

# R Notebook

Neil yetz & Gemma Wallace

## Kevin's R code

```
dfhyp= NA
dferr= NA
alpha=.05
effect= NA           #enter the minimum effect you are testing
sse=100              #Don't change this
mse=((1/effect)-1)*sse/dferr
noncen=sse/mse
qf((1-alpha),dfhyp,dferr,noncen)
```

```
## [1] NA
```

## 1a Applied to Bret et al. (Right Wing Authoritarianism)

```
dfhyp=1
dferr=161
alpha=.05
effect=.01           #enter the minimum effect you are testing
sse=100
mse=((1/effect)-1)*sse/dferr
noncen=sse/mse
qf((1-alpha),dfhyp,dferr,noncen)
```

```
## [1] 8.683388
```

The authors need an F-value of 8.683388 to reach a significant effect at a minimum effect size of .01.

## 1b

With their F-value of 4.81. They had enough power to reject the comparison of the nil (F-value = 3.89) With their F-value of 4.81. They did not have enough power to reject the comparison of 1% or less of the variance (F = 8.61)

## 1c

They would need a sample size of at least 122 (dferror = n - k) to have a power of .80. They would need a sample size of at least 302 to reject the 1% or less of the variance and have a power of .80.

## Load libraries

```
library(tidyverse)
```

```
## -- Attaching packages -----
## v ggplot2 3.3.0    v purrr  0.3.3
## v tibble  3.0.0    v dplyr  0.8.5
## v tidyr   1.0.2    v stringr 1.4.0
## v readr   1.3.1    v forcats 0.5.0

## Warning: package 'ggplot2' was built under R version 3.6.3
## Warning: package 'tibble' was built under R version 3.6.3
## Warning: package 'tidyr' was built under R version 3.6.3
## Warning: package 'dplyr' was built under R version 3.6.3
## Warning: package 'forcats' was built under R version 3.6.3

## -- Conflicts -----
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
```

```
library(BayesFactor)
```

```
## Warning: package 'BayesFactor' was built under R version 3.6.3
## Loading required package: coda
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
## The following objects are masked from 'package:tidyr':
##
##   expand, pack, unpack
##
## *****
## Welcome to BayesFactor 0.9.12-4.2. If you have questions, please contact Richard Morey (richarddmorey@stanford.edu)
##
## Type BFManual() to open the manual.
## *****
```

## read in retirement.csv

```
retirement <- read_csv("retirement.csv")
```

```
## Parsed with column specification:
## cols(
##   occupation = col_double(),
##   sex = col_double(),
##   mental = col_double()
## )
```

## Factor the categorical variables

```
retirement <- mutate(retirement,
  sex.f = factor(sex,
    levels = c(1,2),
    labels = c("Female", "Male")),
  occupation.f = factor(occupation,
    levels = c(1,2,3,4,5,6),
    labels = c("Prof", "Manag", "nonmanual", "Skilled", "Semi-Sk"))
```

## Frequentist ANOVA

```
summary(aov(lm(mental ~ sex.f*occupation.f, data = retirement)))
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## sex.f          1    0.2    0.206    0.256    0.613
## occupation.f    5   45.9    9.187   11.396 7.44e-11 ***
## sex.f:occupation.f  5    6.0    1.202    1.491    0.189
## Residuals     1898 1530.0    0.806
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
sex_eta <- 0.2 / (1530 + .2 + 45.9 + 6)
occ_eta <- 45.9 / (1530 + .2 + 45.9 + 6)
int_et  <- 6.0 / (1530 + .2 + 45.9 + 6)
```

```
sex_eta
```

```
## [1] 0.0001264143
```

```
occ_eta
```

```
## [1] 0.02901207
```

```
int_et
```

```
## [1] 0.003792428
```

## Bayes ANOVA: “all”

```
m1 <- anovaBF(mental ~ sex.f*occupation.f, data = retirement, whichModels = "all")
```

```
## Warning: data coerced from tibble to data frame
```

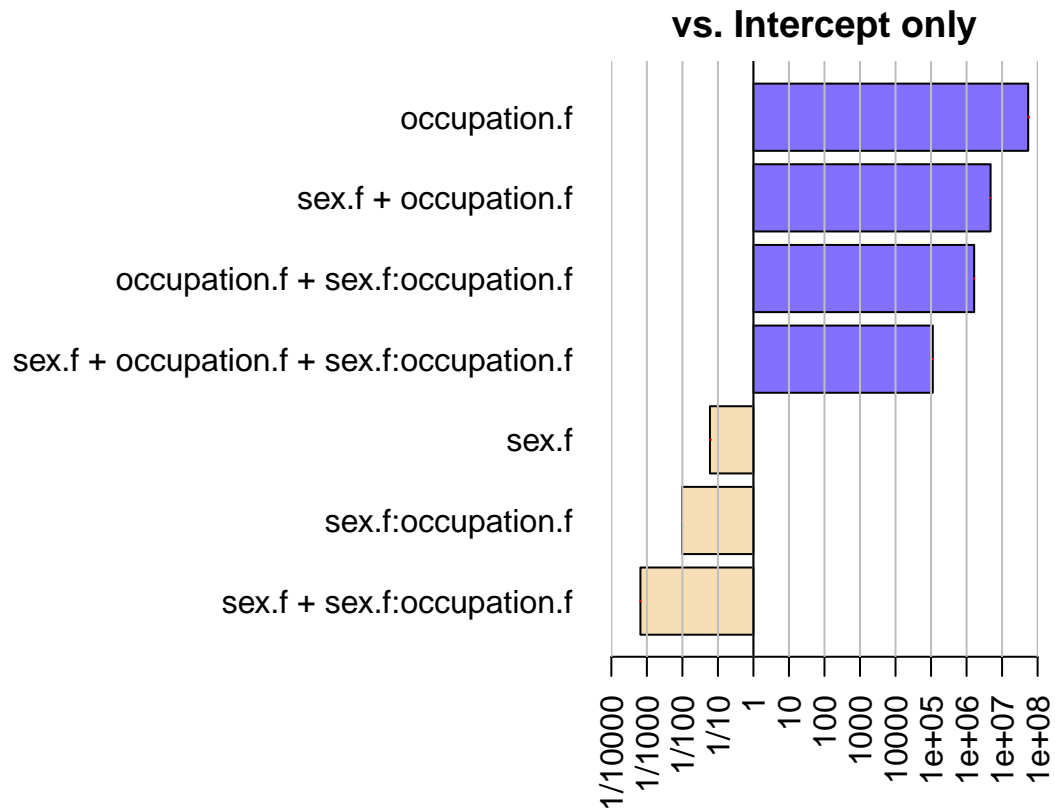
```
m1
```

```
## Bayes factor analysis
```

```
## -----
```

```
## [1] sex.f : 0.05966566 ±0%
## [2] occupation.f : 54417793 ±0.01%
## [3] sex.f:occupation.f : 0.009737589 ±0.1%
## [4] sex.f + occupation.f : 4750752 ±1.4%
## [5] sex.f + sex.f:occupation.f : 0.0006576211 ±1.3%
## [6] occupation.f + sex.f:occupation.f : 1639816 ±1.18%
## [7] sex.f + occupation.f + sex.f:occupation.f : 112035.6 ±1.3%
```

```
##
## Against denominator:
##   Intercept only
## ---
## Bayes factor type: BFlinearModel, JZS
plot(m1)
```

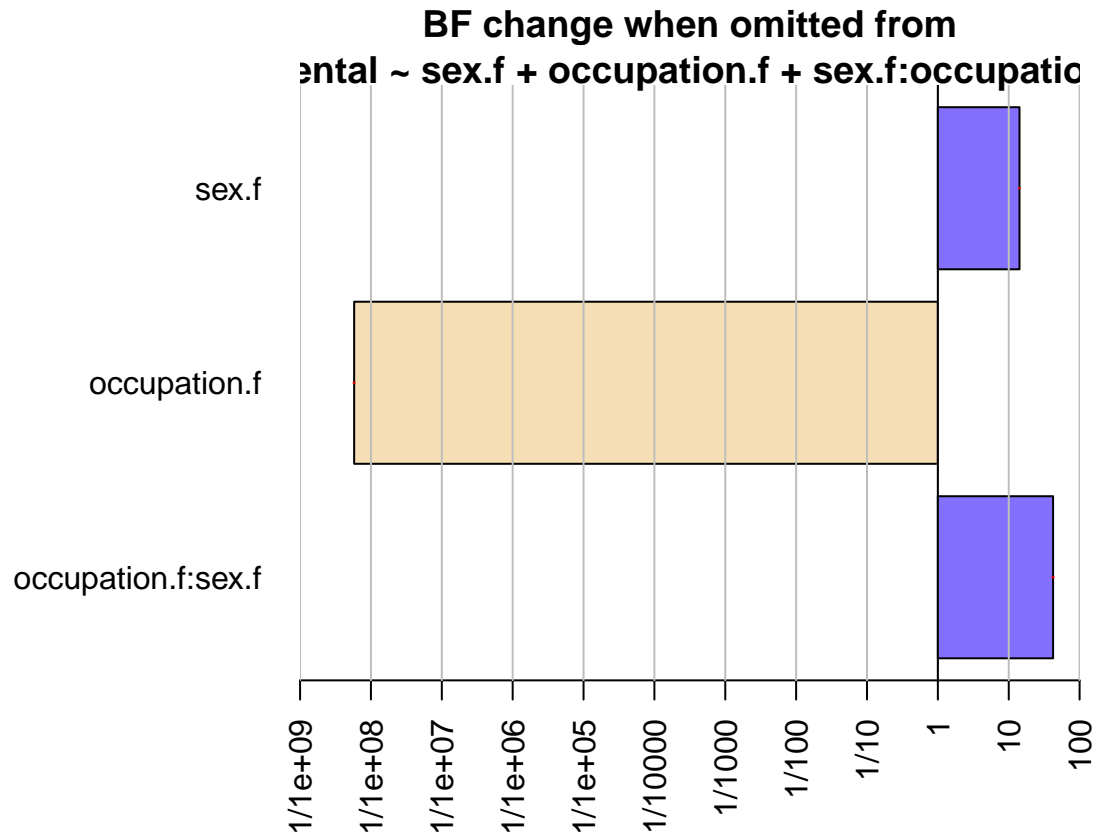


```
#Bayes ANOVA: "top"
m2 <- anovaBF(mental ~ sex.f*occupation.f, data = retirement, whichModels = "top")
```

```
## Warning: data coerced from tibble to data frame
m2
```

```
## Bayes factor top-down analysis
## -----
## When effect is omitted from sex.f + occupation.f + sex.f:occupation.f , BF is...
## [1] Omit occupation.f:sex.f : 42.25136 ±2.5%
## [2] Omit occupation.f      : 5.795131e-09 ±2.32%
## [3] Omit sex.f           : 14.18332 ±2.03%
##
## Against denominator:
##   mental ~ sex.f + occupation.f + sex.f:occupation.f
## ---
## Bayes factor type: BFlinearModel, JZS
```

```
plot(m2)
```



## Bayes ANOVA: “bottom”

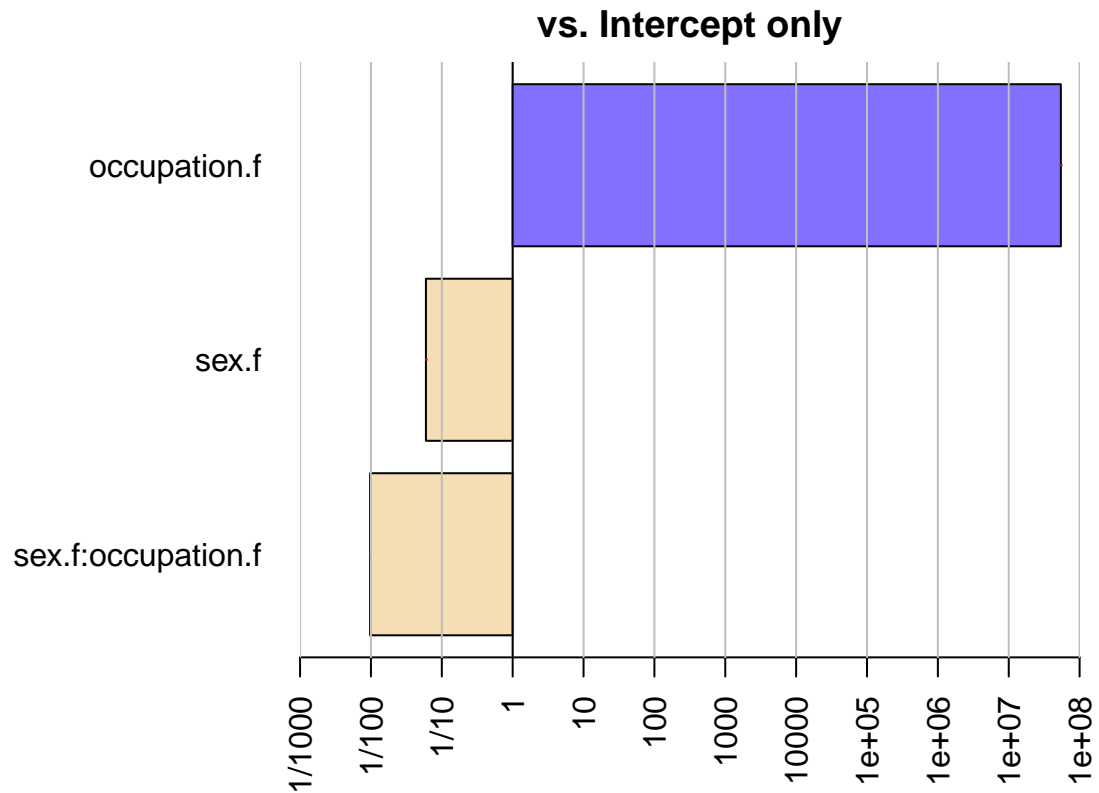
```
m3 <- anovaBF(mental ~ sex.f*occupation.f, data = retirement, whichModels = "bottom")
```

```
## Warning: data coerced from tibble to data frame
```

```
m3
```

```
## Bayes factor analysis
## -----
## [1] sex.f          : 0.05966566 ±0%
## [2] occupation.f   : 54417793 ±0.01%
## [3] sex.f:occupation.f : 0.009737589 ±0.1%
##
## Against denominator:
##   Intercept only
## ---
## Bayes factor type: BFlinearModel, JZS
```

```
plot(m3)
```



## Try it yourself

1a

```
dfhyp=1
dferr=230
alpha=.05
effect=.01 #enter the minimum effect you are testing
sse=100
mse=(((1/effect)-1)*sse)/dferr
noncen=sse/mse
qf((1-alpha),dfhyp,dferr,noncen)
```

```
## [1] 10.17986
```

1b

compared to null = 3.88 compared to 1% = 9.58

1c

At Nil the needed sample size is 71 (dferror = n - 1) At 1% The needed samples size is 121 (dferror = n - 1)

## Part 2

```
slp <- read_csv("slpdata.csv")
```

### Factor categorical predictors

```
slp <- mutate(slp,
              sex.f = factor(sex, levels = c(1,2), labels = c("male", "female")),
              cond.f = factor(cond, levels = c(1,2,3), labels= c("selfhelp", "group", "group_and_partners"))
)
```

### Frequentist ANOVA

```
anova <- aov(sleep ~ sex.f*cond.f, data=slp)
summary(anova)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## sex.f          1  16182   16182  206.572 <2e-16 ***
## cond.f         2  24971   12485  159.386 <2e-16 ***
## sex.f:cond.f   2    593     297   3.787 0.0232 *
## Residuals     594 46531      78
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### Eta squared calculations

```
sex      <- 16182 / (46531 + 16182 + 24971 + 593)
condition <- 24971 / (46531 + 16182 + 24971 + 593)
interaction <- 593 / (46531 + 16182 + 24971 + 593)
```

```
sex
```

```
## [1] 0.1833094
```

```
condition
```

```
## [1] 0.282871
```

```
interaction
```

```
## [1] 0.006717492
```

### Bayesian ANOVA with all models

```
Bayesm1 <- anovaBF(sleep ~ sex.f*cond.f, data=slp, whichModels = 'all')
```

```
## Warning: data coerced from tibble to data frame
```

```
Bayesm1
```

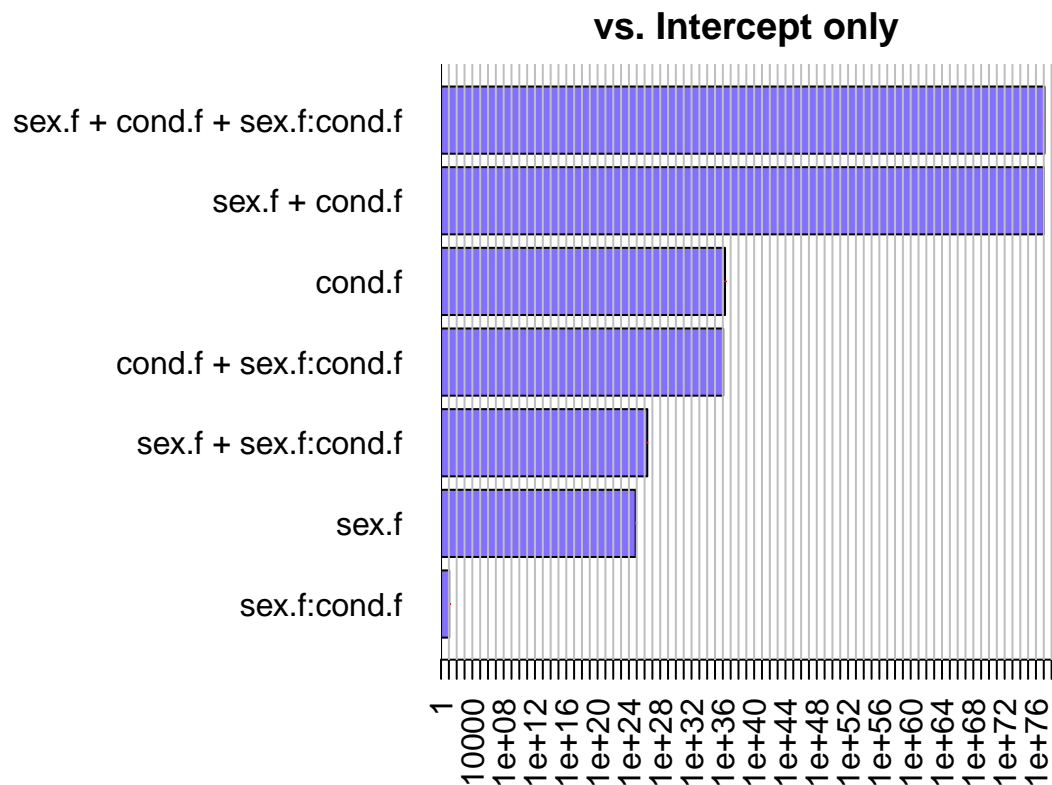
```
## Bayes factor analysis
```

```
## -----
```

```
## [1] sex.f              : 7.223375e+24 ±0%
## [2] cond.f             : 1.908767e+36 ±0.01%
## [3] sex.f:cond.f       : 11.04142      ±0.03%
## [4] sex.f + cond.f     : 1.012823e+77 ±1.15%
## [5] sex.f + sex.f:cond.f : 2.250371e+26 ±2.84%
```

```
## [6] cond.f + sex.f:cond.f      : 1.120565e+36 ±1.48%
## [7] sex.f + cond.f + sex.f:cond.f : 1.230544e+77 ±2.69%
##
## Against denominator:
##   Intercept only
## ---
## Bayes factor type: BFlinearModel, JZS
```

```
plot(Bayesm1)
```



## Bayesian ANOVA top-down approach

```
Bayesm2 <- anovaBF(sleep ~ sex.f*cond.f, data=slp, whichModels = "top")
```

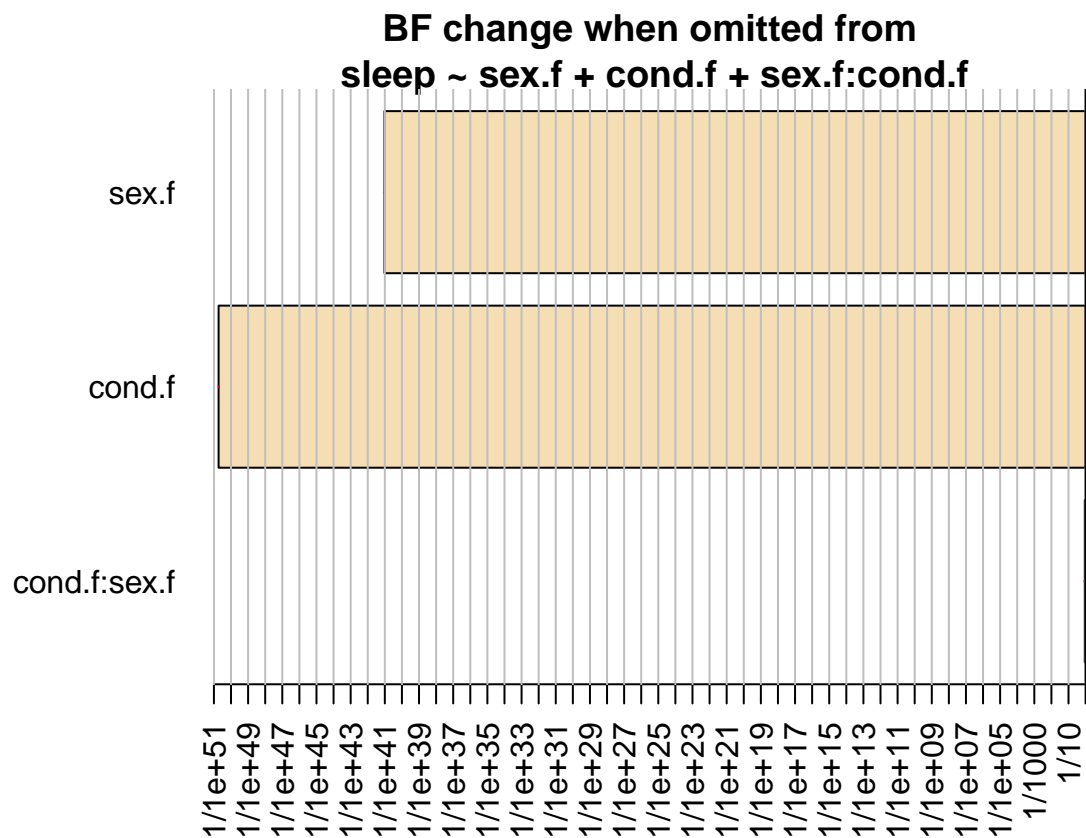
```
## Warning: data coerced from tibble to data frame
```

```
Bayesm2
```

```
## Bayes factor top-down analysis
## -----
## When effect is omitted from sex.f + cond.f + sex.f:cond.f , BF is...
## [1] Omit cond.f:sex.f : 0.8989903 ±7.24%
## [2] Omit cond.f      : 1.875716e-51 ±2.11%
## [3] Omit sex.f      : 9.448965e-42 ±2.31%
##
## Against denominator:
##   sleep ~ sex.f + cond.f + sex.f:cond.f
```



```
## ---
## Bayes factor type: BFlinearModel, JZS
plot(Bayesm2)
```



## Bayesian ANOVA bottom-up approach

```
Bayesm3 <- anovaBF(sleep ~ sex.f*cond.f, data=slp, whichModels = "bottom")
```

```
## Warning: data coerced from tibble to data frame
```

```
Bayesm3
```

```
## Bayes factor analysis
## -----
## [1] sex.f      : 7.223375e+24 ±0%
## [2] cond.f    : 1.908767e+36 ±0.01%
## [3] sex.f:cond.f : 11.04142 ±0.03%
##
## Against denominator:
##   Intercept only
## ---
## Bayes factor type: BFlinearModel, JZS
```

```
plot(Bayesm3)
```

