

Informative hypotheses evaluation

Bayesian model selection

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ANOVA and Beyond, Example Analyses with R and JASP

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bain

1. 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.

Bayes Factor

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.

Bayes Factor

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

Bayes Factor

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.

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

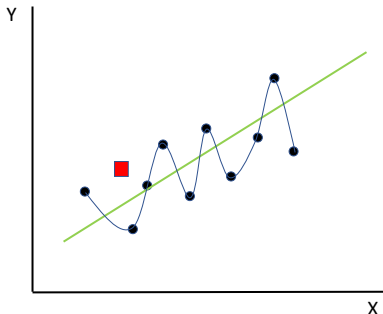
2 orderings of three means: 1-2-3 and 1-3-2, less parsimonious.

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

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

Bayes Factor

Balancing Fit and Complexity



The straight line results from a linear regression model with 3 parameters (intercept, slope, residual variance).

The other line results from a polynomial regression models with 11 parameters (intercept, nine slopes, residual variance).

The red square is a new observation that is added to the original 10 observations.

What is the predictive value of both models?

Bayes Factor

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

$BF_{ij'}$ evaluating H_i versus $H_{j'} : \mu_1 = \mu_2 = \mu_3$

BF_{ic} evaluating H_i versus $H_c : \text{not } H_i$

Bayes Factor

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 $BF_{ij'}$
3. Compare "my theory" with "not my theory" using BF_{ic}

	f_i	c_i	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

Bayes Factor

Descriptives

Gender Role Match Effect

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

$$H_2 : (166, 163) > (158, 154, 155, 164) \text{ and}$$

$$(157, 152) > (157, 150, 143, 149)$$

Gender Role Mismatch Effect

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

$$H_4 : (158, 155) > (166, 154, 163, 164) \text{ and}$$

$$(157, 143) > (157, 150, 152, 149)$$

Bayes Factor

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 update**, that is, collect more data and recompute the Bayes factor
4. One **can compare** more than two hypotheses (see extra comments later on)
5. "Something is going on and **we do know what!**"
6. 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"

Bayes Factor

Interpreting (the Size of) the Bayes Factor

When is the Bayes factor large enough?

1. Guidelines by Jeffreys (1969) and Kass and Raftery (1995), e.g., < 3 is ignorable, > 3 is positive evidence, > 10 is strong evidence ...
2. Will lead to a return of sloppy science and publication bias (when used without pre-registration or a pre-registered report)
3. Where does the 3 come from?

Bayes Factor

Interpreting (the Size of) the Bayes Factor

When is the Bayes factor large enough?

1. Before collecting or accessing the data, formulate informative hypotheses (and decide how large you would like the Bayes factor to be).
2. Insert this information in a pre-registration or pre-registered report.
3. Collect data and evaluate hypotheses.
 - Is one good and the best with a "large" Bayes factor: nice!
 - Are the Bayes factors "not large enough": follow up research or updating is needed.
 - Is none good: BIG news, well-constructed hypotheses have been rejected!

Extra: PMPs

Posterior Model Probabilities, e.g., $PMP(H_i | \text{data})$ and $PMP(H_c | \text{data})$ quantify the support in the data for each hypothesis.

$$\frac{PMP(H_i | \text{data})}{PMP(H_c | \text{data})} = \text{BF}_{ic} \times \frac{PRI(H_i)}{PRI(H_c)}, \quad (1)$$

where $PRI(H_i)$ and $PRI(H_c)$ denote the *prior* probabilities, that is, an evaluation of the support for the hypotheses *before* observing the data.

Usually equal prior model probabilities are used (which means that the PMP's convey the same information as the Bayes factors), but this is not a requirement.

PMPs

Bayesian Error Probabilities

PMPs can be interpreted as Bayesian error probabilities, that is, the Bayesian counterparts of the Type I and Type II errors.

	f_i	c_i	BF_{iu}	PMP_i	PRI_i
H_1 : Sex Match	.0039	.012	.32	.04	1/5
H_2 : Gender Role Match	.0725	.012	5.85	.81	1/5
H_3 : Sex Mismatch	.0007	.012	.06	.01	1/5
H_4 : Gender Role Mismatch	.0001	.012	.01	.00	1/5
H_u :				.14	1/5

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 .

PMPs

Replacing H_u by H_c

	f_i	c_i	BF_{iu}	PMP_i	PRI_i
H_1 : Sex Match	.0039	.012	.32	.04	1/5
H_2 : Gender Role Match	.0725	.012	5.85	.84	1/5
H_3 : Sex Mismatch	.0007	.012	.06	.00	1/5
H_4 : Gender Role Mismatch	.0001	.012	.01	.00	1/5
H_c :	.9200	.9500	.97	.12	1/5

Where H_c denotes the complement H_1 through H_4 , that is, "not one of these four hypotheses".

PMPs

The Number of Hypotheses and PMPs

Look what happens if we compare many hypotheses, the PMPs become smaller and smaller, and thus the Bayesian error probabilities become larger and larger:

	f_i	c_i	BF_{iu}	PMP_i	PR_i
H_1 : Sex Match	.0039	.012	.32	.013	1/13
H_2 : Gender Role Match	.0725	.012	5.85	.270	1/13
H_3 : Sex Mismatch	.0007	.012	.06	.003	1/13
H_4 : Gender Role Mismatch	.0001	.012	.01	.000	1/13
H_5 : Lets try this one too	.0521	.012	2.61	.180	1/13
...					
H_{12} : Don't miss something	.0164	.012	1.36	.040	1/13
H_u :				.047	1/13

PMPs

The Number of Hypotheses and PMPs

The same results as two slides up are in fact obtained by assigning PMPs of 0 to each hypothesis that is NOT considered:

	f_i	c_i	BF_{iu}	PMP_i	PR_i
H_1 : Sex Match	.0039	.012	.32	.04	1/5
H_2 : Gender Role Match	.0725	.012	5.85	.81	1/5
H_3 : Sex Mismatch	.0007	.012	.06	.01	1/5
H_4 : Gender Role Mismatch	.0001	.012	.01	.00	1/5
H_5 : Lets try this one too	.0521	.012	2.61	.18	0
...					
H_{12} : Don't miss something	.0164	.012	1.36	.04	0
H_u :				.14	1/5

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

Informative Hypotheses

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).

Informative Hypotheses

Example 1: ANOVA

```
library(bain)
sesamesim$site <- as.factor(sesamesim$site)
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)
```

Informative Hypotheses

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

Informative Hypotheses

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

Informative Hypotheses

Example 1: ANOVA

sesame[®]

Descriptives T-Tests ANOVA Mixed Models Regression Frequencies Factor Bain R (Beta)

Bain ANOVA

Dependent Variable: **postrumb**

Fixed Factors: **site**

Tables:
☐ Bayes factor matrix
☒ Descriptives
Credible interval 95.0 %

Plots:
☐ Posterior probabilities
☐ Descriptives plot

Additional Options:
Seed 100

Model Constraints:
Place each hypothesis on a new line. For example:
factorLow = factorMed = factorHigh
factorLow < factorMed < factorHigh
where factor is the factor name and Low/Med/High are the factor level names.
Read the help file for further instructions.

site1 = site2 = site3 = site4 = site5
site2 > site3 > site1 > site3 > site4

Results

Bain ANOVA

Hypothesis Legend

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

Bain ANOVA

	BF.c	PMP a	PMP b
H1	1.151e-11	7.338e-13	6.899e-13
H2	17.784	1.000	0.940
Hu			0.060

Note: BF.c denotes the Bayes factor of the hypothesis in the row versus its complement. Posterior model probabilities (a, excluding the unconstrained hypothesis; b, including the unconstrained hypothesis) are based on equal prior model probabilities.

Descriptive Statistics

	N	Mean	SD	SE	95% Credible Interval	
					Lower	Upper
site1	60	29.667	11.427	1.447	26.830	32.503
site2	55	38.982	12.991	1.512	36.019	41.945
site3	64	23.188	11.361	1.401	20.441	25.934
site4	43	25.326	8.941	1.710	21.975	28.677
site5	18	31.722	8.512	2.942	26.543	36.901

Informative Hypotheses

Example 2: ANOVA Interaction Effect

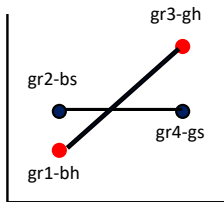
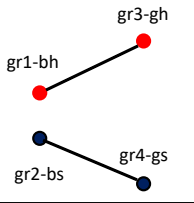
Dependent variable: Knowledge of numbers.

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

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

Informative Hypotheses

Example 2: ANOVA Interaction Effect



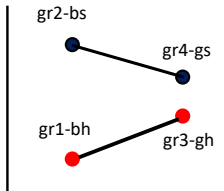
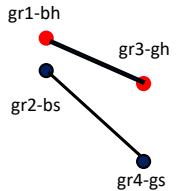
$H_i :$

$$gr2 - gr1 > gr4 - gr3$$

and

$$gr2 > gr1$$

$$gr2 > gr4$$



Informative Hypotheses

Example 2: ANOVA Interaction Effect

```
sesamesim$gr <- as.factor(sesamesim$gr)
anov <- lm(postnumb~gr-1,sesamesim)
results <- bain(anov,
"gr2 - gr1 > gr4 - gr3 & gr2 > gr1 & gr2 > gr4")
```

Informative Hypotheses

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
Hu						0.235	
Hc	0.078	0.717	0.109				0.032

Hypotheses:

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

Informative Hypotheses

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

Informative Hypotheses

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

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

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

Informative Hypotheses

Example 4: Multiple Regression

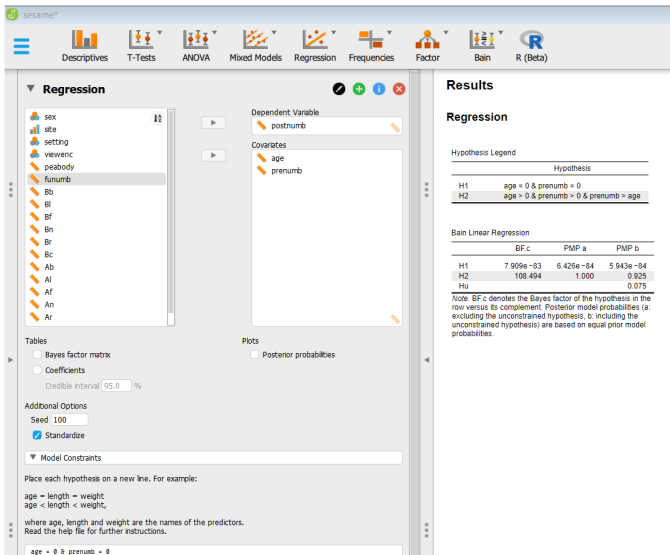
$$\text{postnumb}_i = \beta_0 + \beta_1 \times \text{age}_i + \beta_2 \times \text{prenumb}_i + \epsilon_i$$

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

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

Informative Hypotheses

Example 4: Multiple Regression



Regression

Dependent Variable: postnumb

Covariates: age, prenumb

Results

Regression

Hypothesis Legend

	Hypothesis
H1	age = 0 & prenumb = 0
H2	age > 0 & prenumb > 0 & prenumb > age

Bayes Linear Regression

	BF.c	PMP a	PMP b
H1	7.909e-83	6.426e-84	5.943e-84
H2	108.494	1.000	0.925
Hu			0.075

Note: BF.c denotes the Bayes factor of the hypothesis in the row versus its complement. Posterior model probabilities (a. excluding the unconstrained hypothesis, b. including the unconstrained hypothesis) are based on equal prior model probabilities.

Place each hypothesis on a new line. For example:

age = length + weight
age < length + weight,

where age, length and weight are the names of the predictors.
Read the help file for further instructions.

age = 0 & prenumb = 0

Informative Hypotheses

Example 5: About Equality Constraints

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

Informative Hypotheses

Example 5: About Equality Constraints

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

Informative Hypotheses

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
Hu						0.120	
Hc	0.336	0.909	0.370				0.048

Hypotheses:

H1: $-2 < \text{sex1} - \text{sex2} < 2$

Informative Hypotheses

Example 6: Structural Equation Modelling

```
library(bain)
library(lavaan)

model <- '
    A  =~ Ab + Al + Af + An + Ar + Ac
    B  =~ Bb + 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~B > A~peabody > A~age = 0"

set.seed(100)
y1 <- bain(fit, hypotheses, standardize = TRUE)
```

Hands-on/Demo: BMS

- Let's practice. Go to `https://github.com/rebeccakuiper/Tutorials:`
 1. Click on green button called Code.
 2. Download zip (last option in list).
 3. Unzip it on your machine (that folder is now your working directory).
- Start Rstudio. 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 (`lm()`).
- Specify hypotheses (make up your own).
Note: Use names used in the model.
- Run `bain()`.
- Inspect and interpret output.

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The End

BMS

Thanks for listening!

Are there any questions?

Websites

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

www.uu.nl/staff/RMKuiper/Software

www.uu.nl/staff/RMKuiper/Websites%20%2F%20Shiny%20apps

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

What's next

- Model selection using information criteria
- Possibly: Evidence synthesis / Support aggregation

Depending on time and wishes:

- Some extra information
- Demo in R
- Demo in JASP

We end with:

- Lab

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A Closer Look at the Bayes Factor

A Closer Look at the Bayes Factor

Three Simple Hypotheses

Consider the hypotheses:

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

$$H_2 : \mu_1 > \mu_2$$

$$H_3 : \mu_1, \mu_2$$

A Closer Look at the Bayes Factor

Information in the Data about the Two Means

	N	Mean	SD	SE	95% Credible Interval	
					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

$$g(\mu_1, \mu_2 \mid \text{data}) \approx \mathcal{N} \left(\begin{bmatrix} m_1 \\ m_2 \end{bmatrix}, \begin{bmatrix} se_1^2 = \frac{SD_1^2}{N_1} & 0 \\ 0 & se_2^2 = \frac{SD_2^2}{N_2} \end{bmatrix} \right),$$

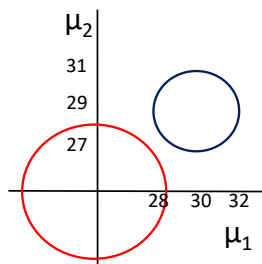
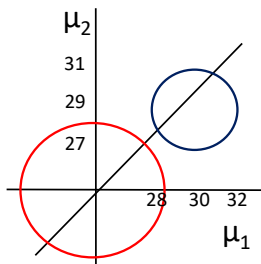
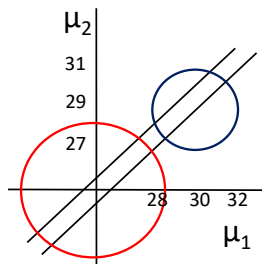
A Closer Look at the Bayes Factor

Posterior Distribution, Prior Distribution, and Hypotheses

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

$$H_2: \mu_1 > \mu_2$$

$$H_u: \mu_1, \mu_2$$



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

$$BF_{12} = 5/1.5 = 3.33$$

A Closer Look at the Bayes Factor

Fit and Complexity

1. The fit of a hypothesis is the proportion of the posterior distribution in agreement with the hypothesis.
2. The complexity of a hypothesis is the proportion of the prior distribution in agreement with the hypothesis.

A Closer Look at the Bayes Factor

The Prior Distribution

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

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

Choices for J for the example at hand:

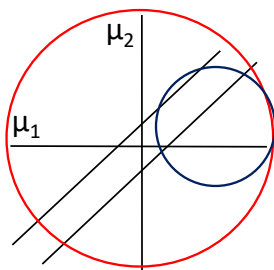
- Default in `bain`: number of independent constraints, that is, 1, this is a conservative choice (NB. $.5 * J$)
- Minimal training sample size, that is, 4, because four observations are needed to estimate two means and variances
- J_{ref} , which renders $BF_{0u} = 19$ if the effect size in the sample equals 0

A Closer Look at the Bayes Factor

Prior Sensitivity for = Constrained Hypotheses

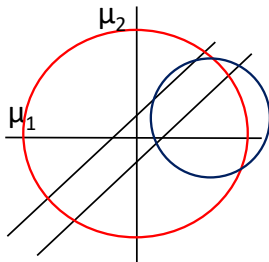
$$H_1: \mu_1 \approx \mu_2$$

$J = 1$



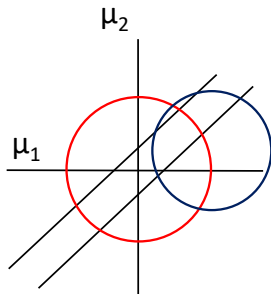
$$BF_{1u} = .2/.01 = 20$$

$J = 2$



$$BF_{1u} = .2/.05 = 4$$

$J = 3$



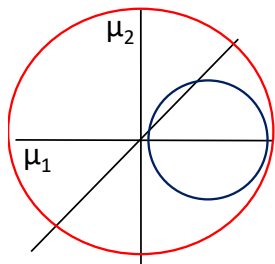
$$BF_{1u} = .2/.2 = 1$$

A Closer Look at the Bayes Factor

Prior In-Sensitivity for $> <$ Constrained Hypotheses

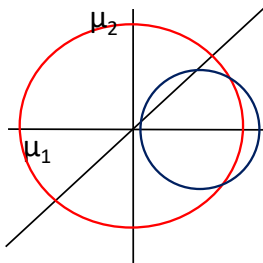
$$H_2: \mu_1 > \mu_2$$

J=1



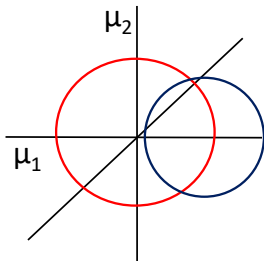
$$BF_{2u} = .9/.5 = 1.8$$

J=2



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

J=3



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

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

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