

Informative hypotheses evaluation

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Table of Contents

Example Null hypothesis (H_0) vs Informative hypothesis (H_m)

Generalized Order-Restricted Information Criterion (GORIC)

GORIC weights

Examples with R code

Failsafe/Safeguard hypotheses: Unconstrained & Complement

GORICA

GORIC(A) in JASP

End & Extra

ANOVA Example: Comparisons of 3 Means

Palmer and Gough (2007) examined the difference in the attribution of importance of defective education as an explanation for criminal behavior between three types of “offenders”:

(1) non-offenders, (2) property offenders, and (3) person offenders.

ANOVA

$$y_j = \mu_1 d_{1j} + \mu_2 d_{2j} + \mu_3 d_{3j} + \epsilon_j,$$

where μ_i ($i = 1, 2, 3$) is the mean in group i ,
 d_{ij} is a dummy variable denoting group membership,
 ϵ_j is an error term and $\epsilon_j \sim N(0, \sigma^2)$.

$(n_i = 20, 20, 31)$

Hypotheses of interest

Palmer and Gough (2007) expect that

- non-offenders (1) attribute more importance to defective education for explaining crime than the other two offenders;
i.e., $\mu_1 > \mu_2$ and $\mu_1 > \mu_3$,
- property offenders (2) attribute more importance to defective education than person offenders (3);
i.e., $\mu_2 > \mu_3$.

$$H_1 : \quad \mu_1 > \mu_2 > \mu_3.$$

Note that ‘<’ denotes “smaller than” and ‘>’ denotes “larger than”.

Conclusions w.r.t. hypothesis of interest $H_1 : \mu_1 > \mu_2 > \mu_3$

With post-hoc test (e.g., Bonferroni) and on basis of the sample means, we could say a bit more.

But, what if

- $\mu_1 \neq \mu_2, \mu_1 \neq \mu_3, \mu_2 = \mu_3,$
- $\bar{y}_1 > \bar{y}_2,$

which implies $\mu_1 > \mu_2 = \mu_3$.

But also not interested in this.

Furthermore, inconsistent results are possible (like in this data example):

$\mu_1 \neq \mu_3, \mu_1 = \mu_2,$ and $\mu_2 = \mu_3,$

which is logically impossible, since latter two imply $\mu_1 = \mu_3$.

Using planned contrasts would overcome this, but still = restrictions then.

NHST on Palmer & Gough (2007) Data

```
PandG_data <- read.table("Data_PalmerAndGough.txt",  
                          header=TRUE)  
PandG_data$group <- factor(PandG_data$group)  
pairwise.t.test(PandG_data$Importance, PandG_data$group,  
                p.adj = 'bonferroni')  
  
##  
## Pairwise comparisons using t tests with pooled SD  
##  
## data: PandG_data$Importance and PandG_data$group  
##  
##      1      2  
## 2 0.191 -  
## 3 0.011 1.000  
##  
## P value adjustment method: bonferroni
```


Confirmatory methods

Most researchers are able to specify “order-restricted” / “informative” / “theory-based” hypotheses, like $H_1 : \mu_1 > \mu_2 > \mu_3$.
Use prior knowledge and/or expertise in hypothesis.

Methods to evaluate theory-based hypotheses

- Hypothesis testing: F_{bar} (\bar{F}) test
(renders p-value and can test only one theory-based hypothesis)
- Confirmatory model selection using information criteria:
GORIC and GORICA
- (Confirmatory) Bayesian model selection (BMS)

Note: ‘model’ refers to hypothesis.

GORIC on Palmer & Gough (2007) Data

$$H_0 : \mu_1 = \mu_2 = \mu_3,$$

$$H_1 : \mu_1 > \mu_2 > \mu_3,$$

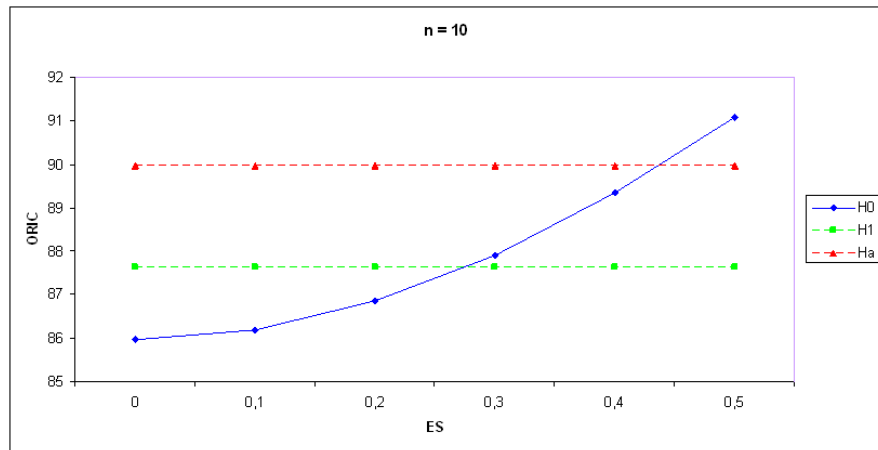
$$H_u : \mu_1, \mu_2, \mu_3.$$

GORIC

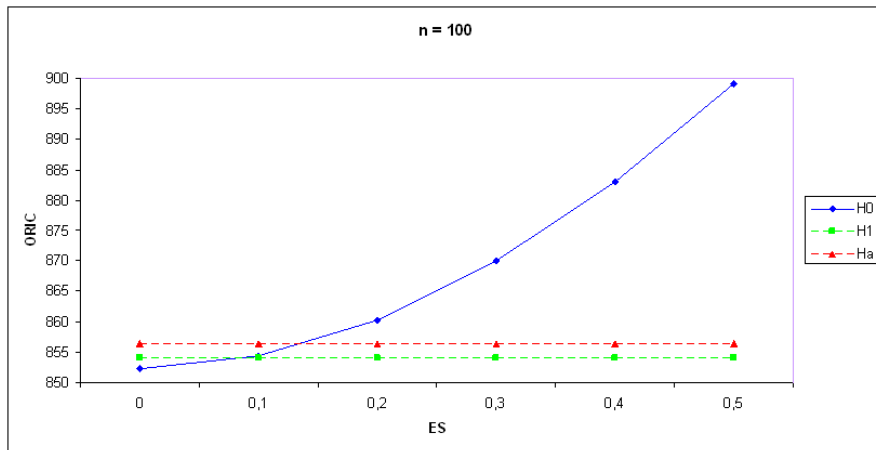
Model	Fit	Complexity	GORIC	GORIC weights
H_0	-196.36	2.00	396.71	0.02
H_1	-191.89	2.81	389.41	0.75
H_u	-191.89	4.00	391.79	0.23

Confirmatory methods have more “power” than their exploratory counterparts (cf. one-sided testing).

Confirmation more power: 1 data set. GORIC values for 3 groups, effect size ES , and $n = 10$ observations per group



Confirmation more power: 1 data set. GORIC values for 3 groups, effect size ES , and $n = 100$ observations per group



Confirmatory methods - some of my references

- Kuiper, R. M., and Hoijtink, H. (2010). Comparisons of Means Using Exploratory and Confirmatory Approaches. *Psychological Methods*, 15(1), 69–86.
- Kuiper, R. M., Klugkist, I., and Hoijtink, H. (2010). A Fortran 90 Program for Confirmatory Analysis of Variance. *Journal of Statistical Software*, 34(8), 1–31.
- Kuiper, R.M., Hoijtink, H. and Silvapulle, M.J. (2011). An Akaike type information criterion for model selection under inequality constraints. *Biometrika*, 98, 495-501. (GORIC)
- Kuiper, R.M., Nederhof, T., and Klugkist, I. (2015). Properties of hypothesis testing techniques and (Bayesian) model selection for exploration-based and theory-based (order-restricted) hypotheses. *British Journal of Mathematical and Statistical Psychology*, 68(2), 220 – 245.
- Altınışık, Y., Van Lissa, C. J., Hoijtink, H., Oldehinkel, A. J., and Kuiper, R. M. (2021). Evaluation of inequality constrained hypotheses using a generalization of the AIC. *Psychological Methods*, 26(5), 599–621.
<https://doi.org/10.1037/met0000406> (GORICA)

Table of Contents

Example Null hypothesis (H_0) vs Informative hypothesis (H_m)

Generalized Order-Restricted Information Criterion (GORIC)

GORIC weights

Examples with R code

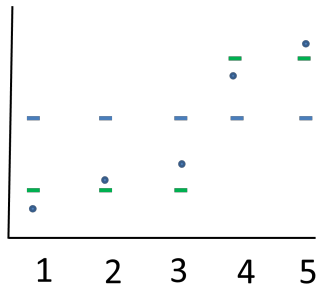
Failsafe/Safeguard hypotheses: Unconstrained & Complement

GORICA

GORIC(A) in JASP

End & Extra

Intermezzo: Balance Fit and Complexity



$$\mu_1 = \mu_2 = \mu_3 = \mu_{\text{low}}$$

$$\mu_4 = \mu_5 = \mu_{\text{high}}$$

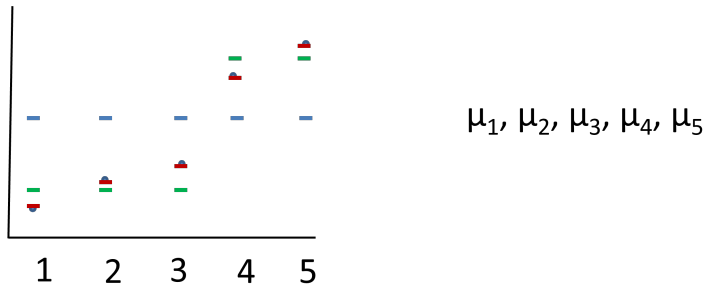
parameters:

2 mean parameters (i.e., μ_{low} and μ_{high})

Fit:

Better than with one parameter, even good fit.

Intermezzo: Balance Fit and Complexity



parameters: 5 mean parameter (complex)
Fit: Better than with two parameters, even best possible fit.

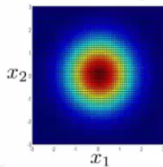
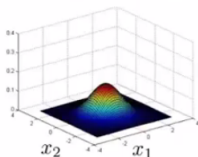
Thus: Best fit (= highest likelihood), but also most complex (= highest penalty).

In this example: Two means may be best trade-off between fit & complexity.

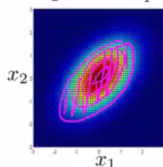
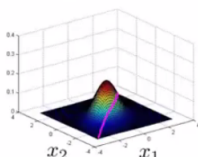
Intermezzo: Contour plot ctd.

Multivariate Gaussian (Normal) examples

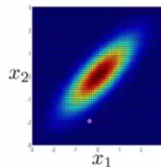
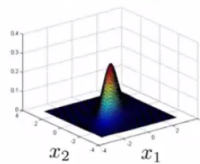
$$\mu = \begin{bmatrix} 0 \\ 0 \end{bmatrix} \Sigma = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$$



$$\mu = \begin{bmatrix} 0 \\ 0 \end{bmatrix} \Sigma = \begin{bmatrix} 1 & 0.5 \\ 0.5 & 1 \end{bmatrix}$$



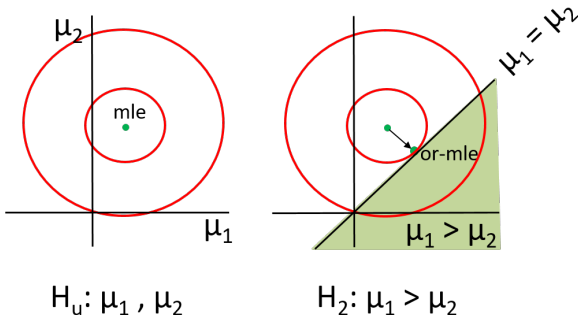
$$\mu = \begin{bmatrix} 0 \\ 0 \end{bmatrix} \Sigma = \begin{bmatrix} 1 & 0.8 \\ 0.8 & 1 \end{bmatrix}$$



Andreas

Idea fit

order-restricted maximum likelihood (or-ml)



mle not in H_2 : Find highest likelihood in allowable (= green) space.
The resulting estimated mean $\hat{\mu} = (\hat{\mu}_1, \hat{\mu}_2)$ is referred to as or-ml.

GORIC on Palmer & Gough (2007) Data

$$H_0 : \mu_1 = \mu_2 = \mu_3,$$

$$H_1 : \mu_1 > \mu_2 > \mu_3,$$

$$H_2 : \mu_1 > \mu_2 < \mu_3,$$

$$H_3 : \mu_1 < \mu_2 < \mu_3,$$

$$H_u : \mu_1, \mu_2, \mu_3.$$

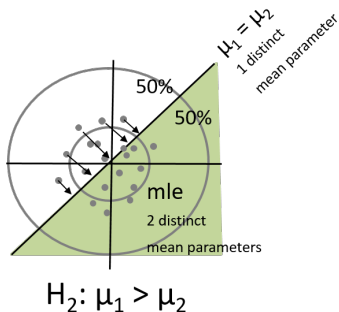
```
## group1 group2 group3
## 11.95  9.75  8.77
```

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_0	-196.36	2.00	396.71	0.01
H_1	-191.89	2.81	389.41	0.56
H_2	-192.34	3.19	391.05	0.25
H_3	-196.36	2.81	398.34	0.01
H_u	-191.89	4.00	391.79	0.17

Idea complexity

penalty (PT)



Note: sampling from null distribution: $H_0 : \mu_1 = \mu_2 = 0$.

complexity $H_2 = PT_2 = 1 + 0.5 \times 1 + 0.5 \times 2 = 2.5$.

PT = number of expected distinct parameters (under H_0).

Idea complexity

loose interpretation

$$H_1 : \mu_1 > \mu_2 > \mu_3$$

contains 1 ordering of three means, 1-2-3.

Thus, not complex (i.e., parsimonious).

$$H_2 : \mu_1 > \mu_2, \mu_3$$

contains 2 orderings of three means: 1-2-3 and 1-3-2.

Thus, more complex (less parsimonious).

$$H_u : \mu_1, \mu_2, \mu_3$$

contains all six possible orderings of three means.

Thus, is most complex one (least parsimonious).

GORIC on Palmer & Gough (2007) Data

$$H_0 : \mu_1 = \mu_2 = \mu_3,$$

$$H_1 : \mu_1 > \mu_2 > \mu_3,$$

$$H_2 : \mu_1 > \mu_2 < \mu_3,$$

$$H_3 : \mu_1 < \mu_2 < \mu_3,$$

$$H_u : \mu_1, \mu_2, \mu_3.$$

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_0	-196.36	2.00	396.71	0.01
H_1	-191.89	2.81	389.41	0.56
H_2	-192.34	3.19	391.05	0.25
H_3	-196.36	2.81	398.34	0.01
H_u	-191.89	4.00	391.79	0.17

GORIC: Lowest value is best

GORIC is like AIC expected distance from the truth (KL-distance). Hence, smallest value is best.

$$H_u : \quad \mu_1, \mu_2, \mu_3.$$

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_0	-196.36	2.00	396.71	0.02
H_1	-191.89	2.81	389.41	0.75
H_u	-191.89	4.00	391.79	0.23

Hands-on/Demo (1a): GORIC

Start Rstudio and let's practice.

- Go to <https://github.com/rebeccakuiper/Tutorials>:
 1. Click on green button called Code.
 2. Download zip (last option in list).
 3. Unzip it on your machine (that folder is now your working directory).
- Start Rstudio. Optional: make project.
- Open 'Tutorial_GORIC_restriktor_ANOVA.html', 'PalmerAndGough_and_Lucas.R', and 'Hands-on_1_GORIC_Unc_ANOVA_restriktor.R' (in 'Hands-on files').
- Install packages and load them.
- Read and inspect data. Use Data_PalmerAndGough.txt (in 'data').
- Run model (`lm()`).
- Specify hypotheses (make up your own).
Note: Use names used in the model.
- Run `goric()`.
- Inspect and interpret output.
Note: 'GORIC weights' will be explained later on.

Table of Contents

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Interpretation: GORIC weights

GORIC values

GORIC values cannot be interpreted, only compared:
Smallest is best.

GORIC weights (w_m) and ratios ($w_m/w_{m'}$)

w_m quantifies how much H_m is more supported than others in set.
 $w_m/w_{m'}$ quantifies relative support of H_m vs $H_{m'}$.
 The bigger, the better.

Reference:

Kuiper, R.M., Hoijtink, H. and Silvapulle, M.J. (2012). Generalization of the order restricted information criterion for multivariate normal linear models. *Journal of Statistical Planning and Inference*, 142, 2454-2463.

Illustration of the GORIC weights (w_m)

$$H_0 : \mu_1 = \mu_2 = \mu_3,$$

$$H_1: \mu_1 > \mu_2 > \mu_3,$$

$$H_u : \quad \mu_1, \mu_2, \mu_3.$$

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_0	-196.36	2.00	396.71	0.02
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Table of Contents

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R code: Data and fit object

Palmer & Gough

```
# Data
PandG_data <- read.table("Data_PalmerAndGough.txt",
                          header=TRUE)
PandG_data$group <- factor(PandG_data$group)

# fit object (needed as input for gorica function)
fit.PandG <- lm(Importance ~ group - 1, data = PandG_data)
```

R code: Hypotheses

Palmer & Gough

$$H_0 : \mu_1 = \mu_2 = \mu_3$$

$$H_1 : \mu_1 = \mu_2 > \mu_3$$

$$H_u : \quad \mu_1, \mu_2, \mu_3$$

Hypotheses

```
H0 <- 'group1 = group2 = group3'
```

```
H1 <- 'group1 > group2 > group3'
```

R code: GORIC

Palmer & Gough

$$H_0 : \mu_1 = \mu_2 = \mu_3$$

$$H_1: \mu_1 = \mu_2 > \mu_3$$

$$H_u : \quad \mu_1, \mu_2, \mu_3$$

```
# GORIC (using goric function in restriktor package)
library(restriktor)
set.seed(123) # Set seed value
goric.PandG <- goric(fit.PandG,
                     hypotheses = list(H0, H1))
```


Another illustration: one-way ANOVA

Lucas: 5 groups

Lucas (2003) investigated difference between female and male leadership w.r.t. influence of the leader.

Five experimental groups:

1. a randomly selected male leader
2. a randomly selected female leader
3. male leader selected via task
4. female leader selected via task
5. female leader selected via task + institutionalized female leadership via movie

(Two informative) hypotheses of interest

$$H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5 \text{ (include only when of interest),}$$
$$H_1 : \mu_5 = \mu_3 > \{\mu_1, \mu_4\} > \mu_2,$$
$$H_2 : \mu_3 > \mu_1 > \mu_4 = \mu_5 > \mu_2,$$
$$H_u : \mu_1, \mu_2, \mu_3, \mu_4, \mu_5 \text{ (included as failsafe).}$$

Descriptive statistics of Lucas' Data

Group	Mean Influence	SD	n
1 (male, random)	2.33	1.86	30
2 (female, random)	1.33	1.15	30
3 (male, selected)	3.20	1.79	30
4 (female, selected)	2.23	1.45	30
5 (female, selected+)	3.23	1.50	30

R code: Data and fit object

Lucas

```
# Data
```

```
lucas_data <- read.table("Data_Lucas.txt", header=TRUE)
```

```
lucas_data$group <- factor(lucas_data$group)
```

```
# fit object (needed as input for goric function)
```

```
fit.lucas <- lm(Influence ~ group - 1, data = lucas_data)
```

R code: Hypotheses

Lucas

$$H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5,$$

$$H_1 : \mu_5 = \mu_3 > \{\mu_1, \mu_4\} > \mu_2$$

$$H_2 : \mu_3 > \mu_1 > \mu_4 = \mu_5 > \mu_2,$$

$$H_u : \mu_1, \mu_2, \mu_3, \mu_4, \mu_5.$$

Hypotheses

```
H0 <- 'group1 = group2 = group3 = group4 = group5'
```

```
H1 <- 'group5 = group3 > group1 > group2;  
      group3 > group4 > group2'
```

```
H2 <- 'group3 > group1 > group4 = group5 > group2'
```

R code: GORIC

Lucas

$$H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5,$$

$$H_1 : \mu_5 = \mu_3 > \{\mu_1, \mu_4\} > \mu_2$$

$$H_2 : \mu_3 > \mu_1 > \mu_4 = \mu_5 > \mu_2,$$

$$H_u : \mu_1, \mu_2, \mu_3, \mu_4, \mu_5.$$

```
# GORIC (using goric function in restriktor package)
library(restriktor)
set.seed(123) # Set seed value
goric.lucas <- goric(fit.lucas,
                     hypotheses = list(H0, H1, H2))
```


GORIC on Lucas' Data: GORIC weights (w_m)

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_0	-292.27	2.00	588.54	0.00
H_1	-278.05	3.20	562.49	0.92
H_2	-281.76	3.14	569.79	0.02
H_u	-278.05	6.00	568.10	0.06

H_1 is $.921/.024 \approx 38.6$ (∞) times more supported than H_2 (H_0 , resp.). Thus, there is quite some evidence that H_1 is the best of this set.

Note:

H_1 is $.921/.056 \approx 16.5 > 1$ times more supported than H_ν .

Hence, H_1 not weak and thus comparable to the other informative hypotheses (as explained next).

Hands-on/Demo (1b): GORIC weights

Start Rstudio and let's practice.

- If needed: Start Rstudio again (optional: make project) and then also load packages again.
- Read and inspect data.
Use Data_Lucas.txt and/or Data_PalmerAndGough.txt.
- Run model (`lm()`).
- Specify hypotheses (make up your own).
Note: Use names used in the model.
- Run `goric()`.
- Inspect and interpret output: Focus on GORIC weights.

Include “unconstrained” hypothesis

If set of hypotheses does not contain a reasonable/good one:
Select the best of set of weak hypotheses.
E.g.: $w_0 = .2$ and $w_1 = .8$.

Prevent choosing a weak hypothesis

Include unconstrained hypothesis H_u (or H_a):

$$\begin{aligned} H_0 : & \quad \mu_1 = \mu_2 = \mu_3, \\ H_1 : & \quad \mu_1 > \mu_2 > \mu_3, \\ H_u : & \quad \mu_1, \mu_2, \mu_3, \\ & \quad (\text{i.e., no restrictions}). \end{aligned}$$

H_u highest fit but also most complex, thus failsafe/safeguard.

E.g.: $w_0 = .02$, $w_1 = .08$, and $w_\mu = .90$.

What if another hypothesis is true?

What if another informative hypothesis is true?

The failsafe hypothesis will be preferred over the informative hypotheses in the set, if the sample size is large enough.

E.g.: $w_0 = .02$, $w_1 = .08$, and $w_\mu = .90$.

Use of H_u : Palmer & Gough (2007) Data

$$H_0 : \mu_1 = \mu_2 = \mu_3,$$

$$H_1 : \mu_1 > \mu_2 > \mu_3,$$

$$H_u : \mu_1, \mu_2, \mu_3.$$

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_0	-196.36	2.00	396.71	0.02
H_1	-191.89	2.81	389.41	0.75
H_u	-191.89	4.00	391.79	0.23

If at least one informative hypothesis not weak ($w_1 > w_u$ or $w_1/w_u > 1$), then compare informative hypotheses.

Hence: H_u is only a failsafe not another hypothesis of interest.

H_1 vs H_u : Palmer & Gough (2007) Data

What if only one informative hypothesis:

$$H_1 : \mu_1 > \mu_2 > \mu_3,$$

$$H_u : \mu_1, \mu_2, \mu_3.$$

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_1	-191.89	2.81	389.41	.77
H_u	-191.89	4.00	391.79	.23

H_1 is $.77/.23 \approx 3.3$ times more supported than H_u .

BUT: H_u includes H_1 .

So, support for H_u contains support for H_1 .

H_1 vs H_u : Palmer & Gough (2007) Data

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_1	-191.89	2.81	389.41	0.77
H_u	-191.89	4.00	391.79	0.23

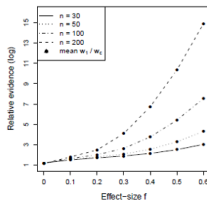
Unconstrained is always true, so will always receive support.
Support for H_u contains support for H_1 (if any).

Now: Fit H_1 and H_u the same;
thus, GORIC weights are based on only complexity.

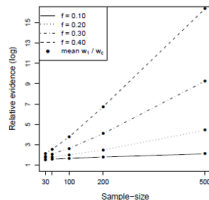
Consequently, $.77/.23 \approx 3.3$ is an upper bound.

Alternative failsafe: Complement of H_m using GORIC

vs complement

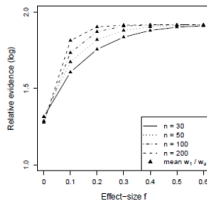


(a)

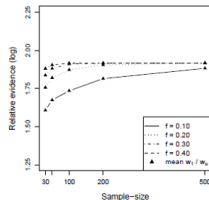


(b)

vs unconstrained



(c)



(d)

R code: complement

Palmer & Gough

$$H_1 : \mu_1 > \mu_2 > \mu_3,$$

$$H_c : \text{not } H_1.$$

GORIC

```
H1 <- 'group1 > group2 > group3'  
# GORIC (using goric function in restriktor package)  
library(restriktor)  
set.seed(123) # Set seed value  
goric.lucas_C <- goric(fit.PandG,  
                        hypotheses = list(H1),  
                        comparison = 'complement')
```

Palmer & Gough (2007): H_1 vs H_c

$$H_c : \quad \text{not } H_1.$$

GORIC

Model	Fit	Complexity	GORICA	GORICA weights
H1	-191.89	2.81	389.41	0.79
complement	-192.34	3.69	392.05	0.21

H_1 is $.79/.21 \approx 3.8$ times more supported than its complement, that is, any other hypothesis.

Hands-on/Demo (2): GORIC - H_m vs complement

Start Rstudio and let's practice.

- If needed: Start Rstudio again (optional: make project) and then also load packages again.
- Optional: Open 'Tutorial_GORIC_restriktor_ANOVA.html', 'PalmerAndGough_and_Lucas.R', and **'Hands-on_2_GORIC_Compl_ANOVA_restriktor.R'**.
- Read and inspect data.
Use Data_Lucas.txt and/or Data_PalmerAndGough.txt.
- Run model (lm()).
- Specify hypotheses (make up your own). E.g., for Lucas:

$$H_1 : \mu_5 = \mu_3 > \{\mu_1, \mu_4\} > \mu_2$$

Note: Use names used in the model.

- Run goric(); now, add:
`comparison = "complement"`

- Inspect and interpret output.

Table of Contents

Example Null hypothesis (H_0) vs Informative hypothesis (H_m)

Generalized Order-Restricted Information Criterion (GORIC)

GORIC weights

Examples with R code

Failsafe/Safeguard hypotheses: Unconstrained & Complement

GORICA

GORIC(A) in JASP

End & Extra

GORICA

Similarities with GORIC

- Form: $GORICA_m = -2 \text{ fit} + 2 \text{ complexity}$.
- Broad type of restrictions.

Differences compared to GORIC

- Uses asymptotic expression of the likelihood (is a normal):
can therefore be easily applied to all types of statistical models.
Disadvantage: might work less well in case of small samples.
- Does not need data set; mle's and their covariance matrix suffice.
- Can leave out nuisance parameters (i.e., not part of hypotheses).

Note

In case of normal linear models and/or not too small samples:
GORICA weights = GORIC weights.

R code: GORICA

Palmer & Gough

$$H_1 : \mu_1 > \mu_2 > \mu_3,$$

$$H_c : \text{not } H_1.$$

GORICA: type = "gorica"

```

H1 <- 'group1 > group2 > group3'
# GORICA (using goric function in restriktor package)
library(restriktor)
set.seed(123) # Set seed value
gorica.lucas_C <- goric(fit.PandG,
                        hypotheses = list(H1),
                        comparison = 'complement',
                        type = "gorica")
    
```

GORICA on Palmer & Gough (2007) Data

$$\begin{aligned} H_1 : & \quad \mu_1 > \mu_2 > \mu_3, \\ H_c : & \quad \text{not } H_1. \end{aligned}$$

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H1	-1.96	1.81	7.55	0.79
complement	-2.39	2.69	10.15	0.21

H_1 is $.79/.21 \approx 3.8$ times more supported than its complement, that is, any other hypothesis.

Note: GORIC weights are the same.

Hands-on/Demo (3): GORICA - H_m vs complement

Start Rstudio and let's practice.

- If needed: Start Rstudio again (optional: make project) and then also load packages again.
- Optional: Open 'Tutorial_GORIC_restriktor_ANOVA.html', 'PalmerAndGough_and_Lucas.R', and **'Hands-on_3_GORICA_UncAndCompl_ANOVA_restriktor.R'**.
- Read and inspect data.
Use Data_Lucas.txt and/or Data_PalmerAndGough.txt.
- Run model (lm()).
- Specify hypotheses (make up your own). E.g., for Lucas:

$$H_1 : \quad \mu_5 = \mu_3 > \{\mu_1, \mu_4\} > \mu_2$$

Note: Use names used in the model (or overwrite those).

- Run goric(); now, add:
`type = "gorica"`
- Inspect and interpret output.

Table of Contents

Example Null hypothesis (H_0) vs Informative hypothesis (H_m)

Generalized Order-Restricted Information Criterion (GORIC)

GORIC weights

Examples with R code

Failsafe/Safeguard hypotheses: Unconstrained & Complement

GORICA

GORIC(A) in JASP

End & Extra

GORIC in JASP: Palmer & Gough

Descriptives

T-Tests

ANOVA

Mixed Models

Regression

Frequencies

Factor

Bain

SEM

R (Beta)

Order Restricted Hypotheses

Enter each restriction of one hypothesis on a new line, e.g.,
factorLow == factorMid
factorMid < factorHigh
where 'factor' is the factor (or covariate) name and 'Low'/'Mid'/'High' are the factor level names.
Click on the 'plus' icon to add more hypotheses.
Click the information icon for more examples.

Syntax settings

Set for all models

☐ Include intercept
☐ Show available coefficients

☐ Model summary
☐ Marginal means
☐ Informed hypothesis tests

Model 1

+

group1 > group2 > group3

Ctrl + Enter to apply. Click on the blue button above for help on the restriction syntax

☐ Summary for Model 1
☐ Marginal means for Model 1
☐ Informed hypothesis tests for Model 1

Results

ANOVA

ANOVA - Importance

Cases	Sum of Squares	df	Mean Square	F	p
group	123.960	2	61.980	4.554	0.014
Residuals	925.418	68	13.609		

Note. Type III Sum of Squares

Order Restricted Hypotheses

Model Comparison

Model Comparison Table

Model	Log-likelihood	Penalty	GORIC	Weight	Weights ratio
Model 1	-191.893	2.814	389.415	0.789	3.731
Complement	-192.338	3.686	392.048	0.211	1.000

Note. Weights ratios indicate the relative weight for each model against the "complement" model. GORIC = Generalized Order-Restricted Information Criterion (Kuiper, Hoijtink, & Silvapulle, 2011).

70/97

GORIC in JASP: Lucas

Descriptives

T-Tests

ANOVA

Mixed Models

Regression

Frequencies

Factor

Bain

SEM

R (Beta)

Order Restricted Hypotheses

Results

Enter each restriction of one hypothesis on a new line, e.g.,
factorLow == factorMid
factorMid < factorHigh
where 'factor' is the factor (or covariate) name and 'Low'/'Mid'/'High' are the factor level names.
Click on the 'plus' icon to add more hypotheses.
Click the information icon for more examples.

Syntax settings

Set for all models

Include intercept

Show available coefficients

Model summary

Marginal means

Informed hypothesis tests

Model 1

group5 = group3 > group1 > group2
group3 > group4 > group2

Ctrl + Enter to apply. Click on the blue button above for help on the restriction syntax

Summary for Model 1

Marginal means for Model 1

Informed hypothesis tests for Model 1

ANOVA - Influence

Cases	Sum of Squares	df	Mean Square	F	p
group	74.700	4	18.675	7.567	< .001
Residuals	357.835	145	2.468		

Note. Type III Sum of Squares

Order Restricted Hypotheses

Model Comparison

Model	Log-likelihood	Penalty	GORIC	Weight	Weights ratio
Model 1	-278.051	3.197	562.495	0.930	13.357
Complement	-278.048	5.791	567.680	0.070	1.000

Note. Weights ratios indicate the relative weight for each model against the "complement" model. GORIC = Generalized Order-Restricted Information Criterion (Kuiper, Hoijtink, & Silvapulle, 2011).

72/97

GORIC and GORICA in JASP

	GORIC R	GORIC JASP	GORICA R	GORICA JASP
ANOVA	✓	✓	✓	
RM-ANOVA			✓	✓
Regression	✓	Not yet	✓	
SEM		Future?	✓	Future?
Other model		Future?	✓	Future?

GORIC and GORICA in JASP

GORIC or GORICA in the following statistical models (as part of that model)

GORIC

- Order Restricted Hypotheses
- Post Hoc Tests
- Descriptives Plots
- Raincloud Plots
- Marginal Means

ANOVA

Cases	Sum of Squares	df	Mean Square	F	p
Note: Type III Sum of Squares					

GORIC

- Order Restricted Hypotheses
- Post Hoc Tests
- Descriptives Plots
- Raincloud Plots
- Marginal Means

ANCOVA

Cases	Sum of Squares	df	Mean Square	F	p
Note: Type III Sum of Squares					

GORICA

- Assumption Checks
- Contrasts
- Order Restricted Hypotheses
- Post Hoc Tests
- Descriptives Plots
- Raincloud Plots
- Marginal Means
- Simple Main Effects

Repeated Measures ANOVA

Cases	Sum of Squares	df	Mean Square	F	p
Note: Type III Sum of Squares					

ANCOVA

- Dependent Variable
- Fixed Factors
- Covariates
- WLS Weights

Table of Contents

Example Null hypothesis (H_0) vs Informative hypothesis (H_m)

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GORIC weights

Examples with R code

Failsafe/Safeguard hypotheses: Unconstrained & Complement

GORICA

GORIC(A) in JASP

End & Extra

The End

Thanks for listening!

Are there any questions?

Websites

<https://github.com/rebeccakuiper/Tutorials>
www.uu.nl/staff/RMKuiper/Software
www.uu.nl/staff/RMKuiper/Websites%20%2F%20Shiny%20apps%20informative-hypotheses.sites.uu.nl/software/goric/

E-mail

r.m.kuiper@uu.nl

What's next

Depending on time and wishes:

- Some notes
- Demo in R
- Demo in JASP
- Evidence synthesis / Support aggregation

We end with:

- Lab
- Discussion

Note on using complement

Complement not always higher weight

In case H_m is almost true, but not true:

1. H_m does not have maximum fit (but much lower penalty).
2. Support for H_m is less when evaluating it against its complement (than H_μ).

This is of course a good thing, since H_m is not true.

Explanation:

Penalty of H_c is smaller than that of H_u .

Against H_μ , you choose H_m 'sooner' because of low penalty for H_m .

Note on hypotheses

1. Only include hypotheses with sound theoretical and/or empirical basis.
Often a null hypothesis is not of interest.
2. Keep the number of hypotheses included as small as possible.
3. This is a subjective endeavor, aim for inter-peer / inter-subjective agreement.

Note on possibilities multiple studies

- Update GORIC(A) and GORIC(A) weights:
More data collected, (re-)calculate the GORIC(A) weights.
- Update hypotheses:
First data set (or a part of it) generates one or more hypotheses.
Other data set (or part) used to determine evidence / support.
See this html tutorial and/or this R script tutorial.
- Aggregate evidence for hypotheses:
Aggregate the support for theories (diverse designs allowed).
Bear in mind: Meta-analysis aggregates parameter estimates or effect sizes which need to be comparable (often same designs required).
See this html tutorial and/or this R script tutorial.

Note on BF as an IC

The fit in GORICA refers to the maximum log likelihood. The fit in BF refers to the maximum likelihood.

Notably, BF can be written as an IC (and vice versa):

$$\begin{aligned} -2 \log BF_{1u} &= -2 \log \frac{f_1}{c_1} \\ &= -2 \log f_1 + 2 \log c_1 \\ &= -2 \log \text{fit } H_1 + 2 \log \text{complexity } H_1. \end{aligned}$$

Note: complexity value in BF depends on prior.

Note on GORIC weights vs BF and PMPs

$w_m/w_{m'} = \text{relative weight} \sim \text{Bayes factor } (BF_{mm'}).$

$w_m \sim \text{posterior model probability (PMP)}.$

1 - w_m = conditional error probability.

Note: w_m depends on set of hypotheses.

Note on conditional error probability

using PMPS and GORIC(A) weights

H_m	weights
H_1 : Sex Match	.04
H_2 : Gender Role Match	.81
H_3 : Sex Mismatch	.01
H_4 : Gender Role Mismatch	.00
H_u :	.14

The conditional error probability for preferred hypotheses H_2 is $1 - .81 = .19$.

Note on conditional error probability

using PMPS and GORIC(A) weights

What if we compare many hypotheses?

H_m	weights
H_1 : Sex Match	.013
H_2 : Gender Role Match	.270
H_3 : Sex Mismatch	.003
H_4 : Gender Role Mismatch	.000
H_5 : Lets try this one too	.180
...	...
H_{12} : Don't miss something	.040
H_u :	.047

The conditional error probability for H_2 becomes $1 - .27 = .77$ (was .19).

namely, included additional hypotheses may obtain some support.
Hence, the conditional error probabilities becomes larger.

Note on conditional error probability

using PMPS and GORIC(A) weights

Hypotheses that overlap can also share support (like H_u does).

My advise:

Only use error probabilities if one hypothesis versus its complement.

(Or when you are sure that there is no overlap in hypotheses)

H_m	weights
H_2 : Gender Role Match	.82
H_c : complement H_2	.18

Extra material

- **Logistic Regression Modeling**
 - Article: <https://doi.org/10.1037/met0000406>
- **GORICA on SEM**
 - Article: <https://www.tandfonline.com/doi/full/10.1080/10705511.2020.1836967>.
 - R scripts: https://github.com/rebeccakuiper/GORICA_in_SEM.
- **GORICA on cross-lagged panel model (CLPM)** – Article: <https://doi.org/10.1111/bjep.12455>.
 - R scripts: https://github.com/rebeccakuiper/GORICA_in_SEM.
- **GORICA on Random-Intercept CLPM (RI-CLPM)**
 - Article: Chuenjai Sukpan and Rebecca M. Kuiper (submitted 2023). How to evaluate causal dominance hypotheses in lagged effects models.
 - R scripts: <https://github.com/Chuenjai/Causal-dominance>.
- **GORICA on CTmeta**
 - Article: <https://doi.org/10.1080/10705511.2020.1823228>.
 - R scripts: https://github.com/rebeccakuiper/GORICA_on_CTmeta.
- **GORICA on Meta-analysis**
 - Article: <https://doi.org/10.3390/e24111525>.
 - R scripts: https://github.com/rebeccakuiper/GORICA_on_MetaAn.

Note: On github site, go to Code (green button) and download zip

Simulation study

Properties of Methods: Simulation study

1. All methods (e.g., (G)ORIC and BMS) programmed in Fortran.
2. Generate data sets with know structure (conditions).
3. Apply methods to all data sets (within one condition).
4. Summarize results (per condition):
proportion of (correct) chosen hypotheses.

Reference:

Kuiper, R.M., Nederhof, T., and Klugkist, I. (2015). Properties of hypothesis testing techniques and (Bayesian) model selection for exploration-based and theory-based (order-restricted) hypotheses. *British Journal of Mathematical and Statistical Psychology*, 68(2), 220 – 245.

Population Values in Simulated Data Sets when $k = 3$

Values of Population Means (μ_i) and Standard Deviations (σ_i)
Used to Simulate 1000 Data Sets

$k = 3$	Case Number ('ES')	μ_1	μ_2	μ_3	ES (Cohen)
	0	0.00	0.00	0.00	
	1	-0.10	0.00	0.10	.1
	2	-0.20	0.00	0.20	.2
	3	-0.30	0.00	0.30	.3
	4	-0.40	0.00	0.40	.4
	5	-0.50	0.00	0.50	.5
		σ_1	σ_2	σ_3	
	0 - 5	1.00	1.00	1.00	

NB in Case 0 $H_{30C} : \mu_1 = \mu_2 = \mu_3$ is true
in Cases 1 to 5 $H_{31C} : \mu_1 < \mu_2 < \mu_3$ is true.

Results Exploration vs Confirmatory ($k = 3$ and $n = 50$)

$H_{30E} : \mu_1 = \mu_2 = \mu_3$	$H_{30C} : \mu_1 = \mu_2 = \mu_3$
$H_{31E} : \mu_1 = \mu_2, \mu_3$	$H_{31C} : \mu_1 < \mu_2 < \mu_3$
$H_{32E} : \mu_1, \mu_2 = \mu_3$	$H_{32C} : \mu_1 = \mu_2 < \mu_3$
$H_{33E} : \mu_1 = \mu_3, \mu_2$	$H_{33C} : \mu_1 < \mu_2 > \mu_3$
$H_{34E} : \mu_1, \mu_2, \mu_3$	$H_{34C} : \mu_1, \mu_2, \mu_3$

'ES'	Method	H_{30E}	H_{31E}	H_{32E}	H_{33E}	H_{34E}
0	PCIC: AIC	0.658	0.113	0.115	0.112	0.002
2	PCIC: AIC	0.201	0.356	0.358	0.028	0.057
5	PCIC: AIC	0.000	0.135	0.136	0.000	0.729

'ES'	Method	H_{30C}	H_{31C}	H_{32C}	H_{33C}	H_{34C}
0	ORIC	0.662	0.065	0.119	0.120	0.034
2	ORIC	0.148	0.506	0.311	0.029	0.006
5	ORIC	0.000	0.955	0.044	0.001	0.000

Results Confirmation ($k = 3$ and $n = 50$)

$$H_{30C} : \mu_1 = \mu_2 = \mu_3$$

$$H_{31C} : \mu_1 < \mu_2 < \mu_3$$

$$H_{32C} : \mu_1 = \mu_2 < \mu_3$$

$$H_{33C} : \mu_1 < \mu_2 > \mu_3$$

$$H_{34C} : \mu_1, \mu_2, \mu_3$$

'ES'	Method	'Prior'	H_{30C}	H_{31C}	H_{32C}	H_{33C}	H_{34C}
0	ORIC		0.662	0.065	0.119	0.120	0.034
0	BMS	3	0.865	0.012	0.075	0.036	0.012
0	BMS	2	0.774	0.022	0.124	0.058	0.022
0	BMS	1	0.656	0.047	0.147	0.120	0.033
2	ORIC		0.148	0.506	0.311	0.029	0.006
2	BMS	3	0.299	0.299	0.371	0.031	0.001
2	BMS	2	0.252	0.328	0.381	0.040	0.000
2	BMS	1	0.125	0.494	0.321	0.063	0.000
5	ORIC		0.000	0.955	0.044	0.001	0.000
5	BMS	3	0.000	0.887	0.112	0.001	0.000
5	BMS	2	0.001	0.890	0.107	0.002	0.000
5	BMS	1	0.000	0.928	0.070	0.002	0.000

Results Confirmation ($k = 3$ and $n = 50$)

$H_{30C} : \mu_1 = \mu_2 = \mu_3$

$H_{31C} : \mu_1 < \mu_2 < \mu_3$

$H_{32C} : \mu_1 = \mu_2 < \mu_3$

$H_{33C} : \mu_1 < \mu_2 > \mu_3$

$H_{34C} : \mu_1, \mu_2, \mu_3$

1 – **Type I error** (here):

not preferring the true null hypothesis,
given the set of hypotheses (!).

'ES'	Method	'Prior'	H_{30C}	H_{31C}	H_{32C}	H_{33C}	H_{34C}
0	ORIC		0.662	0.065	0.119	0.120	0.034
0	BMS	3	0.865	0.012	0.075	0.036	0.012
0	BMS	2	0.774	0.022	0.124	0.058	0.022
0	BMS	1	0.656	0.047	0.147	0.120	0.033
2	ORIC		0.148	0.506	0.311	0.029	0.006
2	BMS	3	0.299	0.299	0.371	0.031	0.001
2	BMS	2	0.252	0.328	0.381	0.040	0.000
2	BMS	1	0.125	0.494	0.321	0.063	0.000
5	ORIC		0.000	0.955	0.044	0.001	0.000
5	BMS	3	0.000	0.887	0.112	0.001	0.000
5	BMS	2	0.001	0.890	0.107	0.002	0.000
5	BMS	1	0.000	0.928	0.070	0.002	0.000

Results Confirmation ($k = 3$ and $n = 50$)

$H_{30C} : \mu_1 = \mu_2 = \mu_3$

$H_{31C} : \mu_1 < \mu_2 < \mu_3$

$H_{32C} : \mu_1 = \mu_2 < \mu_3$

$H_{33C} : \mu_1 < \mu_2 > \mu_3$

$H_{34C} : \mu_1, \mu_2, \mu_3$

1 – **Type II error** (here):

not preferring the true hypothesis,
given the set of hypotheses (!).

'ES'	Method	'Prior'	H_{30C}	H_{31C}	H_{32C}	H_{33C}	H_{34C}
0	ORIC		0.662	0.065	0.119	0.120	0.034
0	BMS	3	0.865	0.012	0.075	0.036	0.012
0	BMS	2	0.774	0.022	0.124	0.058	0.022
0	BMS	1	0.656	0.047	0.147	0.120	0.033
2	ORIC		0.148	0.506	0.311	0.029	0.006
2	BMS	3	0.299	0.299	0.371	0.031	0.001
2	BMS	2	0.252	0.328	0.381	0.040	0.000
2	BMS	1	0.125	0.494	0.321	0.063	0.000
5	ORIC		0.000	0.955	0.044	0.001	0.000
5	BMS	3	0.000	0.887	0.112	0.001	0.000
5	BMS	2	0.001	0.890	0.107	0.002	0.000
5	BMS	1	0.000	0.928	0.070	0.002	0.000

Extra: Prior choice for BMS

Prior

$$P(\mu, \sigma^2) = P(\mu_1) \times \dots \times P(\mu_k) \times P(\sigma^2),$$

where $P(\mu_i) = P(\mu) \forall i = 1, \dots, k$.

$P(\mu)$ is a data-based normal distribution, with parameters β_0 and τ_0^2 , and $P(\sigma^2)$ an inverse chi-squared distribution (see Klugkist et al., 2005)

β_0 and τ_0^2 data-based hyperparameters

For each μ_i ($i = 1, \dots, k$) a credibility interval is computed:
estimated group mean \pm $PV \times$ *the group standard error*.

The credibility interval for μ_i is represented by " $[LB_i, UB_i]$ ".

Lowest lower bound: LB_{min} .

Highest upper bound: UB_{max} .

Then, $\beta_0 = \frac{LB_{min} + UB_{max}}{2}$ and $\tau_0^2 = \left[\frac{UB_{max} - LB_{min}}{2} \right]^2$.

Three types of prior vagueness: BMS PV 1, BMS PV 2 and BMS PV 3