

Informative hypotheses evaluation

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Table of Contents

Example Null hypothesis (H0) vs Informative hypothesis (Hm)

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

Example Palmer and Gough (P&G)

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

Example Palmer and Gough (P&G)

Palmer and Gough (2007) expect that

- non-offenders (1) attribute more importance to defective education for explaining crime than the other two offenders (2 & 3):
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., $\mu_2 > \mu_3$.

This leads to the theory-based hypothesis:

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

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

ANOVA Example: Comparisons of 3 Means

Simple, hypothetical example

Examine the difference in happiness
between three types of “treatments”:
(1) new treatment, (2) current treatment, and (3) no treatment.

Theory-based hypothesis:

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

where “>” denotes “larger than”.

Testing the null hypothesis

Example 3 means

Test H_0 with ANOVA F test:

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

$$H_a : \quad \text{not } H_0.$$

Then, reject or not-reject ('accept') H_0 .

But, often not interested in H_0 !

Cannot say anything about $H_1 : \mu_1 > \mu_2 > \mu_3$.

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

Example 3 means

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 P&G 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

Example Palmer and Gough

```
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
```


Exploration and Confirmation

Exploration (like in post hoc tests and possibly AIC)

Test all possible pairs/subsets of means whether significant different (“,”) or not (“=”).

For example, when $k = 3$:

$$H_{0E} : \mu_1 = \mu_2 = \mu_3$$

$$H_{1E} : \mu_1 = \mu_2, \mu_3$$

$$H_{2E} : \mu_1, \mu_2 = \mu_3$$

$$H_{3E} : \mu_1 = \mu_3, \mu_2$$

$$H_a : \mu_1, \mu_2, \mu_3$$

When $k = 5$, there are even 52 hypotheses.

Confirmation

Limited set: Compare only prespecified hypotheses including order restrictions ($<$, $>$, but also $=$).

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

Example Palmer and Gough, that is, 3 means

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

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

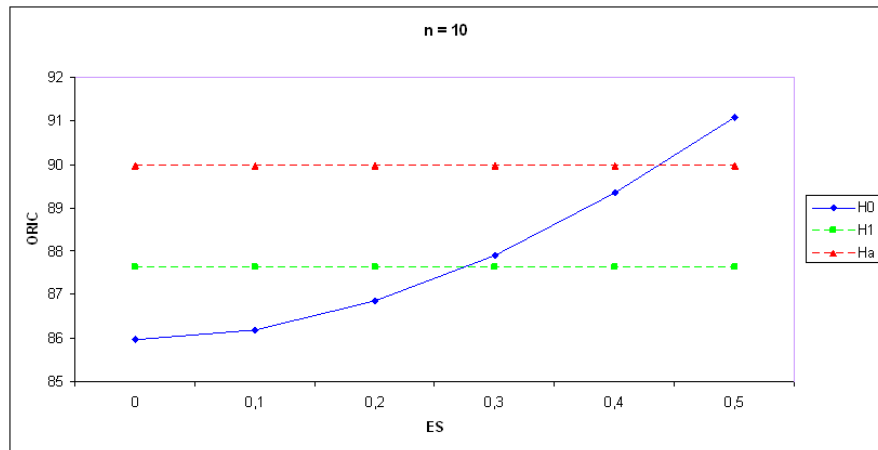
$$H_u : \mu_1, \mu_2, \mu_3.$$

GORIC

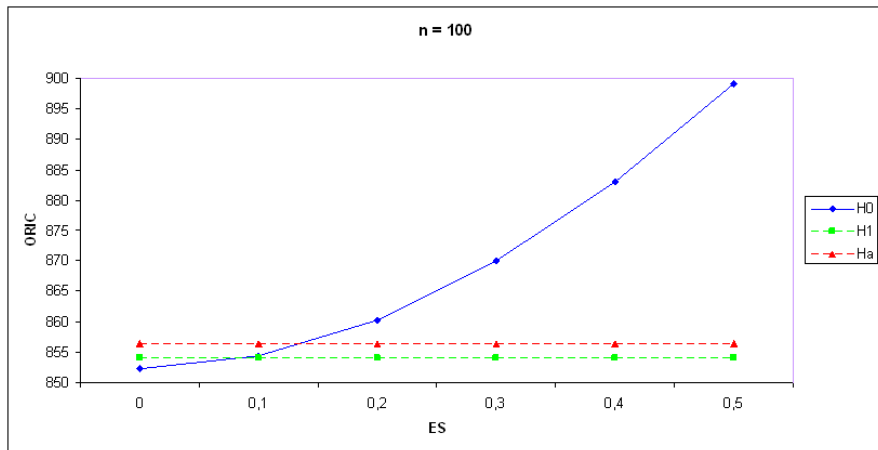
Model	Fit	Complexity	GORIC	GORIC weights
H_0	-196.36	2.00	396.71	0.02
H_1	-191.89	2.81	389.41	0.75
H_u	-191.89	4.00	391.79	0.23

Confirmatory methods (e.g., GORIC) have more “power” than their exploratory counterparts (e.g., AIC; cf. one- vs two-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

Generalized Order-Restricted Information Criterion (GORIC)

GORIC weights

Examples with R code

GORICA

GORIC(A) in JASP

End & Extra

Generalized Order-Restricted Information Criterion

GORIC

'IC' = $-2 \text{ fit} + 2 \text{ complexity}$

Fit = Maximized order-restricted log likelihood

Maximized log likelihood based on parameters in agreement with H_m .

Complexity = Penalty

Represents: Expected number of distinct parameters.

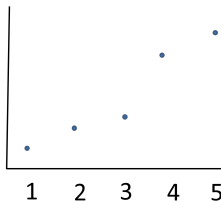
Here, expected number of distinct mean values plus 1 (because of the unknown variance term).

Details: Function of level probabilities.

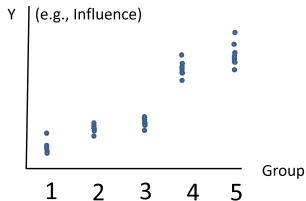
Intermezzo: Balance Fit and Complexity (1/6)

Example 5 means

Data for 5 groups – Oversimplified representation

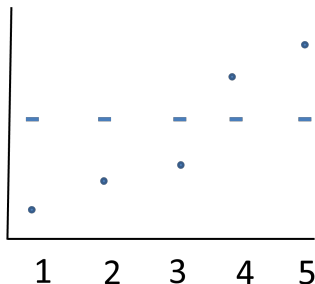


Data for 5 groups – Better representation (scatter of data points)



Intermezzo: Balance Fit and Complexity (2/6)

Example 5 means



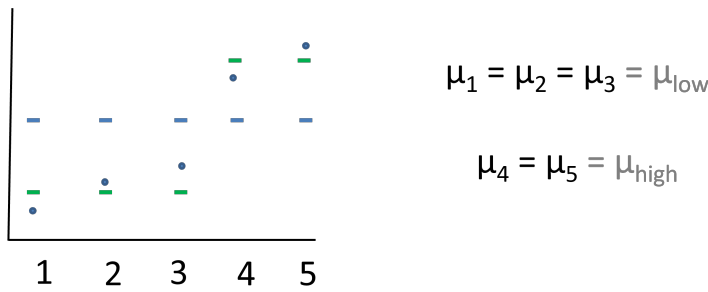
$$\mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5 = \mu$$

parameters: 1 mean parameter (i.e., μ)

Fit: Bad fit

Intermezzo: Balance Fit and Complexity (3/6)

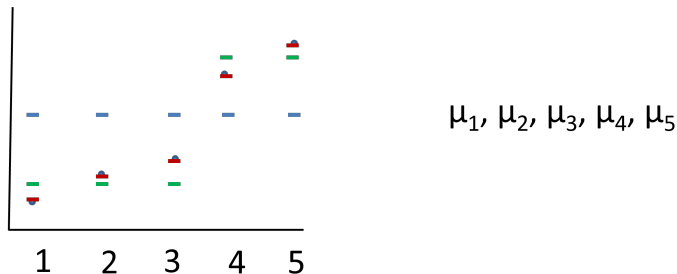
Example 5 means



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 (4/6)

Example 5 means



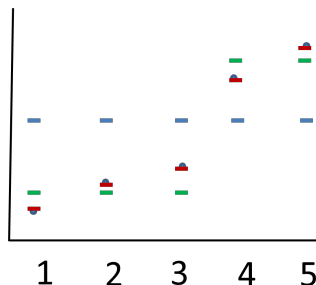
parameters: 5 mean parameter (complex)

Fit: Better than with two parameters, even best possible fit.

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

Intermezzo: Balance Fit and Complexity (6/6)

From “Example 5 means” to ‘Example 2 means’

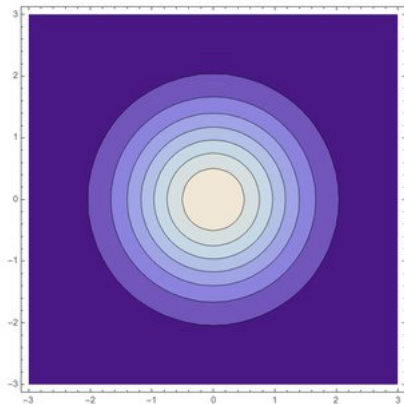
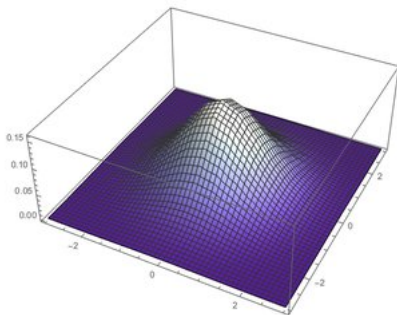


In theory-based hypotheses, we also incorporate **order-restrictions** (e.g., $\mu_1 < \mu_2$). Then, helpful to look at likelihood using **contour plots** (not scatter plot, as done here).

For ease, I will next use **2 means** (instead of 5).

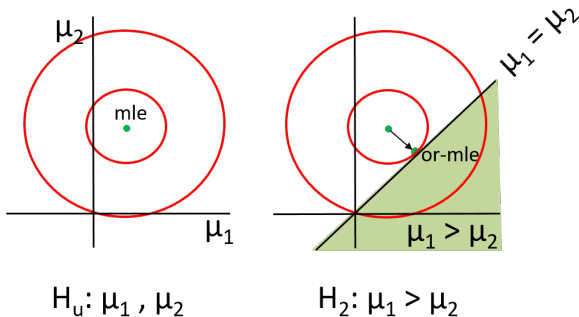
Intermezzo: Contour plot (1/2)

Example 2 means



Idea fit: order-restricted maximum likelihood (or-ml)

Example 2 means



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.

Idea fit

Example Palmer and Gough, that is, 3 means

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

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

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

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

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

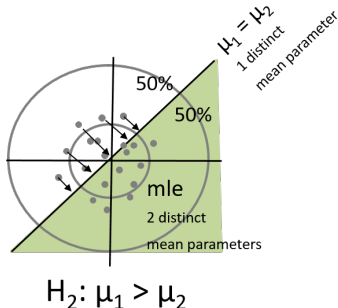
```
## group1 group2 group3
## 11.95  9.75  8.77
```

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)

Example 2 means



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

Example Palmer and Gough, that is, 3 means

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

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).

Idea complexity

Example Palmer and Gough, that is, 3 means

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

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

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

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

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

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

$$IC_m = -2 \text{ fit}_m + 2 \text{ complexity}_m$$

Broad type of restrictions

More or less: any linear restriction.

e.g., the interaction $H_1 : \mu_1 - \mu_2 < \mu_3 - \mu_4$.

Note

If no inequalities ($<$ and/or $>$), then (G)ORIC = AIC.

Reference:

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

Example Palmer and Gough

H_0 : $\mu_1 = \mu_2 = \mu_3$ (include only when of interest)

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

H_2 : $\mu_1 > \mu_2 < \mu_3$ (if competing theory/hypothesis)

H_u : μ_1, μ_2, μ_3 .

GORIC

Model	Fit	Complexity	GORIC
H_0	-196.36	2.00	396.71
H_1	-191.89	2.81	389.41
H_2	-192.34	3.19	391.05
H_u	-191.89	4.00	391.79

Hands-on/Demo (1a): GORIC

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 dir.).
- Start Rstudio. Optional: make project.
- Open 'Tutorial_GORIC_restriktor_ANOVA.html',
'PalmerAndGough_and_Lucas.R', and/or
'**Hands-on_1_GORIC**_Unc_ANOVA_restriktor.R' (Hands-on files').
- Install packages and load them.
- Read and inspect data.
Use **Data_PalmerAndGough.txt** and/or Data_Lucas.txt.
- 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 next.



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)

Example Palmer and Gough

H_0 : $\mu_1 = \mu_2 = \mu_3$ (include only when of interest)

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

H_2 : $\mu_1 > \mu_2 < \mu_3$ (if competing theory/hypothesis)

H_u : μ_1, μ_2, μ_3 .

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_1	-191.89	2.81	389.41	0.57
H_2	-192.34	3.19	391.05	0.25
H_u	-191.89	4.00	391.79	0.17

H_1 is $0.57 / 0.25 \approx 2.26$ times more supported than H_2 .

Table of Contents

Generalized Order-Restricted Information Criterion (GORIC)

GORIC weights

Examples with R code

GORICA

GORIC(A) in JASP

End & Extra

R code: Hypotheses

Palmer & Gough

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

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

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

```
# Hypotheses
H1 <- 'group1 > group2 > group3'
H2 <- 'group1 > group2 < group3'
# and the unconstrained
# (default in case of multiple hypotheses)
```

R code: GORIC

Palmer & Gough

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

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

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

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

GORIC output and interpretation

Palmer & Gough

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

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

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

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_1	-191.89	2.81	389.41	0.57
H_2	-192.34	3.19	391.05	0.25
H_u	-191.89	4.00	391.79	0.17

H_1 and H_2 are not weak (nl, better than H_u).

H_1 is $0.57 / 0.25 \approx 2.26$ times more supported than H_2 .

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

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, group4) > group2'
```

```
# Stated otherwise:
```

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

```
#           group3 > group4 > group2'
```

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

```
# and the unconstrained (default here)
```

R code: GORIC

Lucas

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

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

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

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


GORIC output

Lucas

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

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

$$H_\mu : \quad \mu_1, \mu_2, \mu_3, \mu_4, \mu_5.$$

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_1	-278.05	3.46	563.02	0.90
H_2	-281.76	3.14	569.79	0.03
H_u	-278.05	6.00	568.10	0.07

GORIC weights (w_m)

Lucas

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_1	-278.05	3.46	563.02	0.90
H_2	-281.76	3.14	569.79	0.03
H_u	-278.05	6.00	568.10	0.07

H_1 is $0.9 / 0.03 \approx 29.59$ times more supported than H_2 .

Thus, there is quite some evidence that H_1 is the best of this set.

Note:

H_1 is $0.9 / 0.07 > 1$ times more supported than H_u .

Hence, H_1 not weak and thus comparable to the other (weak and non-weak) informative hypotheses (as explained in a bit).

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

Let's practice.

- If needed: Start Rstudio again (optional: make project) and then also load packages again.
- Read and inspect data.
- 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.

Table of Contents

Generalized Order-Restricted Information Criterion (GORIC)

GORIC weights

Examples with R code

Failsafe/Safeguard hypotheses: Unconstrained & Complement

GORICA

GORIC(A) in JASP

End & Extra

Include “unconstrained” hypothesis

If set of hypotheses does not contain a reasonable/good one:
Select the best of set of weak hypotheses.

E.g.: $w_1 = .8$ and $w_2 = .2$.

Prevent choosing a weak hypothesis

Include unconstrained hypothesis H_u (or H_a):

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

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

$$H_u : \quad \mu_1, \mu_2, \mu_3, \\ \text{(i.e., no restrictions).}$$

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

E.g.: $w_1 = .08$, $w_2 = .02$, and $w_u = .90$.

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.: $w_1 = .08$, $w_2 = .02$, and $w_u = .90$.

Use of H_u

Palmer & Gough

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

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

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

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_1	-191.89	2.81	389.41	0.57
H_2	-192.34	3.19	391.05	0.25
H_u	-191.89	4.00	391.79	0.17

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

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

H_1 vs H_u

Palmer & Gough

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	0.77
H_u	-191.89	4.00	391.79	0.23

H_1 is $0.77 / 0.23 \approx 3.27$ times more supported than H_2 .

BUT: H_u includes H_1 .

So, support for H_u contains support for H_1 .

H_1 vs H_u ctd.

Palmer & Gough

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, $0.77 / 0.23 \approx 3.27$ is an upper bound.

H_1 vs H_u : Upper bound

Based on simulation

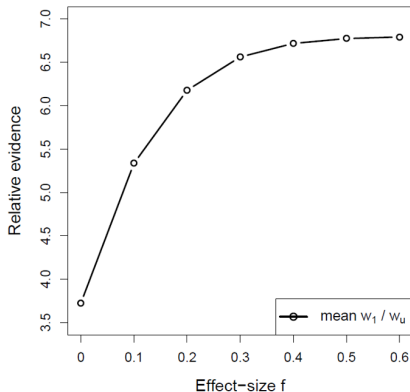


Figure: IC weights can have an upper bound, when informative hypothesis has maximum fit (i.e., is fully in agreement with the data).

Alternative failsafe: Complement of H_m

Alternatively (in the case of one hypothesis of interest)

Evaluate hypothesis of interest against its complement;
that is, all other possible hypotheses.

More powerful than against the unconstrained
if H_m has maximum fit.

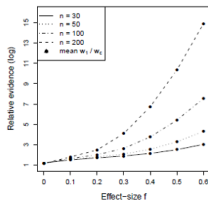
Reference:

Vanbrabant, L., Van Loey, N., and Kuiper, R. M. (2020). Evaluating a Theory-Based Hypothesis Against Its Complement Using an AIC-Type Information Criterion With an Application to Facial Burn Injury. *Psychological Methods*, 25(2), 129-142.
<https://doi.org/10.1037/met0000238>

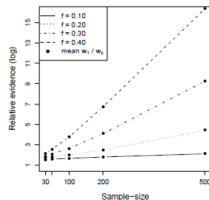
Alternative failsafe: Complement of H_m

Based on simulation

vs complement

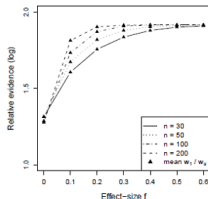


(a)

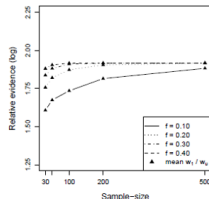


(b)

vs unconstrained



(c)



(d)

R code: complement

Palmer & Gough

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

$H_c :$ not H_1 .

GORIC

```
H1 <- 'group1 > group2 > group3'  
# vs its complement (default in case of one hypothesis)  
#  
# GORIC (using goric function in restriktor package)  
library(restriktor)  
set.seed(123) # Set seed value  
goric.PandG_1c <- goric(fit.PandG,  
                        hypotheses = list(H1))
```

H_1 vs H_c

Palmer & Gough

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

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

GORIC

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

H_1 is $0.79 / 0.21 \approx 3.73$ times more supported than its complement, that is, any other hypothesis (i.e., any other ordering).

Note on use of safeguard hypotheses (1/2)

- Unconstrained (H_u) is failsafe.
If at least one hypothesis (H_m) not weak (i.e., better than H_u), then compare that with the other, competing hypotheses ($H_{m'}$).
Note: Do not compare H_m with H_u (since support is bounded).
- Complement (H_c) acts as competing hypothesis.
Note 1: Relative support H_m vs $H_{m'}$ same as in case above.
Note 2: Can compare H_m with H_c .

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

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/or '**Hands-on_2_GORIC_Compl_ANOVA_restriktor.R**'.
- Read and inspect data.
Use Data_PalmerAndGough.txt and/or **Data_Lucas.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.

- Run goric()
- Inspect and interpret output.

Table of Contents

Generalized Order-Restricted Information Criterion (GORIC)

GORIC weights

Examples with R code

GORICA

GORIC(A) in JASP

End & Extra

GORICA

GORIC: Normal linear models

GORIC can easily be applied to normal linear models (e.g., ANOVA models or regression models).

GORIC: Other statistical models

In case of other statistical models (e.g., a SEM model), more cumbersome to calculate maximized order-restricted log likelihood and thus GORIC.

GORICA: All statistical models

Therefore, GORICA: asymptotic expression for GORIC.
Can be used for all types of statistical models.

Reference:

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

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 : not H_1 .

GORICA: type = "gorica"

```
H1 <- 'group1 > group2 > group3'  
# vs its complement (default in case of one hypothesis)  
#  
# GORICA (using goric function in restriktor package)  
library(restriktor)  
set.seed(123) # Set seed value  
gorica.PandG_C <- goric(fit.PandG,  
                        hypotheses = list(H1),  
                        type = "gorica") # needed if lm object
```

GORICA

Palmer & Gough

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

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

GORIC

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

H_1 is $0.79 / 0.21 \approx 3.67$ times more supported than its complement, that is, any other hypothesis.

Note: GORIC weights are the same (ratio may differ a bit).

Hands-on/Demo (3): GORICA

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/or '**Hands-on_3_GORICA_UncAndCompl_ANOVA_restriktor.R**'.
- Read and inspect data.
Use Data_PalmerAndGough.txt and/or **Data_Lucas.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 (since lm object):
`type = "gorica"`
- Inspect and interpret output.

Table of Contents

Generalized Order-Restricted Information Criterion (GORIC)

GORIC weights

Examples with R code

GORICA

GORIC(A) in JASP

End & Extra

GORIC in JASP: instructions

Palmer & Gough

- Open JASP and 'Data_PalmerAndGough_JASP.txt'.
Check measurement levels.
- Go to ANOVA and denote variables of interest.
- Go to Order Restrictions tab.
- Specify hypotheses. For example,

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

$$JASP : \quad group1 > group2 > group3$$

- Press Ctrl+Enter. Inspect and interpret output.

More in (demo and) lab.

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)

The screenshot displays the JASP software interface with three statistical model windows open: ANOVA, ANCOVA, and Repeated Measures ANOVA. In each window, the 'Order Restricted Hypotheses' option is highlighted with a red circle. The ANOVA window also shows the 'GORIC' label. The ANCOVA window shows the 'ANCOVA' label. The Repeated Measures ANOVA window shows the 'Repeated Measures ANOVA' label. The right-hand pane shows the 'ANCOVA' model settings, including the 'Dependent Variable' (id), 'Fixed Factors' (sex, age, viewcat, swelling, treat, prebody, prelat, preform, pronumb, prevelat, preclat, postbody, postlat, postform, postnumb, postclat, postvelat), 'Covariates', and 'WLS Weights'. The 'Display' section is also visible, showing options for 'Descriptive statistics', 'Estimates of effect size', 'Work-Save maximum p-value', and 'Model'.

ANOVA

Order Restricted Hypotheses

GORIC

ANOVA

Cases Sum of Squares df Mean Square F p

Note: Type III Sum of Squares

ANCOVA

Order Restricted Hypotheses

GORIC

ANCOVA

Cases Sum of Squares df Mean Square F p

Note: Type III Sum of Squares

Repeated Measures ANOVA

Order Restricted Hypotheses

GORICA

Repeated Measures ANOVA

Within Subjects Effects

Cases Sum of Squares df Mean Square F p

Note: Type III Sum of Squares

Between Subjects Effects

Cases Sum of Squares df Mean Square F p

Note: Type III Sum of Squares

ANCOVA

Dependent Variable

Fixed Factors

Covariates

WLS Weights

Display

☐ Descriptive statistics

☐ Estimates of effect size

☐ Work-Save maximum p-value

☐ Model

☐ Assumption Checks

☐ Contrasts

Order Restricted Hypotheses

Table of Contents

Generalized Order-Restricted Information Criterion (GORIC)

GORIC weights

Examples with R code

GORICA

GORIC(A) in JASP

End & Extra

Your hypothesis of interest

If you have your own data

Before:

- What is your research question?
- What is your theory / expectation?
- What is your statistical hypothesis?
- Is there a competing statistical hypothesis?

Additionally:

- Are you able to specify your statistical hypothesis/-es?
- How will you evaluate it/them?

The End

GORIC(A)

Thanks for listening!

Are there any questions?

Websites

<https://github.com/rebeccakuiper/Tutorials>

www.uu.nl/staff/RMKuiper/Software

www.uu.nl/staff/RMKuiper/Extra2

informative-hypotheses.sites.uu.nl/software/goric/

E-mail

r.m.kuiper@uu.nl

Note on comparable estimates

Until now: comparing means.

Continuous predictors

If compare relative strength/importance of parameters (e.g., $\beta_1 > \beta_2$), then make sure comparable:
e.g., standardize continuous predictors.

Multiple outcomes

If compare parameters across outcomes, then (also) standardize outcomes.

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_u).

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) values & weights.
More data collected: (re-)calculate.
- 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.
Download 'Tutorial_GORIC_restriktor_UpdateHypo.html' and/or
'Hands-on_4_GORIC_UpdateHypo_restriktor.R' from
<https://github.com/rebeccakuiper/Tutorials>.
- 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).

Download 'Tutorial_GORIC_restriktor_evSyn.html' and/or
'Hands-on_4_GORIC_evSyn_restriktor.R' from

<https://github.com/rebeccakuiper/Tutorials>.

Extra material (1/2)

- Logistic Regression Modeling
 - Article: doi.org/10.1037/met0000406
- GORICA on SEM
 - Article: www.tandfonline.com/doi/full/10.1080/10705511.2020.1836967.
 - R scripts: github.com/rebeccakuiper/GORICA_in_SEM.
- GORICA on cross-lagged panel model (CLPM)
 - Article: doi.org/10.1111/bjep.12455.
 - R scripts: github.com/rebeccakuiper/GORICA_in_CLPM.
- GORICA on Random-Intercept CLPM (RI-CLPM)
 - Article: Sukpan, C. and Kuiper, R.M. (2023). How to evaluate causal dominance hypotheses in lagged effects models.
 - R scripts: github.com/rebeccakuiper/GORICA%20in%20RI-CLPM.
- GORICA for EffectLiteR
 - R scripts: <https://github.com/rebeccakuiper/Tutorials/tree/main/GORICA%20for%20EffectLiteR>.

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

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

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

ratio GORIC weights ($w_m/w_{m'}$) \sim Bayes factor ($BF_{mm'}$).

GORIC weight (w_m) \sim posterior model probability (PMP).

1 - w_m = conditional error probability.

Like PMP, w_m depends on set of hypotheses.

using PMPS and GORIC(A) weights

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

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 $n = 50$)

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

'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

