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

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Contents

Tutorial GORICA on SEM

This is a tutorial for using GORICA for Structural Equation Models. The GORICA is an information criterion that can be used to evaluate theory-driven hypotheses.

Below, you will find two examples for the use of the goric() function in the restriktor R package. The first example covers Confirmatory Factor Analysis, while the second example covers Multigroup Regression.
More details can be found in:
Kuiper, R. (2021). AIC-type Theory-Based Model Selection for Structural Equation Models. Structural Equation Modeling. https://doi.org/10.1080/10705511.2020.1836967
Here, I will use the restriktor package; in this article, the gorica package is used in the main text.
R scripts can be found on 'https://github.com/rebeccakuiper/Tutorials/tree/main/GORICA%20in%20SEM'.

Example 1: Confirmatory Factor Analysis

First, install and call the `lavaan` library to conduct CFA 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.

```
# 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)

# Additionally, load the gorica library to obtain the data set 'sesamesim' if
```

```r
# (!require('gorica')) install.packages('gorica')
library(gorica)
```

The second step involves specifying the confirmatory factor model. Because the goric() function cannot use the default labeling, make sure to give your own labels to estimates by including them in the `lavaan` model.

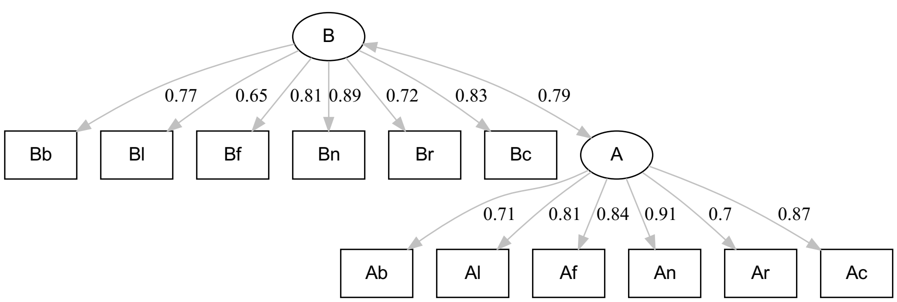
```r
model1 <- "
    A =~ A1*Ab + A2*Al + A3*Af + A4*An + A5*Ar + A6*Ac
    B =~ B1*Bb + B2*Bl + B3*Bf + B4*Bn + B5*Br + B6*Bc
"
```

Next, we can fit the confirmatory factor model using the `lavaan` sem() function.

```r
fit1 <- sem(model1, data = sesamesim, std.lv = TRUE)
```

We can also plot said model using `lavaanPlot`.

```r
# if (!require('lavaanPlot')) install.packages('lavaanPlot')
library(lavaanPlot)
lavaanPlot(model = fit1, node_options = list(shape = "box", fontname = "Helvetica"),
    edge_options = list(color = "grey"), coefs = T, stand = T, covs = T)
```



To call the goric() function, we need to formulate the hypothesis of interest. The GORICA selects the best hypothesis out of a given set. Here, since we only have a single hypothesis, we will compare it to its complement.

In this case, the hypothesis of interest consists of 12 order restrictions. Note that when specifying the hypothesis we repeat the labeling using when specifying the lavaan model object. Also note that restrictions are connected by the character `;` (or `,` or `&`).

```r
H1.1 <- "
A1 > .6; A2 > .6; A3 > .6; A4 > .6; A5 > .6; A6 > .6;
B1 > .6; B2 > .6; B3 > .6; B4 > .6; B5 > .6; B6 > .6
"
```

After specifying the hypothesis of interest, we can call the goric() function. Here we use GORICA by specifying `type = "gorica"` as an argument. Additionally, because we need standardized estimates to obtain a meaningful comparison, we specify `standardized = TRUE`. Finally, because we are interested in comparing the hypothesis of interest to its complement, we also specify `comparison = "complement"`.

```r
# Calculate GORICA values and weights for H1.1 and its complement ().
set.seed(100)

results1 <- goric(fit1, hypotheses = list(H1.1 = H1.1), comparison = "complement",
    type = "gorica", standardized = TRUE)

summary(results1)
```

```
restriktor (0.5-50): generalized order-restricted information criterion approximation:

Results:
        model  loglik  penalty   gorica  loglik.weights  penalty.weights  gorica.weights
1        H1.1  33.581    8.139  -50.884           0.669            0.977           0.988
2  complement  32.879   11.886  -41.985           0.331            0.023           0.012
---
The order-restricted hypothesis 'H1.1' has 85.56 times more support than its complement.


Ratio GORICA-weights:
            vs. H1.1  vs. complement
H1.1           1.000          85.561
complement     0.012           1.000
---

Ratio loglik-weights:
            vs. H1.1  vs. complement
H1.1           1.000           2.017
complement     0.496           1.000
---

Ratio penalty-weights:
            vs. H1.1  vs. complement
H1.1           1.000          42.417
complement     0.024           1.000
---

order-restricted hypotheses:

H1.1:
A1 > .6; A2 > .6; A3 > .6; A4 > .6; A5 > .6; A6 > .6;
B1 > .6; B2 > .6; B3 > .6; B4 > .6; B5 > .6; B6 > .6
```

From the comparison of hypotheses, it seems that the hypothesis H1.1 is better supported by the data than its complement.

The default way of calculating the penalty scores in goric() is slower when the number of parameters is large. Here, there are 12 parameters; so, we may want to use: `mix_weights = "boot"`. This means that the function will use bootstrapping in the calculation of the so-called level probabilities (LPs) needed in the penalties.

The results of course do not change, but the computation time may decrease.

```r
# if (!require('parallel')) install.packages('parallel') library(parallel)
# nrCPUcores <- detectCores(all.tests = FALSE, logical = TRUE) Increasing the
# number of cores does not always help, so for now: nrCPUcores <- 1
```

We repeat the same analysis with bootstrapping:

```r
set.seed(100)

results1_b <- goric(fit1, hypotheses = list(H1.1 = H1.1), comparison = "complement",
    type = "gorica", standardized = TRUE, mix_weights = "boot")

summary(results1_b)
```

```
restriktor (0.5-50): generalized order-restricted information criterion approximation:

Results:
        model  loglik  penalty   gorica  loglik.weights  penalty.weights  gorica.weights
1        H1.1  33.581    8.152  -50.857           0.669            0.977           0.988
2  complement  32.879   11.884  -41.990           0.331            0.023           0.012
---
The order-restricted hypothesis 'H1.1' has 84.26 times more support than its complement.


Ratio GORICA-weights:
            vs. H1.1  vs. complement
H1.1           1.000          84.260
complement     0.012           1.000
---

Ratio loglik-weights:
            vs. H1.1  vs. complement
H1.1           1.000           2.017
complement     0.496           1.000
---

Ratio penalty-weights:
            vs. H1.1  vs. complement
H1.1           1.000          41.773
complement     0.024           1.000
---

order-restricted hypotheses:

H1.1:
A1 > .6; A2 > .6; A3 > .6; A4 > .6; A5 > .6; A6 > .6;
B1 > .6; B2 > .6; B3 > .6; B4 > .6; B5 > .6; B6 > .6
```

As you can see from the summary of the results, we arrive at the same GORICA weights as earlier.

Example 2: Multiple Group Regression

As for Example 1, ensure that the required libraries are loaded in the R workspace.

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

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

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

# Additionally, load the gorica library to obtain the data set 'sesamesim' if
# (!require('gorica')) install.packages('gorica')
library(gorica)
```

Before specifying the regression model ensure that the variable *sex* in the *sesamesim* data set is a factor with the right labels.

```r
sesamesim$sex <- factor(sesamesim$sex, labels = c("boy", "girl"))
```

Then specify the model being tested, which in this case is a multiple group regression model. Again, because the goric() function cannot use the default labeling, make sure to include your own labels in the model.

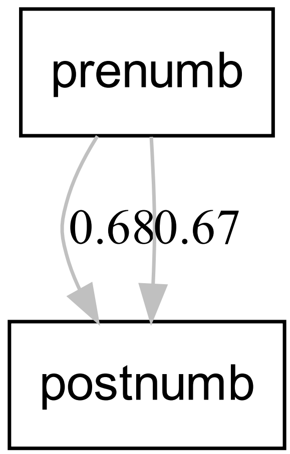
```r
model2 <- "
    postnumb ~ c(Pre_b, Pre_g)*prenumb
"
```

Fit the model using the `lavaan` sem() function and, if desired, use the lavaanPlot() function to obtain a graph of the model.

```r
fit2 <- sem(model2, data = sesamesim, std.lv = TRUE, group = "sex")

# if (!require('lavaanPlot')) install.packages('lavaanPlot') # install this
# package first (once)
library(lavaanPlot)

lavaanPlot(model = fit2, node_options = list(shape = "box", fontname = "Helvetica"),
    edge_options = list(color = "grey"), coefs = T, stand = T, covs = T)
```



Proceed to formulate the hypothesis of interest using the same labels as in the model definition:

```
H2.1 <- "Pre_b < Pre_g"
```

Call the goric() function to evaluate the hypothesis. Again, we request GORICA weights using the argument `type = "gorica"` and, because we have a single hypothesis, we test it against its complement using `comparison = "complement"`. And similarly, because we need standardized estimates for a meaningful comparison, we use `standardized = TRUE`.

```
set.seed(100)

results2 <- goric(fit2, hypotheses = list(H2.1 = H2.1), comparison = "complement",
    type = "gorica", standardized = TRUE)

summary(results2)
```

```
restriktor (0.5-50): generalized order-restricted information criterion approximation:

Results:
        model  loglik  penalty  gorica  loglik.weights  penalty.weights  gorica.weights
1        H2.1   4.420    1.500  -5.841           0.498            0.500           0.498
2  complement   4.428    1.500  -5.856           0.502            0.500           0.502
---
The order-restricted hypothesis 'H2.1' has 0.99 times more support than its complement.


Ratio GORICA-weights:
            vs. H2.1  vs. complement
H2.1           1.000           0.992
complement     1.008           1.000
---
```

```
Ratio loglik-weights:
            vs. H2.1  vs. complement
H2.1           1.000           0.992
complement     1.008           1.000
---

Ratio penalty-weights:
            vs. H2.1  vs. complement
H2.1               1               1
complement         1               1
---

order-restricted hypotheses:

H2.1:
Pre_b < Pre_g
```

The output table shows that the hypothesis of interest and its complement are equally likely, since both have a weight of approximately .50. In other words, both are equally supported.

Since the hypotheses do not overlap and are equally complex (i.e., they have the same penalty value), this implies that their boundary is the preferred hypothesis; that is, H0: Pre_b = Pre_g.

Thus, there is support for the boundary of the hypothesis of interest and its complement, indicating that the relationship between postnumb and prenumb is equally high for girls and boys.