SRM: Implementation in lavaan

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I. Background information
1. Sample descriptives

- 57 families (consisting of two parents and two children)

- Inclusion criteria:
  - Two adults that live together & in the parent role
  - Two children going to school and living with these parents
    - One in the adolescence (between 11 and 18)
    - The other minimum 11 and maximum 25 years old

- Parents
  - 82% two biological parents, 18% reconstituted families

- Children
  - Between 11 and 25 years old (youngest child: $M = 14.26$, $SD = 0.24$; oldest child: $M = 16.25$, $SD = 0.32$), 60% male
2. Effectance measured with SRM

- Interpersonal Sense of Control (ISOC; Cook, 1993)
  - Effectance scale
- Possible sources of dysfunctional interpersonal influence
  - Family effect
  - Actor effect (perceiver effect)
  - Partner effect (target effect)
  - Relationship effect

! Not unidirectional
Cook (1994): A SEM of dyadic relationships within the family system

One measure of the observed variable relationship effect is part of the error-variance.
Cook (1994): A SEM of dyadic relationships within the family system

Figure 2. Measurement model for actor and partner effects. Parameters to be estimated are indicated by an asterisk. Fixed parameters are indicated by a 1.0. Boxes indicate observed relationship measures. Circles indicate latent variables (i.e., factors). The three boxes on the left represent the relationships of person $i$ (as actor) with persons $j$, $m$, and $n$ (as partners), respectively, on occasion $k$. The three boxes on the right represent the relationships of persons $n$, $m$, and $j$ (as actors) with person $i$ (as partner) on occasion $k$. Single-headed arrows indicate the observed variable predicted by the source of variance. Double-headed arrow at the bottom of the diagram indicates actor-partner reciprocity correlation for person $i$, and double-headed arrows at the top indicate dyadic reciprocity correlations.
II. SRM implementation in lavaan
A. Model specification

- **Step 1:** Open R (or R-studio) and install lavaan
- **Step 2:** Read in your data
  - **Preferable:** a logic order of DV’s:
    - E.g. Primary sorted by actor effects (with corresponding partners)
      MF, MC1, MC2, FM, FC1, FC2, C1M, C1F, C1C2, C2M, C2F, C2C1
- **Step 3**: Specify the SRM model
  - SRM components are independent latent variables in a CFA (Cook, 1994)

  ➤ **Step 3a**: The observed measures are forced to load on corresponding SRM components (factor loadings usually fixed to 1)

  **Goal**: how many variance in DV is explained by each of the components?
- **Difference EQS and lavaan**
  - **EQS**: Variance of observed measure is partitioned into corresponding SRM components
    - E.g.: M→C = family + actor M + partner C + M-C relationship
  - **lavaan**: specify latent variable with all corresponding observed measures
    - E.g.: Actor Mother = M→V + M→K1 + M→K2
Specification of SRM components depends on sequence of variables

Our sequence of variables:
• EffMV
• EffMK1
• EffMK2
• EffVM
• EffVK1
• EffVK2
• EffK1M
• EffK1V
• EffK1K2
• EffK2M
• EffK2V
• EffK2K1

Our sequence of SRM components:
• Factor 1 = family effect
• Factor 2 = actor mother
• Factor 3 = actor father
• Factor 4 = actor oldest child
• Factor 5 = actor youngest child
• Factor 6 = partner father
• Factor 7 = partner oldest child
• Factor 8 = partner youngest child
• Factor 9 = partner mother

Legend:
M = mother
V = father
K1 = oldest child
K2 = youngest child
Eff = effectance
Specification of the **model** in lavaan

```r
# Step 3: specify the SRM model
SRM <- ' 
family.effect =~ 1*effMV + 1*effMK1 + 1*effMK2 +  
                   1*effVM + 1*effVK1 + 1*effVK2 +  
                   1*effK1M + 1*effK1V + 1*effK1K2 +  
                   1*effK2M + 1*effK2V + 1*effK2K1  
actor.M =~ 1*effMV + 1*effMK1 + 1*effMK2  
actor.V =~ 1*effVM + 1*effVK1 + 1*effVK2  
actor.K1 =~ 1*effK1M + 1*effK1V + 1*effK1K2  
actor.K2 =~ 1*effK2M + 1*effK2V + 1*effK2K1  
partner.V =~ 1*effMV + 1*effK1V + 1*effK2V  
partner.K1 =~ 1*effMK1 + 1*effVK1 + 1*effK2K1  
partner.K2 =~ 1*effMK2 + 1*effVK2 + 1*effK1K2  
partner.M =~ 1*effVM + 1*effK1M + 1*effK2M
```

**Legend:**
- M = mother
- F = father
- K1 = oldest child
- K2 = youngest child
Step 3b: Reciprocities

Specify covariances:
At the individual level of analysis
- actor.M ~~ partner.M
- actor.V ~~ partner.V
- actor.K1 ~~ partner.K1
- actor.K2 ~~ partner.K2

At the dyadic level of analysis
- effMV ~~ effVM
- effMK1 ~~ effK1M
- effMK2 ~~ effK2M
- effVK1 ~~ effK1V
- effVK2 ~~ effK2V
- effK1K2 ~~ effK2K1

Optional: Intragenerational similarity correlations
- actor.M ~~ actor.V
- actor.K1 ~~ actor.K2
- partner.M ~~ partner.V
- partner.K1 ~~ partner.K2

Legend:
- M = mother
- V = father
- K1 = oldest child
- K2 = youngest child
- Eff = effectance
- F1 = family effect
- F2 = actor M
- F3 = actor V
- F4 = actor K1
- F5 = actor K2
- F6 = partner V
- F7 = partner K1
- F8 = partner K2
- F9 = partner M
**Step 4:** fit the model with the data

```r
SRM <-
family.effect =~ 1*effMV + 1*effMK1 + 1*effMK2 +
1*effVM + 1*effVK1 + 1*effVK2 +
1*effK1M + 1*effK1V + 1*effK1K2 +
1*effK2M + 1*effK2V + 1*effK2K1
actor.M =~ 1*effMV + 1*effMK1 + 1*effMK2
actor.V =~ 1*effVM + 1*effVK1 + 1*effVK2
actor.K1 =~ 1*effK1M + 1*effK1V + 1*effK1K2
actor.K2 =~ 1*effK2M + 1*effK2V + 1*effK2K1
partner.V =~ 1*effMV + 1*effK1V + 1*effK2V
partner.K1 =~ 1*effK1M + 1*effVK1 + 1*effK1K2
partner.K2 =~ 1*effMK2 + 1*effVK2 + 1*effK1K2
partner.M =~ 1*effVM + 1*effK1M + 1*effK2M

# RECIPROCITIES #
# At the individual level of analysis
actor.M ~~ partner.M
actor.V ~~ partner.V
actor.K1 ~~ partner.K1
actor.K2 ~~ partner.K2

# At the dyadic level of analysis
effMV ~~ effVM
effMK1 ~~ effK1M
effMK2 ~~ effK2M
effVK1 ~~ effK1V
effVK2 ~~ effK2V
effK1K2 ~~ effK2K1
```

`fit <- lavaan(SRM, data=Eff, mimic="EQS", auto.var=TRUE)`  => *fit model with data*

`summary(fit, fit.measures=T)` => *summary about the fit*
B. Output
Step 1: Does your model fit the data?

lavaan (0.5-10) converged normally after 45 iterations

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of observations</td>
<td>57</td>
</tr>
<tr>
<td>Estimator</td>
<td>ML</td>
</tr>
<tr>
<td>Minimum Function Chi-square</td>
<td>44.790</td>
</tr>
<tr>
<td>Degrees of freedom</td>
<td>47</td>
</tr>
<tr>
<td><strong>P-value</strong></td>
<td>0.565</td>
</tr>
</tbody>
</table>

Chi-square test baseline model:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Minimum Function Chi-square</td>
<td>281.560</td>
</tr>
<tr>
<td>Degrees of freedom</td>
<td>66</td>
</tr>
<tr>
<td><strong>P-value</strong></td>
<td>0.000</td>
</tr>
</tbody>
</table>

Full model versus baseline model:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Comparative Fit Index (CFI)</td>
<td>1.000</td>
</tr>
<tr>
<td>Tucker-Lewis Index (TLI)</td>
<td>1.014</td>
</tr>
</tbody>
</table>

Loglikelihood and Information Criteria:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Loglikelihood user model (H0)</td>
<td>-801.824</td>
</tr>
<tr>
<td>Loglikelihood unrestricted model (H1)</td>
<td>-779/029</td>
</tr>
<tr>
<td>Number of free parameters</td>
<td>31</td>
</tr>
<tr>
<td>Akaike (AIC)</td>
<td>1665.647</td>
</tr>
<tr>
<td>Bayesian (BIC)</td>
<td>1728.982</td>
</tr>
<tr>
<td>Sample-size adjusted Bayesian (BIC)</td>
<td>1631.531</td>
</tr>
</tbody>
</table>

Root Mean Square Error of Approximation:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>RMSEA</strong></td>
<td>0.000</td>
</tr>
</tbody>
</table>

90 Percent Confidence Interval      | 0.000 0.080 |
P-value RMSEA <= 0.05                | 0.786  |

Standardized Root Mean Square Residual:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>SRMR</strong></td>
<td>0.096</td>
</tr>
</tbody>
</table>

Parameter estimates:

<table>
<thead>
<tr>
<th>Information Standard Errors</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Expected Standard</td>
<td></td>
</tr>
</tbody>
</table>
A bad fit?

- Modification indices

\[ \text{MI} \leftarrow \text{modindices(fit)} \]
\[ \text{sortedModInd} \leftarrow \text{MI[order(-MI$\mi$),]} ; \text{sortedModInd[1:10,]} \]

<table>
<thead>
<tr>
<th>lhs</th>
<th>op</th>
<th>rhs</th>
<th>mi</th>
<th>epc</th>
<th>sepc.lv</th>
<th>sepc.all</th>
<th>sepc.nox</th>
</tr>
</thead>
<tbody>
<tr>
<td>effMK2</td>
<td>~</td>
<td>effK1K2</td>
<td>6.126</td>
<td>-0.179</td>
<td>-0.179</td>
<td>-0.190</td>
<td>-0.190</td>
</tr>
<tr>
<td>partner.K2</td>
<td>=</td>
<td>effVK2</td>
<td>5.983</td>
<td>1.282</td>
<td>0.477</td>
<td>0.604</td>
<td>0.604</td>
</tr>
<tr>
<td>actor.V</td>
<td>~</td>
<td>partner.M</td>
<td>5.800</td>
<td>-0.117</td>
<td>-1.071</td>
<td>-1.071</td>
<td>-1.071</td>
</tr>
<tr>
<td>family.effect</td>
<td>~</td>
<td>effVK2</td>
<td>5.294</td>
<td>2.839</td>
<td>0.477</td>
<td>0.604</td>
<td>0.604</td>
</tr>
<tr>
<td>effK2V</td>
<td>~</td>
<td>effK2K1</td>
<td>4.809</td>
<td>-0.222</td>
<td>-0.222</td>
<td>-0.220</td>
<td>-0.220</td>
</tr>
<tr>
<td>actor.K2</td>
<td>~</td>
<td>effK2M</td>
<td>4.295</td>
<td>0.362</td>
<td>0.277</td>
<td>0.265</td>
<td>0.265</td>
</tr>
<tr>
<td>partner.M</td>
<td>~</td>
<td>effVK1</td>
<td>4.158</td>
<td>-2.501</td>
<td>-0.437</td>
<td>-0.552</td>
<td>-0.552</td>
</tr>
<tr>
<td>effK2M</td>
<td>~</td>
<td>effK2V</td>
<td>3.882</td>
<td>0.208</td>
<td>0.208</td>
<td>0.219</td>
<td>0.219</td>
</tr>
<tr>
<td>actor.K2</td>
<td>~</td>
<td>effK2K1</td>
<td>3.742</td>
<td>-0.347</td>
<td>-0.265</td>
<td>-0.239</td>
<td>-0.239</td>
</tr>
<tr>
<td>family.effect</td>
<td>~</td>
<td>partner.K2</td>
<td>3.701</td>
<td>0.069</td>
<td>1.101</td>
<td>1.101</td>
<td>1.101</td>
</tr>
</tbody>
</table>
Which modifications?

Possible hierarchy:

1. Negative variances?
   => fix corresponding correlations to zero

2. Theoretically fundated
   (e.g. intragenerational similarities,...)

3. Set factor free in DV (i.e. not fix to 1)
   - Interpret in the output (i.e. smaller or larger than 1?)

4. Let two factors correlate without theoretical fundation
   - Interpret - with caution - the output
### Step 2: Parameter estimation

**Variances:**

| Parameter       | Estimate | Std.err | Z-value | P(>|z|) |
|-----------------|----------|---------|---------|---------|
| family.effect   | 0.028    | 0.043   | 0.656   | 0.512   |
| actor.M        | 0.411    | 0.105   | 3.903   | 0.000   |
| actor.V        | 0.388    | 0.096   | 4.057   | 0.000   |
| actor.K1       | 0.451    | 0.120   | 3.757   | 0.000   |
| actor.K2       | 0.586    | 0.141   | 4.167   | 0.000   |
| partner.V      | 0.006    | 0.041   | 0.143   | 0.886   |
| partner.K1     | 0.061    | 0.038   | 1.588   | 0.112   |
| partner.K2     | 0.138    | 0.048   | 2.855   | 0.004   |
| partner.M      | 0.030    | 0.047   | 0.650   | 0.516   |
| effMV          | 0.480    | 0.119   | 4.024   | 0.000   |
| effMK1         | 0.190    | 0.071   | 2.658   | 0.008   |
| effMK2         | 0.255    | 0.083   | 3.066   | 0.002   |
| effVM          | 0.415    | 0.107   | 3.897   | 0.000   |
| effVK1         | 0.149    | 0.060   | 2.506   | 0.012   |
| effVK2         | 0.068    | 0.054   | 1.259   | 0.208   |
| effK1M         | 0.457    | 0.124   | 3.692   | 0.000   |
| effK1V         | 0.377    | 0.110   | 3.428   | 0.001   |
| effK1K2        | 0.448    | 0.128   | 3.508   | 0.000   |
| effK2M         | 0.446    | 0.120   | 3.711   | 0.000   |
| effK2V         | 0.212    | 0.086   | 2.467   | 0.014   |
| effK2K1        | 0.555    | 0.139   | 3.977   | 0.000   |

- **Variance is positive**
  - one-sided testing (lavaan shows two sided p-values)
    - significant: $Z > 1.65$, $p < .05$
    - marginally significant: $Z > 1.29$, $p < .10$
  - When variances are negative
    - fix them to zero!
• Significant variance
  = significant source of variance in each observed measure that loads on this factor.

• `parameterEstimates(fit)`
  – Gives the estimate of each SRM component

```
> parameterEstimates(fit)

     lhs op rhs   est  se  z    pvalue ci.lower  ci.upper
 1 family.eff ~ effMV 1.000 0.000 NA     NA  1.000    1.000
 2 family.eff ~ effMK1 1.000 0.000 NA     NA  1.000    1.000
 3 family.eff ~ family.eff 0.028 0.043 0.656  0.512 -0.056  0.113
 4 actor.M ~ actor.M  0.411 0.105 3.903   0.000  0.204    0.617
 5 actor.V ~ actor.V  0.388 0.096 4.057   0.000  0.201    0.576
```

Interpretation:
Lecture Prof. Dr. W.L. Cook
### Step 3: Reciprocities

In order to interpret: **both** corresponding factors need to be significant (cfr. Step 2)!

| Covariances                      | Estimate | Std.err | Z-value | P(>|z|) |
|----------------------------------|----------|---------|---------|---------|
| actor.M ~ partner.M              | 0.017    | 0.048   | 0.363   | 0.717   |
| actor.V ~ partner.V              | 0.034    | 0.043   | 0.785   | 0.432   |
| actor.K1 ~ partner.K1            | 0.030    | 0.048   | 0.619   | 0.536   |
| actor.K2 ~ partner.K2            | 0.033    | 0.058   | 0.565   | 0.572   |
| effMV ~ effVM                    | -0.061   | 0.076   | -0.802  | 0.423   |
| effMK1 ~ effK1M                  | 0.073    | 0.066   | 1.110   | 0.267   |
| effMK2 ~ effK2M                  | -0.078   | 0.069   | -1.129  | 0.259   |
| effVK1 ~ effK1V                  | -0.064   | 0.055   | -1.167  | 0.243   |
| effVK2 ~ effK2V                  | -0.041   | 0.045   | -0.897  | 0.370   |
| effK1K2 ~ effK2K1                | 0.201    | 0.098   | 2.051   | 0.040   |

**Interpretation:**
Lecture Prof. Dr. W.L. Cook