Getting the most out of your family data with fSRM The Social Belations Model

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Lara.Stas@UGent.be The Social Relations Model

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Outline

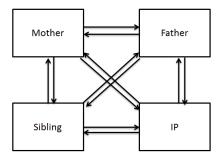
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Example: Case Study: X, 14 years old

- Aggressive problems in family context
- No problems at school
- Disturbed family dynamics?

Network of Relationship Inventory (Furman & Buhrmester, 1985):

- Negative interaction subscale



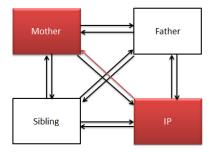
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Example: Case Study: X, 14 years old

- Aggressive problems in family context
- No problems at school
- Disturbed family dynamics?

e.g. How much do you and your mother get annoyed with each other's behavior?

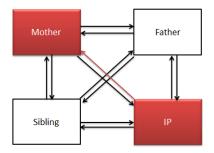


Example: Case Study: X, 14 years old

- Aggressive problems in family context
- No problems at school
- Disturbed family dynamics?

Result NRI :

X reports a lot of negativity in relation to his mother



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X reports about negativity in relation to his mother.

Actor effect:

How much negativity does this child report in

general?

Partner effect

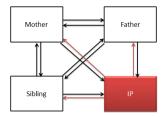
How negative is this mother perceived?

Relationship effect

Is it specific to their relationship?

• Family effect

Is it something specific to the family culture?



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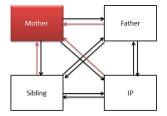
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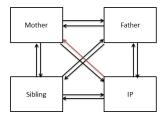
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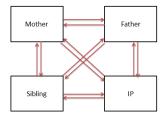
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The SRM is perfectly suitable for

Perform case studies

! need normative sample

(e.g. What are abnormal dynamics within this particular family?)

Examining one group

(e.g. Do mothers differ in terms of negativity?)

Comparing two groups

(e.g. Is there a difference between mothers with or without a child with externalizing problem behavior?)

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Additional questions that can be answered:

• At the individual level of analyses: What you give is what you get?

(i.e. correlation between actor and partner effect of the same person)

• At the dyadic level of analyses:

Are there bidirectional effects?

(i.e. correlation between the two relationship effects of the same dyad)

• Within generations:

Are there intragenerational similarities?

(i.e. correlation between actor or partner effects of the individuals of the same generation)

A (1) > A (2) > A (2) > A

Confirmatory Factor Analysis

SRM components are specified as latent variables in a CFA.

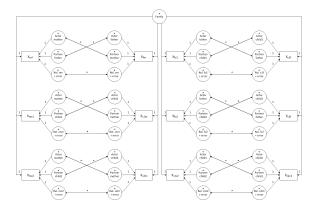


Figure : Boxes represent observed dyadic measurements, circles latent variables. Parameters that are fixed are indicated by '1', free parameters by an asterisk. Every indicator is connected with the corresponding latent variable by a single headed arrow. Double headed arrows represent reciprocities.

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Family researchers often find it hard to perform the analyses

R.f.m ~ .means.R.f.m*1 R.f.y ~ .means.R.f.y*1 R.m.c ~ .means.R.m.c*1 R.m.f ~ .means.R.m.f*1 R.m.y ~ .means.R.m.y*1 R.y.c ~ .means.R.y.c*1 R.y.f ~ .means.R.y.c*1 R.y.m ~ .means.R.y.c*1

set means of observed variables to zero _____ann = 0-1 ____ann = 0-1 y___ann = 0-1

```
# Met Constraints on Means I or lown: fileNilleDist
Means A.c. + means A.f. + means A.f. +
Means F.c. + means P.f + means F.m +
means R.c. + means P.f + means F.m +
means R.c. + means R.c. + means R.c. + means
Means R.c. + means R.f. + means R.c. + means
means R.c. + means R.f. + means R.m.y =
means R.f. + means R.m.f + means R.m.y.
means R.f. + means R.m.f + means R.m.y.
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means R.c. + means R.f. + means R.y. =
means R.c. + means R.f. + means R.y. =
means R.c. + means R.f. + means R.y. =
means R.c. + means R.f. + means R.y. =
means R.c. + means R.f. + means R.y. =
means R.c. + means R.f. + means R.g. + means R.f. +
```

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Family effect:

FE =~ 1*c_f_anx + 1*c_m_anx + 1*c_y_anx + $1 \star f$ c anx + $1 \star f$ m anx + $1 \star f$ v anx + 1*m_c_anx + 1*m_f_anx + 1*m_y_anx + 1*y_c_anx + 1*y_f_anx + 1*y_m_anx # Actor effects: A.c =~ $1 \star c$ f anx + $1 \star c$ m anx + $1 \star c$ v anx A.f =~ $1 \pm f$ c anx + $1 \pm f$ m anx + $1 \pm f$ v anx A.m =~ 1*m_c_anx + 1*m_f_anx + 1*m_y_anx A.y =~ 1*y_c_anx + 1*y_f_anx + 1*y_m_anx # Partner effects: P.c =~ $1 \star f$ c anx + $1 \star m$ c anx + $1 \star v$ c anx P.f =~ 1*c_f_anx + 1*m_f_anx + 1*y_f_anx P.m =~ 1*c_m_anx + 1*f_m_anx + 1*y_m_anx P.y =~ 1*c_y_anx + 1*f_y_anx + 1*m_y_anx # Relationship effects: R.c.f =~ 1* c f anx R.c.m =~ 1* c_m_anx R.c.v =~ 1* c v anx R.f.c =~ 1* f c anx R.f.m =~ 1* f_m_anx R.f.v =~ 1* f v anx R.m.c =~ 1* m c anx R.m.f =~ 1* m_f_anx R.m.v =~ 1* m v anx

R.y.c =~ 1* y_c_anx R.y.f =~ 1* y_f_anx R.y.m =~ 1* y_m_anx

Generalized reciprocity: A.c ~~ P.c

A.f ~~ P.f A.m ~~ P.m A.y ~~ P.y # Dyadic reciprocity: R.c.f ~~ R.f.c B.C.m.~~ B.m.C R.c.y ~~ R.y.c R.f.m ~~ R.m.f R.f.y ~~ R.y.f R.m.v ~~ R.v.m c_f_anx ~~ 0*c_f_anx c m anx ~~ 0+c m anx c v anx ~~ 0*c v anx f_c_anx ~~ 0*f_c_anx f m anx ~~ 0+f m anx f v anx ~~ 0*f v anx m_c_anx ~~ 0+m_c_anx m f anx ~~ 0+m f anx m_y_anx ~~ 0+m_y_anx y_c_anx ~~ 0*y_c_anx v f anx ~~ 0*v f anx y_m_anx ~~ 0*y_m_anx ## Compute structured means # Define labels for subsequent constraints FE ~ .means.FE+1 A.c ~ .means.A.c+1 A.f ~ .means.A.f+1 A.m ~ .means.A.m+1 A.v ~ .means.A.v*1 P.c ~ .means.P.c*1 P.f ~ .means.P.f *1 P.m ~ .means.P.m*1 P.y ~ .means.P.y*1 R.c.f ~ .means.R.c.f*1

R.c.m ~ .means.R.c.m*1

R.c.y ~ .means.R.c.y*1

R.f.c ~ .means.R.f.c*1

 $\begin{array}{l} {\rm R, f, m} \ \sim \ .means. R, f, m + 1 \\ {\rm R, f, y} \ \sim \ .means. R, m, v + 1 \\ {\rm R, m, c} \ \sim \ .means. R, m, c + 1 \\ {\rm R, m, y} \ \sim \ .means. R, m, c + 1 \\ {\rm R, m, y} \ \sim \ .means. R, m, y + 1 \\ {\rm R, y, c} \ \sim \ .means. R, y, c + 1 \\ {\rm R, y, f} \ \sim \ .means. R, y, c + 1 \\ {\rm R, y, f} \ \sim \ .means. R, y, m + 1 \end{array}$

set means of observed variables to zero c f anx ~ 0*1 c_m_anx ~ 0 * 1 c v anx ~ 0+1 f_c_anx ~ 0 * 1 $f_m_anx \sim 0 \star 1$ f v anx ~ 0+1 $m_c_anx \sim 0 \star 1$ $m_f_anx \sim 0 \star 1$ m v anx ~ 0+1 y_c_anx ~ 0*1 v f anx $\sim 0 \pm 1$ v m anx ~ 0+1 # set constraints on means for identifiability .means.A.c + .means.A.f + .means.A.m + .means.A.y -- 0 .means.P.c + .means.P.f + .means.P.m + .means.P.y -- 0 .means.R.c.f + .means.R.c.m + .means.R.c.y -- 0

```
means R.t.: + means R.t.: + means R.t.y = 
means R.R.c. + means R.m.f + means R.f.y = 0
means R.m.c + means R.m.f + means R.m.y = 0
means R.y.c. + means R.m.c + means R.y.r = 0
means R.f.c + means R.m.f + means R.y.r = 0
means R.c.m + means R.m.f + means R.y.r = 0
means R.c.m + means R.f.y + means R.y.r = 0
```

Family researchers often find it hard to perform the analyses

<pre># Fmaily affect Fm =- 1+cmank + 1+vmank + 1+vmank # Actor effect: A.c == 1+cmank + 1+cmank # Actor effect:</pre>	<pre># Dyadic reciprocity: R.c.f R.f.c R.c.m R.m.c R.c.y R.m.c R.f.m R.m.f R.f.y R.m.f R.f.y R.y.f R.m.y R.y.m</pre>	$ \begin{array}{llllllllllllllllllllllllllllllllllll$
With fSRM:		

 $fSRM(DV \sim actor.id, partner.id | family.id, means = T, data = dat)$

R.F.M	<pre>FE ~ .means.FE+1 A.C ~ .means.A.c+1 A.f ~ .means.A.f+1 A.m ~ .means.A.m+1 A.y ~ .means.A.m+1 P.C ~ .means.P.C+1 P.f ~ .means.P.C+1 P.m ~ .means.P.m+1 P.y ~ .means.P.m+1 P.y ~ .means.R.c+1</pre>	<pre>* set constraints on means for identifiability .means.A.c + .means.A.f + .means.A.m + .means.P.y -= 0 .means.P.c + .means.P.f + .means.P.m + .means.P.y -= 0 .means.R.c.f + .means.R.c.m + .means.R.c.y -= 0 .means.R.f.c + .means.R.c.m + .means.R.f.y -= 0 .means.R.f.c + .means.R.f. + .means.R.f.y -= 0 .means.R.f.y.c + .means.R.f. + .means.R.f.y -= 0</pre>

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fSRM will help!

- User-friendly R-package
- Based on lavaan (Rosseel, 2012)
- Easily insert, transform and analyze data in R
- Goes beyond the standard SRM analyses

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Outline

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Study of Eichelsheim et al. (2001)

- Patterns of negativity (NRI)
- Families with and without adolescent with externalizing problem behavior
- Group comparison clinical (n = 120) and nonclinical (n = 153) sample
- Simulated dataset

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Outline

Lara.Stas@UGent.be The Social Relations Model

fSRM: A user-friendly R-package for SRM analyses

Easily insert your data in R

76 Inserting and transforming your data			
Read in your datafile			
Select CSV file			
Select TXT file			
Select SPSS File			
Do you want to transform your data from wide to long format?			
Transform my data			
Which SRM labels do you prefer in the output?			
Family effect?	FE		
Actor/Perceiver effect?	A		
Partner/Target effect?	P		
Relationship effect?	R		
Confirm output format			
OK			
Please deal with missing data in an appropriate way before using these functions.			



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fSRM: A user-friendly R-package for SRM analysesEasy to transform a dataset to long format

76 Inserting and transforming your data	
Read in your datafile Select CSV file Select SPTS file Select SPTS File	
Do you want to transform your data from wide to long format? Transform my data	
Which SRM labels do you prefer in the output?	
Family effect? Actor/Perceiver effect? Partner/Target effect? Relationship effect?	FE A
Confirm output format	
ок	
Please deal with missing data in an appropriate way before using these fun	etions.

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fSRM: A user-friendly R-package for SRM analysesEasy to transform a dataset to long format

76 Inserting and trans	sforming your data			
Read in your datafile	Select CSV file Select TXT file Select SPSS File			
Do you want to transform your data from wide to long format? Transform my data				
Which SRM labels do y	you prefer in the output?			
Family effect?		FE		
Actor/Perceiver effect	?	A		
Partner/Target effect?		P		
Relationship effect?		R		
	Confirm output format			
	ок			
Please deal with missing	data in an appropriate way before using these fu	netions.		

	family_ID	mfanx	mcanx	myanx		
1	1	1.000000	1.500000	1.5000	99	
2	2	2.166667	2.000000	2.1666	67	
3	3	1.166667	1.333333	1.0000	99	
		~	$\overline{\mathbf{v}}$			
	family.id	variable	value	actor.id	partner.id	inc
1	1	mfanx	1.000000	n f		an
2	2	mfanx	2.166667	n f		an
3	3	mfanx	1.166667	n	f	an
			•••			
209	1	mcanx	1.500000	m	c	an
			2,000000		c	an
210	2	mcanx	2.000000	-		
210 211	3	mcanx	1.333333		c	an
						an
			1.333333			
211	3	mcanx	1.333333	m	c	anx anx anx

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fSRM: A **user-friendly** R-package for SRM analyses

Easy to transform a dataset to long format

76 Inserting and trans	forming your data	- • ×
Read in your datafile	Select CSV file Select TXT file Select SPSS File	
Do you want to transfo	orm your data from wide to long format?	
	Transform my data	
Which SRM labels do y	you prefer in the output?	
Family effect?		FE
Actor/Perceiver effect	2	A
Partner/Target effect?		Ρ
Relationship effect?		R
	Confirm output format	
	ок	
Please deal with missing	data in an appropriate way before using these functi	ionz.

74 Transformation of the dataset				
If present, enter the variable name that contains the identificat	ince of			
the different families.	1015 01			
the different groups.				
Specify the column numbers of the dyadic measuren	nents in your original d	ataset		
Paramining Longin 11, 11 and 16 an extend of 14, 1				
E.g. variables 1 until 9, 11, 13 and 15 are entered as 1:9, 1	1, 13, 13			
Based on the variable names of the dvadic measurements, define the position of the characters of				
the rater in the dyadic measurement?	From	To		
	From	To		
the person being rated in the dyadic measurement?	From	10		
the indicators (if present)	From	To		
ОК	Cancel			

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fSRM: A user-friendly R-package for SRM analyses

• The labels in the output can be customized

76 Inserting and transforming your data	
Read in your datafile Select CSV file Select TXT file	
Select SPSS File	
Transform my data	
Which SRM labels do you prefer in the output?	
Family effect?	FE
Actor/Perceiver effect?	A
Partner/Target effect?	Ρ
Relationship effect?	R
Confirm output format	
<u>ok</u>	
Please deal with missing data in an appropriate way before using these function	945.

3 1 4 3 1

```
# Load the package
install.packages("fSRM")
library("fSRM")
```

Load data and select clinical group data(two.groups) clinical <- subset(two.groups, group==1)</pre>

```
# Run the basic SRM analysis
fSRM.1gr <- fSRM(neg1/neg2 ~ actor.id * partner.id |
family.id, data = clinical)</pre>
```

Only SRM variance are requested

Two indicators ⇒ SRM relationship partitioned from error

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SRM with roles (latent) (Roles: C1, C2, FA, MO ; DVs = neg1 neg2) :

Model summary:

lavaan (0.5-12) converged normally after 65 iterations

Number of observations	120
Estimator	ML
Minimum Function Test Statistic	110.720
Degrees of freedom	113
P-value (Chi-square)	0.543

Model Fit:

CH2 (df=113) = 110.72, p = 0.543 CFI = 1 TLI / NNFI = 1.011 RMSEA = 0 [0:0.044]; Test of close fit: p(data | true value == .05) = 0.979

Variance decomposition:

component	estimate	se	z	p.value	ci.lower	ci.upper
1 FE ~~ FE	0.019	0.018	1.058	0.290	-0.016	0.054
2 A.C1 ~~ A.C1		0.040		0.033	0.007	0.165
3 A.C2 ~~ A.C2	0.138	0.045	3.090	0.002	0.051	0.226
4 A.FA ~~ A.FA	0.010	0.026	0.385	0.700	-0.042	0.062
5 A.MO ~~ A.MO	0.009	0.028	0.321	0.749	-0.045	0.063
6 P.C1 ~~ P.C1	0.078	0.034	2.306	0.021	0.012	0.143
7 P.C2 ~~ P.C2	0.061	0.033	1.836	0.066	-0.004	0.126
8 P.FA ~~ P.FA	0.079	0.035	2.294	0.022	0.012	0.147
9 P.MO ~~ P.MO	0.014	0.032	0.448	0.654	-0.048	0.076
10 R.C1.C2 ~~ R.C1.C2	0.507	0.114	4.435	0.000	0.283	0.731
11 R.C1.FA ~~ R.C1.FA	0.234	0.077	3.038	0.002	0.083	0.385
12 R.C1.MO ~~ R.C1.MO	0.275	0.085	3.230	0.001	0.108	0.441
13 R.C2.C1 ~~ R.C2.C1	0.204	0.091	2.243	0.025	0.026	0.382
14 R.C2.FA ~~ R.C2.FA	0.177	0.076	2.327	0.020	0.028	0.327
15 R.C2.MO ~~ R.C2.MO	0.329	0.087	3.779	0.000	0.159	0.500
16 R.FA.C1 ~~ R.FA.C1	0.225	0.064	3.514	0.000	0.099	0.350
17 R.FA.C2 ~~ R.FA.C2	0.078	0.059	1.319	0.187	-0.038	0.195
18 R.FA.MO ~~ R.FA.MO	0.169	0.072	2,360	0.018	0.029	0.310
19 R.MO.C1 ~~ R.MO.C1	0.109	0.063	1.731	0.083	-0.014	0.232
20 R.MO.C2 ~~ R.MO.C2		0.075		0.004	0.071	0.365
21 R.MO. FA ~~ R.MO. FA		0.065		0.002	0.070	0.325

Information about the model fit

Information about the SRM variances

SRM with roles (latent) (Roles: C1, C2, FA, MO ; DVs = neg1 neg2) :

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Variance decomposition:

component	estimate	se	z	p.value	ci.lower	ci.upper				
1 FE ~~ FE	0.019	0.018	1.058	0.290	-0.016	0.054				
2 A.C1 ~~ A.C1	0.086	0.040	2.131	0.033	0.007	0.165				
3 A.C2 ~~ A.C2	0.138	0.045	3.090	0.002	0.051	0.226				
4 A.FA ~~ A.FA	0.010	0.026	0.385	0.700	-0.042	0.062				
5 A.MO ~~ A.MO	0.009	0.028	0.321	0.749	-0.045	0.063				
6 P.C1 ~~ P.C1	0.078	0.034	2.306	0.021	0.012	0.143				
7 P.C2 ~~ P.C2	0.061	0.033	1.836	0.066	-0.004	0.126				
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10 R.C1.C2 ~~ R.C1.C2	0.507	0.114	4.435	0.000	0.283	0.731				
11 R.C1.FA ~~ R.C1.FA	0.234	0.077	3.038	0.002	0.083	0.385				
12 R.C1.MO ~~ R.C1.MO	0.275	0.085	3.230	0.001	0.108	0.441				
13 R.C2.C1 ~~ R.C2.C1	0.204	0.091	2.243	0.025	0.026	0.382				
14 R.C2.FA ~~ R.C2.FA	0.177	0.076	2.327	0.020	0.028	0.327				
15 R.C2.MO ~~ R.C2.MO	0.329	0.087	3.779	0.000	0.159	0.500				
16 R.FA.C1 ~~ R.FA.C1	0.225	0.064	3.514	0.000	0.099	0.350				
17 R.FA.C2 ~~ R.FA.C2	0.078	0.059	1.319	0.187	-0.038	0.195				
18 R.FA.MO ~~ R.FA.MO	0.169	0.072	2.360	0.018	0.029	0.310				
19 R.MO.C1 ~~ R.MO.C1	0.109	0.063	1.731	0.083	-0.014	0.232				
20 R.MO.C2 ~~ R.MO.C2	0.218	0.075	2.901	0.004	0.071	0.365				
21 R.MO.FA ~~ R.MO.FA	0.197	0.065	3.030	0.002	0.070	0.325				

Information about the model fit

• Good fit according to the χ^2 (p > 0.05)

Information about the SRM variances

SRM with roles (latent) (Roles: C1, C2, FA, MO ; DVs = neg1 neg2) :

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Minimum Function Test Statistic	110.720
Degrees of freedom	113
P-value (Chi-square)	0.543

Model Fit:

Chi2 (df=113) = 110.72, p = 0.543 CFI = 1 TII / NNFI = 1.011 RMSEA = 0 [0;0.044]; Test of close fit: p(data | true value == .05) = 0.979

Variance decomposition:

component	estimate	se	z	p.value	ci.lower	ci.upper
1 FE ~~ FE	0.019	0.018	1.058	0.290	-0.016	0.054
2 A.C1 ~~ A.C1		0.040		0.033	0.007	0.165
3 A.C2 ~~ A.C2	0.138	0.045	3.090	0.002	0.051	0.226
4 A.FA ~~ A.FA	0.010	0.026	0.385	0.700	-0.042	0.062
5 A.MO ~~ A.MO	0.009	0.028	0.321	0.749	-0.045	0.063
6 P.C1 ~~ P.C1	0.078	0.034	2.306	0.021	0.012	0.143
7 P.C2 ~~ P.C2	0.061	0.033	1.836	0.066	-0.004	0.126
8 P.FA ~~ P.FA	0.079	0.035	2.294	0.022	0.012	0.147
9 P.MO ~~ P.MO	0.014	0.032	0.448	0.654	-0.048	0.076
10 R.C1.C2 ~~ R.C1.C2	0.507	0.114	4.435	0.000	0.283	0.731
11 R.C1.FA ~~ R.C1.FA	0.234	0.077	3.038	0.002	0.083	0.385
12 R.C1.MO ~~ R.C1.MO	0.275	0.085	3.230	0.001	0.108	0.441
13 R.C2.C1 ~~ R.C2.C1	0.204	0.091	2.243	0.025	0.026	0.382
14 R.C2.FA ~~ R.C2.FA	0.177	0.076	2.327	0.020	0.028	0.327
15 R.C2.MO ~~ R.C2.MO	0.329	0.087	3.779	0.000	0.159	0.500
16 R.FA.C1 ~~ R.FA.C1	0.225	0.064	3.514	0.000	0.099	0.350
17 R.FA.C2 ~~ R.FA.C2	0.078	0.059	1.319	0.187	-0.038	0.195
18 R.FA.MO ~~ R.FA.MO	0.169	0.072	2.360	0.018	0.029	0.310
19 R.MO.C1 ~~ R.MO.C1	0.109	0.063	1.731	0.083	-0.014	0.232
20 R.MO.C2 ~~ R.MO.C2	0.218	0.075	2,901	0.004	0.071	0.365
21 R.MO.FA ~~ R.MO.FA		0.065		0.002	0.070	0.325

Information about the model fit

Information about the SRM variances

 e.g., some target adolescents experience more negativity in relation to his/her family members than others

	Family	Actor	Partner	Relationship	Error	explained
C1_C2	2	7	5	41	45	55
C1_FA	2	10	10	29	49	51
C1_MO	2	11	2	34	51	49
C2_C1	2	14	8	20	57	43
C2_FA	2	17	10	22	49	51
C2_MO	2	14	1	34	48	52
FA_C1	3	2	12	35	48	52
FA_C2	3	2	11	14	69	31
FA_MO	3	2	2	25	69	31
M0_C1	3	1	12	17	67	33
MO_C2	2	1	8	27	62	38
MO_FA	3	1	11	29	56	44
mean	2	7	8	27	56	44

4 Generalized reciprocity (actor-partner covariances):

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	component	estimate	se	z	p.value	ci.lower	ci.upper	r
1	A.C1 ~~ P.C1	0.031	0.028	1.083	0.279	-0.025	0.086	0.377
2	A.C2 ~~ P.C2	-0.014	0.029	-0.474	0.635	-0.071	0.043	-0.150
3	A.FA ~~ P.FA	0.012	0.024	0.482	0.630	-0.036	0.060	0.414
4	A.MO ~~ P.MO	0.013	0.023	0.555	0.579	-0.033	0.059	NA

component	estimate	se	z	p.value	ci.lower	ci.upper	r
1 R.C1.C2 ~~ R.C2.C1	0.238 0	0.076	3.144	0.002	0.089	0.386	0.739
2 R.C1.FA ~~ R.FA.C1	0.129 0	0.053	2.456	0.014	0.026	0.232	0.563
3 R.C1.MO ~~ R.MO.C1	-0.049 0	0.053	-0.930	0.352	-0.152	0.054	-0.283
4 R.C2.FA ~~ R.FA.C2	0.139 0	0.049	2.834	0.005	0.043	0.236	NA
5 R.C2.MO ~~ R.MO.C2	0.113 0	0.058	1.934	0.053	-0.001	0.227	0.421
6 R.FA.MO ~~ R.MO.FA	0.134 0	0.051	2.660	0.008	0.035	0.233	0.736

Relative importance of each SRM component

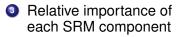
- per observed relationship
- averaged

Generalized reciprocities

Oyadic reciprocities

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	Family	Actor	Partner	Relationship	Error	explained
C1_C2	2	7	5	41	45	55
C1_FA	2	10	10	29	49	51
C1_MO	2	11	2	34	51	49
C2_C1	2	14	8	20	57	43
C2_FA	2	17	10	22	49	51
C2_MO	2	14	1	34	48	52
FA_C1	3	2	12	35	48	52
FA_C2	3	2	11	14	69	31
FA_MO	3	2	2	25	69	31
MO_C1	3	1	12	17	67	33
MO_C2	2	1	8	27	62	38
MO_FA	3	1	11	29	56	44
mean	2	7	8	27	56	44

Generalized reciprocity (actor-partner covariances):

	component	estimate	se	z	p.value	ci.lower	ci.upper	r
1	A.C1 ~~ P.C1	0.031	0.028	1.083	0.279	-0.025	0.086	0.377
2	A.C2 ~~ P.C2	-0.014	0.029	-0.474	0.635	-0.071	0.043	-0.150
3	A.FA ~~ P.FA	0.012	0.024	0.482	0.630	-0.036	0.060	0.414
4	A.MO ~~ P.MO	0.013	0.023	0.555	0.579	-0.033	0.059	NA

Dyadic reciprocity (relationship covariances): Mean r = 0.491 (out of bounds estimates set to NA)

component	estimate	se	z	p.value	ci.lower	ci.upper	r
1 R.C1.C2 ~~ R.C2.C1	0.238	0.076	3.144	0.002	0.089	0.386	0.739
2 R.C1.FA ~~ R.FA.C1	0.129	0.053	2.456	0.014	0.026	0.232	0.563
3 R.C1.MO ~~ R.MO.C1	-0.049	0.053	-0.930	0.352	-0.152	0.054	-0.283
4 R.C2.FA ~~ R.FA.C2	0.139	0.049	2.834	0.005	0.043	0.236	NA
5 R.C2.MO ~~ R.MO.C2	0.113	0.058	1.934	0.053	-0.001	0.227	0.421
6 R.FA.MO ~~ R.MO.FA	0.134	0.051	2.660	0.008	0.035	0.233	0.736

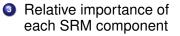
Generalized reciprocities

 Not what you give is what you get

Dyadic reciprocities

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	Family	Actor	Partner	Relationship	Error	explained
C1_C2	2	7	5	41	45	55
C1_FA	2	10	10	29	49	51
C1_MO	2	11	2	34	51	49
C2_C1	2	14	8	20	57	43
C2_FA	2	17	10	22	49	51
C2_MO	2	14	1	34	48	52
FA_C1	3	2	12	35	48	52
FA_C2	3	2	11	14	69	31
FA_MO	3	2	2	25	69	31
MO_C1	3	1	12	17	67	33
MO_C2	2	1	8	27	62	38
MO_FA	3	1	11	29	56	44
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Generalized reciprocity (actor-partner covariances):

	component	estimate	se	z	p.value	ci.lower	ci.upper	r
1	A.C1 ~~ P.C1	0.031	0.028	1.083	0.279	-0.025	0.086	0.377
2	A.C2 ~~ P.C2	-0.014	0.029	-0.474	0.635	-0.071	0.043	-0.150
3	A.FA ~~ P.FA	0.012	0.024	0.482	0.630	-0.036	0.060	0.414
4	A.MO ~~ P.MO	0.013	0.023	0.555	0.579	-0.033	0.059	NA

Dyadic reciprocity (relationship covariances): Mean r = 0.491 (out of bounds estimates set to NA)

component	estimate	se	z	p.value	ci.lower	ci.upper	r
1 R.C1.C2 ~~ R.C2.C1	0.238	0.076	3.144	0.002	0.089	0.386	0.739
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3 R.C1.MO ~~ R.MO.C1	-0.049	0.053	-0.930	0.352	-0.152	0.054	-0.283
4 R.C2.FA ~~ R.FA.C2	0.139	0.049	2.834	0.005	0.043	0.236	NA
5 R.C2.MO ~~ R.MO.C2	0.113	0.058	1.934	0.053	-0.001	0.227	0.421
6 R.FA.MO ~~ R.MO.FA	0.134	0.051	2.660	0.008	0.035	0.233	0.736

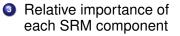
Generalized reciprocities

Oyadic reciprocities

- Unique negativity of target adolescent towards father, and vice versa, correlate
- Mother is the exception in relation to her children

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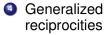
	Family	Actor	Partner	Relationship	Error	explained
C1_C2	2	7	5	41	45	55
C1_FA	2	10	10	29	49	51
C1_MO	2	11	2	34	51	49
C2_C1	2	14	8	20	57	43
C2_FA	2	17	10	22	49	51
C2_MO	2	14	1	34	48	52
FA_C1	3	2	12	35	48	52
FA_C2	3	2	11	14	69	31
FA_MO	3	2	2	25	69	31
M0_C1	3	1	12	17	67	33
MO_C2	2	1	8	27	62	38
MO_FA	3	1	11	29	56	44
mean	2	7	8	27	56	44

Generalized reciprocity (actor-partner covariances):

	component	estimate	se	z	p.value	ci.lower	ci.upper	r
1	A.C1 ~~ P.C1	0.031	0.028	1.083	0.279	-0.025	0.086	0.377
2	A.C2 ~~ P.C2	-0.014	0.029	-0.474	0.635	-0.071	0.043	-0.150
3	A.FA ~~ P.FA	0.012	0.024	0.482	0.630	-0.036	0.060	0.414
4	A.MO ~~ P.MO	0.013	0.023	0.555	0.579	-0.033	0.059	NA

Dyadic reciprocity (relationship covariances): Mean r = 0.491 (out of bounds estimates set to NA)

component	estimate	se	z	p.value	ci.lower	ci.upper	r
1 R.C1.C2 ~~ R.C2.C1	0.238	0.076	3.144	0.002	0.089	0.386	0.739
2 R.C1.FA ~~ R.FA.C1	0.129	0.053	2.456	0.014	0.026	0.232	0.563
3 R.C1.MO ~~ R.MO.C1	-0.049	0.053	-0.930	0.352	-0.152	0.054	-0.283
4 R.C2.FA ~~ R.FA.C2	0.139	0.049	2.834	0.005	0.043	0.236	NA
5 R.C2.MO ~~ R.MO.C2	0.113	0.058	1.934	0.053	-0.001	0.227	0.421
6 R.FA.MO ~~ R.MO.FA	0.134	0.051	2.660	0.008	0.035	0.233	0.736



Oyadic reciprocities

- Unique negativity of target adolescent towards father, and vice versa, correlate
- Mother is the exception in relation to her children

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- Mean SRM components
- Intragenerational similarities
- Pairwise comparisons of actor (or partner) effects between two roles

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- Mean SRM components
- Intragenerational similarities
- Pairwise comparisons of actor (or partner) effects between two roles

```
fSRM.extra <- fSRM(neg1/neg2 ~ actor.id * partner.id |
            family.id, data = clinical,
            means = T,</pre>
```

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Mean SRM components

Intragenerational similarities

• Pairwise comparisons of actor (or partner) effects between two roles

```
fSRM.extra <- fSRM(neg1/neg2 ~ actor.id * partner.id |
            family.id, data = clinical,
            means = T,
            IGSIM=list(c("MO", "FA"), c("C1", "C2")),</pre>
```

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- Mean SRM components
- Intragenerational similarities
- Pairwise comparisons of actor (or partner) effects between two roles

```
fSRM.extra <- fSRM(neg1/neg2 ~ actor.id * partner.id |
    family.id, data = clinical,
    means = T,
    IGSIM=list(c("MO", "FA"), c("C1", "C2")),
    pairwise = TRUE)</pre>
```

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6 Intragenerational similarity:

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component	estimate se	z p.value	ci.lower	ci.upper	r
107 A.FA ~~ A.MO	-0.008 0.022	-0.364 0.716	-0.051	0.035	NA
108 P.FA ~~ P.MO	0.056 0.028	1.994 0.046	0.001	0.111	NA
109 A.C1 ~~ A.C2	0.008 0.030	0.272 0.786	-0.050	0.067	0.088
110 P.C1 ~~ P.C2	-0.013 0.025	-0.512 0.609	-0.061	0.035	-0.183

Intragenerational similarities

7 Mean structure: Indices starting with 'C.' are pairwise comparisons between roles

_								
			estimate				ci.lower	
	1	FE			68.029		1.801	1.908
	2	A.C1			10.076	0.000	0.308	0.457
	3	A.C2	0.149		3.693	0.000	0.070	0.229
	4	A. FA			-8.778	0.000	-0.353	
	5	A.MO	-0.243			0.000	-0.310	-0.177
	6	P.C1	0.312		8.179	0.000	0.237	0.387
	7	P.C2	0.151		4.042	0.000	0.078	0.224
	8	P.FA	-0.239	0.036	-6.627	0.000	-0.309	-0.168
	9	P.MO	-0.224			0.000	-0.292	
	10	R.C1.C2	0.168	0.040	4.212	0.000	0.090	0.246
	11	R.C1.FA			-2.637	0.008	-0.173	-0.025
	12	R.C1.MO	-0.069	0.040	-1.734	0.083	-0.147	0.009
	13	R.C2.C1	0.276		7.507	0.000	0.204	0.348
	14	R.C2.FA			-3.889	0.000	-0.207	-0.068
	15	R.C2.MO			-3.608	0.000	-0.213	-0.063
	16	R. FA. C1			-3.588	0.000	-0.181	-0.053
	17	R. FA. C2	-0.090	0.035	-2.564	0.010	-0.159	-0.021
	18	R.FA.MO	0.207	0.039	5.362	0.000	0.131	0.283
	19	R.MO.C1	-0.159	0.034	-4.649	0.000	-0.226	-0.092
	20	R.MO.C2	-0.078	0.035	-2.229	0.026	-0.146	-0.009
-	21	R.MO.FA	0.237	0.035	6.682	0.000	0.167	0.306
		C.means.A.C1.C2	0.233			0.000	0.107	
-		C.means.P.C1.C2				0.007		
		C.means.A.C1.FA				0.000	0.559	
		C.means.P.C1.FA			8.941	0.000	0.430	0.671
		C.means.A.C1.MO			10.448	0.000	0.509	
		C.means.P.C1.MO	0.536		8.611	0.000	0.414	
		C.means.A.C2.FA	0.438		7.048	0.000	0.316	0.560
		C.means.P.C2.FA	0.390		6.215	0.000	0.267	
	30	C.means.A.C2.MO	0.393		6.362	0.000	0.272	
		C.means.P.C2.MO			6.339		0.259	
	32	C.means.A.FA.MO			-0.916		-0.143	
	33	C.means.P.FA.MO	-0.015	0.053	-0.278	0.781	-0.119	0.089

Mean SRM components

Pairwise comparisons

🕤 Intragenerational similarity

component	estimate	se	z	p.value	ci.lower	ci.upper	r
107 A.FA - A.MO	-0.008	0.022	-0.364	0.716	-0.051	0.035	NA
108 P.FA ~~ P.MO	0.056	0.028	1.994	0.046	0.001	0.111	NA
109 A.C1 ~~ A.C2	0.008	0.030	0.272	0.786	-0.050	0.067	0.088
110 P.C1 ~~ P.C2	-0.013	0.025	-0.512	0.609	-0.061	0.035	-0.183

🕜 Mean structure: Indices starting with 'C.' are pairwise comparisons between roles

-								
		factor	estimate	se			ci.lower	
	1	FE	1.854	0.027	68.029	0.000	1.801	1.908
	2	A.C1	0.383	0.038	10.076	0.000	0.308	0.457
	3	A.C2	0.149	0.040	3.693	0.000	0.070	0.229
	4	A.FA	-0.289	0.033	-8.778	0.000	-0.353	-0.224
	5	A.MO	-0.243	0.034	-7.211	0.000	-0.310	-0.177
	6	P.C1	0.312	0.038	8.179	0.000	0.237	0.387
	7	P.C2	0.151	0.037	4.042	0.000	0.078	0.224
	8	P.FA	-0.239	0.036	-6.627	0.000	-0.309	-0.168
	9	P.MO	-0.224	0.035	-6.441	0.000	-0.292	-0.156
	10	R.C1.C2			4.212	0.000	0.090	0.246
	11	R.C1.FA	-0.099	0.038	-2.637	0.008		-0.025
	12	R.C1.MO			-1.734	0.083		0.009
	13	R.C2.C1	0.276			0.000	0.204	0.348
	14	R.C2.FA			-3.889	0.000		-0.068
	15	R.C2.MO			-3.608	0.000	-0.213	-0.063
	16	R. FA. C1	-0.117	0.033	-3.588	0.000	-0.181	-0.053
	17	R. FA. C2			-2.564	0.010	-0.159	-0.021
	18	R.FA.MO	0.207		5.362	0.000	0.131	0.283
	19	R.MO.C1	-0.159	0.034	-4.649	0.000	-0.226	-0.092
	20	R.MO.C2	-0.078	0.035	-2.229	0.026	-0.146	-0.009
_	21	R.MO.FA	0.237	0.035	6.682	0.000	0.167	0.306
8	22	C.means.A.C1.C2		0.065		0.000		0.360
-	23	C.means.P.C1.C2		0.059		0.007	0.045	0.277
	24	C.means.A.C1.FA	0.672	0.058	11.671	0.000	0.559	0.785
	25	C.means.P.C1.FA	0.551	0.062	8.941	0.000	0.430	0.671
	26	C.means.A.C1.MO	0.626	0.060	10.448	0.000	0.509	0.744
		C.means.P.C1.MO	0.536		8.611	0.000	0.414	0.658
		C.means.A.C2.FA				0.000	0.316	0.560
		C.means.P.C2.FA				0.000	0.267	0.513
		C.means.A.C2.MO	0.393			0.000	0.272	0.514
	31	C.means.P.C2.MO	0.375			0.000	0.259	
	32	C.means.A.FA.MO			-0.916		-0.143	0.052
	33	C.means.P.FA.MO	-0.015	0.053	-0.278	0.781	-0.119	0.089

Intragenerational similarities

> Good child - bad child? (not significant)

Mean SRM components

Pairwise comparisons

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component	estimate	se	z	p.value	ci.lower	ci.upper	r
107 A.FA ~~ A.MO	-0.008	0.022	-0.364	0.716	-0.051	0.035	NA
108 P.FA ~~ P.MO	0.056	0.028	1.994	0.046	0.001	0.111	NA
109 A.C1 ~~ A.C2	0.008	0.030	0.272	0.786	-0.050	0.067	0.088
110 P.C1 ~~ P.C2	-0.013	0.025	-0.512	0.609	-0.061	0.035	-0.183

 Intragenerational similarities

Mean structure: Indices starting with 'C.' are pairwise comparisons between roles

_		estimate				ci.lower	
1	FE			68.029	0.000	1.801	1.908
2	A.C1			10.076	0.000	0.308	0.457
3	A.C2		0.040	3.693	0.000	0.070	0.229
4	A.FA			-8.778	0.000	-0.353	-0.224
5	A.MO			-7.211	0.000	-0.310	-0.177
6	P.C1	0.312		8.179	0.000	0.237	0.387
7	P.C2		0.037		0.000	0.078	0.224
8	P.FA			-6.627	0.000		
9	P.MO			-6.441	0.000	-0.292	-0.156
10	R.C1.C2	0.168		4.212	0.000	0.090	0.246
11	R.C1.FA			-2.637	0.008	-0.173	-0.025
12	R.C1.MO			-1.734	0.083	-0.147	0.009
13	R.C2.C1	0.276		7.507	0.000	0.204	0.348
14	R.C2.FA	-0.138	0.035	-3.889	0.000	-0.207	-0.068
15	R.C2.MO	-0.138	0.038	-3.608	0.000	-0.213	-0.063
16	R.FA.C1			-3.588	0.000	-0.181	-0.053
17	R.FA.C2			-2.564	0.010	-0.159	-0.021
18	R.FA.MO		0.039	5.362	0.000	0.131	0.283
19	R.MO.C1	-0.159			0.000	-0.226	-0.092
20	R.MO.C2			-2.229	0.026	-0.146	-0.009
21	R.MO.FA	0.237		6.682	0.000	0.167	0.306
	C.means.A.C1.C2	0.233	0.065	3.613	0.000	0.107	0.360
	C.means.P.C1.C2		0.059	2.716	0.007	0.045	0.277
	C.means.A.C1.FA			11.671	0.000	0.559	0.785
25	C.means.P.C1.FA	0.551	0.062	8.941	0.000	0.430	0.671
26	C.means.A.C1.MO	0.626	0.060	10.448	0.000	0.509	0.744
27	C.means.P.C1.MO	0.536	0.062	8.611	0.000	0.414	0.658
28	C.means.A.C2.FA	0.438	0.062	7.048	0.000	0.316	0.560
29	C.means.P.C2.FA	0.390	0.063	6.215	0.000	0.267	0.513
30	C.means.A.C2.MO	0.393	0.062	6.362	0.000	0.272	0.514
31	C.means.P.C2.MO	0.375	0.059	6.339	0.000	0.259	0.491
32	C.means.A.FA.MO	-0.045	0.050	-0.916	0.360	-0.143	0.052
33	C.means.P.FA.MO	-0.015	0.053	-0.278	0.781	-0.119	0.089

Mean SRM components

Pairwise comparisons

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component	estimate	se	z	p.value	ci.lower	ci.upper	r
107 A.FA ~~ A.MO							NA
108 P.FA ~~ P.MO	0.056	0.028	1.994	0.046	0.001	0.111	NA
109 A.C1 ~~ A.C2	0.008	0.030	0.272	0.786	-0.050	0.067	0.088
110 P.C1 ~~ P.C2	-0.013	0.025	-0.512	0.609	-0.061	0.035	-0.183

 Intragenerational similarities

m Mean structure: Indices starting with 'C.' are pairwise comparisons between roles

-								
		factor	estimate	se	z		ci.lower	ci.upper
	1	FE			68.029		1.801	1.908
	2	A.C1			10.076	0.000	0.308	0.457
	3	A.C2		0.040	3.693	0.000	0.070	0.229
	4	A. FA			-8.778	0.000	-0.353	
	5	A.MO	-0.243			0.000	-0.310	
	6	P.C1	0.312		8.179		0.237	0.387
	7	P.C2			4.042	0.000	0.078	
	8	P.FA			-6.627			
	9	P.MO			-6.441	0.000	-0.292	-0.156
	10	R.C1.C2	0.168		4.212	0.000	0.090	
	11	R.C1.FA			-2.637	0.008	-0.173	
	12	R.C1.MO			-1.734	0.083	-0.147	
	13	R.C2.C1			7.507	0.000	0.204	
	14	R.C2.FA			-3.889	0.000	-0.207	
	15	R.C2.MO			-3.608	0.000	-0.213	-0.063
	16	R. FA. C1			-3.588	0.000	-0.181	-0.053
	17	R.FA.C2			-2.564	0.010	-0.159	
	18	R.FA.MO		0.039	5.362	0.000	0.131	0.283
	19	R.MO.C1	-0.159		-4.649	0.000	-0.226	
	20	R.MO.C2			-2.229	0.026	-0.146	-0.009
-	21	R.MO.FA			6.682	0.000	0.167	0.306
		C.means.A.C1.C2			3.613	0.000	0.107	
-		C.means.P.C1.C2		0.059			0.045	
		C.means.A.C1.FA			11.671	0.000	0.559	
		C.means.P.C1.FA	0.551		8.941	0.000	0.430	
		C.means.A.C1.MO			10.448	0.000	0.509	
		C.means.P.C1.MO	0.536		8.611	0.000	0.414	
		C.means.A.C2.FA	0.438		7.048	0.000	0.316	0.560
		C.means.P.C2.FA	0.390		6.215	0.000	0.267	
		C.means.A.C2.MO	0.393		6.362	0.000	0.272	0.514
		C.means.P.C2.MO	0.375		6.339		0.259	
		C.means.A.FA.MO			-0.916	0.360	-0.143	0.052
	33	C.means.P.FA.MO	-0.015	0.053	-0.278	0.781	-0.119	0.089

Mean SRM components

Pairwise comparisons between the actor (and partner) effects of two roles

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Differences in negativity between problematic and nonproblematic families?

- SRM with two indicators
- Two groups
- Differences in variances and means?

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Differences in negativity between problematic and nonproblematic families?

- SRM with two indicators
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- Differences in variances and means?

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Differences in negativity between problematic and nonproblematic families?

- SRM with two indicators
- Two groups
- Differences in variances and means?

```
fSRM.2gr <- fSRM(neg1/neg2 ~ actor.id * partner.id |
    family.id,
    data = two.groups, group="group",
    means = T, diff=TRUE)</pre>
```

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Difference of means between groups (1-2)

	component	diff	se	z	p.value	ci.lower	ci.upper
1077	.meanDiff.FE		0.028		0.000	0.147	0.257
1078	.meanDiff.A.Cl	0.293	0.049	5.998	0.000	0.197	0.388
1079	.meanDiff.A.C2	-0.178	0.053	-3.374	0.001	-0.281	-0.074
1080	.meanDiff.A.FA	-0.148	0.043	-3.407	0.001	-0.233	-0.063
1081	.meanDiff.A.MO	0.033	0.043	0.759	0.448	-0.052	0.117
1082	.meanDiff.P.C1			6.263	0.000	0.195	0.373
1083	.meanDiff.P.C2				0.516	-0.121	0.061
1084	.meanDiff.P.FA				0.680	-0.112	0.073
1085	.meanDiff.P.MO				0.483	-0.123	0.058
1086	.meanDiff.R.C1.C2			-0.782	0.434	-0.129	0.056
1087	.meanDiff.R.C1.FA			1.030	0.303	-0.041	0.131
1088	.meanDiff.R.C1.MO				0.860	-0.099	0.083
1089	.meanDiff.R.C2.C1			-0.341	0.733	-0.108	0.076
1090	.meanDiff.R.C2.FA			-0.251	0.802	-0.096	0.075
1091	.meanDiff.R.C2.MO	0.027	0.047	0.571	0.568	-0.066	0.120
1092	.meanDiff.R.FA.C1		0.039	0.259	0.796	-0.067	0.087
1093	.meanDiff.R.FA.C2		0.042	0.206	0.837	-0.074	0.091
1094	.meanDiff.R.FA.MO	-0.019	0.046	-0.408	0.683	-0.109	0.072
		0.006	0.042	0.143	0.887	-0.076	0.087
1096	.meanDiff.R.MO.C2	0.028	0.044	0.647	0.518	-0.057	0.114
1097	.meanDiff.R.MO.FA	-0.034	0.045	-0.761	0.447	-0.122	0.054

Output for each group

Difference between groups

Difference of variances between groups (1-2)

	component	diff	se	z	p.value	ci.lower	ci.upper
1098	.varDiff.FE	0.020	0.022	0.917	0.359	-0.023	0.063
1099	.varDiff.A.C1	0.026	0.045	0.567	0.570	-0.063	0.114
1100	.varDiff.A.C2	0.046	0.054	0.850	0.395	-0.060	0.153
1101	.varDiff.A.FA	-0.039	0.032	-1.196	0.232	-0.103	0.025
1102	.varDiff.A.MO	-0.031	0.034	-0.914	0.361	-0.096	0.035
1103	.varDiff.P.C1	0.057	0.038	1.513	0.130	-0.017	0.132
1104	.varDiff.P.C2	0.023	0.039	0.586	0.558	-0.053	0.099
1105	.varDiff.P.FA	0.014	0.040	0.355	0.722	-0.064	0.092
1106	.varDiff.P.MO	-0.056	0.040	-1.410	0.159	-0.133	0.022
1107	.varDiff.R.C1.C2	0.254	0.125	2.028	0.043	0.008	0.500

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Difference of means between groups (1-2)

_	component	diff	se	z	p.value	ci.lower	ci.upper
1077	.meanDiff.FE	0.202	0.028	7.182	0.000	0.147	0.257
1078	.meanDiff.A.C1	0.293	0.049	5.998	0.000	0.197	0.388
1079	.meanDiff.A.C2	-0.178	0.053	-3.374	0.001	-0.281	-0.074
1080	.meanDiff.A.FA		0.043	-3.407	0.001	-0.233	-0.063
1081	.meanDiff.A.MO	0.033	0.043	0.759	0.448	-0.052	0.117
1082	.meanDiff.P.C1		0.045	6.263	0.000	0.195	0.373
1083	.meanDiff.P.C2				0.516	-0.121	0.061
1084	.meanDiff.P.FA			-0.413	0.680	-0.112	0.073
1085	.meanDiff.P.MO			-0.701	0.483	-0.123	0.058
1086	.meanDiff.R.C1.C2	-0.037	0.047	-0.782	0.434	-0.129	0.056
1087	.meanDiff.R.C1.FA	0.045		1.030	0.303	-0.041	0.131
1088	.meanDiff.R.C1.MO	-0.008		-0.176	0.860	-0.099	0.083
1089	.meanDiff.R.C2.C1		0.047	-0.341	0.733	-0.108	0.076
1090	.meanDiff.R.C2.FA		0.044	-0.251	0.802	-0.096	0.075
1091	.meanDiff.R.C2.MO	0.027	0.047	0.571	0.568	-0.066	0.120
1092	.meanDiff.R.FA.C1		0.039	0.259	0.796	-0.067	0.087
1093	.meanDiff.R.FA.C2	0.009	0.042	0.206	0.837	-0.074	0.091
1094	.meanDiff.R.FA.MO	-0.019	0.046	-0.408	0.683	-0.109	0.072
1095	.meanDiff.R.MO.C1	0.006	0.042	0.143	0.887	-0.076	0.087
1096	.meanDiff.R.MO.C2	0.028	0.044	0.647	0.518	-0.057	0.114
1097	.meanDiff.R.MO.FA	-0.034	0.045	-0.761	0.447	-0.122	0.054

Difference of variances between groups (1-2)

	component	diff	se	z	p.value	ci.lower	ci.upper
1098	.varDiff.FE	0.020	0.022	0.917	0.359	-0.023	0.063
1099	.varDiff.A.C1	0.026	0.045	0.567	0.570	-0.063	0.114
1100	.varDiff.A.C2	0.046	0.054	0.850	0.395	-0.060	0.153
1101	.varDiff.A.FA	-0.039	0.032	-1.196	0.232	-0.103	0.025
1102	.varDiff.A.MO	-0.031	0.034	-0.914	0.361	-0.096	0.035
1103	.varDiff.P.C1	0.057	0.038	1.513	0.130	-0.017	0.132
1104	.varDiff.P.C2	0.023	0.039	0.586	0.558	-0.053	0.099
1105	.varDiff.P.FA	0.014	0.040	0.355	0.722	-0.064	0.092
1106	.varDiff.P.MO	-0.056	0.040	-1.410	0.159	-0.133	0.022
1107	.varDiff.R.C1.C2	0.254	0.125	2.028	0.043	0.008	0.500

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Output for each group

• Difference between groups

- More family negativity in problematic families
- Target adolescent reports more negativity

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Difference of means between groups (1-2)

	component	diff	se	z	p.value	ci.lower	ci.upper	
1077	.meanDiff.FE	0.202	0.028	7.182	0.000	0.147	0.257	
1078	.meanDiff.A.C1	0.293	0.049	5.998	0.000	0.197	0.388	
1079	.meanDiff.A.C2	-0.178	0.053	-3.374	0.001	-0.281	-0.074	
1080	.meanDiff.A.FA			-3.407	0.001	-0.233	-0.063	
1081	.meanDiff.A.MO		0.043	0.759	0.448	-0.052	0.117	
1082	.meanDiff.P.C1		0.045	6.263	0.000	0.195	0.373	
1083	.meanDiff.P.C2				0.516	-0.121	0.061	
1084	.meanDiff.P.FA				0.680	-0.112	0.073	
1085	.meanDiff.P.MO				0.483	-0.123	0.058	
1086	.meanDiff.R.C1.C2			-0.782	0.434	-0.129	0.056	
1087	.meanDiff.R.C1.FA		0.044	1.030	0.303	-0.041	0.131	
1088	.meanDiff.R.C1.MO			-0.176	0.860	-0.099	0.083	
1089	.meanDiff.R.C2.C1			-0.341	0.733	-0.108	0.076	
1090	.meanDiff.R.C2.FA	-0.011	0.044	-0.251	0.802	-0.096	0.075	
1091	.meanDiff.R.C2.MO	0.027	0.047	0.571	0.568	-0.066	0.120	
1092	.meanDiff.R.FA.C1	0.010	0.039	0.259	0.796	-0.067	0.087	
1093	.meanDiff.R.FA.C2		0.042	0.206	0.837	-0.074	0.091	
1094	.meanDiff.R.FA.MO	-0.019	0.046	-0.408	0.683	-0.109	0.072	
1095	.meanDiff.R.MO.C1	0.006	0.042	0.143	0.887	-0.076	0.087	
1096	.meanDiff.R.MO.C2	0.028	0.044	0.647	0.518	-0.057	0.114	
1097	.meanDiff.R.MO.FA	-0.034	0.045	-0.761	0.447	-0.122	0.054	

Difference of variances between groups (1-2)

	component	diff	se	z	p.value	ci.lower	ci.upper
1098	.varDiff.FE		0.022	0.917	0.359	-0.023	0.063
1099	.varDiff.A.C1	0.026	0.045	0.567	0.570	-0.063	0.114
1100	.varDiff.A.C2	0.046	0.054	0.850	0.395	-0.060	0.153
1101	.varDiff.A.FA	-0.039	0.032	-1.196	0.232	-0.103	0.025
1102	.varDiff.A.MO	-0.031	0.034	-0.914	0.361	-0.096	0.035
1103	.varDiff.P.C1	0.057	0.038	1.513	0.130	-0.017	0.132
1104	.varDiff.P.C2	0.023	0.039	0.586	0.558	-0.053	0.099
1105	.varDiff.P.FA	0.014	0.040	0.355	0.722	-0.064	0.092
1106	.varDiff.P.MO	-0.056	0.040	-1.410	0.159	-0.133	0.022
1107	.varDiff.R.C1.C2	0.254	0.125	2.028	0.043	0.008	0.500

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Output for each group

Difference between groups

- More family negativity in problematic families
- Target adolescent reports more negativity

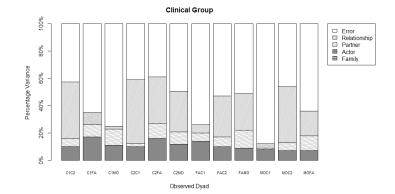
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Some other features of the package:

- SRM in three person family
 - Specify which component to drop (default: family factor)
- Improve model fit
 - Modification indices
 - Fix negative or nonsignificant effects to zero
- Investigate difference over roles same component
- Handle missing data
- Different kind of plots

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e.g., Barplot for relative variance decomposition



Lara.Stas@UGent.be The Social Relations Model

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