(solve(I-beta) ** gamma ** GroMean, name = "FacMean")
ManMean <- mxAlgebra(t(lamba ** FacMean), "ManMean")
Pracatica
Dual_change_score_model.R