Informative hypotheses evaluation Bayesian model selection

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ANOVA and Beyond, Example Analyses with R and JASP

bain

 Hoijtink, H., Mulder, J., van Lissa, C., and Gu, X. (2018). A tutorial on testing hypotheses using the Bayes factor. Psychological Methods, 24, 539-556.

Balancing Fit and Complexity

The Bayes factor quantifies the relative support in the data for two hypotheses, for example,

$$H_i: \mu_1 > \mu_2 > \mu_3$$

$$H_{u}: \mu_{1}, \mu_{2}, \mu_{3}$$

with

$$BF_{iu} = \frac{f_i}{c_i} = \frac{\text{fit } H_i}{\text{complexity } H_i}$$

that is, after observing the data H_i is BF_{iu} times as likely as H_u , for example, .2, 5, 10.

Balancing Fit and Complexity

A (very) loose interpretation of the meaning of fit

$$H_i: \mu_1 > \mu_2 > \mu_3$$
 if $\bar{x}_1 = 7 \& \bar{x}_2 = 4 \& \bar{x}_3 = 2$ the fit is good if $\bar{x}_1 = 2 \& \bar{x}_2 = 4 \& \bar{x}_3 = 7$ the fit is bad

Balancing Fit and Complexity

A (very) loose interpretation of the meaning of complexity

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

very parsimonious, the means have to be exactly equal.

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

one ordering of three means: 1-2-3, thus is parsimonious.

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

2 orderings of three means: 1-2-3 and 1-3-2, less parsimonious.

$$H_{u}: \mu_{1}, \mu_{2}, \mu_{3}$$

contains all six possible orderings of three means, not parsimonious.

Balancing Fit and Complexity

Three forms of Hypotheses and Bayes factors involving $H_i: \mu_1 > \mu_2 > \mu_3$

 BF_{iu} evaluating H_i versus H_u : μ_1, μ_2, μ_3

 $BF_{ii'}$ evaluating H_i versus $H_{i'}$: $\mu_1 = \mu_2 = \mu_3$

 BF_{ic} evaluating H_i versus H_c : not H_i

Interpreting (the Size of) the Bayes Factor

- 1. Select the best of a set of hypotheses using BF_{iu}
- 2. Compare two competing hypotheses using $BF_{ii'}$
- 3. Compare "my theory" with "not my theory" using BF_{ic}

	f _i	Ci	BF_{iu}	BF_{ic}
H ₁ : Sex Match	.0039	.012	.32	.32
H ₂ : Gender Role Match	.0725	.012	5.85	6.44
H ₃ : Sex Mismatch	.0007	.012	.06	.06
H ₄ : Gender Role Mismatch	.0001	.012	.01	.01

Descriptives

Gender Role Match Effect

$$H_2: (\mu_1, \mu_5) > (\mu_2, \mu_3, \mu_4, \mu_6) \text{ and } (\mu_7, \mu_{11}) > (\mu_8, \mu_9, \mu_{10}, \mu_{12})$$

$$H_2: (166, 163) > (158, 154, 155, 164)$$
 and

Gender Role Mismatch Effect

$$H_4: (\mu_2, \mu_4) > (\mu_1, \mu_3, \mu_5, \mu_6)$$
 and $(\mu_8, \mu_{10}) > (\mu_7, \mu_9, \mu_{11}, \mu_{12})$

$$H_4: (158, 155) > (166, 154, 163, 164)$$
 and

Interpreting (the Size of) the Bayes Factor

- 1. The Bayes factor **is** a measure of support (also for the null-hypothesis)
- 2. The Bayes factor **can be indecisive**. A value around 1 denotes "the data don't tell us which hypothesis to prefer"
- 3. One can compare more than two hypotheses
- 4. "Something is going on and we do know what!"
- The Bayes factor selects the best of the hypotheses under consideration. Note that the "true" hypothesis may not be among them, and that all hypotheses may be "wrong"

Note on hypotheses

H_i 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_i and H_c .

Subjectivity of Bayesian Hypotheses Evaluation

- 1. Which hypotheses to evaluate?
- 2. How to formalize hypotheses? E.g. $(\mu_1, \mu_2) > (\mu_3, \mu_4)$ or $\mu_1 = \mu_2 > \mu_3 = \mu_4$
- 3. The (implicit) choice for equal prior model probabilities
- 4. The specification of the prior distribution

Bayesian Informative Hypotheses Evaluation (bain)

ANOVA and Beyond, Example Analyses with R and JASP

Enc

Extra

Example 1: ANOVA

What is the relation between "knowledge of numbers after watching Sesame Street for a year"

and

site from which the child originates (1 = disadvantaged inner city, 2 = advantaged suburban, 3 = advantaged rural, 4 = disadvantaged rural, 5 = disadvantaged Spanish speaking).

Example 1: ANOVA

```
library (bain)
sesamesim$site <- as.factor(sesamesim$site)</pre>
anov <- lm(postnumb~site-1, sesamesim)
coef(anov)
set.seed(100)
results <- bain(anov,
                "site1=site2=site3=site4=site5;
                 site2>site5>site1>site3>site4")
print(results)
summary (results, ci = 0.95)
```

Example 1: ANOVA

coef(anov) renders

```
site1 site2 site3 site4 site5
29.66667 38.98182 23.18750 25.32558 31.72222
```

summary(results) renders

```
Parameter n Estimate lb ub

1 site1 60 29.66667 26.82991 32.50343

2 site2 55 38.98182 36.01892 41.94472

3 site3 64 23.18750 20.44082 25.93418

4 site4 43 25.32558 21.97466 28.67650

5 site5 18 31.72222 26.54303 36.90141
```

Example 1: ANOVA

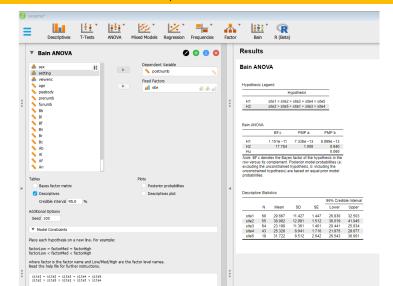
The main output is

```
Fit Com BF.u BF.c PMPa PMPb PMPc
H1 0.000 0.000 0.000 0.000 0.000 0.000 0.000
H2 0.121 0.008 14.559 16.428 1.000 0.936 0.943
Hu 0.064
Hc 0.879 0.992 0.886 0.057
```

Hypotheses:

H1: site1=site2=site3=site4=site5
H2: site2>site5>site1>site3>site4

Example 1: ANOVA



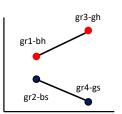
Example 2: ANOVA Interaction Effect

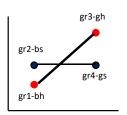
Dependent variable: Knowledge of numbers.

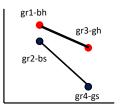
Factors: sex (boy, girl) and setting (watching at home, watching at school).

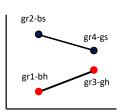
Gr: 1=boyhome, 2= boyschool, 3= girlhome, 4=girlschool.

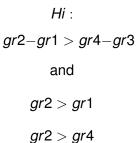
Example 2: ANOVA Interaction Effect











Example 2: ANOVA Interaction Effect

```
sesamesim$gr <- as.factor(sesamesim$gr)</pre>
anov <- lm(postnumb~gr-1, sesamesim)</pre>
results <- bain(anov,
"qr2 - qr1 > qr4 - qr3 & qr2 > qr1 & qr2 > qr4")
```

Example 2: ANOVA Interaction Effect

The main output is

```
Fit.
        Com BF.u BF.c PMPa PMPb PMPc
H1 0.922 0.283 3.262 29.984 1.000 0.765 0.968
                                  0.235
H11
Hc 0.078 0.717 0.109
                                        0.032
```

Hypotheses:

```
H1: gr2-gr1>gr4-gr3&gr2>gr1&gr2>gr4
```

How to write down an hypothesis

bain can handle hypotheses build using constraints on (linear combinations) of parameters. Suppose the parameter names are "a", "b", "c".

Step 1: Construct the elements of the linear combination. E.g. "a" or "a + 2" or "3 * a" or "2 * a + 4"

Step 2: Constrain the resultsing elements. E.g. a > b > c

or
$$a > b + 2 \& b > c + 2$$

or
$$2 * a > b + c & b > 0 & c > 0$$

or
$$a > (b, c) \& b - c > 0$$

Example 3: Repeated Measures

Development of depression

	Measurement					
	8 years	12 years	16 years	20 years		
Men	μ_1	μ_2	μ_3	μ_{4}		
Women	μ_5	μ_{6}	μ_7	μ_{8}		

$$H_1: \mu_5 - \mu_1 > \mu_6 - \mu_2 > \mu_7 - \mu_3 < \mu_8 - \mu_4$$

$$H_2: \mu_6 - \mu_5 < \mu_7 - \mu_6 > \mu_8 - \mu_7$$

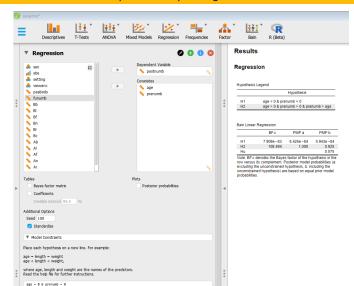
Example 4: Multiple Regression

$$postnumb_i = \beta_0 + \beta_1 \times age_i + \beta_2 \times prenumb_i + \epsilon_i$$

$$H_1: \beta_1 > 0, \beta_2 > 0, \beta_1 < \beta_2$$

Note: β_1 and β_2 are only comparable if age and prenumb are standardized

Example 4: Multiple Regression



Is the difference in number knowledge relevantly different between boys and girls?

Example 5: About Equality Constraints

```
sesamesim$sex <- as.factor(sesamesim$sex)</pre>
anov <- lm(postnumb~sex-1, sesamesim)
results \leftarrow bain(anov, "-2 < sex1 - sex2 < 2")
```

Example 5: About Equality Constraints

```
sex1 sex2
30.09565 28.85600
```

```
Fit
      Com BF.u BF.c PMPa PMPb PMPc
H1 0.664 0.091 7.304 19.735 1.000 0.880 0.952
                                0.120
Hи
Hc 0.336 0.909 0.370
                                      0.048
```

Hypotheses:

H1: -2 < sex1 - sex2 < 2

Example 6: Structural Equation Modelling

```
library (bain)
library (lavaan)
model <- '
    A = Ab + Al + Af + An + Ar + Ac
    B = Rb + Bl + Bf + Bn + Br + Bc
    A ~ B + age + peabody'
fit <- sem(model, data = sesamesim, std.lv = TRUE)
hypotheses <- "A~B = A~peabody = A~age = 0;
                A \sim B > A \sim peabody > A \sim age = 0"
set.seed(100)
y1 <- bain(fit, hypotheses, standardize = TRUE)</pre>
```

Hands-on/Demo: BMS

Let's practice.

- If needed: Start Rstudio again (optional: make project).
- Open 'Hands-on_1_BMS_Unc_ANOVA_bain.R' (in 'Hands-on files').
- Install packages and load them.
- Read and inspect data. Use Data_Lucas.txt.
- Run model (Im()).
- Specify hypotheses (make up your own).
 Note: Use names used in the model.
- Run bain().
- Inspect and interpret output.

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Extra



Your hypothesis of interest

If you have your own data

Before:

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

Additionally:

- Are you able to specify your statistical hypothesis/-es?
- How will you evaluate it/them? (preference GORIC(A) or BMS or both?)

What's next

Depending on time and wishes:

- Some extra information
- Demo in JASP (GORIC(A) and/or BMS)
- Demo in R (GORIC(A) and/or BMS)

We end with:

• Lab: https://github.com/rebeccakuiper/ EMLaR---Informative-Hypothesis-Evaluation



The End

Thanks for listening!

Are there any questions?

Websites

https://github.com/rebeccakuiper/Tutorials www.uu.nl/staff/RMKuiper/Software www.uu.nl/staff/RMKuiper/Extra2 informative-hypotheses.sites.uu.nl/software/goric/

E-mail

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Extra

Bayes Factor (BF)

comparing two informative hypotheses

The BF quantifies the relative support in the data for two hypotheses.

$$BF_{12} = \frac{BF_{1u}}{BF_{2u}} = \frac{f_1/f_2}{c_1/c_2}$$

using

$$BF_{iu} = \frac{f_i/f_u}{c_i/c_u} = \frac{f_i}{c_i}$$

Three Simple Hypotheses

Consider the hypotheses:

$$H_1: \mu_1 \approx \mu_2$$
, that is, $|\mu_1 - \mu_2| < .1$

$$H_2: \mu_1 > \mu_2$$

$$H_3: \mu_1, \mu_2$$

Information in the Data about the Two Means

					95% Credible Interval	
	Ν	Mean	SD	SE	Lower	Upper
sex1	115	30.096	13.058	1.175	27.793	32.398
sex2	125	28.856	12.162	1.127	26.647	31.065

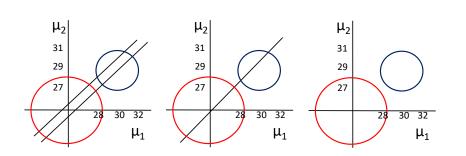
$$g(\mu_1,\mu_2\mid ext{data}) pprox \mathcal{N}\left(\left[egin{array}{c} m_1 \ m_2 \end{array}
ight], \left[egin{array}{ccc} se_1^2 = rac{SD_1^2}{N_1} & 0 \ 0 & se_2^2 = rac{SD_2^2}{N_2} \end{array}
ight]
ight),$$

Posterior Distribution, Prior Distribution, and Hypotheses

$$H_1: \mu_1 \approx \mu_2$$

$$H_2$$
: $\mu_1 > \mu_2$

$$\boldsymbol{H}_{u}\!:\boldsymbol{\mu}_{1}$$
 , $\boldsymbol{\mu}_{2}$



$$BF_{1u} = f_1/c_1 = .25/.05 = 5$$
 $BF_{2u} = f_2/c_2 = .75/.5 = 1.5$ $BF_{12} = 5/1.5 = 3.33$

Fit and Complexity

- The fit of a hypothesis is the proportion of the posterior distribution in agreement with the hypothesis.
 Note: posterior = likelihood × prior.
- 2. The **complexity** of a hypothesis is the proportion of the **prior** distribution in agreement with the hypothesis.

The Prior Distribution

$$h(\mu_1, \mu_2 \mid \text{data}) \approx \mathcal{N}\left(\left[\begin{array}{c} m \\ m \end{array} \right], \left[\begin{array}{cc} \frac{SD_1^2}{J} & 0 \\ 0 & \frac{SD_2^2}{J} \end{array} \right] \right),$$

where μ_1 and μ_2 have the same prior mean m, and where J denotes the size of the training sample.

Possible choices for *J* for the example at hand:

- use the default in bain: J = the number of independent constraints, here, 1. This is a conservative choice. Sensitivity check: e.g., J, 2*J, and 3*J (fraction = 1, 2, and 3, resp.).
- or use J = the minimal training sample size, here, 4 because four observations are needed to estimate two means and two variances.
- or use J = Jref, which renders $BF_{0u} = 19$ if the effect size in the sample equals 0.

Posterior Distribution (f), Prior Distribution (c), and Hypotheses Prior Sensitivity for = Constrained Hypotheses

Here, used bain: J = 1.

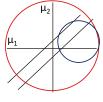
Sensitivity check: J, 2*J, and 3*J (i.e., fraction = 1, 2, and 3).

$$H_1{:}\; \mu_1\approx \mu_2$$

$$J = 1$$

$$2*J = 2$$

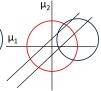
$$3*J = 3$$







$$BF_{111} = .2/.05 = 4$$



$$BF_{1u} = .2/.2 = 1$$

Posterior Distribution (f), Prior Distribution (c), and Hypotheses Prior In-Sensitivity for > < Constrained Hypotheses

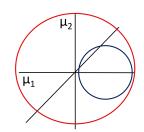
$$H_2$$
: $\mu_1 > \mu_2$

$$J = 1$$

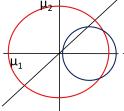
$$2*J = 2$$



 μ_2



 $BF_{2u} = .9/.5 = 1.8$





$$\mu_1$$

$$BF_{2u} = .9/.5 = 1.8$$

$$BF_{2u} = .9/.5 = 1.8$$