Hands-on introduction to (one) approach for evaluating informative hypotheses

Information criteria

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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

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

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 $\epsilon_j \sim N(0, \sigma^2)$.

$(n_i = 20, 20, 31)$

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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:

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

Note that "$<$" denotes "smaller than" and "$>$" denotes "larger than".

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Testing the null hypothesis

Example 3 means

Test H_0 with ANOVA F test:

$$\begin{aligned} H_0 : &\quad \mu_1 = \mu_2 = \mu_3, \\ H_a : &\quad \text{not } H_0. \end{aligned}$$

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

But, often not interested in H_0!

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

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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

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

which implies $\mu_1 > \mu_2 = \mu_3$.
But also not interested in this.

Furthermore, inconsistent results are possible (like in P&G example):
$\mu_1 = \mu_2$, $\mu_2 = \mu_3$, and $\mu_1 \neq \mu_3$,
which is logically impossible, since the first two imply $\mu_1 = \mu_3$.
Using planned contrasts would overcome this, but still = restrictions then.

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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)

Evaluate all possible pairs/subsets of means whether significant different (“,”) or not (“=”).
For example, when $k = 3$:

$$
\begin{aligned}
H_{0E} &: \mu_1 = \mu_2 = \mu_3 \\
H_{1E} &: \mu_1 = \mu_2, \mu_3 \\
H_{2E} &: \mu_1, \mu_2 = \mu_3 \\
H_{3E} &: \mu_1 = \mu_3, \mu_2 \\
H_a &: \ \mu_1, \ \mu_2, \ \mu_3
\end{aligned}
$$

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

Confirmation

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

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Limited set: Evaluate 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: Fbar ($\bar{F}$) 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.

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GORIC

Example Palmer and Gough, that is, 3 means

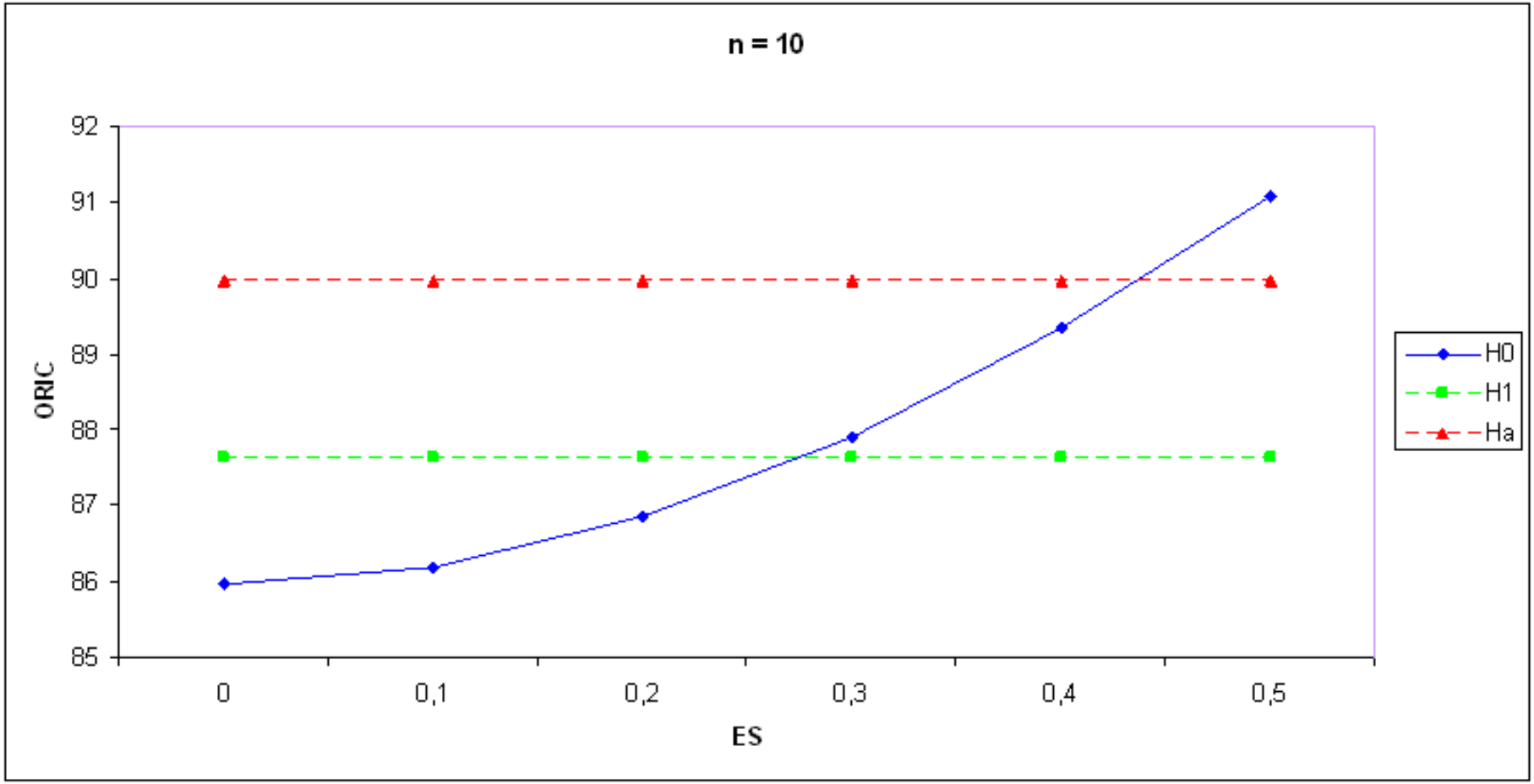
$$
\begin{aligned}
H_0 : &\quad \mu_1 = \mu_2 = \mu_3, \\
H_1 : &\quad \mu_1 > \mu_2 > \mu_3, \\
H_u : &\quad \mu_1,\ \mu_2,\ \mu_3.
\end{aligned}
$$

GORIC – will be explained later

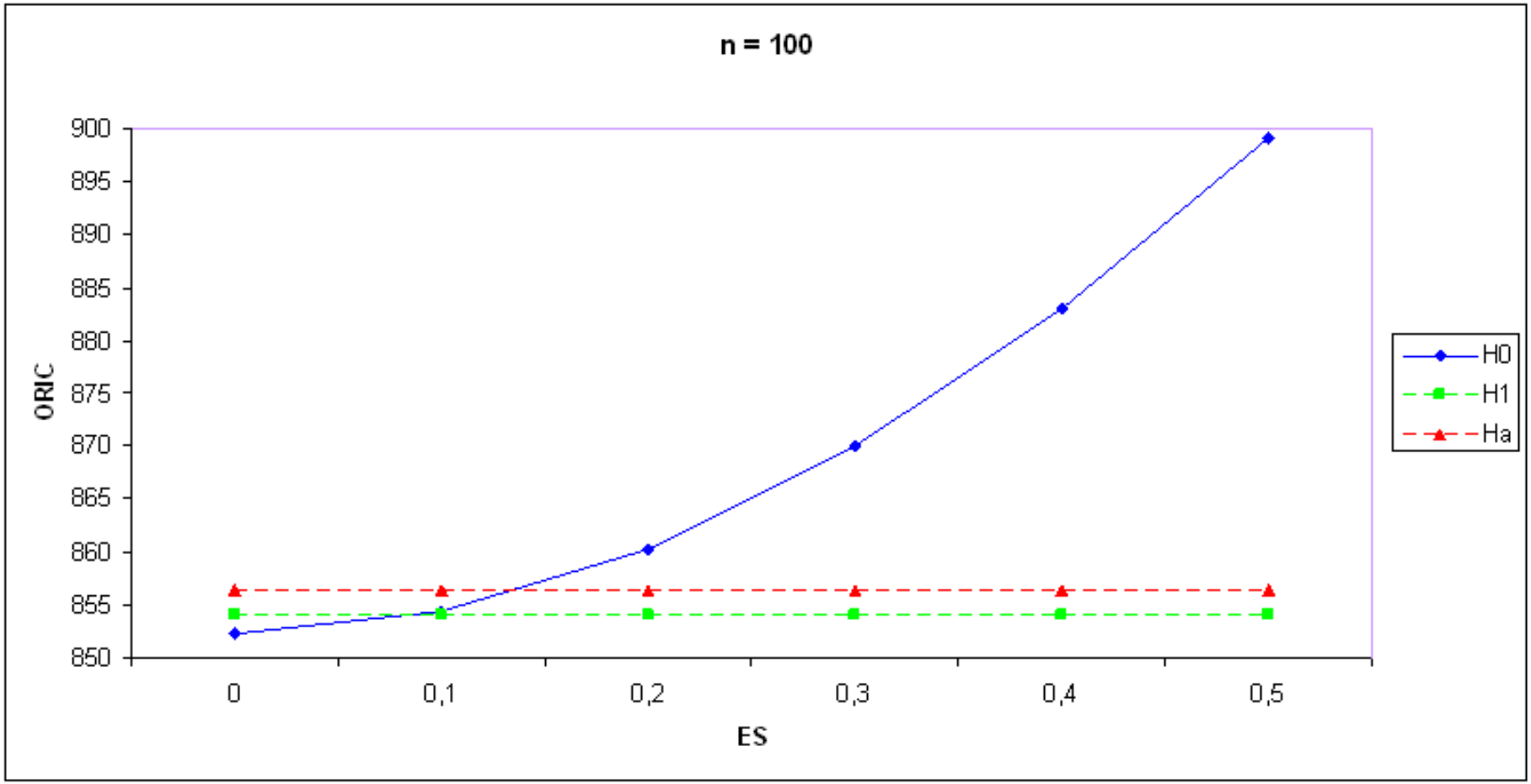
Model	Fit	Complexity	GORIC	GORIC weights
H_0	-196.36	2.00	396.71	0.02
H_1	-191.89	2.81	389.41	0.75
H_u	-191.89	4.00	391.79	0.23

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 $\mathbf{n} = \mathbf{10}$ observations per group



Confirmation more power: 1 data set. GORIC values for 3 groups, effect size *ES*, and $\mathbf{n} = \mathbf{100}$ 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)

ANOVA Example: Comparisons of 3 Means

Simple, hypothetical example

Examine the difference in happiness
between three types of "treatments":
(A) treatment A, (B) treatment B, and (C) no treatment / control.

DIY: Think of one or more theory-based hypotheses.
(in terms of μ_A, μ_B, and/or μ_C.)

ANOVA Example: Comparisons of 3 Means

Simple, hypothetical example

Examine the difference in happiness
between three types of "treatments":
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Possible (sets of) theory-based hypothesis/-es:

$$H_1: \quad \mu_A > \mu_B > \mu_C.$$

$$H_1: \quad \mu_A > \mu_B > \mu_C,$$
$$H_2: \quad \mu_B > \mu_A > \mu_C.$$

$$H_1: \quad \{\mu_A, \mu_B\} > \mu_C.$$

Your hypothesis of interest

If/When you have your own data

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

Notably, think outside of the H_0-box...

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GORIC(A) in JASP

End & Extra

Information criteria (ICs)

An IC, like AIC and GORIC, balances fit and complexity:

Describe data as good as possible (fit)
with fewest number of parameters (simplicity / non-complexity).

Generalized Order-Restricted Information Criterion

GORIC

'IC' = -2 fit + 2 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/free parameters.
Here, expected number of distinct mean values plus 1 (because of the unknown variance term).
Details: Function of level probabilities.

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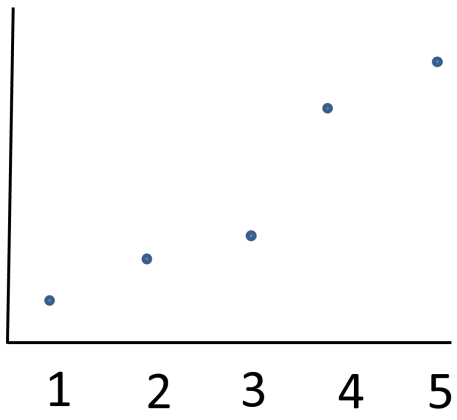
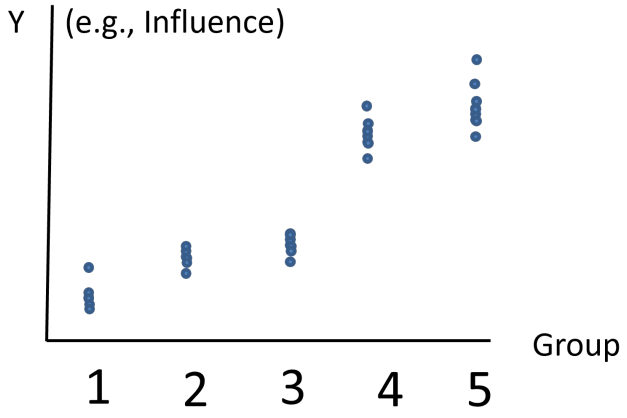
Intermezzo: Balance Fit and Complexity (1/6)

Example 5 means

Data for 5 groups – Oversimplified representation

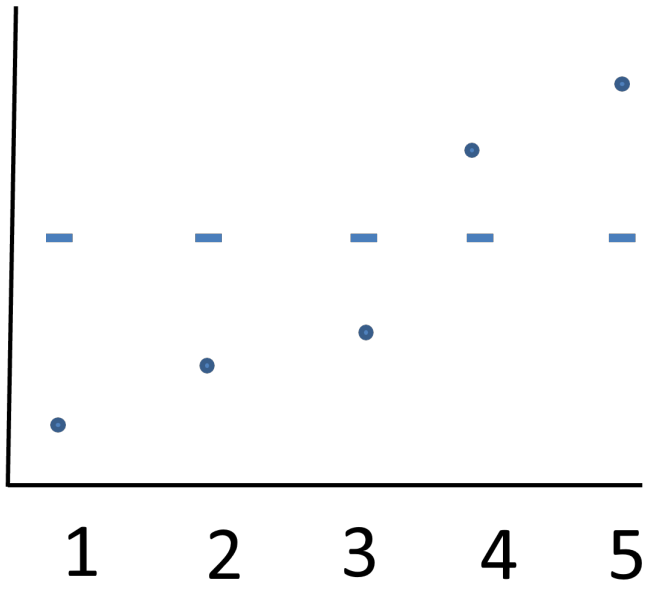


Data for 5 groups – Better representation (scatter of data points)



Intermezzo: Balance Fit and Complexity (2/6)

Example 5 means

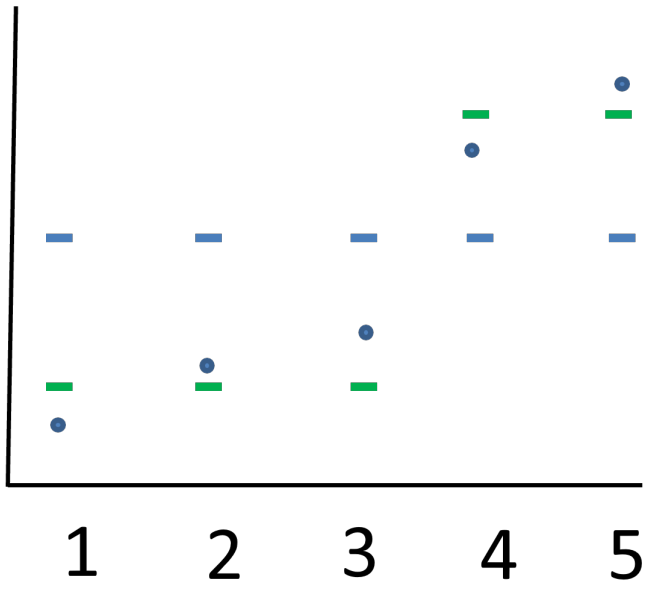


$$\mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5 = \mu$$

# parameters:	1 mean parameter (i.e., μ)
Fit:	Bad fit

Intermezzo: Balance Fit and Complexity (3/6)

Example 5 means



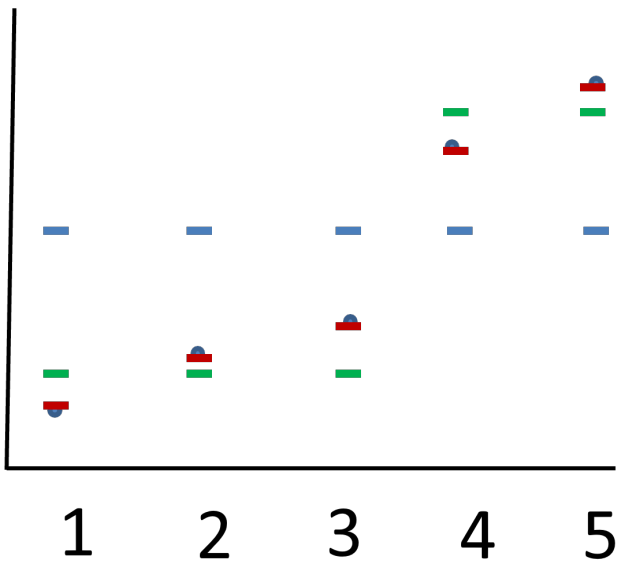
$$\mu_1 = \mu_2 = \mu_3 = \mu_{low}$$

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

# 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 (4/6)

Example 5 means



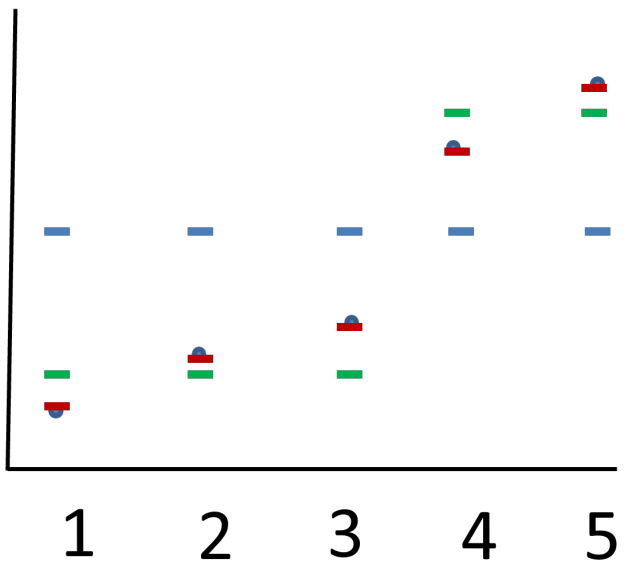
$\mu_1, \mu_2, \mu_3, \mu_4, \mu_5$

# 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 (5/6)

Example 5 means



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$\mu_1 = \mu_2 = \mu_3 = \mu_{low}$ &
$\mu_4 = \mu_5 = \mu_{high}$

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

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

Intermezzo: Balance Fit and Complexity (6a/6)

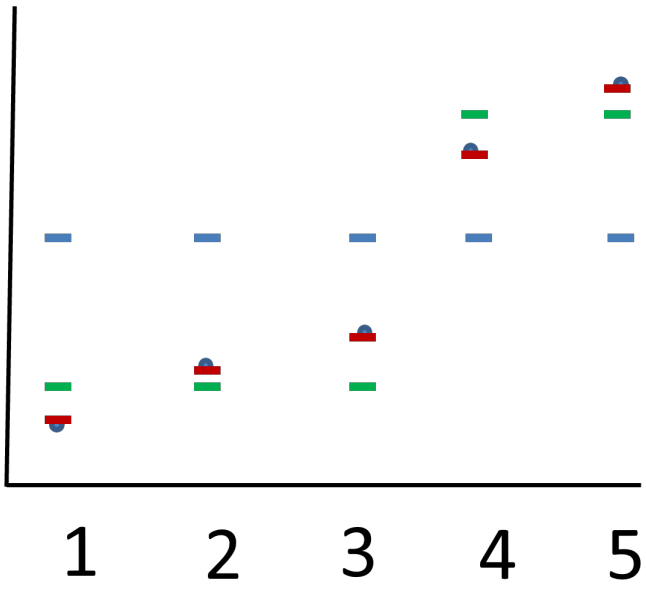
Order-restrictions

Previous slides demonstrated balancing fit and complexity for equality ('=') restrictions.

For inequality/order ('<', '>', and possible some '=') restrictions, the calculation of the fit and complexity is more complex :-), but the idea of balancing is the same.

Intermezzo: Balance Fit and Complexity (6b/6)

Order-restrictions: From "Example 5 means' to 'Example 2 means'

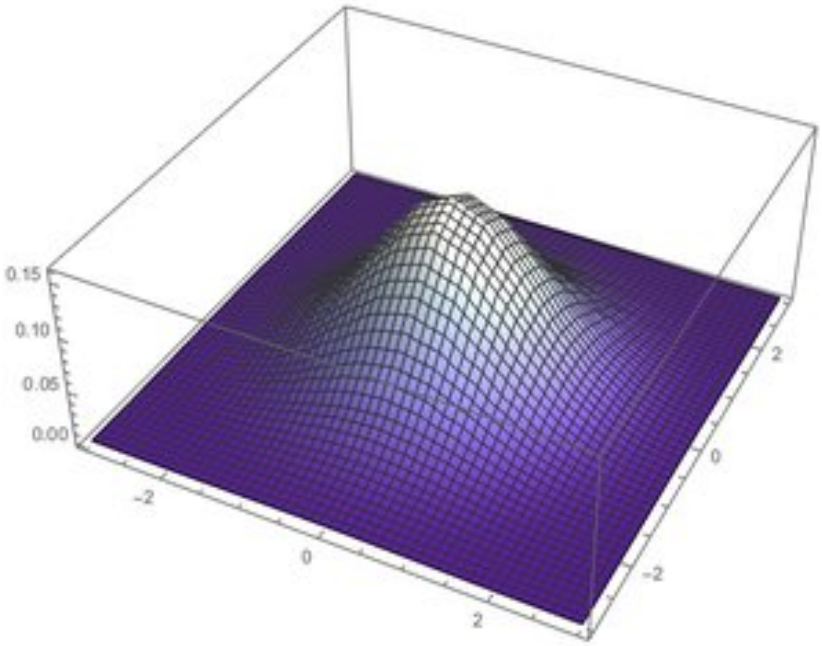


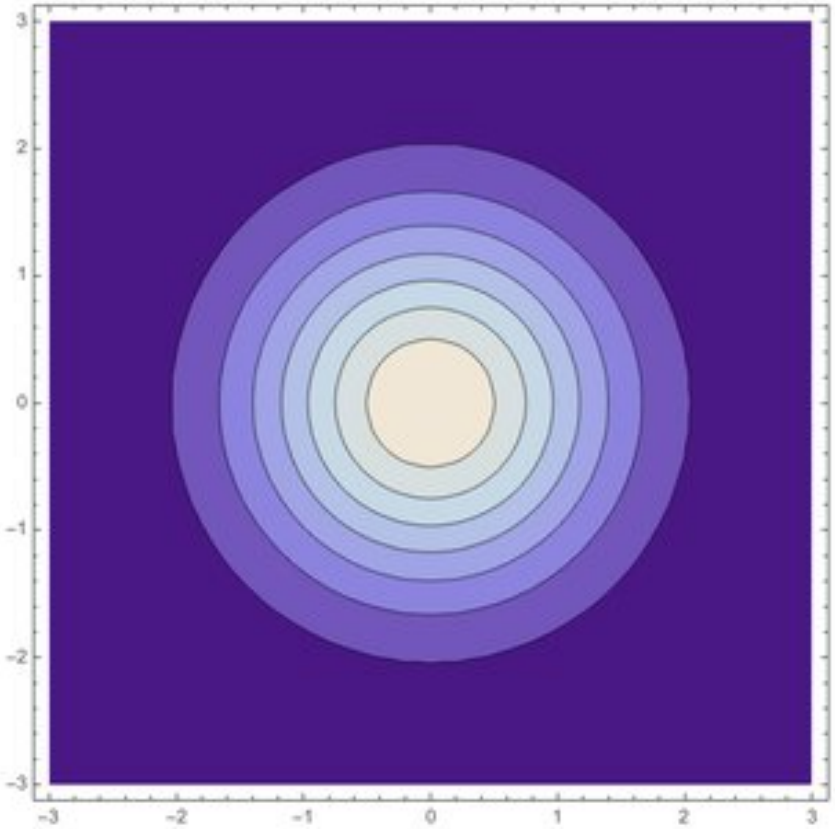
In theory-based hypotheses, we also incorporate **order-restrictions** (e.g., $\mu_1 < \mu_2$).
Then, helpful to look at likelihood using **contour plots** (not scatter plot, as done here).

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

Intermezzo: Contour plot (1/2)

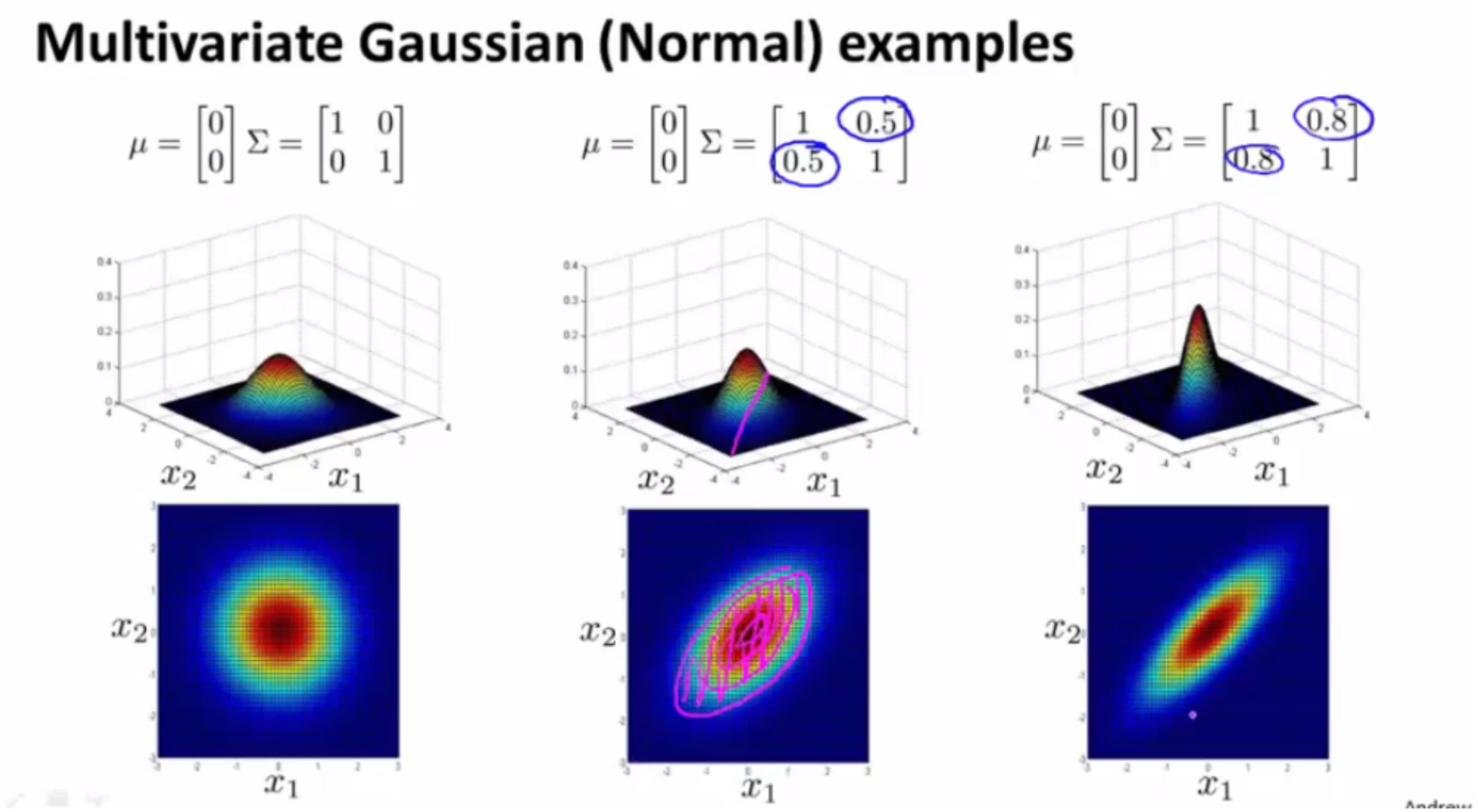
Example 2 means





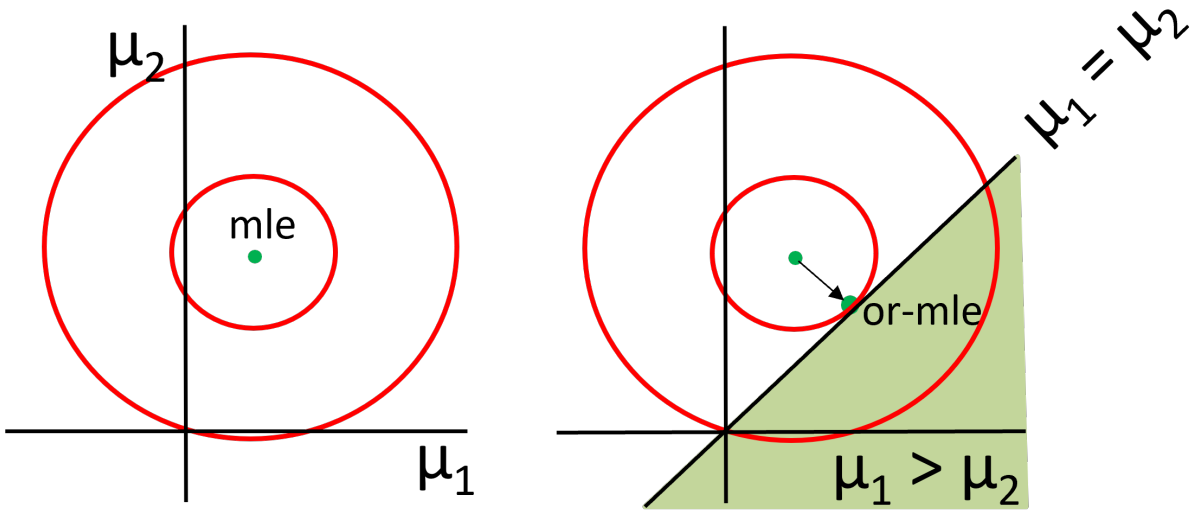
Intermezzo: Contour plot (2/2)

Example 2 means



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

Example 2 means (with or-mle $\neq$ mle)

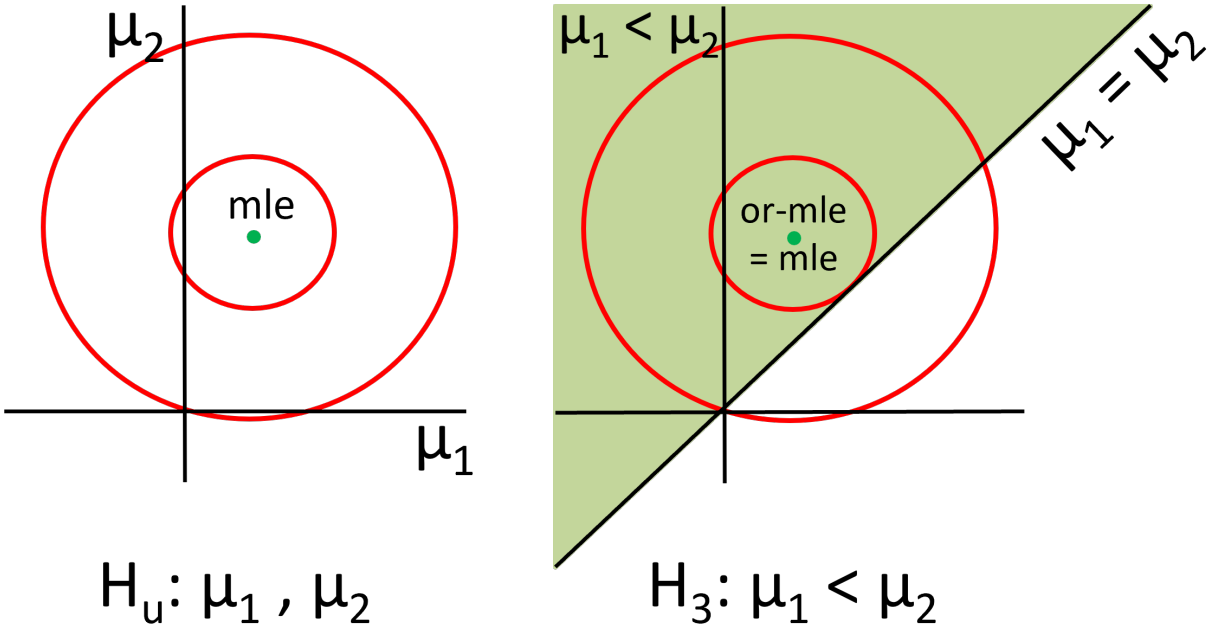


H_u: μ_1 , μ_2 H_2: $\mu_1 > \mu_2$

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-mle.

Note: if in agreement, or-mle = mle

Example 2 means with or-mle = mle



mle in H_3: highest likelihood is in allowable (= green) space.
Hence, or-mle = mle.

Idea fit

Example Palmer and Gough, that is, 3 means

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H_1 &: \quad \mu_1 > \mu_2 > \mu_3, \\
H_2 &: \quad \mu_1 > \mu_2 < \mu_3, \\
H_3 &: \quad \mu_1 < \mu_2 < \mu_3, \\
H_u &: \quad \mu_1,\ \mu_2,\ \mu_3.
\end{aligned}
$$

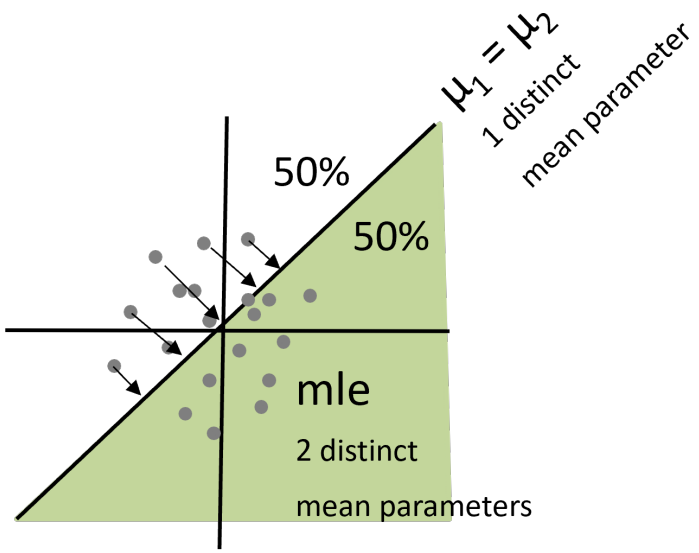
```
## group1 group2 group3
##  11.95   9.75   8.77
```

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

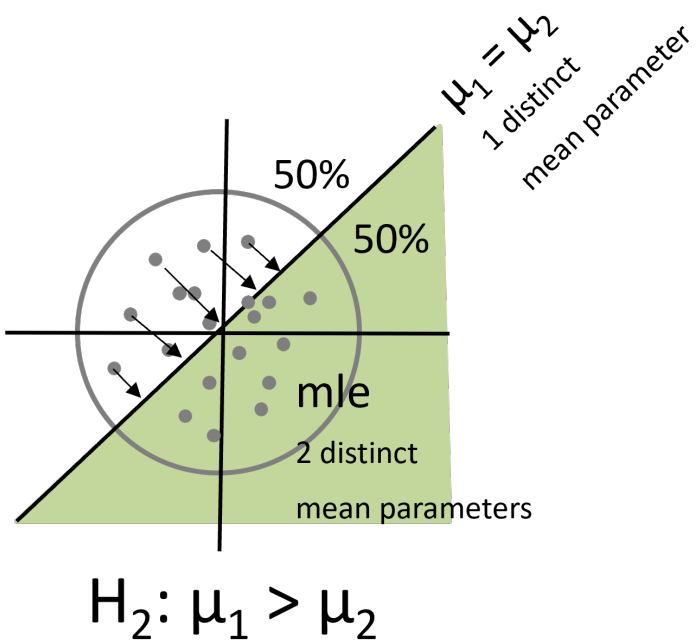


H_2: $\mu_1 > \mu_2$

Note: sampling from distribution with $\mu_1 = \mu_2 = 0$.
Complexity H_2 is $PT_2 = 1 + 0.5 \times 1 + 0.5 \times 2 = 2.5$.
PT = number of expected distinct/free parameters.

Idea complexity: penalty (PT)

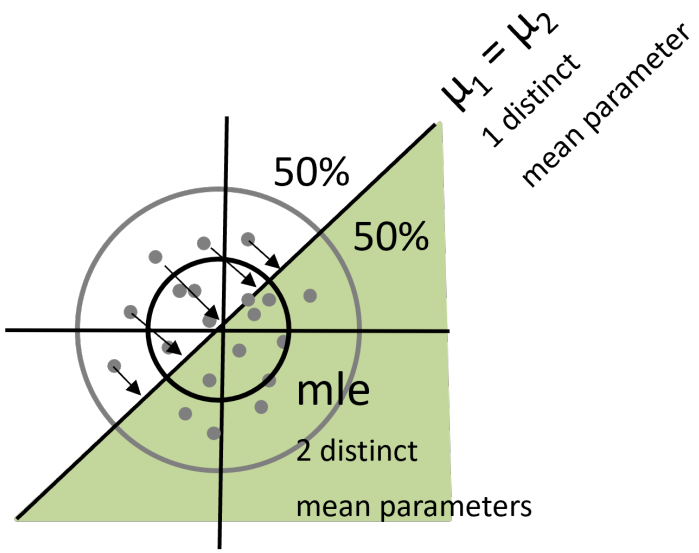
Example 2 means: Contour distribution



Sampling from distribution with $\mu_1 = \mu_2 = 0$. (Note: not likelihood!)
Contour denotes distribution for a variance value.
Choice variance does not matter, see next slide.

Idea complexity: penalty (PT)

Example 2 means: PT value independent from choice variance

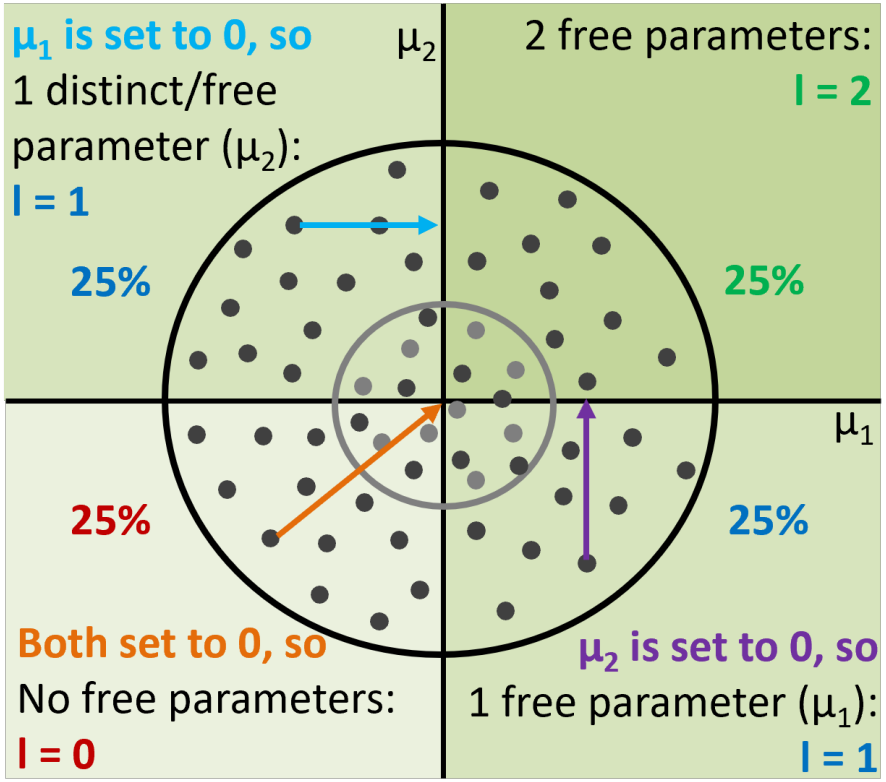


H_2: $\mu_1 > \mu_2$

For both variance values, that is, for both contours:
Complexity H_2 is $PT_2 = 1 + 0.5 \times 1 + 0.5 \times 2 = 2.5$.
PT = number of expected distinct/free parameters.

Extra: Levels and level probabilities

Example 2 means



H_4: $\mu_1 > 0$, $\mu_2 > 0$

Level (l): number of distinct/free parameters.
Level probability (LP_l): probability that there are l levels.
$PT_4 = 1 + 0.25 \times 0 + (0.25 + 0.25) \times 1 + 0.25 \times 2 = 2.$

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

$$
\begin{aligned}
H_0 : &\quad \mu_1 = \mu_2 = \mu_3, \\
H_1 : &\quad \mu_1 > \mu_2 > \mu_3, \\
H_2 : &\quad \mu_1 > \mu_2 < \mu_3, \\
H_3 : &\quad \mu_1 < \mu_2 < \mu_3, \\
H_u : &\quad \mu_1,\ \mu_2,\ \mu_3.
\end{aligned}
$$

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

$IC_m = -2\ fit_m + 2\ complexity_m$

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: Lowest value is best

GORIC is like AIC expected distance from the truth (KL-distance).
One wants smallest distance.

Or: One wants the smallest 'misfit + complexity'.
Note: GORIC = -2 fit + 2 complexity = 2 misfit + 2 complexity

Hence, smallest value is best.

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Note: GORIC = -2 fit + 2 complexity = 2 misfit + 2 complexity

Hence, smallest value is best.

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

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

GORIC

Model	Fit	Complexity	GORIC
H_0	-196.36	2.00	396.71
H_1	-191.89	2.81	389.41
H_2	-193.70	2.81	393.03
H_u	-191.89	4.00	391.79

Hands-on/Demo (1a): GORIC

- 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.

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GORIC(A) in JASP

End & Extra

Interpretation: GORIC weights

GORIC values

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

GORIC weights (w_m)

w_m quantifies relative support for H_m versus others in the set.
Values between 0 and 1, and they sum to 1.
The bigger, the better.

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

$w_m/w_{m'}$ quantifies relative support of H_m vs $H_{m'}$.
Values between 0 and infinity:
* If < 1, lack of support for H_m (nl. $w_{m'}/w_m$, support for $H_{m'}$).
* If > 1, support for H_m.

Interpretation: GORIC weights

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

$w_m/w_{m'}$ quantifies relative support of H_m vs $H_{m'}$.
Values between 0 and infinity:
* If < 1, lack of support for H_m (nl. $w_{m'}/w_m$, support for $H_{m'}$).
* If > 1, support for H_m.

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

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

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_1	-191.89	2.81	389.41	0.68
H_2	-193.70	2.81	393.03	0.11
H_u	-191.89	4.00	391.79	0.21

H_1 is 0.68 / 0.11 $\approx$ 6.11 times more supported than H_2.

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.

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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 goric function)
fit.PandG <- lm(Importance ~ group - 1, data = PandG_data)
```

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 goric function)
fit.PandG <- lm(Importance ~ group - 1, data = PandG_data)
```

R code: Hypotheses

Palmer & Gough

$$
\begin{aligned}
H_1: &\quad \mu_1 > \mu_2 > \mu_3 \\
H_2: &\quad \mu_2 > \mu_1 > \mu_3 \\
H_u: &\quad \mu_1,\ \mu_2,\ \mu_3
\end{aligned}
$$

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

R code: GORIC

Palmer & Gough

$$
\begin{aligned}
H_1 : &\quad \mu_1 > \mu_2 > \mu_3 \\
H_2 : &\quad \mu_2 > \mu_1 > \mu_3 \\
H_u : &\quad \mu_1,\ \mu_2,\ \mu_3
\end{aligned}
$$

```
# 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

$$H_1: \quad \mu_1 > \mu_2 > \mu_3$$
$$H_2: \quad \mu_2 > \mu_1 > \mu_3$$
$$H_u: \quad \mu_1,\ \mu_2,\ \mu_3$$

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_1	-191.89	2.81	389.41	0.68
H_2	-193.70	2.81	393.03	0.11
H_u	-191.89	4.00	391.79	0.21

H_1 and H_2 are not weak (nl, better than Hu - will be explained in a bit).
H_1 is 0.68 / 0.11 $\approx$ 6.11 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

(Two informative) hypotheses of interest

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

(Two informative) hypotheses of interest

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

$$
\begin{aligned}
H_0: &\quad \mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5 \\
H_1: &\quad \mu_5 = \mu_3 > \{\mu_1, \mu_4\} > \mu_2 \\
H_2: &\quad \mu_3 > \mu_1 > \mu_4 = \mu_5 > \mu_2 \\
H_u: &\quad \mu_1,\ \mu_2,\ \mu_3,\ \mu_4,\ \mu_5
\end{aligned}
$$

```
# 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

$$
\begin{aligned}
H_1: &\quad \mu_5 = \mu_3 > \{\mu_1, \mu_4\} > \mu_2 \\
H_2: &\quad \mu_3 > \mu_1 > \mu_4 = \mu_5 > \mu_2 \\
H_u: &\quad \mu_1,\ \mu_2,\ \mu_3,\ \mu_4,\ \mu_5
\end{aligned}
$$

```
# 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

$$
\begin{aligned}
H_1: &\quad \mu_5 = \mu_3 > \{\mu_1, \mu_4\} > \mu_2 \\
H_2: &\quad \mu_3 > \mu_1 > \mu_4 = \mu_5 > \mu_2, \\
H_u: &\quad \mu_1,\ \mu_2,\ \mu_3,\ \mu_4,\ \mu_5.
\end{aligned}
$$

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).

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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):

$$\begin{aligned} H_1 : &\quad \mu_1 > \mu_2 > \mu_3, \\ H_2 : &\quad \mu_2 > \mu_1 > \mu_3 \\ H_u : &\quad \mu_1, \mu_2, \mu_3, \\ &\quad \text{(i.e., } \textit{no restrictions}\text{).} \end{aligned}$$

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

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

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):

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Include "unconstrained" hypothesis

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

Include unconstrained hypothesis H_u (or H_a):

$$\begin{aligned} H_1 : &\quad \mu_1 > \mu_2 > \mu_3, \\ H_2 : &\quad \mu_2 > \mu_1 > \mu_3 \\ H_u : &\quad \mu_1, \mu_2, \mu_3, \\ &\quad \text{(i.e., } \textit{no restrictions}\text{).} \end{aligned}$$

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

$$
\begin{aligned}
H_1 : &\quad \mu_1 > \mu_2 > \mu_3, \\
H_2 : &\quad \mu_2 > \mu_1 > \mu_3 \\
H_u : &\quad \mu_1,\ \mu_2,\ \mu_3.
\end{aligned}
$$

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_1	-191.89	2.81	389.41	0.68
H_2	-193.70	2.81	393.03	0.11
H_u	-191.89	4.00	391.79	0.21

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.

Use of H_u

Palmer & Gough

$$
\begin{aligned}
H_1 : &\quad \mu_1 > \mu_2 > \mu_3, \\
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If at least one informative hypothesis not weak (i.e., $w_m > w_u$ or $w_m/w_u > 1$), then compare informative hypotheses.
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Use of H_u

Palmer & Gough

$$
\begin{aligned}
H_1 : &\quad \mu_1 > \mu_2 > \mu_3, \\
H_2 : &\quad \mu_2 > \mu_1 > \mu_3 \\
H_u : &\quad \mu_1,\ \mu_2,\ \mu_3.
\end{aligned}
$$

GORIC

Model	Fit	Complexity	GORIC	GORIC weights	without Hu
H_1	-191.89	2.81	389.41	0.68	0.86
H_2	-193.70	2.81	393.03	0.11	0.14
H_u	-191.89	4.00	391.79	0.21	NA

H_1 is not weak and is 0.68 / 0.11 = 0.86 / 0.14 $\approx$ 6.11 times more supported than competing hypothesis H_2.

H_1 vs H_u

Palmer & Gough

What if only one informative hypothesis:

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

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_u.

BUT: H_u includes H_1.

So, support for H_u contains support for H_1.

H_1 vs H_u

Palmer & Gough

What if only one informative hypothesis:

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

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_u.
BUT: H_u includes H_1.
So, support for H_u contains support for H_1.

H_1 vs H_u

Palmer & Gough

What if only one informative hypothesis:

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

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_u.
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 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

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Palmer & Gough

GORIC

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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

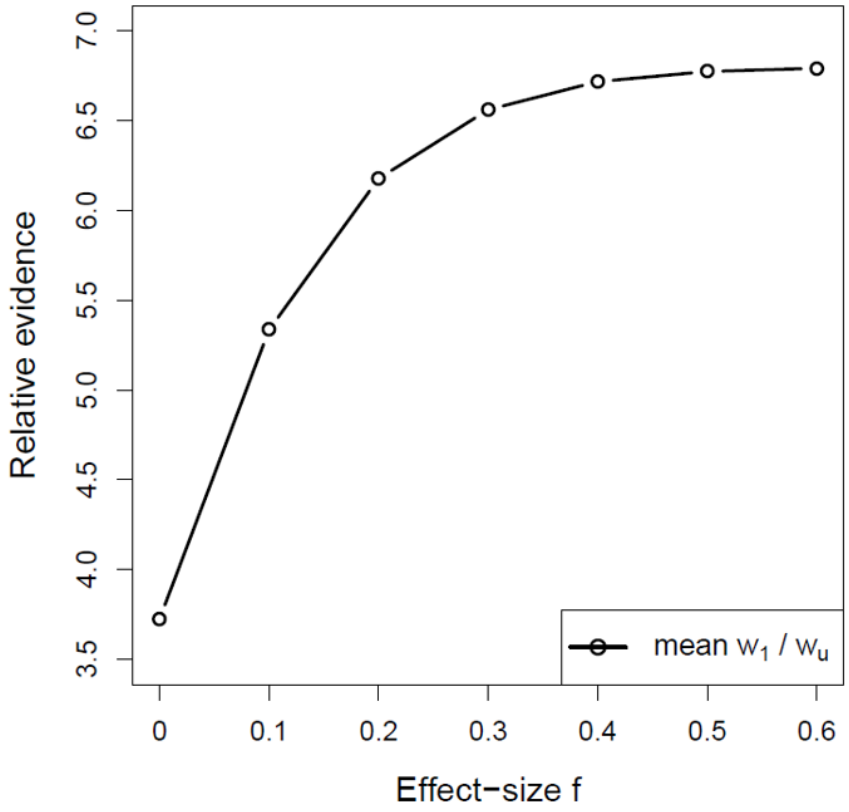


Figure: IC weights can have an upper bound, when informative hypothesis has maximum fit (i.e., is fully in agreement with the data).

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.

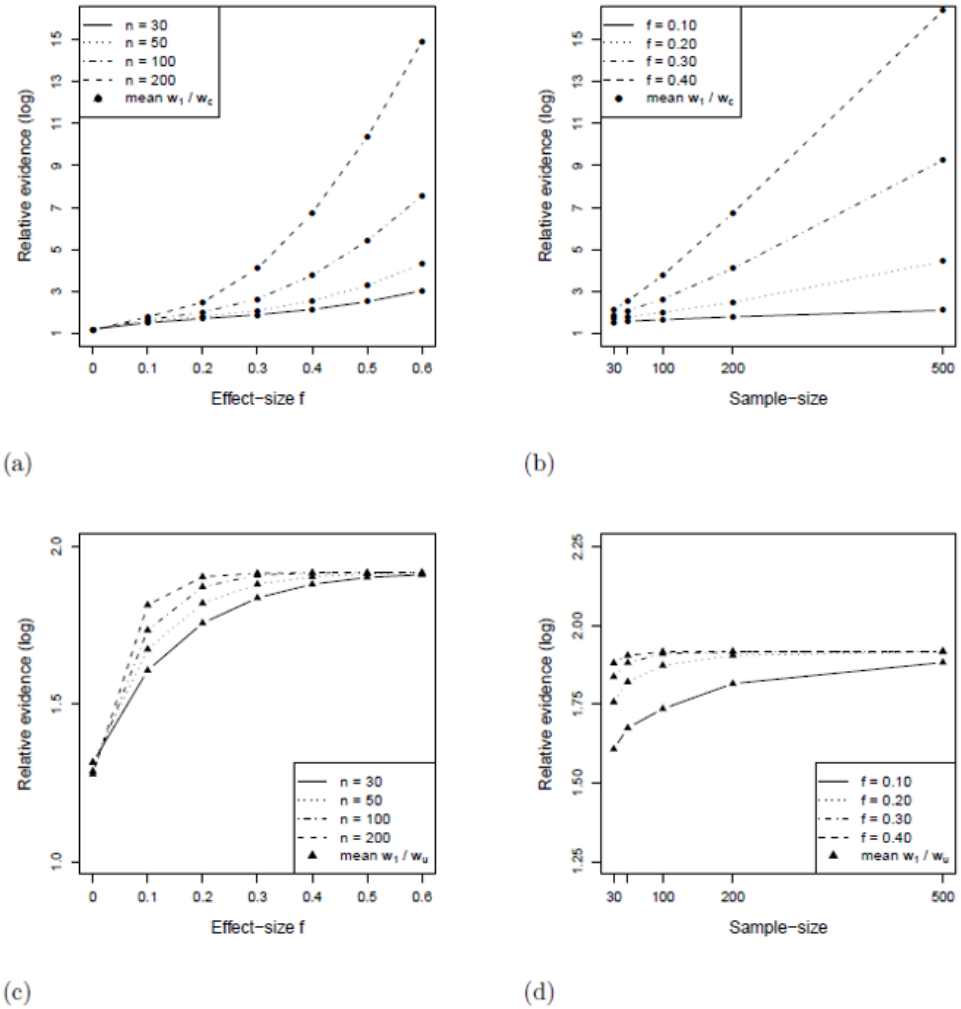
Reference:
Vanbrabant, L., Van Loey, N., and Kuiper, R. M. (2020). Evaluating a Theory-Based Hypothesis Against Its Complement Using an AIC-Type Information Criterion With an Application to Facial Burn Injury. *Psychological Methods, 25(2)*, 129-142.
https://doi.org/10.1037/met0000238

Alternative failsafe: Complement of H_m

Based on simulation

vs complement

vs unconstrained



Note: unconstrained vs complement

H_1 contains 1 ordering of means:

1. $\mu_1 > \mu_2 > \mu_3$

H_c contains 5 orderings of means:

2. $\mu_1 > \mu_3 > \mu_2$
3. $\mu_2 > \mu_1 > \mu_3$
4. $\mu_2 > \mu_3 > \mu_1$
5. $\mu_3 > \mu_1 > \mu_2$
6. $\mu_3 > \mu_2 > \mu_1$

H_u combines H_1 and H_c, and thus consists of all 6 possble orderings.

Note: unconstrained vs complement

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H_u combines H_1 and H_c, and thus consists of all 6 possble orderings.

R code: complement

Palmer & Gough

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

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

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

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.

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Note on use of safeguard hypotheses (2/2)

My advise and default in goric function:

- If multiple informative, theory-based hypotheses:
  Goal: Comparison of informative, theory-based hypotheses.
  Safeguard: Unconstrained.

- If one informative, theory-based hypothesis (H_m):
  Goal: Compare H_m with all other possibilities / theories.
  Safeguard: Its complement.

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My advise and default in goric function:

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Extra: complement & 'Heq' (1/4)

Palmer & Gough

H_1 and H_c do not really overlap, but they do share a border.
The border is defined by boundary hypotheses, that is, all possible hypotheses where ≥ 1 inequalities ('<', '>') are replaced by '='.

If one wishes to also evaluate the boundary hypothesis were all inequalities are replaced by equalities (H_{eq}):

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

then one can use 'Heq = TRUE',
as demonstrated on the next slide.

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then one can use 'Heq = TRUE',
as demonstrated on the next slide.

Extra: complement & 'Heq' (2/4)

Palmer & Gough

R code

```
#Heq: mu1 = mu2, mu3 -> Heq = T(RUE)
H1 <- 'group1 > group2' #mu1 > mu2, mu3
# 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=H1),
                        Heq = T)
```

Extra: complement & 'Heq' (3/4)

Palmer & Gough

R output (partly)

```
## restriktor (0.6-50): generalized order-restricted information criterion:
##
## Results:
##         model    loglik  penalty    goric  loglik.weights  penalty.weights
## 1         Heq  -193.703    3.000  393.406           0.123            0.452
## 2          H1  -191.893    3.500  390.786           0.753            0.274
## 3  complement  -193.703    3.500  394.406           0.123            0.274
##    goric.weights  goric.weights_without_heq
## 1          0.188
## 2          0.698                      0.859
## 3          0.114                      0.141
##
## Conclusion:
## - The order-restricted hypothesis H1 is the best in the set, as it has the h
##   * 'H1' is 6.109 times more supported than 'complement'.
```

Extra: complement & 'Heq' (4/4)

Note

H_{eq} is only one boundary hypothesis, and the most strict one.

I would only include H_{eq} when you a priori want to evaluate this (possibly to rule it out).

When the truth lies on the border of H_1 and H_c,
then the loglik.weights are approximate equal.
If you find this, then I would go into an exploration phase
(and evaluate all (or some) boundary hypotheses).

Extra: complement & 'Heq' (4/4)

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ANOVA Example alternative

Comparisons of 3 Means with minimal/meaningful differences

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

Theory-based hypothesis using minimal or meaningful differences:

$$H_1: \quad \mu_1 - \mu_2 > 0.1 \quad \& \quad \mu_2 - \mu_3 > 0.2,$$

where "$>$" denotes "larger than".

Note:
Could also formulate competing hypotheses based on effect size cut-offs (for say, small, medium, and large effects).

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Example GORIC minimal/meaningful difference

Based on Palmer & Gough (2007) Data

$$H_1: \quad \mu_1 - \mu_2 > 0.1 \quad \& \quad \mu_2 - \mu_3 > 0.2,$$
$$H_c: \quad \text{not } H_1.$$

GORIC

Model	Fit	Complexity	GORIC	GORIC weights
H_1	-191.89	2.81	389.41	0.76
H_c	-192.18	3.69	391.72	0.24

H_1 is 0.76 / 0.24 $\approx$ 3.17 times more supported than its complement H_c, that is, any other hypothesis.

Example GORIC minimal/meaningful difference

Based on Palmer & Gough (2007) Data

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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.

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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.
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GORICA

Similarities with GORIC

- Form: $GORICA_m = -2\ fit + 2\ complexity$.
- 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).

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In case of normal linear models or, otherwise, for not too small samples: GORICA weights = GORIC weights.

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In case of normal linear models or, otherwise, for not too small samples: GORICA weights = GORIC weights.

R code: GORICA

Palmer & Gough

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

GORICA: type = "gorica" (not default for lm objects)

```
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

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

Model	Fit	Complexity	GORICA	GORICA weights
H1	-1.90	1.81	7.42	0.79
complement	-2.34	2.69	10.06	0.21

H_1 is 0.79 / 0.21 $\approx$ 3.74 times more supported than its complement, that is, any other hypothesis.

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

GORICA

Palmer & Gough

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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.

Power improvement

Power improvement via

- Using order restrictions
  (cf. one-sided vs two-sided testing).
- Having limited set of hypotheses.
  Note: Null hypothesis can be one of them, but only if of interest!
  Try to think outside of the null-hypothesis box :-).
- (if:) Specifying restrictions for multiple outcomes within each informative hypothesis.

If you do not have a priori expectations and sample size is large enough:
1) You could use part of your data to generate one or more hypotheses.
2) This/These can then be evaluated in the other part of the data.

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GORIC(A) in JASP

End & Extra

GORIC in JASP: instructions

Palmer & Gough

- Extract data file 'Data_PalmerAndGough_JASP.txt' from 'data_JASP' subfolder (`github.com/rebeccakuiper/Tutorials`).
- Open JASP and 'Data_PalmerAndGough_JASP.txt'. Check measurement levels.
- Go to ANOVA and denote variables of interest.
- Go to Order Restricted Hypotheses tab.
- Specify hypotheses. For example,

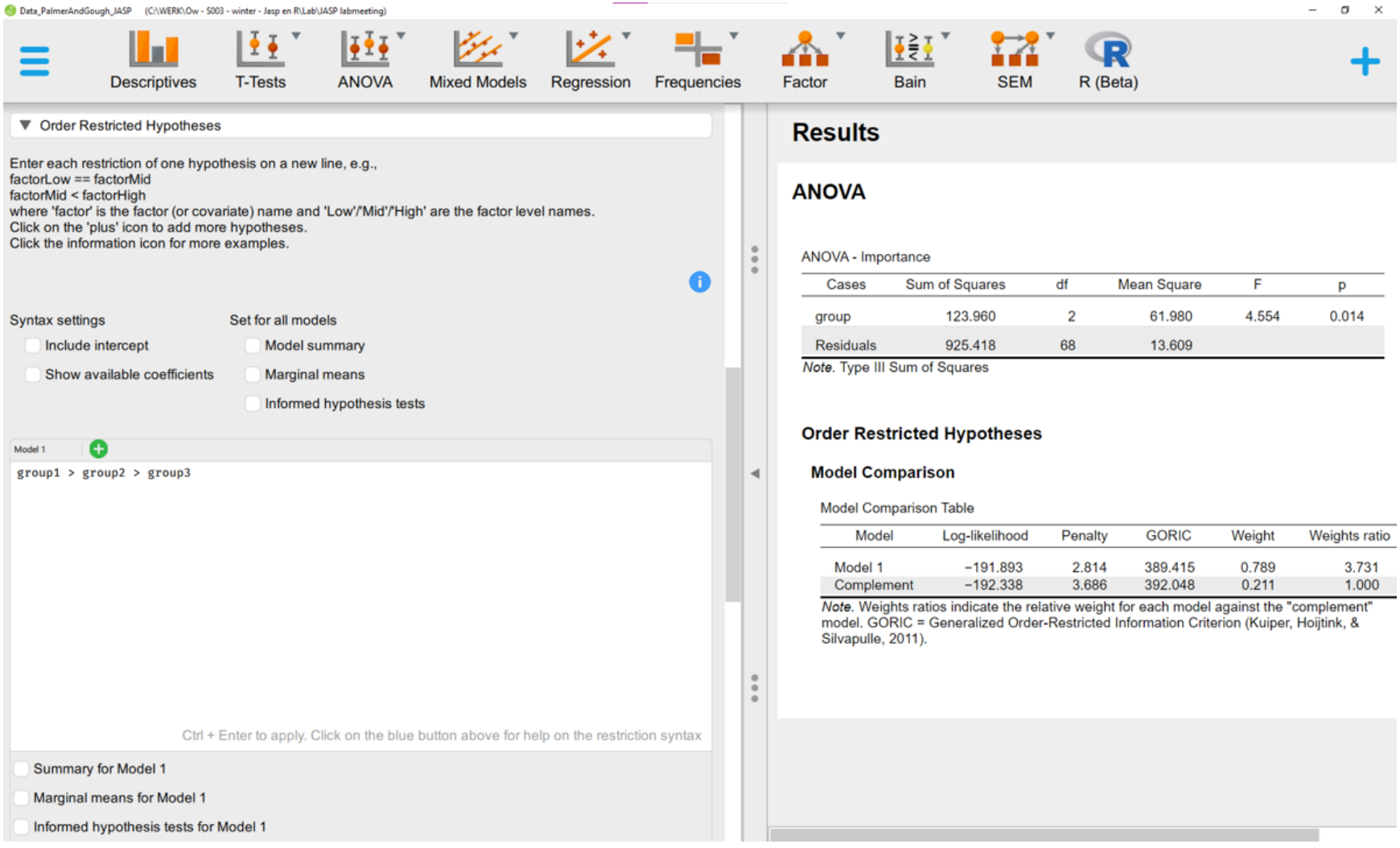
$$\begin{aligned} H_1: &\quad \mu_1 > \mu_2 > \mu_3 \\ JASP: &\quad group1 > group2 > group3 \end{aligned}$$

- Press Ctrl+Enter. Inspect and interpret output.

More in (demo and) lab.

GORIC in JASP: screenshot

Palmer & Gough



GORIC in JASP: instructions

Lucas

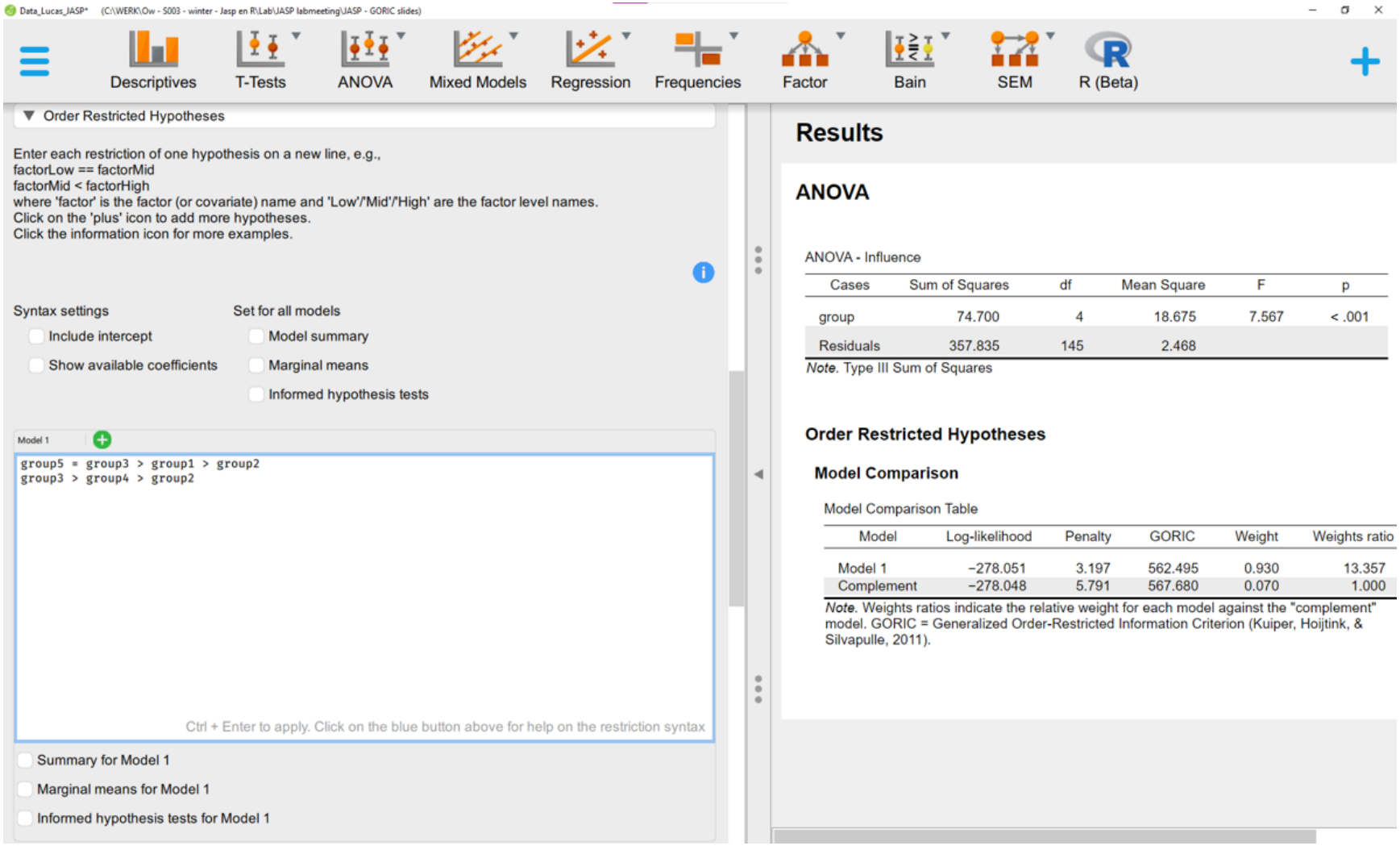
- Open JASP.
  Use 'Data_Lucas_JASP.txt' ('data_JASP' subfolder).
  Check measurement levels.
- Go to ANOVA and denote variables of interest.
- Go to Order Restricted Hypotheses tab.
- Specify hypotheses. For example,

$$
\begin{aligned}
H_1: &\quad \mu_5 = \mu_3 > \{\mu_1, \mu_4\} > \mu_2 \\
JASP: &\quad group5 = group3 > group1 > group2 \\
&\quad group3 > group4 > group2
\end{aligned}
$$

- Press Ctrl+Enter. Inspect and interpret output.

GORIC in JASP: screenshot

Lucas

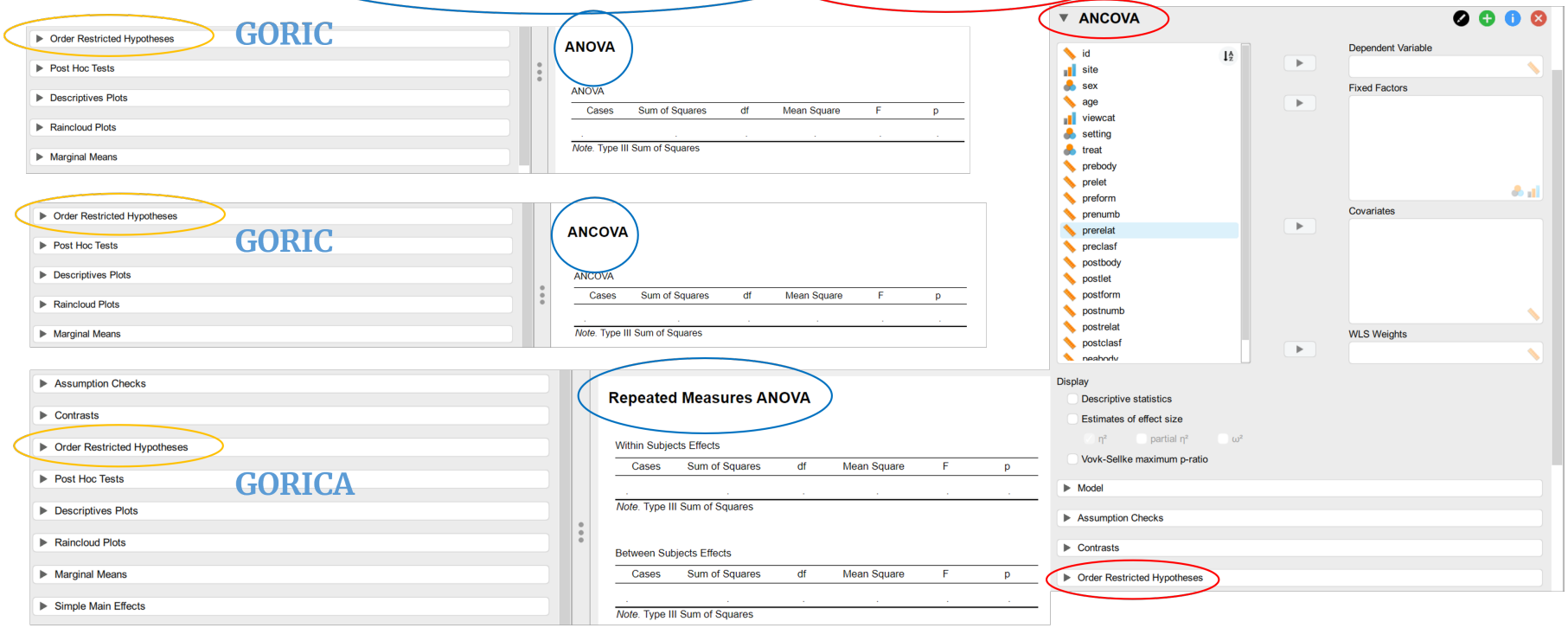


GORIC and GORICA in JASP

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

GORIC and GORICA in JASP

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



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End & Extra

More information GORIC(A) output

More information GORIC(A) output:

- 'Guidelines_output_GORIC.html'
- Possibly: 'Guidelines_GORIC-Benchmarks'

from `https://github.com/rebeccakuiper/Tutorials`.
On github site, go to Code (green button) and download zip.

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/Extra1
www.uu.nl/staff/RMKuiper/Extra2
informative-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
- Check out decision trees files (github.com/rebeccakuiper/Tutorials)
- Check out benchmarks function (via tutorial and/or hands-on file)

We end with:

- Lab

Notes

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

Note on type of hypotheses

Absolute strength

Compare strength/importance of parameters: $\beta_1 > \beta_2$.
Compare absolute strength/importance of parameters:
$abs(\beta_1) > abs(\beta_2)$.

About-equality

Equality: $\beta_1 = \beta_2$.
About-equality: $-0.01 < \beta_1 - \beta_2 < 0.01$.

Minimum difference

Difference: $abs(\beta_1) > abs(\beta_2)$.
Minimum difference: $abs(\beta_1) - abs(\beta_2) > 0.01$.

Note on type of hypotheses: Magnitude-hypotheses

Hypotheses can regard height of effect size.
In the case of Cohen's d, one could evaluate:

$$H_1 : d < 0,$$
$$H_2 : d > 0,$$
$$H_3 : d > 0.2,$$
$$H_4 : d > 0.5,$$
$$H_5 : d > 0.8.$$

Now, overlapping hypotheses.

$$H_1 : d < 0,$$
$$H_2 : 0 < d < 0.2,$$
$$H_3 : 0.2 < d < 0.5,$$
$$H_4 : 0.5 < d < 0.8,$$
$$H_5 : d > 0.8.$$

Now, range restrictions (complexity as if equalities).

Or better: One of these versus its complement.

Or incorporate such cut-off values when inspecting ordering of parameters (say, means).

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.
  If no expectations (or no support), use exploration and confirmation:
  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`.

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

Extra material (1/2)

- GORICA on logistic Regression Model
  - 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.

Extra material (2/2)

- GORICA on CTmeta
  - Article: doi.org/10.1080/10705511.2020.1823228.
  - R scripts: github.com/rebeccakuiper/GORICA_on_CTmeta.
- GORICA on Meta-analysis
  - Article: doi.org/10.3390/e24111525.
  - R scripts: github.com/rebeccakuiper/GORICA_on_MetaAn.

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 is related 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.

Note on conditional error probability (1/3)

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 (2/3)

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 (3/3)

using PMPS and GORIC(A) weights

What does conditional error probability reflect when hypotheses overlap?
Notably, when hypotheses overlap they can also share/divide support (like H_u does with any hypothesis).

My advise:
Only use error probabilities if one hypothesis versus its complement.
(Or when you are sure that there is no overlap in hypotheses;
and they preferably do cover all possibilities)

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 $n = 50$)

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

$H_{31E} : \mu_1 = \mu_2,\ \mu_3$ $\quad$ $H_{31C} : \mu_1 < \mu_2 < \mu_3$

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

$H_{33E} : \mu_1 = \mu_3,\ \mu_2$ $\quad$ $H_{33C} : \mu_1 < \mu_2 > \mu_3$

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

'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):
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
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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):
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
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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

$P(\boldsymbol{\mu}, \sigma^2) = P(\mu_1) \times \ldots \times P(\mu_k) \times P(\sigma^2)$,
where $P(\mu_i) = P(\mu)\ \forall\ i = 1, \ldots, k$.
$P(\mu)$ 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 $(i = 1, \ldots, k)$ 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 $\tau_0^2 = [\frac{UB_{max}-LB_{min}}{2}]^2$.
Three types of prior vagueness: BMS PV 1, BMS PV 2 and BMS PV 3