

Longitudinal Structural Equation Modeling

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Summer School – Using R for personality research

August 23–28, 2014

Bertinoro, Italy

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1 Longitudinal Structural Equation Modeling

1.1 Longitudinal Data Analysis

- longitudinal data analysis is the analysis of *change* in an outcome (or several outcomes) over time
- longitudinal data analysis studies the changes within individuals and the factors that influence change
- longitudinal data is collected in almost every discipline: health, social and behavioural sciences, biological and agricultural sciences, economics, marketing, ...
- data is collected in studies using longitudinal designs
- longitudinal data are (by nature) multivariate, and have a complex random-error structure that must be accounted for in the analysis

simple dataset with 4 time points

- 12 subjects, each one has 4 scores on the ‘McCarthy Scales of Children’s Abilities’ (source: Maxwell & Delaney, 2004, Table 11.5)
- 4 time points: 30, 36, 42 and 48 months

```
> MD11.5 <-  
+   read.table("http://www.da.ugent.be/datasets/MaxwellDelaney11.5.dat",  
+             header=TRUE)  
> MD11.5
```

	age30	age36	age42	age48
1	108	96	110	122
2	103	117	127	133
3	96	107	106	107
4	84	85	92	99
5	118	125	125	116
6	110	107	96	91
7	129	128	123	128
8	90	84	101	113
9	84	104	100	88
10	96	100	103	105
11	105	114	105	112
12	113	117	132	130

data characteristics: the mean structure

- the observed (within-subjects) cell means:

```
> colMeans(MD11.5)
```

```
age30 age36 age42 age48  
  103   107   110   112
```

- we can consider the 4 time points as the 4 levels of a within-subjects factor 'A'
 - typical research question: is there a (significant) difference between the four time points (on average)?
- or we can consider 'time' (in months) as a continuous variable, with four observed values (30, 36, 42 and 48 months)
 - typical research question: is there a (significant) linear/quadratic/. . . effect of 'time'?
- and last but not least: what about individual differences? do all subjects follow the same pattern?

data characteristics: the covariance structure

- often, the focus of the analysis is on the means; however, we should also take into account the (complex) correlation structure of the data

```
> round(cor(MD11.5), 2)
```

```
      age30 age36 age42 age48
age30  1.00  0.79  0.70  0.60
age36  0.79  1.00  0.76  0.47
age42  0.70  0.76  1.00  0.85
age48  0.60  0.47  0.85  1.00
```

- the variances are important too, so in practice, we need to model the variance-covariance matrix:

```
> round(cov(MD11.5), 1)
```

```
      age30 age36 age42 age48
age30 188.0 154.4 127.4 121.2
age36 154.4 200.5 143.6  97.5
age42 127.4 143.6 178.0 168.1
age48 121.2  97.5 168.1 218.0
```

data characteristics: the covariance structure (2)

- typical research questions related to variances/covariances:
 - do the variances change over time?
 - can we detect a particular structure/pattern in the covariance structure?
- modeling the covariances in an adequate way is an important component of longitudinal data analysis

plotting the data

- learn how to plot your data: both average trends, individual trends, . . .
- you may need to ‘reshape’ your data (from wide to long format, or from long to wide format)

reshape data from 'wide' to 'long' format + plot

```
> library(reshape)
> MD11.5$subject <- factor(paste("subject", 1:nrow(MD11.5), sep=""))
> MD11.5.long <- melt(MD11.5, id.var="subject", variable_name="A")
> MD11.5.long$age <- as.numeric(MD11.5.long$A) - 1
> names(MD11.5.long)[3] <- "y"
> head(MD11.5.long)
```

	subject	A	y	age
1	subject1	age30	108	0
2	subject2	age30	103	0
3	subject3	age30	96	0
4	subject4	age30	84	0
5	subject5	age30	118	0
6	subject6	age30	110	0

```
> library(lattice)
> p1 <- xyplot(y ~ A, groups=subject, data=MD11.5.long, type=c("l", "g"))
> p2 <- xyplot(y ~ A, data=MD11.5.long, type=c("a", "g"))

> print(p1, split=c(1,1,1,2), more=TRUE); print(p2, split=c(1,2,1,2))
```


classic analysis: paired t-test

- Student's (1908) paired t -test
- only two time-points (say, age30 and age36)
- we treat 'age' as categorical
- R code:

```
> t.test(MD11.5$age30, MD11.5$age36, paired=TRUE)
```

Paired t-test

```
data: MD11.5$age30 and MD11.5$age36
t = -1.551, df = 11, p-value = 0.1492
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -9.676458  1.676458
sample estimates:
mean of the differences
      -4
```

classic analysis: repeated measures ANOVA

- one of the earliest statistical methods for the analysis of change
- based on the analysis of variance (ANOVA) paradigm, as originally developed by R. A. Fisher
- the mixed-effects ANOVA model (random intercept only):

$$Y_{ij} = \mathbf{X}'_{ij}\boldsymbol{\beta} + b_i + e_{ij}, \quad i = 1, \dots, N, \quad j = 1, \dots, J$$

- N is the number of observations; J is the number of repeated measures
 - \mathbf{X}_{ij} is the design matrix; $\boldsymbol{\beta}$ a vector of regression parameters
 - b_i is a random intercept; $b_i \sim N(0, \sigma_b^2)$
 - $e_{ij} \sim N(0, \sigma_e^2)$
- the implied ‘compound symmetry’ structure for the covariance (of the repeated measures within an observation) is very restrictive

- R code:

```
> fit <- aov(y ~ A + Error(subject), data=MD11.5.long)
> summary(fit)
```

```
Error: subject
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Residuals	11	6624	602.2		

```
Error: Within
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
A	3	552	184.00	3.027	0.0432 *
Residuals	33	2006	60.79		

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- corrections (to the degrees of freedom of the F -test) have been proposed by Greenhouse & Geisser (1959) and Huynh & Feldt (1976)
 - $F(1.83, 20.12) = 3.027, p = 0.075$ (Greenhouse & Geisser)
 - $F(2.18, 23.94) = 3.027, p = 0.063$ (Huynh & Feldt)

sidenote: compound symmetry

- a covariance-matrix has a ‘compound symmetry’ structure if
 1. all variances are equal: $\text{Var}(Y_l) = \text{Var}(Y_m)$ for every pair (l, m)
 2. all covariances are equal: $\text{Cov}(Y_l, Y_m) = \rho$ for every pair $l \neq m$
- example:

```
> C <- matrix(2, ncol=4, nrow=4)
> diag(C) <- 10
> C
```

```
      [,1] [,2] [,3] [,4]
[1,]  10   2   2   2
[2,]   2  10   2   2
[3,]   2   2  10   2
[4,]   2   2   2  10
```

classic analysis: repeated measures MANOVA

- different tradition: repeated measures MANOVA (Box, 1950; Geisser, 1963; Potthof & Roy, 1964)
- based on the multivariate linear model:

$$\mathbf{Y}_i = \mathbf{X}'_i \boldsymbol{\beta} + \mathbf{e}_i$$

- error covariance (of the repeated measures) is ‘unstructured’ (all elements are freely estimated)
- multivariate tests (Wilks’ lambda)
- no random effects
- the original response vector is linearly transformed into a ‘difference’ vector, reflecting the fact that we are interested in the differences among the responses; different types of transformations are possible

- R code:

```
> d12 <- c(1, -1, 0, 0)
> d23 <- c(0, 1, -1, 0)
> d34 <- c(0, 0, 1, -1)
> M <- cbind(d12, d23, d34)
> M
```

```
      d12 d23 d34
[1,]    1    0    0
[2,]   -1    1    0
[3,]    0   -1    1
[4,]    0    0   -1
```

```
> fit <- lm( cbind(age30, age36, age42, age48) ~*~ M ~ 1, data=MD11.5)
> anova(fit, test="Wilks")
```

Analysis of Variance Table

```
              Df  Wilks approx F num Df den Df Pr(>F)
(Intercept)  1 0.57251   2.2401      3      9 0.1528
Residuals   11
```

limitations of the classic approaches

- issues with repeated measures ANOVA:
 - correlations among repeated measurement often decay with increasing separation in time
 - the assumption of constant variance across time is often unrealistic
 - complete data only (no missing values)
- issues with repeated measures MANOVA:
 - balanced data only (everyone is measured at the same time points)
 - complete data only (no missing values)
 - no time-varying covariates
- time is treated as an (unordered) categorical variable

the linear mixed model

- the linear mixed model (Laird-ware notation):

$$\mathbf{y}_i = \mathbf{X}_i\boldsymbol{\beta} + \mathbf{Z}_i\mathbf{b}_i + \boldsymbol{\epsilon}_i \quad i = 1, 2, \dots, N$$

- more flexibility in the covariance structure for $\boldsymbol{\epsilon}_i$
- no restrictions on the design matrices (\mathbf{X}_i and \mathbf{Z}_i)
- efficient estimation using likelihood-based models (ML and REML)
- can handle unbalanced data, missing data, time-varying covariates, time-invariant covariates
- outside the SEM world, this is the golden standard
- special case: growth curve models (Wishart 1938, Box 1950, Potthof & Roy, 1964)
- can be generalized to account for non-Gaussian responses

- R code:

```
> library(lme4)
> fit.lmer <- lmer(y ~ 1 + age + (1 + age | subject), data=MD11.5.long)
> summary(fit.lmer)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: y ~ 1 + age + (1 + age | subject)
Data: MD11.5.long
```

```
REML criterion at convergence: 345.5595
```

```
Random effects:
```

Groups	Name	Variance	Std.Dev.	Corr
subject	(Intercept)	169.85	13.033	
	age	14.53	3.812	-0.41
Residual		34.82	5.901	

```
Number of obs: 48, groups: subject, 12
```

```
Fixed effects:
```

	Estimate	Std. Error	t value
(Intercept)	103.500	4.023	25.726
age	3.000	1.338	2.241

```
Correlation of Fixed Effects:
```

```
(Intr)
age -0.475
```

1.2 The SEM approach to longitudinal data analysis

- long history, mostly for ‘balanced data’: same number of time points for each observation
 - repeated measures models
 - panel models, simplex models, autoregressive models
 - growth curve models (random coefficient models)
 - hybrid models (growth curve + autoregressive)
 - latent-state, latent-trait models
 - latent difference scores models
 - ...
- multilevel SEM
 - combines ‘mixed models’ with path analysis and latent variables
 - allows for unbalanced data
 - relatively new, active research; major software package: Mplus

1.3 Repeated measures models (using SEM)

- how do the *means* change over time (on average)
- we treat ‘time’ as a categorical variable with t levels
- SEM version of repeated measures ANOVA
- but much more flexible:
 - the (error) covariance structure is not restricted to compound symmetry
 - we can use latent variables (instead of observed variables), and study the differences between latent means
- if we use latent variables, we first need to establish measurement invariance across time

the naive approach

- what is wrong with this approach?

```
> library(lavaan)
> model <- '
+   age30 ~ i1*1
+   age36 ~ i2*1
+   age42 ~ i3*1
+   age48 ~ i4*1
+
+   age30 ~~ v1*age30
+   age36 ~~ v2*age36
+   age42 ~~ v3*age42
+   age48 ~~ v4*age48
+ '
> fit <- lavaan(model, data = MD11.5)
> lavTestWald(fit, constraints = 'i1 == i2; i2 == i3; i3 == i4')
```

`$stat`
[1] 3.058521

`$df`
[1] 3

`$p.value`
[1] 0.3826902

adding correlated residuals

- we allow the residuals to be correlated:

```
> model <- '  
+   age30 ~ i1*1; age36 ~ i2*1; age42 ~ i3*1; age48 ~ i4*1  
+  
+   age30 ~~ v1*age30  
+   age36 ~~ v2*age36  
+   age42 ~~ v3*age42  
+   age48 ~~ v4*age48  
+  
+   age30 ~~ age36 + age42 + age48  
+   age36 ~~ age42 + age48  
+   age42 ~~ age48  
+ '  
> fit <- lavaan(model, data = MD11.5)  
> lavTestWald(fit, constraints = 'i1 == i2; i2 == i3; i3 == i4')  
  
$stat  
[1] 8.960391  
  
$df  
[1] 3  
  
$p.value  
[1] 0.02982217
```

alternative test: LRT

- specify a null model with equal intercepts/means

```

> model.equal <- '
+   age30 ~ i1*1; age36 ~ i1*1; age42 ~ i1*1; age48 ~ i1*1
+
+   age30 ~~ v1*age30
+   age36 ~~ v2*age36
+   age42 ~~ v3*age42
+   age48 ~~ v4*age48
+
+   age30 ~~ age36 + age42 + age48
+   age36 ~~ age42 + age48
+   age42 ~~ age48
+ '
> fit.equal <- lavaan(model.equal, data = MD11.5)
> anova(fit, fit.equal)

```

Chi Square Difference Test

	Df	AIC	BIC	Chisq	Chisq diff	Df diff	Pr(>Chisq)
fit	0	367.65	374.44	0.0000			
fit.equal	3	368.34	373.68	6.6927	6.6927	3	0.08236 .

Signif. codes:	0	***	0.001	**	0.01	*	0.05 . 0.1 1

compound symmetry

- the classical repeated measures ANOVA implies a compound symmetry structure for the residuals:

```
> model <- '
+   age30 ~ i1*1; age36 ~ i2*1; age42 ~ i3*1; age48 ~ i4*1
+
+   age30 ~~ v1*age30
+   age36 ~~ v1*age36
+   age42 ~~ v1*age42
+   age48 ~~ v1*age48
+
+   age30 ~~ c*age36 + c*age42 + c*age48
+   age36 ~~ c*age42 + c*age48
+   age42 ~~ c*age48
+ '
> fit <- lavaan(model, data = MD11.5)
> summary(fit)
```

lavaan (0.5-17.700) converged normally after 21 iterations

Number of observations	12
Estimator	ML
Minimum Function Test Statistic	17.066
Degrees of freedom	8

P-value (Chi-square) 0.029

Parameter estimates:

Information		Expected			
Standard Errors		Standard			
		Estimate	Std.err	Z-value	P(> z)
Covariances:					
age30	~~				
age36	(c)	124.069	56.434	2.198	0.028
age42	(c)	124.069	56.434	2.198	0.028
age48	(c)	124.069	56.434	2.198	0.028
age36	~~				
age42	(c)	124.069	56.434	2.198	0.028
age48	(c)	124.069	56.434	2.198	0.028
age42	~~				
age48	(c)	124.069	56.434	2.198	0.028
Intercepts:					
age30	(i1)	103.000	3.871	26.610	0.000
age36	(i2)	107.000	3.871	27.643	0.000
age42	(i3)	110.000	3.871	28.418	0.000
age48	(i4)	112.000	3.871	28.935	0.000
Variances:					
age30	(v1)	179.792	57.193		
age36	(v1)	179.792	57.193		

```

age42 (v1) 179.792 57.193
age48 (v1) 179.792 57.193

```

```

> model.equal <- '
+   age30 ~ i1*1; age36 ~ i1*1; age42 ~ i1*1; age48 ~ i1*1
+
+   age30 ~~ v1*age30
+   age36 ~~ v1*age36
+   age42 ~~ v1*age42
+   age48 ~~ v1*age48
+
+   age30 ~~ c*age36 + c*age42 + c*age48
+   age36 ~~ c*age42 + c*age48
+   age42 ~~ c*age48
+ '
> fit.equal <- lavaan(model.equal, data = MD11.5)
> anova(fit, fit.equal)

```

Chi Square Difference Test

	Df	AIC	BIC	Chisq	Chisq diff	Df diff	Pr(>Chisq)
fit	8	368.71	371.62	17.066			
fit.equal	11	371.47	372.92	25.817	8.751	3	0.03279 *

Signif. codes:	0	***	0.001	**	0.01	*	0.05 . 0.1 1

- compare this to:

```
> fit.aov <- aov(y ~ 1 + A + Error(subject), data=MD11.5.long)
> summary(fit.aov)
```

Error: subject

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Residuals	11	6624	602.2		

Error: Within

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
A	3	552	184.00	3.027	0.0432 *
Residuals	33	2006	60.79		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

- here we get an F-statistic, while lavaan is using a chi-square statistic

alternative parameterization, using random intercept

- instead of specifying the compound symmetry structure directly, we can postulate a random effect (random intercept)
- this is the ‘growth curve’ approach

```
> model.A <- '  
+   int =~ 1*age30 + 1*age36 + 1*age42 + 1*age48  
+  
+   # intercepts (fixed effects)  
+   int ~ 0  
+   age30 ~ i1*1  
+   age36 ~ i2*1  
+   age42 ~ i3*1  
+   age48 ~ i4*1  
+  
+   # random intercept  
+   int ~~ int  
+  
+   # force same variance for all (compound symmetry)  
+   age30 ~~ v1*age30  
+   age36 ~~ v1*age36  
+   age42 ~~ v1*age42  
+   age48 ~~ v1*age48  
+ '
```

```
> fit.A <- lavaan(model.A, data=MD11.5)
> summary(fit.A, standardized = TRUE)
```

lavaan (0.5-17.700) converged normally after 21 iterations

Number of observations	12
Estimator	ML
Minimum Function Test Statistic	17.066
Degrees of freedom	8
P-value (Chi-square)	0.029

Parameter estimates:

Information				Expected		
Standard Errors				Standard		
	Estimate	Std.err	Z-value	P(> z)	Std.lv	Std.all
Latent variables:						
int =~						
age30	1.000				11.139	0.831
age36	1.000				11.139	0.831
age42	1.000				11.139	0.831
age48	1.000				11.139	0.831
Intercepts:						
int	0.000				0.000	0.000
age30 (i1)	103.000	3.871	26.610	0.000	103.000	7.682

age36	(i2)	107.000	3.871	27.643	0.000	107.000	7.980
age42	(i3)	110.000	3.871	28.418	0.000	110.000	8.204
age48	(i4)	112.000	3.871	28.935	0.000	112.000	8.353

Variances:

int		124.069	56.434			1.000	1.000
age30	(v1)	55.722	13.134			55.722	0.310
age36	(v1)	55.722	13.134			55.722	0.310
age42	(v1)	55.722	13.134			55.722	0.310
age48	(v1)	55.722	13.134			55.722	0.310

> fitted(fit)\$cov

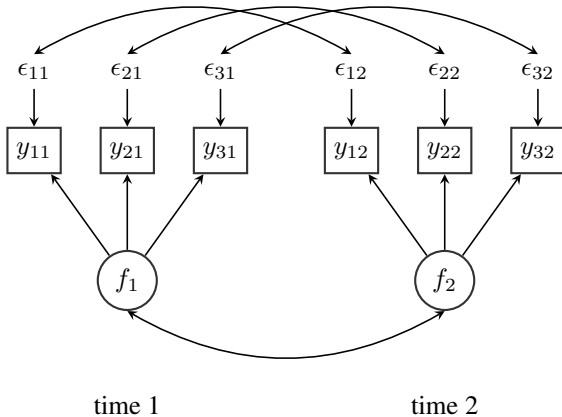
	age30	age36	age42	age48
age30	179.792			
age36	124.069	179.792		
age42	124.069	124.069	179.792	
age48	124.069	124.069	124.069	179.792

repeated measures ANOVA in SEM

- we can mimic the classical repeated measures ANOVA in a SEM framework
- using two time-points only, this is the SEM equivalent of the paired t -test
- but we can relax the compound symmetry restriction
 - we can allow for an unstructured covariance structure
 - or we could impose an autoregressive AR(1) structure
 - ...
- but above all, we can replace the observed variables by latent variables

repeated measures using latent variables

- example with 2 time points:



comments

- first of all, we need to establish measurement invariance across time points
 - it is tempting to do this using a multiple group analysis, using the time points as group levels, but this will not allow us to specify correlated residuals among the corresponding variables (and the time points are not independent)
 - therefore, we need to use labels for the different time points (for factor loadings and intercepts of observed variables), and impose the equality constraints by using the same label for the different time points
- since we wish to compare the latent means, we need ‘strong invariance’:
 - equal factor loadings
 - equal intercepts/means of the observed variables
- usually, we allow the residuals variances of the corresponding variables across time to be correlated

- if we have more than two time points, we can allow for all possible correlations among the repeated latent variables (this corresponds to the ‘unstructured’ assumption)
- the latent mean/intercept of the first time point is fixed to zero, while we estimate the latent mean/intercept of the other time points (although alternative coding schemes are possible)

example

- example from Todd Little's book (Longitudinal SEM, 2013): table 3.8 and figure 3.10 (but with equality constraints)
- the latent variable 'positive affect' is measured by three indicators (Glad, Cheerful and Happy): 823 children in grades 7 en 8 responded to questions like "In the past 2 weeks, I have felt . . ." (with 4 response categories: almost never, seldom, often, almost always)
- measured at two time points: in the fall of two successive school years
- main question: is there a significant difference in (self-reported) 'positive affect' between the two time points?
- this is the SEM equivalent of the paired t -test

R code: reading in the sample statistics

```
> MEAN <- c(3.06893, 2.92590, 3.11013, 3.02577, 2.85656, 3.09346)
> SDS <- c(0.84194, 0.88934, 0.83470, 0.84081, 0.90864, 0.83984)
> lower <- '
+ 1.00000
+ 0.55226 1.00000
+ 0.56256 0.60307 1.00000
+ 0.31889 0.35898 0.27757 1.00000
+ 0.24363 0.35798 0.31889 0.56014 1.00000
+ 0.32217 0.36385 0.32072 0.56164 0.59738 1.00000 '
> COV <- getCov(lower, sds=SDS, names = c("Glad1", "Cheer1", "Happy1",
+ "Glad2", "Cheer2", "Happy2"))
> COV
```

	Glad1	Cheer1	Happy1	Glad2	Cheer2	Happy2
Glad1	0.7088630	0.4135162	0.3953488	0.2257459	0.1863819	0.2278048
Cheer1	0.4135162	0.7909256	0.4476782	0.2684330	0.2892800	0.2717608
Happy1	0.3953488	0.4476782	0.6967241	0.1948053	0.2418595	0.2248294
Glad2	0.2257459	0.2684330	0.1948053	0.7069615	0.4279434	0.3965998
Cheer2	0.1863819	0.2892800	0.2418595	0.4279434	0.8256266	0.4558680
Happy2	0.2278048	0.2717608	0.2248294	0.3965998	0.4558680	0.7053312

R code: setting up a longitudinal CFA

```
> model <- '  
+   posAffect1 =~ 1*Glad1 + ch*Cheer1 + ha*Happy1  
+   posAffect2 =~ 1*Glad2 + ch*Cheer2 + ha*Happy2  
+  
+   # intercepts  
+   Glad1 ~ igl*1  
+   Glad2 ~ igl*1  
+   Cheer1 ~ ich*1  
+   Cheer2 ~ ich*1  
+   Happy1 ~ iha*1  
+   Happy2 ~ iha*1  
+  
+   # residual covariances  
+   Glad1 ~~ Glad2  
+   Cheer1 ~~ Cheer2  
+   Happy1 ~~ Happy2  
+  
+   # latent means  
+   posAffect1 ~ 0*1 # baseline  
+   posAffect2 ~ 1 # difference compared to baseline  
+ '  
> fit <- cfa(model, sample.cov = COV,  
+           sample.mean = MEAN,  
+           sample.nobs = 823)  
> summary(fit, fit.measures = TRUE, standardized = TRUE)
```

lavaan (0.5-17.700) converged normally after 36 iterations

Number of observations	823
Estimator	ML
Minimum Function Test Statistic	20.279
Degrees of freedom	9
P-value (Chi-square)	0.016

Model test baseline model:

Minimum Function Test Statistic	1761.666
Degrees of freedom	15
P-value	0.000

User model versus baseline model:

Comparative Fit Index (CFI)	0.994
Tucker-Lewis Index (TLI)	0.989

Loglikelihood and Information Criteria:

Loglikelihood user model (H0)	-5381.011
Loglikelihood unrestricted model (H1)	-5370.871
Number of free parameters	18
Akaike (AIC)	10798.022
Bayesian (BIC)	10882.855

Sample-size adjusted Bayesian (BIC) 10825.694

Root Mean Square Error of Approximation:

RMSEA 0.039
 90 Percent Confidence Interval 0.016 0.062
 P-value RMSEA <= 0.05 0.763

Standardized Root Mean Square Residual:

SRMR 0.019

Parameter estimates:

Information				Expected		
Standard Errors				Standard		
	Estimate	Std.err	Z-value	P(> z)	Std.lv	Std.all
Latent variables:						
posAffect1 =~						
Glad1	1.000				0.603	0.715
Cheer1 (ch)	1.150	0.046	25.063	0.000	0.693	0.780
Happy1 (ha)	1.076	0.043	25.208	0.000	0.648	0.777
posAffect2 =~						
Glad2	1.000				0.607	0.723
Cheer2 (ch)	1.150	0.046	25.063	0.000	0.698	0.768
Happy2 (ha)	1.076	0.043	25.208	0.000	0.653	0.780

Covariances:

Glad1	~~						
Glad2		0.032	0.015	2.074	0.038	0.032	0.092
Cheer1	~~						
Cheer2		0.017	0.016	1.047	0.295	0.017	0.053
Happy1	~~						
Happy2		-0.011	0.014	-0.800	0.424	-0.011	-0.041
posAffect1	~~						
posAffect2		0.202	0.021	9.840	0.000	0.553	0.553

Intercepts:

Glad1	(igl)	3.067	0.027	114.088	0.000	3.067	3.639
Glad2	(igl)	3.067	0.027	114.088	0.000	3.067	3.652
Cheer1	(ich)	2.915	0.029	99.814	0.000	2.915	3.283
Cheer2	(ich)	2.915	0.029	99.814	0.000	2.915	3.204
Happy1	(iha)	3.123	0.027	115.351	0.000	3.123	3.740
Happy2	(iha)	3.123	0.027	115.351	0.000	3.123	3.726
psAffc1		0.000				0.000	0.000
psAffc2		-0.040	0.025	-1.617	0.106	-0.066	-0.066

Variances:

Glad1		0.347	0.022			0.347	0.489
Cheer1		0.308	0.024			0.308	0.391
Happy1		0.277	0.021			0.277	0.397
Glad2		0.336	0.022			0.336	0.477
Cheer2		0.340	0.025			0.340	0.411
Happy2		0.275	0.021			0.275	0.392
posAffect1		0.363	0.029			1.000	1.000

posAffect2	0.369	0.030	1.000	1.000
-------------------	--------------	--------------	--------------	--------------

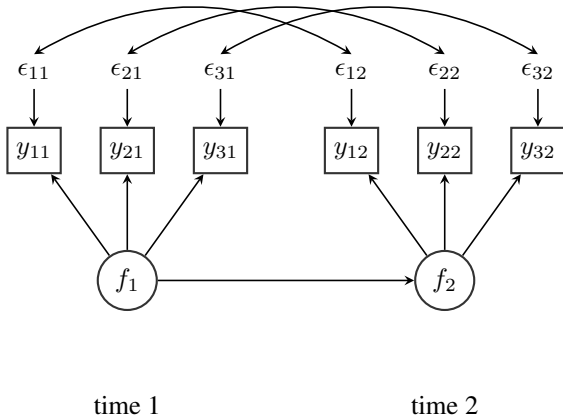
- answer: there is NO significant difference between the two time points

1.4 Panel models for longitudinal data

- panel models postulate *directional* (regression) relationships among the repeated measures
- the ‘covariance’ is replaced by a ‘regression’
- both within repeated variables (autoregressive) and between repeated variables (cross-lagged)
- focus on the model-implied covariance/correlation structure
- the means are usually ignored
- some subtypes:
 - autoregressive models (the simplex model)
 - cross-lagged models
 - latent autoregressive/cross-lagged models
 - ...

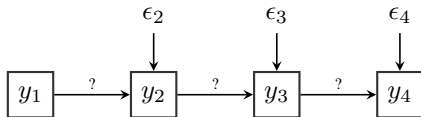
example panel model with a single latent variable

- example with 2 time points:



autoregressive models

- each time point is regressed on a previous time point (first order) , or an even further time point (second order, third order, ...)
- alternative names: Markov models, simplex models, panel models, ...
- earliest development dates back to the seminal work of Guttman (1954)
- example first-order univariate autoregressive model:



The simplex change process

- basic assumption: if individuals are changing at a steady rate, the pattern of correlations from one time point to the next should follow a *simplex pattern*
- key characteristic of a simplex pattern: correlations decrease in magnitude as a function of distance from the diagonal of the correlation matrix
- example of a 'Guttman simplex pattern' (correlation = 0.9):

	y1	y2	y3	y4
y1	1.000			
y2	0.900	1.000		
y3	0.810	0.900	1.000	
y4	0.729	0.810	0.900	1.000

- example of a 'Guttman simplex pattern' (correlation = 0.5):

	y1	y2	y3	y4
y1	1.000			
y2	0.500	1.000		
y3	0.250	0.500	1.000	
y4	0.125	0.205	0.500	1.000

- the simplex model assumes that external (eg. environmental or contextual) influences are minimal, and can be ignored
 - typical example in psychology: early cognitive development
 - counterexample: social adjustment in school (often strongly influenced by contextual influences)
- questions we can answer with panel models:
 - are the effects (regression coefficients) the same across time points?
 - * makes more sense if the time span between variables is the same
 - * if yes, this would suggest that the process does not change over time
 - are the residual variances the same across time points?
 - * often unrealistic
 - do we have correlated residuals? if so, are they the same across time points?

example: McCarthy Scales of Children's Abilities

- a first-order autoregressive model

```
> library(lavaan)
> model.age <- '
+   # first order
+   age36 ~ age30
+   age42 ~ age36
+   age48 ~ age42
+ '
> fit <- sem(model.age, data = MD11.5, fixed.x = FALSE)
> summary(fit, standardized = TRUE)
```

lavaan (0.5-17.700) converged normally after 14 iterations

Number of observations	12
Estimator	ML
Minimum Function Test Statistic	7.661
Degrees of freedom	3
P-value (Chi-square)	0.054

Parameter estimates:

Information	Expected
Standard Errors	Standard

	Estimate	Std.err	Z-value	P(> z)	Std.lv	Std.all
Regressions:						
age36 ~						
age30	0.821	0.181	4.540	0.000	0.821	0.795
age42 ~						
age36	0.716	0.177	4.054	0.000	0.716	0.760
age48 ~						
age42	0.944	0.167	5.669	0.000	0.944	0.853
Variances:						
age36	67.650	27.618			67.650	0.368
age42	68.863	28.113			68.863	0.422
age48	54.328	22.179			54.328	0.272
age30	172.333	70.355			172.333	1.000

```
> round(cor(MD11.5[,c("age30", "age36", "age42", "age48")]), 3)
```

```

      age30 age36 age42 age48
age30 1.000 0.795 0.696 0.599
age36 0.795 1.000 0.760 0.466
age42 0.696 0.760 1.000 0.853
age48 0.599 0.466 0.853 1.000

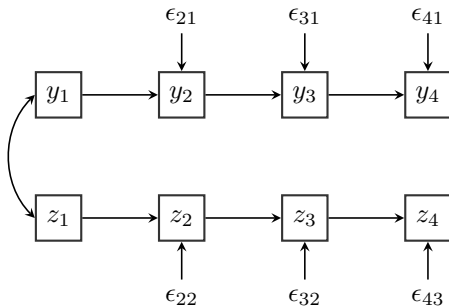
```


extensions

- higher-order models:
 - AR(2): T_3 is regressed on T_2 and T_1
 - AR(p): $T_{(p+1)}$ is regressed on the p previous time points
- if we interpret a residual as part of the variable at time t that is not explained by the previous variable(s), we can use this residual as an additional predictor of the next variable:
 - without AR(1), this is a first-order moving average model MA(1)
 - with AR(1), this is an autoregressive first-order moving average model, ARMA(1)
 - typically effects of the moving averages are invariant over time (Box-Jenkins time series)

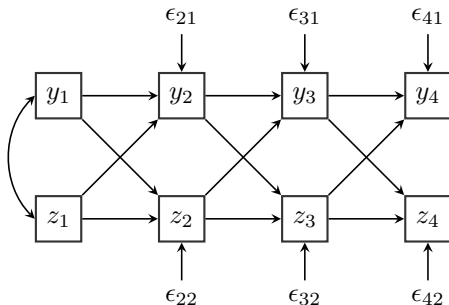
multivariate panel models

- in a multivariate panel model, we have more than one outcome, measured at (the same) t time points
- example: a bivariate panel/simplex model where Y is a measure of mathematical achievement, and Z is a measure of reading ability (4 time points: grade 3, grade 4, grade 5 and grade 6)



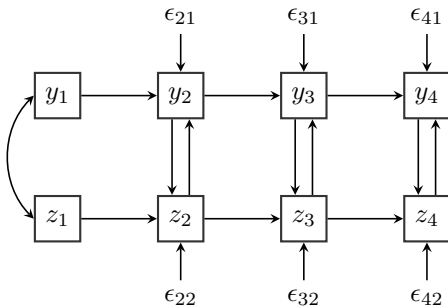
crosslagged effects

- what is the directional effect of one variable on the other?
 - do the two variables develop independently of each other?
 - or does Y exert a greater influence on Z , or vice versa?



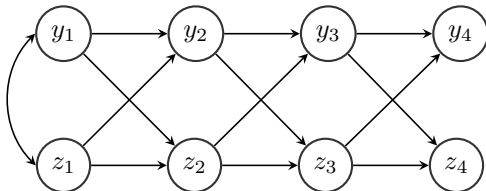
contemporaneous effects

- sometimes, the crossed effects between two variables are not lagged, but contemporaneous (exerting an effect at the same time point)
- this can be unidirectional, or reciprocal
- not everyone believes this approach is useful (in addition: often convergence issues)



panel model with latent variables

- if the ‘repeated’ outcomes are not directly observable, we may replace them with a latent variable with a proper measurement model
- but first, we need to establish ‘measurement invariance’ for the latent variables across time



- in this diagram, the observed indicators have been omitted

strengths and limitations of panel models

- panel models can be very useful for examining the relations of two (or more) variables (observed or latent) over time
- often, we are equally interested in the lack of relations over time
- panel models do not tell us anything about group level tendencies (overall increase or decrease of the scores)
- panel models do not tell us anything about individual tendencies

1.5 Growth curve models

- ‘time’ is typically considered as a continuous variable
- two components:
 - fixed effects: what is the nature of the average trend (linear, quadratic)
 - random effects: individual differences
- in addition, we may try to explain these individual differences by taking into account:
 - time-invariant covariates (age, gender, ...)
 - time-varying covariates (measured at each time point)
- closely related to ‘mixed models’ (linear mixed models, generalized mixed models)
 - limited to balanced data
 - but we can add indirect paths and latent variables
- focus on the mean structure (not the covariance structure)

some references

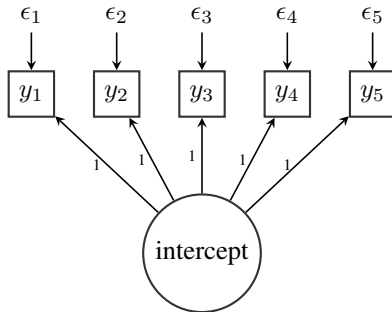
- Bollen, K.A., & Curran, P.J. (2006). *Latent curve models: A structural equation perspective*. John Wiley & Sons.
- Duncan, T.E., Duncan, S.C., & Strycker, L.A. (2006). *An introduction to latent variable growth curve modeling: Concepts, issues, and applications*. Routledge Academic.
- Preacher, K.J., Wichman, A.L., MacCallum, R.C., & Briggs, N.E. (2008). *Latent Growth Curve Modeling*. Quantitative Applications in the Social Sciences, No. 157, Sage.

from latent variable to random effect

- a random effect is simply a latent variable with the following properties:
 - the repeated measures are the indicators of the latent variable
 - the factor loadings are fixed to a specific pattern
 - the intercepts of the observed repeated measures are fixed to zero
 - the mean/intercept of the latent variable is freely estimated
 - the (residual) variance of the latent variable is freely estimated
- typical patterns for the factor loadings:
 - by fixing all factor loadings to unity, we obtain a random intercept
 - by fixing all factor loadings to a linear scale (eg. 0, 1, 2, 3, ...) we obtain a random slope
 - by fixing all factor loadings to a quadratic scale (eg. 0, 1, 4, 9, ...), we obtain a random quadratic effect
 - ...

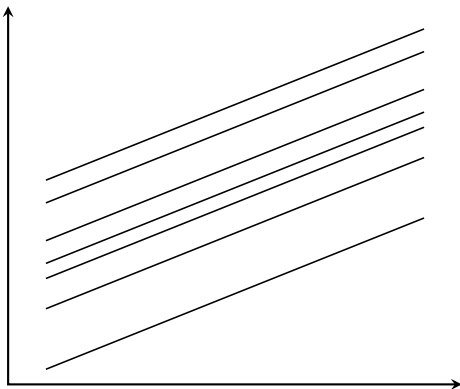
random intercept

- creating a random intercept:



random intercept only, positive linear trend

- a random-intercept-only model assumes that all individuals follow the same trend, but with a different initial point (intercept)



R code

- when using the `sem()` or `cfa()` fitting functions, you need to manually set the intercepts of the observed repeated variables to zero, and free the latent intercept:

```
> model <- '  
+   # random intercept  
+   int =~ 1*y1 + 1*y2 + 1*y3 + 1*y4 + 1*y5  
+  
+   # zero intercepts  
+   y1 + y2 + y3 + y4 + y5 ~ 0*1  
+  
+   # free latent intercept  
+   int ~ 1  
+ '
```

- the `growth()` fitting function does this automatically (for all latent variables):

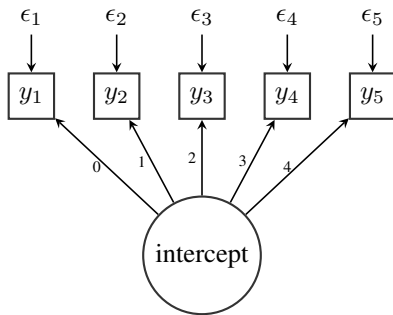
```
> model <- '  
+   # random intercept  
+   int =~ 1*y1 + 1*y2 + 1*y3 + 1*y4 + 1*y5  
+ '
```

- when both ‘regular’ latent variables, and ‘random effects’ are used in the same model, it is perhaps better to use the lavaan() function:

```
> model <- '  
+   # random intercept  
+   int =~ 1*y1 + 1*y2 + 1*y3 + 1*y4 + 1*y5  
+  
+   # free latent intercept and variance  
+   int ~ 1  
+   int ~~ int  
+  
+   # add residual variances  
+   y1 ~~ y1; y2 ~~ y2; y3 ~~ y3; y4 ~~ y4; y5 ~~ y5  
+ '
```

random slope

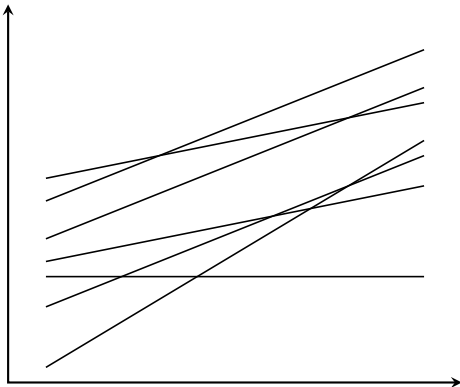
- creating a random slope:



- here, the 'reference' point is the first time point; another coding scheme (-4, -3, -2, -1, 0) treats the last time point as the reference point
- this will not affect model fit, but it will change the interpretation of the parameters

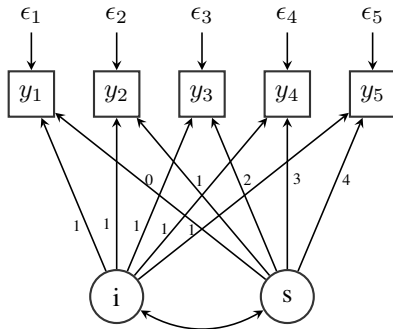
random intercept and random slope

- different intercepts, different slopes



a typical growth curve model

- random intercept and random slope



- $y_t = (\text{initial time at time 1}) + (\text{growth per unit time}) * \text{time} + \text{error}$
- $y_t = \text{intercept} + \text{slope} * \text{time} + \text{error}$

example: McCarthy Scales of Children's Abilities

- random intercept, but fixed slope

```
> model.int <- '  
+   int    =~ 1*age30 + 1*age36 + 1*age42 + 1*age48  
+   slope =~ 0*age30 + 1*age36 + 2*age42 + 3*age48  
+  
+   # intercepts (fixed effects)  
+   int    ~ 1  
+   slope  ~ 1  
+  
+   # random intercept  
+   int    ~~ int  
+  
+   # fixed slope  
+   slope  ~~ 0*slope # no variance  
+   int    ~~ 0*slope # no covariance  
+  
+   # force same variance for all (compound symmetry)  
+   age30  ~~ v1*age30  
+   age36  ~~ v1*age36  
+   age42  ~~ v1*age42  
+   age48  ~~ v1*age48  
+ '  
> fit.int <- lavaan(model.int, data=MD11.5)  
> summary(fit.int)
```

lavaan (0.5-17.700) converged normally after 56 iterations

Number of observations	12
Estimator	ML
Minimum Function Test Statistic	17.280
Degrees of freedom	10
P-value (Chi-square)	0.068

Parameter estimates:

Information	Expected
Standard Errors	Standard

	Estimate	Std.err	Z-value	P(> z)
Latent variables:				
int =~				
age30	1.000			
age36	1.000			
age42	1.000			
age48	1.000			
slope =~				
age30	0.000			
age36	1.000			
age42	2.000			
age48	3.000			

Covariances:

```

int ~~
  slope                0.000

Intercepts:
  int                 103.500    3.688    28.063    0.000
  slope                3.000     0.967     3.104     0.002
  age30                 0.000
  age36                 0.000
  age42                 0.000
  age48                 0.000

Variances:
  int                 123.986    56.435
  slope                0.000
  age30 (v1)          56.056    13.212
  age36 (v1)          56.056    13.212
  age42 (v1)          56.056    13.212
  age48 (v1)          56.056    13.212

```

- compare this to the output of `lmer()`:

```
> fit <- lmer(y ~ 1 + age + (1 | subject), data=MD11.5.long, REML=FALSE)
> summary(fit)
```

```
Linear mixed model fit by maximum likelihood ['lmerMod']
Formula: y ~ 1 + age + (1 | subject)
Data: MD11.5.long
```

AIC	BIC	logLik	deviance
364.9290	372.4138	-178.4645	356.9290

Random effects:

Groups	Name	Variance	Std.Dev.
subject	(Intercept)	123.99	11.135
Residual		56.06	7.487

Number of obs: 48, groups: subject, 12

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	103.5000	3.6881	28.063
age	3.0000	0.9666	3.104

Correlation of Fixed Effects:

(Intr)	
age	-0.393

plausible values for the random intercepts

- the `predict()` function computes (estimated) individual values for the latent variables (here random effects):

```
> predict(fit.int)
```

```
      int slope
[1,] 104.398   3
[2,] 114.281   3
[3,]  99.906   3
[4,]  87.328   3
[5,] 115.180   3
[6,]  97.211   3
[7,] 120.571   3
[8,]  93.617   3
[9,]  90.922   3
[10,] 97.211   3
[11,] 104.398   3
[12,] 116.977   3
```

- random intercept, random slope

```
> model.slope <- '  
+   int    =~ 1*age30 + 1*age36 + 1*age42 + 1*age48  
+   slope =~ 0*age30 + 1*age36 + 2*age42 + 3*age48  
+  
+   # intercepts (fixed effects)  
+   int    ~ 1  
+   slope  ~ 1  
+  
+   # random intercept, random slope  
+   int    ~~ int  
+   slope  ~~ slope  
+   int    ~~ slope  
+  
+   # force same variance for all (compound symmetry)  
+   age30  ~~ v1*age30  
+   age36  ~~ v1*age36  
+   age42  ~~ v1*age42  
+   age48  ~~ v1*age48  
+ '  
> fit.slope <- lavaan(model.slope, data=MD11.5)  
> summary(fit.slope)
```

lavaan (0.5-17.700) converged normally after 85 iterations

Number of observations

12

Estimator	ML
Minimum Function Test Statistic	12.610
Degrees of freedom	8
P-value (Chi-square)	0.126

Parameter estimates:

Information	Expected
Standard Errors	Standard

	Estimate	Std.err	Z-value	P(> z)
Latent variables:				
int =~				
age30	1.000			
age36	1.000			
age42	1.000			
age48	1.000			
slope =~				
age30	0.000			
age36	1.000			
age42	2.000			
age48	3.000			

Covariances:

int ~~				
slope	-17.682	19.168	-0.922	0.356

Intercepts:

```

int          103.500    3.852    26.870    0.000
slope        3.000     1.281     2.341    0.019
age30        0.000
age36        0.000
age42        0.000
age48        0.000

```

Variiances:

```

int          153.668    73.024
slope        12.743     8.293
age30 (v1)   34.817    10.051
age36 (v1)   34.817    10.051
age42 (v1)   34.817    10.051
age48 (v1)   34.817    10.051

```

```
> anova(fit.int, fit.slope)
```

Chi Square Difference Test

```

          Df    AIC    BIC Chisq Chisq diff Df diff Pr(>Chisq)
fit.slope  8 364.26 367.17 12.61
fit.int   10 364.93 366.87 17.28      4.6704      2    0.09679 .
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1 1

```


- compare this to the output of lmer():

```
> fit <- lmer(y ~ 1 + age + (1 + age | subject), data=MD11.5.long, REML=FALSE)
> summary(fit)
```

```
Linear mixed model fit by maximum likelihood ['lmerMod']
Formula: y ~ 1 + age + (1 + age | subject)
Data: MD11.5.long
```

	AIC	BIC	logLik	deviance
	364.2587	375.4859	-176.1293	352.2587

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
subject	(Intercept)	153.67	12.396	
	age	12.74	3.570	-0.40
Residual		34.82	5.901	

Number of obs: 48, groups: subject, 12

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	103.500	3.852	26.870
age	3.000	1.281	2.341

Correlation of Fixed Effects:

(Intr)	
age	-0.475

plausible values for the random intercepts and slopes

- (estimated) individual values for both random effects:

```
> predict(fit.slope)
```

```
      int  slope
[1,] 101.922  4.684
[2,] 107.922  7.569
[3,]  99.582  3.115
[4,]  84.612  4.356
[5,] 119.082  0.721
[6,] 106.437 -3.360
[7,] 124.863  0.614
[8,]  87.851  6.579
[9,]  92.584  1.527
[10,]  96.980  2.974
[11,] 106.168  1.840
[12,] 113.997  5.382
```

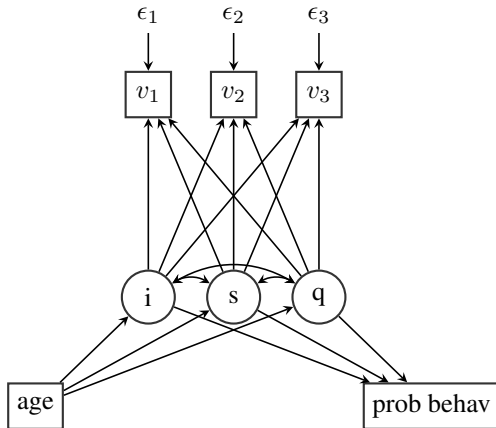
comments

- in the previous examples, we forced the residual variances to be equal, but this was just to mimic the default behavior of the linear mixed model
- in general, it is often better to leave the residual variances free
- a quadratic random effect can be added by simply adding another latent variable with quadratic factor loadings (0, 1, 4, 9); similar for cubic and higher effects
- the random effects are exogenous (no incoming arrows); we call this the *unconditional* growth curve model
- instead of fixing the linear scale (as in 0, 1, 2, 3), we may estimate some of the factor loading (as in 0, 1, ?, ?): this allows for more flexible shapes (not necessarily linear)
- custom shapes (i.e. piecewise curves) are also possible

second example (optional)

- example from Chapter 3 from the book ‘An introduction to latent variable growth curve modeling’ (Duncan et. al. 2006); sample statistics from table 3.4; model from example 3.4
- repeated measures: alcohol use at three time points (V1, V2, V3)
- possible consequence: problem behaviour
- possible predictor of growth factors: age
- we will model the time trend by a quadratic curve: this is perhaps a bit too ambitious, since we only have three time points; the price we have to pay is to fix the residual variances of the repeated measure to zero
- orthogonal coding of the intercept/slope/quadratic components

Path diagram



R code

```

> lower <- ' 0.481
+           0.401 0.539
+           0.168 0.044 0.120
+           0.311 0.343 0.516 -0.002 '
> COV3.4 <- getCov(x=lower, diag=FALSE,
+                 sds=c(7.388, 8.000, 8.043, 0.379, 0.790),
+                 names=c("v1","v2","v3","age", "probelmbehav"))
> MEAN3.4 <- c(8.265, 10.084, 10.888, 15.363, 0.026)
> model3.4 <- '
+   int    =~ 0.577*v1 + 0.577*v2 + 0.577*v3
+   linear  =~ (-0.707)*v1 + 0*v2 + 0.707*v3
+   quadratic =~ 0.408*v1 + (-0.816)*v2 + 0.408*v3
+
+   # random effects: means and variances
+   int ~ 1; int ~~ int
+   linear ~ 1; linear ~~ linear
+   quadratic ~ 1; quadratic ~~ quadratic
+
+   # fix error variances to zero
+   v1 ~~ 0*v1
+   v2 ~~ 0*v2
+   v3 ~~ 0*v3
+
+   # effect of age
+   int + linear + quadratic ~ age
+   age ~ 1

```

```

+   age ~~ age
+
+   # sequelae of change
+   probelmbehav ~ 1 + int + linear + quadratic
+   probelmbehav ~~ probelmbehav
+
+   # correlated residuals
+   int ~~ linear
+   int ~~ quadratic
+   linear ~~ quadratic
+ '
> fit3.4 <- lavaan(model3.4, sample.cov=COV3.4, sample.mean=MEAN3.4,
+                 sample.nobs=358, mimic="EQS")
> summary(fit3.4, standardized=TRUE)

```

lavaan (0.5-17.700) converged normally after 246 iterations

Number of observations	358
Estimator	ML
Minimum Function Test Statistic	2.974
Degrees of freedom	1
P-value (Chi-square)	0.085

Parameter estimates:

Information	Expected
Standard Errors	Standard

	Estimate	Std.err	Z-value	P(> z)	Std.lv	Std.all
Latent variables:						
int =~						
v1	0.577				6.299	0.853
v2	0.577				6.299	0.787
v3	0.577				6.299	0.783
linear =~						
v1	-0.707				-4.231	-0.573
v2	0.000				0.000	0.000
v3	0.707				4.231	0.526
quadratic =~						
v1	0.408				2.176	0.295
v2	-0.816				-4.352	-0.544
v3	0.408				2.176	0.271
Regressions:						
int ~						
age	3.900	1.511	2.582	0.010	0.357	0.135
linear ~						
age	-0.515	0.835	-0.617	0.537	-0.086	-0.033
quadratic ~						
age	1.619	0.740	2.189	0.029	0.304	0.115
probelmbehav ~						
int	0.035	0.003	10.609	0.000	0.380	0.481
linear	0.023	0.006	3.821	0.000	0.136	0.172
quadratic	0.018	0.007	2.758	0.006	0.098	0.124

Covariances:

int ~~						
linear	6.972	3.444	2.024	0.043	0.108	0.108
quadratic	-6.614	3.053	-2.166	0.030	-0.115	-0.115
linear ~~						
quadratic	-0.573	1.678	-0.341	0.733	-0.018	-0.018

Intercepts:

int	-43.020	23.214	-1.853	0.064	-3.940	-3.940
linear	9.768	12.837	0.761	0.447	1.632	1.632
quadratic	-25.291	11.370	-2.224	0.026	-4.742	-4.742
age	15.363	0.020	765.898	0.000	15.363	40.536
probelmbehav	-0.596	0.066	-9.091	0.000	-0.596	-0.755
v1	0.000				0.000	0.000
v2	0.000				0.000	0.000
v3	0.000				0.000	0.000

Variances:

int	117.010	8.758	13.360	0.000	0.982	0.982
linear	35.781	2.678	13.360	0.000	0.999	0.999
quadratic	28.072	2.101	13.360	0.000	0.987	0.987
v1	0.000				0.000	0.000
v2	0.000				0.000	0.000
v3	0.000				0.000	0.000
age	0.144	0.011	13.360	0.000	0.144	1.000
probelmbehav	0.449	0.034	13.360	0.000	0.449	0.719

comments

- in the model, we have not included a direct effect of age on subsequent problem behavior (hence we have 1 degree of freedom)
- age only affects the constant and the quadratic growth factors
- but all three latent growth factors are significant predictors of problem behavior
- the main conclusion of this model was that the effect of ‘age’ on problem behavior was mediated through its effect on the developmental parameters (the growth factors); adding a direct effect of age on problem behavior did not significantly improve the fit

autoregressive latent trajectory (ALT) models

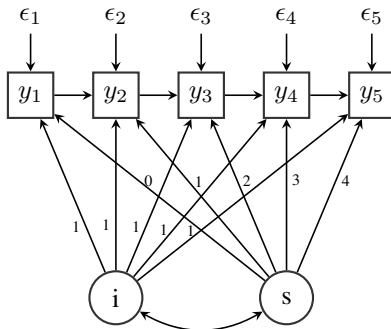
- Bollen & Curran, in a series of papers (1999, 2000, 2001, 2004) proposed a hybrid model they called the ‘autoregressive latent trajectory’ (ALT) model; best reference:

Bollen, K.A., & Curran, P.J. (2004). Autoregressive latent trajectory (ALT) models: a synthesis of two traditions. *Sociological Methods & Research*, 32(3), 336-383.

- it is a growth curve model, combined with an autoregressive structure for the repeated measures
- can be used when there is interest in both continuous underlying trajectories and time-specific influences across constructs
- the authors described this approach as ‘The Best of Both Worlds’
- nevertheless, the approach has been criticized because the interpretation is not always clear

example ALT model

- combination of a growth curve model with a random intercept, a random slope, and an autoregressive structure for the repeated measures



Longitudinal Structural Equation Modeling Principles and Effective Practices. Todd D. Little. Featuring actual datasets as illustrative examples, this book reveals numerous ways to apply structural equation modeling (SEM) to any repeated-measures study. read more ». Bestseller. View larger. Longitudinal Structural Equation Modeling. Todd D. Little Foreword by Noel A. Card. Hardcover+e-book. Featuring actual datasets as illustrative examples, this book reveals numerous ways to apply structural equation modeling (SEM) to any repeated-measures study. Initial chapters lay the groundwork for modeling a longitudinal change process, from measurement, design, and specification issues to model evaluation and interpretation.