Tutorial

Shiny app 'Bayesian evidence synthesis'

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

Open app: Top

http://127.0.0.1:7384 | Open in Browser | Publish

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

Input

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 parameter estimates**, 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 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).

```
1
```

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 parameter estimates as given in previous input. Within a hypothesis, multiple restrictions are combined by a '&'. If you want to label lines, use headers starting with a '#'.
For example (if M = 1),
Hypothesis 1
b1 > b2 > b3 > b4 & b1 - b2 > 2*(b3 - b4).

Output

Evidence per study and per hypotheses of interest (using R package bain)

Bayes factors (BFs)

```
NULL
```

BF_{mc} = Bayes factor for hypothesis of interest (H_m) versus its complement (compl.H_m)

BF_{mu} = Bayes factor for hypothesis of interest (H_m) versus the unconstrained hypothesis (H_u)

Posterior model probabilities (PMPs)

```
NULL
```

PMP_{mc} = Posterior model probability for hypothesis of interest (H_m) versus its complement (compl.H_m)

PMP_{mu} = Posterior model probability for hypothesis of interest (H_m) versus the other hypotheses in the set.

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

Bayes factors (BFs)

```
NULL
```

c resp. u: (updated or final) BF for H_m versus compl.H_m resp. H_u

inclUnc: the unconstrained hypothesis (i.e., H_u) is added to the set

Posterior model probabilities (PMPs)

```
NULL
```

c resp. u: (updated or final) PMP for H_m versus compl.H_m resp. the other hypotheses in the set

inclUnc: the unconstrained hypothesis (i.e., H_u) is added to the set

Open app: Bottom

c resp. u: (updated or final) BF for H_m versus compl.H_m resp. H_u

inclUnc: the unconstrained hypothesis (i.e., H_u) is added to the set

c resp. u: (updated or final) PMP for H_m versus compl.H_m resp. the other hypotheses in the set

inclUnc: the unconstrained hypothesis (i.e., H_u) is added to the set

Select the tab delimited .txt file that contains the covariance matrices of the 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).

1

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 parameter estimates as given in previous input. Within a hypothesis, multiple restrictions are combined by a '&'. If you want to label lines, use headers starting with a '#'.
For example (if M = 1),
Hypothesis 1
b1 > b2 > 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 > b3 > b4 & b1 - b2 > 2*(b3 - b4)
Study 2
Hypothesis 1
b_1 > b_2 > b_3

Browse... | No file selected

Select the tab delimited .txt file that contains the number of observations (N). Currently, the program assumes that studies with group structures, like ANOVAs, have group sizes that are approximately equal. For such models, fill in the total number of observations and not the (average) group size.
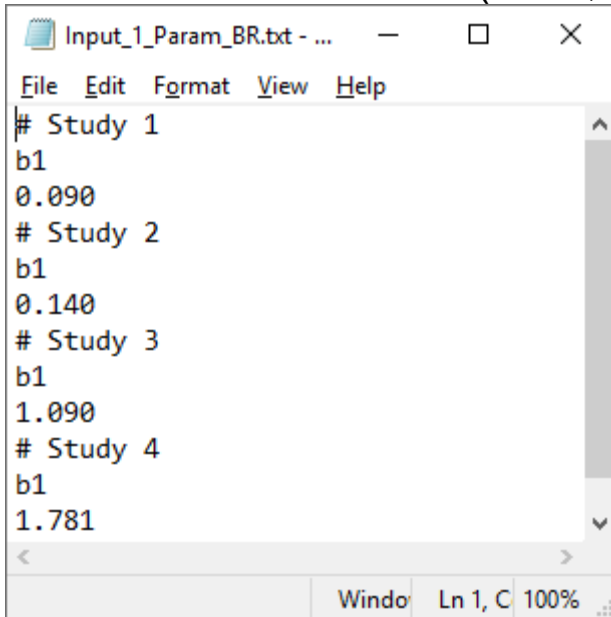
Browse... | No file selected

Input: **One-parameter** example
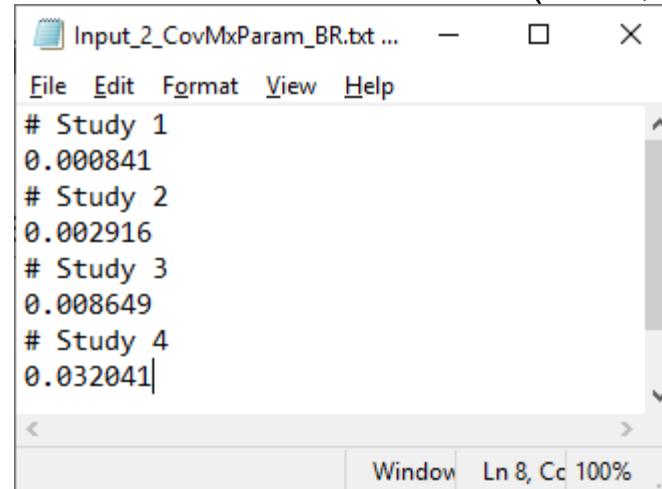
Combine evidence from S=4 studies

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%
```
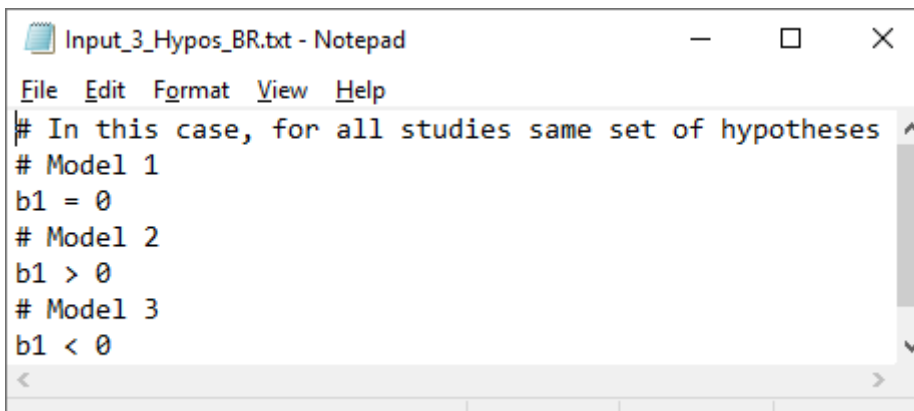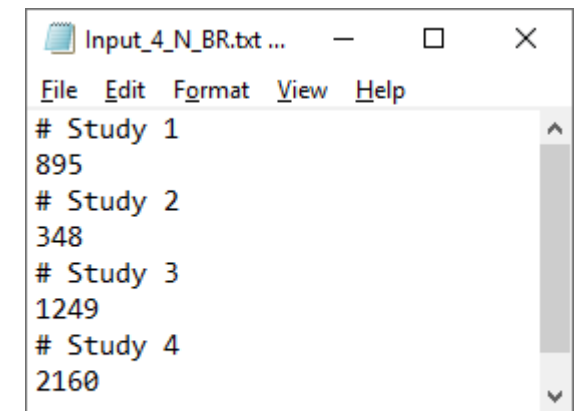
Their covariance matrix (here, variance):

```
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.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
```

N per study

```
Input_4_N_BR.txt ...    —    □    ×

File  Edit  Format  View  Help
# Study 1
895
# Study 2
348
# Study 3
1249
# Study 4
2160
```

Example input: Top (zoomed in)

Aggregating Bayesian evidence from multiple studies (with diverse designs), using as input: **Standardized parameter estimates and their covariance matrix** **Bayes Factors** *By us*

Input

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 parameter estimates, 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 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).

| 3 | ⯅⯆ |

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 | ▼ |

Output

Evidence per study and per hypotheses of interest (using R package bain)

Bayes factors (BFs)

| NULL |

BF_{mc} = Bayes factor for hypothesis of interest (H_m) versus its complement (compl.H_m)

BF_{mu} = Bayes factor for hypothesis of interest (H_m) versus the unconstrained hypothesis (H_u)

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

Bayes factors (BFs)

| NULL |

c resp. u: (updated or final) BF for H_m versus compl.H_m resp. H_u

inclUnc: the unconstrained hypothesis (i.e., H_u) is added to the set

Posterior model pr

| NULL |

PMP_{mc} = Posterior m

PMP_{mu} = Posterior m

Posterior model pr

| NULL |

c resp. u: (updated o

inclUnc: the unconst

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.

Example input: Bottom (zoomed in)

c resp. u: (updated or final) BF for H$_m$ versus compl.H$_m$ resp. H$_u$

inclUnc: the unconstrained hypothesis (i.e., H$_u$) is added to the set

c resp. u: (updated or final) PMP f

inclUnc: the unconstrained hypoth

Select the tab delimited .txt file that contains the covariance matrices of the 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).

1	

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 parameter estimates as given in previous input. Within a hypothesis, multiple restrictions are combined by a '&'. If you want to label lines, use headers starting with a '#'.
For example (if M = 1),
Hypothesis 1
b1 > b2 > 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 > b3 > b4 & b1 - b2 > 2*(b3 - b4)
Study 2
Hypothesis 1
b_1 > b_2 > b_3

Browse...	No file selected

Select the tab delimited .txt file that contains the number of observations (N). Currently, the program assumes that studies with group structures, like ANOVAs, have group sizes that are approximately equal. For such models, fill in the total number of observations and not the (average) group size.

Browse...	No file selected

If you upload the file with sample sizes (Ns), then the output will be generated.
Scroll up to see it from the top.

Example input: Running (can take some time)

Select the tab delimited .txt file that contains the **covariance matrices of the 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).

3	▲▼

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 parameter estimates as given in previous input. Within a hypothesis, multiple restrictions are combined by a '&'. If you want to label lines, use headers starting with a '#'.
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Study 1
Hypothesis 1
b1 > b2 > b3 > b4 & b1 - b2 > 2*(b3 - b4)
Study 2
Hypothesis 1
b_1 > b_2 > b_3

Browse...	Input_3_Hypos_BR.txt
Upload complete	

Select the tab delimited .txt file that contains the **number of observations** (N). Currently, the program assumes that studies with group structures, like ANOVAs, have group sizes that are approximately equal. For such models, fill in the total number of observations and not the (average) group size.

Browse...	Input_4_N_BR.txt
Upload complete	

c resp. u: (updated or final) BF for H_m versus compl.H_m resp. H_u

inclUnc: the unconstrained hypothesis (i.e., H_u) is added to the set

c resp. u: (updated or final) PMP for H_m versus compl.H_m resp. the other hypotheses in the set

inclUnc: the unconstrained hypothesis (i.e., H_u) is added to the set

Example output: Top

D:/Shiny Apps and R packages/AF_4_Bayesian evidence synthesis - TO DO - Shiny

http://127.0.0.1:7748   Open in Browser   Publish

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

Input

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 parameter estimates**, 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 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).

    3

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 parameter estimates as given in previous input. Within a hypothesis, multiple restrictions are combined by a '&'. If you want to label lines, use headers starting with a '#'.
For example (if M = 1),
Hypothesis 1
b1 > b2 > b3 > b4 & b1 - b2 > 2*(b3 - b4).

Output

Evidence per study and per hypotheses of interest (using R package bain)

Bayes factors (BFs)

```
$BFmc
        H1      compl.H1       H2      compl.H2       H3     compl.H3
Study1 2.424e-01 1.045e+03 9.573e-04 2.424e-01 1.045e+03 9.573e-04
Study2 6.475e-01 2.090e+02 4.786e-03 6.475e-01 2.090e+02 4.786e-03
Study3 5.237e-29 2.292e+13 5.008e-32 5.237e-29 2.292e+13 5.008e-32
Study4 1.480e-20 2.292e+13 1.264e-23 1.480e-20 2.292e+13 1.264e-23

$BFmu
        H1      H2      H3
Study1 2.424e-01 1.998 1.913e-03
Study2 6.475e-01 1.990 9.526e-03
Study3 5.237e-29 2.000 1.002e-31
Study4 1.480e-20 2.000 2.529e-23
```

BF_{mc} = Bayes factor for hypothesis of interest (H_m) versus its complement (compl.H_m)

BF_{mu} = Bayes factor for hypothesis of interest (H_m) versus the unconstrained hypothesis (H_u)

Posterior model probabilities (PMPs)

```
$PMPmc
        H1 compl.H1      H2 compl.H2      H3 compl.H3
Study1 1.951e-01    0.8049 0.9990 9.564e-04 9.564e-04    0.9990
Study2 3.930e-01    0.6070 0.9952 4.763e-03 4.763e-03    0.9952
Study3 5.237e-29    1.0000 1.0000 4.363e-14 5.008e-32    1.0000
Study4 1.480e-20    1.0000 1.0000 4.363e-14 1.264e-23    1.0000

$PMPmu
        H1      H2      H3
Study1 1.081e-01 0.8911 8.530e-04
Study2 2.446e-01 0.7518 3.598e-03
Study3 2.619e-29 1.0000 5.008e-32
Study4 7.401e-21 1.0000 1.264e-23
```

PMP_{mc} = Posterior model probability for hypothesis of interest (H_m) versus its complement (compl.H_m)

PMP_{mu} = Posterior model probability for hypothesis of interest (H_m) versus the other hypotheses in the set.

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

Bayes factors (BFs)

```
$updatedBFs_c
        H1      compl.H1       H2      compl.H2       H3     compl.H3
T=0 1.000e+00 1.000e+00 1.000e+00 1.000e+00 1.000e+00 1.000e+00
T=1 2.424e-01 1.045e+03 9.573e-04 2.424e-01 1.045e+03 9.573e-04
T=2 1.569e-01 2.183e+05 4.581e-06 1.569e-01 2.183e+05 4.581e-06
T=3 8.219e-30 5.003e+18 2.294e-37 8.219e-30 5.003e+18 2.294e-37
T=4 1.217e-49 1.147e+32 2.901e-60 1.217e-49 1.147e+32 2.901e-60

$updatedBFs_u
        H1      H2      H3
T=0 1.000e+00 1.000 1.000e+00
T=1 2.424e-01 1.998 1.913e-03
T=2 1.569e-01 3.977 1.822e-05
T=3 8.219e-30 7.954 1.825e-36
T=4 1.217e-49 15.909 4.615e-59

$updatedBFs_u_inclUnc
        H1      H2      H3 Hu
T=0 1.000e+00 1.000 1.000e+00  1
T=1 2.424e-01 1.998 1.913e-03  1
T=2 1.569e-01 3.977 1.822e-05  1
```

Posterior model probabilities (PMPs)

```
$updatedPMPs_c
        H1 compl.H1      H2 compl.H2  H3  compl.H3
T=0 5.000e-01    0.5000 5.000e-01    0.5000 0.5 5.000e-01
T=1 2.320e-04    0.9998 3.934e-03    0.9961 1.0 9.164e-07
T=2 7.189e-07    0.9620 2.919e-05    1.0000 2.099e-11
T=3 1.643e-48    1.0000 2.792e-08    1.0000 1.0 4.586e-56
T=4 1.061e-81    1.0000 2.385e-11    1.0000 1.0 2.530e-92

$updatedPMPs_u
        H1      H2      H3
T=0 3.333e-01 0.3333 3.333e-01
T=1 1.081e-01 0.8911 8.530e-04
T=2 3.796e-02 0.9620 4.407e-06
T=3 1.033e-30 1.0000 2.294e-37
T=4 7.647e-51 1.0000 2.901e-60

$updatedPMPs_u_inclUnc
        H1      H2      H3      Hu
T=0 2.500e-01 0.2500 2.500e-01 0.25000
T=1 7.475e-02 0.6162 5.899e-04 0.30842
T=2 3.057e-02 0.7747 3.549e-06 0.19478
```

Example output: Top (zoomed in)

First: Study-specific output

Output

Evidence per study and per hypotheses of interest (using R package bain)

Bayes factors (BFs)

```
$BFmc
          H1  compl.H1        H2  compl.H2        H3  compl.H3
Study1 2.424e-01 1.045e+03 9.573e-04 2.424e-01 1.045e+03 9.573e-04
Study2 6.475e-01 2.090e+02 4.786e-03 6.475e-01 2.090e+02 4.786e-03
Study3 5.237e-29 2.292e+13 5.008e-32 5.237e-29 2.292e+13 5.008e-32
Study4 1.480e-20 2.292e+13 1.264e-23 1.480e-20 2.292e+13 1.264e-23


$BFmu
          H1    H2        H3
Study1 2.424e-01 1.998 1.913e-03
Study2 6.475e-01 1.990 9.526e-03
Study3 5.237e-29 2.000 1.002e-31
Study4 1.480e-20 2.000 2.529e-23
```

BF_{mc} = Bayes factor for hypothesis of interest (H_m) versus its complement (compl.H_m)

BF_{mu} = Bayes factor for hypothesis of interest (H_m) versus the unconstrained hypothesis (H_u)

Posterior model probabilities (PMPs)

```
$PMPmc
          H1 compl.H1    H2  compl.H2        H3 compl.H3
Study1 1.951e-01    0.8049 0.9990 9.564e-04 9.564e-04    0.9990
Study2 3.930e-01    0.6070 0.9952 4.763e-03 4.763e-03    0.9952
Study3 5.237e-29    1.0000 1.0000 4.363e-14 5.008e-32    1.0000
Study4 1.480e-20    1.0000 1.0000 4.363e-14 1.264e-23    1.0000


$PMPmu
          H1    H2        H3
Study1 1.081e-01 0.8911 8.530e-04
Study2 2.446e-01 0.7518 3.598e-03
Study3 2.619e-29 1.0000 5.008e-32
Study4 7.401e-21 1.0000 1.264e-23
```

PMP_{mc} = Posterior model probability for hypothesis of interest (H_m) versus its complement (co

PMP_{mu} = Posterior model probability for hypothesis of interest (H_m) versus the other hypothes

Example output: Bottom

http://127.0.0.1:7748 | Open in Browser

Select the tab delimited .txt file that contains the covariance matrices of the 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).

3

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 parameter estimates as given in previous input. Within a hypothesis, multiple restrictions are combined by a '&'. If you want to label lines, use headers starting with a '#'.
For example (if M = 1),
Hypothesis 1
b1 > b2 > 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 > b3 > b4 & b1 - b2 > 2*(b3 - b4)
Study 2
Hypothesis 1
b_1 > b_2 > b_3

Browse... | Input_3_Hypos_BR.txt
Upload complete

Select the tab delimited .txt file that contains the number of observations (N). Currently, the program assumes that studies with group structures, like ANOVAs, have group sizes that are approximately equal. For such models, fill in the total number of observations and not the (average) group size.

Browse... | Input_4_N_BR.txt
Upload complete

BF_{mc} = Bayes factor for hypothesis of interest (H_m) versus its complement (compl.H_m)

BF_{mu} = Bayes factor for hypothesis of interest (H_m) versus the unconstrained hypothesis (H_u)

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

Bayes factors (BFs)

```
$updatedBFs_c
          H1   compl.H1       H2   compl.H2       H3   compl.H3
T=0 1.000e+00  1.000e+00 1.000e+00  1.000e+00 1.000e+00  1.000e+00
T=1 2.424e-01  1.045e+03 9.573e-04 2.424e-01  1.045e+03 9.573e-04
T=2 1.569e-01  2.183e+05 4.581e-06 1.569e-01  2.183e+05 4.581e-06
T=3 8.219e-30  5.003e+18 2.294e-37 8.219e-30  5.003e+18 2.294e-37
T=4 1.217e-49  1.147e+32 2.901e-60 1.217e-49  1.147e+32 2.901e-60


$updatedBFs_u
          H1      H2       H3
T=0 1.000e+00  1.000 1.000e+00
T=1 2.424e-01  1.998 1.913e-03
T=2 1.569e-01  3.977 1.822e-05
T=3 8.219e-30  7.954 1.825e-36
T=4 1.217e-49 15.909 4.615e-59


$updatedBFs_u_inclUnc
          H1      H2       H3 Hu
T=0 1.000e+00  1.000 1.000e+00  1
T=1 2.424e-01  1.998 1.913e-03  1
T=2 1.569e-01  3.977 1.822e-05  1
T=3 8.219e-30  7.954 1.825e-36  1
T=4 1.217e-49 15.909 4.615e-59  1


$FinalBF_c
         H1   compl.H1       H2   compl.H2       H3   compl.H3
1.217e-49  1.147e+32 2.901e-60 1.217e-49  1.147e+32 2.901e-60


$FinalBF_u
       H1      H2       H3
1.217e-49 1.591e+01 4.615e-59


$FinalBF_u_inclUnc
       H1      H2       H3       Hu
1.217e-49 1.591e+01 4.615e-59 1.000e+00
```

c resp. u: (updated or final) BF for H_m versus compl.H_m resp. H_u

inclUnc: the unconstrained hypothesis (i.e., H_u) is added to the set

---

PMP_{mc} = Posterior model probability for hypothesis of interest (H_m) versus its complement (compl.H_m)

PMP_{mu} = Posterior model probability for hypothesis of interest (H_m) versus the other hypotheses in the set.

Posterior model probabilities (PMPs)

```
$updatedPMPs_c
          H1 compl.H1       H2 compl.H2  H3  compl.H3
T=0 5.000e-01   0.5000 5.000e-01   0.5000 0.5 5.000e-01
T=1 2.320e-04   0.9998 3.934e-03   0.9961 1.0 9.164e-07
T=2 7.189e-07   1.0000 2.919e-05   1.0000 1.0 2.099e-11
T=3 1.643e-48   1.0000 2.792e-08   1.0000 1.0 4.586e-56
T=4 1.061e-81   1.0000 2.385e-11   1.0000 1.0 2.530e-92


$updatedPMPs_u
          H1      H2       H3
T=0 3.333e-01 0.3333 3.333e-01
T=1 1.081e-01 0.8911 8.530e-04
T=2 3.796e-02 0.9620 4.407e-06
T=3 1.033e-30 1.0000 2.294e-37
T=4 7.647e-51 1.0000 2.901e-60


$updatedPMPs_u_inclUnc
          H1      H2       H3       Hu
T=0 2.500e-01 0.2500 2.500e-01 0.25000
T=1 7.475e-02 0.6162 5.899e-04 0.30842
T=2 3.057e-02 0.7747 3.549e-06 0.19478
T=3 9.178e-31 0.8883 2.038e-37 0.11168
T=4 7.195e-51 0.9409 2.730e-60 0.05914


$FinalPMP_c
          H1   compl.H1       H2 compl.H2       H3  compl.H3
1.061e-81  1.000e+00 2.385e-11 1.000e+00 1.000e+00 2.530e-92


$FinalPMP_u
       H1      H2       H3
7.647e-51 1.000e+00 2.901e-60


$FinalPMP_u_inclUnc
       H1      H2       H3       Hu
7.195e-51 9.409e-01 2.730e-60 5.914e-02
```

c resp. u: (updated or final) PMP for H_m versus compl.H_m resp. the other hypotheses in the set

inclUnc: the unconstrained hypothesis (i.e., H_u) is added to the set

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

BF_{mc} = Bayes factor for hypothesis of interest (H_m) versus its complement (compl.H_m)

BF_{mu} = Bayes factor for hypothesis of interest (H_m) versus the unconstrained hypothesis (H_u)

PMP_{mc} = Posterior model probability for hypothesis of interest (H_m) versus its complement (compl.H_m)

PMP_{mu} = Posterior model probability for hypothesis of interest (H_m) versus the other hypotheses in the set.

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

Bayes factors (BFs)

Against its own complement. So, look at pairs

```
$updatedBFs_c
            H1  compl.H1        H2  compl.H2        H3  compl.H3
T=0 1.000e+00 1.000e+00 1.000e+00 1.000e+00 1.000e+00 1.000e+00
T=1 2.424e-01 1.045e+03 9.573e-04 2.424e-01 1.045e+03 9.573e-04
T=2 1.569e-01 2.183e+05 4.581e-06 1.569e-01 2.183e+05 4.581e-06
T=3 8.219e-30 5.003e+18 2.294e-37 8.219e-30 5.003e+18 2.294e-37
T=4 1.217e-49 1.147e+32 2.901e-60 1.217e-49 1.147e+32 2.901e-60
```

Against H_u.

```
$updatedBFs_u
            H1        H2        H3
T=0 1.000e+00    1.000 1.000e+00
T=1 2.424e-01    1.998 1.913e-03
T=2 1.569e-01    3.977 1.822e-05
T=3 8.219e-30    7.954 1.825e-36
T=4 1.217e-49   15.909 4.615e-59
```

Against H_u, also includes H_u

```
$updatedBFs_u_inclUnc
            H1        H2        H3 Hu
T=0 1.000e+00    1.000 1.000e+00  1
T=1 2.424e-01    1.998 1.913e-03  1
T=2 1.569e-01    3.977 1.822e-05  1
T=3 8.219e-30    7.954 1.825e-36  1
T=4 1.217e-49   15.909 4.615e-59  1
```

```
$FinalBF_c
        H1  compl.H1        H2  compl.H2        H3  compl.H3
1.217e-49 1.147e+32 2.901e-60 1.217e-49 1.147e+32 2.901e-60
```

```
$FinalBF_u
        H1        H2        H3
1.217e-49 1.591e+01 4.615e-59
```

```
$FinalBF_u_inclUnc
        H1        H2        H3        Hu
1.217e-49 1.591e+01 4.615e-59 1.000e+00
```

Corresponding PMPs:

Posterior model probabilities (PMPs)

Look at pairs

```
$updatedPMPs_c
            H1 compl.H1        H2 compl.H2  H3  compl.H3
T=0 5.000e-01    0.5000 5.000e-01    0.5000 0.5 5.000e-01
T=1 2.320e-04    0.9998 3.934e-03    0.9961 1.0 9.164e-07
T=2 7.189e-07    1.0000 2.919e-05    1.0000 1.0 2.099e-11
T=3 1.643e-48    1.0000 2.792e-08    1.0000 1.0 4.586e-56
T=4 1.061e-81    1.0000 2.385e-11    1.0000 1.0 2.530e-92
```

Look at whole set

```
$updatedPMPs_u
            H1        H2        H3
T=0 3.333e-01 0.3333 3.333e-01
T=1 1.081e-01 0.8911 8.530e-04
T=2 3.796e-02 0.9620 4.407e-06
T=3 1.033e-30 1.0000 2.294e-37
T=4 7.647e-51 1.0000 2.901e-60
```

Look at whole set, includes H_u

```
$updatedPMPs_u_inclUnc
            H1        H2        H3        Hu
T=0 2.500e-01 0.2500 2.500e-01 0.25000
T=1 7.475e-02 0.6162 5.899e-04 0.30842
T=2 3.057e-02 0.7747 3.549e-06 0.19478
T=3 9.178e-31 0.8883 2.038e-37 0.11168
T=4 7.195e-51 0.9409 2.730e-60 0.05914
```

```
$FinalPMP_c
        H1  compl.H1        H2  compl.H2        H3  compl.H3
1.061e-81 1.000e+00 2.385e-11 1.000e+00 1.000e+00 2.530e-92
```

```
$FinalPMP_u
        H1        H2        H3
7.647e-51 1.000e+00 2.901e-60
```

```
$FinalPMP_u_inclUnc
        H1        H2        H3        Hu
7.195e-51 9.409e-01 2.730e-60 5.914e-02
```

Combined evidence for each 'update'

Combined evidence after all 'updates'

c resp. u: (updated or final) BF for H_m versus compl.H_m resp. H_u

inclUnc: the unconstrained hypothesis (i.e., H_u) is added to the set

c resp. u: (updated or final) PMP for H_m versus compl.H_m resp. the other hypotheses in the set

inclUnc: the unconstrained hypothesis (i.e., H_u) is added to the set