Tutorial

Shiny app 'GoricEvSyn':
GORIC(A) evidence synthesis

https://utrecht-university.shinyapps.io/GoricEvSyn/

Open app: Top

Aggregating evidence from multiple studies (with diverse designs), using as input: **(Standardized) parameter estimates and their covariance matrix**   GORICA or GORIC values   *By using this app you agree with the Terms of Usage*   Contact

Click here to open a folder with a tutorial and folders with example input files

Input

Choose your **type of evidence synthesis approach**.
In case of an equal-evidence approach, aggregating evidence from 5 studies with n=100 observations is the same as obtaining evidence from 1 study (as if it was possible) with n=500 observations (like meta-analysis does).
In the added-evidence approach, the aggregated evidence from 5 studies is stronger than as if the data were combined (as if that was possible).

```
Equal-evidence approach                                    ▼
```

Fill in the **number of studies**, that is, the integer S (>= 2).

```
2
```

Select the tab delimited .txt file that contains the **names and values of the (standardized) parameter estimates of interest**, each on one line. Do this for each study. If you want to seperate or label the lines, use headers starting with a '#'. For example,
\# Study 1
b1 b2 b3 b4
1.70 1.20 0.50 0.10
\# Study 2
b_1 b_2 b_3
1.75 0.90 0.25

```
Browse...    No file selected
```

Select the tab delimited .txt file that contains the **covariance matrices of the (standardized) parameter estimates**. For Study s, this matrix consists of k_s rows and k_s columns, with k_s the number of parameters in Study s. Do this for each study, by writing them below each other. If you want to seperate or label the matrices, use headers starting with a '#'.

```
Browse...    No file selected
```

Fill in the **number of hypotheses**, that is, the integer M (>= 1), excluding the unconstrained and the complement of hypothesis H_m (m=1,...,M).
In case M > 1, the unconstrained hypothesis (representing all possible theories) is included. In case, M = 1, one can choose below which safeguard/competing hypothesis should be included.

```
1
```

Choose your **type of competing hypothesis** to evaluate your hypothesis of interest against.
Since you have one hypothesis of interest (M = 1), you can choose to use the complement of the hypothesis of interest (i.e., all the other possible theories exept

Output

H_u denotes the unconstrained hypothesis, which covers all possible theories (including the ones in the evaluation).

H_{cm} denotes the complement of Hypothesis H_m, which covers the remaining theories (hence, excluding the one in H_m).

Evidence per study and per hypotheses of interest (using goric function from R package restriktor)

GORICA values

```
NULL
```

GORICA weights

```
NULL
```

$GORICA_m$ = GORICA value for hypothesis H_m.

LL_m and PT_m are log likelihood and penalty value for hypothesis H_m, respectively.

$GORICA.weight_m$ = GORICA weight for hypothesis H_m.

$rel.GORICA.weight_{mu}$ or $rel.GORICA.weight_{mc}$ = ratio of GORICA weights (i.e., relative evidence) for Hypothesis H_m versus the unconstrained hypothesis (H_u) or versus its complement (H_{cm}), respectively.

Aggregated evidence over all studies (updated per study and the final overall evidence)

GORICA values

```
NULL
```

GORICA weights

```
NULL
```

$Final.rel.GORICA.weights$ = matrix of final GORICA weights ratios (i.e., relative evidence) for each Hypothesis H_m versus each of the hypotheses.

k_s columns, with k_s the number of parameters in Study s. Do this for each study, by writing them below each other. If you want to seperate or label the matrices, use headers starting with a '#'.

Browse...   No file selected

Fill in the **number of hypotheses**, that is, the integer M (>= 1), excluding the unconstrained and the complement of hypothesis H_m (m=1,...,M).
In case M > 1, the unconstrained hypothesis (representing all possible theories) is included. In case, M = 1, one can choose below which safeguard/competing hypothesis should be included.

1

Choose your **type of competing hypothesis** to evaluate your hypothesis of interest against.
Since you have one hypothesis of interest (M = 1), you can choose to use the complement of the hypothesis of interest (i.e., all the other possible theories exept the one that is specified) or the unconstrained (i.e., all possible theories, including the one specified).

Complement (Hc)   ▾

Do all studies have the same hypotheses-specification **same hypotheses-specification** (and thus also the same number of parameter estimates with the same names)?

yes   ▾

Select the tab delimited .txt file that contains the **hypotheses of interest** H_m (m=1,...,M), which are specified using the names of the (standardized) parameter estimates as given in previous input. Within a hypothesis, multiple restrictions are combined by a ';', restrictions should be pairwise (i.e., b1 > b2; b2 > b3 instead of b1 > b2 > b3), and equalities are denoted by '==' (not '='). If you want to label lines, use headers starting with a '#'.
Note: In case of comparing parameter estimates of continuous variables, one should use the standardized parameter estimates (e.g., by standardizing the continuous variables).
For example (if M = 1),
Hypothesis 1
b1 > b2; b2 > b3; b3 > b4; b1 - b2 > 2*(b3 - b4)
If sets of hypotheses vary over studies, then do this for each study below each other (and use, if necessary, the study-specific parameter names). For example (if M = 1 and S = 2),
Study 1
Hypothesis 1
b1 > b2; b2 > b3; b3 > b4; b1 - b2 > 2*(b3 - b4)
Study 2
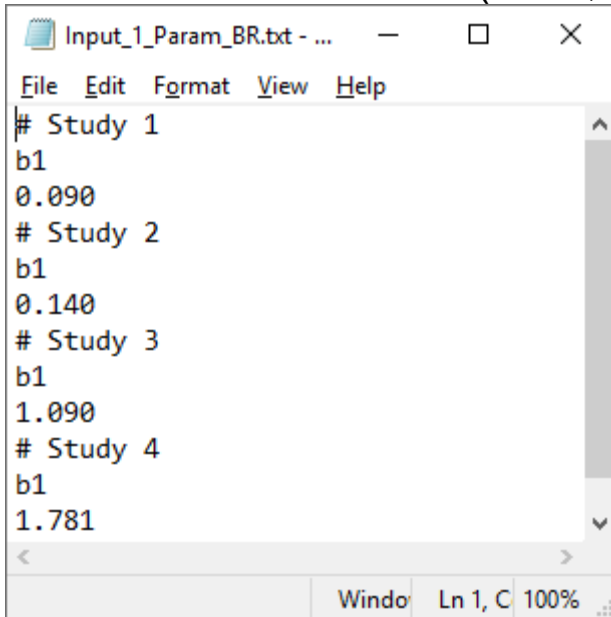# Hypothesis 1
b_1 > b_2; b2 > b_3

Browse...   No file selected
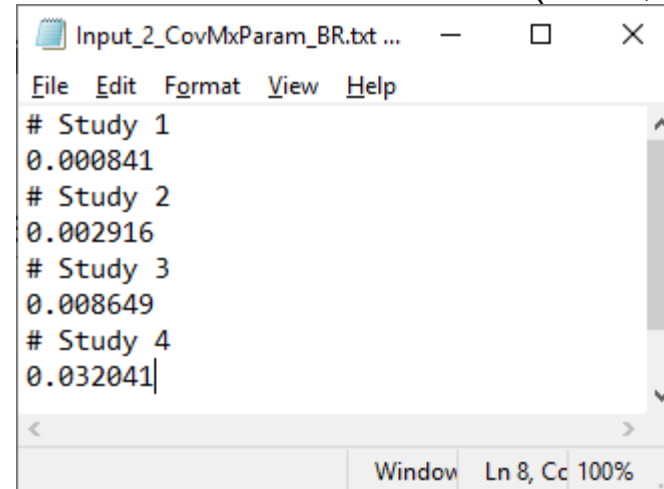
Input: **One-parameter** example with three hypotheses

Combine evidence from S=4 studies
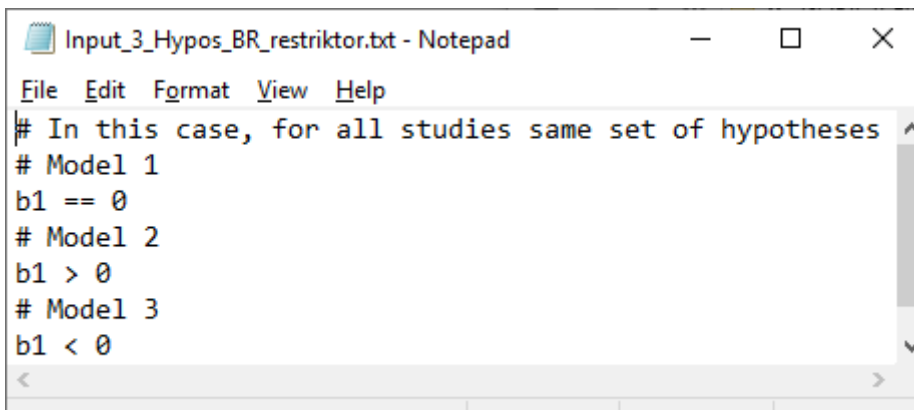
Parameter estimates (here, one):

```
Input_1_Param_BR.txt - ...     —   □   ×
File  Edit  Format  View  Help
# Study 1
b1
0.090
# Study 2
b1
0.140
# Study 3
b1
1.090
# Study 4
b1
1.781

                    Windo   Ln 1, C  100%
```

Their covariance matrix (here, variance):

```
Input_2_CovMxParam_BR.txt ...     —   □   ×
File  Edit  Format  View  Help
# Study 1
0.000841
# Study 2
0.002916
# Study 3
0.008649
# Study 4
0.032041

                Window   Ln 8, Cc  100%
```

Hypotheses (same for each)

```
Input_3_Hypos_BR_restriktor.txt - Notepad     —   □   ×
File  Edit  Format  View  Help
# In this case, for all studies same set of hypotheses
# Model 1
b1 == 0
# Model 2
b1 > 0
# Model 3
b1 < 0
```

Example input: Top (zoomed in)

D:/Shiny Apps and R packages/_4-2_GoricEvSyn - Release 1 - Shiny

http://127.0.0.1:7141   Open in Browser

n=100 observations is the same as obtaining evidence from 1 study (as if it was possible) with n=500 observations (like meta-analysis does).
In the added-evidence approach, the aggregated evidence from 5 studies is stronger than as if the data were combined (as if that was possible).

Added-evidence approach

Fill in the number of studies, that is, the integer S (>= 2).

4

Select the tab delimited .txt file that contains the **names and values of the (standardized) parameter estimates of interest**, each on one line. Do this for each study. If you want to seperate or label the lines, use headers starting with a '#'. For example,
Study 1
b1 b2 b3 b4
1.70 1.20 0.50 0.10
Study 2
b_1 b_2 b_3
1.75 0.90 0.25

Browse...   Input_1_Param_BR.txt
Upload complete

Select the tab delimited .txt file that contains the **covariance matrices of the (standardized) parameter estimates**. For Study s, this matrix consists of k_s rows and k_s columns, with k_s the number of parameters in Study s. Do this for each study, by writing them below each other. If you want to seperate or label the matrices, use headers starting with a '#'.

Browse...   Input_2_CovMxParam_BR.txt
Upload complete

Fill in the **number of hypotheses**, that is, the integer M (>= 1), excluding the unconstrained and the complement of hypothesis H_m (m=1,...,M).
In case M > 1, the unconstrained hypothesis (representing all possible theories) is included. In case, M = 1, one can choose below which safeguard/competing hypothesis should be included.

3

Choose your **type of competing hypothesis** to evaluate your hypothesis of interest against.
Since you have multiple hypotheses of interest (M > 1), you may need a safeguard-hypothesis such that not the best out of a set of weak hypotheses is chosen. You can choose to use the unconstrained (i.e., all possible theories, including the ones specified) as safeguard or to use none if your theories cover all possible theories.

Do all studies have the same hypotheses-specification **same hypotheses-specification** (and thus also the same number of parameter estimates with the same names)?

yes

Evidence per study and per hypotheses of interest (using goric function from R package restriktor)

GORICA values
NULL

GORICA weights
NULL

$GORICA_m$ = GORICA value for hypothesis H_m.

LL_m and PT_m are log likelihood and penalty value for hypothesis H_m, respectively.

GORICA.weight$_m$ = GORICA weight for hypothesis H_m.

rel.GORICA.weight$_{mu}$ or rel.GORICA.weight$_{mc}$ = ratio of GORICA weights (i.e., relat Hm versus the unconstrained hypothesis (H_u) or versus its complement (H_{cm}), respe

Aggregated evidence over all studies (updated per study and the final overall evidence)

GORICA values
NULL

GORICA weights
NULL

Final.rel.GORICA.weights = matrix of final GORICA weights ratios (i.e., relative evid versus each of the hypotheses.

Since the three hypotheses cover all possible theories, we do not need a safeguard hypothesis (i.e., "none")

There is an option to specify study-specific hypotheses:
In case of diverse designs (i.e., conceptual replications), hypotheses representing the same theory may differ because of different operationalization and number of variables.

R D:/Shiny Apps and R packages/_4-2_GoricEvSyn - Release 1 - Shiny

http://127.0.0.1:7141 | Open in Browser | ⟳

k_s columns, with k_s the number of parameters in Study s. Do this for each study, by writing them below each other. If you want to seperate or label the matrices, use headers starting with a '#'.

Browse... | Input_2_CovMxParam_BR.txt

Upload complete

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none ▼

Do all studies have the same hypotheses-specification **same hypotheses-specification** (and thus also the same number of parameter estimates with the same names)?

yes ▼

Select the tab delimited .txt file that contains the **hypotheses of interest** H_m (m=1,...,M), which are specified using the names of the (standardized) parameter estimates as given in previous input. Within a hypothesis, multiple restrictions are combined by a ';', restrictions should be pairwise (i.e., b1 > b2; b2 > b3 instead of b1 > b2 > b3), and equalities are denoted by '==' (not '='). If you want to label lines, use headers starting with a '#'.
Note: In case of comparing parameter estimates of continuous variables, one should use the standardized parameter estimates (e.g., by standardizing the continuous variables).
For example (if M = 1),
Hypothesis 1
b1 > b2; b2 > b3; b3 > b4; b1 - b2 > 2*(b3 - b4)
If sets of hypotheses vary over studies, then do this for each study below each other (and use, if necessary, the study-specific parameter names). For example (if M = 1 and S = 2),
Study 1
Hypothesis 1
b1 > b2; b2 > b3; b3 > b4; b1 - b2 > 2*(b3 - b4)
Study 2
Hypothesis 1
b_1 > b_2; b2 > b_3

Browse... | No file selected

If you upload the file with hypotheses, then the output will be generated.
Scroll up to see it from the top.

Example output: Top

Aggregating evidence from multiple studies (with diverse designs), using as input: | **(Standardized) parameter estimates and their covariance matrix** | GORICA or GORIC values | *By using this app you agree with the Terms of Usage* | Contact

Input

Click here to open a folder with a tutorial and folders with example input files

Input

Choose your **type of evidence synthesis approach**.
In case of an equal-evidence approach, aggregating evidence from 5 studies with n=100 observations is the same as obtaining evidence from 1 study (as if it was possible) with n=500 observations (like meta-analysis does).
In the added-evidence approach, the aggregated evidence from 5 studies is stronger than as if the data were combined (as if that was possible).

Added-evidence approach ▾

Fill in the **number of studies**, that is, the integer S (>= 2).

4

Select the tab delimited .txt file that contains the **names and values of the (standardized) parameter estimates of interest**, each on one line. Do this for each study. If you want to seperate or label the lines, use headers starting with a '#'. For example,
Study 1
b1 b2 b3 b4
1.70 1.20 0.50 0.10
Study 2
b_1 b_2 b_3
1.75 0.90 0.25

Browse... | Input_1_Param_BR.txt
Upload complete

Select the tab delimited .txt file that contains the **covariance matrices of the (standardized) parameter estimates**. For Study s, this matrix consists of k_s rows and k_s columns, with k_s the number of parameters in Study s. Do this for each study, by writing them below each other. If you want to seperate or label the matrices, use headers starting with a '#'.

Browse... | Input_2_CovMxParam_BR.txt
Upload complete

Fill in the **number of hypotheses**, that is, the integer M (>= 1), excluding the unconstrained and the complement of hypothesis H_m (m=1,...,M).
In case M > 1, the unconstrained hypothesis (representing all possible theories) is included. In case, M = 1, one can choose below which safeguard/competing hypothesis should be included.

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Choose your **type of competing hypothesis** to evaluate your hypothesis of interest against.
Since you have multiple hypotheses of interest (M > 1), you may need a safeguard-hypothesis such that not the best out of a set of weak hypotheses is chosen. You

Output

H_u denotes the unconstrained hypothesis, which covers all possible theories (including the ones in the evaluation).

H_{cm} denotes the complement of Hypothesis H_m, which covers the remaining theories (hence, excluding the one in H_m).

Evidence per study and per hypotheses of interest (using goric function from R package restriktor)

GORICA values

```
$GORICA_m
          H1      H2       H3
Study1   6.388 -2.24304   7.388
Study2   4.722 -0.99967   5.722
Study3 136.456  0.08757 137.456
Study4  99.394  1.39714 100.394

$LL_m
          H1     H2      H3
Study1  -2.194 2.6215  -2.194
Study2  -1.361 1.9998  -1.361
Study3 -67.228 1.4562 -67.228
Study4 -48.697 0.8014 -48.697

$PT_m
        H1  H2  H3
Study1   1 1.5 1.5
Study2   1 1.5 1.5
Study3   1 1.5 1.5
Study4   1 1.5 1.5
```

GORICA weights

```
$GORICA.weight_m
            H1     H2       H3
Study1 1.308e-02 0.9790 7.931e-03
Study2 5.241e-02 0.9158 3.179e-02
Study3 2.443e-30 1.0000 1.482e-30
Study4 5.251e-22 1.0000 3.185e-22
```

$GORICA_m$ = GORICA value for hypothesis H_m.

LL_m and PT_m are log likelihood and penalty value for hypothesis H_m, respectively.

$GORICA.weight_m$ = GORICA weight for hypothesis H_m.

rel.GORICA.weight$_{mu}$ or rel.GORICA.weight$_{mc}$ = ratio of GORICA weights (i.e., relative evidence) for Hypothesis H_m versus the unconstrained hypothesis (H_u) or versus its complement (H_{cm}), respectively.

Aggregated evidence over all studies (updated per study and the final overall evidence)

GORICA values

```
$Approach
[1] Added-evidence approach

$Updated.GORICA_m
          H1      H2       H3
Study1   6.388 -2.243    7.388
Study2  11.110 -3.243   13.110
Study3 147.566 -3.155  150.566
Study4 246.960 -1.758  250.960

$Final.GORICA_m
          H1      H2       H3
246.960  -1.758  250.960

$Final.LL_m
```

GORICA weights

```
$Approach
[1] Added-evidence approach

$Updated.GORICA.weight_m
            H1     H2       H3
Study1 1.308e-02 0.979 7.931e-03
Study2 7.636e-04 0.999 2.809e-04
Study3 1.868e-33 1.000 4.167e-34
Study4 9.806e-55 1.000 1.327e-55

$Final.GORICA.weight_m
         H1 H2       H3
Final 9.806e-55  1 1.327e-55

$Final.rel.GORICA.weights
```

Example output: Top (zoomed in)

First: Study-specific output

Output

H_u denotes the unconstrained hypothesis, which covers all possible theories (including the ones in the evaluation).

H_{cm} denotes the complement of Hypothesis H_m, which covers the remaining theories (hence, excluding the one in H_m).

Evidence per study and per hypotheses of interest (using goric function from R package restriktor)

GORICA values

```
$GORICA_m
          H1        H2       H3
Study1   6.388  -2.24304    7.388
Study2   4.722  -0.99967    5.722
Study3 136.456   0.08757  137.456
Study4  99.394   1.39714  100.394


$LL_m
          H1       H2        H3
Study1   -2.194  2.6215    -2.194
Study2   -1.361  1.9998    -1.361
Study3  -67.228  1.4562   -67.228
Study4  -48.697  0.8014   -48.697


$PT_m
        H1  H2   H3
Study1   1  1.5  1.5
Study2   1  1.5  1.5
Study3   1  1.5  1.5
Study4   1  1.5  1.5
```

GORICA weights

```
$GORICA.weight_m
            H1        H2        H3
Study1 1.308e-02 0.9790 7.931e-03
Study2 5.241e-02 0.9158 3.179e-02
Study3 2.443e-30 1.0000 1.482e-30
Study4 5.251e-22 1.0000 3.185e-22
```

$GORICA_m$ = GORICA value for hypothesis H_m.

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GORICA.weight$_m$ = GORICA weight for hypothesis H_m.

rel.GORICA.weight$_{mu}$ or rel.GORICA.weight$_{mc}$ = ratio of GORICA weights (i.e., relative evidence) for Hypothesis H_m versus the unconstrained hypothesis (H_u) or versus its complement (H_{cm}), respectively.

Example output: Bottom

Upload complete

Select the tab delimited .txt file that contains the **covariance matrices of the (standardized) parameter estimates**. For Study s, this matrix consists of k_s rows and k_s columns, with k_s the number of parameters in Study s. Do this for each study, by writing them below each other. If you want to seperate or label the matrices, use headers starting with a '#'.

Browse...	Input_2_CovMxParam_BR.txt

Upload complete

Fill in the **number of hypotheses**, that is, the integer M (>= 1), excluding the unconstrained and the complement of hypothesis H_m (m=1,...,M).
In case M > 1, the unconstrained hypothesis (representing all possible theories) is included. In case, M = 1, one can choose below which safeguard/competing hypothesis should be included.

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Choose your **type of competing hypothesis** to evaluate your hypothesis of interest against.
Since you have multiple hypotheses of interest (M > 1), you may need a safeguard-hypothesis such that not the best out of a set of weak hypotheses is chosen. You can choose to use the unconstrained (i.e., all possible theories, including the ones specified) as safeguard or to use none if your theories cover all possible theories.

none   ▾

Do all studies have the same hypotheses-specification **same hypotheses-specification** (and thus also the same number of parameter estimates with the same names)?

yes   ▾

Select the tab delimited .txt file that contains the **hypotheses of interest H_m** (m=1,...,M), which are specified using the names of the (standardized) parameter estimates as given in previous input. Within a hypothesis, multiple restrictions are combined by a ';', restrictions should be pairwise (i.e., b1 > b2; b2 > b3 instead of b1 > b2 > b3), and equalities are denoted by '==' (not '='). If you want to label lines, use headers starting with a '#'.
Note: In case of comparing parameter estimates of continuous variables, one should use the standardized parameter estimates (e.g., by standardizing the continuous variables).
For example (if M = 1),
\# Hypothesis 1
b1 > b2; b2 > b3; b3 > b4; b1 - b2 > 2*(b3 - b4)
If sets of hypotheses vary over studies, then do this for each study below each other (and use, if necessary, the study-specific parameter names). For example (if M = 1 and S = 2),
\# Study 1
\# Hypothesis 1
b1 > b2; b2 > b3; b3 > b4; b1 - b2 > 2*(b3 - b4)
\# Study 2
\# Hypothesis 1
b_1 > b_2; b2 > b_3

Browse...	Input_3_Hypos_BR_restriktor.txt

$GORICA_m$ = GORICA value for hypothesis H_m.

LL_m and PT_m are log likelihood and penalty value for hypothesis H_m, respectively.

$GORICA.weight_m$ = GORICA weight for hypothesis H_m.

$rel.GORICA.weight_{mu}$ or $rel.GORICA.weight_{mc}$ = ratio of GORICA weights (i.e., relative evidence) for Hypothesis H_m versus the unconstrained hypothesis (H_u) or versus its complement (H_{cm}), respectively.

Aggregated evidence over all studies (updated per study and the final overall evidence)

GORICA values

```
$Approach
[1] Added-evidence approach

$Updated.GORICA_m
          H1     H2      H3
Study1   6.388 -2.243   7.388
Study2  11.110 -3.243  13.110
Study3 147.566 -3.155 150.566
Study4 246.960 -1.758 250.960


$Final.GORICA_m
    H1     H2     H3
246.960 -1.758 250.960


$Final.LL_m
        H1     H2     H3
Final -119.5  6.879 -119.5


$Final.PT_m
      H1 H2 H3
Final  4  6  6
```

GORICA weights

```
$Approach
[1] Added-evidence approach

$Updated.GORICA.weight_m
            H1       H2       H3
Study1 1.308e-02 0.979 7.931e-03
Study2 7.636e-04 0.999 2.809e-04
Study3 1.868e-33 1.000 4.167e-34
Study4 9.806e-55 1.000 1.327e-55


$Final.GORICA.weight_m
          H1 H2       H3
Final 9.806e-55  1 1.327e-55


$Final.rel.GORICA.weights
        vs H1     vs H2     vs H3
H1 1.000e+00 9.806e-55 7.389e+00
H2 1.020e+54 1.000e+00 7.535e+54
H3 1.353e-01 1.327e-55 1.000e+00
```

Final.rel.GORICA.weights = matrix of final GORICA weights ratios (i.e., relative evidence) for each Hypothesis H_m versus each of the hypotheses.

Example output: Bottom (zoomed in) with comments in blue

$GORICA_m$ = GORICA value for hypothesis H_m.

LL_m and PT_m are log likelihood and penalty value for hypothesis H_m, respectively.

$GORICA.weight_m$ = GORICA weight for hypothesis H_m.

$rel.GORICA.weight_{mu}$ or $rel.GORICA.weight_{mc}$ = ratio of GORICA weights (i.e., relative evidence) for Hypotheses H_m versus the unconstrained hypothesis (H_u) or versus its complement (H_{cm}), respectively.

Aggregated evidence over all studies (updated per study and the final overall evidence)

GORICA values

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$Approach
[1] Added-evidence approach

$Updated.GORICA_m
            H1      H2       H3
Study1   6.388  -2.243    7.388
Study2  11.110  -3.243   13.110
Study3 147.566  -3.155  150.566
Study4 246.960  -1.758  250.960


$Final.GORICA_m
     H1       H2       H3
246.960  -1.758  250.960

$Final.LL_m
         H1       H2      H3
Final -119.5  6.879  -119.5

$Final.PT_m
      H1 H2 H3
Final  4  6  6
```

GORICA weights

```
$Approach
[1] Added-evidence approach

$Updated.GORICA.weight_m
            H1       H2        H3
Study1 1.308e-02 0.979 7.931e-03
Study2 7.636e-04 0.999 2.809e-04
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Study4 9.806e-55 1.000 1.327e-55


$Final.GORICA.weight_m
            H1 H2        H3
Final 9.806e-55  1 1.327e-55

$Final.rel.GORICA.weights
           vs H1     vs H2     vs H3
H1 1.000e+00 9.806e-55 7.389e+00
H2 1.020e+54 1.000e+00 7.535e+54
H3 1.353e-01 1.327e-55 1.000e+00
```
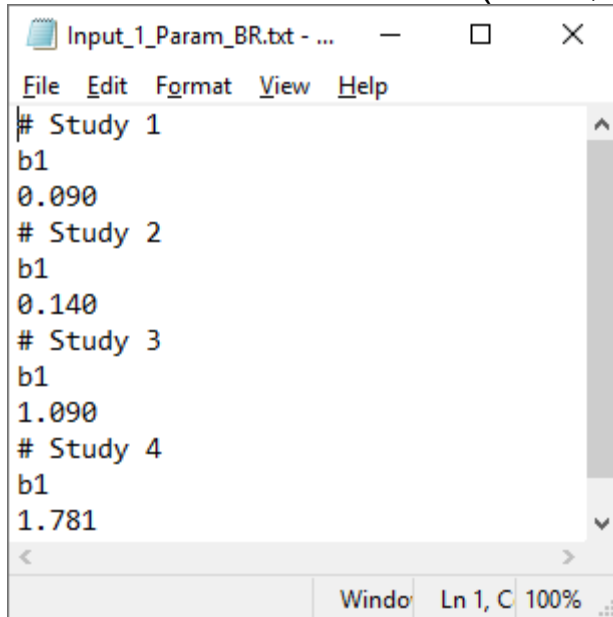
Final.rel.GORICA.weights = matrix of final GORICA weights ratios (i.e., relative evidence) for each Hypothesis versus each of the hypotheses.

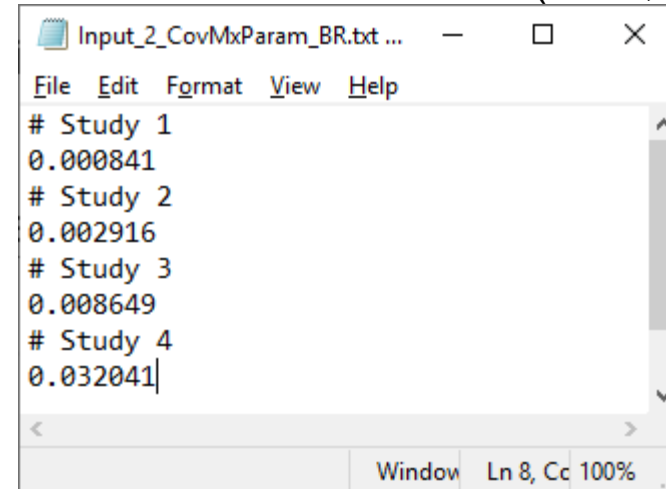*Combined evidence for each 'update'*

Combined evidence after all 'updates'

Input: **One-parameter** example with 1 hypothesis (against complement)

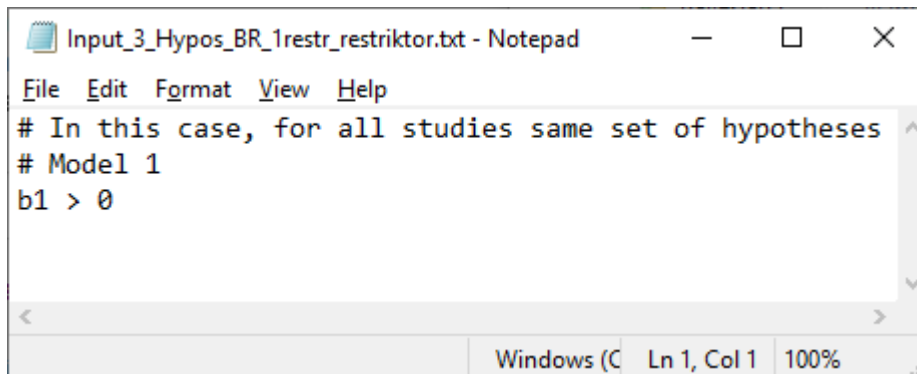Combine evidence from S=4 studies

Parameter estimates (here, one):

Input_1_Param_BR.txt - ...   —   □   ✕

File   Edit   Format   View   Help

```
# Study 1
b1
0.090
# Study 2
b1
0.140
# Study 3
b1
1.090
# Study 4
b1
1.781
```

Windo   Ln 1, C   100%

Their covariance matrix (here, variance):

Input_2_CovMxParam_BR.txt ...   —   □   ✕

File   Edit   Format   View   Help

```
# Study 1
0.000841
# Study 2
0.002916
# Study 3
0.008649
# Study 4
0.032041
```

Window   Ln 8, Cc 100%

Hypotheses (same for each)

Input_3_Hypos_BR_1restr_restriktor.txt - Notepad   —   □   ✕

File   Edit   Format   View   Help

```
# In this case, for all studies same set of hypotheses
# Model 1
b1 > 0
```

Windows (C   Ln 1, Col 1   100%

D:/Shiny Apps and R packages/_4-2_GoricEvSyn - Release 1 - Shiny

http://127.0.0.1:7141 | Open in Browser | Republish ⚙

k_s columns, with k_s the number of parameters in Study s. Do this for each study, by writing them below each other. If you want to seperate or label the matrices, use headers starting with a '#'.

Browse... | Input_2_CovMxParam_BR.txt

Upload complete

Fill in the number of hypotheses, that is, the integer M (>= 1), excluding the unconstrained and the complement of hypothesis H_m (m=1,...,M).
In case M > 1, the unconstrained hypothesis (representing all possible theories) is included. In case, M = 1, one can choose below which safeguard/competing hypothesis should be included.

1

Choose your type of competing hypothesis to evaluate your hypothesis of interest against.
Since you have one hypothesis of interest (M = 1), you can choose to use the complement of the hypothesis of interest (i.e., all the other possible theories exept the one that is specified) or the unconstrained (i.e., all possible theories, including the one specified).

Complement (Hc) ▼

Do all studies have the same hypotheses-specification same hypotheses-specification (and thus also the same number of parameter estimates with the same names)?

yes ▼

Select the tab delimited .txt file that contains the hypotheses of interest H_m (m=1,...,M), which are specified using the names of the (standardized) parameter estimates as given in previous input. Within a hypothesis, multiple restrictions are combined by a ';', restrictions should be pairwise (i.e., b1 > b2; b2 > b3 instead of b1 > b2 > b3), and equalities are denoted by '==' (not '='). If you want to label lines, use headers starting with a '#'.
Note: In case of comparing parameter estimates of continuous variables, one should use the standardized parameter estimates (e.g., by standardizing the continuous variables).
For example (if M = 1),
Hypothesis 1
b1 > b2; b2 > b3; b3 > b4; b1 - b2 > 2*(b3 - b4)
If sets of hypotheses vary over studies, then do this for each study below each other (and use, if necessary, the study-specific parameter names). For example (if M = 1 and S = 2),
Study 1
Hypothesis 1
b1 > b2; b2 > b3; b3 > b4; b1 - b2 > 2*(b3 - b4)
Study 2
Hypothesis 1
b_1 > b_2; b2 > b_3

Browse... | Input_3_Hypos_BR_1restr_restriktor.txt

Upload complete

Aggregated evidence over all studies (updated per study and the final overall evidence)

GORICA values

```
$Approach
[1] Added-evidence approach

$Updated.GORICA_m
          H1      Hc1
Study1 -2.243    7.388
Study2 -3.243   13.110
Study3 -3.155  150.566
Study4 -1.758  250.960

$Final.GORICA_m
         H1      Hc1
 -1.758 250.960

$Final.LL_m
         H1      Hc1
Final 6.879  -119.5

$Final.PT_m
        H1 Hc1
Final   6   6
```

GORICA weights

```
$Approach
[1] Added-evidence approach

$Updated.GORICA.weight_m
           H1        Hc1
Study1 0.9920  8.036e-03
Study2 0.9997  2.811e-04
Study3 1.0000  4.167e-34
Study4 1.0000  1.327e-55

$Final.GORICA.weight_m
          H1       Hc1
Final  1   1.327e-55

$Final.rel.GORICA.weights
        vs H1      vs Hc1
H1   1.000e+00  7.535e+54
Hc1  1.327e-55  1.000e+00
```

Final.rel.GORICA.weights = matrix of final GORICA weights ratios (i.e., relative evidence) for each Hypothesis H_m versus each of the hypotheses.

Example output: Bottom (zoomed in) with comments in blue

GORICA$_m$ = GORICA value for hypothesis H$_m$.

LL$_m$ and PT$_m$ are log likelihood and penalty value for hypothesis H$_m$, respectively.

GORICA.weight$_m$ = GORICA weight for hypothesis H$_m$.

rel.GORICA.weight$_{mu}$ or rel.GORICA.weight$_{mc}$ = ratio of GORICA weights (i.e., relative evidence) for Hypothesis H$_m$ versus the unconstrained hypothesis (H$_u$) or versus its complement (H$_{cm}$), respectively.

Aggregated evidence over all studies (updated per study and the final overall evidence)

GORICA values

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```

GORICA weights

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[1] Added-evidence approach

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Study2 0.9997 2.811e-04
Study3 1.0000 4.167e-34
Study4 1.0000 1.327e-55
```

```
$Final.GORICA_m
    H1     Hc1
 -1.758 250.960

$Final.LL_m
       H1     Hc1
Final 6.879 -119.5

$Final.PT_m
      H1 Hc1
Final  6   6
```

```
$Final.GORICA.weight_m
         H1       Hc1
Final   1 1.327e-55

$Final.rel.GORICA.weights
         vs H1    vs Hc1
H1  1.000e+00 7.535e+54
Hc1 1.327e-55 1.000e+00
```

Final.rel.GORICA.weights = matrix of final GORICA weights ratios (i.e., relative evidence) for each Hypothesis versus each of the hypotheses.

Combined evidence for each 'update'

Combined evidence after all 'updates'