

# How to evaluate theory-based hypotheses in a lavaan model using the GORICA

Rebecca M. Kuiper

07 november 2025

## Contents

Packages	1
Example 1: Confirmatory Factor Analysis	2
Example 2: Multiple Group CFA	3
Example 3: Structural equation modeling (SEM)	3
Example 4: Multilevel SEM	4
Example 5: linear growth model with a time-varying covariate	5
Example 6: Mediation	6

This is a tutorial for applying the AIC-type criterion GORICA to a lavaan object. The GORICA is an information criterion that can be used to evaluate theory-driven, informative, order-restricted hypotheses. The GORICA selects the best hypothesis out of a given set. Below, you will find examples for the use of the `goric` function in the `restriktor` R package when you have a lavaan object.

Note: For (more) information (tutorials and example R scripts) is available from [https://github.com/r\\_ebeccakuiper/Tutorials](https://github.com/r_ebeccakuiper/Tutorials), including a tutorial regarding interpreting the GORIC(A) output (called ‘Guidelines\_output\_GORIC’).

## Packages

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

```
# 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)
```

## Example 1: Confirmatory Factor Analysis

In this example, we will look at the Confirmatory Factor Analysis (CFA) lavaan example (<https://www.lavaan.ugent.be/tutorial/cfa.html>).

To specify your hypotheses in terms of model parameters, it is often handy (and sometimes even necessary) to give your own labels to estimates by including them in the `lavaan` model.

```
# specify the model, using own labeling
HS.model <- " visual =~ lambda_v1*x1 + lambda_v2*x2 + lambda_v3*x3
              textual =~ lambda_t1*x4 + lambda_t2*x5 + lambda_t3*x6
              speed   =~ lambda_s1*x7 + lambda_s2*x8 + lambda_s3*x9 "
```

Next, we need to formulate the hypothesis of interest. Let us say that the hypothesis is that all factor loadings are at least (in absolute sense) .6. Notably, it is also possible to compare the height of (absolute values of) factor loadings. Since we are interested in one theory-based hypothesis, we compare it to its complement (reflecting all the other possibilities); which is done by default (i.e., by default: `comparison = "complement"`).

```
# Hypotheses
H1_cfa <- "
abs(lambda_v1) > .6; abs(lambda_v2) > .6; abs(lambda_v3) > .6;
abs(lambda_t1) > .6; abs(lambda_t2) > .6; abs(lambda_t3) > .6;
abs(lambda_s1) > .6; abs(lambda_s2) > .6; abs(lambda_s3) > .6;
"
# vs its complement (default)
```

Then, we fit the confirmatory factor analysis (CFA) model using the `cfa` function from `lavaan`:

```
# fit the model fixing the variances of all the latent variables in a CFA model
# to unity (std.lv = TRUE; https://www.lavaan.ugent.be/tutorial/syntax2.html)
fit_cfa <- cfa(HS.model, data = HolzingerSwineford1939, std.lv = TRUE)
```

Now, we can call the `goric` function. Here, we use GORICA (i.e.,`type = "gorica"`) by default, because of entering a `lavaan` object. Notably, if one needs standardized estimates to obtain a meaningful comparison, add `standardized = TRUE`.

```
# Calculate GORICA values and weights for H1_cfa and its complement.

set.seed(100) # Needed for reproducibilty & sensitivity check
results_cfa <- goric(fit_cfa, hypotheses = list(H1_cfa = H1_cfa))
```

```
restriktor Message: The covariance matrix of the estimates was obtained via 'vcov()'. This is the biased
# summary(results_cfa)
results_cfa
```

```
restriktor (0.6-20): generalized order-restricted information criterion approximation:
```

Results:

	model	loglik	penalty	gorica	loglik.weights	penalty.weights	gorica.weights
1	H1_cfa	15.546	5.172	-20.749	0.296	0.977	0.948
2	complement	16.414	8.943	-14.944	0.704	0.023	0.052

Conclusion:

The order-restricted hypothesis 'H1\_cfa' has 18.22 times more support than its complement.

Conclusion: The order-restricted hypothesis 'H1\_cfa' has 18.22 times more support than its complement.

## Example 2: Multiple Group CFA

In this example, we will extend the CFA with a multiple-group structure (cf. <https://www.lavaan.ugent.be/tutorial/groups.html>). There are two groups: 1. Pasteur and 2. Grant-White. Each will have their own parameter estimates and thus also need their own labeling. In this example, we will evaluate whether the factor loadings in the second group are higher than the corresponding ones in the first group (i.e., in the first group lower than in the second).

```
# specify the model, using own labeling (per group!)
HS.model_mgcfa <- "
visual   =~ c(lambda_v1_P, lambda_v1_GW)*x1 + c(lambda_v2_P, lambda_v2_GW)*x2 + c(lambda_v3_P, lambda_v3_GW)*x3
textual  =~ c(lambda_t1_P, lambda_t1_GW)*x4 + c(lambda_t2_P, lambda_t2_GW)*x5 + c(lambda_t3_P, lambda_t3_GW)*x6
speed    =~ c(lambda_s1_P, lambda_s1_GW)*x7 + c(lambda_s2_P, lambda_s2_GW)*x8 + c(lambda_s3_P, lambda_s3_GW)*x9"
# Hypotheses
H1_mgcfa <- "
abs(lambda_v1_P) < abs(lambda_v1_GW); abs(lambda_v2_P) < abs(lambda_v2_GW); abs(lambda_v3_P) < abs(lambda_v3_GW);
abs(lambda_t1_P) < abs(lambda_t1_GW); abs(lambda_t2_P) < abs(lambda_t2_GW); abs(lambda_t3_P) < abs(lambda_t3_GW);
abs(lambda_s1_P) < abs(lambda_s1_GW); abs(lambda_s2_P) < abs(lambda_s2_GW); abs(lambda_s3_P) < abs(lambda_s3_GW)"
# vs its complement (default)

# fit the model fixing the variances of all the latent variables in a CFA model
# to unity (std.lv = TRUE; https://www.lavaan.ugent.be/tutorial/syntax2.html)
fit_mgcfa <- cfa(HS.model_mgcfa, data = HolzingerSwineford1939, group = "school",
                   std.lv = TRUE)

# Calculate GORICA values and weights
set.seed(100) # Needed for reproducibility & sensitivity check
results_mgcfa <- goric(fit_mgcfa, hypotheses = list(H1_mgcfa = H1_mgcfa))
```

restriktor Message: The covariance matrix of the estimates was obtained via 'vcov()'. This is the biased default.

```
# summary(results_mgcfa)
results_mgcfa
```

restriktor (0.6-20): generalized order-restricted information criterion approximation:

Results:

	model	loglik	penalty	gorica	loglik.weights	penalty.weights	gorica.weights
1	H1_mgcfa	24.950	14.170	-21.561	0.119	0.978	0.855
2	complement	26.948	17.943	-18.011	0.881	0.022	0.145

Conclusion:

The order-restricted hypothesis 'H1\_mgcfa' has 5.90 times more support than its complement.

Conclusion: The order-restricted hypothesis 'H1\_mgcfa' has 5.90 times more support than its complement.

## Example 3: Structural equation modeling (SEM)

In this example, we will look at the structural equation modeling (SEM) lavaan example (cf. <https://www.lavaan.ugent.be/tutorial/sem.html>).

Here, we assume that we are interested in (some of) the regression parameters; so, we only need to label these. We want to compare the strengths of the predictive relationships; hence, we need standardized estimates for a meaningful comparison; that is, add `standardized = TRUE`. We expect that the predictive relationship of

ind60 for dem60 is (in absolute sense) higher than that for dem65.

```
# specify the model, using own labeling
model_sem <- "
  # measurement model
  ind60 =~ x1 + x2 + x3
  dem60 =~ y1 + y2 + y3 + y4
  dem65 =~ y5 + y6 + y7 + y8
  # regressions
  dem60 ~ beta_dem60_ind60*ind60
  dem65 ~ beta_dem65_ind60*ind60 + dem60
  # residual correlations
  y1 ~~ y5
  y2 ~~ y4 + y6
  y3 ~~ y7
  y4 ~~ y8
  y6 ~~ y8
"
# Hypotheses
H1_sem <- "
abs(beta_dem60_ind60) > abs(beta_dem65_ind60)
"
# vs its complement (default)

# fit the model
fit_sem <- sem(model_sem, data = PoliticalDemocracy)

# Calculate GORICA values and weights
set.seed(100) # Needed for reproducibility & sensitivity check
results_sem <- goric(fit_sem, hypotheses = list(H1_sem = H1_sem), standardized = TRUE)
```

restriktor Message: The covariance matrix of the estimates was obtained via 'vcov()'. This is the biased default.

```
# summary(results_sem)
results_sem
```

restriktor (0.6-20): generalized order-restricted information criterion approximation:

Results:

	model	loglik	penalty	gorica	loglik.weights	penalty.weights	gorica.weights
1	H1_sem	3.113	1.500	-3.226	0.862	0.500	0.862
2	complement	1.279	1.500	0.443	0.138	0.500	0.138

Conclusion:

The order-restricted hypothesis 'H1\_sem' has 6.26 times more support than its complement.

Conclusion: The order-restricted hypothesis 'H1\_sem' has 6.06 times more support than its complement.

## Example 4: Multilevel SEM

In this example, we will look at the multilevel/two-level SEM lavaan example (cf. <https://www.lavaan.ugent.be/tutorial/multilevel.html>).

Here, we assume that we are interested in (some of) the regression parameters; so, we only need to label these.

We want to compare the strengths of the predictive relationships; hence, we need standardized estimates for a meaningful comparison; that is, add `standardized = TRUE`. We expect that the order of the (absolute) height in predictive relationships for fw is x1, x2, x3.

```
# specify the model, using own labeling
model_msem <- "
  level: 1
    fw =~ y1 + y2 + y3
    fw ~ beta_1*x1 + beta_2*x2 + beta_3*x3
  level: 2
    fb =~ y1 + y2 + y3
    fb ~ w1 + w2
"
# Hypotheses
H1_msem <- "
abs(beta_1) > abs(beta_2) > abs(beta_3)
"
# vs its complement (default)

# fit the model
fit_msem <- sem(model = model_msem, data = Demo.twolevel, cluster = "cluster")

# Calculate GORICA values and weights
set.seed(100) # Needed for reproducibility & sensitivity check
results_msem <- goric(fit_msem, hypotheses = list(H1_msem = H1_msem), standardized = TRUE)
```

restriktor Message: The covariance matrix of the estimates was obtained via 'vcov()'. This is the biased # summary(results\_msem)  
results\_msem

restriktor (0.6-20): generalized order-restricted information criterion approximation:

Results:

	model	loglik	penalty	gorica	loglik.weights	penalty.weights	gorica.weights
1	H1_msem	9.146	1.827	-14.637	0.995	0.700	0.998
2	complement	3.848	2.673	-2.350	0.005	0.300	0.002

Conclusion:

The order-restricted hypothesis 'H1\_msem' has 465.55 times more support than its complement.

Conclusion: The order-restricted hypothesis 'H1\_msem' has 465.55 times more support than its complement.

## Example 5: linear growth model with a time-varying covariate

In this example, we will look at the linear growth model with a time-varying covariate lavaan example (cf. <https://www.lavaan.ugent.be/tutorial/growth.html>).

Here, we assume that we are interested in the two intercepts; so, we only need to label these. For this, we now need extra code. We expect that the intercept of the slope s is (in absolute sense) higher than the intercept of the intercept i.

```
# specify the model, using own labeling a linear growth model with a
# time-varying covariate
```

```

model_growth <- "
# intercept and slope with fixed coefficients
i =~ 1*t1 + 1*t2 + 1*t3 + 1*t4
s =~ 0*t1 + 1*t2 + 2*t3 + 3*t4
# regressions
i ~ x1 + x2
s ~ x1 + x2
# time-varying covariates
t1 ~ c1
t2 ~ c2
t3 ~ c3
t4 ~ c4
# Extra: Label intercepts
i ~ intercept_i * 1
s ~ intercept_s * 1
"

# Hypotheses
H1_growth <- "
abs(intercept_s) > abs(intercept_i)
"
# vs its complement (default)

# fit the model
fit_growth <- growth(model_growth, data = Demo.growth)

# Calculate GORICA values and weights
set.seed(100) # Needed for reproducibility & sensitivity check
results_growth <- goric(fit_growth, hypotheses = list(H1_growth = H1_growth), standardized = TRUE)

```

restriktor Message: The covariance matrix of the estimates was obtained via 'vcov()'. This is the biased

```
# summary(results_growth)
results_growth
```

restriktor (0.6-20): generalized order-restricted information criterion approximation:

Results:

	model	loglik	penalty	gorica	loglik.weights	penalty.weights	gorica.weights
1	H1_growth	3.977	1.500	-4.954	1.000	0.500	1.000
2	complement	-47.034	1.500	97.068	0.000	0.500	0.000

Conclusion:

The order-restricted hypothesis 'H1\_growth' has 14251239710235289453804.00 times more support than its

Conclusion: The order-restricted hypothesis 'H1\_growth' has many more (nl., 14251239710235289453804.00) times more support than its complement.

## Example 6: Mediation

In this example, we will look at the mediation lavaan example (cf. <https://www.lavaan.ugent.be/tutorial/mediation.html>).

Let us say we want to evaluate whether there is partial mediation or full mediation. It can be helpful to

specify what you believe is the minimum effect. Here, we assume that an (in)direct effect between -0.1 and 0.1 can be seen as no effect. Note: More examples can be found on <https://github.com/rebeccakuiper/Tutorials/tree/main/GORICA%20for%20mediation>.

```
# Create data
set.seed(1234)
X <- rnorm(100)
M <- 0.5 * X + rnorm(100)
Y <- 0.7 * M + rnorm(100)
Data <- data.frame(X = X, Y = Y, M = M)

# specify the model, using own labeling
model_med <- " # direct effect
                  Y ~ c*X
                  # mediator
                  M ~ a*X
                  Y ~ b*M
                  # indirect effect (a*b)
                  indirect := a*b
                  # direct effect (c)
                  direct := c
"
# Hypotheses
H_part <- "abs(indirect) > 0.1; abs(direct) > 0.1"
H_full <- "abs(indirect) > 0.1; -0.1 < direct < 0.1"
# and unconstrained as failsafe (default)

# fit the model
fit_med <- sem(model_med, data = Data)
# summary(fit_med, standardized = TRUE)

# Calculate GORICA values and weights Based on object
set.seed(100) # Needed for reproducibility & sensitivity check
results_med <- goric(fit_med, hypotheses = list(H_part = H_part, H_full = H_full),
                      standardized = TRUE)
```

restriktor Message: The covariance matrix of the estimates was obtained via 'vcov()'. This is the biased default.

```
# summary(results_med)
```

```
results_med
```

restriktor (0.6-20): generalized order-restricted information criterion approximation:

Results:

	model	loglik	penalty	gorica	loglik.weights	penalty.weights	gorica.weights	gorica.weight
1	H_part	8.382	3.922	-8.919	0.249	0.349	0.262	
2	H_full	8.795	3.500	-10.590	0.376	0.532	0.604	
3	unconstrained	8.795	5.000	-7.590	0.376	0.119	0.135	

Conclusion:

- The order-restricted hypothesis 'H\_full' is the best in the set, as it has the highest GORIC(A) weight
- Since 'H\_full' has a higher GORIC(A) weight than the unconstrained hypothesis, it is not considered weakly supported.
- \* 'H\_full' is 2.306 times more supported than 'H\_part'.

```

# # Based on extracted estimates # Extract standardized estimates of the
# defined parameters and their var-cov matrix label_names <- c('direct',
# 'indirect') est <-
# as.vector(standardizedSolution(fit_med)['est.std'])$est.std names(est) <-
# standardizedSolution(fit_med)$label est <- est[label_names] #est VCOV <-
# lavInspect(fit_med, 'vcov.def.std.all')[label_names, label_names] # VCOV
# matrix of parameters # GORICA set.seed(123) # for reproducibility & possibly
# sensitivity check results_med <- goric(est, VCOV = VCOV, hypotheses =
# list(H_part = H_part, H_full = H_full)) #summary(results_med) results_med

```

Conclusion: - The order-restricted hypothesis ‘H\_full’ is the best in the set, as it has the highest GORIC(A) weight. - Since ‘H\_full’ has a higher GORIC(A) weight than the unconstrained hypothesis, it is not considered weak. We can now inspect the relative support for ‘H\_full’ against the other order-restricted hypotheses: \* ‘H\_full’ is 2.306 times more supported than ‘H\_part’.