PSY 653 Module 11: Testing the hypothesis that something important happened
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Try it Yourself Activity

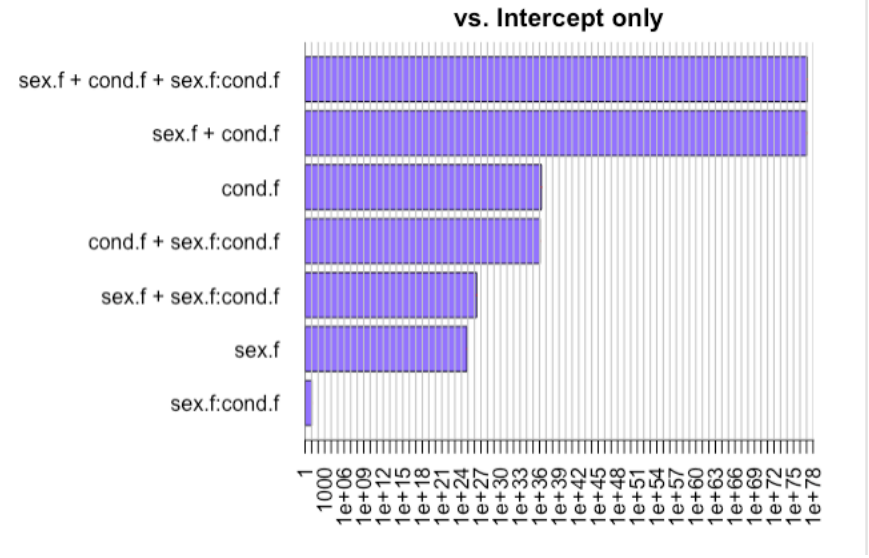
Part 1: Practice identifying minimum effects

1. A study that predicted differences in GPA from number of hours spent studying, and found a squared correlation of .103, which was significant, with F(1,230) = 3.26.
    a. Determine the critical *F* value for testing the hypothesis that RWA accounts for 1% or less of the variance in responses for the analysis that is highlighted
        i. This will require you to enter the appropriate values in the R script for df, F and execute the script

```
## 1a Determine critical vaue of F
```{r}
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
```

The authors' F value of 3.26 does not exceed the critical value of F (10.17986), indicating that their model did not identify a significant minimum effect for explaining 1% of the variance in Y.

b. Using Appendix B from Murphy, Myors & Wolach (2014), what can you say about the power of this study for rejecting
    ii. The traditional null hypothesis

With their F-value of 3.26, the authors were not able to reject the null hypothesis (required F-value = 3.88).

    iii. The hypothesis that studying time accounts for 1% or less of the variance in responses

With their F-value of 3.26, the authors were not able to reject the hypothesis that number of hours spent studying explained of 1% or less of the variance in GPA (required F-value = 9.58)

c. Use Appendix C from Murphy, Myors & Wolach (2014). Assuming that the effect size reported here is an accurate reflection of the population, approximately what sample size would you need to have power of .80 for rejecting

iv. The traditional null hypothesis

The authors need a sample size of 71 (df_{error} = n-1) to achieve a power level of 0.80 for rejecting the null hypothesis.

v. The hypothesis that studying time accounts for 1% or less of the variance in responses

The authors need a sample size of 121 to achieve a power level of 0.80 to reject the hypothesis that number of hours spend studying explains 1% or less of the variance in GPA.

Part 2: Practice bayesian analyses

2. Read in the datafile "slpdata.csv".

```
## Part 2
```{r,message=FALSE}
slp <- read_csv("slpdata.csv")
```
```

a. Factor sex identity and treatment condition, to code all levels of these variables

```
### Factor categorical variables
```{r}
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_partner"))
            )
```
```

b. Conduct a regular (i.e., frequentist) ANOVA in which sex identity, condition (cond), and their interaction predict sleep efficiency.

```
### Frequentist ANOVA
```{r}
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
```{r}
sex    <-  16182/ (46531 + 16182 + 24971 + 593)
condition    <- 24971 / (46531 + 16182 + 24971 + 593)
interaction     <-  593 / (46531 + 16182 + 24971 + 593)

sex
condition
interaction
```
```

```
[1] 0.1833094
[1] 0.282871
[1] 0.006717492
```

Results from the frequentist ANOVA indicate that both main effects as well as the interaction term significantly predict sleep hygiene. The main effect of sex explains ~18% of the variance in sleep efficiency, the main effect of condition explains ~28% of the variance in sleep efficiency, and the interaction term explains ~0.6% of the variance in sleep efficiency.

c. Use the BayesFactor package to do a comparable analysis (Use the anovaBF function)
    i. Interpret and compare the results

```
## Bayesian ANOVA with all models
```{r}
Bayesm1 <- anovaBF(sleep ~ sex.f*cond.f, data=slp,whichModels = 'all')
Bayesm1
plot(Bayesm1)
```
```

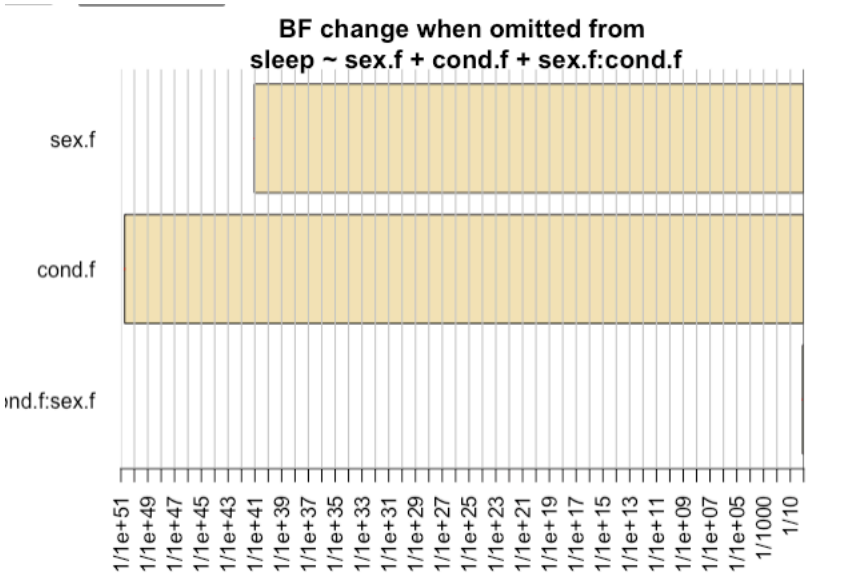
```
  |======================================================================================================
Bayes factor analysis
--------------
[1] sex.f                       : 7.223375e+24 ±0%
[2] cond.f                      : 1.908767e+36 ±0.01%
[3] sex.f:cond.f                : 11.04142     ±0.03%
[4] sex.f + cond.f              : 1.018488e+77 ±1.14%
[5] sex.f + sex.f:cond.f        : 2.135045e+26 ±1.29%
[6] cond.f + sex.f:cond.f       : 1.123194e+36 ±1.48%
[7] sex.f + cond.f + sex.f:cond.f : 1.191637e+77 ±1.89%

Against denominator:
  Intercept only
---
Bayes factor type: BFlinearModel, JZS
```



Comparing the Bayes factors of all of the possible models: models that include the main effects of sex and condition have large Bayes factors, with decisive evidence that both main effects predict sleep efficiency (BF>100). There is strong evidence that the interaction term predicts sleep efficiency (BF between 10-30).

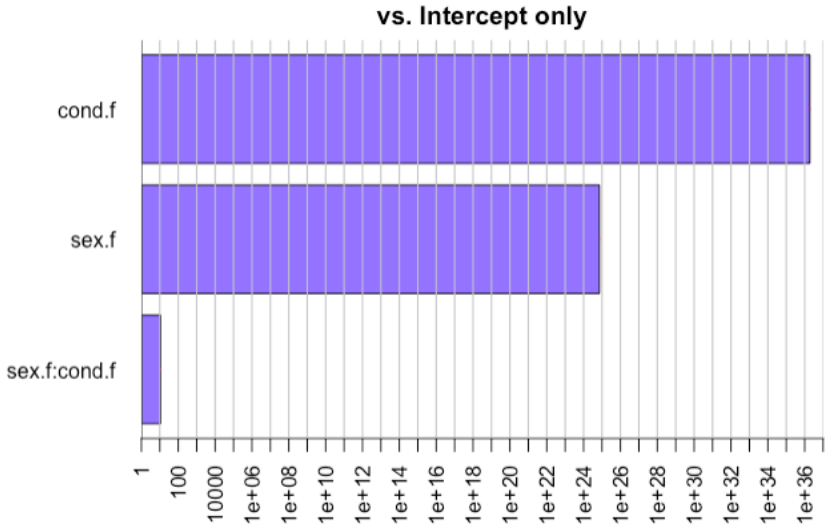
```r
## Bayesian ANOVA top-down approach
```{r}
Bayesm2 <- anovaBF(sleep ~ sex.f*cond.f, data=slp, whichModels = "top")
Bayesm2
plot(Bayesm2)
```
```


```
  |======================================================================
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 : 0.8139254    ±3.19%
[2] Omit cond.f       : 1.889831e-51 ±6.08%
[3] Omit sex.f        : 9.102183e-42 ±3.13%

Against denominator:
  sleep ~ sex.f + cond.f + sex.f:cond.f
---
Bayes factor type: BFlinearModel, JZS
```



Comparing the Bayes factors for models when each effect is eliminated one at a time: Removing each main effect leaves a model with a much smaller Bayes factor that supports the null hypothesis. Condition has a larger impact on model Bayes factor than sex. Removing the interaction term doesn't have a large effect on model Bayes factor.

```
## Bayesian ANOVA bottom-up approch
```{r}
Bayesm3 <- anovaBF(sleep ~ sex.f*cond.f, data=slp,whichModels = "bottom")
Bayesm3
plot(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
```



Comparing change in model Bayes factor when each effect is added one at a time: Adding each main effect yields a model with a much larger Bayes factor that supports the alternative hypothesis (that X predicts Y). Condition has a larger impact on model Bayes factor than sex. Adding the interaction term doesn't have a large effect on model Bayes factor.

Comparing frequentist and Bayesian ANOVAS:
Both sets of analyses indicate that all three effects (sleep, condition, and their interaction) predict sleep efficiency. Condition has the strongest impact on sleep efficiency (largest eta

squared and Bayes factor). The interaction term contributed least to the prediction of sleep efficiency (smallest eta squared and smallest Bayes factor).