

# Longitudinal Data Analysis using Mplus and R

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# Plan for today

- Objectives of longitudinal research
- Role of time scores/factor loadings in LGCM
- Growth Curve Models
  - No growth, linear and quadratic LGCM
  - Spline/Piecewise/Multiphase LGCM
  - Adding time-invariant and time-varying (dynamical) predictors, and (distal) outcomes
  - Multi-group LGCM and invariance testing
  - Multi (Parallel) process LGCM

# Objectives of longitudinal research

1. Identification of intraindividual (within-person) changes (and stability)
  - Is there change over time on average?
    - ✓ Growth models can address various linear and nonlinear patterns of intraindividual change
2. Analysis of causes (determinants) of intraindividual change
  - What factors/mechanisms – time-varying/dynamical predictors – drive change?
    - ✓ Inclusion of time-varying (dynamical) predictors in growth models
3. Identification of interindividual differences (or similarity) in intraindividual change
  - Do different individuals change in different ways?
    - ✓ Growth models are structured to address interindividual differences in the growth factors
4. Analysis of causes (determinants) of interindividual differences in intraindividual change
  - What factors explain between-person differences in change?
    - ✓ Inclusion of time-invariant covariates in growth models, multigroup LGCM, Growth mixture models
5. Interrelationships in change
  - Does change in one variable related (*precede, covary and/or follow* ) to change in another variable?
  - Correlating slopes of X and Y could provide evidence that one variable is changing in the same people as another variable – correlated changes! Or common changes!
    - ✓ Multi (parallel & sequentially contingent) process LGCM

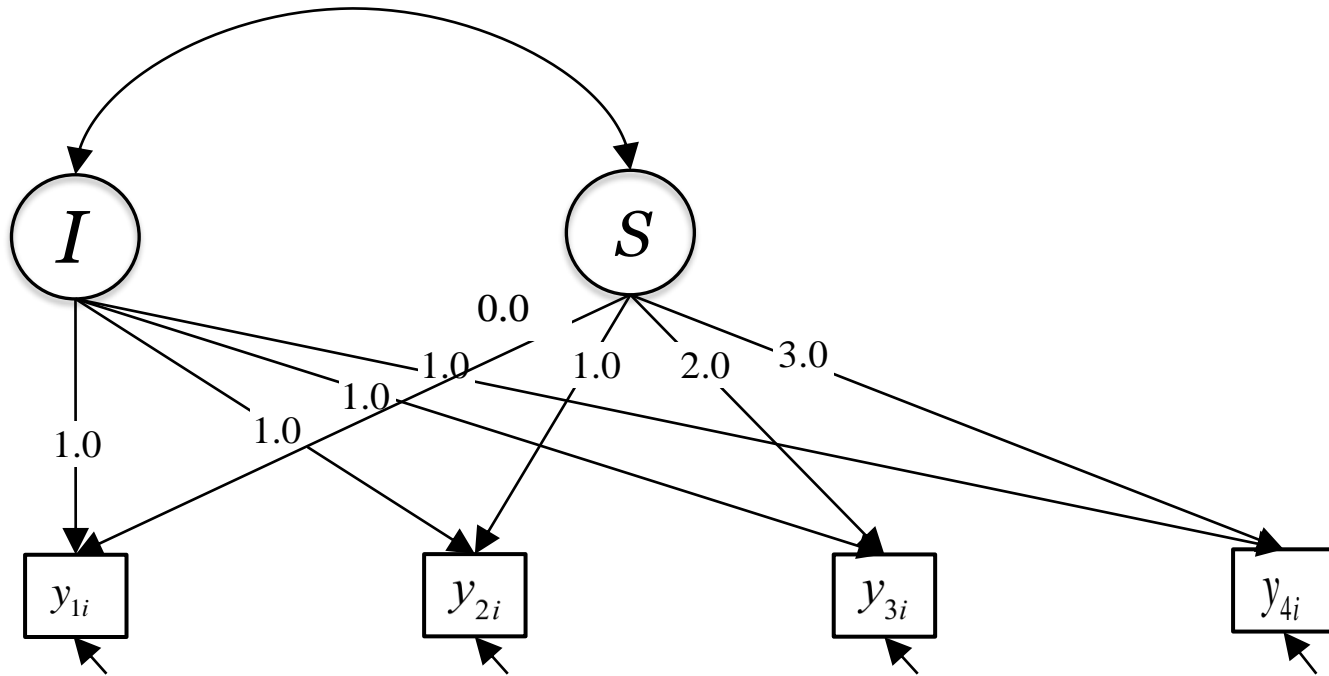
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# Modelling change over time



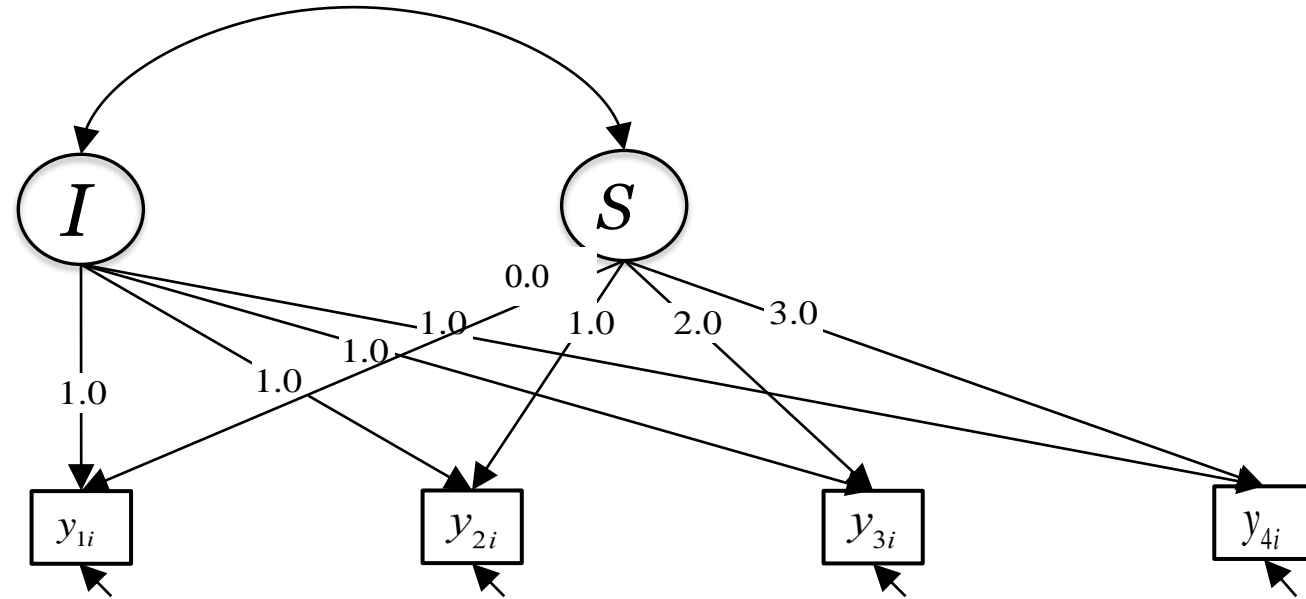
# Modelling change over time

- Role of time scores
  - Time of observation as factor loading
  - Time scores determine
    1. Form/shape of growth process
    2. Centering point of growth process
    3. Scaling of growth factors

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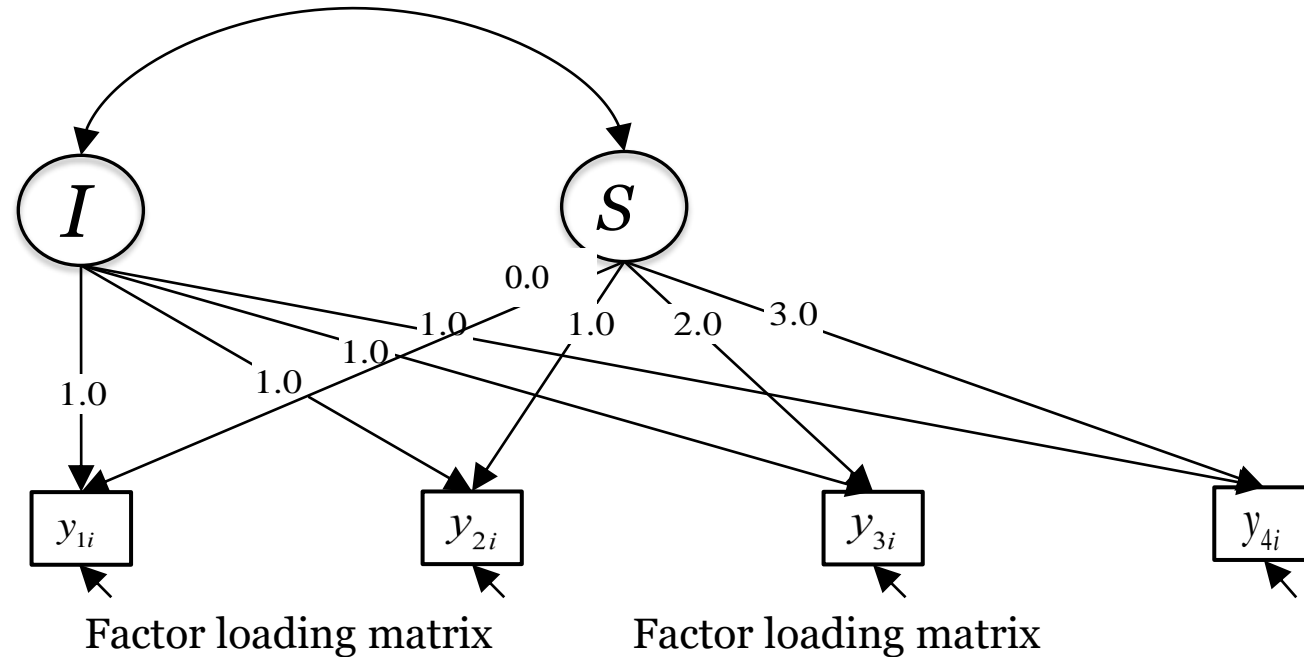




# Modelling change over time

## • Role of time scores

- Time of observation as factor loading
- Time scores determine
  1. Form/shape of growth process
  2. Centering point of growth process
  3. Scaling of growth factors



1 0 Time 1  
1 1 Time 2  
1 2 Time 3  
1 3 Time 4

1 -3 Time 1  
1 -2 Time 2  
1 -1 Time 3  
1 0 Time 4

I S | y1@0 y2@1 y3@2 y4@3

I S | y1@-3 y2@-2 y3@-1 y4@0

I S | y1@-1 y2@0 y3@1 y4@2; centering at Time 2

# Factor loadings should be proportionate to time intervals/spacing

Factor loading matrix

1	0	Time 1
1	1	Time 2
1	2	Time 3
1	3	Time 4

Factor loading matrix

1	0	Month 1
1	1	Month 6
1	2	Month 12
1	3	Month 18
1	4	Month 24

Factor loading matrix  
(unequal time interval)

1	0	Month 1
1	1	Month 2
1	2	Month 3
1	3	Month 4
1	4	Month 5
1	5	Month 6
1	6	Month 7

Factor loading matrix

1	-5	Month 1
1	-4	Month 2
1	-3	Month 3
1	-2	Month 4
1	-1	Month 5
1	0	Month 6

I S | y1@0 y2@1 y3@2 y4@3)

I S | y1@0 y2@1 y3@2 y4@3 y5@4

I S | y1@0 y2@6 y3@12 y4@18 y5@24

Either one is correct, same model fit indices

I S | y1@0 y2@1 y3@3 y4@4 y5@6 [No observations on Months 3 & 6, time scores specified to match observed time points]

I S | y1@-5 y2@-4 y3@-3 y4@-2 y5@-1 y6@0 [End of observation defined as centering point; intercept status; predicted level of y at end of obs.]

Free time score/Unspecified LGCM/Model estimated time score = empirically determines shape of outcome growth

I S | y1@0 y2@1 y3\* y4\* y5\*

Latent basis model/Unstructured growth model

I S | y1@0 y2\* y3\* y4@1

- Freely estimated parameters represent the proportion of predicted overall change that occurred up to a specific point in time eg Time 2, for y2\*
- The Slope growth factor represents the total amount of change from the first to the last timepoints

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1	6	Month 7

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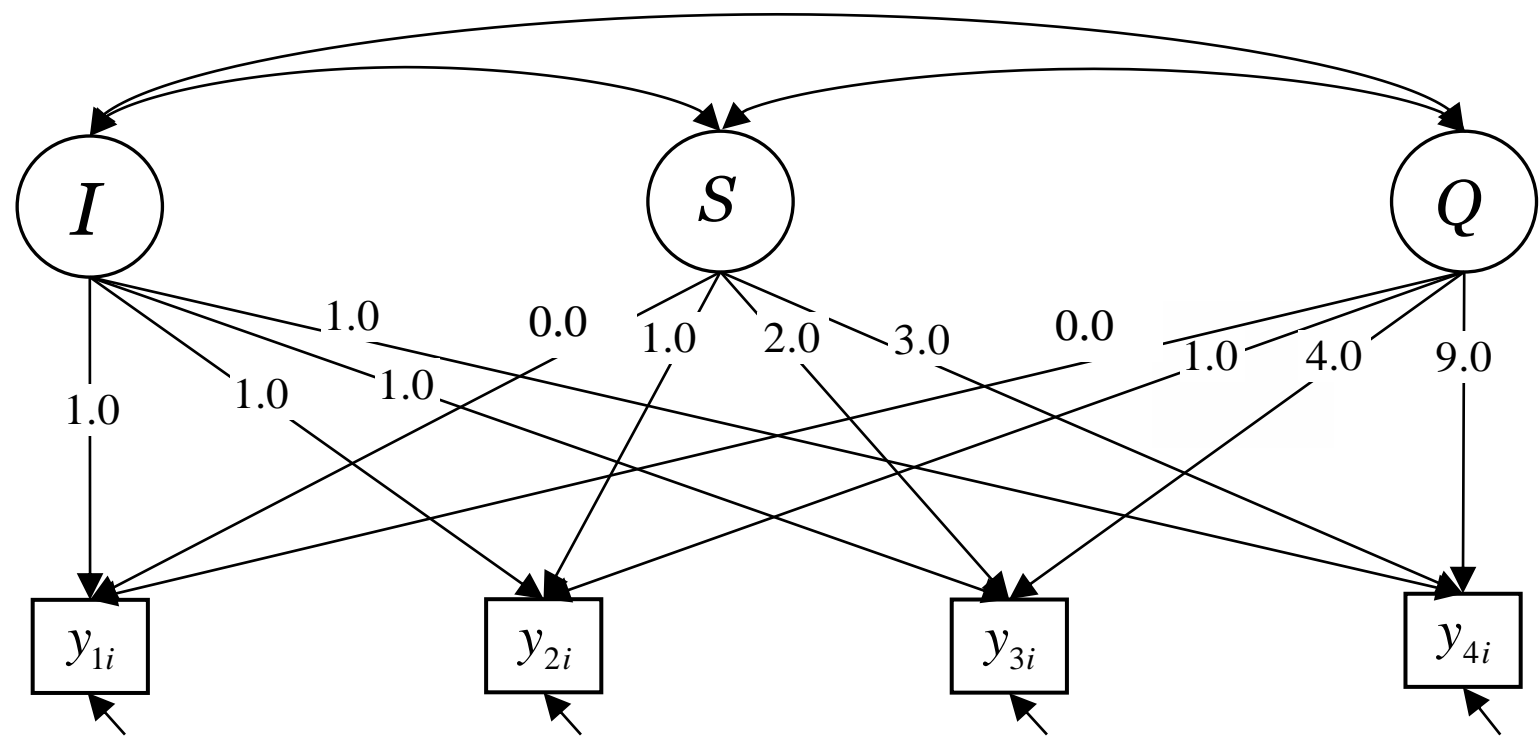
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- 14
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# Non-linear change (e.g., quadratic)



Factor loading matrix

1	0	0	Time 1
1	1	1	Time 2
1	2	4	Time 3
1	3	9	Time 4

(I S Q| y1@0 y2@1 y3@2 y4@3)

# Dataset

Variable Names	Time 1 (2015)	Time 2 (2016)	Time 3 (2018)	Time 4 (2019)	Time 5 (2021)
Id	personid				
Female	female				
Parental drug use	pdu1				
Adverse childhood environment	ace1				
Worry	worry1				
Loneliness	lone1	lone2	lone3	lone4	lone5
Anxiety symptoms	anx1	anx2	anx3	anx4	anx5
Depression symptoms	dep1	dep2	dep3	dep4	dep5
Hostility	host1	host2	host3	host4	host5
Peer conflict					percon5
Peer conflict					percon5b
Substance use					subs5
Substance use					subs5b
Difficulty sleeping					sleep5
Difficulty sleeping					sleep5b



## Things to do before fitting growth models to longitudinal data

### 1. Examine univariate and bivariate

► Code

	vars	n	mean	sd	median	trimmed	mad	min	max	range	st
lone1	1	398	1.46	0.46	1.32	1.38	0.34	1	3.75	2.75	1.
lone2	2	395	1.47	0.52	1.31	1.38	0.31	1	5.00	4.00	2.
lone3	3	390	1.53	0.52	1.36	1.44	0.37	1	3.78	2.78	1.
lone4	4	413	1.35	0.47	1.22	1.25	0.25	1	4.92	3.92	3.
lone5	5	409	1.32	0.39	1.20	1.24	0.25	1	3.43	2.43	2.

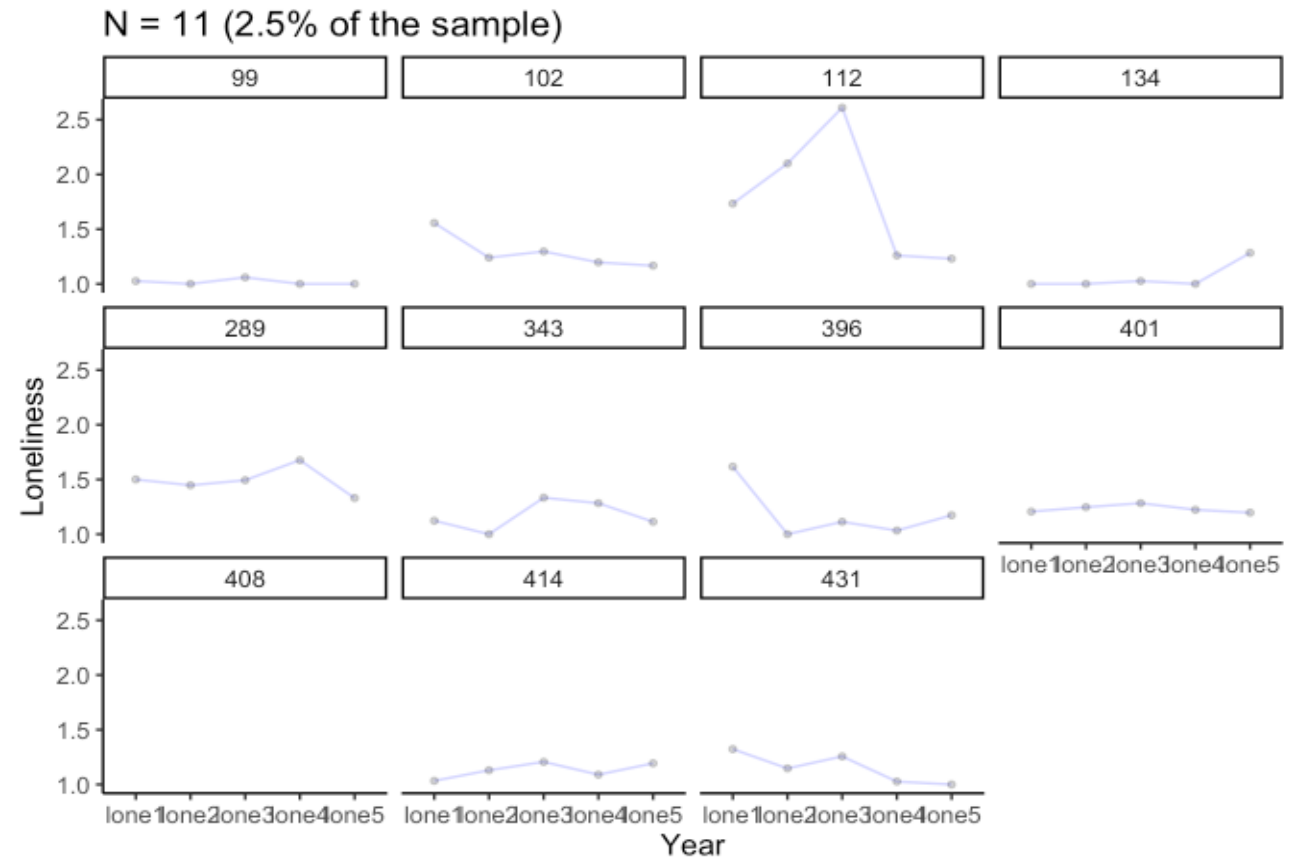
The means and standard deviations show a simple pattern with increases in the feeling of loneliness from T1 through to T3 and begins to decline afterwards though to T5 coupled with increases in variation and then a decline after T3.

### 5. Examine separate individual longitudinal plots

► Code

Warning: Removed 5 rows containing missing values (``geom_line()``).

Warning: Removed 5 rows containing missing values (``geom_point()``).

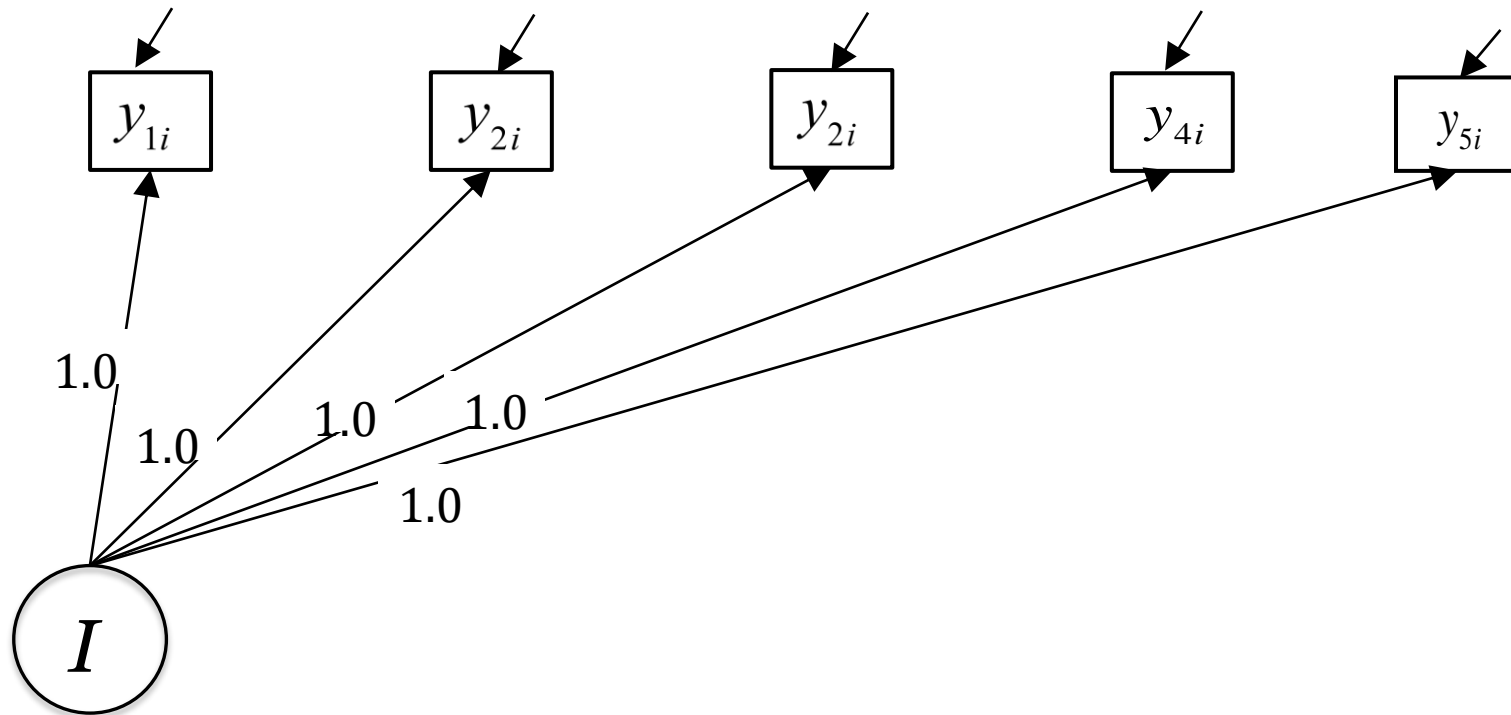


# Objectives of longitudinal research

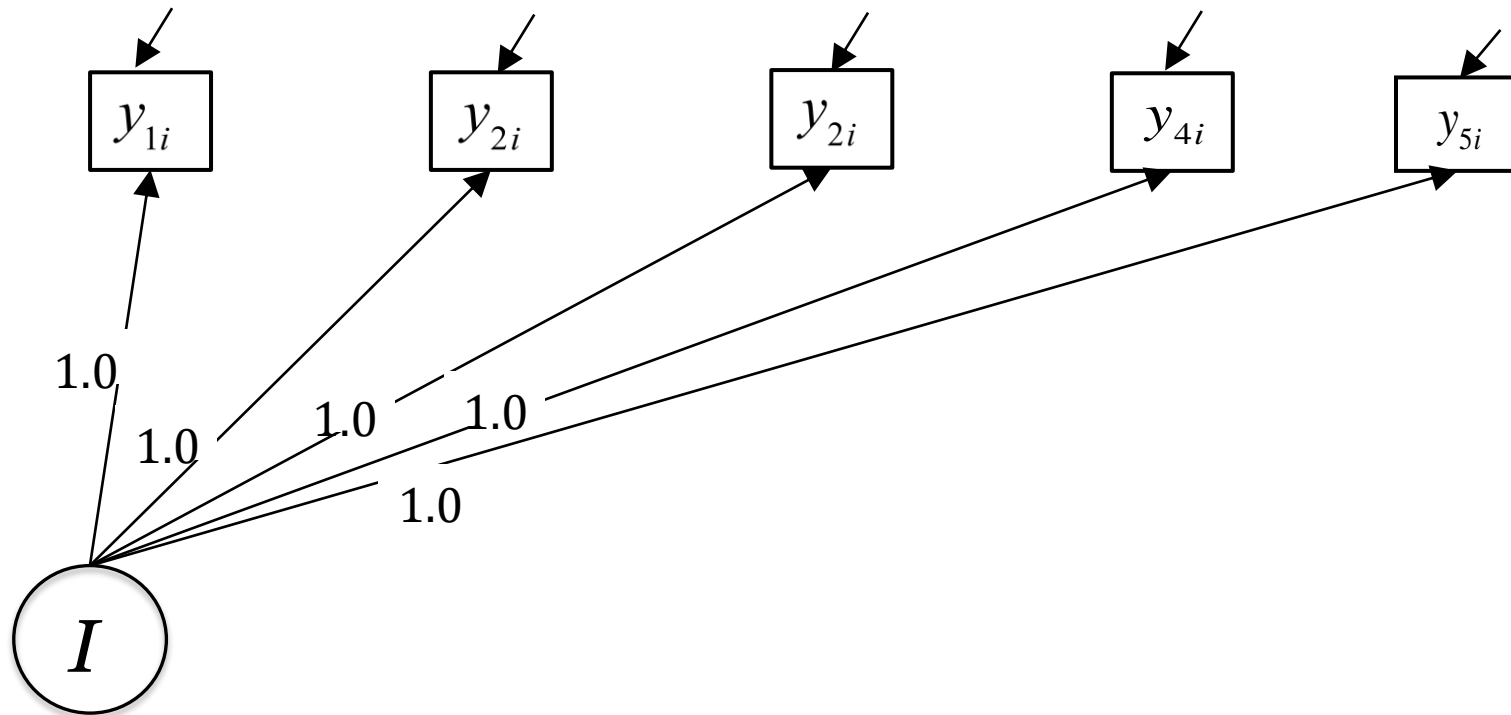
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- What does the overall trajectory of loneliness look like?
  - Is there change over time on average?
    - What growth function characterizes change over time/shape of growth?

# No growth/Intercept only model



# No growth/Intercept only model



```
26 # 001_No growth model
27 nogrowth <- 'i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5'
28 fit_nogrowth <- growth(nogrowth, data = data)
29 summary(fit_nogrowth, fit.measures = TRUE)
30 ..
```

```
001_No_change_No_growth_Intercept_only_model

TITLE: 001_No_change_No_growth_Intercept_only_model

DATA:
FILE IS data.dat;
LISTWISE = ON;

VARIABLE:
NAMES ARE
id |female pdu1 ace1 worry1
lone1 lone2 lone3 lone4 lone5
anx1 anx2 anx3 anx4 anx5
dep1 dep2 dep3 dep4 dep5
host1 host2 host3 host4 host5
percon5 percon5b subs5 subs5b sleep5 sleep5b;

USEVARIABLES ARE
lone1 lone2 lone3 lone4 lone5;

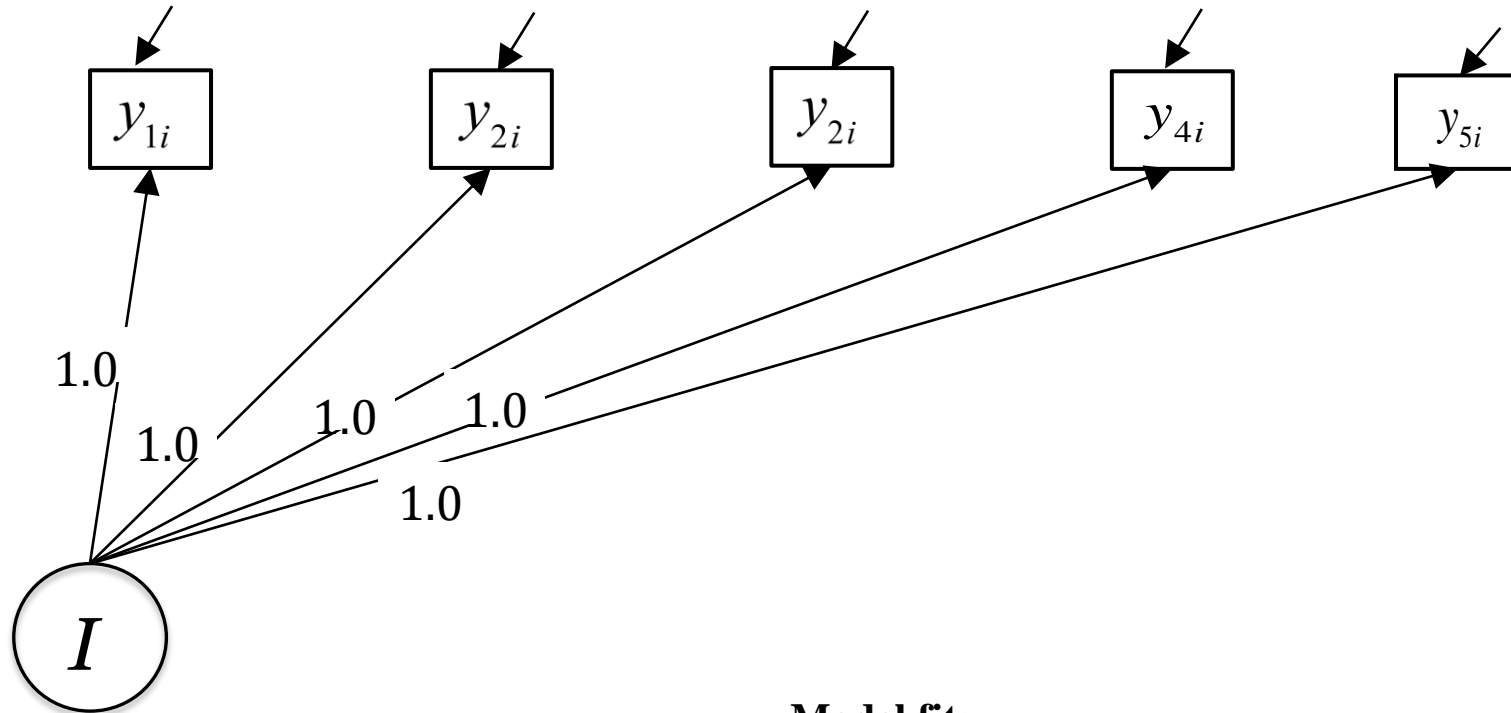
MISSING ARE ALL (-999);

ANALYSIS:
ESTIMATOR = ML;

MODEL:
I|lone1@1 lone2@1 lone3@1 lone4@1 lone5@1;
!I|lone1-lone5@1;

OUTPUT:
SAMPSTAT;
```

# No growth/Intercept only model



## RESULTS

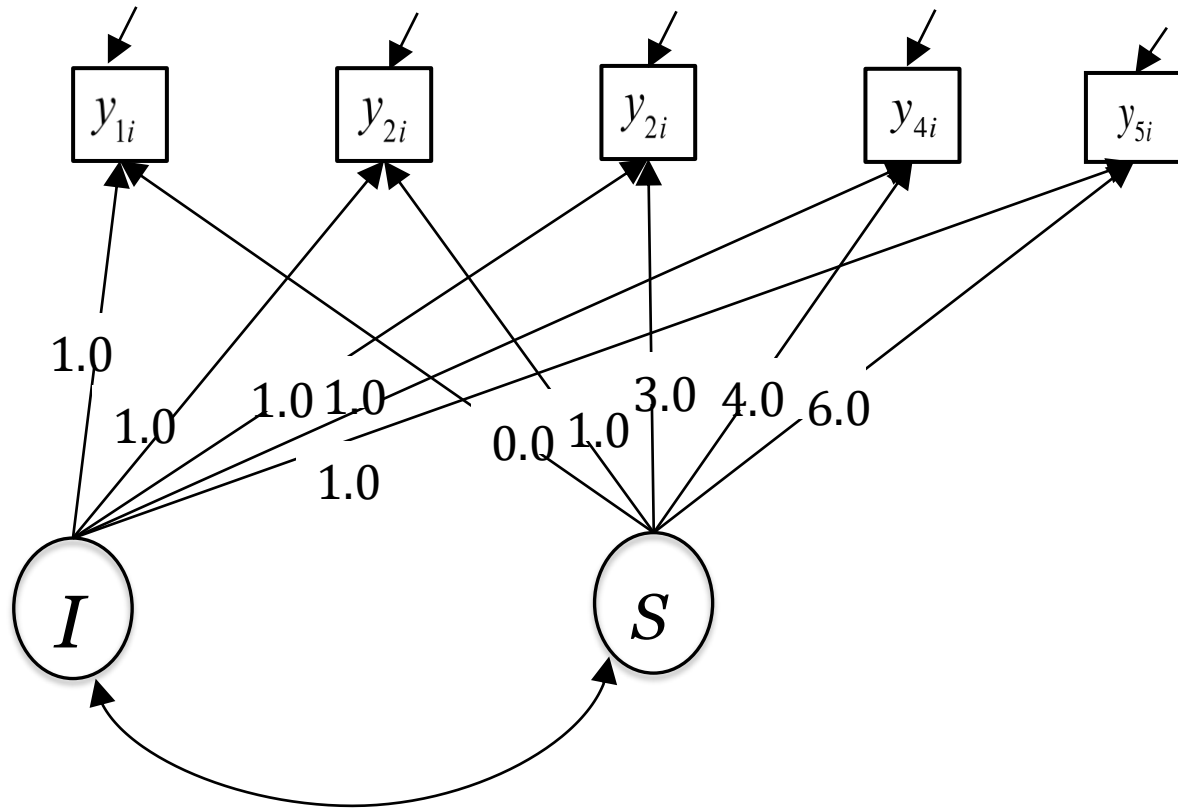
### Model fit:

( $\chi^2 = 186.433$ ,  $df = 13$ ;  $p < .001$ ;  $RMSEA = .204$ , [90% CI = 0.179, 0.230];  $CFI = .607$ ;  $TLI = .698$ )

### Parameter estimates:

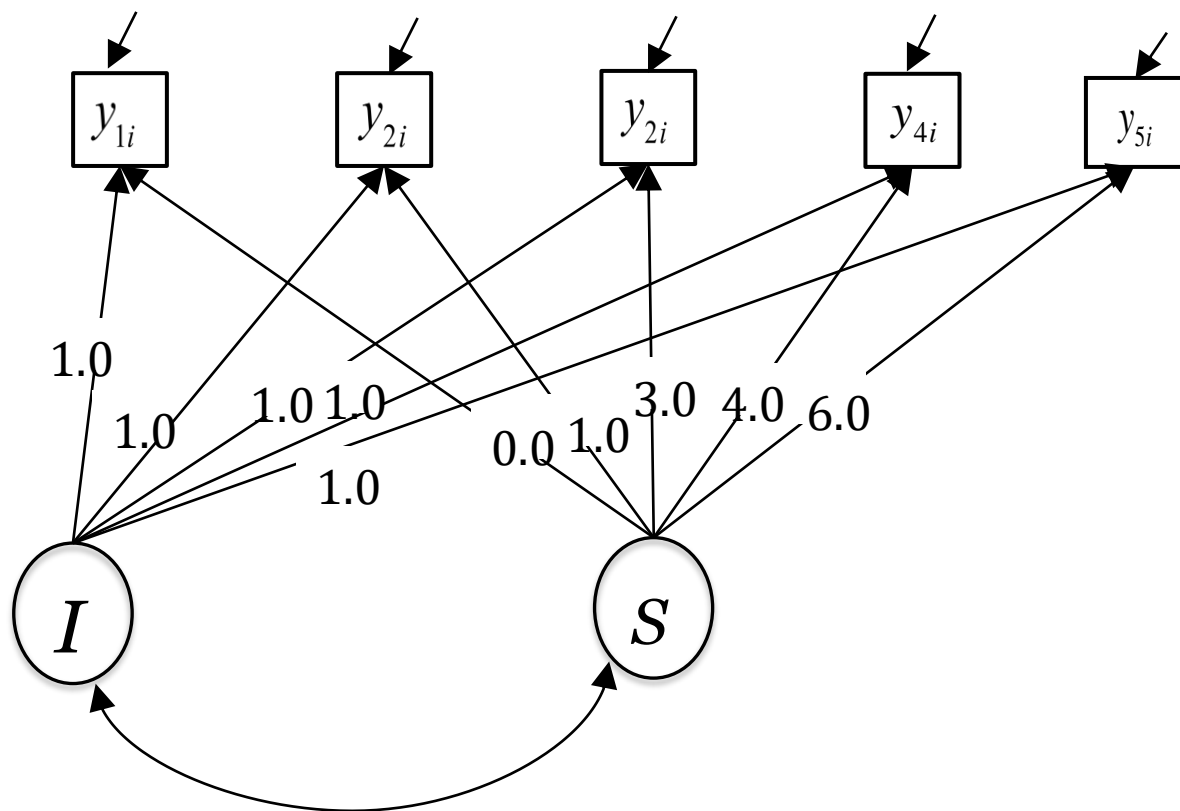
Intercept:	1.398***
Intercept variance:	0.075***
Residual variance:	0.092 – 1.167, all***

# Linear growth



Unconditional Linear LGCM

# Linear growth



```

32 # 002_Linear growth model
33 linear <- ' i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5
34           s =~ 0*lone1 + 1*lone2 + 3*lone3 + 4*lone4 + 6*lone5'
35 fit_linear <- growth(linear, data = data)
36 summary(fit_linear, fit.measures = TRUE)

```

002\_Linear\_growht\_curve\_model

TITLE: 002\_Linear\_growht\_curve\_model

DATA:

FILE IS data.dat;  
LISTWISE = ON;

VARIABLE:

NAMES ARE

id female pdu1 ace1 worry1  
lone1 lone2 lone3 lone4 lone5  
anx1 anx2 anx3 anx4 anx5  
dep1 dep2 dep3 dep4 dep5  
host1 host2 host3 host4 host5  
percon5 percon5b subs5 subs5b sleep5 sleep5b;

USEVARIABLES ARE

lone1 lone2 lone3 lone4 lone5;

MISSING ARE ALL (-999);

ANALYSIS:

ESTIMATOR = ML;

MODEL:

I S|lone1@0 lone2@1 lone3@3 lone4@4 lone5@6;

OUTPUT:

SAMPSTAT;

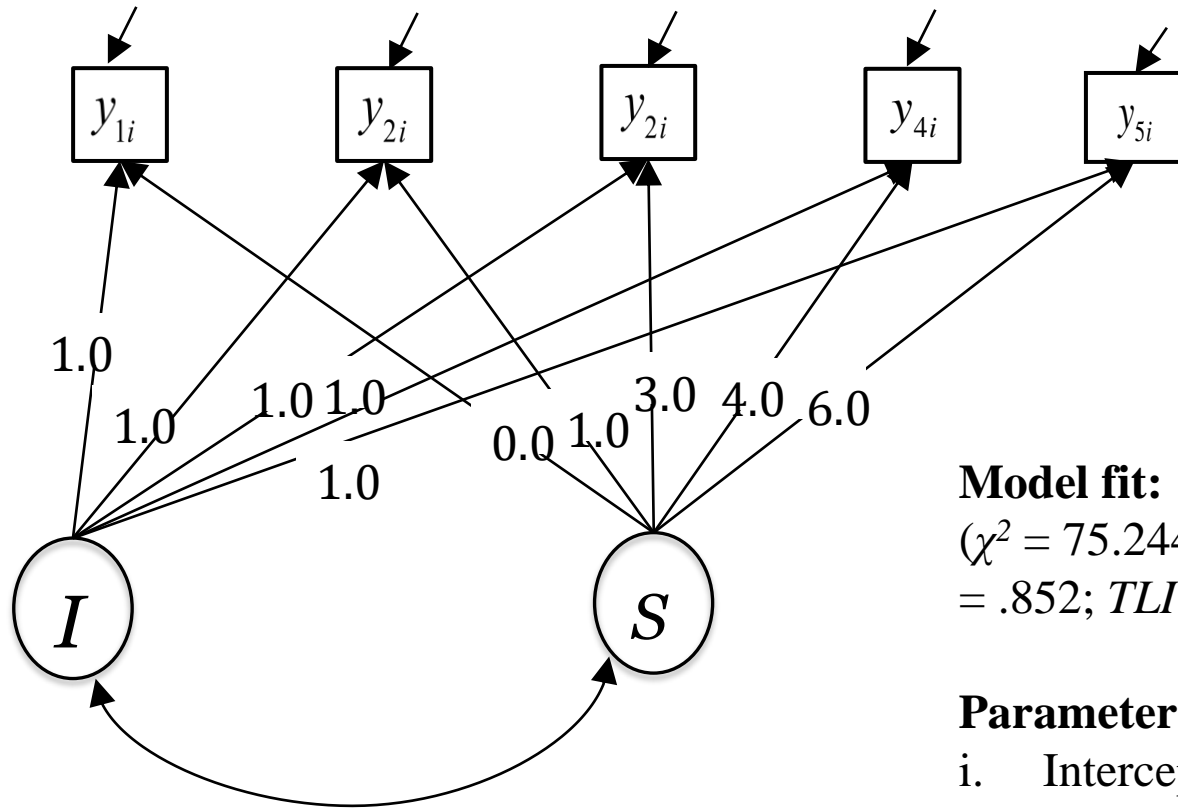
PLOT:

TYPE = PLOT3;

SERIES = lone1 - lone5(S);



# Linear growth



Unconditional Linear LGCM

## RESULTS

### Model fit:

( $\chi^2 = 75.244$ ,  $df = 10$ ;  $p < .001$ ;  $RMSEA = .143$ , [90% CI = 0.113, 0.174];  $CFI = .852$ ;  $TLI = .852$ )

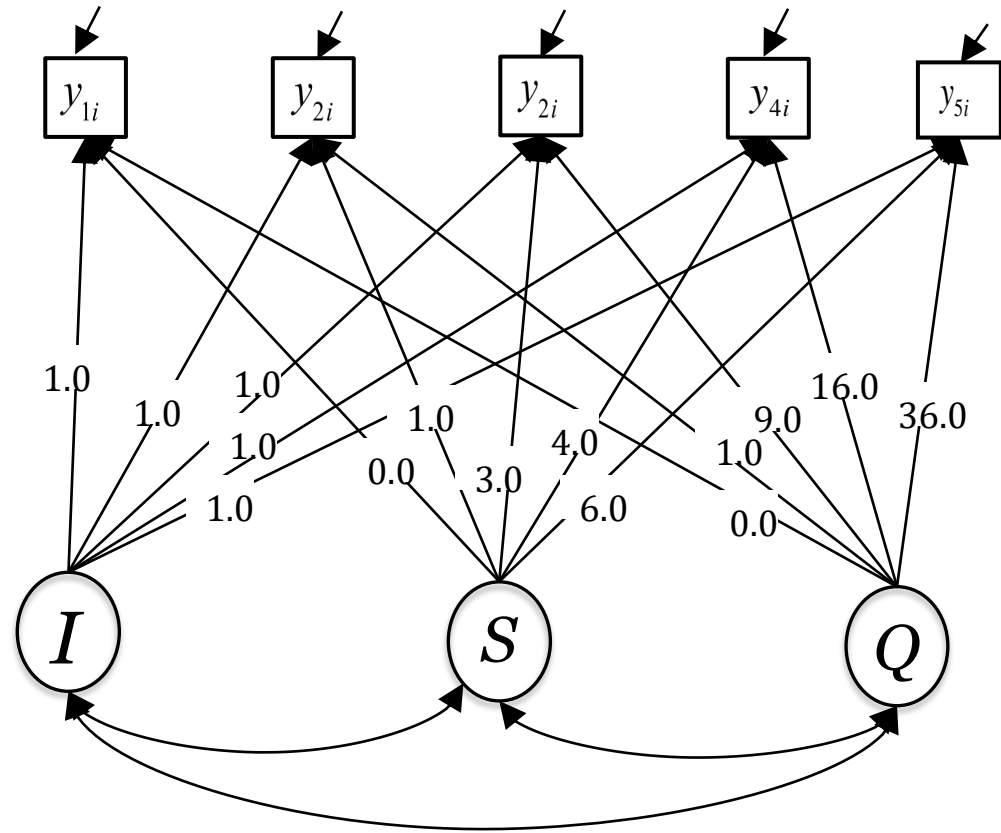
### Parameter estimates:

- i. Intercept: 1.466\*\*\*
- ii. Slope: -0.025\*\*\*

### (Co)Variances:

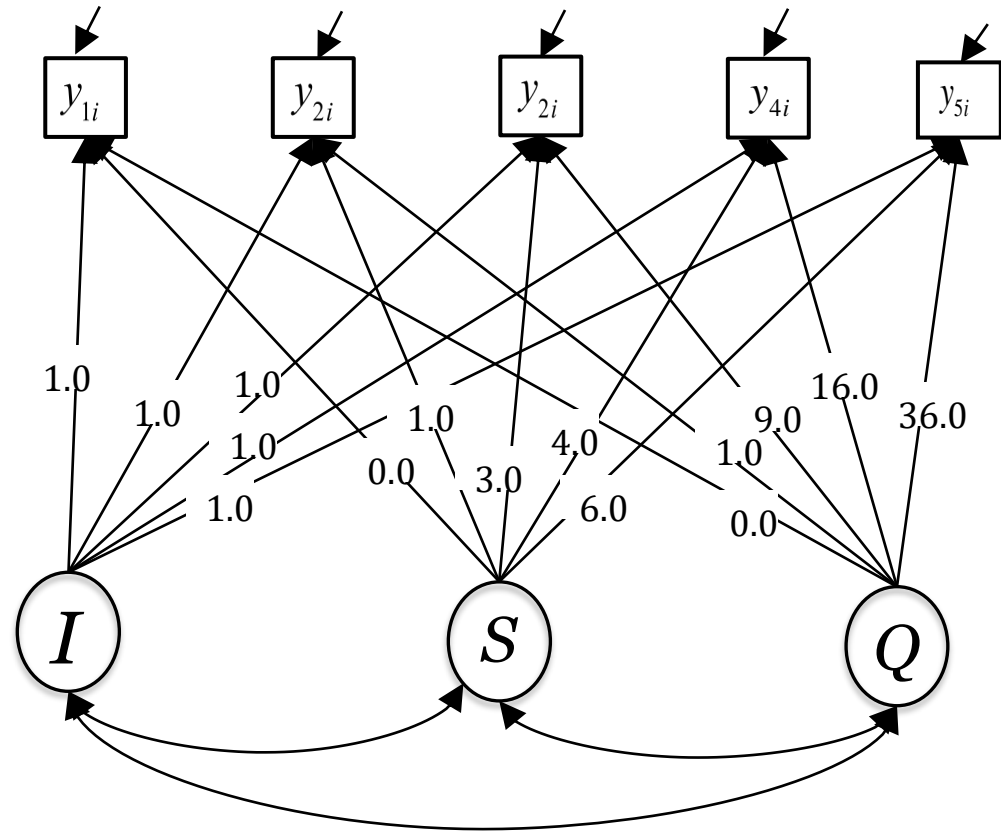
- i. Intercept: 0.139\*\*\*
- ii. Slope: 0.003\*\*\*
- iii. Intercept WITH Slope: -0.015\*\*\*

# Quadratic growth



Unconditional Quadratic LGCM

# Quadratic growth



```

40 # 003_Quadratic growth model
41 quadratic <- ' i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5
42               s =~ 0*lone1 + 1*lone2 + 3*lone3 + 4*lone4 + 6*lone5
43               q =~ 0*lone1 + 1*lone2 + 9*lone3 + 16*lone4 + 36*lone5'
44 fit_quadratic <- growth(quadratic, data = data)
45 summary(fit_quadratic, fit.measures = TRUE)

```

003\_Quadratic\_growht\_curve\_model

TITLE: 003\_Quadratic\_growht\_curve\_model

DATA:

FILE IS data.dat;  
LISTWISE = ON;

VARIABLE:

NAMES ARE

id female pdu1 ace1 worry1  
lone1 lone2 lone3 lone4 lone5  
anx1 anx2 anx3 anx4 anx5  
dep1 dep2 dep3 dep4 dep5  
host1 host2 host3 host4 host5  
percon5 percon5b subs5 subs5b sleep5 sleep5b;

USEVARIABLES ARE

lone1 lone2 lone3 lone4 lone5;

MISSING ARE ALL (-999);

ANALYSIS:

ESTIMATOR = ML;

MODEL:

I S Q|lone1@0 lone2@1 lone3@3 lone4@4 lone5@6;

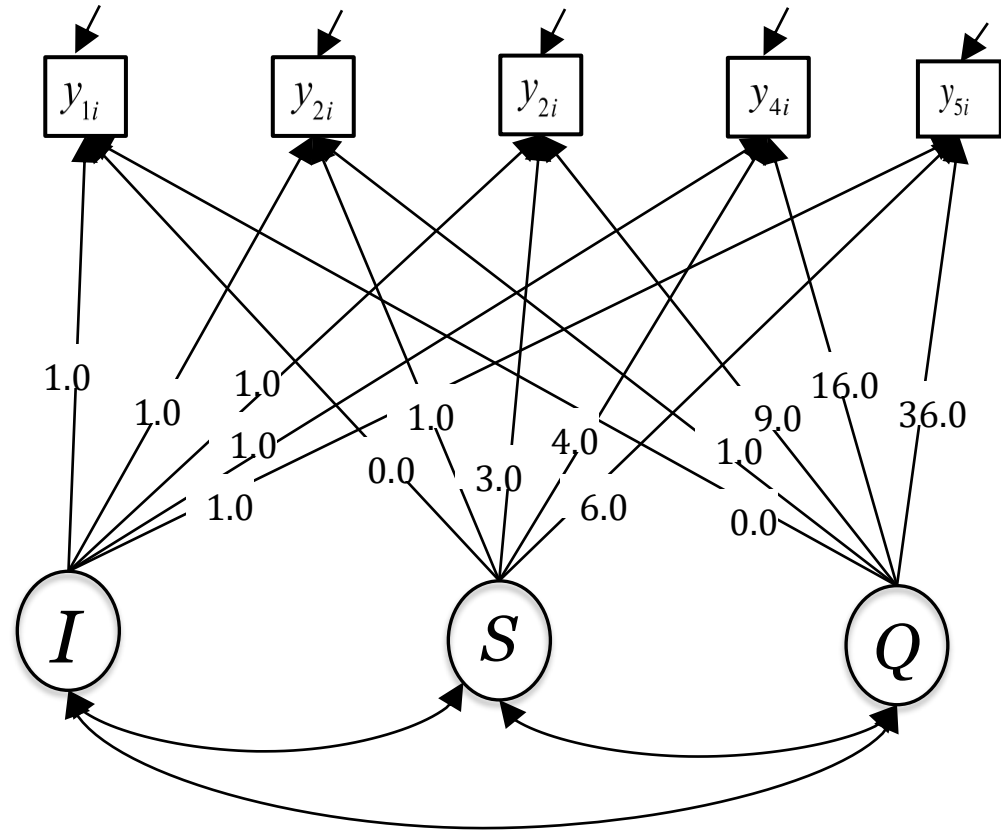
OUTPUT:

SAMPSTAT;

PLOT:

TYPE = PLOT3;  
SERIES = lone1 - lone5(S);

# Quadratic growth



Unconditional Quadratic LGCM

## RESULTS

### Model fit:

( $\chi^2 = 46.671$ ,  $df = 6$ ;  $p < .001$ ;  $RMSEA = .145$ , [90% CI = 0.108, 0.185];  $CFI = .908$ ;  $TLI = .846$ )

### Parameter estimates:

- i. Intercept: 1.466\*\*\*
- ii. Slope: 0.017
- iii. Quadratic: -0.007\*\*

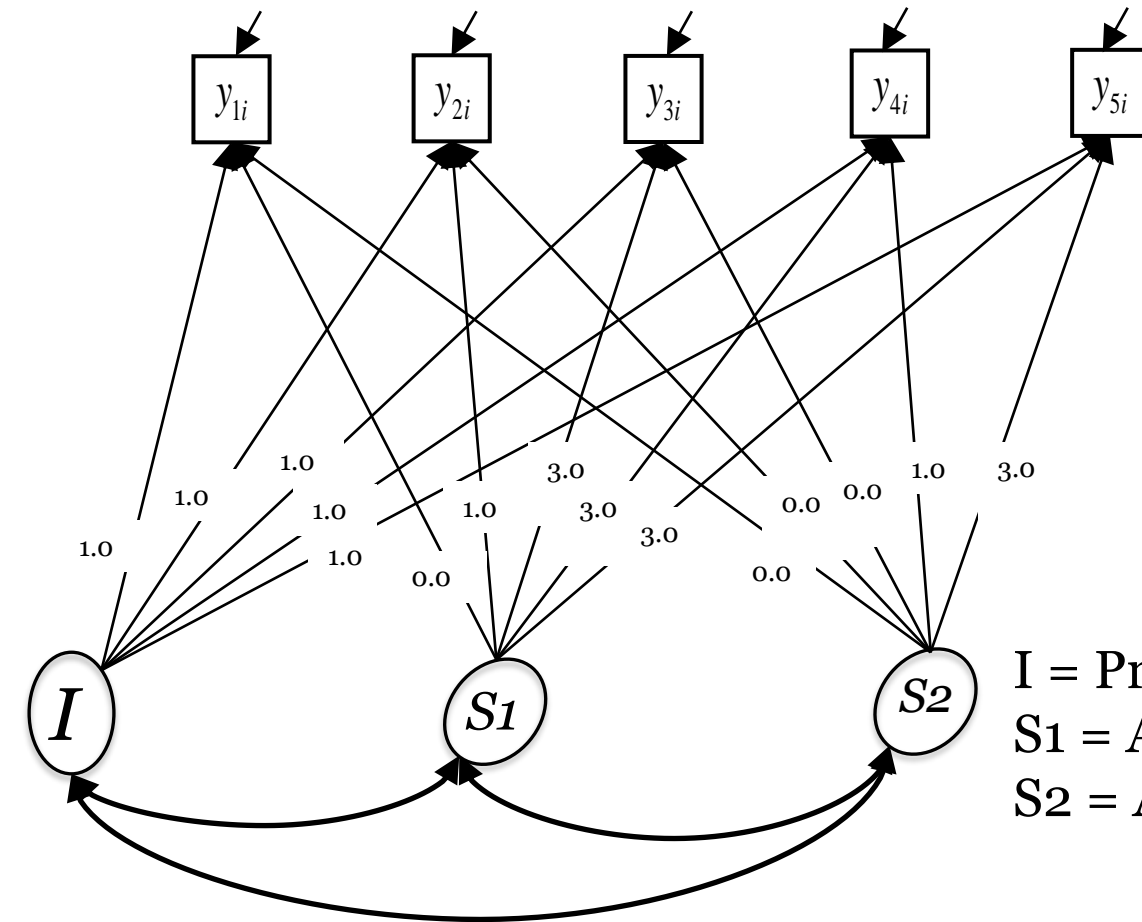
### (Co)Variances:

- i. Intercept: 0.148\*\*\*
- ii. Slope: 0.003\*\*
- iii. Quadratic: 0.000
- iv. Intercept WITH Slope: -0.020\*
- v. Intercept WITH Quadratic: 0.000
- vi. Slope WITH Quadratic: -0.002

# Spline/Piecewise/Multiphase/Slope-segmented LGCM

- When theoretical reasons suggest to separate time/development into discrete phases
  - Trajectory of loneliness before divorce and after divorce
  - Trajectory of depression before and after intervention
  - Pre-crawling and post-crawling in children
  - Childhood and adolescence
- Different phases of development are captured by more than one slope growth factor
  - Knots or transition points show where one phase is ending, and another phase is beginning

# Bilinear Spline/Piecewise/Multiphase LGCM - 1



Intercept at Time 1, knot at Time 3

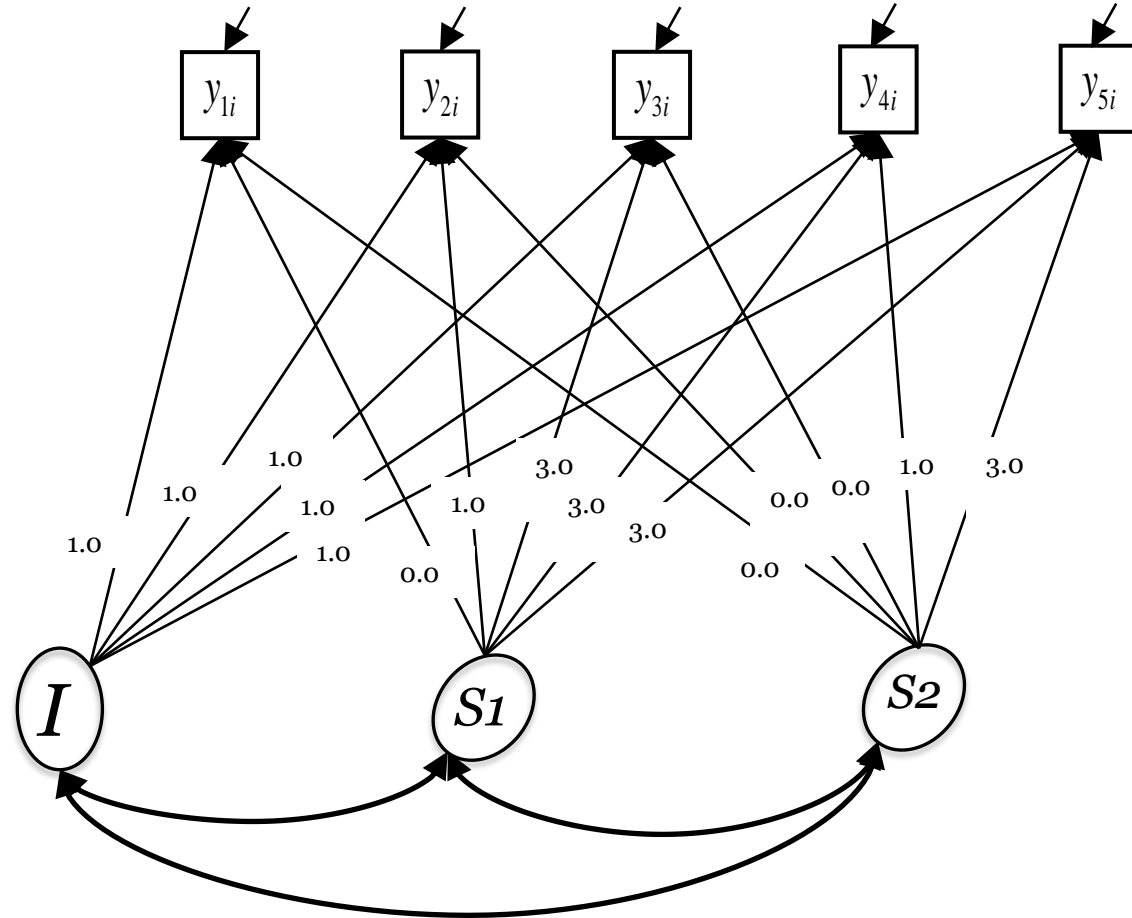
1	0	0	Time 1, 2015
1	1	0	Time 2, 2016
1	3	0	Time 3, 2018
1	3	1	Time 4, 2019
1	3	3	Time 5, 2021

I = Predicted average value of outcome in 2015

S1 = Average rate of change in outcome from 2015 through 2018

S2 = Average rate of change in outcome from 2018 through 2021

# Bilinear Spline/Piecewise/Multiphase LGCM - 1



Intercept at Time 1, knot at Time 3

I = Predicted average value of outcome **in 2015**

S1 = Average rate of change in outcome from **2015 through 2018**

S2 = Average rate of change in outcome from **2018 through 2021**

004\_1\_Bilinear\_spline\_growht\_curve\_model

TITLE: 004\_Bilinear\_spline\_growht\_curve\_model

DATA:

FILE IS data.dat;

LISTWISE = ON;

VARIABLE:

NAMES ARE

id female pdu1 ace1 worry1

lone1 lone2 lone3 lone4 lone5

anx1 anx2 anx3 anx4 anx5

dep1 dep2 dep3 dep4 dep5

host1 host2 host3 host4 host5

percon5 percon5b subs5 subs5b sleep5 sleep5b;

USEVARIABLES ARE

lone1 lone2 lone3 lone4 lone5;

MISSING ARE ALL (-999);

ANALYSIS:

ESTIMATOR = ML;

MODEL:

I S1|lone1@0 lone2@1 lone3@3 lone4@3 lone5@3;!Slope 1

I S2|lone1@0 lone2@0 lone3@0 lone4@1 lone5@3;!Slope 2

OUTPUT:

SAMPSTAT;

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```
51 # 004_1_Bilinear/Spline growth curve model
52
53 bilinear <- ' i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5
54             s1 =~ 0*lone1 + 1*lone2 + 3*lone3 + 3*lone4 + 3*lone5
55             s2 =~ 0*lone1 + 0*lone2 + 0*lone3 + 1*lone4 + 3*lone5'
56 fit_bilinear <- growth(bilinear, data = data)
57 summary(fit_bilinear, fit.measures = TRUE)
```

# Bilinear Spline/Piecewise/Multiphase LGCM - 1

Intercept at Time 1, knot at Time 3

1	0	0	Time 1, 2015
1	1	0	Time 2, 2016
1	3	0	Time 3, 2018
1	3	1	Time 4, 2019
1	3	3	Time 5, 2021

I = Predicted average value of outcome **in 2015**  
S1 = Average rate of change in outcome from **2015 through 2018**  
S2 = Average rate of change in outcome from **2018 through 2021**

## RESULTS

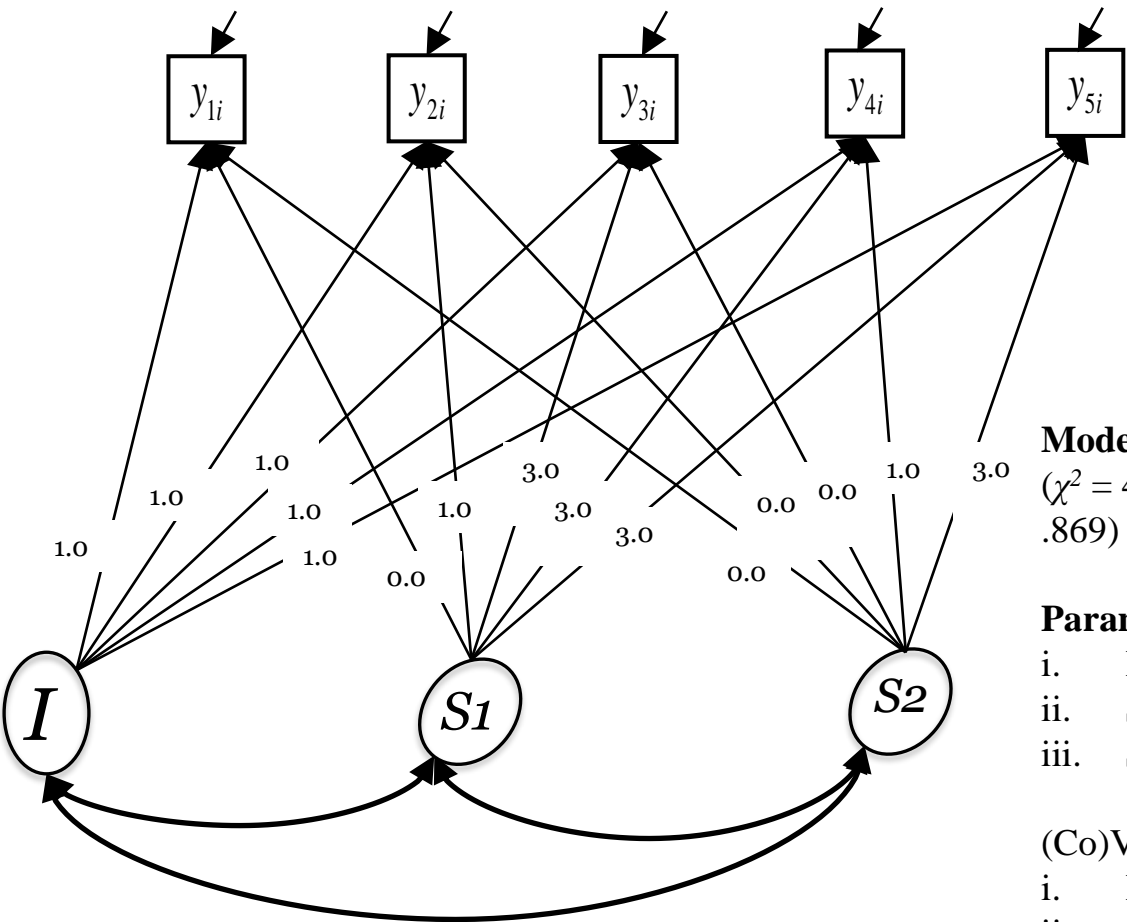
**Model fit:**  
( $\chi^2 = 40.781$ ,  $df = 6$ ;  $p < .001$ ;  $RMSEA = .134$ , [90% CI = 0.097, 0.175];  $CFI = .921$ ;  $TLI = .869$ )

**Parameter estimates:**

i.	Intercept:	1.444***
ii.	Slope 1:	0.007
iii.	Slope 2:	-0.059***

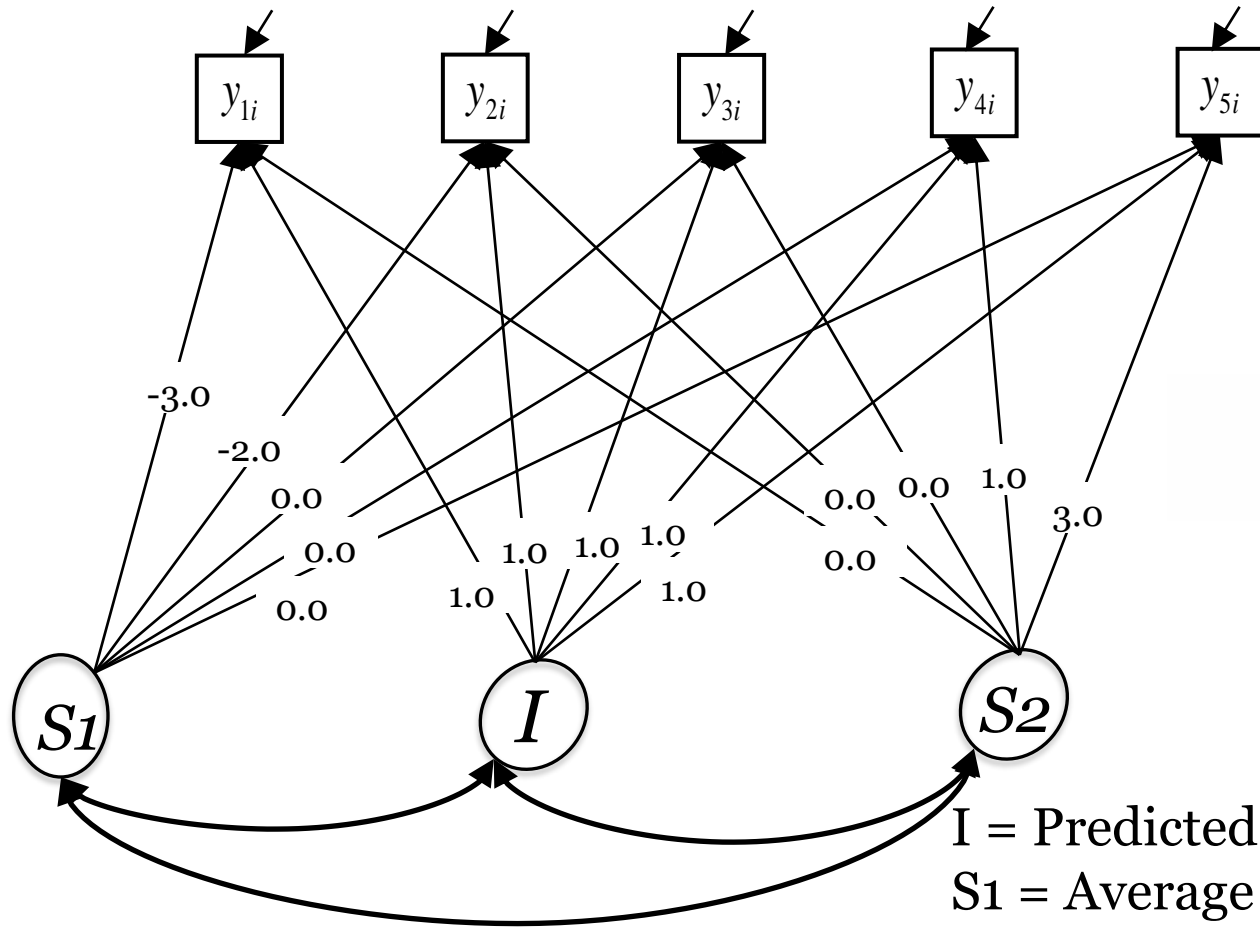
(Co)Variances:

i.	Intercept:	0.140***
ii.	Slope 1:	0.001**
iii.	Slope 2:	0.002
iv.	Intercept WITH Slope 1:	-0.015**
v.	Intercept WITH Slope 2	-0.019***
vi.	Slope 1 WITH Slope 2	0.000





# Spline/Piecewise/Multiphase LGCM - 2



Intercept at Time 3, knot at Time 3

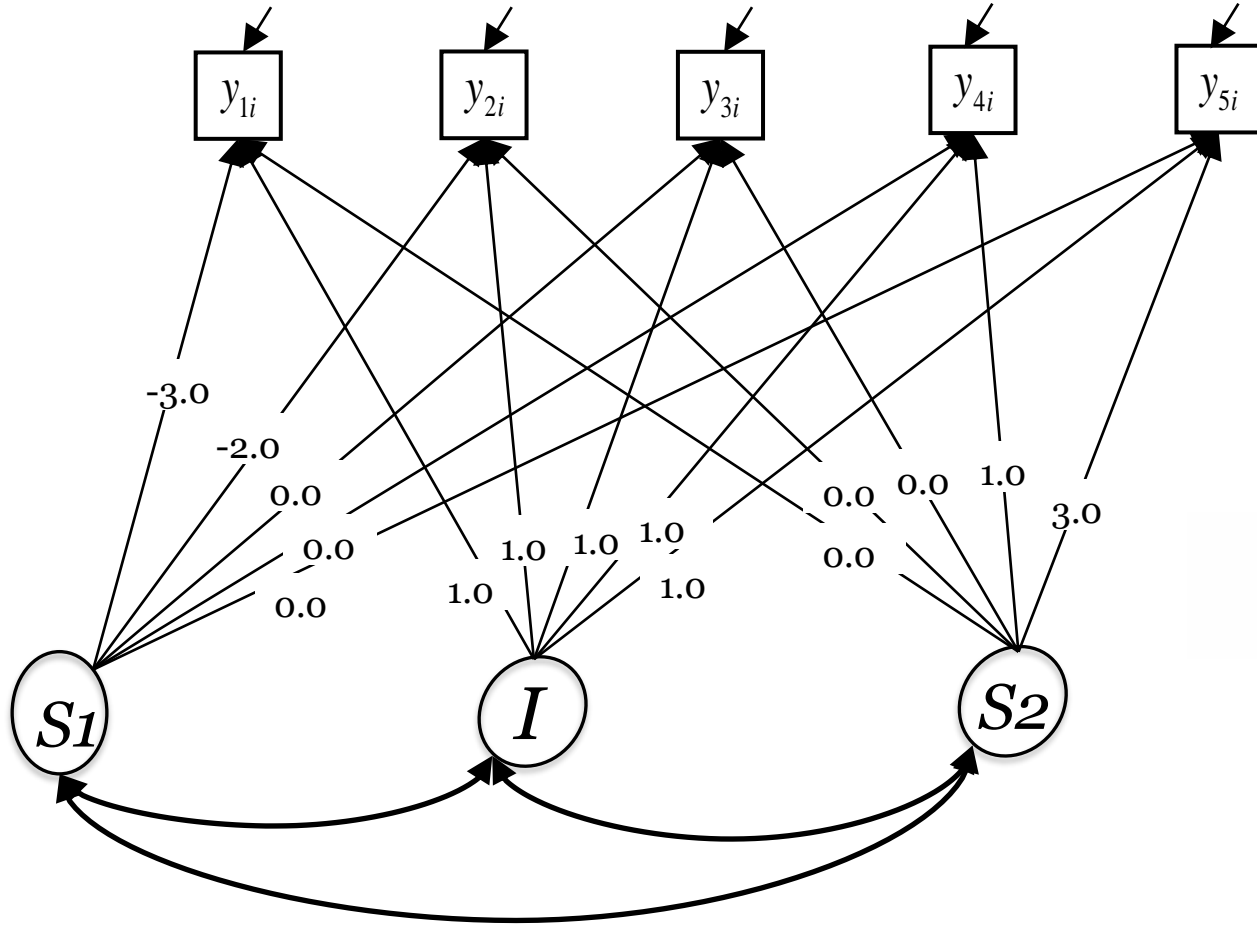
-3	1	0	Time 1, 2015
-2	1	0	Time 2, 2016
0	1	0	Time 3, 2018
0	1	1	Time 4, 2019
0	1	3	Time 5, 2021

I = Predicted average value of outcome in 2018

S1 = Average rate of change in outcome prior to 2018

S2 = Average rate of change in outcome from 2018 through 2021

# Spline/Piecewise/Multiphase LGCM - 2



Intercept at Time 3, knot at Time 3

I = Predicted average value of **outcome in 2018**

S1 = Average rate of change in outcome **prior to 2018**

S2 = Average rate of change in outcome from **2018 through 2021**

004\_2\_Bilinear\_spline\_growht\_curve\_model\_2

TITLE: 002\_Bilinear\_spline\_growht\_curve\_model

DATA:

FILE IS data.dat;  
LISTWISE = ON;

VARIABLE:

NAMES ARE

id female pdul acel worry1  
lone1 lone2 lone3 lone4 lone5  
anx1 anx2 anx3 anx4 anx5  
dep1 dep2 dep3 dep4 dep5  
host1 host2 host3 host4 host5  
percon5 percon5b subs5 subs5b sleep5 sleep5b;

USEVARIABLES ARE

lone1 lone2 lone3 lone4 lone5;

MISSING ARE ALL (-999);

ANALYSIS:

ESTIMATOR = ML;

MODEL:

I S1|lone1@-3 lone2@-2 lone3@0 lone4@0 lone5@0;!Slope 1  
I S2|lone1@0 lone2@0 lone3@0 lone4@1 lone5@3;!Slope 2

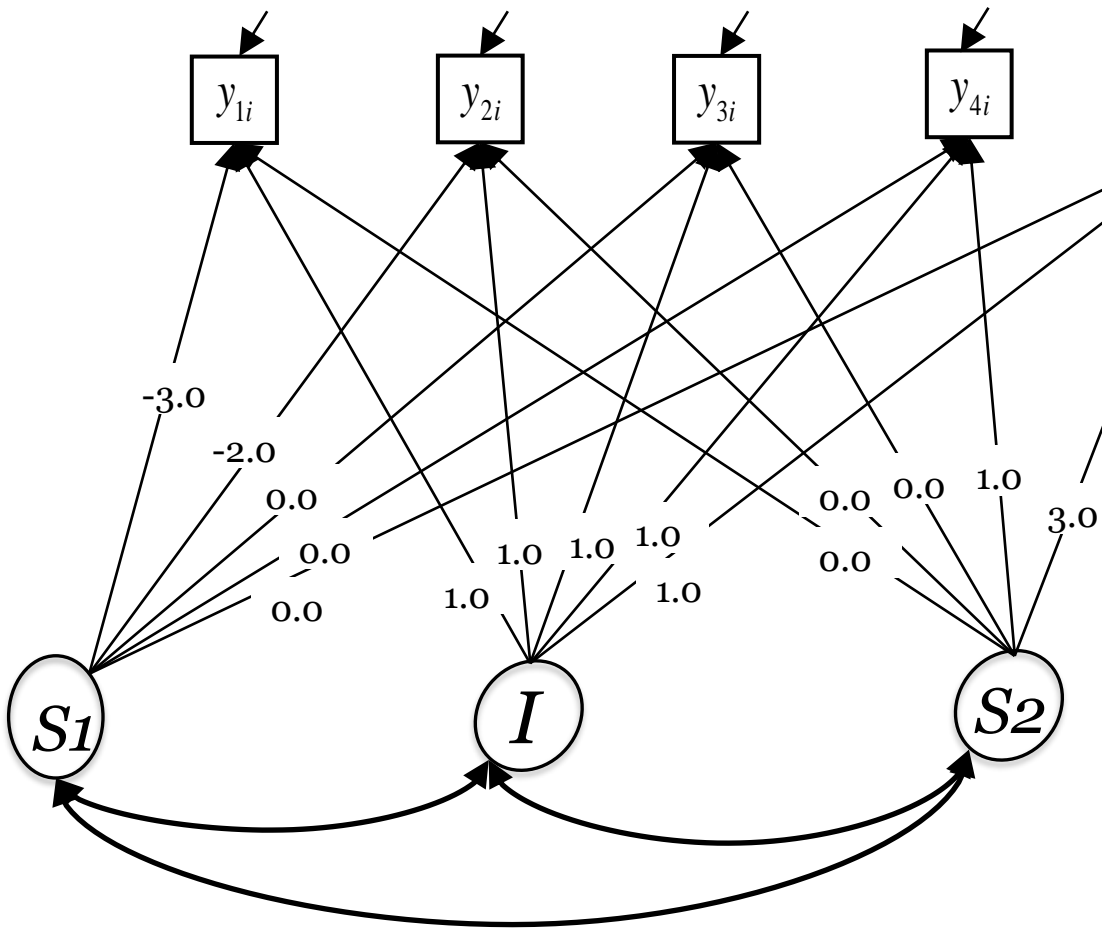
OUTPUT:

SAMPSTAT;

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```
60 # 004_2_Bilinear/Spline growth curve model - 2
61 bilinear_2 <- ' i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5
62             s1 =~ -3*lone1 + -2*lone2 + 0*lone3 + 0*lone4 + 0*lone5
63             s2 =~ 0*lone1 + 0*lone2 + 0*lone3 + 1*lone4 + 3*lone5'
64 fit_bilinear_2 <- growth(bilinear_2, data = data)
65 summary(fit_bilinear_2, fit.measures = TRUE)
```

# Spline/Piecewise/Multiphase LGCM - 2



Intercept at Time 3, knot at Time 3

-3	1	0	Time 1, 2015
-2	1	0	Time 2, 2016
0	1	0	Time 3, 2018
0	1	1	Time 4, 2019
0	1	3	Time 5, 2021

I = Predicted average value of **outcome in 2018**  
S1 = Average rate of change in outcome **prior to 2018**  
S2 = Average rate of change in outcome **from 2018 through 2021**

## RESULTS

### Model fit:

( $\chi^2 = 40.781$ ,  $df = 6$ ;  $p < .001$ ;  $RMSEA = .134$ , [90% CI = 0.097, 0.175];  $CFI = .921$ ;  $TLI = .869$ )

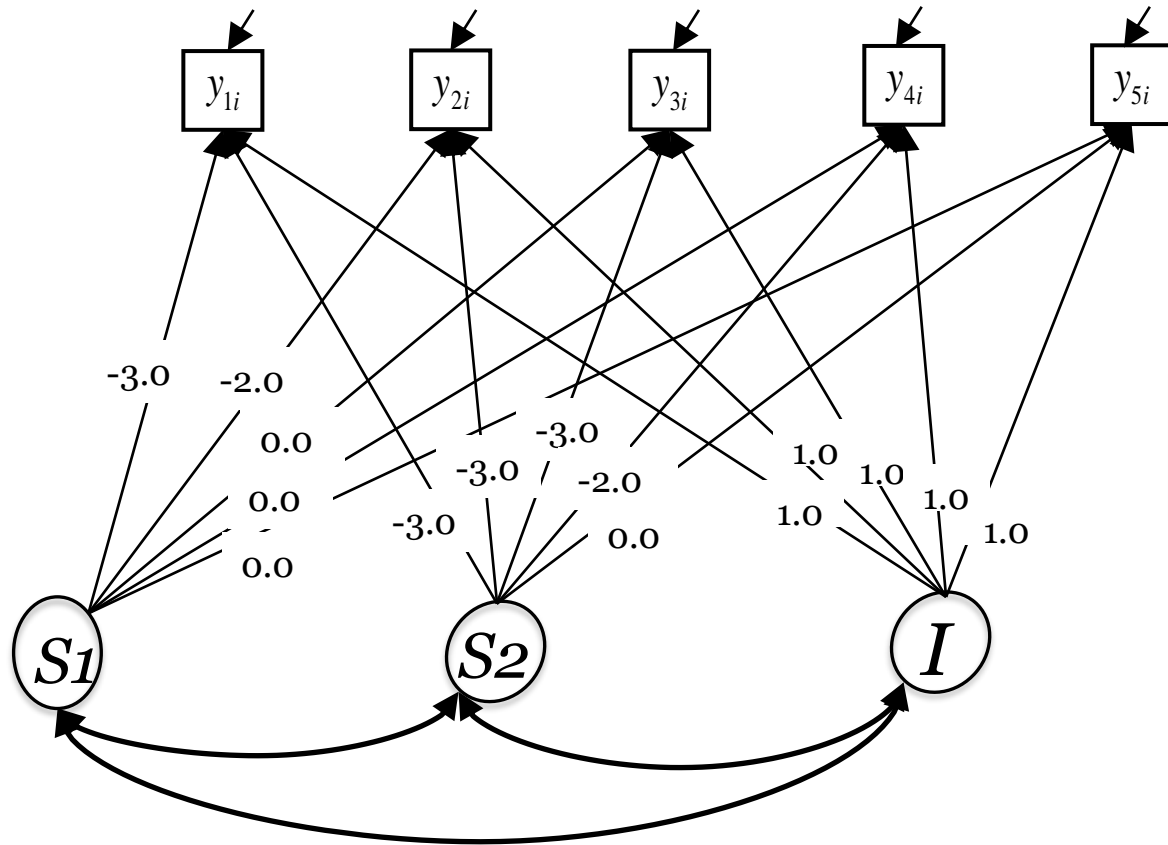
### Parameter estimates:

i.	Intercept:	1.465***
ii.	Slope 1:	0.007
iii.	Slope 2:	-0.059***

### (Co)Variances:

i.	Intercept:	0.126***
ii.	Slope 1:	0.008**
iii.	Slope 2:	0.002
iv.	Intercept WITH Slope 1:	0.010*
v.	Intercept WITH Slope 2	-0.018**
vi.	Slope 1 WITH Slope 2	0.000

# Spline/Piecewise/Multiphase LGCM - 3



Intercept at Time 5, knot at Time 3

-3	-3	1	Time 1, 2015
-2	-3	1	Time 2, 2016
0	-3	1	Time 3, 2018
0	-2	1	Time 4, 2019
0	0	1	Time 5, 2021

I = Predicted average value of outcome at end of observation in 2021

S1 = Average rate of change in outcome prior to 2018

S2 = Average rate of change in between 2018 to 2021

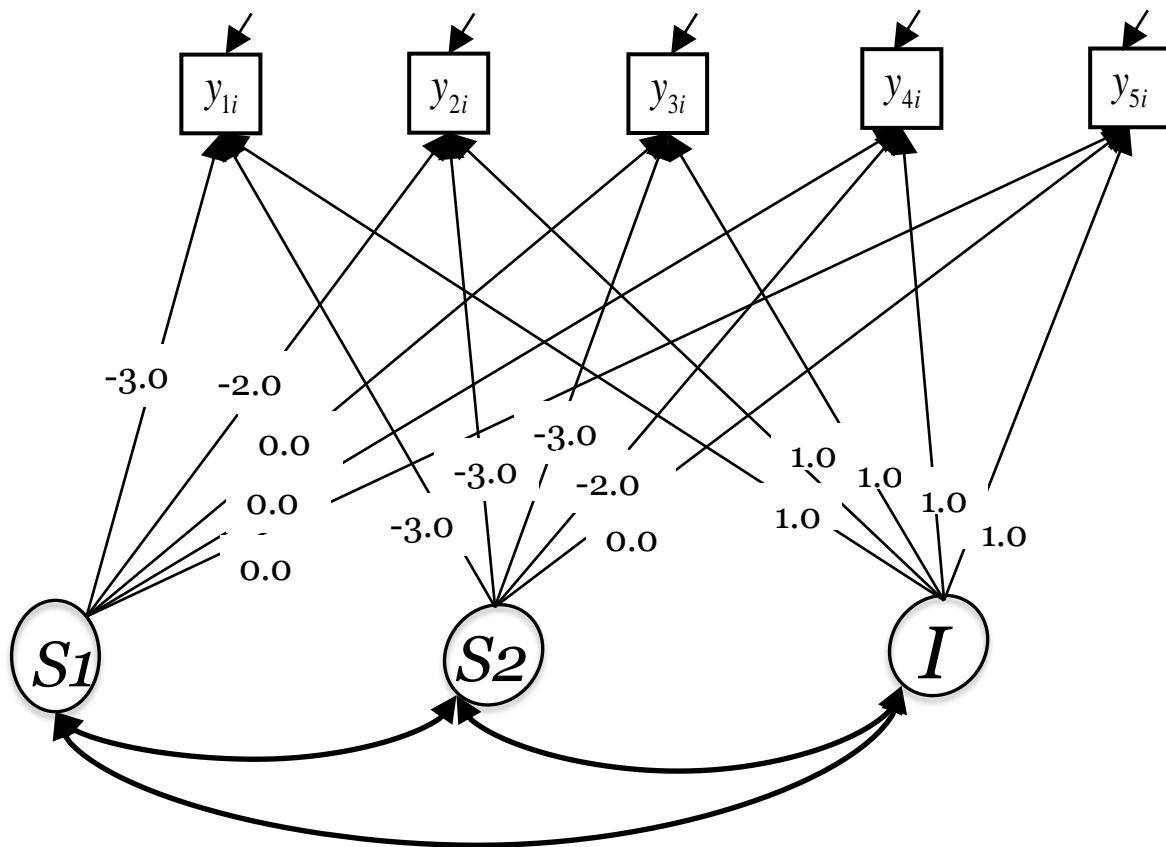
# Spline/Piecewise/Multiphase LGCM - 3

Intercept at Time 5, knot at Time 3

I = Predicted average value of outcome at end of observation in 2021

S1 = Average rate of change in outcome prior to 2018

S2 = Average rate of change in outcome from 2018 through 2021



```
004_3_Bilinear_spline_growht_curve_model_3
TITLE: 002_Bilinear_spline_growht_curve_model
DATA:
FILE IS data.dat;
LISTWISE = ON;

VARIABLE:
NAMES ARE
id female pdul acel worry1
lone1 lone2 lone3 lone4 lone5
anx1 anx2 anx3 anx4 anx5
dep1 dep2 dep3 dep4 dep5
host1 host2 host3 host4 host5
percon5 percon5b subs5 subs5b sleep5 sleep5b;

USEVARIABLES ARE
lone1 lone2 lone3 lone4 lone5;

MISSING ARE ALL (-999);

ANALYSIS:
ESTIMATOR = ML;

MODEL:
I S1|lone1@-3 lone2@-3 lone3@-3 lone4@-2 lone5@0;!Slope 1
I S2|lone1@-3 lone2@-2 lone3@0 lone4@0 lone5@0;!Slope 2

OUTPUT:
SAMPSTAT;
```

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```
68 # 004_3_Bilinear/Spline growth curve model - 3
69 bilinear_3 <- ' i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5
70           s1 =~ -3*lone1 + -3*lone2 + -3*lone3 + -2*lone4 + 0*lone5
71           s2 =~ -3*lone1 + -2*lone2 + 0*lone3 + 0*lone4 + 0*lone5'
72 fit_bilinear_3 <- growth(bilinear_3, data = data)
73 summary(fit_bilinear_3, fit.measures = TRUE)
```

# Spline/Piecewise/Multiphase LGCM - 3

Intercept at Time 5, knot at Time 3

-3	-3	1	Time 1, 2015
-2	-3	1	Time 2, 2016
0	-3	1	Time 3, 2018
0	-2	1	Time 4, 2019
0	0	1	Time 5, 2021

I = Predicted average value of outcome at end of observation in 2021

S1 = Average rate of change in outcome prior to 2018

S2 = Average rate of change in outcome from 2018 through 2021

## RESULTS

### Model fit:

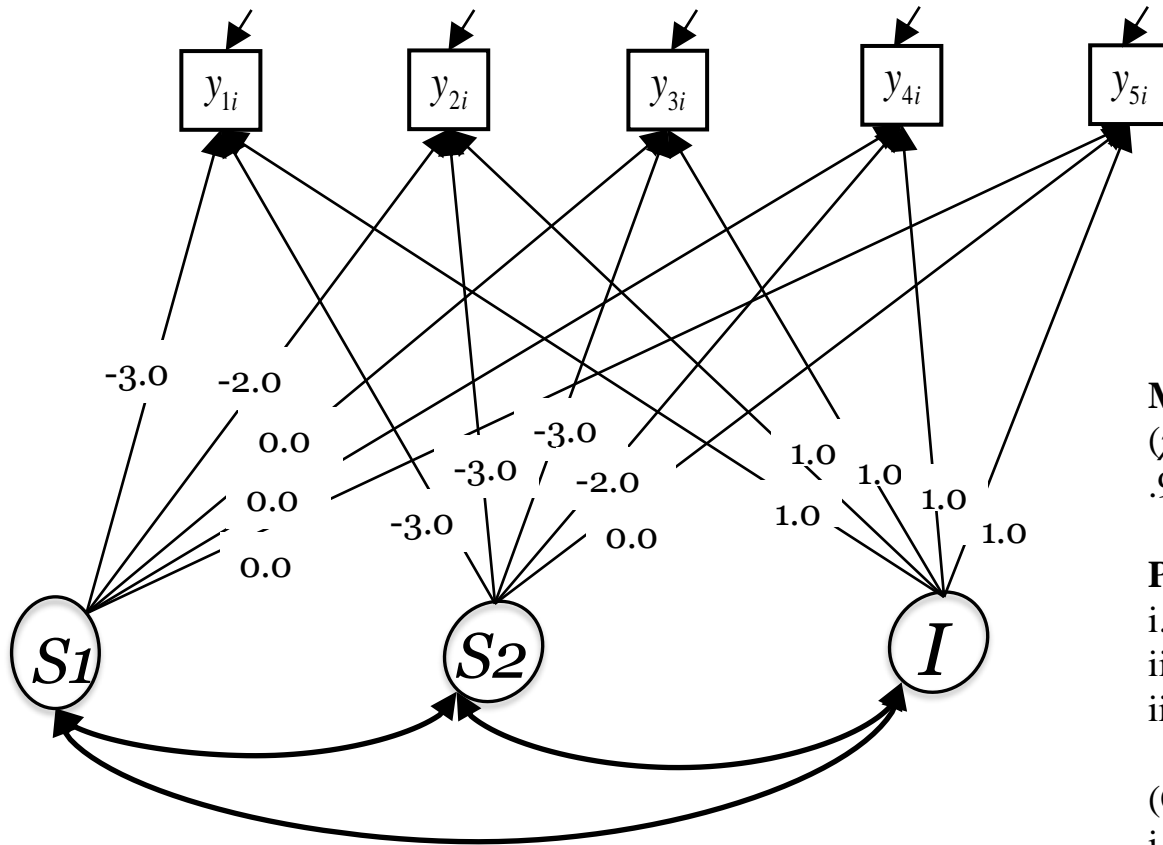
( $\chi^2 = 40.781$ ,  $df = 6$ ;  $p < .001$ ;  $RMSEA = .134$ , [90% CI = 0.097, 0.175];  $CFI = .921$ ;  $TLI = .869$ )

### Parameter estimates:

i.	Intercept:	1.288***
ii.	Slope 1:	-0.059***
iii.	Slope 2:	0.007

### (Co)Variances:

i.	Intercept:	0.036
ii.	Slope 1:	0.002
iii.	Slope 2:	0.008**
iv.	Intercept WITH Slope 1:	-0.012
v.	Intercept WITH Slope 2	0.011**
vi.	Slope 1 WITH Slope 2	0.000



# Model comparisons and selection

Model		Compared with	$\chi^2$	$df$	$RMSEA$	$CFI$	$TLI$
M1	No growth		186.443	13	.204[0.179, 0.230]	.607	.698
M2	Linear growth	M1	75.244	10	.143[0.113, 0.174]	.852	.852
M3	Quadratic growth	M2	46.671	6	.145[0.108, 0.185]	.908	.846
M4	Bilinear spline growth	NON-NESTED!	40.781	6	.134[0.097, 0.175]	.921	.869

## Model Comparison

	Model M1 No growth	Model M2 Linear growth	Model M3 Quadratic growth	Model M4 Bilinear spline
Parameters	7	10	14	
-2LL	1629.268	1518.080	1489.508	
AIC	1643.269	1538.080	1517.507	1511.809
BIC	1669.669	1575.796	1570.308	1564.418
$\Delta$ parameters	-	3	4	
$\Delta$ -2LL	-	111.19***	28.573***	

- Do not compare nested models whose fit indices do not reach acceptable, e.g. M1 and M2
- Bilinear is a non-nested model with M1-M3
  - So use AIC and BIC

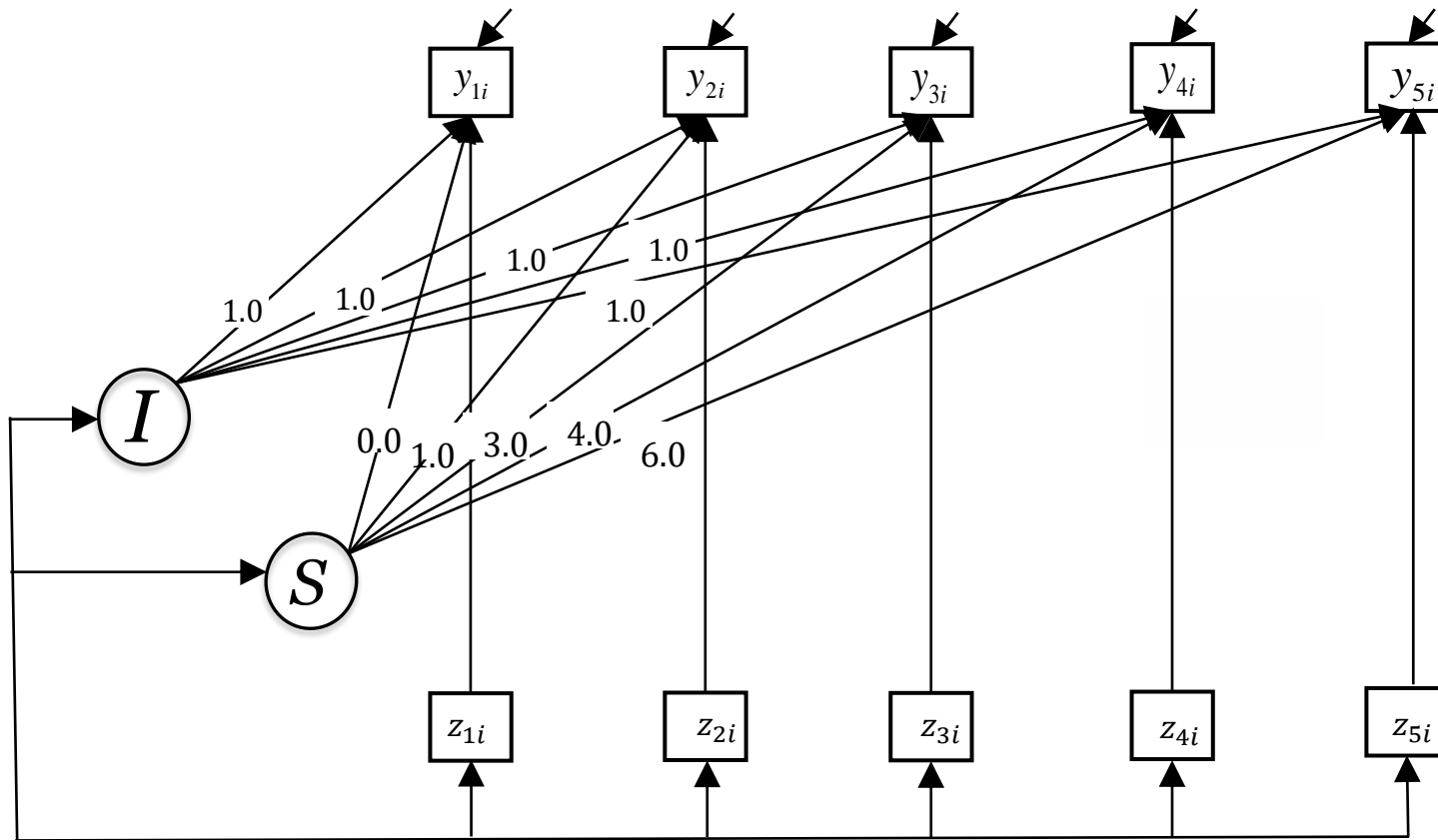
# Objectives of longitudinal research

1. Identification of intraindividual (within-person) changes (and stability)
  - Is there change over time on average?
    - ✓ Growth models can address various linear and nonlinear patterns of intraindividual change
2. Analysis of causes (determinants) of intraindividual change
  - What factors/mechanisms – time-varying/dynamical predictors – drive change?
    - ✓ Inclusion of time-varying (dynamical) predictors in growth models
3. Identification of interindividual differences (or similarity) in intraindividual change
  - Do different individuals change in different ways?
    - ✓ Differences between groups of persons in the way people change
4. Analysis of causes (determinants) of interindividual differences in intraindividual change
  - What factors explain between-person differences in change?
    - ✓ Inclusion of time-invariant covariates in growth models, multigroup LGCM, Growth mixture models
5. Interrelationships in change
  - Does change in one variable relate (*precede, covary and/or follow* ) to change in another variable?
  - Correlating slopes of X and Y could provide evidence that one variable is changing in the same people as another variable – correlated changes! Or common changes!
    - ✓ Multi (parallel & sequentially contingent) process LGCM



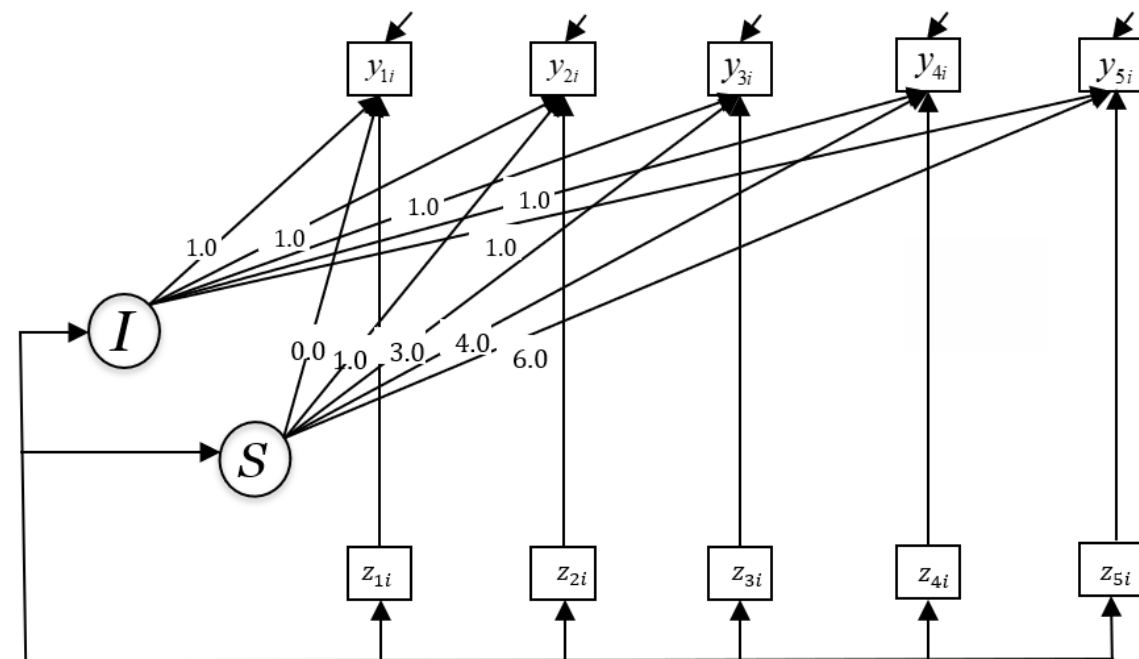
- What dynamics or factors drive within-person changes?
  - Does hostility affect the trajectory of loneliness?
    - Loneliness is more elevated than usual when someone is more hostile than usual?

# Conditional Linear LGCM, LGCM with Time-varying covariates



- TVC is exogenous to the developmental process
- The effect of TVC is a within-person effect which influences an individual's change trajectory
- Flexibility in SEM allows correlating TVC with  $I$  and  $S$  – growth factors.
  - Convergence problems
    - *Fix covariance between TVC with  $I$  and  $S$  to zero*

# Conditional Linear LGCM, LGCM with Time-varying covariates



```
005_Linear_growht_curve_model_with_time_varying_covariate
TITLE: 005_Linear_growht_curve_model_with_time_varying_covariate

DATA:
FILE IS data.dat;
LISTWISE = ON;

VARIABLE:
NAMES ARE
id female pdul ace1 worry1
lone1 lone2 lone3 lone4 lone5
anx1 anx2 anx3 anx4 anx5
dep1 dep2 dep3 dep4 dep5
host1 host2 host3 host4 host5
percon5 percon5b subs5 subs5b sleep5 sleep5b;

USEVARIABLES ARE
lone1 lone2 lone3 lone4 lone5
host1 host2 host3 host4 host5;

MISSING ARE ALL (-999);

ANALYSIS:
ESTIMATOR = ML;

MODEL:
I S|lone1@0 lone2@1 lone3@3 lone4@4 lone5@6;!Growth for loneliness

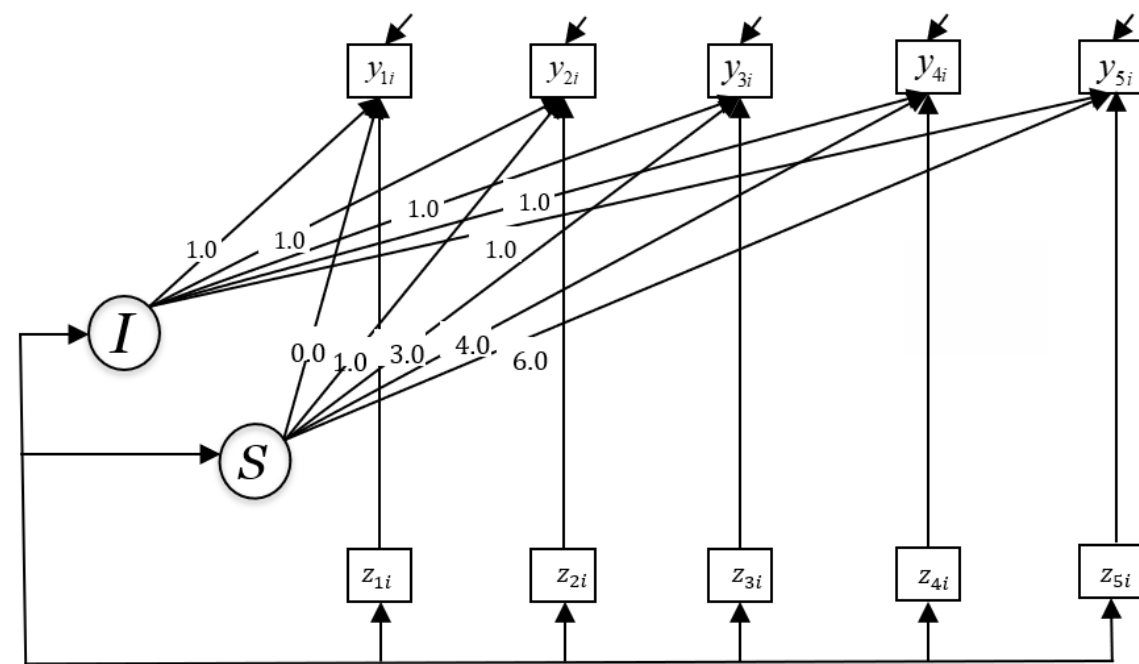
!Regress loneliness on time-varying covariate
lone1 ON host1;!By adding labels to the parameter estimates
lone2 ON host2;!you can test whether TVC effects are constant over time
lone3 ON host3;
lone4 ON host4;
lone5 ON host5;

!However, if you already assume constant effect of TVC over time
!and do not want to test, you can use this model specification
!lone1 ON host1(a);!By adding the same label (a) to the parameter estimates
!lone2 ON host2(a);!you constrain the effects to be constant across time
!lone3 ON host3(a);
!lone4 ON host4(a);
!lone5 ON host5(a);

!Fix TVC covariance with intercept and slope to zero
I S WITH host1-host5@0;

OUTPUT:
SAMPSTAT;
```

# Conditional Linear LGCM, LGCM with Time-varying covariates

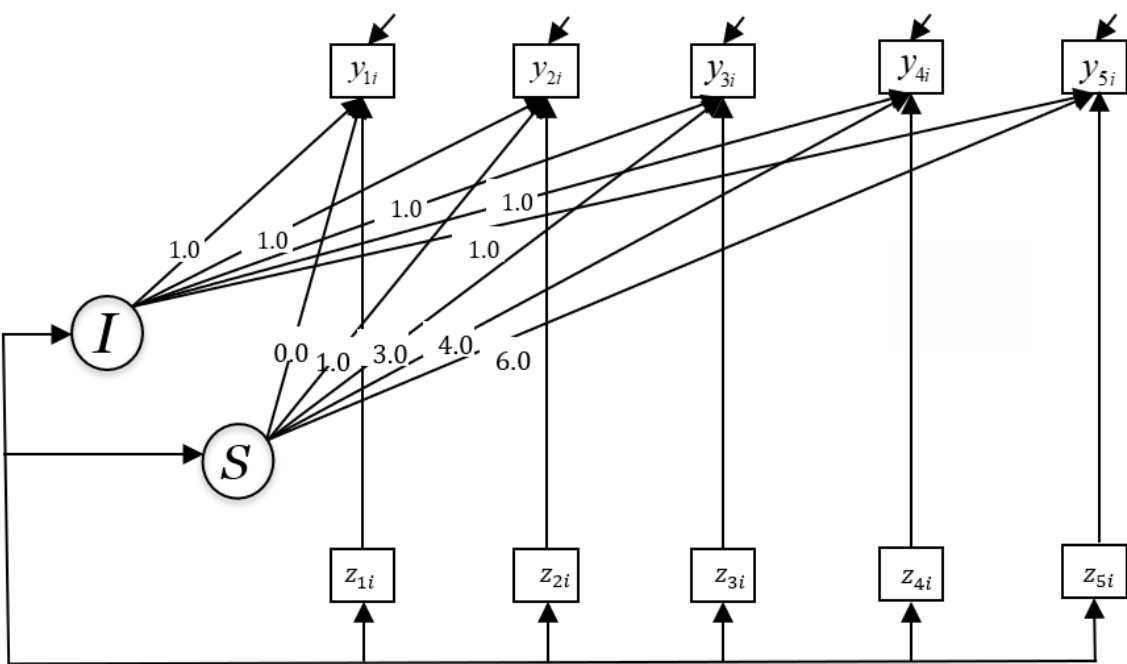


```

87 # 005_Linear growth curve model with time-varying covariates
88 timevaryingcov <- ' i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5
89                      s =~ 0*lone1 + 1*lone2 + 3*lone3 + 4*lone4 + 6*lone5
90 # Time-varying covariates
91 lone1 ~ host1           #lone1 ~ eq*host1
92 lone2 ~ host2           #lone2 ~ eq*host2
93 lone3 ~ host3           #lone3 ~ eq*host3
94 lone4 ~ host4           #lone4 ~ eq*host4
95 lone5 ~ host5           #lone5 ~ eq*host5
96
97 #Estimate the means of the TVC
98 host1 ~ 1
99 host2 ~ 1
100 host3 ~ 1
101 host4 ~ 1
102 host5 ~ 1
103
104 #Estimate covariance between TVC
105 host1 ~~ host2 + host3 + host4 + host5
106 host2 ~~ host3 + host4 + host5
107 host3 ~~ host4 + host5
108 host4 ~~ host5'
109
110 fit_timevaryingcov <- growth(timevaryingcov, data = data)
111 summary(fit_timevaryingcov, fit.measures = TRUE)

```

# Conditional Linear LGCM, LGCM with Time-varying covariates



## RESULTS

### Model fit:

( $\chi^2 = 103.191$ ,  $df = 30$ ;  $p < .001$ ;  $RMSEA = .087$ , [90% CI = 0.069, 0.106];  $CFI = .972$ ;  $TLI = .967$ )

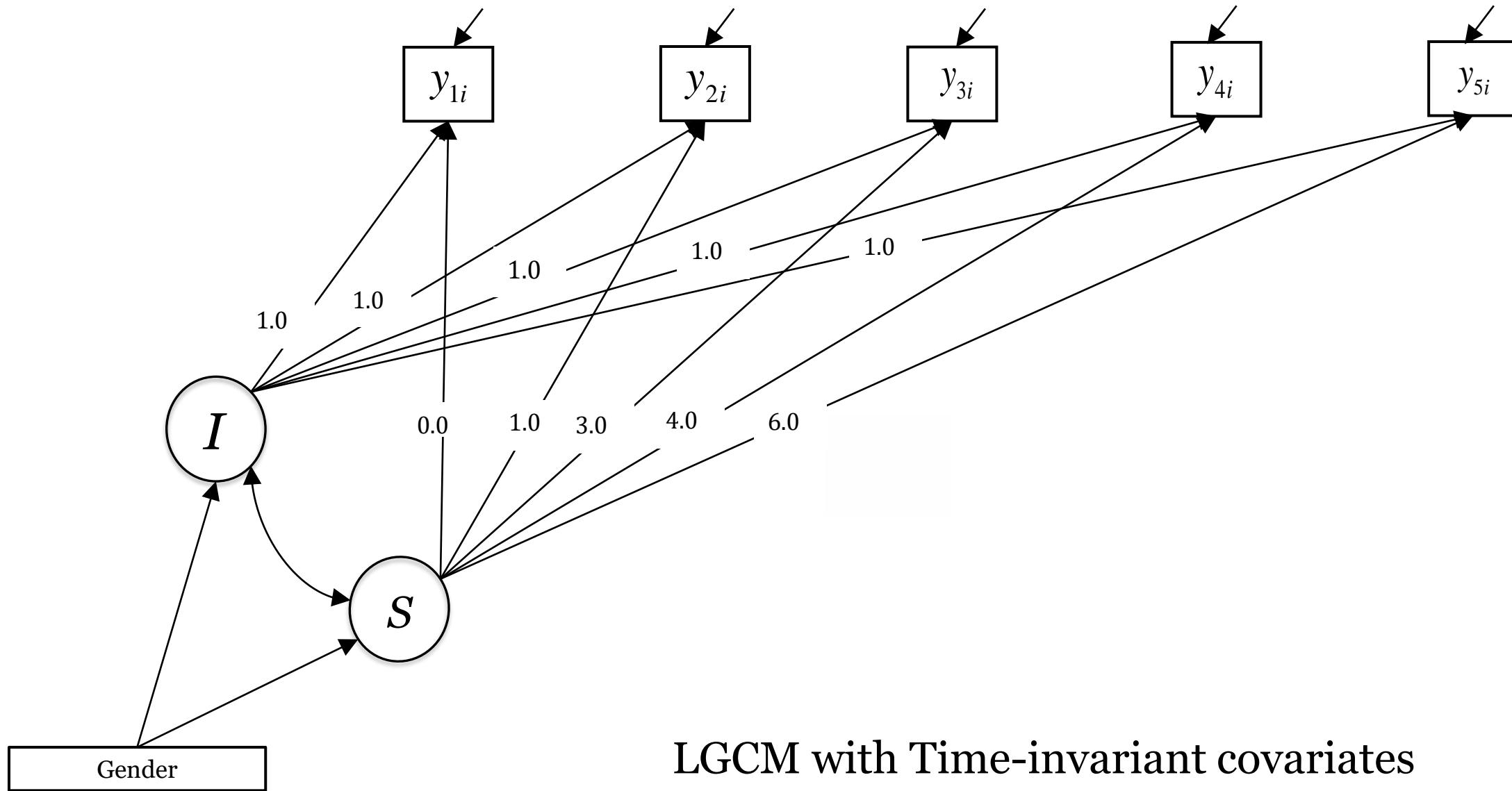
### Parameter estimates:

i.	Intercept:	0.414***
ii.	Slope 1:	-0.010
TVC		
i.	Hostility:	0.719 – 0.737
(Co)Variances:		
i.	Intercept:	0.028***
ii.	Slope 1:	0.001***
iii.	Intercept WITH Slope:	-0.003***
iv.	TVC WITH TVC:	0.036 – 0.161***

# Objectives of longitudinal research

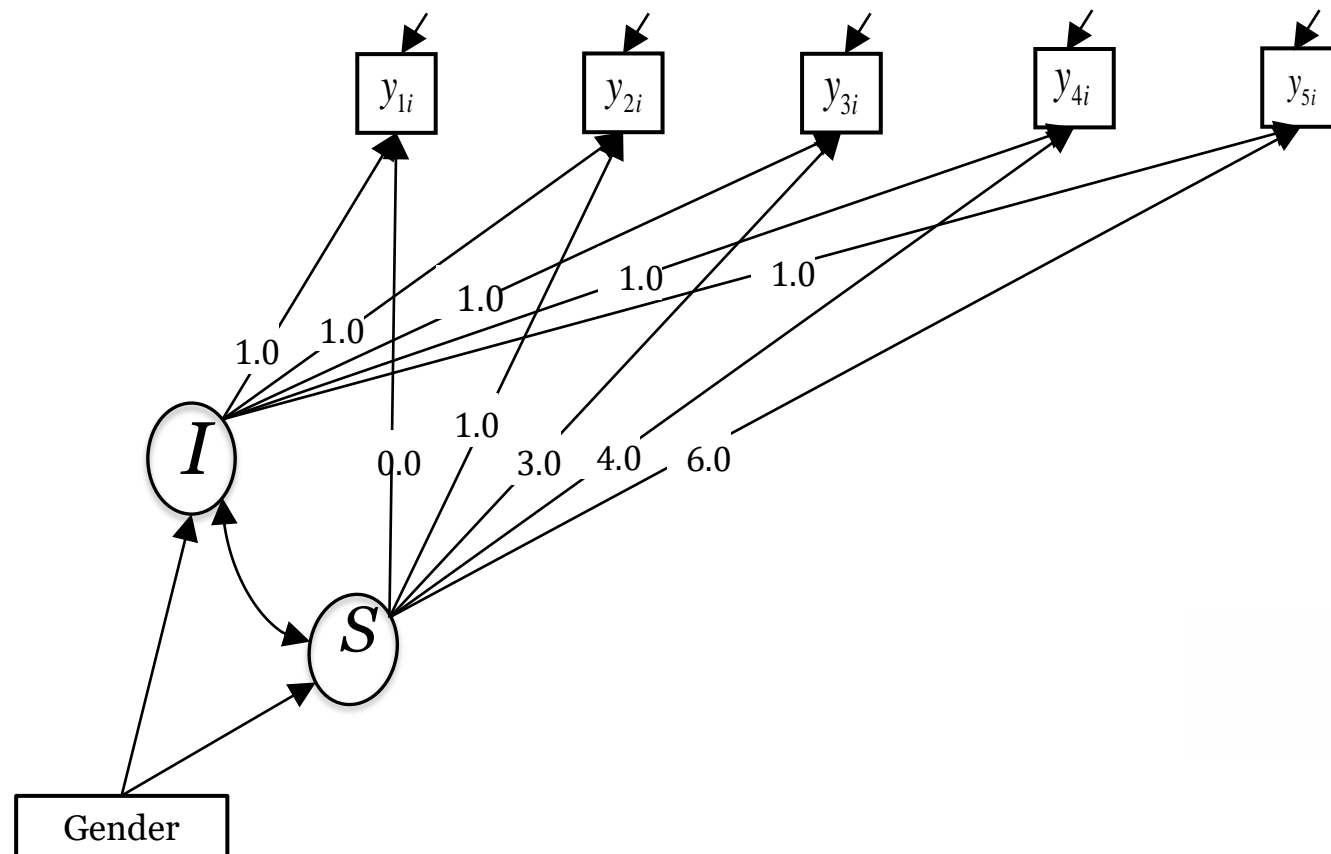
1. Identification of intraindividual (within-person) changes (and stability)
  - Is there change over time on average?
    - ✓ Growth models can address various linear and nonlinear patterns of intraindividual change
2. Analysis of causes (determinants) of intraindividual change
  - What factors/mechanisms – time-varying/dynamical predictors – drive change?
    - ✓ Inclusion of time-varying (dynamical) predictors in growth models
3. Identification of interindividual differences (or similarity) in intraindividual change
  - Do different individuals change in different ways?
    - ✓ Differences between groups of persons in the way people change
4. Analysis of causes (determinants) of interindividual differences in intraindividual change
  - What factors explain between-person differences in change?
    - ✓ Inclusion of time-invariant covariates in growth models, multigroup LGCM, Growth mixture models
5. Interrelationships in change
  - Does change in one variable relate (*precede, covary and/or follow* ) to change in another variable?
  - Correlating slopes of X and Y could provide evidence that one variable is changing in the same people as another variable – correlated changes! Or common changes!
    - ✓ Multi (parallel & sequentially contingent) process LGCM

- Do girls have different intercept and slope of the feeling of loneliness from boys ?
  - Does gender influence between-person differences in the trajectory of loneliness?



LGCM with Time-invariant covariates





LGCM with Time-invariant covariates

```

006_Linear_growht_curve_model_with_time_invariant_covariates
TITLE: 006_Linear_growht_curve_model_with_time_invariant_covariate

DATA:
FILE IS data.dat;
LISTWISE = ON;

VARIABLE:
NAMES ARE
id female pdul acel worry1
lone1 lone2 lone3 lone4 lone5
anx1 anx2 anx3 anx4 anx5
dep1 dep2 dep3 dep4 dep5
host1 host2 host3 host4 host5
percon5 percon5b subs5 subs5b sleep5 sleep5b;

USEVARIABLES ARE
lone1 lone2 lone3 lone4 lone5 female;

MISSING ARE ALL (-999);

ANALYSIS:
ESTIMATOR = ML;

MODEL:
I S|lone1@0 lone2@1 lone3@3 lone4@4 lone5@6;

!Regress growth factors on the time-invariant covariate
I S ON female;

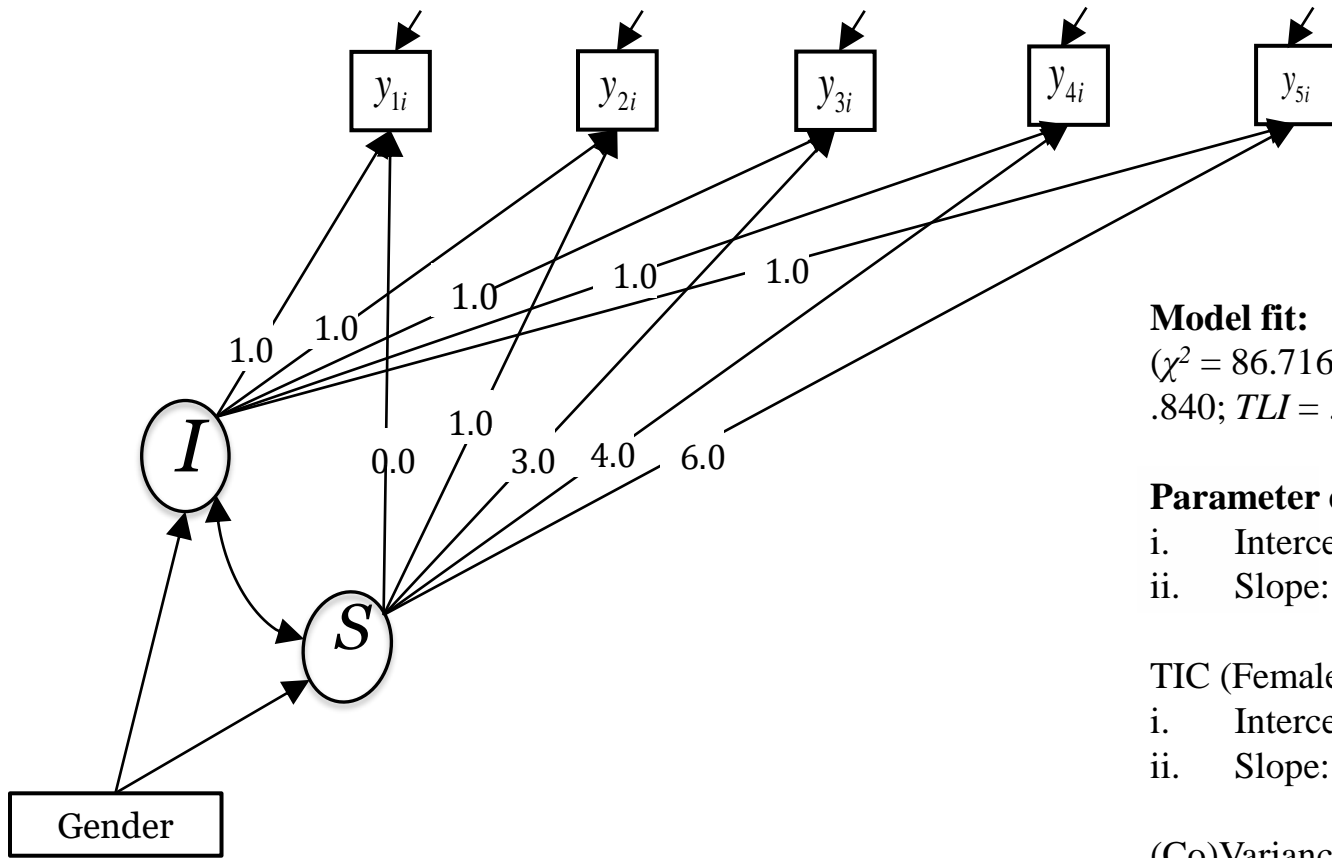
OUTPUT:
SAMPSTAT;

```

```

114 # 006_Linear growth curve model with time invariant covariates
115 timeinvar <- ' i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5
116               s =~ 0*lone1 + 1*lone2 + 3*lone3 + 4*lone4 + 6*lone5
117
118 # Time invariant covariates
119 i ~ female
120 s ~ female'
121 fit_timeinvar <- growth(timeinvar, data = data)
122 summary(fit_timeinvar, fit.measures = TRUE)

```



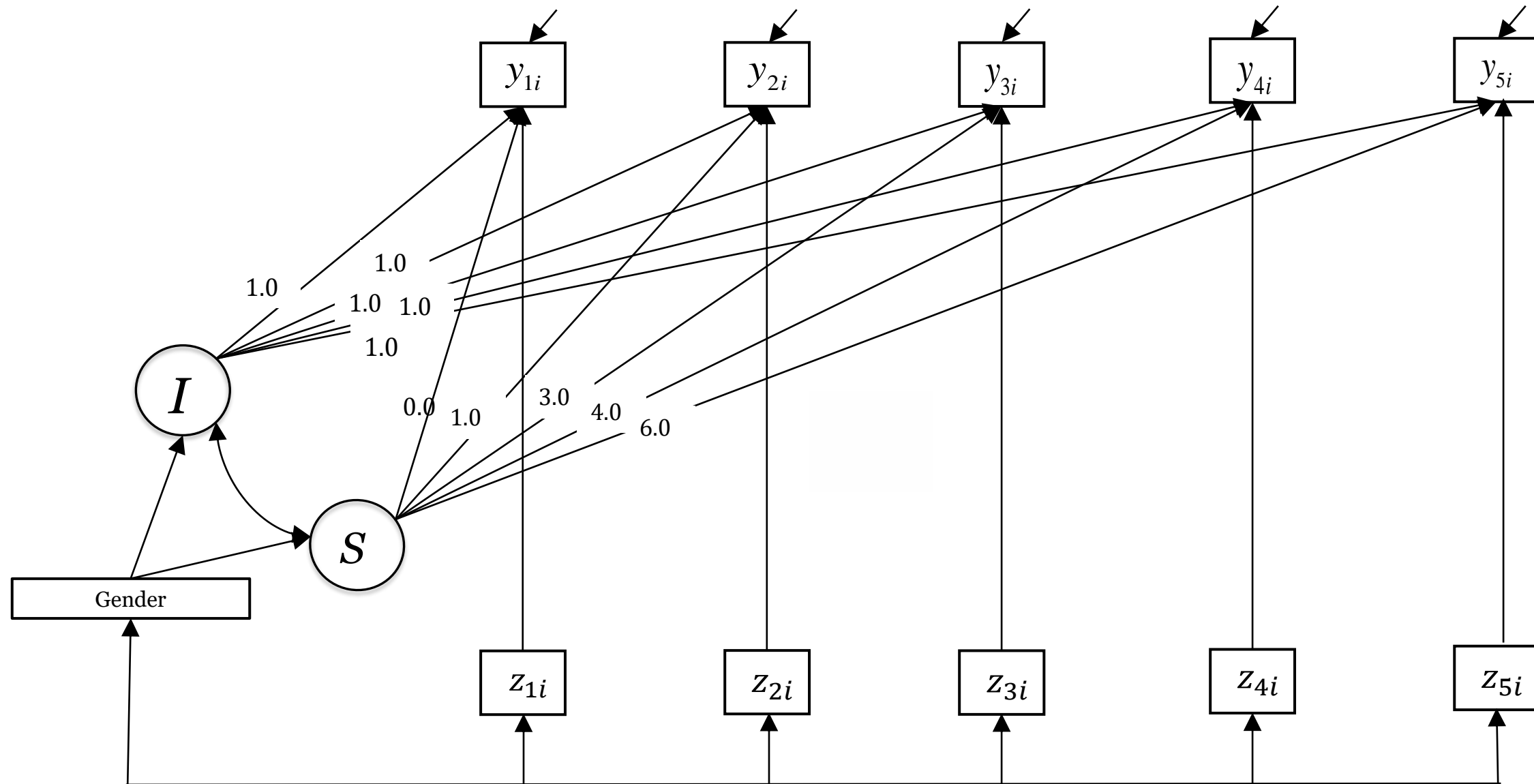
LGCM with Time-invariant covariates

**RESULTS**

**Model fit:**  
 $(\chi^2 = 86.716, df = 13; p < .001; RMSEA = .133, [90\% CI = 0.107, 0.160]; CFI = .840; TLI = .815)$

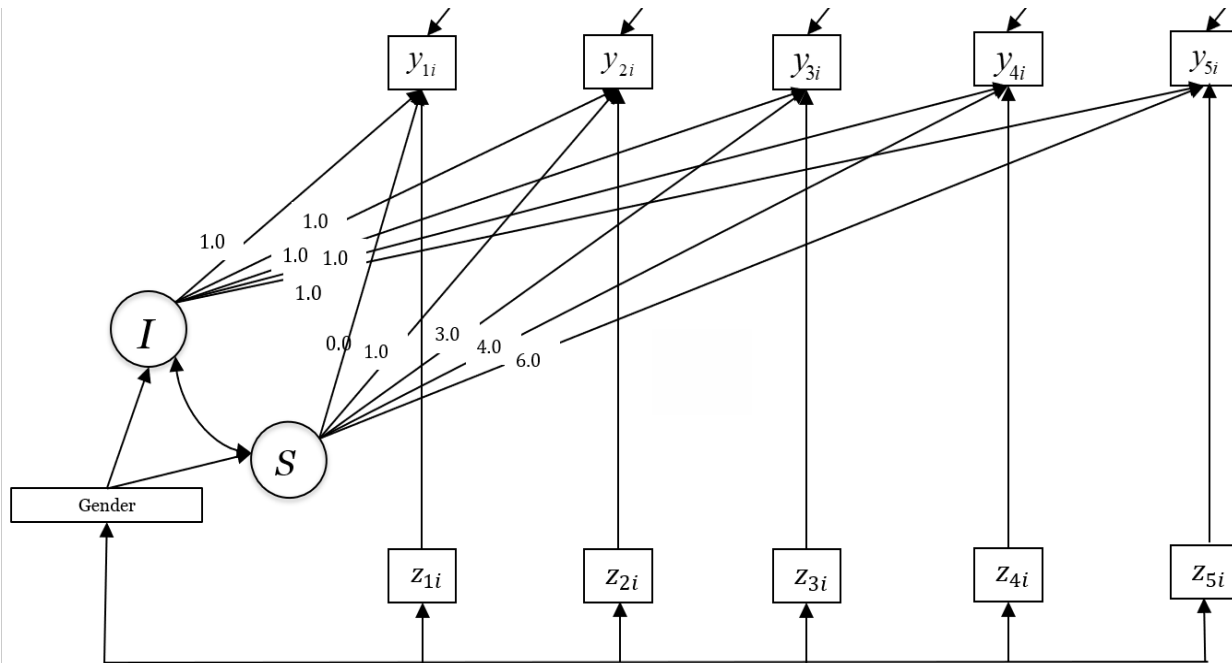
**Parameter estimates:**

i.	Intercept:	1.526***
ii.	Slope:	-0.029***
TIC (Female)		
i.	Intercept:	-0.132**
ii.	Slope:	0.007
(Co)Variances:		
i.	Intercept:	0.134***
ii.	Slope:	0.003***
iii.	Intercept WITH Slope:	-0.015***



LGCM with Time-invariant and time-varying covariates

# LGCM with Time-invariant and time-varying covariates



```
007_Linear_growht_curve_model_with_time-invariant and time-v
TITLE: 007_Linear_growht_curve_model_with_time-invariant and time-v

DATA:
FILE IS data.dat;
LISTWISE = ON;

VARIABLE:
NAMES ARE
id female pdul acel worry1
lone1 lone2 lone3 lone4 lone5
anx1 anx2 anx3 anx4 anx5
dep1 dep2 dep3 dep4 dep5
host1 host2 host3 host4 host5
percon5 percon5b subs5 subs5b sleep5 sleep5b;

USEVARIABLES ARE
lone1 lone2 lone3 lone4 lone5
host1 host2 host3 host4 host5
female;

MISSING ARE ALL (-999);

ANALYSIS:
ESTIMATOR = ML;

MODEL:
I S|lone1@0 lone2@1 lone3@3 lone4@4 lone5@6;

!Regress growth factors on time-invariant covariates
I S ON female;

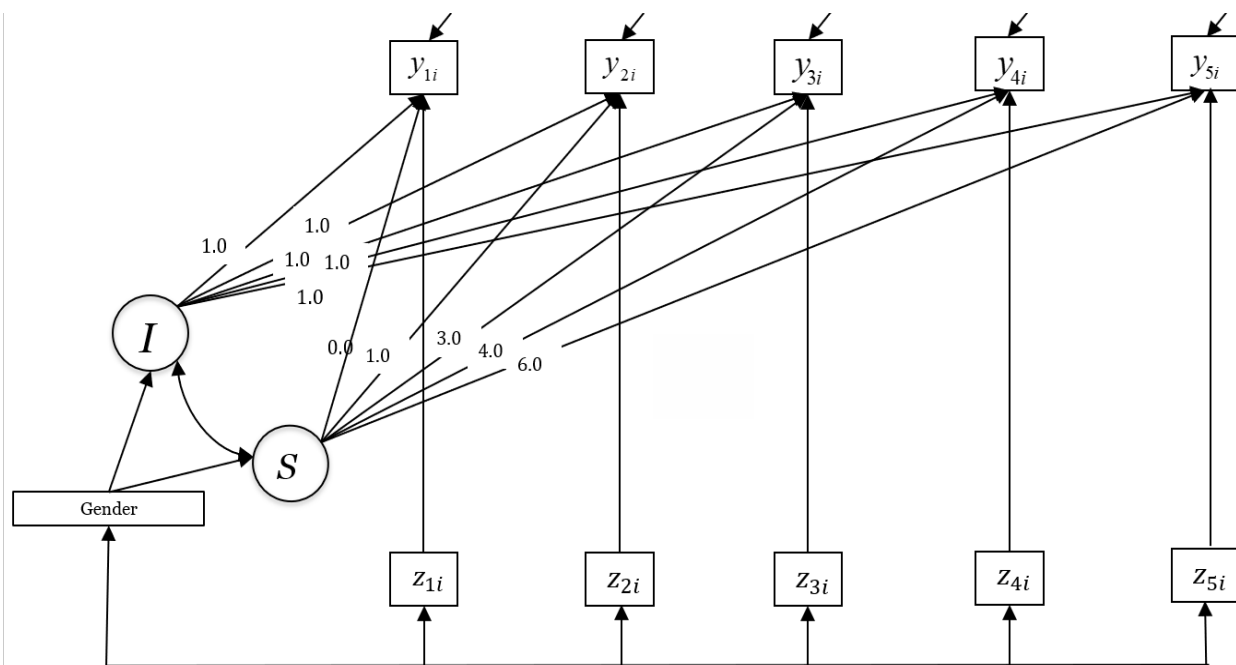
!Regress loneliness on TVC
lone1 ON host1(a);!Constrain TVC effect to be equal across time
lone2 ON host2(a);
lone3 ON host3(a);
lone4 ON host4(a);
lone5 ON host5(a);

!Fix TVC covariance with intercept and slope to zero
I S WITH host1-host5@0;

!Estimate the covaraince between covariates
female WITH host1-host5;

OUTPUT:
SAMPSTAT;
```

## LGCM with Time-invariant and time-varying covariates



```

125 # 007_Linear growth curve model with time invariant and time-varying covariates
126 timeinvar_timevar <- ' i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5
127                        s =~ 0*lone1 + 1*lone2 + 3*lone3 + 4*lone4 + 6*lone5
128 # Time-varying covariates held equal
129 lone1 =~ eq*host1
130 lone2 =~ eq*host2
131 lone3 =~ eq*host3
132 lone4 =~ eq*host4
133 lone5 =~ eq*host5
134
135 # Time invariant covariates
136 i =~ female
137 s =~ female
138
139 #Estimate the means of TVC and TIC
140 host1 =~ 1
141 host2 =~ 1
142 host3 =~ 1
143 host4 =~ 1
144 host5 =~ 1
145 female =~ 1
146
147 #Estimate covariances between TIC with TVC
148 female =~ host1 + host2 + host3 + host4 + host5
149 host1 =~ host2 + host3 + host4 + host5
150 host2 =~ host3 + host4 + host5
151 host3 =~ host4 + host5
152 host4 =~ host5
153
154 #Fix covariances between TVC and growth factors to zero
155 i =~ 0*host1
156 i =~ 0*host2
157 i =~ 0*host3
158 i =~ 0*host4
159 i =~ 0*host5
160
161 s =~ 0*host1
162 s =~ 0*host2
163 s =~ 0*host3
164 s =~ 0*host4
165 s =~ 0*host5
166
167 '
168 fit_timeinvar_timevar <- growth(timeinvar_timevar, data = data)
169 summary(fit_timeinvar_timevar, fit.measures = TRUE)

```

## RESULTS

### Model fit:

( $\chi^2 = 106.720$ ,  $df = 37$ ;  $p < .001$ ;  $RMSEA = .077$ , [90% CI = 0.060, 0.094];  $CFI = .973$ ;  $TLI = .971$ )

### Parameter estimates:

i. Intercept: 0.456\*\*\*  
ii. Slope: -0.009\*\*

### TIC (Female)

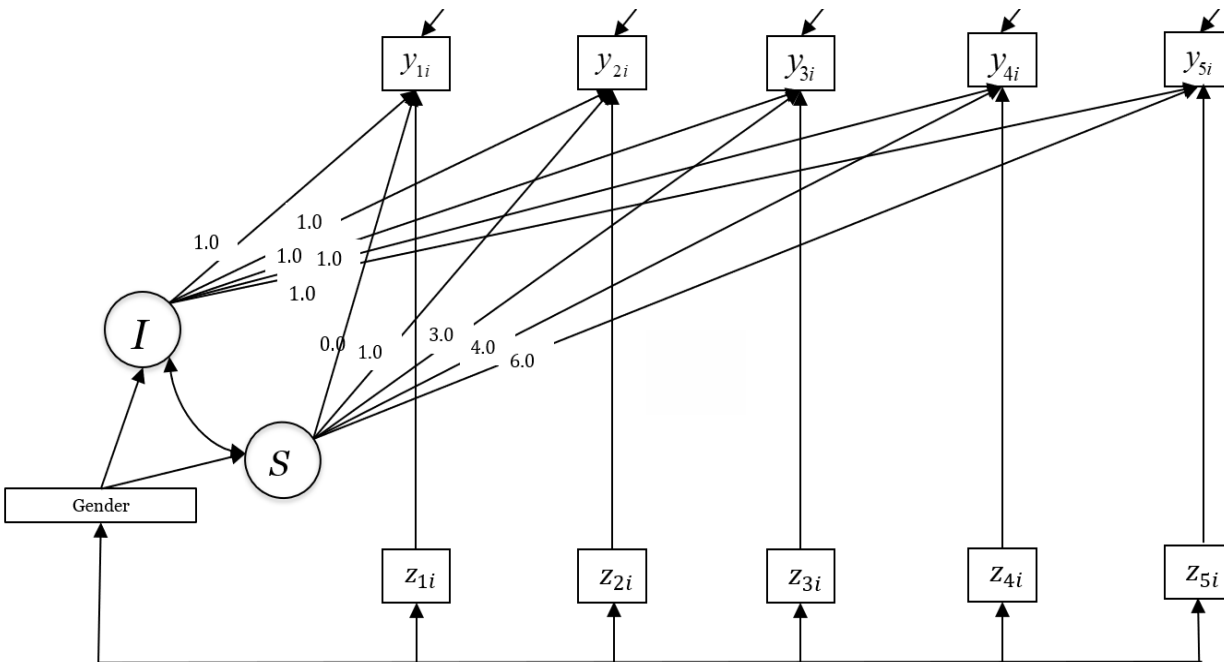
i. Intercept: -0.131\*\*  
ii. Slope: 0.008

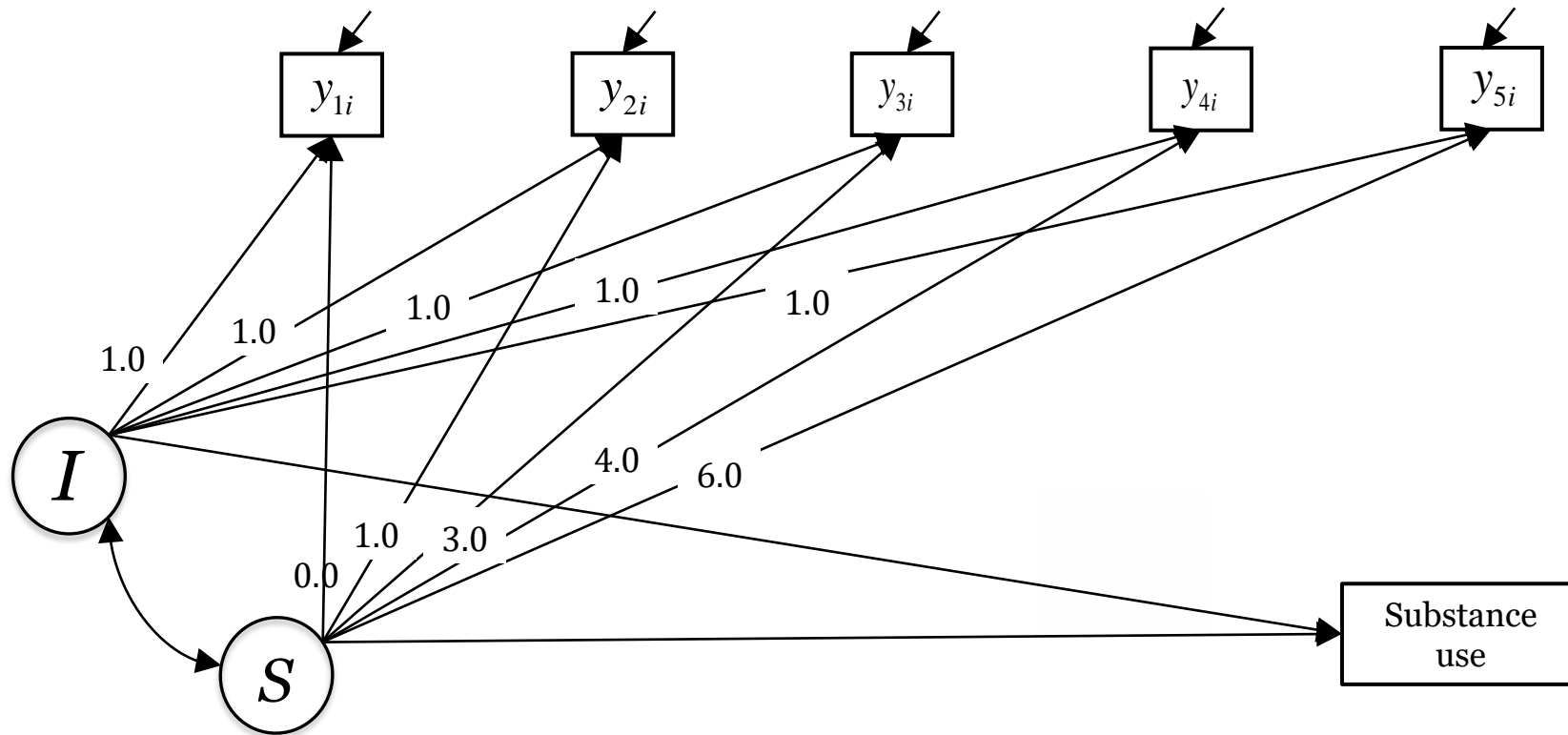
### TVC

Host .731\*\*\*

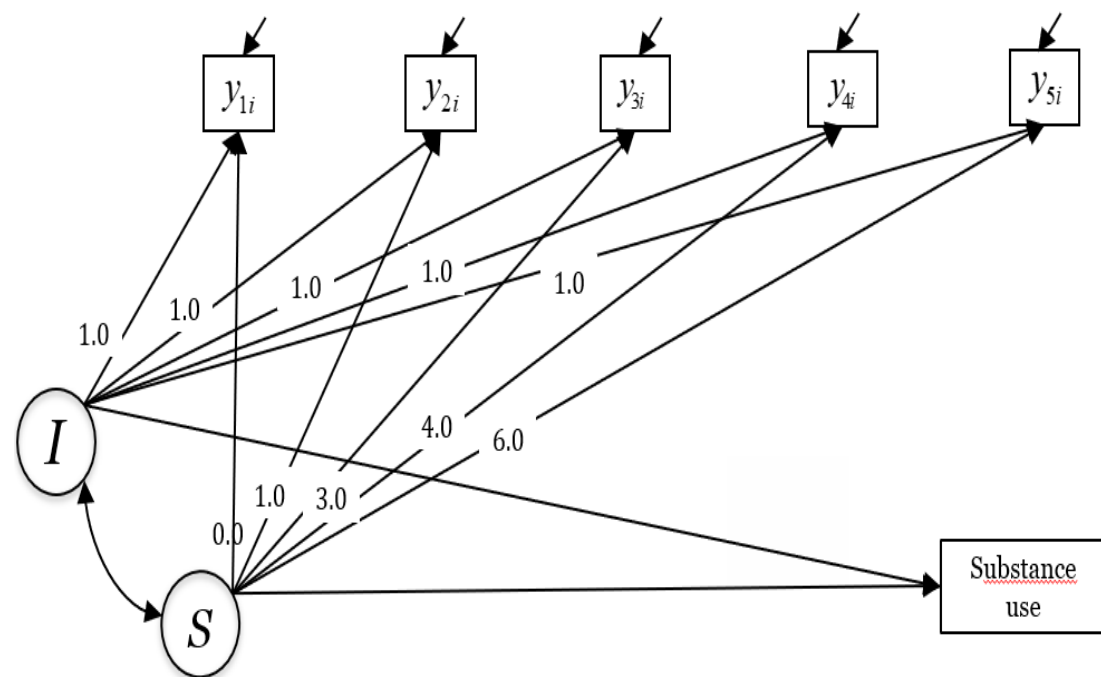
### (Co)Variances:

i. Intercept: 0.023\*\*\*  
ii. Slope: 0.001\*\*\*  
iii. Intercept WITH Slope: -0.002\*\*\*  
iv. TVC WITH TVC: 0.037 – 0.161\*\*\*





LGCM growth factors predicting distal outcome



LGCM growth factors predicting distal outcome

```

172 # 008_Linear growth curve model with growth factors predicting distal outcome
173 distal <- ' i =~ 1*lonel + 1*lonel2 + 1*lonel3 + 1*lonel4 + 1*lonel5
174           s =~ 0*lonel + 1*lonel2 + 3*lonel3 + 4*lonel4 + 6*lonel5
175
176 # Time invariant covariates
177 subs5 ~ i + s
178
179 #Estimate the intercept of subs
180 subs5 ~ 1'
181 fit_distal <- growth(distal, data = data)
182 summary(fit_distal, fit.measures = TRUE)

```

008\_Linear\_growht\_curve\_model\_with\_growth\_factors\_predicting\_distal\_outcome

TITLE: 008\_Linear\_growht\_curve\_model\_with\_growth\_factors\_predicting\_distal\_outcome

#### DATA:

FILE IS data.dat;

LISTWISE = ON;

#### VARIABLE:

NAMES ARE

id female pdul ace1 worry1

lonel lone2 lone3 lone4 lone5

anx1 anx2 anx3 anx4 anx5

dep1 dep2 dep3 dep4 dep5

host1 host2 host3 host4 host5

percon5 percon5b subs5 subs5b sleep5 sleep5b;

USEVARIABLES ARE

lonel lone2 lone3 lone4 lone5 subs5;

MISSING ARE ALL (-999);

#### ANALYSIS:

ESTIMATOR = ML;

#### MODEL:

I S|lonel@0 lone2@1 lone3@3 lone4@4 lone5@6;

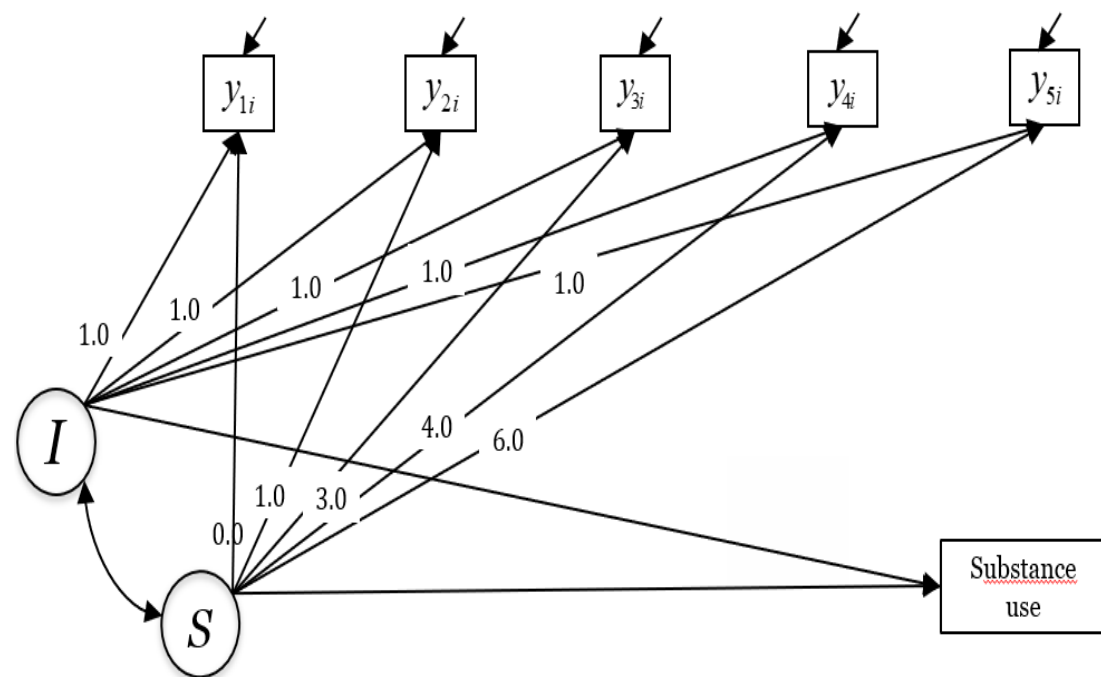
!Regress distal outcome on growth factors and time-invariant predictors

subs5 ON I S;

#### OUTPUT:

SAMPSTAT;





LGCM growth factors predicting distal outcome

## RESULTS

### Model fit:

( $\chi^2 = 74.672$ ,  $df = 13$ ;  $p < .001$ ;  $RMSEA = .128$ , [90% CI = 0.101, 0.157];  $CFI = .854$ ;  $TLI = .832$ )

### Parameter estimates:

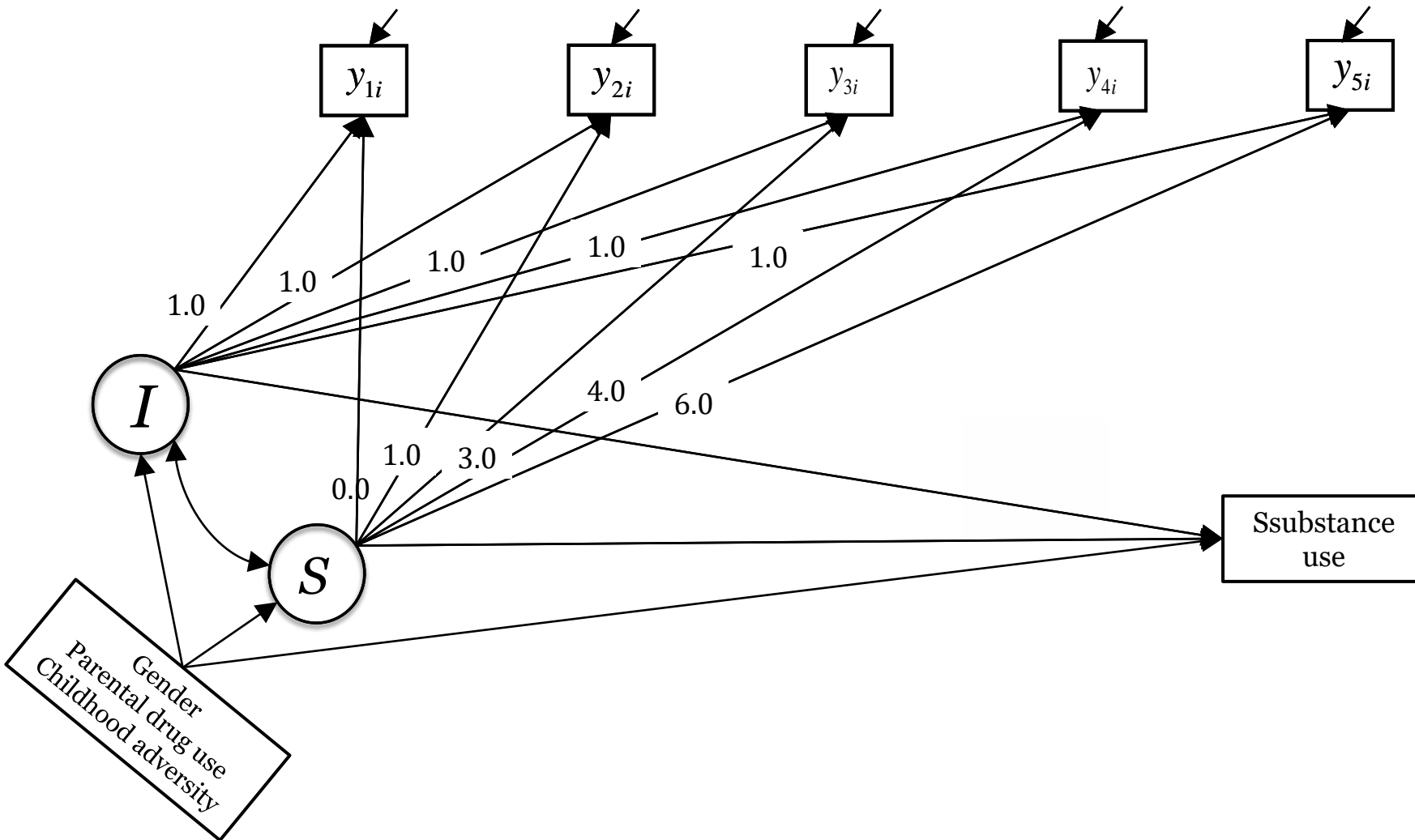
- i. Intercept: 1.466\*\*\*
- ii. Slope: -0.023\*\*\*

### Distal outcome (substance use)

- i. Intercept: 0.896\*
- ii. Slope: 5.889

### (Co)Variances:

- i. Intercept: 0.142\*\*\*
- ii. Slope: 0.003\*\*\*
- iii. Intercept WITH Slope: -0.015\*\*\*



LGCM with Time-invariant covariates and distal outcome

# Multigroup LGCM

- How is it different from using time-invariant covariate model?
  - Time-invariant covariate (TIC) models examine the difference in the average growth trajectory
  - TIC models do not examine aspects of the growth model related to
    - Group differences in the
      - i. Average trajectory and invariance testing
      - ii. Variability and covariability of growth trajectories
      - iii. Unexplained within-person variability
- Multigroup LGCM models can examine differences in any aspect of growth trajectory for known, measured or predefined groups
  - Growth mixture models are used for unknown or unmeasured groups that may exist as subpopulations in the data

# Multigroup LGCM

- What factors account for between-person differences in the trajectory of loneliness between boys and girls?
  - i. Do boys and girls *significantly* differ in their trajectories of loneliness?
    - What is the extent of differences in the average trajectory of boys and girls?
    - What is the extent of variability around the individual trajectories of boys and girls?

# Model comparisons

## Model Comparison for the Multiple-Group LGCM

	Model M1 Invariance model	Model M2 Means model	Model M3 Means and covariances model	Model M4 Means, covariances and residual variances model
Parameters				
-2LL				
$\Delta$ parameters				
$\Delta$ -2LL				

### Sequence of testing

- M1: Constrain all parameters (growth factor means, growth factor variances and covariances, and residual variances) to be identical across groups
- M2: Freely estimate growth factor means across groups, while keeping constraints on the growth factor variances and covariance, and residual variances
- M3: Freely estimate growth factor means, growth factor variances and covariances, while keeping the constraints on the residual variances
- M4: Freely estimate growth factor means, growth factor variances and covariances, and residual variances across the groups

### Questions to answer

- M1 vs. M2: Tests whether the groups differ in their average trajectory
- M2 vs. M3: Tests the extent of between-person differences in the trajectories of groups
- M3 vs. M4: Tests the extent of within-person variability around individual trajectories
  - If all models fit equally well (i.e., no significant results from the LRT) then choose the model with the smallest number of parameters, M1 – most parsimonious model as it is the most constrained/reduced form

# Sequence of testing

- M1: Constrain all parameters (growth factor means, growth factor variances and covariances, and residual variances) to be identical across groups

009\_1\_Multigroup\_LGCM\_M1\_Invariance\_model

MODEL:

```
I S|lone1@0 lone2@1 lone3@3 lone4@4 lone5@6;
```

```
!Estimate means of growth factors and label them
```

```
[I] (INT);
```

```
[S] (SLP);
```

```
!Estimate variances of growth factors
```

```
I (INT_V);
```

```
S (SLP_V);
```

```
!Estimate covariance of growth factors
```

```
I WITH S (IS_COV);
```

```
!Estimate residual variance and constrain them equal
```

```
lone1-lone5 (RES);
```

```
!Sequentially testing models means specific parameters are o  
!For those parameters, we will begin by constraining them to  
!Those parameters are (MEANS OF GROWTH FACTORS, CO/VARIANCES  
!In subsequent models, we will freely estimate those paramet
```

MODEL MALES:

```
!Growth factor means for males
```

```
[I] (INT); !The INT label will make the males' intercept g
```

```
[S] (SLP); !The labelling for all the parameters will make
```

```
!Growth factor variances for males
```

```
I (INT_V);
```

```
S (SLP_V);
```

```
!Growth factor covariance for males
```

```
I WITH S (IS_COV);
```

```
!Residual variances for males
```

```
lone1-lone5 (RES);
```

MODEL FEMALES:

```
!Growth factor means for females
```

```
[I] (INT); !The INT label will make the females' intercept
```

```
[S] (SLP);
```

```
!Growth factor variances for females
```

```
I (INT_V);
```

```
S (SLP_V);
```

```
!Growth factor covariance for females
```

```
I WITH S (IS_COV);
```

```
!Residual variances for females
```

```
lone1-lone5 (RES);
```

OUTPUT:

```
SAMPSTAT;
```

```
189 # 009_1_Multigroup LGCM M1 Invariance model  
190 multigroupM1 <- ' i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5  
191                  s =~ 0*lone1 + 1*lone2 + 3*lone3 + 4*lone4 + 6*lone5  
192 #Growth factor means constrained equal  
193 i ~ c(int, int)*1  
194 s ~ c(slp, slp)*1  
195  
196 #Growth factor variances held equal  
197 i =~ c(vint, vint)*i  
198 s =~ c(vslp, vslp)*s  
199  
200 #Growth factor covariances held equal  
201 i =~ c(cvf, cvf)*s  
202  
203 #Residual variances of observed items held equal  
204 lone1 =~ c(res, res)*lone1  
205 lone2 =~ c(res, res)*lone2  
206 lone3 =~ c(res, res)*lone3  
207 lone4 =~ c(res, res)*lone4  
208 lone5 =~ c(res, res)*lone5  
209 '  
210 fit_multigroupM1 <- growth(multigroupM1, data = data, group = "female")  
211 summary(fit_multigroupM1, fit.measures = TRUE)  
212
```

## Sequence of testing

- M2: Freely estimate growth factor means across groups, while keeping constraints on the growth factor variances and covariance, and residual

009\_2\_Multigroup\_LGCM\_M2\_Growth\_factor\_means

```
lone1 lone2 lone3 lone4 lone5;

GROUPING = FEMALE (0 = MALES 1 = FEMALES);
MISSING ARE ALL (-999);

ANALYSIS:
  ESTIMATOR = ML;

MODEL:
  I S|lone1@0 lone2@1 lone3@3 lone4@4 lone5@6;

  [I] (INT);
  [S] (SLP);

  I (INT_V);
  S (SLP_V);

  I WITH S (IS_COV);

  lone1-lone5 (RES);

MODEL MALES:
  [I] (INT_M); !Free growth factor means by using
  [S] (SLP_M);

  I (INT_V);
  S (SLP_V);

  I WITH S (IS_COV);

  lone1-lone5 (RES);

MODEL FEMALES:
  [I] (INT_F); !Different labels are used to free
  [S] (SLP_F);

  I (INT_V);
  S (SLP_V);

  I WITH S (IS_COV);

  lone1-lone5 (RES);
```

```
214 # 009_2_Multigroup LGCM M2 Free factor means
215 multigroupM2 <- ' i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5
216                  s =~ 0*lone1 + 1*lone2 + 3*lone3 + 4*lone4 + 6*lone5
217 #Growth factor means freely estimated
218 i ~ c(intm, intf)*1
219 s ~ c(slpm, slpf)*1
220
221 #Growth factor variances held equal
222 i =~ c(vint, vint)*i
223 s =~ c(vslp, vslp)*s
224
225 #Growth factor covariances held equal
226 i =~ c(cvf, cvf)*s
227
228 #Residual variances of observed items held equal
229 lone1 =~ c(res, res)*lone1
230 lone2 =~ c(res, res)*lone2
231 lone3 =~ c(res, res)*lone3
232 lone4 =~ c(res, res)*lone4
233 lone5 =~ c(res, res)*lone5
234 '
235 fit_multigroupM2 <- growth(multigroupM2, data = data, group = "female")
236 summary(fit_multigroupM2, fit.measures = TRUE)
```

## Sequence of testing

- M3: Freely estimate growth factor means, growth factor variances and covariances, while keeping the constraints on the residual variances

```
GROUPING = FEMALE (0 = MALES 1 = FEMALES);
```

```
MISSING ARE ALL (-999);
```

### ANALYSIS:

```
ESTIMATOR = ML;
```

### MODEL:

```
I S|lone1@0 lone2@1 lone3@3 lone4@4 lone5@6;
```

```
[I] (INT);
```

```
[S] (SLP);
```

```
I (INT_V);
```

```
S (SLP_V);
```

```
I WITH S (IS_COV);
```

```
lone1-lone5 (RES);
```

### MODEL MALES:

```
[I S];!First: Growth factor means are freely estimated
```

```
I S;!Second: Growth factor variances are freely estimated
```

```
I WITH S;!Second: Growth factor covariances are freely estimated
```

```
lone1-lone5 (RES);
```

### MODEL FEMALES:

```
[I S];!First: Growth factor means are freely estimated
```

```
I S;!Second: Growth factor variances are freely estimated
```

```
I WITH S;!Second: Growth factor covariances are freely estimated
```

```
lone1-lone5 (RES);
```

### OUTPUT:

```
SAMPSTAT;
```

```
239 # 009_3_Multigroup LGCM M3 Free factor means and co/variances
240 multigroupM3 <- ' i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5
241                  s =~ 0*lone1 + 1*lone2 + 3*lone3 + 4*lone4 + 6*lone5
242 #Growth factor means freely estimated
243 i ~ c(intm, intf)*1
244 s ~ c(slpf, slpf)*1
245
246 #Growth factor variances freely estimated
247 i =~ c(vinm, vinf)*i
248 s =~ c(vslm, vslf)*s
249
250 #Growth factor covariances freely estimated
251 i =~ c(covm, covf)*s
252
253 #Residual variances of observed items held equal
254 lone1 =~ c(res, res)*lone1
255 lone2 =~ c(res, res)*lone2
256 lone3 =~ c(res, res)*lone3
257 lone4 =~ c(res, res)*lone4
258 lone5 =~ c(res, res)*lone5
259 '
260 fit_multigroupM3 <- growth(multigroupM3, data = data, group = "female")
261 summary(fit_multigroupM3, fit.measures = TRUE)
```



## Sequence of testing

- M4: Freely estimate growth factor means, growth factor variances and covariances, and residual variances across the groups

```
GROUPING = FEMALE (0 = MALES 1 = FEMALES);
```

```
MISSING ARE ALL (-999);
```

### ANALYSIS:

```
ESTIMATOR = ML;
```

### MODEL:

```
I S|lone1@0 lone2@1 lone3@3 lone4@4 lone5@6;
```

```
[I] (INT);
```

```
[S] (SLP);
```

```
I (INT_V);
```

```
S (SLP_V);
```

```
I WITH S (IS_COV);
```

```
lone1-lone5 (RES);
```

### MODEL MALES:

```
[I S] (INT_M SLP_M);!First: Growth factor means are freely estimated
```

```
I S;!Second: Growth factor variances are freely estimated
```

```
I WITH S;!Second: Growth factor covariances are freely estimated
```

```
lone1-lone5;!Third, residual variances freely estimated
```

### MODEL FEMALES:

```
[I S] (INT_F SLP_F);!First: Growth factor means are freely estimated
```

```
I S;!Second: Growth factor variances are freely estimated
```

```
I WITH S;!Second: Growth factor covariances are freely estimated
```

```
lone1-lone5;!Third: residual variances freely estimated
```

### !MODEL TEST:

```
! 0 = INT_M - INT_F;
```

### OUTPUT:

```
SAMPSTAT;
```

```
264 # 009_4_Multigroup LGCM M4 Free factor means and co/variances
265 multigroupM4 <- ' i =~ 1*lone1 + 1*lone2 + 1*lone3 + 1*lone4 + 1*lone5
266                  s =~ 0*lone1 + 1*lone2 + 3*lone3 + 4*lone4 + 6*lone5
267 #Growth factor means freely estimated
268 i ~ c(intm, intf)*1
269 s ~ c(slpm, slpf)*1
270
271 #Growth factor variances freely estimated
272 i ~~ c(vinm, vinf)*i
273 s ~~ c(vslm, vslf)*s
274
275 #Growth factor covariances freely estimated
276 i ~~ c(covm, covf)*s
277
278 #Residual variances of observed items freely estimated
279 lone1 ~~ c(rsm1, rsf1)*lone1
280 lone2 ~~ c(rsm2, rsf2)*lone2
281 lone3 ~~ c(rsm3, rsf3)*lone3
282 lone4 ~~ c(rsm4, rsf4)*lone4
283 lone5 ~~ c(rsm5, rsf5)*lone5
284 '
285 fit_multigroupM4 <- growth(multigroupM4, data = data, group = "female")
286 summary(fit_multigroupM4, fit.measures = TRUE)
```

## Sequence of testing

- M1: Constrain all parameters (growth factor means, growth factor variances and covariances, and residual variances) to be identical across groups
- M2: Freely estimate growth factor means across groups, while keeping constraints on the growth factor variances and covariance, and residual variances
- M3: Freely estimate growth factor means, growth factor variances and covariances, while keeping the constraints on the residual variances
- M4: Freely estimate growth factor means, growth factor variances and covariances, and residual variances across the groups

## Questions to answer

- M1 vs. M2: Tests whether the groups differ in their average trajectory
- M2 vs. M3: Tests the extent of between-person differences in the trajectories of groups
- M3 vs. M4: Tests the extent of within-person variability around individual trajectories
  - If all models fit equally well (i.e., no significant results from the LRT) then choose the model with the smallest number of parameters, M1 – most parsimonious model as it is the most constrained/reduced form

```
292 #The `anova` function in `lavaan` computes the LRT for nested models.  
293 compare_groups <- anova(fit_multigroupM1, fit_multigroupM2, fit_multigroupM3, fit_multigroupM4)  
294 compare_groups  
295
```

```
298 # Test of parameter constraints  
299 constint = 'intm - intf == 0'  
300 lavTestWald(fit_multigroupM4, constraints = constint)  
301  
302 constslp = 'slpm - slpf ==0'  
303 lavTestWald(fit_multigroupM4, constraints = constslp)  
...
```

# Multigroup LGCM

[illegible]

# Model comparisons

## Model Comparison for the Multiple-Group LGCM

	Model M1 Invariance model	Model M2 Means model	Model M3 Means and covariances model	Model M4 Means, covariances and residual variances model
Parameters	6	8	11	12
-2LL	1553.446	1542.510	1532.416	1448.148
$\Delta$ parameters	-	2	3	1
$\Delta$ -2LL	-	10.936**	10.094*	8.046**

### Questions to answer

- M1 vs. M2: Tests whether the groups differ in their average trajectory
- M2 vs. M3: Tests the extent of between-person differences in the trajectories of groups
- M3 vs. M4: Tests the extent of within-person variability around individual trajectories

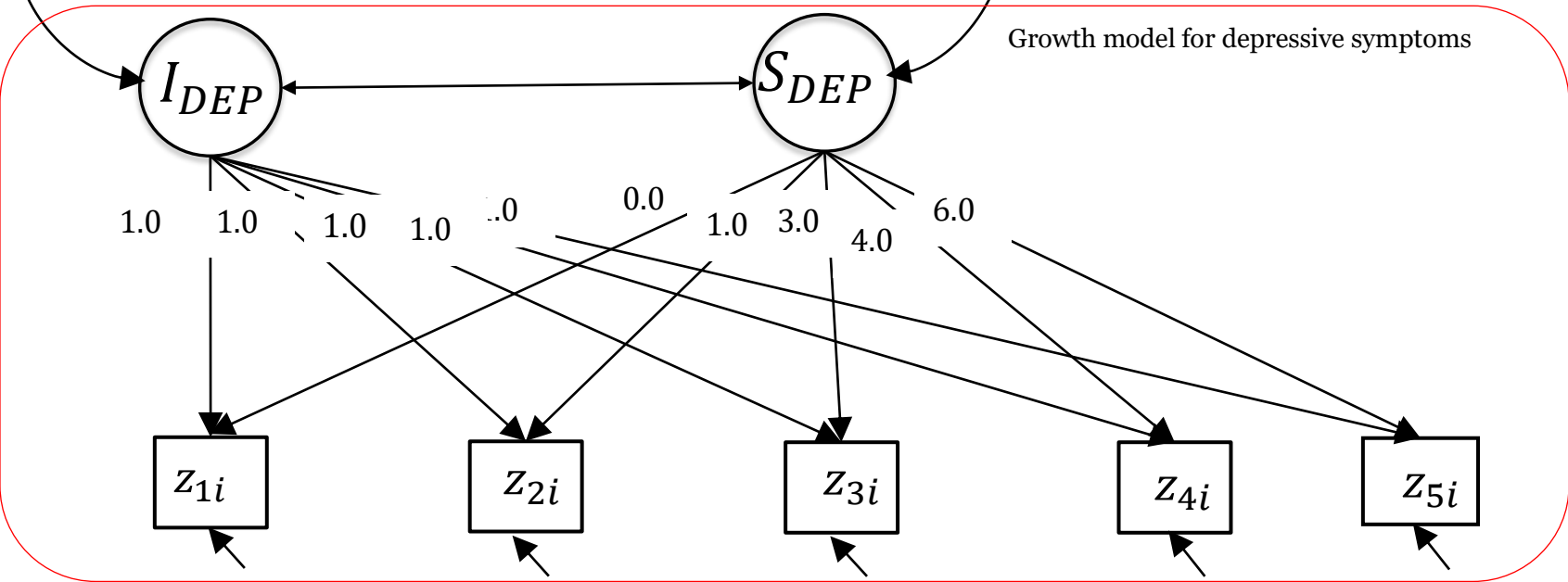
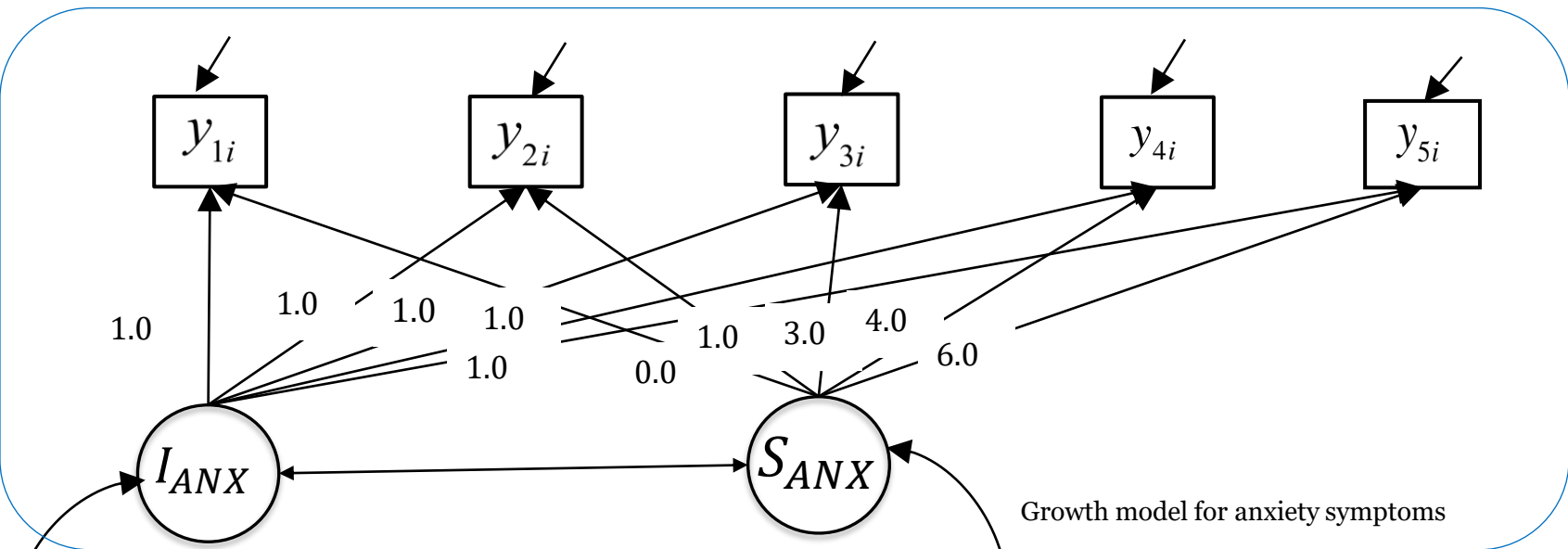
Males and females differ in their average growth trajectories of loneliness, the extent of between-person differences in those trajectories and the extent of variability around their individual trajectories

# Objectives of longitudinal research

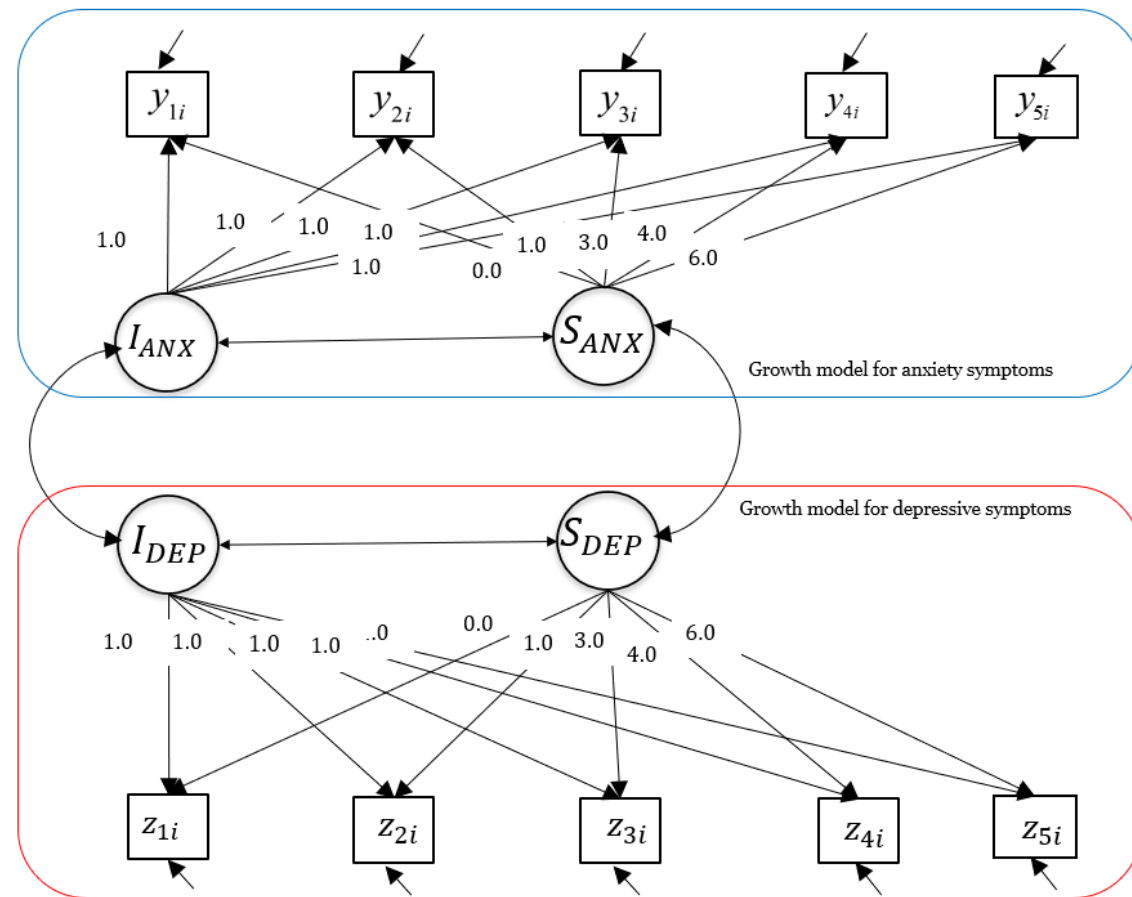
1. Identification of intraindividual (within-person) changes (and stability)
  - Is there change over time on average?
    - ✓ Growth models can address various linear and nonlinear patterns of intraindividual change
2. Analysis of causes (determinants) of intraindividual change
  - What factors/mechanisms – time-varying/dynamical predictors – drive change?
    - ✓ Inclusion of time-varying (dynamical) predictors in growth models
3. Identification of interindividual differences (or similarity) in intraindividual change
  - Do different individuals change in different ways?
    - ✓ Differences between groups of persons in the way people change
4. Analysis of causes (determinants) of interindividual differences in intraindividual change
  - What factors explain between-person differences in change?
    - ✓ Inclusion of time-invariant covariates in growth models, multigroup LGCM, Growth mixture models
5. Interrelationships in change
  - Does change in one variable relate (*precede, covary and/or follow* ) to change in another variable?
  - Correlating slopes of X and Y could provide evidence that one variable is changing in the same people as another variable – correlated changes! Or common changes!
    - ✓ Multi (parallel & sequentially contingent) process LGCM

# Multi Process LGCM

- Simultaneously model multiple outcomes
  1. Parallel LGCM
    - Covariance between two intercepts
      - Information about association between the two outcomes at the beginning of observation period
    - Covariance between two slopes
      - How rate of change in the two outcomes are associated with each other
  2. Sequential LGCM
    - Change in one subdomain, e.g. Anxiety symptoms (T1-T5) is correlated with change in another subdomain, e.g. depressive symptoms (T6-T10)



- Study distinct but related subdomains
- Developmental associations (co-development) between anxiety and depressive symptoms
- Non-directional associations represent co-development/occurrence



```
USEVARIABLES ARE
    anx1 anx2 anx3 anx4 anx5
    dep1 dep2 dep3 dep4 dep5;
```

```
MISSING ARE ALL (-999);
```

#### ANALYSIS:

```
ESTIMATOR = ML;
```

```
MODEL = NOCOV; !Suppress Mplus default correlations between the growth factor.
!That way, you have control over what variables you want to co
```

#### MODEL:

```
I_ANX S_ANX|anx1@0 anx2@1 anx3@3 anx4@4 anx5@6; !anxiety symptoms growth
I_DEP S_DEP|dep1@0 dep2@1 dep3@3 dep4@4 dep5@6; !depressive symptoms
```

```
!Correlate the growth factors
```

```
I_ANX WITH S_ANX;
```

```
I_DEP WITH S_DEP;
```

```
I_ANX WITH I_DEP;
```

```
S_ANX WITH S_DEP;
```

#### OUTPUT:

```
SAMPSTAT;
```

```
309 # 010_1_Parallel growth curve models - anxiety and depression symptoms
310 parallel <- ' ia =~ 1*anx1 + 1*anx2 + 1*anx3 + 1*anx4 + 1*anx5
311              sa =~ 0*anx1 + 1*anx2 + 3*anx3 + 4*anx4 + 6*anx5
312              id =~ 1*dep1 + 1*dep2 + 1*dep3 + 1*dep4 + 1*dep5
313              sd =~ 0*dep1 + 1*dep2 + 3*dep3 + 4*dep4 + 6*dep5
314 #Growth factor correlations
315 ia =~ id + sa
316 sd =~ id + sa
317 ia =~ 0*sd
318 id =~ 0*sa
319 '
320 fit_parallel <- growth(parallel, data = data)
321 summary(fit_parallel, fit.measures = TRUE)
```



## RESULTS

### Model fit:

( $\chi^2 = 820.887$ ,  $df = 43$ ;  $p < .001$ ;  $RMSEA = .237$  [90% CI = 0.223, 0.252];  $CFI = .584$ ;  $TLI = .564$ )

### Parameter estimates:

Anxiety symptoms

i. Intercept: 1.397\*\*\*  
ii. Slope: -0.032\*\*\*

Depression symptoms

i. Intercept: 1.545\*\*\*  
ii. Slope: -0.014\*\*

(Co)Variances:

Anxiety symptoms

i. Intercept: 0.097\*\*\*  
ii. Slope: 0.002\*\*\*

Depression symptoms

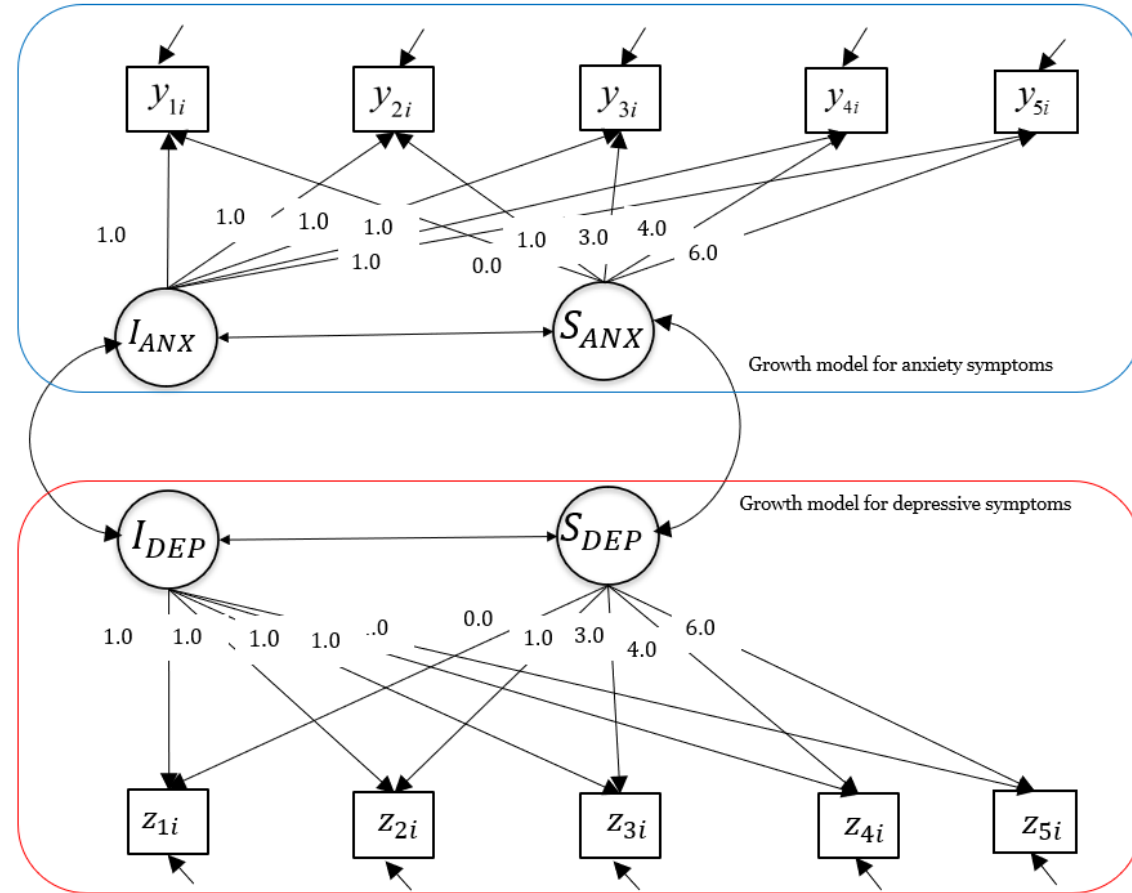
i. Intercept: 0.171\*\*\*  
ii. Slope: 0.002\*\*

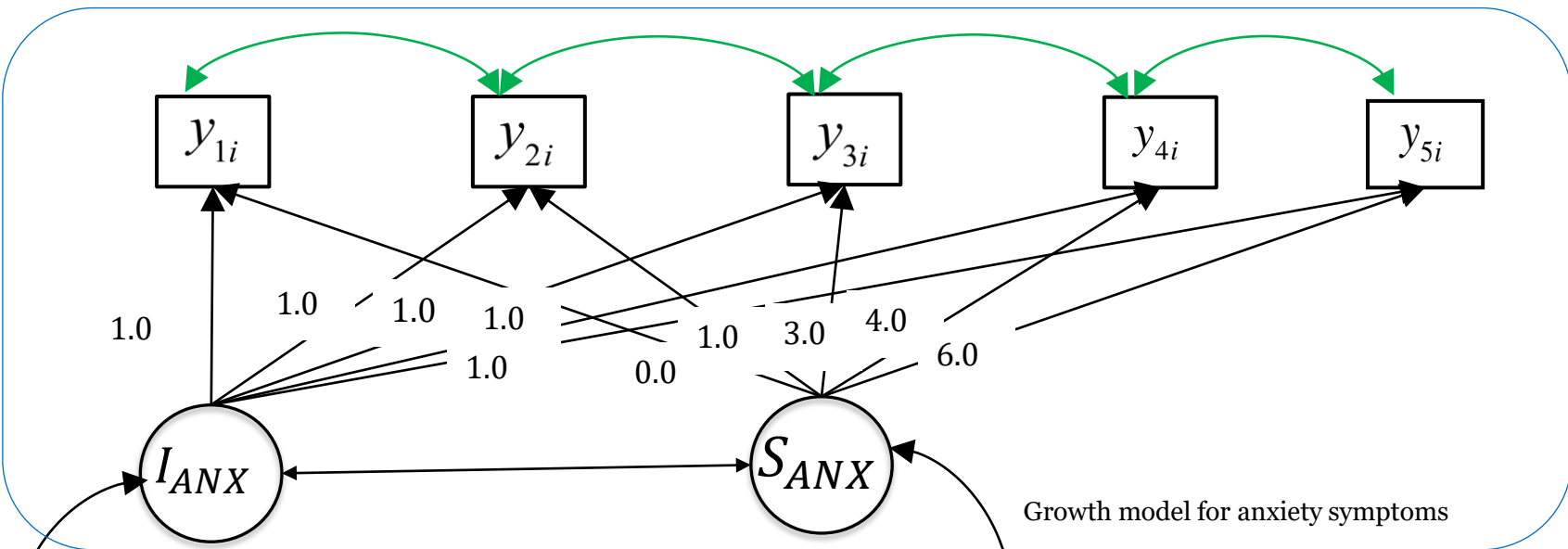
iii. I\_ANX WITH S\_ANX 0.000

iv. I\_ANX WITH I\_DEP 0.125\*\*\*

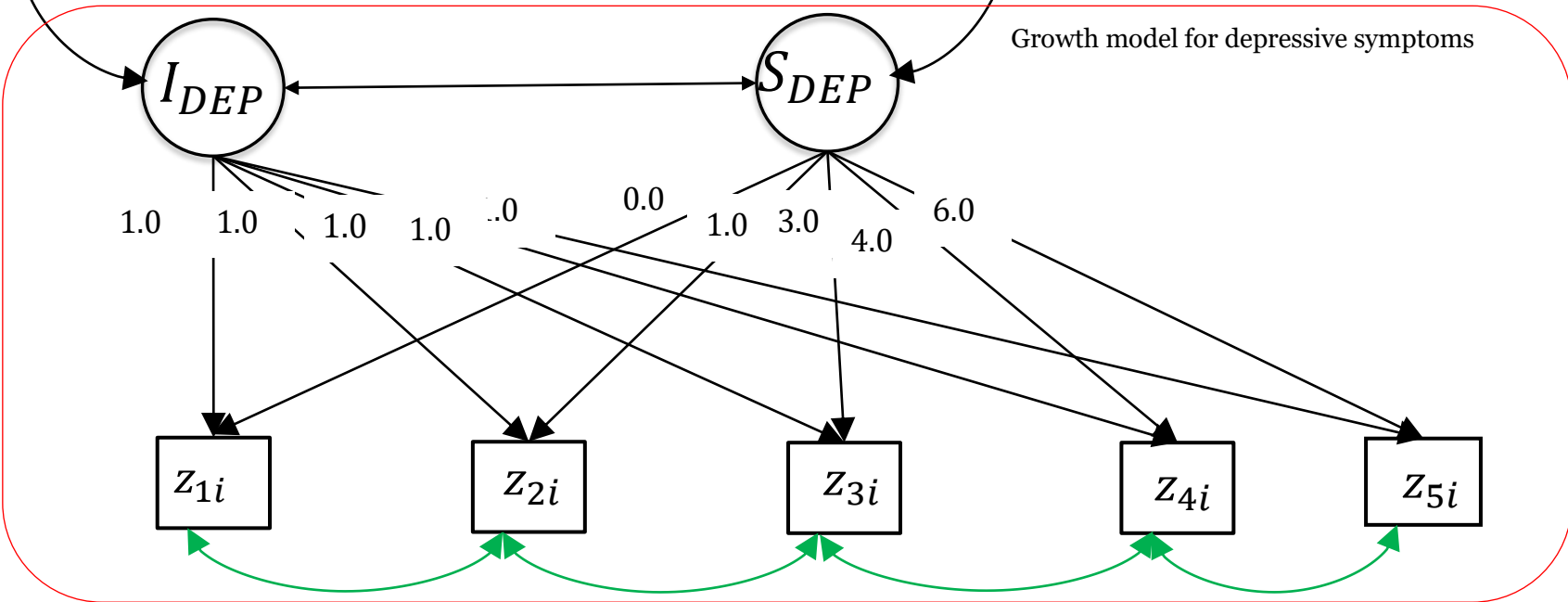
v. I\_DEP WITH S\_DEP 0.005

vi. S\_ANX WITH S\_DEP 0.004\*\*\*

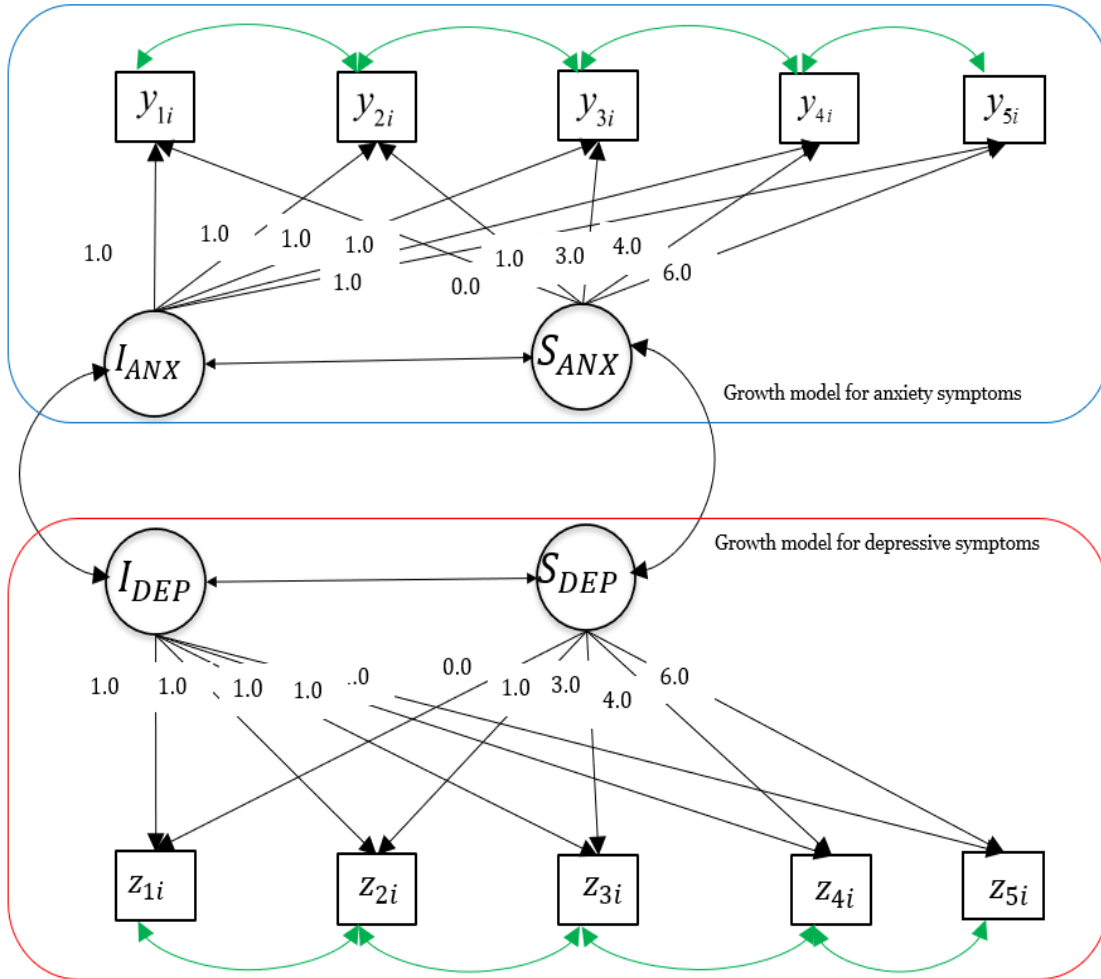




- Each measure consist of
  - Item-specific variance component
  - Time-specific variance component



- Item-specific variance component** = measurement error (within subdomain error correlations – autocorrelated errors)
  - Autocorrelated error capture unique and methodological biases within a measure (e.g., due to repeated administration, reporting biases)



USEVARIABLES ARE

```
anx1 anx2 anx3 anx4 anx5
dep1 dep2 dep3 dep4 dep5;
```

MISSING ARE ALL (-999);

ANALYSIS:

ESTIMATOR = ML;

MODEL = NOCOV; !Suppress Mplus default correlations between the growth factors  
!That way, you have control over what variables you want to correlate

MODEL:

```
I_ANX S_ANX|anx1@0 anx2@1 anx3@3 anx4@4 anx5@6;!anxiety symptoms growth
I_DEP S_DEP|dep1@0 dep2@1 dep3@3 dep4@4 dep5@6;!depressive symptoms
```

!Correlate the growth factors

```
I_ANX WITH S_ANX;
```

```
I_DEP WITH S_DEP;
```

```
I_ANX WITH I_DEP;
```

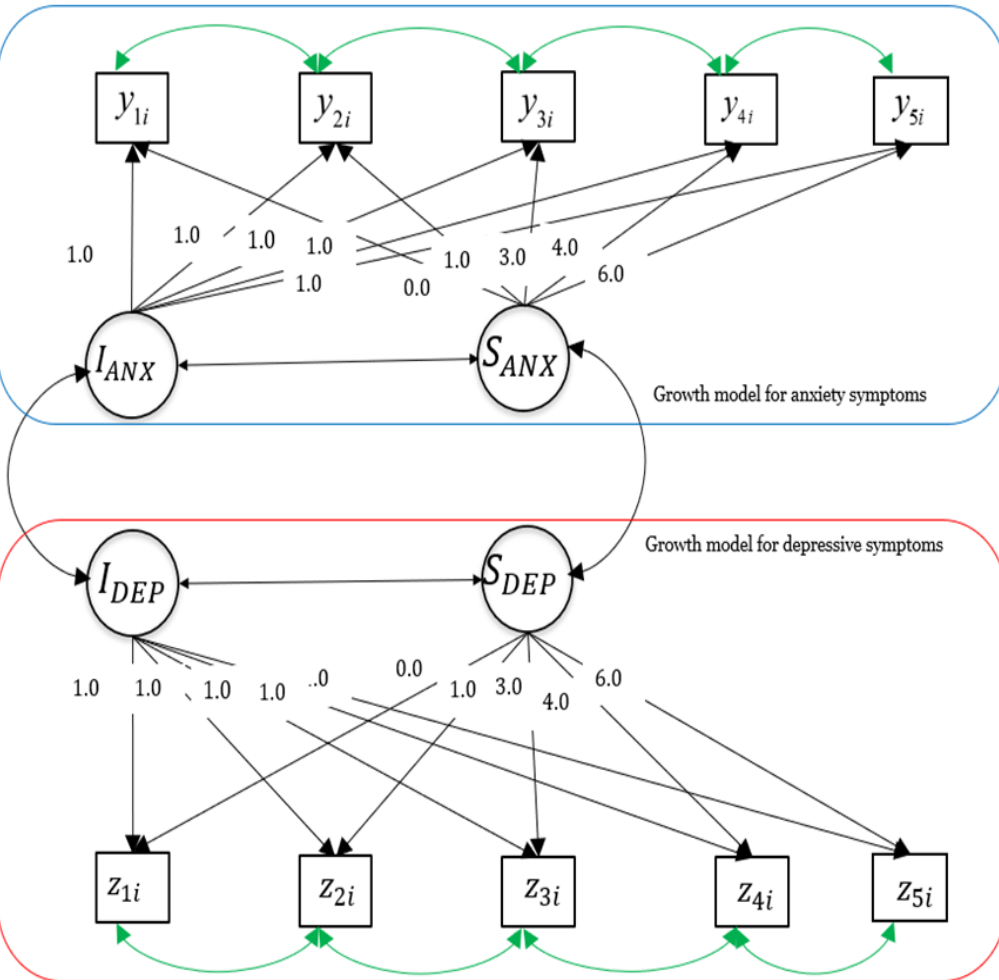
```
S_ANX WITH S_DEP;
```

!Within subdomain autocorrelations

```
anx1 anx2 anx3 anx4 PWITH anx2 anx3 anx4 anx5 (an); !PWITH means pair with
dep1 dep2 dep3 dep4 PWITH dep2 dep3 dep4 dep5 (dp);
```

OUTPUT:

```
SAMPSTAT;
```



```

324 # 010_2_Parallel growth curve models - anxiety and depression symptoms with autocorrelations
325 parallelautocor <- ' ia =~ 1*anx1 + 1*anx2 + 1*anx3 + 1*anx4 + 1*anx5
326                      sa =~ 0*anx1 + 1*anx2 + 3*anx3 + 4*anx4 + 6*anx5
327                      id =~ 1*dep1 + 1*dep2 + 1*dep3 + 1*dep4 + 1*dep5
328                      sd =~ 0*dep1 + 1*dep2 + 3*dep3 + 4*dep4 + 6*dep5
329 #Growth factor correlations
330 ia =~ id + sa
331 sd =~ id + sa
332 ia =~ 0*sd
333 id =~ 0*sa
334
335 #Autocorrelations
336 anx1 =~ eqa*anx2
337 anx2 =~ eqa*anx3
338 anx3 =~ eqa*anx4
339 anx4 =~ eqa*anx5
340
341 dep1 =~ eqd*dep2
342 dep2 =~ eqd*dep3
343 dep3 =~ eqd*dep4
344 dep4 =~ eqd*dep5
345 '
346 fit_parallelautocor <- growth(parallelautocor, data = data)
347 summary(fit_parallelautocor, fit.measures = TRUE)

```

## RESULTS

### Model fit:

( $\chi^2 = 813.952$ ,  $df = 41$ ;  $p < .001$ ;  $RMSEA = .242$  [90% CI = 0.228, 0.257];  $CFI = .586$ ;  $TLI = .546$ )

### Parameter estimates:

#### Anxiety symptoms

- i. Intercept: 1.395\*\*\*
- ii. Slope: -0.031\*\*\*

#### Depression symptoms

- i. Intercept: 1.544\*\*\*
- ii. Slope: -0.014\*\*

#### (Co)Variances:

#### Anxiety symptoms

- i. Intercept: 0.084\*\*\*
- ii. Slope: 0.001

#### Depression symptoms

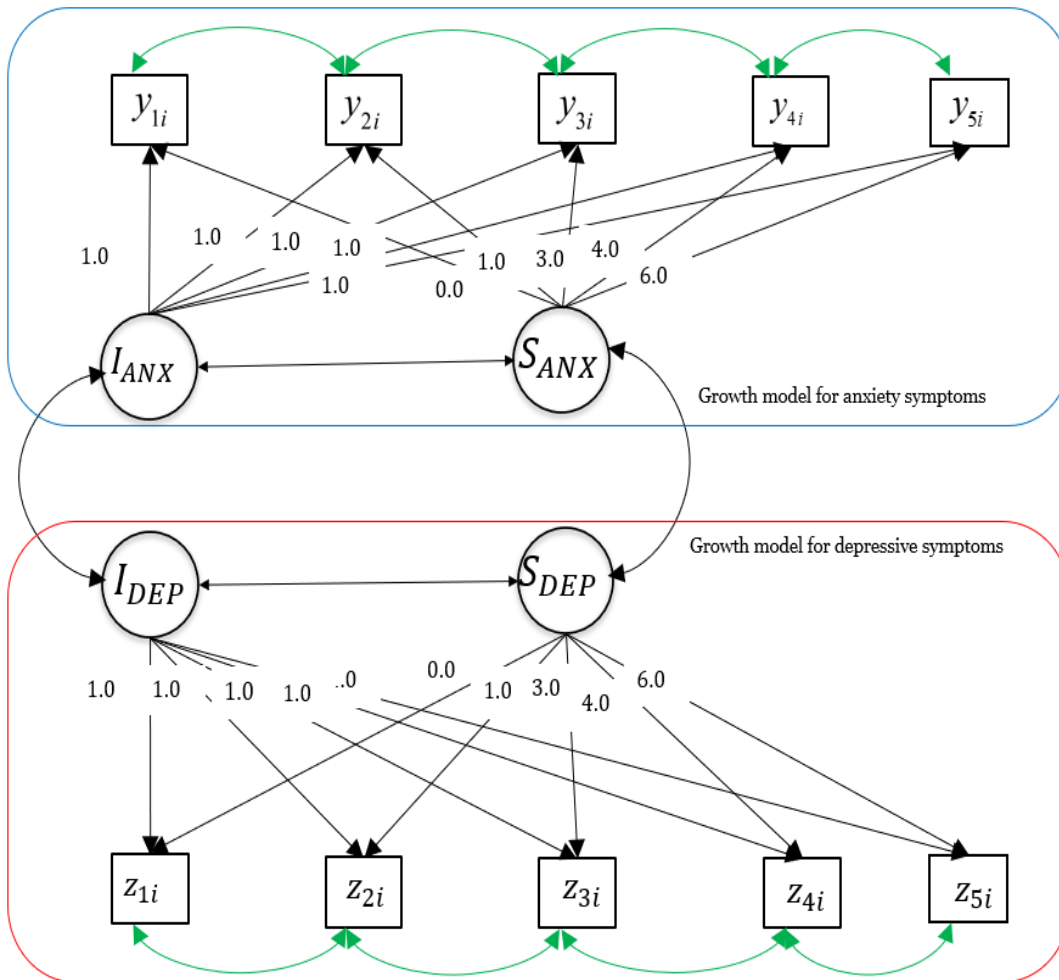
- i. Intercept: 0.156\*\*\*
- ii. Slope: 0.001

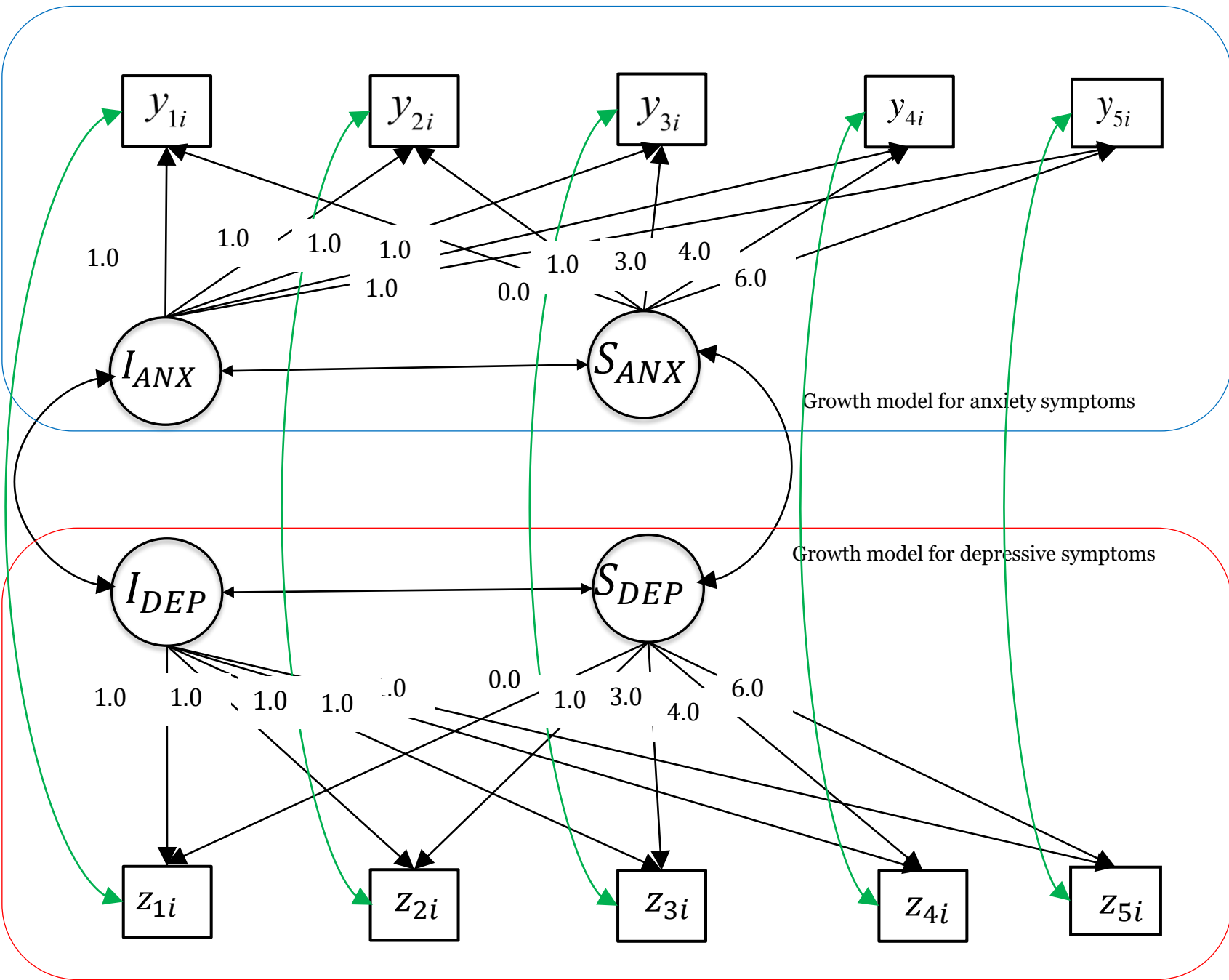
- iii. I\_ANX WITH S\_ANX 0.003
- iv. I\_ANX WITH I\_DEP 0.124\*\*\*

- v. I\_DEP WITH S\_DEP 0.007\*
- vi. S\_ANX WITH S\_DEP 0.004\*\*\*

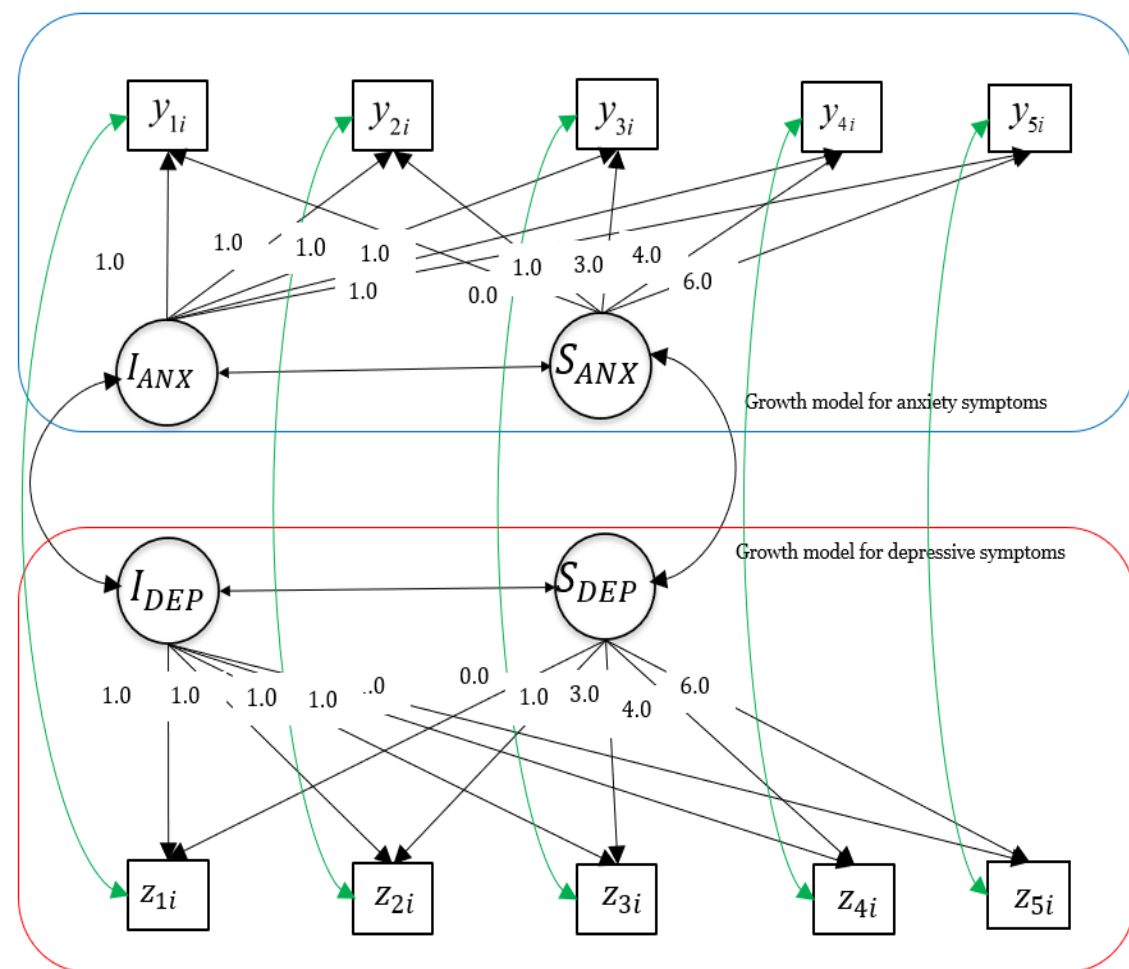
#### Autocorrelations

- i. Anxiety 0.012\*
- ii. Depression 0.013





- Each measure consist of
  - Item-specific variance component
  - Time-specific variance component
- ii. **Time-specific variance component** = between subdomains
  - Attributed to time-specific trends/patterns reporting biases (e.g., reporting lower level of symptoms at first timepoint)



USEVARIABLES ARE

```

    anx1 anx2 anx3 anx4 anx5
    dep1 dep2 dep3 dep4 dep5;

```

MISSING ARE ALL (-999);

ANALYSIS:

ESTIMATOR = ML;

MODEL = NOCOV; !Suppress Mplus default correlations between the growth  
!That way, you have control over what variables you want

MODEL:

```

I_ANX S_ANX|anx1@0 anx2@1 anx3@3 anx4@4 anx5@6; !anxiety symptoms growth
I_DEP S_DEP|dep1@0 dep2@1 dep3@3 dep4@4 dep5@6; !depressive symptoms

```

!Correlate the growth factors

```

I_ANX WITH S_ANX;
I_DEP WITH S_DEP;

```

```

I_ANX WITH I_DEP;
S_ANX WITH S_DEP;

```

!Cross subdomain correlations

```

anx1 anx2 anx3 anx4 anx5 PWITH dep1 dep2 dep3 dep4 dep5 (cros); !Label

```

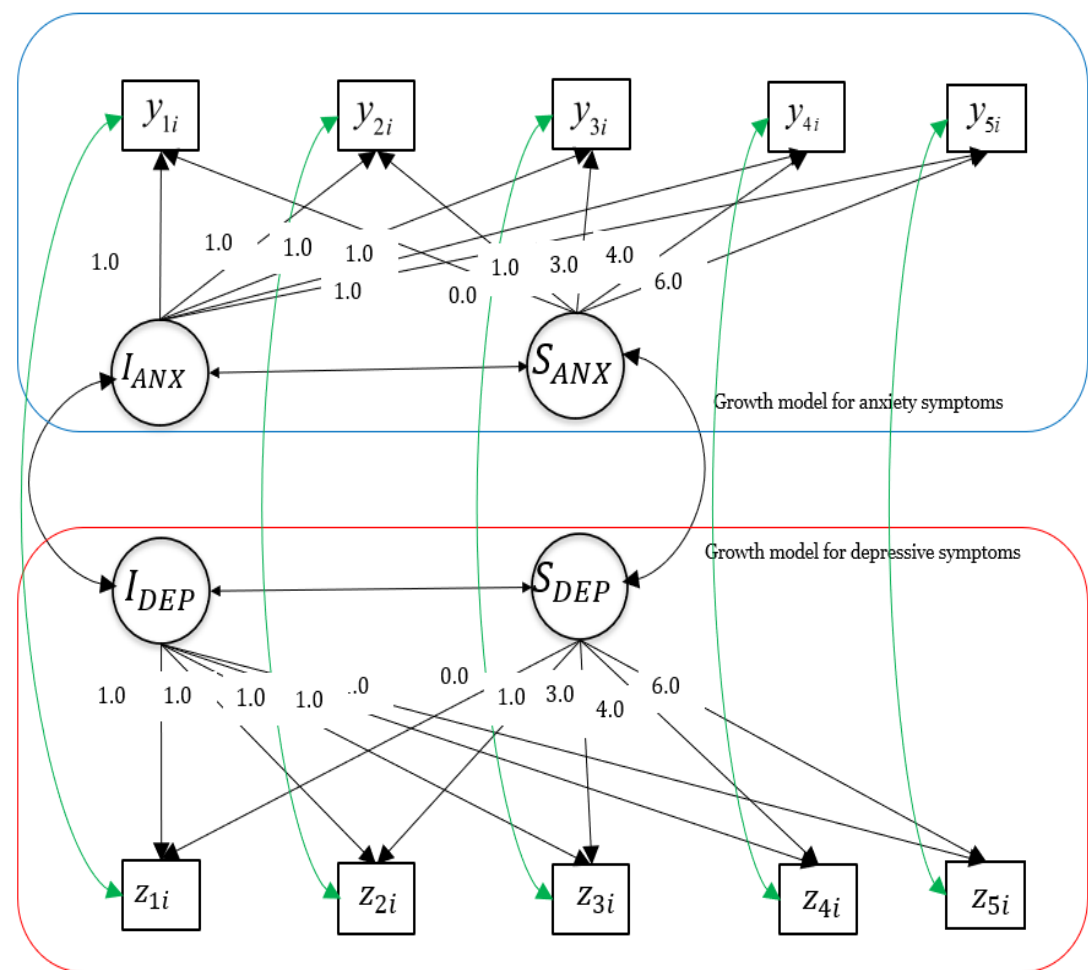
OUTPUT:

```

SAMPSTAT;

```





```

350 # 010_3_Parallel growth curve models - anxiety and depression symptoms with cross
351 parallelcross <- ' ia =~ 1*anx1 + 1*anx2 + 1*anx3 + 1*anx4 + 1*anx5
352                  sa =~ 0*anx1 + 1*anx2 + 3*anx3 + 4*anx4 + 6*anx5
353                  id =~ 1*dep1 + 1*dep2 + 1*dep3 + 1*dep4 + 1*dep5
354                  sd =~ 0*dep1 + 1*dep2 + 3*dep3 + 4*dep4 + 6*dep5
355 #Growth factor correlations
356 ia =~ id + sa
357 sd =~ id + sa
358 ia =~ 0*sd
359 id =~ 0*sa
360
361 #Cross domain correlations
362 anx1 =~ eq*dep1
363 anx2 =~ eq*dep2
364 anx3 =~ eq*dep3
365 anx4 =~ eq*dep4
366 anx5 =~ eq*dep5
367 '
368 fit_parallelcross <- growth(parallelcross, data = data)
369 summary(fit_parallelcross, fit.measures = TRUE)

```



## RESULTS

### Model fit:

( $\chi^2 = 178.746$ ,  $df = 42$ ;  $p < .001$ ;  $RMSEA = .101$ [90% CI = 0.086, 0.116];  $CFI = .927$ ;  $TLI = .922$ )

### Parameter estimates:

#### Anxiety symptoms

Intercept:

1.399\*\*\*

Slope:

-0.030\*\*\*

#### Depression symptoms

Intercept:

1.552\*\*\*

Slope:

-0.013\*

### Variances:

#### Anxiety symptoms

Intercept:

0.085\*\*\*

Slope:

0.001\*

#### Depression symptoms

Intercept:

0.144\*\*\*

Slope:

0.000

### Covariances:

i. I\_ANX WITH S\_ANX

-0.004\*\*

ii. I\_ANX WITH I\_DEP

0.082\*\*\*

iii. I\_DEP WITH S\_DEP

-0.002

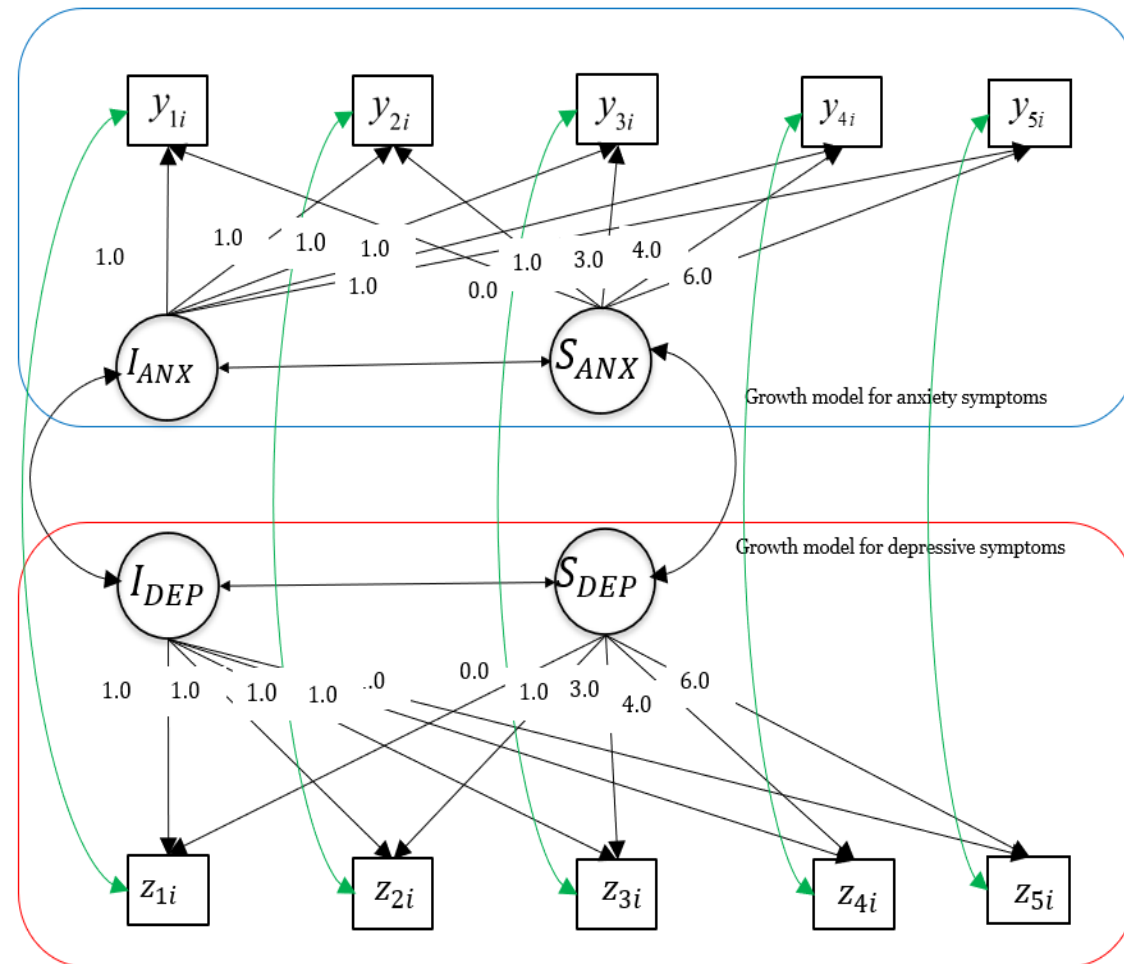
iv. S\_ANX WITH S\_DEP

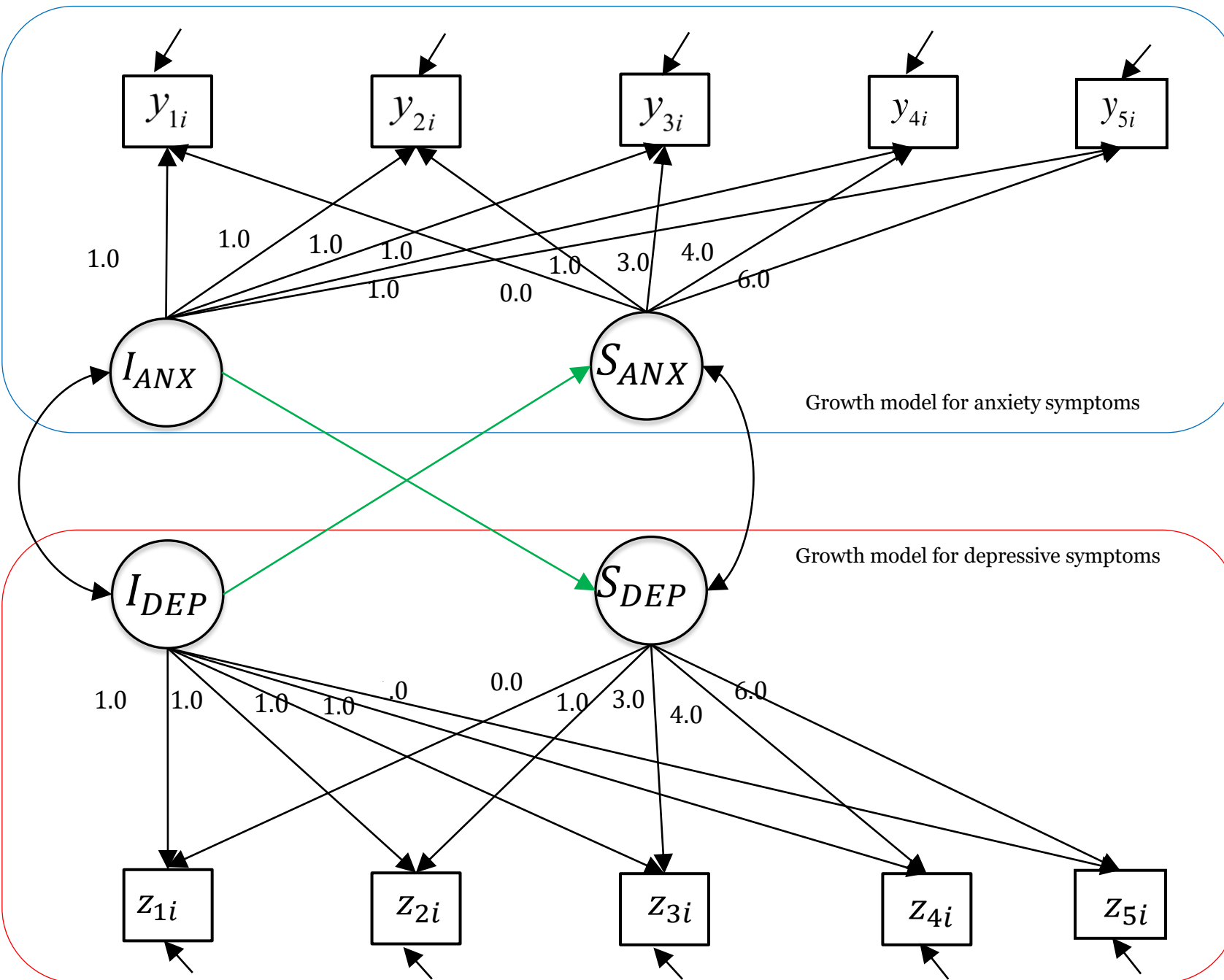
0.000

### Cross-domain correlations

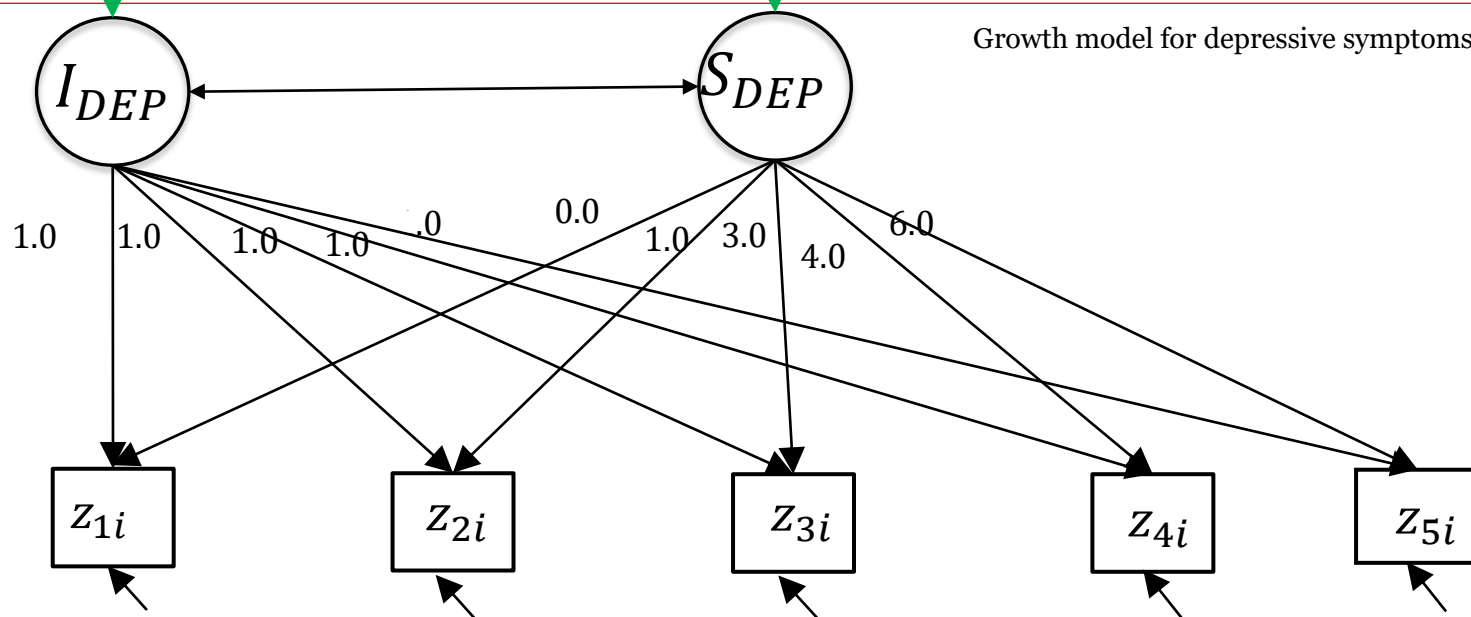
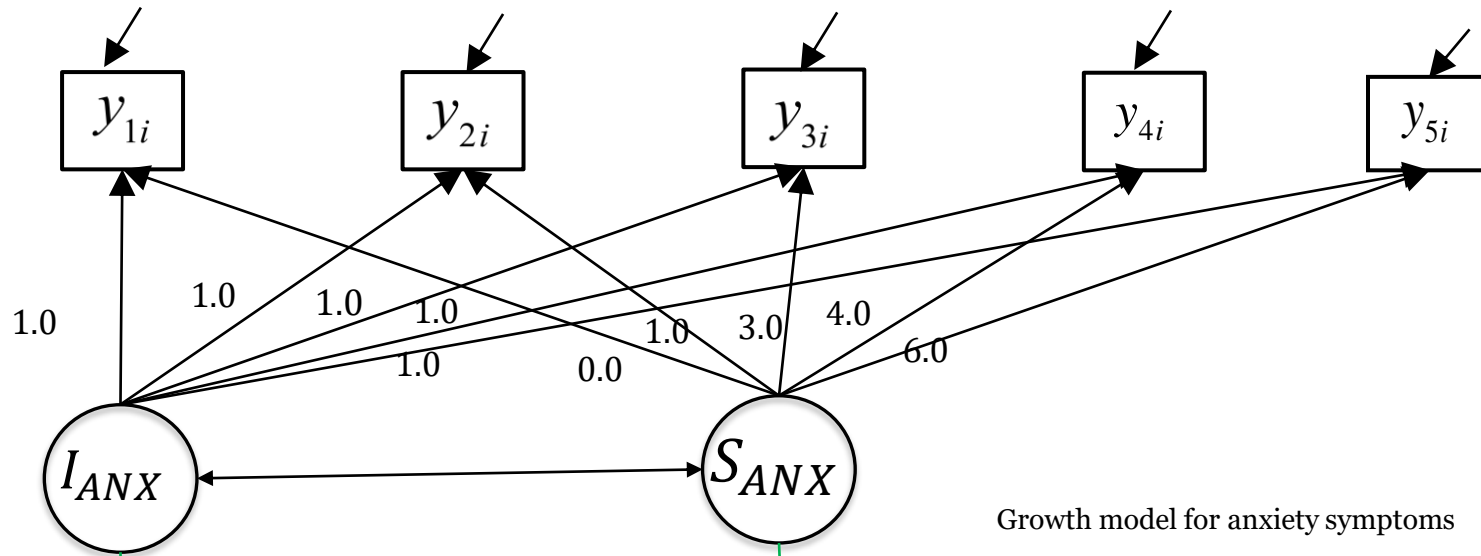
i. Anxiety - Depression

0.098\*\*\*



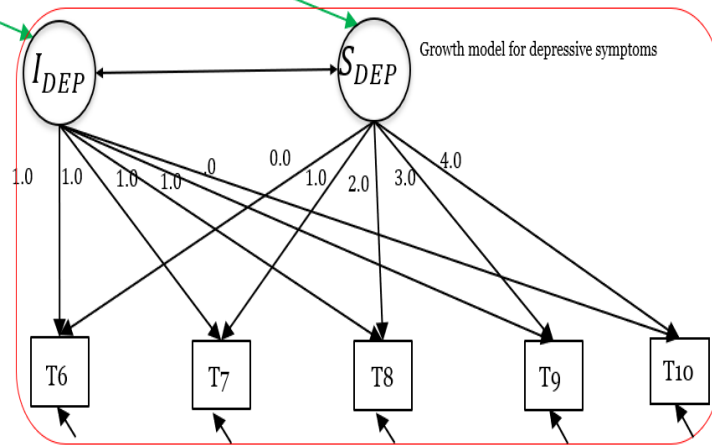
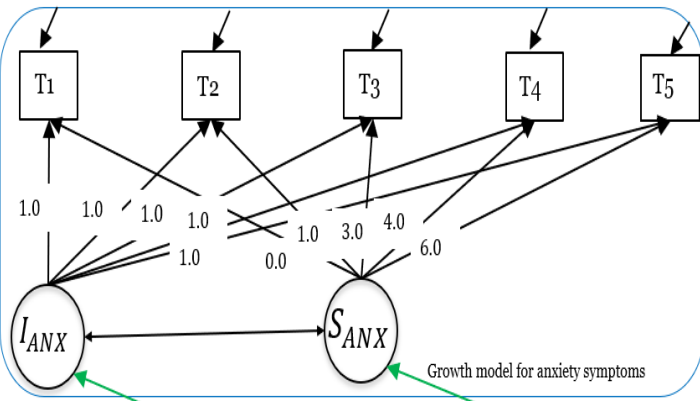


- Parallel growth process with regressions of the slope growth factor
  - Higher initial levels of anxiety symptoms influence the growth rate of depressive symptoms?
  - Higher initial levels of depression symptoms influence the growth rate of anxiety symptoms



- Parallel growth process with uni-directional effects
  - Evidence of co-development
  - Influence of growth factors of one subdomain on the growth factors of another subdomain





USEVARIABLES ARE

anx1 anx2 anx3 anx4 anx5

dep6 dep7 dep8 dep9 dep10; !Time of observations modified for ped

MISSING ARE ALL (-999);

ANALYSIS:

ESTIMATOR = ML;

MODEL = NOCOV; !Suppress Mplus default correlations between the grow

!That way, you have control over what variables you w

MODEL:

I\_ANX S\_ANX|anx1@0 anx2@1 anx3@3 anx4@4 anx5@6; !anxiety symptoms gr

I\_DEP S\_DEP|dep6@0 dep7@1 dep8@2 dep9@3 dep10@4; !Equidistant time s

!Correlate the growth factors

I\_ANX WITH S\_ANX;

I\_DEP WITH S\_DEP;

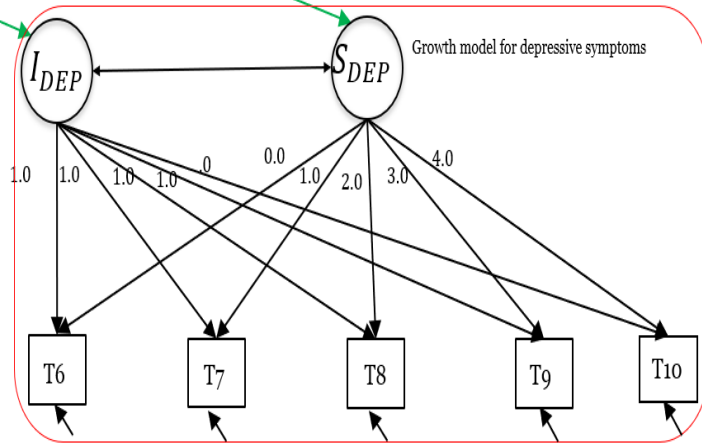
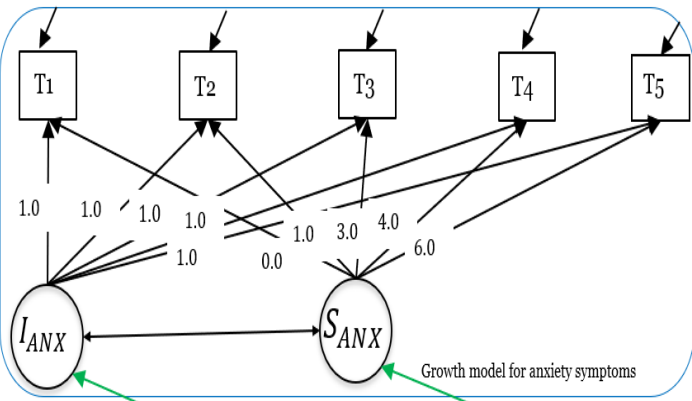
!Add sequqntially contingent growth factors

I\_ANX WITH I\_DEP;

S\_ANX WITH S\_DEP;

OUTPUT:

SAMPSTAT;



```

375 # 011_Sequentially contingent growth curve model anxiety t1-t5 predicting depress
376 sequential <- ' ia ≈ 1*anx1 + 1*anx2 + 1*anx3 + 1*anx4 + 1*anx5
377                  sa ≈ 0*anx1 + 1*anx2 + 3*anx3 + 4*anx4 + 6*anx5
378                  id ≈ 1*dep6 + 1*dep7 + 1*dep8 + 1*dep9 + 1*dep10
379                  sd ≈ 0*dep6 + 1*dep7 + 2*dep8 + 3*dep9 + 4*dep10
380
381 #Growth factor correlations
382 ia ≈ sa
383 id ≈ sd
384 ia ≈ 0*sd
385 id ≈ 0*sa
386
387 #Correlate growth factors across domain (may use regressions depending on theory)
388 ia ≈ id
389 sa ≈ sd
390 '
391 #Rename multiple columns using rename()
392 # We rename them to pretend that these variables are actually measured
393 # at a later date.
394 library(dplyr)
395 data <- data %>%
396   rename("dep6" = "dep1",
397          "dep7" = "dep2",
398          "dep8" = "dep3",
399          "dep9" = "dep4",
400          "dep10" = "dep5")
401
402 fit_sequential <- growth(sequential, data = data)
403 summary(fit_sequential, fit.measures = TRUE)

```

## RESULTS

### Model fit:

( $\chi^2 = 825.260$ ,  $df = 43$ ;  $p < .001$ ;  $RMSEA = .238$ [90% CI = 0.224, 0.252];  $CFI = .581$ ;  $TLI = .562$ )

### Parameter estimates:

Anxiety symptoms

- i. Intercept: 1.397\*\*\*
- ii. Slope: -0.032\*\*\*

Depression symptoms

- i. Intercept: 1.546\*\*\*
- ii. Slope: -0.021\*\*

(Co)Variances:

Anxiety symptoms

- i. Intercept: 0.097\*\*\*
- ii. Slope: 0.002\*\*\*

Depression symptoms

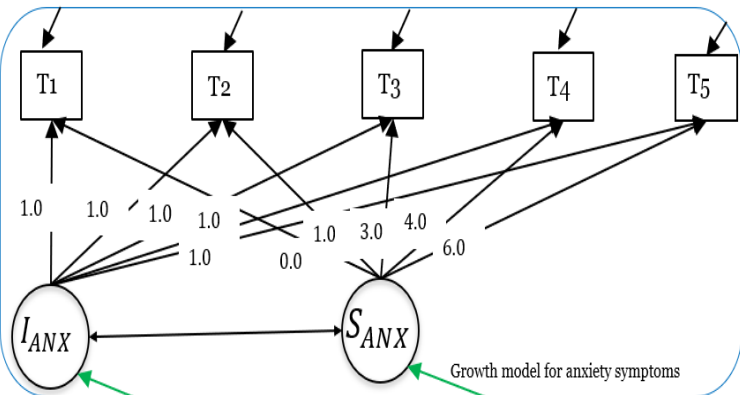
- i. Intercept: 0.171\*\*\*
- ii. Slope: 0.005\*\*

iii. I\_ANX WITH S\_ANX 0.000

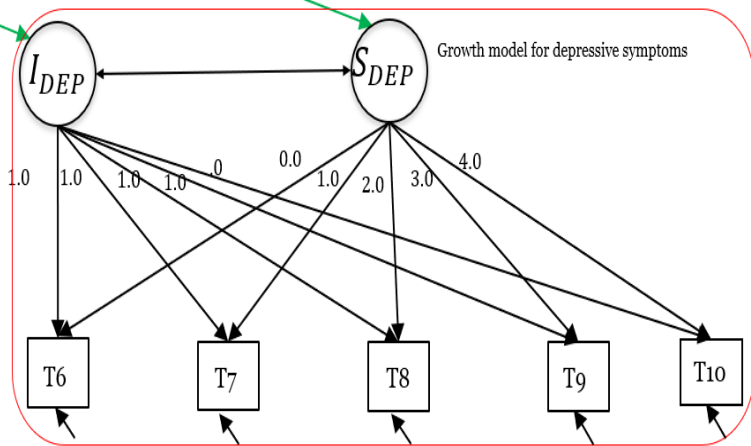
iv. I\_ANX WITH I\_DEP 0.124\*\*\*

v. I\_DEP WITH S\_DEP 0.007

vi. S\_ANX WITH S\_DEP 0.005\*\*\*



Growth model for anxiety symptoms



Growth model for depressive symptoms

# Course/workshop evaluations

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