

How to evaluate theory-based hypotheses in a (RI-)CLPM using the GORICA

Rebecca M. Kuiper

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This is a tutorial for using GORICA for (Random Intercept) Cross-lagged Panel Models ((RI-)CLPMs). The GORICA is an information criterion that can be used to evaluate theory-driven hypotheses.

(RI-)CLPMs are a type of statistical models used in longitudinal data research to analyze the relations between variables measured at multiple time points. Panel data can be analyzed at the construct level and the dimension level. In the construct level model, the focus is on the latent constructs that the observed variables represent. In the dimension model, the focus is on the observed variables themselves, rather than the latent constructs.

Here, two examples are presented for the use of the `goric` function in the `restriktor` package to evaluate hypotheses about a CLPM. These are based on the analysis in:

Snijders, I., Wijnia, L., Kuiper, R. M., Rikers, R. M. J. P., & Loyens, S. M. M. (2021). Relationship quality in higher education and the interplay with student engagement and loyalty. *British Journal of Educational Psychology*. <https://doi.org/10.1111/bjep.12455>

The first example covers analysis at the construct level, while the second example covers analysis at the dimension level.

Other example files for evaluating (causal dominance) hypotheses in RI-CLPMs can be found on ‘<https://github.com/rebeccakuiper/Tutorials/tree/main/GORICA%20in%20RI-CLPM>’.

Note: For (more) information regarding interpreting the GORIC(A) output, see ‘Guidelines_output_GORIC’ (<https://github.com/rebeccakuiper/Tutorials>).

Example 1: Construct Level Analysis

R packages

First, install and call the `lavaan` library to create a CLPM and the `restriktor` library to load the `goric` function. If needed, it is possible to view the description of the function with the `?` operator or the `help` command.

The code presented here also requires the `tidyverse` package for data manipulation.

```
# To install restriktor in R:
# if (!require("restriktor")) install.packages("restriktor")

# To install restriktor from github:
# if (!require("devtools")) install.packages("devtools")
# library(devtools)
# install_github("LeonardV/restriktor")
library(restriktor)

# print docs in the help-tab to view arguments and explanations for the function
# ?goric

# To install lavaan in R:
# if (!require("lavaan")) install.packages("lavaan")
library(lavaan)

# To install tidyverse in R:
# if (!require("tidyverse")) install.packages("tidyverse")
library(tidyverse)
```

Data

Upload the data set to the R environment and select the columns used for analysis. The `id` column is renamed to `ID` and the code in the data set for missing numbers `-999.00` is replaced with `NA`s.

```
data <- read.table("data/CLPM.dat", header = T)
colnames(data)[1] <- "ID"
data <- replace(data , data == -999.00, NA)

data_subset <- select(data,
  THT1_SS,
  TBT1_SS,
  ACOMT1_SS,
  SATT1_SS,
  AB_T1_SS,
  DE_T1_SS,
  VI_T1_SS,
  SLT1_SS,
  TH_T2_SS,
  TB_T2_SS,
  ACOMT2SS,
  SAT_T2SS,
  ABT2_SS,
  DET2_SS,
  VIT2_SS,
  SLT2SS)
```

Measurement invariance

Next, we fit the CLPM using `lavaan`. The ‘RQ’ dimension is split into two sub-dimensions (cf. Snijders et al., 2021). Model 1 is fit to investigate configural invariance. The model is specified and fit in the following two steps.

```
CLPM_M1 <- '

#####
# MEASUREMENT MODEL #
#####

# Factor models for RQ1 at 2 waves.
RQ11 =~ THT1_SS + TBT1_SS
RQ12 =~ TH_T2_SS + TB_T2_SS
#RQ1  =~ 1 * RQ11 + 1 * RQ12

# Factor models for RQ2 at 2 waves.
RQ21 =~ ACOMT1_SS + SATT1_SS
RQ22 =~ ACOMT2SS + SAT_T2SS
#RQ2  =~ 1 * RQ21 + 1 * RQ22

# Factor models for SE at 2 waves.
SE1 =~ AB_T1_SS + DE_T1_SS + VI_T1_SS
SE2 =~ ABT2_SS + DET2_SS + VIT2_SS

#####
# DYNAMICS #
#####

# Specify the lagged effects between the latent variables.
RQ12 + RQ22 + SE2 + SLT2SS ~ RQ11 + RQ21 + SE1 + SLT1_SS

# Estimate the correlations within the same wave.
# T1
RQ11 ~~ RQ21 + SE1 + SLT1_SS
RQ21 ~~ SE1 + SLT1_SS
SE1 ~~ SLT1_SS
# T2
RQ12 ~~ RQ22 + SE2 + SLT2SS
RQ22 ~~ SE2 + SLT2SS
SE2 ~~ SLT2SS

'
```

```
CLPM_M1.fit <- sem(CLPM_M1, data = data_subset, missing = 'ML')
```

When fitting the model R returns the following warning message:

```
Warning message: In lav_object_post_check(object) : lavaan WARNING: covariance matrix of
latent variables is not positive definite;
```

So, we use `lavInspect(fit, "cov.lv")` to investigate further.

```
lavInspect(CLPM_M1.fit, "cov.lv")
```

	RQ11	RQ12	RQ21	RQ22	SE1	SE2
RQ11	7.757					
RQ12	4.985	8.573				
RQ21	8.547	5.629	9.481			
RQ22	5.317	9.563	7.673	11.391		
SE1	4.433	3.928	6.694	6.074	9.840	
SE2	3.768	5.091	5.077	7.265	9.183	11.039

```
lavInspect(CLPM_M1.fit, "cor.lv")
```

	RQ11	RQ12	RQ21	RQ22	SE1	SE2
RQ11	1.000					
RQ12	0.611	1.000				
RQ21	0.997	0.624	1.000			
RQ22	0.566	0.968	0.738	1.000		
SE1	0.507	0.428	0.693	0.574	1.000	
SE2	0.407	0.523	0.496	0.648	0.881	1.000

The correlations between RQ11 & RQ21 and between RQ22 & RQ12 are very high, which is to be expected considered that these two sub-dimensions belong to one dimension. Given that the warning does not point to a model misspecification, we continue the analysis.

```
fitMeasures(CLPM_M1.fit)[c("chisq", "df")]
```

chisq	df
715.867	78.000

The output reports the following: chisq df 715.867 78.000

Based on these results we continue to Model 2, which investigates weak factorial invariance.

```
CLPM_M2 <- '

```

```
#####
# MEASUREMENT MODEL #
#####

# Factor models for RQ1 at 2 waves.
RQ11 =~ L1 * THT1_SS + L2 * TBT1_SS
RQ12 =~ L1 * TH_T2_SS + L2 * TB_T2_SS

# Factor models for RQ2 at 2 waves.
RQ21 =~ L3 * ACOMT1_SS + L4 * SATT1_SS
RQ22 =~ L3 * ACOMT2SS + L4 * SAT_T2SS

# Factor models for SE at 2 waves.
SE1 =~ L5 * AB_T1_SS + L6 * DE_T1_SS + L7 * VI_T1_SS
SE2 =~ L5 * ABT2_SS + L6 * DET2_SS + L7 * VIT2_SS

#####
# DYNAMICS #
#####

# Specify the lagged effects between the latent variables.
RQ12 + RQ22 + SE2 + SLT2SS ~ RQ11 + RQ21 + SE1 + SLT1_SS
```

```

# Estimate the correlations within the same wave.
# T1
RQ11 ~~ RQ21 + SE1 + SLT1_SS
RQ21 ~~ SE1 + SLT1_SS
SE1 ~~ SLT1_SS
# T2
RQ12 ~~ RQ22 + SE2 + SLT2SS
RQ22 ~~ SE2 + SLT2SS
SE2 ~~ SLT2SS

```

```
CLPM_M2.fit <- sem(CLPM_M2, data = data_subset, missing = 'ML')
```

R returns the same warning as before; so, we check the correlations again.

```
lavInspect(CLPM_M2.fit, "cov.lv")
```

	RQ11	RQ12	RQ21	RQ22	SE1	SE2
RQ11	7.734					
RQ12	4.986	8.595				
RQ21	8.460	5.589	9.308			
RQ22	5.342	9.632	7.651	11.528		
SE1	4.481	4.000	6.718	6.212	10.282	
SE2	3.729	5.031	4.984	7.210	9.183	10.540

```
lavInspect(CLPM_M2.fit, "cor.lv")
```

	RQ11	RQ12	RQ21	RQ22	SE1	SE2
RQ11	1.000					
RQ12	0.611	1.000				
RQ21	0.997	0.625	1.000			
RQ22	0.566	0.968	0.739	1.000		
SE1	0.502	0.425	0.687	0.571	1.000	
SE2	0.413	0.529	0.503	0.654	0.882	1.000

Again, there is no sign the model needs revision, so we continue.

```
fitMeasures(CLPM_M2.fit)[c("chisq", "df")]
```

chisq	df
721.021	82.000

We obtain these results: **chisq** **df** 721.021 82.000

We perform a Chi-square difference test to check whether Models 1 and 2 differ significantly.

$Df = 82 - 78 = 4$

Check the constrained factor loadings = $1 + 1 + 2 = 4$

Chi-square difference = $721.021 - 715.867 = 5.154$

<https://www.socscistatistics.com/pvalues/chidistribution.aspx>

The p value is .271858. Hence, the result is not significant at $\alpha = .05$.

When the chi-square test is non-significant, this implies the factor loadings are not significantly different from each other over time. In other words, we can assume weak factorial invariance holds.

So, we move on to strong factorial invariance using Model 3:

```

CLPM_M3 <- '

#####
# MEASUREMENT MODEL #
#####

# Factor models for RQ1 at 2 waves.
RQ11 =~ L1 * THT1_SS + L2 * TBT1_SS
RQ12 =~ L1 * TH_T2_SS + L2 * TB_T2_SS

# Factor models for RQ2 at 2 waves.
RQ21 =~ L3 * ACOMT1_SS + L4 * SATT1_SS
RQ22 =~ L3 * ACOMT2SS + L4 * SAT_T2SS

# Factor models for SE at 2 waves.
SE1 =~ L5 * AB_T1_SS + L6 * DE_T1_SS + L7 * VI_T1_SS
SE2 =~ L5 * ABT2_SS + L6 * DET2_SS + L7 * VIT2_SS

# Constrained intercepts over time
THT1_SS ~ int_th*1
TH_T2_SS ~ int_th*1
TBT1_SS ~ int_tb*1
TB_T2_SS ~ int_tb*1
ACOMT1_SS ~ int_acom*1
ACOMT2SS ~ int_acom*1
SATT1_SS ~ int_sat*1
SAT_T2SS ~ int_sat*1
#
AB_T1_SS ~ int_ab*1
ABT2_SS ~ int_ab*1
DE_T1_SS ~ int_de*1
DET2_SS ~ int_de*1
VI_T1_SS ~ int_vi*1
VIT2_SS ~ int_vi*1
#
SLT1_SS ~ int_sl*1
SLT2SS ~ int_sl*1

# Free latent means on t=2
RQ12 + RQ22 + SE2 + RQ11 + RQ21 + SE1 ~ 1

#####
# DYNAMICS #
#####

# Specify the lagged effects between the latent variables.
RQ12 + RQ22 + SE2 + SLT2SS ~ RQ11 + RQ21 + SE1 + SLT1_SS

# Estimate the correlations within the same wave.
# T1

```

```

RQ11 ~~ RQ21 + SE1 + SLT1_SS
RQ21 ~~ SE1 + SLT1_SS
SE1 ~~ SLT1_SS
# T2
RQ12 ~~ RQ22 + SE2 + SLT2SS
RQ22 ~~ SE2 + SLT2SS
SE2 ~~ SLT2SS

```

```
CLPM_M3.fit <- sem(CLPM_M3, data = data_subset, missing = 'ML')
```

Given the warning, we investigate correlations again.

```
lavInspect(CLPM_M3.fit, "cov.lv")
```

	RQ11	RQ12	RQ21	RQ22	SE1	SE2
RQ11	7.764					
RQ12	5.006	8.632				
RQ21	8.487	5.608	9.328			
RQ22	5.358	9.665	7.670	11.553		
SE1	4.489	4.009	6.727	6.219	10.280	
SE2	3.735	5.042	4.991	7.218	9.181	10.537

```
lavInspect(CLPM_M3.fit, "cor.lv")
```

	RQ11	RQ12	RQ21	RQ22	SE1	SE2
RQ11	1.000					
RQ12	0.611	1.000				
RQ21	0.997	0.625	1.000			
RQ22	0.566	0.968	0.739	1.000		
SE1	0.502	0.426	0.687	0.571	1.000	
SE2	0.413	0.529	0.503	0.654	0.882	1.000

Then, move on to the results of the model:

```
fitMeasures(CLPM_M3.fit)[c("chisq", "df")]
```

chisq	df
725.4913	84.0000

Because Models 2 and 3 are also nested, we perform another Chi-square difference test:

Df = 84 - 82 = 2

Check the constrained parameters = 8 - 6 = 2

Chi-square difference = 725.4913 - 721.021 = 4.4703

<https://www.socscistatistics.com/pvalues/chidistribution.aspx>

The p value is .106976. Hence, the result is not significant: $p > .05$.

If this chi-square difference test is non-significant, this means we can assume that strong factorial invariance holds over time. In that case we could consider investigating whether the means change over time. This is just optional.

Model 4 investigates strong factorial invariance without free latent means, meaning they are constrained over time). We repeat similar steps as above:

```
CLPM_M4 <- '

```

```
#####
```

```

# MEASUREMENT MODEL #
#####

# Factor models for RQ1 at 2 waves.
RQ11 =~ L1 * THT1_SS + L2 * TBT1_SS
RQ12 =~ L1 * TH_T2_SS + L2 * TB_T2_SS

# Factor models for RQ2 at 2 waves.
RQ21 =~ L3 * ACOMT1_SS + L4 * SATT1_SS
RQ22 =~ L3 * ACOMT2SS + L4 * SAT_T2SS

# Factor models for SE at 2 waves.
SE1 =~ L5 * AB_T1_SS + L6 * DE_T1_SS + L7 * VI_T1_SS
SE2 =~ L5 * ABT2_SS + L6 * DET2_SS + L7 * VIT2_SS

# Constrained intercepts over time
THT1_SS ~ int_th*1
TH_T2_SS ~ int_th*1
TBT1_SS ~ int_tb*1
TB_T2_SS ~ int_tb*1
ACOMT1_SS ~ int_acom*1
ACOMT2SS ~ int_acom*1
SATT1_SS ~ int_sat*1
SAT_T2SS ~ int_sat*1
#
AB_T1_SS ~ int_ab*1
ABT2_SS ~ int_ab*1
DE_T1_SS ~ int_de*1
DET2_SS ~ int_de*1
VI_T1_SS ~ int_vi*1
VIT2_SS ~ int_vi*1
#
SLT1_SS ~ int_sl*1
SLT2SS ~ int_sl*1

#####
# DYNAMICS #
#####

# Specify the lagged effects between the latent variables.
RQ12 + RQ22 + SE2 + SLT2SS ~ RQ11 + RQ21 + SE1 + SLT1_SS

# Estimate the correlations within the same wave.
# T1
RQ11 ~~ RQ21 + SE1 + SLT1_SS
RQ21 ~~ SE1 + SLT1_SS
SE1 ~~ SLT1_SS
# T2
RQ12 ~~ RQ22 + SE2 + SLT2SS
RQ22 ~~ SE2 + SLT2SS
SE2 ~~ SLT2SS

```


Fit the model:

```
CLPM_M4.fit <- sem(CLPM_M4, data = data_subset, missing = 'ML')
```

Inspect the correlations:

```
lavInspect(CLPM_M4.fit, "cov.lv")
```

	RQ11	RQ12	RQ21	RQ22	SE1	SE2
RQ11	7.813					
RQ12	4.945	8.645				
RQ21	8.391	5.831	9.761			
RQ22	5.396	9.651	7.340	11.492		
SE1	4.494	4.012	6.627	6.171	10.258	
SE2	3.694	5.065	5.132	7.205	9.182	10.552

```
lavInspect(CLPM_M4.fit, "cor.lv")
```

	RQ11	RQ12	RQ21	RQ22	SE1	SE2
RQ11	1.000					
RQ12	0.602	1.000				
RQ21	0.961	0.635	1.000			
RQ22	0.570	0.968	0.693	1.000		
SE1	0.502	0.426	0.662	0.568	1.000	
SE2	0.407	0.530	0.506	0.654	0.883	1.000

Obtain the results:

```
fitMeasures(CLPM_M4.fit)[c("chisq", "df")]
```

chisq	df
757.1568	90.0000

We proceed with the Chi-squared difference test with the previous model:

$Df = 90 - 84 = 6$

Check the constrained / freed means = 6

Chi-square difference = $757.1568 - 725.4913 = 31.6655$

<https://www.socscistatistics.com/pvalues/chidistribution.aspx>

The p value is .000019. Hence, the result is significant: $p < .05$.

Thus, we reject Model 4 and proceed with Model 3 (i.e., strong factorial invariance - with freed means = CLPM_M3.fit).

We can now move further by specifying the lagged effects between the latent variables.

CLPM

```
clpmModel <- '
#####
# MEASUREMENT MODEL #
#####

# Factor models for RQ1 at 2 waves.
RQ11 =~ L1 * THT1_SS + L2 * TBT1_SS
```

```

RQ12 =~ L1 * TH_T2_SS + L2 * TB_T2_SS

# Factor models for RQ2 at 2 waves.
RQ21 =~ L3 * ACOMT1_SS + L4 * SATT1_SS
RQ22 =~ L3 * ACOMT2SS + L4 * SAT_T2SS

# Factor models for SE at 2 waves.
SE1 =~ L5 * AB_T1_SS + L6 * DE_T1_SS + L7 * VI_T1_SS
SE2 =~ L5 * ABT2_SS + L6 * DET2_SS + L7 * VIT2_SS

# Constrained intercepts over time
TH_T1_SS ~ int_th*1
TH_T2_SS ~ int_th*1
TB_T1_SS ~ int_tb*1
TB_T2_SS ~ int_tb*1
ACOMT1_SS ~ int_acom*1
ACOMT2SS ~ int_acom*1
SATT1_SS ~ int_sat*1
SAT_T2SS ~ int_sat*1
#
AB_T1_SS ~ int_ab*1
ABT2_SS ~ int_ab*1
DE_T1_SS ~ int_de*1
DET2_SS ~ int_de*1
VI_T1_SS ~ int_vi*1
VIT2_SS ~ int_vi*1
#
SLT1_SS ~ int_sl*1
SLT2SS ~ int_sl*1

# Free latent means on t=2
RQ12 + RQ22 + SE2 + RQ11 + RQ21 + SE1 ~ 1

#####
# DYNAMICS #
#####

# Specify the lagged effects between the latent variables.
RQ12 ~ Phi11 * RQ11 + Phi12 * RQ21 + Phi13 * SE1 + Phi14 * SLT1_SS
RQ22 ~ Phi21 * RQ11 + Phi22 * RQ21 + Phi23 * SE1 + Phi24 * SLT1_SS
#
SE2 ~ Phi31 * RQ11 + Phi32 * RQ21 + Phi33 * SE1 + Phi34 * SLT1_SS
SLT2SS ~ Phi41 * RQ11 + Phi42 * RQ21 + Phi43 * SE1 + Phi44 * SLT1_SS

# Estimate the correlations within the same wave.
# T1
RQ11 ~~ RQ21 + SE1 + SLT1_SS
RQ21 ~~ SE1 + SLT1_SS
SE1 ~~ SLT1_SS

```

```
# T2
RQ12 ~~ RQ22 + SE2 + SLT2SS
RQ22 ~~ SE2 + SLT2SS
SE2 ~~ SLT2SS
```

Next, we fit the model with the lagged relations:

```
clpmUnc <- sem(clpmModel, data = data_subset, missing = 'ML')
```

Using the `summary` function we obtain the results of the model fit and estimates. The standardized solution contains the p-values of standardized effects.

```
fitMeasures(clpmUnc)
```

npar	fmin	chisq
68.000	0.220	725.491
srmr	srmr_bentler	srmr_bentler_nomean
0.053	0.053	0.056

```
stdClpmUnc <- standardizedsolution(clpmUnc, type = "std.all", se = TRUE, zstat = TRUE,
pvalue = TRUE, ci = TRUE, level = 0.95, cov.std = TRUE,
remove.eq = TRUE, remove.ineq = TRUE, remove.def = FALSE,
partable = NULL, GLIST = NULL, est = NULL)
```

```
stdClpmUnc
```

	lhs	op	rhs	label	est.std	se	z	pvalue	ci.lower	ci.upper
1	RQ11	==	THT1_SS	L1	0.860	0.010	87.184	0.000	0.841	0.880
2	RQ11	==	TBT1_SS	L2	0.892	0.009	98.450	0.000	0.874	0.909
3	RQ12	==	TH_T2_SS	L1	0.891	0.009	104.577	0.000	0.874	0.907
4	RQ12	==	TB_T2_SS	L2	0.933	0.007	132.024	0.000	0.920	0.947
5	RQ21	==	ACOMT1_SS	L3	0.755	0.015	50.807	0.000	0.726	0.784
6	RQ21	==	SATT1_SS	L4	0.797	0.014	57.832	0.000	0.770	0.824
7	RQ22	==	ACOMT2SS	L3	0.850	0.011	77.025	0.000	0.829	0.872
8	RQ22	==	SAT_T2SS	L4	0.863	0.011	81.286	0.000	0.843	0.884
9	SE1	==	AB_T1_SS	L5	0.843	0.011	74.549	0.000	0.821	0.866
10	SE1	==	DE_T1_SS	L6	0.840	0.012	68.560	0.000	0.816	0.864
11	SE1	==	VI_T1_SS	L7	0.847	0.011	74.234	0.000	0.825	0.869
12	SE2	==	ABT2_SS	L5	0.856	0.012	71.260	0.000	0.833	0.880
13	SE2	==	DET2_SS	L6	0.836	0.013	66.520	0.000	0.811	0.860
14	SE2	==	VIT2_SS	L7	0.858	0.012	72.268	0.000	0.835	0.881
15	THT1_SS	~1		int_th	9.880	0.732	13.505	0.000	8.446	11.314
16	TH_T2_SS	~1		int_th	9.700	0.740	13.105	0.000	8.249	11.150
17	TBT1_SS	~1		int_tb	9.375	0.758	12.376	0.000	7.891	10.860
18	TB_T2_SS	~1		int_tb	9.309	0.774	12.034	0.000	7.793	10.825
19	ACOMT1_SS	~1		int_acom	7.678	0.307	24.994	0.000	7.076	8.281
20	ACOMT2SS	~1		int_acom	7.773	0.317	24.505	0.000	7.151	8.395
21	SATT1_SS	~1		int_sat	8.035	0.325	24.716	0.000	7.398	8.672
22	SAT_T2SS	~1		int_sat	7.824	0.322	24.279	0.000	7.192	8.456
23	AB_T1_SS	~1		int_ab	9.533	0.345	27.664	0.000	8.857	10.208
24	ABT2_SS	~1		int_ab	9.558	0.386	24.730	0.000	8.801	10.316
25	DE_T1_SS	~1		int_de	10.664	0.351	30.340	0.000	9.975	11.353
26	DET2_SS	~1		int_de	10.484	0.396	26.507	0.000	9.709	11.259
27	VI_T1_SS	~1		int_vi	9.709	0.348	27.927	0.000	9.028	10.391
28	VIT2_SS	~1		int_vi	9.714	0.391	24.834	0.000	8.947	10.480

29	SLT1_SS	~1		int_sl	4.075	0.094	43.518	0.000	3.891	4.258
30	SLT2SS	~1		int_sl	3.864	0.098	39.350	0.000	3.672	4.057
31	RQ12	~1			-2.610	1.541	-1.694	0.090	-5.629	0.410
32	RQ22	~1			-2.196	1.921	-1.143	0.253	-5.962	1.569
33	SE2	~1			0.759	1.806	0.420	0.674	-2.782	4.300
34	RQ11	~1			-5.844	0.833	-7.013	0.000	-7.477	-4.210
35	RQ21	~1			-5.302	0.390	-13.588	0.000	-6.067	-4.538
36	SE1	~1			-7.281	0.387	-18.821	0.000	-8.039	-6.523
37	RQ12	~	RQ11	Phi11	0.149	0.542	0.275	0.783	-0.913	1.211
38	RQ12	~	RQ21	Phi12	0.415	0.685	0.606	0.544	-0.927	1.758
39	RQ12	~	SE1	Phi13	0.034	0.147	0.232	0.817	-0.254	0.322
40	RQ12	~	SLT1_SS	Phi14	0.046	0.142	0.324	0.746	-0.233	0.325
41	RQ22	~	RQ11	Phi21	1.721	0.889	1.936	0.053	-0.021	3.462
42	RQ22	~	RQ21	Phi22	-1.808	1.137	-1.591	0.112	-4.036	0.420
43	RQ22	~	SE1	Phi23	0.597	0.223	2.671	0.008	0.159	1.034
44	RQ22	~	SLT1_SS	Phi24	0.517	0.215	2.408	0.016	0.096	0.937
45	SE2	~	RQ11	Phi31	-1.018	0.663	-1.534	0.125	-2.318	0.282
46	SE2	~	RQ21	Phi32	1.319	0.848	1.556	0.120	-0.342	2.981
47	SE2	~	SE1	Phi33	0.752	0.168	4.467	0.000	0.422	1.082
48	SE2	~	SLT1_SS	Phi34	-0.389	0.163	-2.394	0.017	-0.708	-0.071
49	SLT2SS	~	RQ11	Phi41	0.716	0.544	1.316	0.188	-0.351	1.783
50	SLT2SS	~	RQ21	Phi42	-0.708	0.693	-1.023	0.306	-2.066	0.649
51	SLT2SS	~	SE1	Phi43	0.289	0.142	2.027	0.043	0.009	0.568
52	SLT2SS	~	SLT1_SS	Phi44	0.596	0.136	4.388	0.000	0.330	0.862
53	RQ11	~~	RQ21		0.997	0.013	75.177	0.000	0.971	1.023
54	RQ11	~~	SE1		0.502	0.028	17.884	0.000	0.447	0.558
55	RQ11	~~	SLT1_SS		0.675	0.019	34.754	0.000	0.637	0.713
56	RQ21	~~	SE1		0.687	0.026	26.784	0.000	0.637	0.737
57	RQ21	~~	SLT1_SS		0.815	0.017	47.545	0.000	0.782	0.849
58	SE1	~~	SLT1_SS		0.681	0.020	34.112	0.000	0.642	0.720
59	RQ12	~~	RQ22		0.805	0.102	7.909	0.000	0.605	1.004
60	RQ12	~~	SE2		0.484	0.121	3.987	0.000	0.246	0.722
61	RQ12	~~	SLT2SS		0.509	0.068	7.511	0.000	0.376	0.642
62	RQ22	~~	SE2		0.140	0.223	0.628	0.530	-0.297	0.577
63	RQ22	~~	SLT2SS		0.661	0.068	9.773	0.000	0.528	0.794
64	SE2	~~	SLT2SS		0.382	0.173	2.208	0.027	0.043	0.721
65	THT1_SS	~~	THT1_SS		0.260	0.017	15.290	0.000	0.226	0.293
66	TBT1_SS	~~	TBT1_SS		0.205	0.016	12.694	0.000	0.173	0.237
67	TH_T2_SS	~~	TH_T2_SS		0.207	0.015	13.624	0.000	0.177	0.236
68	TB_T2_SS	~~	TB_T2_SS		0.129	0.013	9.748	0.000	0.103	0.155
69	ACOMT1_SS	~~	ACOMT1_SS		0.430	0.022	19.201	0.000	0.387	0.474
70	SATT1_SS	~~	SATT1_SS		0.365	0.022	16.631	0.000	0.322	0.408
71	ACOMT2SS	~~	ACOMT2SS		0.277	0.019	14.767	0.000	0.240	0.314
72	SAT_T2SS	~~	SAT_T2SS		0.254	0.018	13.873	0.000	0.219	0.290
73	AB_T1_SS	~~	AB_T1_SS		0.289	0.019	15.128	0.000	0.251	0.326
74	DE_T1_SS	~~	DE_T1_SS		0.295	0.021	14.329	0.000	0.254	0.335
75	VI_T1_SS	~~	VI_T1_SS		0.283	0.019	14.635	0.000	0.245	0.321
76	ABT2_SS	~~	ABT2_SS		0.267	0.021	12.976	0.000	0.227	0.307
77	DET2_SS	~~	DET2_SS		0.301	0.021	14.345	0.000	0.260	0.343
78	VIT2_SS	~~	VIT2_SS		0.264	0.020	12.971	0.000	0.224	0.304
79	SLT2SS	~~	SLT2SS		0.510	0.064	7.992	0.000	0.385	0.635
80	SLT1_SS	~~	SLT1_SS		1.000	0.000	NA	NA	1.000	1.000
81	RQ11	~~	RQ11		1.000	0.000	NA	NA	1.000	1.000
82	RQ12	~~	RQ12		0.611	0.055	11.157	0.000	0.504	0.719

83	RQ21	~~	RQ21	1.000	0.000	NA	NA	1.000	1.000
84	RQ22	~~	RQ22	0.707	0.164	4.308	0.000	0.385	1.029
85	SE1	~~	SE1	1.000	0.000	NA	NA	1.000	1.000
86	SE2	~~	SE2	0.292	0.099	2.946	0.003	0.098	0.486

GORICA

Next, we select the estimates relative to our hypotheses in order to use the `goric` function.

```
# indices of estimates of interest
indices <- 37:52

# select estimates from the column 'Std.all' in the results summary above
est <- stdClpmUnc[indices, 'est.std']

names(est) <- c("RQ12_RQ11", "RQ12_RQ21", "RQ12_SE1", "RQ12_SL1",
               "RQ22_RQ11", "RQ22_RQ21", "RQ22_SE1", "RQ22_SL1",
               "SE2_RQ11", "SE2_RQ21", "SE2_SE1", "SE2_SL1",
               "SL2_RQ11", "SL2_RQ21", "SL2_SE1", "SL2_SL1"
)

# the covariance matrix for these estimates
vcov <- lavInspect(clpmUnc, "vcov.std.all")[indices-6, indices-6]
```

Next, we specify the hypotheses to be evaluated (which are known before seeing the data). Note the use of the `abs` function: This is because we are interested in the size of the relations and we want to compare absolute effects. In cases where the sign of the values is of interest, one should look at the regular/raw/non-absolute effect (e.g., `estimate_x > .3` or `estimate_y < 0`).

Here, there are two sets of hypotheses, $H1_Q1$ and $H1_Q2$, which focus on different relations in the model. The decisions of whether multiple hypotheses should be split in different sets and how to divide them are driven by theory, and depend on what the researchers intend to evaluate. When multiple hypotheses are included in one set, as in $H1_Q2$, they are handled by the `goric` function as a whole, not individually.

```
# Q1: Phi_21 > Phi_12
H1_Q1 <- "
abs(RQ22_RQ11) > abs(RQ12_RQ21)
"

#
# Q2
H1_Q2 <- "
abs(SE2_RQ11) > abs(RQ12_SE1);
abs(SL2_RQ11) > abs(RQ12_SL1);
abs(SE2_RQ21) > abs(RQ22_SE1);
abs(SL2_RQ21) > abs(RQ22_SL1)
"
```

We obtain the GORICA results for $H1_Q1$ and $H1_Q2$ in two steps (where each is evaluated against their own complement). Note the use of `set.seed` to ensure that the results are reproducible.

```
set.seed(123)

#H1_Q1 vs its complement, using GORICA
goricaResults_Q1 <- goric(est, VCOV = vcov, # then, default: type = "gorica"
                        hypotheses = list(H1_Q1=H1_Q1))

goricaResults_Q1
```

restriktor (0.6-10): generalized order-restricted information criterion approximation:

Results:

	model	loglik	penalty	gorica	loglik.weights	penalty.weights	gorica.weights
1	H1_Q1	22.439	15.500	-13.878	0.632	0.500	0.632
2	complement	21.898	15.500	-12.796	0.368	0.500	0.368

Conclusion:

The order-restricted hypothesis 'H1_Q1' has 1.72 times more support than its complement.

```
#summary(goricaResults_Q1)
```

The output shows that the order-restricted hypothesis $H1_Q1$ has 1.7 times more support than its complement.

```
set.seed(123)
```

```
#H1_Q2 vs its complement, using GORICA
```

```
goricaResults_Q2 <- goric(est, VCOV = vcov,  
                          hypotheses = list(H1_Q2=H1_Q2))
```

```
goricaResults_Q2
```

restriktor (0.6-10): generalized order-restricted information criterion approximation:

Results:

	model	loglik	penalty	gorica	loglik.weights	penalty.weights	gorica.weights
1	H1_Q2	22.439	14.856	-15.167	0.513	0.568	0.581
2	complement	22.387	15.131	-14.512	0.487	0.432	0.419

Conclusion:

The order-restricted hypothesis 'H1_Q2' has 1.39 times more support than its complement.

```
#summary(goricaResults_Q2)
```

Furthermore, the order-restricted hypothesis $H1_Q2$ has 1.4 times more support than its complement.

Note 1: The results hold for the chosen time interval. Hence, the results are time-interval dependent. At the end, more information is given.

Note 2: The log-likelihood (loglik) weights seem to be quite close. This could indicate that one or more of the inequality constraints can be replaced by (about-)equality constraints. One could investigate with the benchmarks function, using 'output_type = "rlw"', whether the loglik weights indeed are close.

For more information, see the guidelines ('Guidelines_output_GORIC.html') and/or the benchmark tutorial on <https://github.com/rebeccakuiper/Tutorials>.

Example 2: Measurement Level Analysis

R packages

First, install and call the `lavaan` library to create a CLPM and the `restriktor` library to load the `goric` function. If needed, it is possible to view the description of the function with the `?` operator or the `help` command.

The code presented here also requires the `tidyverse` package for data manipulation.

```
# To install restriktor in R:
```

```
#if (!require("restriktor")) install.packages("restriktor")
```

```

# To install restriktor from github:
# if (!require("devtools")) install.packages("devtools")
# library(devtools)
# install_github("LeonardV/restriktor")
library(restriktor)

# print docs in the help-tab to view arguments and explanations for the function
#?goric

# To install lavaan in R:
# if (!require("lavaan")) install.packages("lavaan")
library(lavaan)

# To install tidyverse in R:
# if (!require("tidyverse")) install.packages("tidyverse")
library(tidyverse)

```

Data

Upload the data set to the R environment and select the columns used for analysis. The id column is renamed to *ID* and the code in the data set for missing numbers -999.00 is replaced with *NA*s.

```

data <- read.table("data/CLPM.dat", header = T)
colnames(data)[1] <- "ID"
data <- replace(data , data == -999.00, NA)

data_subset <- select(data,
  THT1_SS,
  TBT1_SS,
  ACOMT1_SS,
  SATT1_SS,
  AB_T1_SS,
  DE_T1_SS,
  VI_T1_SS,
  SLT1_SS,
  TH_T2_SS,
  TB_T2_SS,
  ACOMT2SS,
  SAT_T2SS,
  ABT2_SS,
  DET2_SS,
  VIT2_SS,
  SLT2SS)

```

CLPM

Next, we fit the CLPM on sum scores using the *lavaan* package. Here we specify all the relations of the model.

```

clpmModel_2 <- '
#####
# DYNAMICS #
#####

```

```

# Specify the lagged effects between the latent variables.
TH_T2_SS ~ THT1_SS + TBT1_SS + ACOMT1_SS + SATT1_SS + AB_T1_SS + DE_T1_SS + VI_T1_SS + SLT1_SS
TB_T2_SS ~ THT1_SS + TBT1_SS + ACOMT1_SS + SATT1_SS + AB_T1_SS + DE_T1_SS + VI_T1_SS + SLT1_SS
ACOMT2SS ~ THT1_SS + TBT1_SS + ACOMT1_SS + SATT1_SS + AB_T1_SS + DE_T1_SS + VI_T1_SS + SLT1_SS
SAT_T2SS ~ THT1_SS + TBT1_SS + ACOMT1_SS + SATT1_SS + AB_T1_SS + DE_T1_SS + VI_T1_SS + SLT1_SS
#
ABT2_SS ~ THT1_SS + TBT1_SS + ACOMT1_SS + SATT1_SS + AB_T1_SS + DE_T1_SS + VI_T1_SS + SLT1_SS
DET2_SS ~ THT1_SS + TBT1_SS + ACOMT1_SS + SATT1_SS + AB_T1_SS + DE_T1_SS + VI_T1_SS + SLT1_SS
VIT2_SS ~ THT1_SS + TBT1_SS + ACOMT1_SS + SATT1_SS + AB_T1_SS + DE_T1_SS + VI_T1_SS + SLT1_SS
#
SLT2SS ~ THT1_SS + TBT1_SS + ACOMT1_SS + SATT1_SS + AB_T1_SS + DE_T1_SS + VI_T1_SS + SLT1_SS

# Estimate the correlations within the same wave.
# T1
ACOMT1_SS ~~ THT1_SS + TBT1_SS + SATT1_SS + AB_T1_SS + DE_T1_SS + VI_T1_SS + SLT1_SS
THT1_SS ~~ TBT1_SS + SATT1_SS + AB_T1_SS + DE_T1_SS + VI_T1_SS + SLT1_SS
TBT1_SS ~~ SATT1_SS + AB_T1_SS + DE_T1_SS + VI_T1_SS + SLT1_SS
SATT1_SS ~~ AB_T1_SS + DE_T1_SS + VI_T1_SS + SLT1_SS
AB_T1_SS ~~ DE_T1_SS + VI_T1_SS + SLT1_SS
DE_T1_SS ~~ VI_T1_SS + SLT1_SS
VI_T1_SS ~~ SLT1_SS
# T2
TH_T2_SS ~~ TB_T2_SS + SAT_T2SS + ACOMT2SS + ABT2_SS + DET2_SS + VIT2_SS + SLT2SS
TB_T2_SS ~~ SAT_T2SS + ACOMT2SS + ABT2_SS + DET2_SS + VIT2_SS + SLT2SS
SAT_T2SS ~~ ACOMT2SS + ABT2_SS + DET2_SS + VIT2_SS + SLT2SS
ACOMT2SS ~~ ABT2_SS + DET2_SS + VIT2_SS + SLT2SS
ABT2_SS ~~ DET2_SS + VIT2_SS + SLT2SS
DET2_SS ~~ VIT2_SS + SLT2SS
VIT2_SS ~~ SLT2SS

```

We fit the model using the `sem` function:

```
clpmUnc_2 <- sem(clpmModel_2, data = data_subset, missing = 'ML')
```

Using the `summary` function we obtain the results of the model fit and estimates. The standardized solution contains the p-values of standardized effects.

```
fitMeasures(clpmUnc_2)
```

npar	fmin	chisq
152.000	0.000	0.000
srmr	srmr_bentler	srmr_bentler_nomean
0.000	0.000	0.000

```
stdClpmUnc_2 <- standardizedsolution(clpmUnc_2, type = "std.all", se = TRUE, zstat = TRUE,
pvalue = TRUE, ci = TRUE, level = 0.95, cov.std = TRUE,
remove.eq = TRUE, remove.ineq = TRUE, remove.def = FALSE,
partable = NULL, GLIST = NULL, est = NULL)
```

```
stdClpmUnc_2
```

	lhs	op	rhs	est.std	se	z	pvalue	ci.lower	ci.upper
1	TH_T2_SS	~	THT1_SS	0.191	0.094	2.033	0.042	0.007	0.374
2	TH_T2_SS	~	TBT1_SS	0.072	0.098	0.739	0.460	-0.120	0.265

3	TH_T2_SS	~ ACOMT1_SS	-0.017	0.076	-0.225	0.822	-0.167	0.132
4	TH_T2_SS	~ SATT1_SS	0.122	0.093	1.319	0.187	-0.059	0.304
5	TH_T2_SS	~ AB_T1_SS	-0.030	0.083	-0.362	0.718	-0.192	0.132
6	TH_T2_SS	~ DE_T1_SS	0.075	0.101	0.738	0.460	-0.124	0.273
7	TH_T2_SS	~ VI_T1_SS	0.086	0.088	0.981	0.327	-0.086	0.259
8	TH_T2_SS	~ SLT1_SS	0.140	0.086	1.617	0.106	-0.030	0.309
9	TB_T2_SS	~ THT1_SS	0.019	0.092	0.203	0.839	-0.162	0.200
10	TB_T2_SS	~ TBT1_SS	0.384	0.094	4.084	0.000	0.200	0.568
11	TB_T2_SS	~ ACOMT1_SS	0.019	0.074	0.257	0.797	-0.126	0.164
12	TB_T2_SS	~ SATT1_SS	0.051	0.091	0.562	0.574	-0.127	0.230
13	TB_T2_SS	~ AB_T1_SS	-0.106	0.081	-1.299	0.194	-0.265	0.054
14	TB_T2_SS	~ DE_T1_SS	0.037	0.101	0.361	0.718	-0.162	0.235
15	TB_T2_SS	~ VI_T1_SS	0.127	0.087	1.456	0.145	-0.044	0.297
16	TB_T2_SS	~ SLT1_SS	0.142	0.085	1.679	0.093	-0.024	0.308
17	ACOMT2SS	~ THT1_SS	-0.027	0.087	-0.315	0.753	-0.198	0.143
18	ACOMT2SS	~ TBT1_SS	0.002	0.091	0.023	0.981	-0.176	0.180
19	ACOMT2SS	~ ACOMT1_SS	0.329	0.068	4.838	0.000	0.195	0.462
20	ACOMT2SS	~ SATT1_SS	0.018	0.086	0.204	0.838	-0.151	0.186
21	ACOMT2SS	~ AB_T1_SS	0.022	0.076	0.288	0.773	-0.128	0.171
22	ACOMT2SS	~ DE_T1_SS	0.115	0.094	1.230	0.219	-0.068	0.299
23	ACOMT2SS	~ VI_T1_SS	0.078	0.082	0.959	0.337	-0.082	0.238
24	ACOMT2SS	~ SLT1_SS	0.202	0.079	2.547	0.011	0.047	0.357
25	SAT_T2SS	~ THT1_SS	-0.081	0.090	-0.899	0.368	-0.257	0.095
26	SAT_T2SS	~ TBT1_SS	0.126	0.094	1.343	0.179	-0.058	0.310
27	SAT_T2SS	~ ACOMT1_SS	0.033	0.073	0.456	0.648	-0.109	0.176
28	SAT_T2SS	~ SATT1_SS	0.325	0.087	3.751	0.000	0.155	0.494
29	SAT_T2SS	~ AB_T1_SS	-0.088	0.079	-1.111	0.266	-0.242	0.067
30	SAT_T2SS	~ DE_T1_SS	0.098	0.097	1.013	0.311	-0.092	0.288
31	SAT_T2SS	~ VI_T1_SS	0.125	0.084	1.487	0.137	-0.040	0.289
32	SAT_T2SS	~ SLT1_SS	0.147	0.082	1.796	0.073	-0.013	0.308
33	ABT2_SS	~ THT1_SS	0.001	0.079	0.014	0.989	-0.154	0.156
34	ABT2_SS	~ TBT1_SS	0.072	0.085	0.845	0.398	-0.094	0.238
35	ABT2_SS	~ ACOMT1_SS	-0.063	0.064	-0.974	0.330	-0.189	0.064
36	ABT2_SS	~ SATT1_SS	-0.019	0.082	-0.237	0.813	-0.180	0.141
37	ABT2_SS	~ AB_T1_SS	0.645	0.063	10.167	0.000	0.521	0.770
38	ABT2_SS	~ DE_T1_SS	0.118	0.086	1.368	0.171	-0.051	0.286
39	ABT2_SS	~ VI_T1_SS	0.028	0.074	0.378	0.706	-0.116	0.172
40	ABT2_SS	~ SLT1_SS	0.018	0.070	0.259	0.795	-0.120	0.156
41	DET2_SS	~ THT1_SS	-0.124	0.080	-1.550	0.121	-0.280	0.033
42	DET2_SS	~ TBT1_SS	0.214	0.085	2.500	0.012	0.046	0.381
43	DET2_SS	~ ACOMT1_SS	-0.105	0.065	-1.625	0.104	-0.232	0.022
44	DET2_SS	~ SATT1_SS	0.062	0.082	0.751	0.453	-0.100	0.223
45	DET2_SS	~ AB_T1_SS	0.054	0.070	0.771	0.441	-0.083	0.192
46	DET2_SS	~ DE_T1_SS	0.685	0.078	8.737	0.000	0.531	0.838
47	DET2_SS	~ VI_T1_SS	0.037	0.075	0.498	0.619	-0.109	0.184
48	DET2_SS	~ SLT1_SS	-0.051	0.071	-0.708	0.479	-0.190	0.089
49	VIT2_SS	~ THT1_SS	0.025	0.079	0.311	0.756	-0.131	0.180
50	VIT2_SS	~ TBT1_SS	0.151	0.085	1.770	0.077	-0.016	0.318
51	VIT2_SS	~ ACOMT1_SS	-0.155	0.064	-2.417	0.016	-0.281	-0.029
52	VIT2_SS	~ SATT1_SS	-0.021	0.082	-0.255	0.798	-0.183	0.141
53	VIT2_SS	~ AB_T1_SS	0.230	0.069	3.338	0.001	0.095	0.365
54	VIT2_SS	~ DE_T1_SS	0.072	0.088	0.823	0.411	-0.100	0.244
55	VIT2_SS	~ VI_T1_SS	0.574	0.069	8.372	0.000	0.440	0.708
56	VIT2_SS	~ SLT1_SS	-0.074	0.070	-1.057	0.291	-0.212	0.064

57	SLT2SS	~	THT1_SS	-0.026	0.081	-0.318	0.751	-0.184	0.133
58	SLT2SS	~	TBT1_SS	0.021	0.086	0.244	0.807	-0.148	0.190
59	SLT2SS	~	ACOMT1_SS	-0.013	0.066	-0.203	0.839	-0.142	0.116
60	SLT2SS	~	SATT1_SS	0.215	0.082	2.631	0.009	0.055	0.375
61	SLT2SS	~	AB_T1_SS	0.083	0.070	1.186	0.236	-0.054	0.221
62	SLT2SS	~	DE_T1_SS	0.134	0.087	1.537	0.124	-0.037	0.306
63	SLT2SS	~	VI_T1_SS	-0.043	0.075	-0.568	0.570	-0.190	0.104
64	SLT2SS	~	SLT1_SS	0.468	0.068	6.840	0.000	0.334	0.602
65	THT1_SS	~~	ACOMT1_SS	0.611	0.019	31.414	0.000	0.573	0.649
66	TBT1_SS	~~	ACOMT1_SS	0.637	0.018	34.602	0.000	0.601	0.673
67	ACOMT1_SS	~~	SATT1_SS	0.603	0.020	30.608	0.000	0.564	0.641
68	ACOMT1_SS	~~	AB_T1_SS	0.467	0.024	19.248	0.000	0.419	0.515
69	ACOMT1_SS	~~	DE_T1_SS	0.586	0.020	28.750	0.000	0.546	0.626
70	ACOMT1_SS	~~	VI_T1_SS	0.528	0.022	23.450	0.000	0.484	0.572
71	ACOMT1_SS	~~	SLT1_SS	0.651	0.018	36.260	0.000	0.616	0.686
72	THT1_SS	~~	TBT1_SS	0.767	0.013	59.792	0.000	0.742	0.792
73	THT1_SS	~~	SATT1_SS	0.710	0.015	46.179	0.000	0.680	0.741
74	THT1_SS	~~	AB_T1_SS	0.281	0.029	9.855	0.000	0.225	0.337
75	THT1_SS	~~	DE_T1_SS	0.449	0.025	18.208	0.000	0.401	0.498
76	THT1_SS	~~	VI_T1_SS	0.343	0.027	12.482	0.000	0.289	0.397
77	THT1_SS	~~	SLT1_SS	0.592	0.020	29.322	0.000	0.552	0.631
78	TBT1_SS	~~	SATT1_SS	0.740	0.014	52.720	0.000	0.713	0.768
79	TBT1_SS	~~	AB_T1_SS	0.323	0.028	11.659	0.000	0.269	0.377
80	TBT1_SS	~~	DE_T1_SS	0.454	0.024	18.541	0.000	0.406	0.502
81	TBT1_SS	~~	VI_T1_SS	0.377	0.027	14.158	0.000	0.325	0.429
82	TBT1_SS	~~	SLT1_SS	0.594	0.020	29.545	0.000	0.555	0.633
83	SATT1_SS	~~	AB_T1_SS	0.311	0.028	11.178	0.000	0.257	0.366
84	SATT1_SS	~~	DE_T1_SS	0.467	0.024	19.374	0.000	0.420	0.514
85	SATT1_SS	~~	VI_T1_SS	0.390	0.026	14.824	0.000	0.338	0.441
86	SATT1_SS	~~	SLT1_SS	0.621	0.019	32.617	0.000	0.584	0.659
87	AB_T1_SS	~~	DE_T1_SS	0.688	0.016	42.342	0.000	0.656	0.720
88	AB_T1_SS	~~	VI_T1_SS	0.760	0.013	58.074	0.000	0.735	0.786
89	AB_T1_SS	~~	SLT1_SS	0.482	0.024	20.323	0.000	0.435	0.528
90	DE_T1_SS	~~	VI_T1_SS	0.680	0.017	40.772	0.000	0.647	0.712
91	DE_T1_SS	~~	SLT1_SS	0.703	0.016	44.880	0.000	0.672	0.734
92	VI_T1_SS	~~	SLT1_SS	0.535	0.022	24.146	0.000	0.491	0.578
93	TH_T2_SS	~~	TB_T2_SS	0.781	0.019	42.220	0.000	0.745	0.818
94	TH_T2_SS	~~	SAT_T2SS	0.685	0.024	28.242	0.000	0.637	0.732
95	TH_T2_SS	~~	ACOMT2SS	0.643	0.029	22.348	0.000	0.586	0.699
96	TH_T2_SS	~~	ABT2_SS	0.231	0.054	4.268	0.000	0.125	0.338
97	TH_T2_SS	~~	DET2_SS	0.353	0.050	7.097	0.000	0.256	0.451
98	TH_T2_SS	~~	VIT2_SS	0.229	0.055	4.180	0.000	0.122	0.337
99	TH_T2_SS	~~	SLT2SS	0.494	0.041	12.049	0.000	0.414	0.575
100	TB_T2_SS	~~	SAT_T2SS	0.727	0.023	32.276	0.000	0.683	0.772
101	TB_T2_SS	~~	ACOMT2SS	0.698	0.027	26.170	0.000	0.646	0.750
102	TB_T2_SS	~~	ABT2_SS	0.303	0.055	5.496	0.000	0.195	0.412
103	TB_T2_SS	~~	DET2_SS	0.368	0.052	7.086	0.000	0.266	0.470
104	TB_T2_SS	~~	VIT2_SS	0.259	0.057	4.519	0.000	0.147	0.371
105	TB_T2_SS	~~	SLT2SS	0.502	0.043	11.688	0.000	0.418	0.586
106	ACOMT2SS	~~	SAT_T2SS	0.652	0.028	23.001	0.000	0.596	0.708
107	SAT_T2SS	~~	ABT2_SS	0.254	0.054	4.706	0.000	0.148	0.360
108	SAT_T2SS	~~	DET2_SS	0.328	0.051	6.469	0.000	0.229	0.427
109	SAT_T2SS	~~	VIT2_SS	0.249	0.055	4.533	0.000	0.141	0.356
110	SAT_T2SS	~~	SLT2SS	0.494	0.041	12.185	0.000	0.415	0.574

111	ACOMT2SS	~~	ABT2_SS	0.346	0.052	6.706	0.000	0.245	0.447
112	ACOMT2SS	~~	DET2_SS	0.453	0.046	9.769	0.000	0.362	0.544
113	ACOMT2SS	~~	VIT2_SS	0.358	0.052	6.850	0.000	0.256	0.461
114	ACOMT2SS	~~	SLT2SS	0.549	0.039	14.179	0.000	0.474	0.625
115	ABT2_SS	~~	DET2_SS	0.568	0.041	13.762	0.000	0.487	0.648
116	ABT2_SS	~~	VIT2_SS	0.621	0.037	16.797	0.000	0.549	0.693
117	ABT2_SS	~~	SLT2SS	0.314	0.055	5.762	0.000	0.207	0.421
118	DET2_SS	~~	VIT2_SS	0.547	0.044	12.402	0.000	0.461	0.633
119	DET2_SS	~~	SLT2SS	0.508	0.045	11.328	0.000	0.420	0.596
120	VIT2_SS	~~	SLT2SS	0.377	0.054	7.009	0.000	0.272	0.483
121	TH_T2_SS	~~	TH_T2_SS	0.722	0.043	16.911	0.000	0.639	0.806
122	TB_T2_SS	~~	TB_T2_SS	0.646	0.044	14.620	0.000	0.559	0.733
123	ACOMT2SS	~~	ACOMT2SS	0.600	0.044	13.611	0.000	0.513	0.686
124	SAT_T2SS	~~	SAT_T2SS	0.649	0.043	15.050	0.000	0.565	0.734
125	ABT2_SS	~~	ABT2_SS	0.434	0.040	10.971	0.000	0.356	0.511
126	DET2_SS	~~	DET2_SS	0.455	0.041	11.069	0.000	0.374	0.535
127	VIT2_SS	~~	VIT2_SS	0.420	0.038	11.004	0.000	0.345	0.495
128	SLT2SS	~~	SLT2SS	0.464	0.042	11.136	0.000	0.382	0.545
129	THT1_SS	~~	THT1_SS	1.000	0.000	NA	NA	1.000	1.000
130	TBT1_SS	~~	TBT1_SS	1.000	0.000	NA	NA	1.000	1.000
131	ACOMT1_SS	~~	ACOMT1_SS	1.000	0.000	NA	NA	1.000	1.000
132	SATT1_SS	~~	SATT1_SS	1.000	0.000	NA	NA	1.000	1.000
133	AB_T1_SS	~~	AB_T1_SS	1.000	0.000	NA	NA	1.000	1.000
134	DE_T1_SS	~~	DE_T1_SS	1.000	0.000	NA	NA	1.000	1.000
135	VI_T1_SS	~~	VI_T1_SS	1.000	0.000	NA	NA	1.000	1.000
136	SLT1_SS	~~	SLT1_SS	1.000	0.000	NA	NA	1.000	1.000
137	TH_T2_SS	~1		1.839	0.286	6.420	0.000	1.277	2.400
138	TB_T2_SS	~1		1.186	0.275	4.308	0.000	0.646	1.726
139	ACOMT2SS	~1		0.759	0.258	2.941	0.003	0.253	1.265
140	SAT_T2SS	~1		0.925	0.264	3.499	0.000	0.407	1.443
141	ABT2_SS	~1		0.305	0.237	1.284	0.199	-0.160	0.770
142	DET2_SS	~1		1.058	0.244	4.340	0.000	0.580	1.536
143	VIT2_SS	~1		0.466	0.240	1.943	0.052	-0.004	0.937
144	SLT2SS	~1		0.365	0.237	1.540	0.124	-0.100	0.830
145	THT1_SS	~1		4.869	0.111	43.722	0.000	4.651	5.088
146	TBT1_SS	~1		4.140	0.096	43.136	0.000	3.952	4.329
147	ACOMT1_SS	~1		3.686	0.086	42.940	0.000	3.518	3.854
148	SATT1_SS	~1		3.805	0.089	42.896	0.000	3.631	3.979
149	AB_T1_SS	~1		3.429	0.080	42.754	0.000	3.272	3.586
150	DE_T1_SS	~1		4.508	0.102	44.130	0.000	4.308	4.708
151	VI_T1_SS	~1		3.542	0.083	42.581	0.000	3.379	3.705
152	SLT1_SS	~1		4.082	0.094	43.588	0.000	3.899	4.266

In this case, the results shows we obtain a ‘perfect’ model fit, that is because the degrees of freedom are 0, meaning the model is saturated (i.e., you have as much parameters as you have data points).

GORICA

We select the estimates relevant to our hypotheses in order to use the `goric` function.

```
# indices of estimates of interest
indices_2 <- 1:64

# select estimates from the column 'Std.all' in the results summary above
est_2 <- stdClpmUnc_2[indices_2, 'est.std']
```

```

names(est_2) <- c("TH2_TH1", "TH2_TB1", "TH2_ACOM1", "TH2_SAT1", "TH2_AB1", "TH2_DE1", "TH2_VI1", "TH2_SL1",
"TB2_TH1", "TB2_TB1", "TB2_ACOM1", "TB2_SAT1", "TB2_AB1", "TB2_DE1", "TB2_VI1", "TB2_SL1",
"ACOM2_TH1", "ACOM2_TB1", "ACOM2_ACOM1", "ACOM2_SAT1", "ACOM2_AB1", "ACOM2_DE1", "ACOM2_VI1", "ACOM2_SL1",
"SAT2_TH1", "SAT2_TB1", "SAT2_ACOM1", "SAT2_SAT1", "SAT2_AB1", "SAT2_DE1", "SAT2_VI1", "SAT2_SL1",
#
"AB2_TH1", "AB2_TB1", "AB2_ACOM1", "AB2_SAT1", "AB2_AB1", "AB2_DE1", "AB2_VI1", "AB2_SL1",
"DE2_TH1", "DE2_TB1", "DE2_ACOM1", "DE2_SAT1", "DE2_AB1", "DE2_DE1", "DE2_VI1", "DE2_SL1",
"VI2_TH1", "VI2_TB1", "VI2_ACOM1", "VI2_SAT1", "VI2_AB1", "VI2_DE1", "VI2_VI1", "VI2_SL1",
#
"SL2_TH1", "SL2_TB1", "SL2_ACOM1", "SL2_SAT1", "SL2_AB1", "SL2_DE1", "SL2_VI1", "SL2_SL1",
)

# the covariance matrix for these estimates
vcov_2 <- lavInspect(clpmUnc_2, "vcov.std.all")[indices_2, indices_2]

```

Next, we specify the hypotheses to be evaluated. Note the use of the `abs` function; that is because we are interested in the size of the relations and we want to compare absolute effects. In cases where the sign of the values is of interest, one should not use absolute values (e.g., `estimate_x > .3` or `estimate_y < 0`).

Here, there are two sets of hypotheses, $H1_Q1$ and $H1_Q2$, which focus on different relations in the model. The decisions of whether multiple hypotheses should be split in different sets and how to divide them are driven by theory, and depend on what the researchers intend to evaluate. When multiple hypotheses are included in one set they are handled by the `goric` function as a whole, not individually.

```

# Q1
H2_Q1 <- "
abs(ACOM2_TH1) > abs(TH2_ACOM1); abs(SAT2_TH1) > abs(TH2_SAT1);
abs(ACOM2_TB1) > abs(TB2_ACOM1); abs(SAT2_TB1) > abs(TB2_SAT1)
"

# Q2
H2_Q2 <- "
abs(AB2_TH1) > abs(TH2_AB1); abs(DE2_TH1) > abs(TH2_DE1); abs(VI2_TH1) > abs(TH2_VI1); abs(SL2_TH1) > abs(TH2_SL1);
abs(AB2_TB1) > abs(TB2_AB1); abs(DE2_TB1) > abs(TB2_DE1); abs(VI2_TB1) > abs(TB2_VI1); abs(SL2_TB1) > abs(TB2_SL1);
abs(AB2_ACOM1) > abs(ACOM2_AB1); abs(DE2_ACOM1) > abs(ACOM2_DE1); abs(VI2_ACOM1) > abs(ACOM2_VI1); abs(SL2_ACOM1) > abs(ACOM2_SL1);
abs(AB2_SAT1) > abs(SAT2_AB1); abs(DE2_SAT1) > abs(SAT2_DE1); abs(VI2_SAT1) > abs(SAT2_VI1); abs(SL2_SAT1) > abs(SAT2_SL1);
"

```

We obtain the GORICA results for $H2_Q1$ and $H2_Q2$ in two steps. Note the use of `set.seed` to ensure that the results are reproducible.

```

set.seed(123)

#H2_Q1 vs its complement, using GORICA
goricaResults_H2_Q1 <- goric(est_2, VCOV = vcov_2,
                             hypotheses = list(H2_Q1=H2_Q1))

goricaResults_H2_Q1

```

restriktor (0.6-10): generalized order-restricted information criterion approximation:

Results:

	model	loglik	penalty	gorica	loglik.weights	penalty.weights	gorica.weights
1	H2_Q1	134.232	62.451	-143.562	0.483	0.735	0.722
2	complement	134.301	63.473	-141.656	0.517	0.265	0.278

Conclusion:

The order-restricted hypothesis 'H2_Q1' has 2.59 times more support than its complement.

```
#summary(goricaResults_H2_Q1)
```

The output shows that the order-restricted hypothesis $H2_Q1$ has 2.6 times more support than its complement. However, the log-likelihood (loglik) weights seem to be quite close. This could indicate that one or more of the inequality constraints can be replaced by (about-)equality constraints. One could investigate with the benchmarks function, using 'output_type = "rlw"', whether the loglik weights indeed are close. For more information, see the guidelines ('Guidelines_output_GORIC.html') and/or the benchmark tutorial on <https://github.com/rebeccakuiper/Tutorials>.

We can proceed in the same manner for $H2_Q2$; however, because the default method takes too long to calculate the penalty of the GORICA, we use the bootstrap method. When using the bootstrapping the results do not change, but the computation time may decrease.

```
set.seed(123)

##H2_Q2 vs its complement, using GORICA
#goricaResults_H2_Q2 <- gorica(est_2, VCOV = vcov_2,
#                               hypotheses = list(H2_Q2=H2_Q2))
#goricaResults_H2_Q2
##summary(goricaResults_H2_Q2)

# if (!require("parallel")) install.packages("parallel")
#library(parallel)
#
#nrCPUCores <- detectCores(all.tests = FALSE, logical = TRUE)
#
goricaResults_H2_Q2_b <- gorica(est_2, VCOV = vcov_2,
                               hypotheses = list(H2_Q2=H2_Q2),
                               mix_weights = "boot")

goricaResults_H2_Q2_b
```

restriktor (0.6-10): generalized order-restricted information criterion approximation:

Results:

	model	loglik	penalty	gorica	loglik.weights	penalty.weights	gorica.weights
1	H2_Q2	130.969	58.028	-145.881	0.034	0.997	0.933
2	complement	134.301	63.995	-140.612	0.966	0.003	0.067

Conclusion:

The order-restricted hypothesis 'H2_Q2' has 13.94 times more support than its complement.

```
#summary(goricaResults_H2_Q2_b)
```

The order-restricted hypothesis $H2_Q2$ has 14 times more support than its complement.

Note that the results hold for the chosen time interval. Hence, the results are time-interval dependent. Next, more information is given.

Note on time-interval dependency

The parameter estimates in a (RI-)CLPM are time-interval dependent, and thus the GORICA results as well. By using the CTmeta package:

```
# Install and load packages
#
#library(devtools)
#if (!require("CTmeta")) install_github("rebeccakuiper/CTmeta") ##install_github("rebeccakuiper/CTmeta")
library(CTmeta)
##PhiPlot
```

one can plot the lagged-effects parameter estimates for different choices of time intervals. Based on this plot (and/or on other information), one can evaluate the hypotheses using the GORICA for different choices of time intervals.