Reanalysis of 36-Schroeder

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Reference

Schröder, J., Berger, T., Meyer, B., Lutz, W., Späth, C., Michel, P., Rose, M., Hautzinger, M., Hohagen, F., Klein, J. P., & Moritz, S. (2018). Impact and change of attitudes toward Internet interventions within a randomized controlled trial on individuals with depression symptoms. *Depression and Anxiety*", 35(5), 421–430. https://doi.org/10.1002/da.22727

Notes from reading methods section

Secondary analysis of RCT using ANCOVA to assess interaction between attitude toward internet interventions (measured with APOI) and intervention group on the primary outcome patient health (PHQ).

- Dependant variable: PHQ-9diff (difference pre-post in Patient Health Questionnaire; higher means improved)

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- Independent variable: Group
  - Care as usual CAS (n=378)
  - CAS plus deprexis (n=376)
- Covariate: baseline variable
- Design: RCT, 1-way ANCOVA with group (2 levels) as IV and baseline as covariate

Reading data

Data is loaded, reshaped if necessary, and factors are specified.

```
PATH = file.path(path.expand("~"), "Data", "ancova") # ancova project folder
data = read.sav(file.path(PATH, "dataPrimaryStudies",
                          "36-Schroeder", "Schroeder2018DA.sav"), pass="HH2020")
data$group = factor(data$group, levels = c("WLC", "deprexis"))
#summary(data)
```

Descriptives

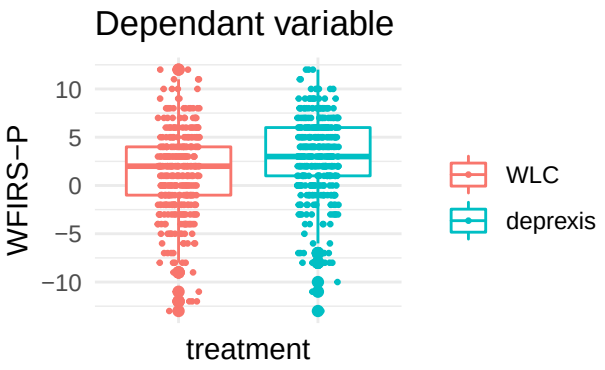
Dependent variable

Mean (SD) of primary outcome per treatment arm. Compare to Table 1, WFIRS-P total score.

```
tapply(data$PHQdif, data$group, function (x) sprintf("%0.2f (%0.2f)", mean(x), sd(x)))
```

```
##           WLC      deprexis
## "1.14 (4.31)" "2.92 (4.06)"
```

```
ggplot(data, aes(y=PHQdif, x=group, color=group)) +
  geom_boxplot() +
  geom_point(position = position_jitter(width = 0.15, height = 0), size=0.5) +
  theme_minimal() +
  theme(axis.text.x = element_blank(), legend.title = element_blank()) +
  xlab("treatment") + ylab("WFIRS-P") + ggtitle("Dependant variable")
```

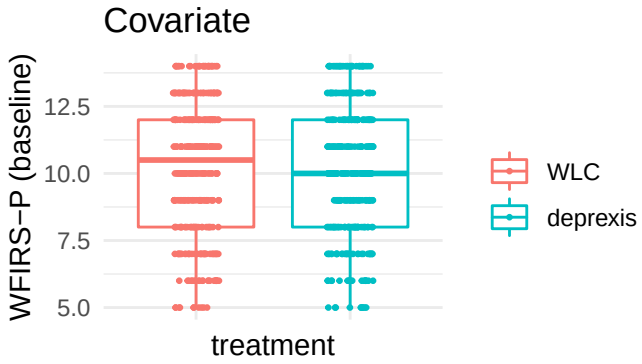


Covariate(s)

```
tapply(data$PHQpre, data$group, function (x) sprintf("%0.2f (%0.2f)", mean(x), sd(x)))
```

```
##            WLC       deprexis
## "10.21 (2.46)" "10.14 (2.42)"
```

```
ggplot(data, aes(y=PHQpre, x=group, color=group)) +
  geom_boxplot() +
  geom_point(position = position_jitter(width = 0.15, height = 0), size=0.5) +
  theme_minimal() +
  theme(axis.text.x = element_blank(), legend.title = element_blank()) +
  xlab("treatment") + ylab("WFIRS-P (baseline)") + ggtitle("Covariate")
```



Main analysis ANCOVA

```
# Orthogonal contrasts
contrasts(data$group) = contr.helmert(2)

fit.ancova = aov(PHQdif ~ PHQpre + APOIpre*group, data = data)
result = Anova(fit.ancova, type=3) # Type III
print(result)
```

```
## Anova Table (Type III tests)
##
## Response: PHQdif
##                Sum Sq  Df F value    Pr(>F)
## (Intercept)     155.8   1  9.6865  0.001927 **
## PHQpre          885.1   1 55.0392 3.209e-13 ***
## APOIpre          30.7   1  1.9077  0.167630
## group            96.8   1  6.0199  0.014372 *
## APOIpre:group   168.7   1 10.4919  0.001252 **
## Residuals     12044.6 749
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Let's visualize the relationship APOI and the outcome per group

They reported a 1.5 point greater symptom reduction per 10 APOI units, trying regression to reproduce this finding. * I scaled the APOI/10 so the estimates are per 10 units * There is a 0.69 points improvement in symptoms per 10 units APOI in the treatment group.

```
data$APOIpre.10 = data$APOIpre/10
summary(lm(PHQdif ~ PHQpre + APOIpre.10*group, data = data))
```

```
##
```

```
## Call:
## lm(formula = PHQdif ~ PHQpre + APOIpre.10 * group, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -15.3579  -2.3830   0.4658   2.8022  10.0050
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -4.14314    1.33121  -3.112  0.00193 **
## PHQpre             0.44602    0.06012   7.419 3.21e-13 ***
## APOIpre.10         0.29181    0.21128   1.381  0.16763
## group1            -2.91642    1.18865  -2.454  0.01437 *
## APOIpre.10:group1  0.68635    0.21189   3.239  0.00125 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.01 on 749 degrees of freedom
## Multiple R-squared:  0.1266, Adjusted R-squared:  0.1219
## F-statistic: 27.14 on 4 and 749 DF,  p-value: < 2.2e-16
```

Comparing ANCOVA in original study with reanalysis

Interaction effect

```
tab.inter = rbind(stats.orig.inter, stats.rep.inter)
rownames(tab.inter) = c("original Study", "reanalysis")
print(t(tab.inter))
```

```
##        original Study reanalysis
## Fvalue "10.492"       "10.49"
## df1    "4"            "1"
## df2    "749"          "749"
## pvalue "0.001"        "0.001"
```

Assumptions

1. Homogeneity of variance

- ANOVA/ANCOVA is fairly robust in terms of the error rate when sample sizes are equal.
- When groups with larger sample sizes have larger variances than the groups with smaller sample sizes, the resulting F-ratio tends to be conservative. That is, it's more likely to produce a non-significant result when a genuine difference does exist in the population.
- Conversely, when the groups with larger sample sizes have smaller variances than the groups with smaller samples sizes, the resulting F-ratio tends to be liberal and can inflate the false positive rate.

```
tapply(data$PHQdif, data$group, sd)
```

```
##      WLC deprexis
## 4.312971 4.058493
```

```r
leveneTest(PHQdif ~ group, data = data)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##        Df F value Pr(>F)
## group   1  1.4057 0.2361
##       752
```

2. Independence between covariate and IV

When the covariate and the experimental effect (independent variable) are not independent the treatment effect is obscured, spurious treatment effects can arise and the interpretation of the ANCOVA is seriously compromised.

We test whether our groups differ on the CV. If the groups do not significantly differ then is appropriate to use the covariate.

```r
fit.cv = aov(PHQdif ~ group, data = data)
Anova(fit.cv, type=3)
```

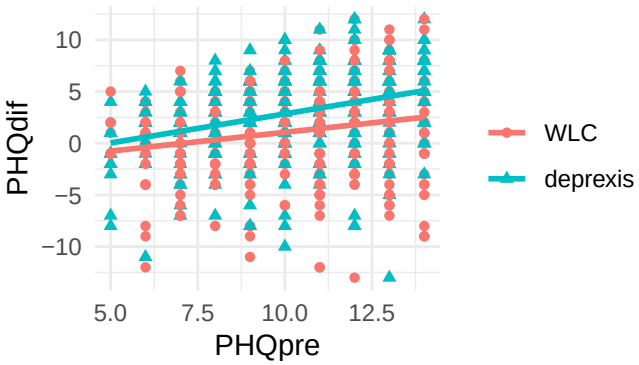
```
## Anova Table (Type III tests)
##
## Response: PHQdif
##              Sum Sq  Df F value    Pr(>F)
## (Intercept)  3107.8   1 177.190 < 2.2e-16 ***
## group         600.8   1  34.255 7.218e-09 ***
## Residuals   13189.6 752
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

3. Homogeneity of regression slopes

```r
fit.hrs = aov(PHQdif ~ PHQpre*group, data = data)
Anova(fit.hrs, type=3)
```

```
## Anova Table (Type III tests)
##
## Response: PHQdif
##               Sum Sq  Df F value    Pr(>F)
## (Intercept)    293.5   1 18.0532 2.419e-05 ***
## PHQpre         959.7   1 59.0242 4.876e-14 ***
## group            0.4   1  0.0246    0.8754
## PHQpre:group    43.8   1  2.6950    0.1011
## Residuals    12194.7 750
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
ggplot(data, aes(y=PHQdif, x=PHQpre, color=group, shape=group)) +
  geom_point() +
  geom_smooth(formula = y ~ x,method=lm, se=FALSE, fullrange=TRUE) +
  theme_minimal() +
  theme(legend.title = element_blank())
```



Notes

- Main finding fully reproduced, but df1 was reported wrong
- They reported a associated 1.5 point greater symptom reduction per 10 APOI units (in treatment arm compared to controls), but I could not reproduce this using a regression with the same model used in the ANCOVA, I found a 0.7-point improvement.
- All assumptions met (equal variances, independence of covariate and homogeneity of regression slopes)

Data was analyzed according to recommendations by Field, Miles, & Field (2012).