PSY.308d.DA5

Prompt

Parents with anxiety disorders tend to have children with anxiety disorders as well (see everything ever written by Bogels, Borelli, Wood, or Rapee). This has led some to hypothesize that anxiety is genetically transmitted. However, you think there might be something else going on. Parental overcontrol, the excess regulation of a child's emotion, cognition, and behavior is strongly related to child anxiety. You wonder if anxious parents are more overcontrolling, leading to child anxiety. You decided to conduct a study to figure this out.

Variables: Parent_Anx: 1-20 (higher scores indicating higher anxiety symptoms) Child_Anx: 1-20 (higher scores indicating higher anxiety symptoms) Parent_OC: 1-20 (higher scores indicating greater use of over-control)

Research Question: Does parental overcontrol mediate the relationship between parent anxiety and child anxiety?

(1) *General assignment:* Conduct the appropriate analysis using bootstrapping techniques. Report the proper assumptions and statistics in the results section. In the discussion section, provide a summary of what you found, discuss the implications, and give at least one limitation and future research direction. Don't forget to include a table for descriptives, correlations, and regression models.

(2) *Conceptual component:* Conduct the same analysis, but use the Sobel test instead of bootstrapping to test the indirect effect. *Report the statistics in your results section.* Provide a summary of what of the findings were for this analysis and compare it to your bootstrapped analysis findings. If the two analyses found different outcomes, determine which results are more appropriate and justify your decision (Hint: What is a known issue with the Sobel test?).

#Prep

```
library(pacman)
p_load(psych, jmv, medmod, lavaan, multilevel)
```

#Read in your data

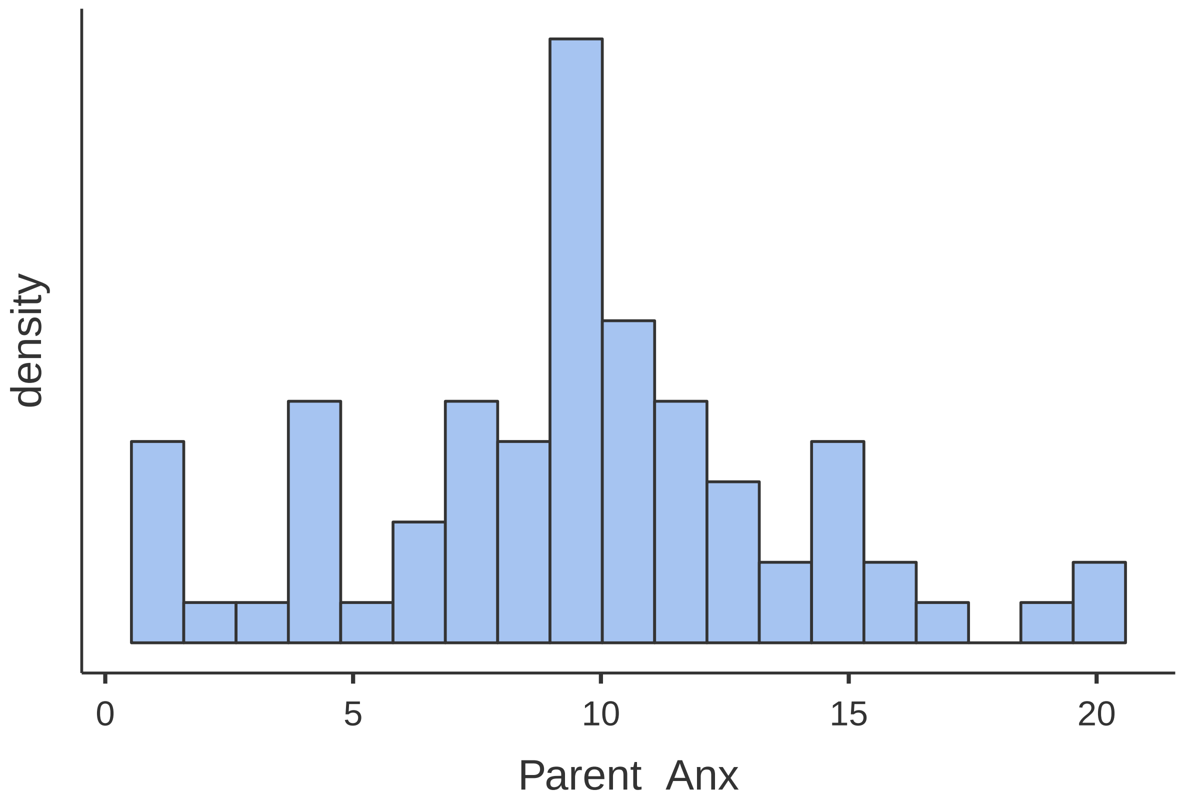
```
datboot <- read.csv("https://www.dropbox.com/s/dsplwa2mppfhmu7/Psy.308d.DA5.csv?dl=1")
```

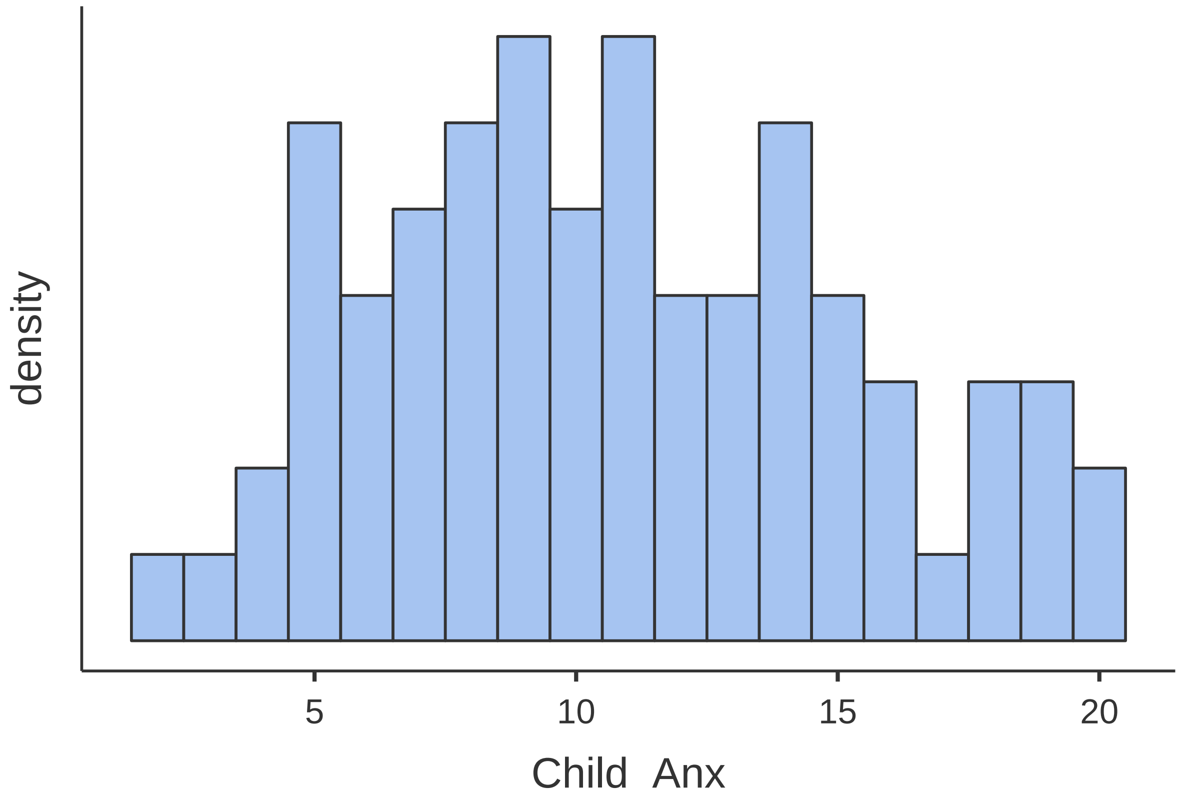
Descriptives

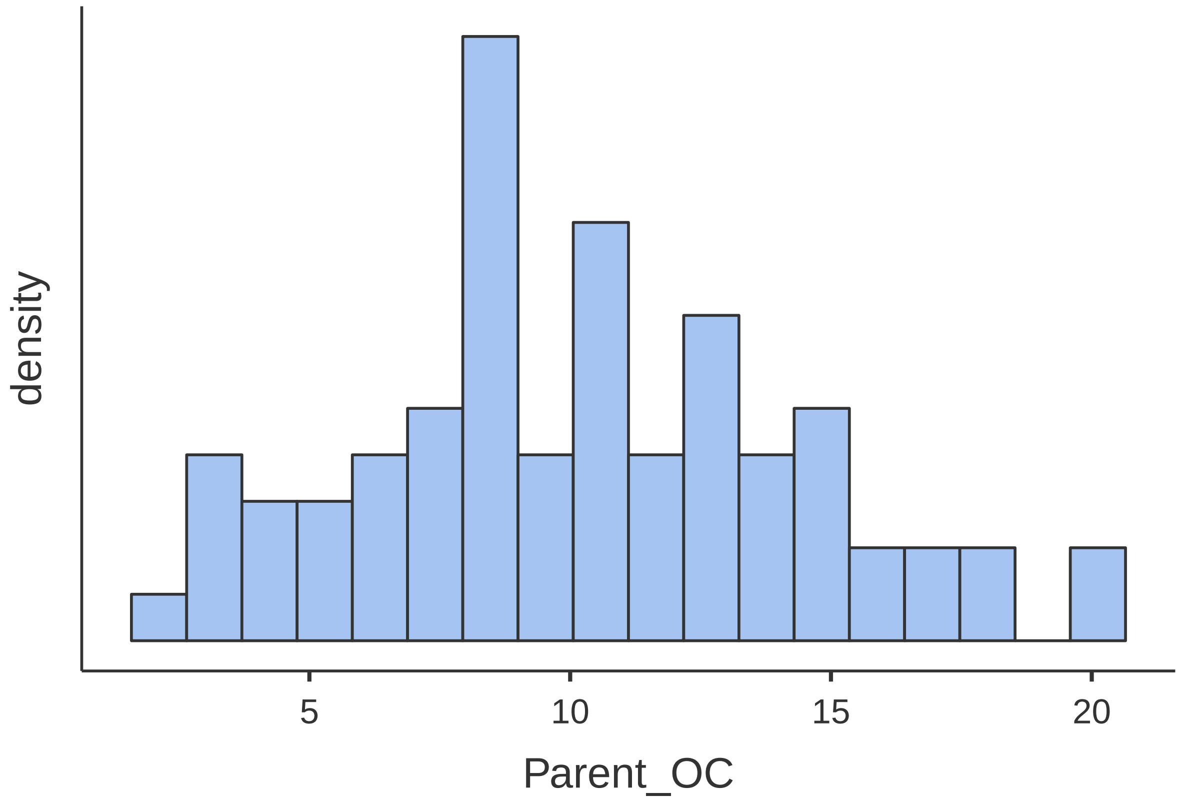
```
desc <- descriptives(datboot,
                     vars = c('Parent_Anx', 'Child_Anx', 'Parent_OC'),
                     hist = TRUE,
                     sd = TRUE,
                     min = TRUE,
                     max = TRUE,
                     skew = TRUE,
                     kurt = TRUE)
desc
```

```
##
##  DESCRIPTIVES
##
##  Descriptives
##  ----------------------------------------------------------------
##                           Parent_Anx    Child_Anx    Parent_OC
##  ----------------------------------------------------------------
##    N                              74           74           74
```

```
##    Missing                       0            0            0
##    Mean                       9.54         10.8         10.3
##    Median                     10.0         10.5         10.5
##    Standard deviation         4.53         4.49         4.31
##    Minimum                       1            2            2
##    Maximum                      20           20           20
##    Skewness                 0.0261        0.254        0.130
##    Std. error skewness       0.279        0.279        0.279
##    Kurtosis                 -0.195       -0.721       -0.542
##    Std. error kurtosis       0.552        0.552        0.552
##  ----------------------------------------------------------------
```




density
5
10
15
20
Child_Anx




```r
cat("\n")
```

```r
corr <- corrMatrix(datboot,
                   vars = c('Parent_Anx', 'Child_Anx', 'Parent_OC'),
                   flag = TRUE)
corr
```

```
##
##  CORRELATION MATRIX
##
##  Correlation Matrix
##  ----------------------------------------------------------------------
##                                 Parent_Anx    Child_Anx    Parent_OC
##  ----------------------------------------------------------------------
##    Parent_Anx    Pearson's r             -        0.618        0.602
##                  p-value                 -       < .001       < .001
##
##    Child_Anx     Pearson's r                          -        0.675
##                  p-value                              -       < .001
##
##    Parent_OC     Pearson's r                                       -
##                  p-value                                           -
##  ----------------------------------------------------------------------
##    Note. * p < .05, ** p < .01, *** p < .001
```

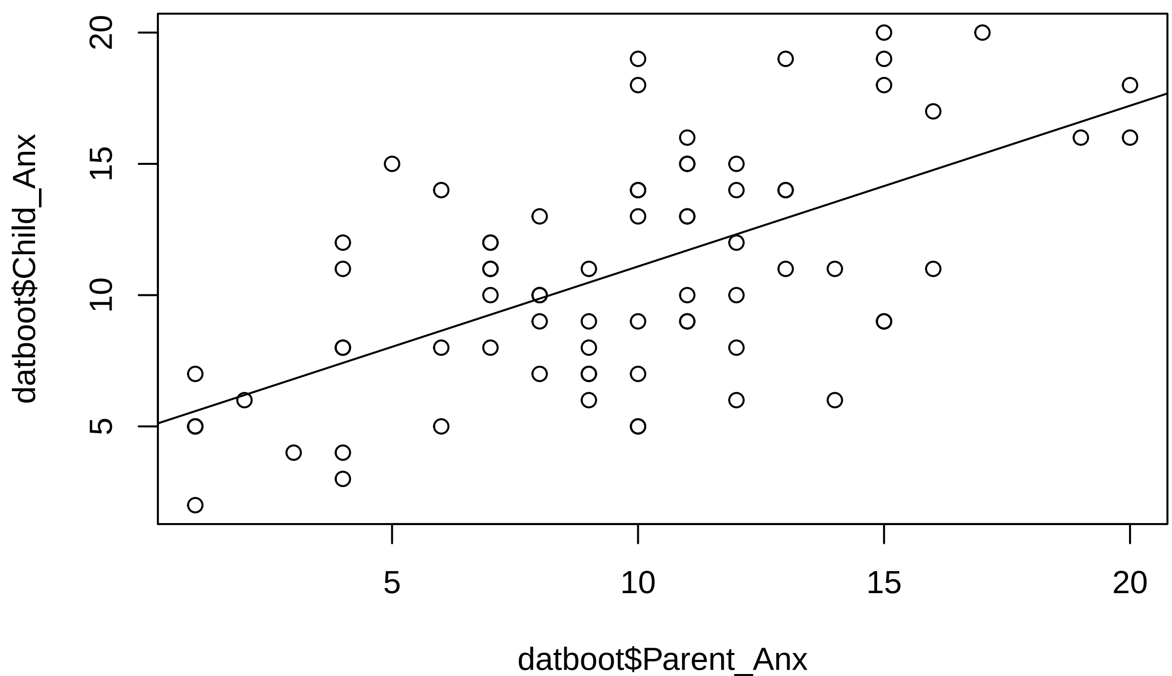
Assumptions:

1. Missing Data - **NONE**

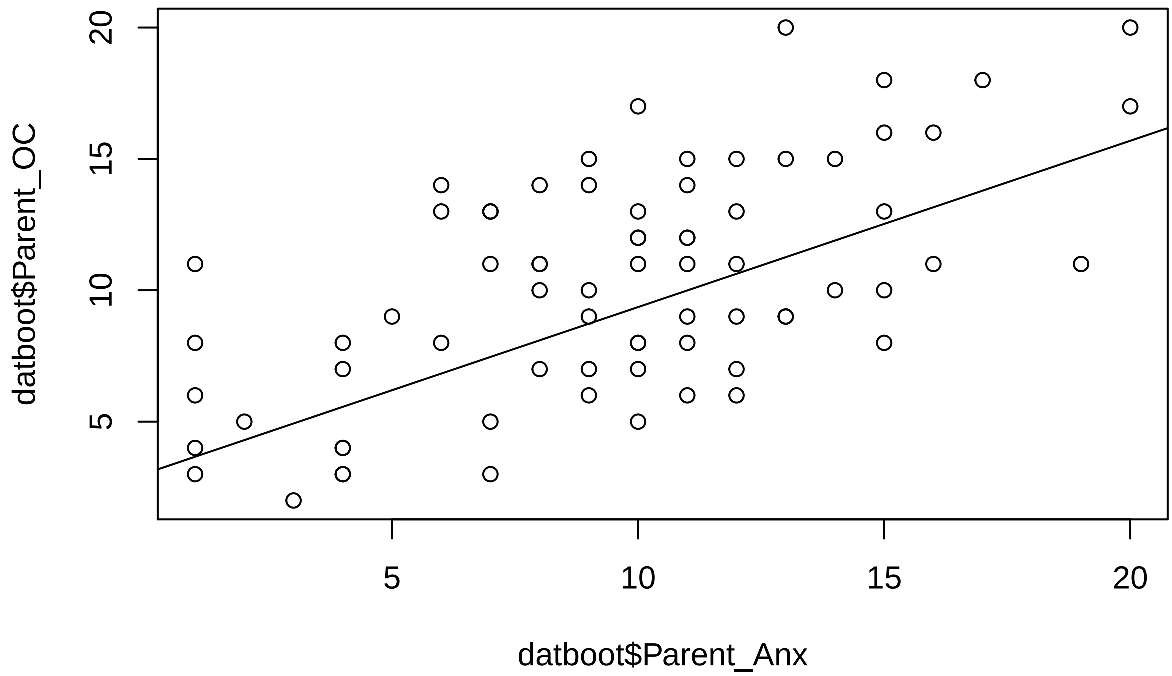
2. Univariate a. Normality **PASSED**, b. Linearity and c. Outliers
3. Multivariate a. Normality **PASSED** and b.Outliers **REMOVED**
4. Heteroscedsticity **PASSED**
5. Multi-collinearity **EXPECTED**

2b. Univariate Linearity

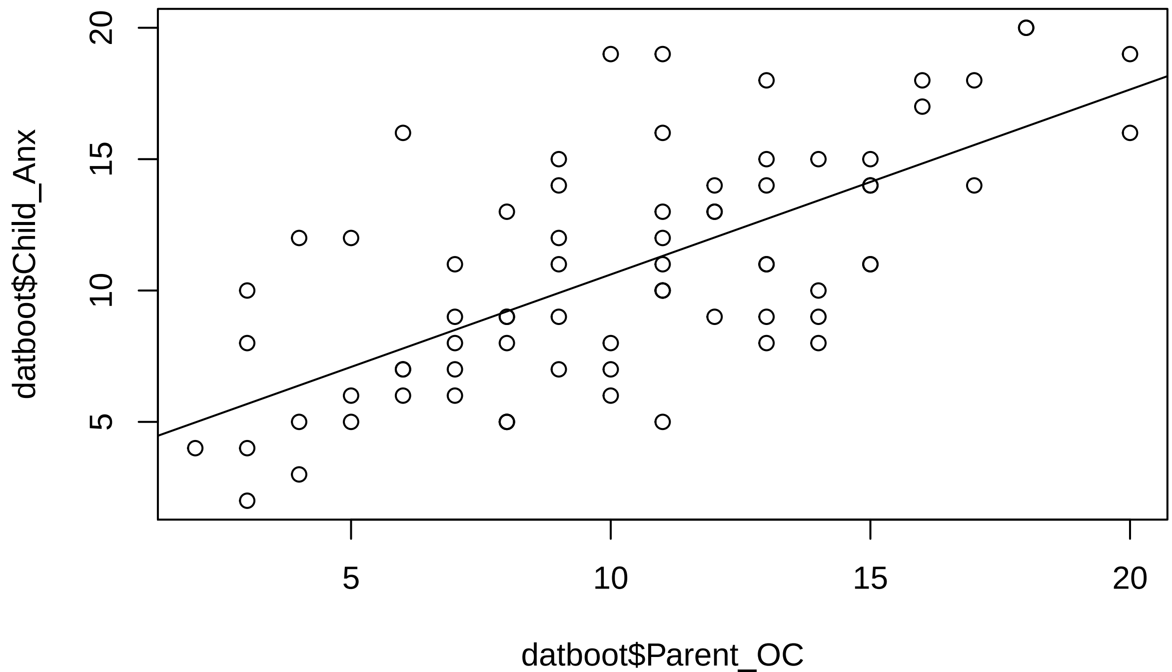
```
# Scatterplots [Assumption 2b]

# Y ~ X [path c]
plot(datboot$Parent_Anx, datboot$Child_Anx, abline(lm(datboot$Child_Anx ~ datboot$Parent_Anx)))
```




```
# M ~ X [path a]
plot(datboot$Parent_Anx, datboot$Parent_OC, abline(lm(datboot$Parent_Anx ~ datboot$Parent_OC)))
```




```r
# Y ~ M [path b]
plot(datboot$Parent_OC, datboot$Child_Anx, abline(lm(datboot$Child_Anx ~ datboot$Parent_OC)))
```



2c. Univariate Outliers

```
#Identify outliers
#scale() converts to z scores - "3" refers to standard deviations
datboot[abs(scale(datboot$Parent_Anx)) > 3, ]
```

```
## [1] Participant Parent_Anx  Parent_OC   Child_Anx
## <0 rows> (or 0-length row.names)
```

```
datboot[abs(scale(datboot$Child_Anx)) > 3, ]
```

```
## [1] Participant Parent_Anx  Parent_OC   Child_Anx
## <0 rows> (or 0-length row.names)
```

```
datboot[abs(scale(datboot$Parent_OC)) > 3, ]
```

```
## [1] Participant Parent_Anx  Parent_OC   Child_Anx
## <0 rows> (or 0-length row.names)
```

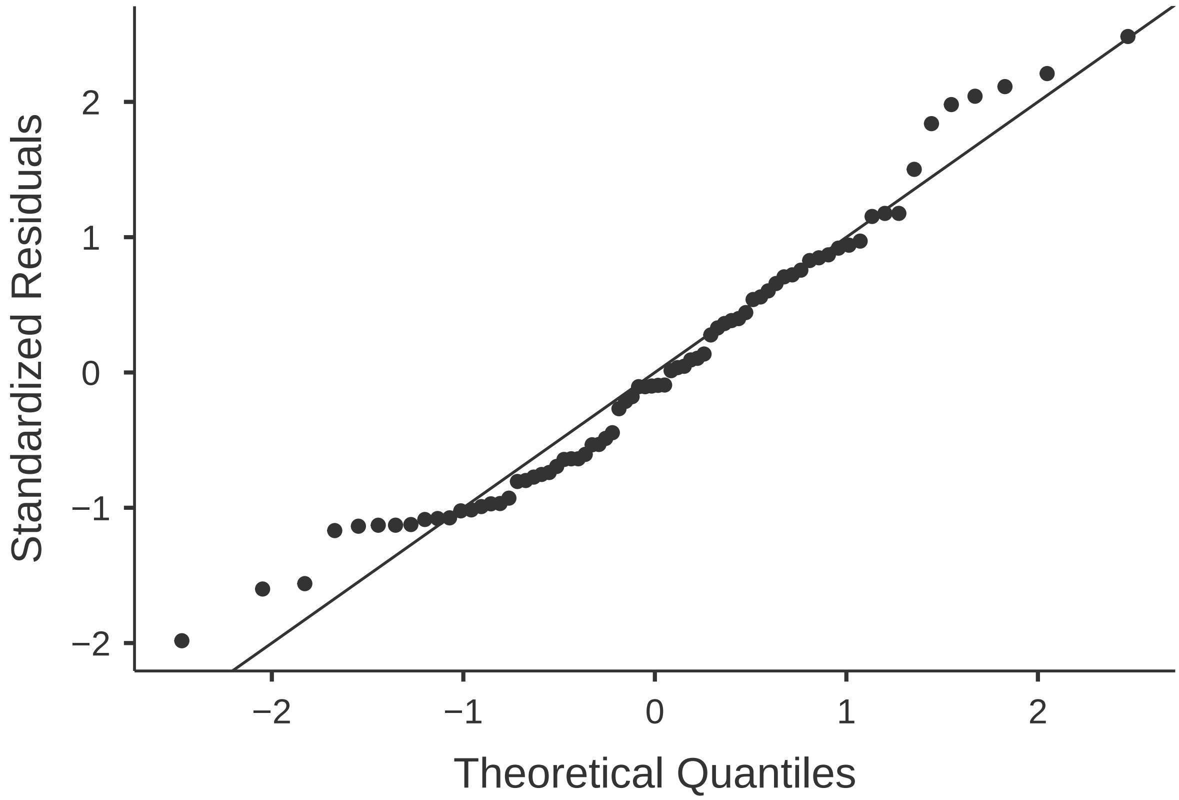
```
#There are a total of 0 independent observations that contain outliers
```

3a. Multivariate Normality

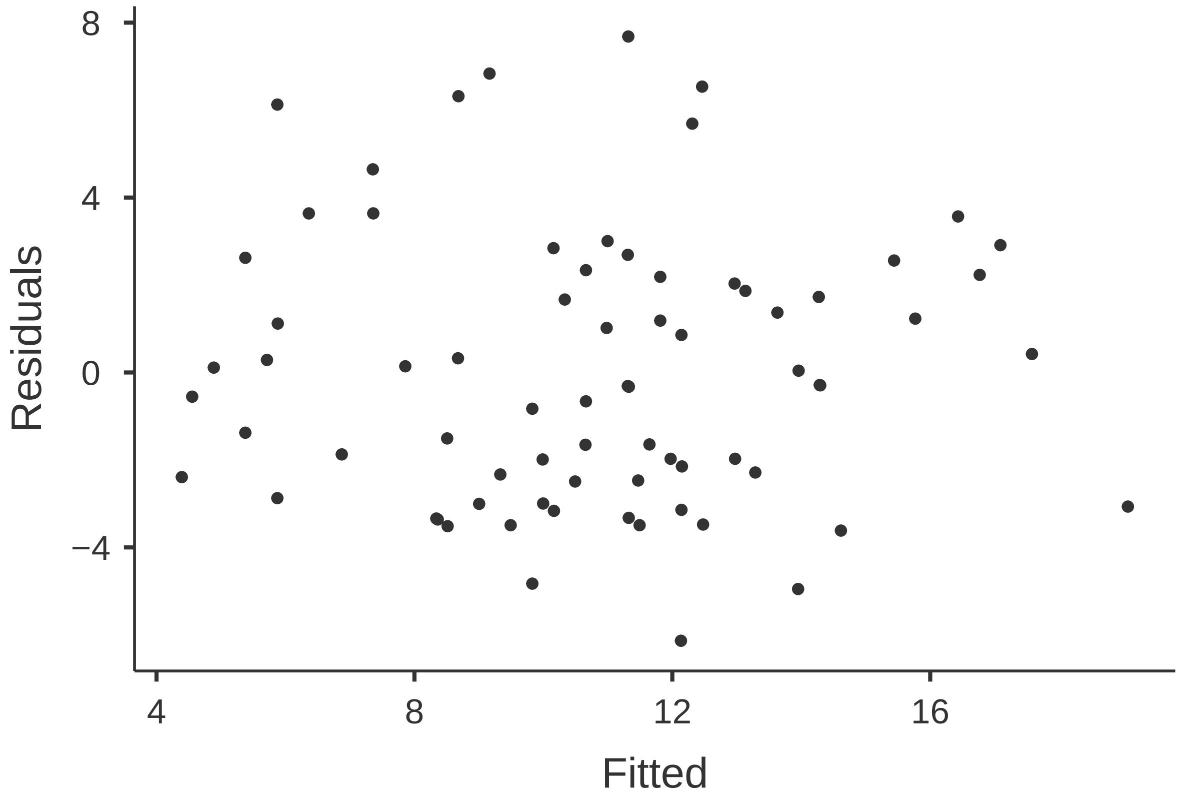
```
#look at residuals and the Q-Q plot for independent variables (should be no relationship)
#Observe Leverage (Mahalanobis' Distance) + Discrepancy (= Influence; Cook's Distance)

# Y ~ X + M
model.multi_norm <- linReg(data = datboot,
                dep = 'Child_Anx',
                covs = c('Parent_Anx', 'Parent_OC'),
```

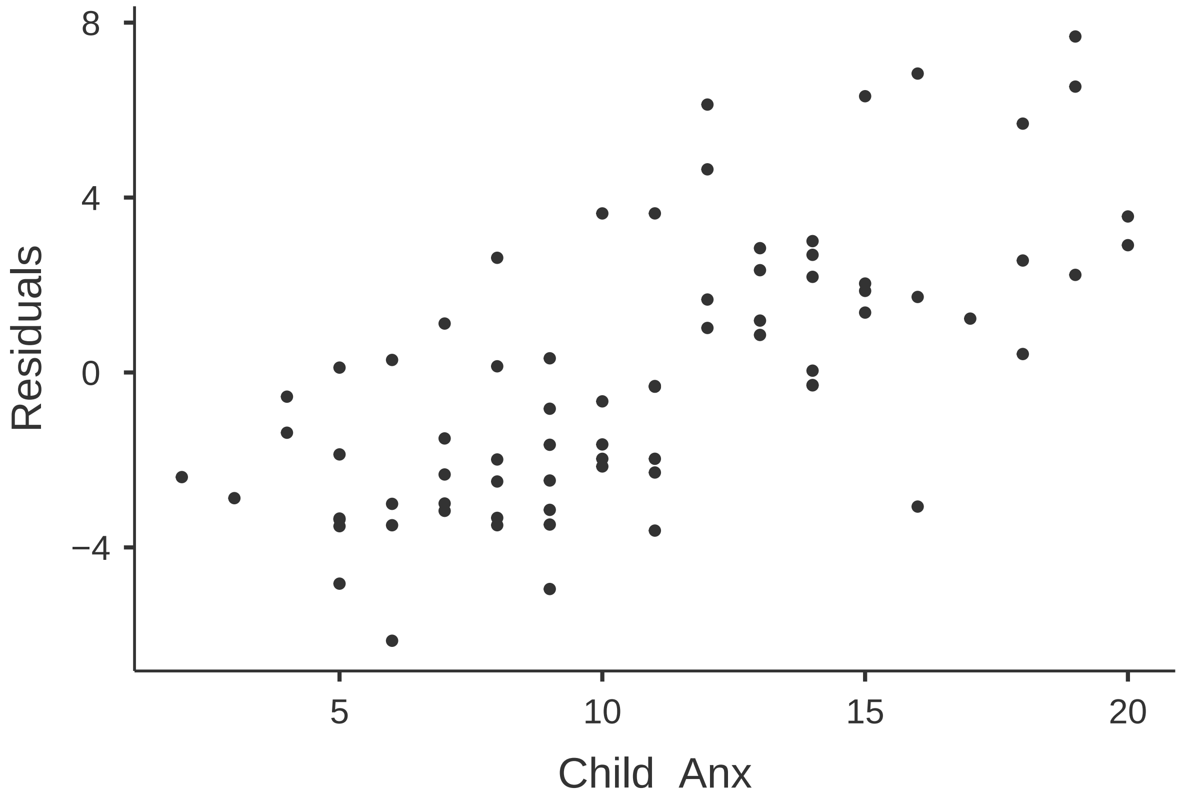
```r
                blocks = list(c('Parent_Anx', 'Parent_OC')),
                modelTest = TRUE,
                r2Adj = TRUE,
                stdEst = TRUE,
                ciStdEst = TRUE,
                qqPlot = TRUE,  ##QQ plot
                resPlots = TRUE) ##residuals plot

model.multi_norm
```

```
##
##  LINEAR REGRESSION
##
##  Model Fit Measures
##  ---------------------------------------------------------------------------
##    Model    R        R²        Adjusted R²    F       df1    df2    p
##  ---------------------------------------------------------------------------
##        1    0.725    0.526           0.512    39.4      2     71    < .001
##  ---------------------------------------------------------------------------
##
##
##  MODEL SPECIFIC RESULTS
##
##  MODEL 1
##
##  Model Coefficients
##  -------------------------------------------------------------------------------------------
##    Predictor     Estimate    SE       t        p         Stand. Estimate    Lower    Upper
##  -------------------------------------------------------------------------------------------
##    Intercept        2.575    0.998    2.58     0.012
##    Parent_Anx       0.328    0.101    3.24     0.002               0.331    0.127    0.535
##    Parent_OC        0.496    0.107    4.65    < .001               0.476    0.272    0.680
##  -------------------------------------------------------------------------------------------
##
##
##  ASSUMPTION CHECKS
```

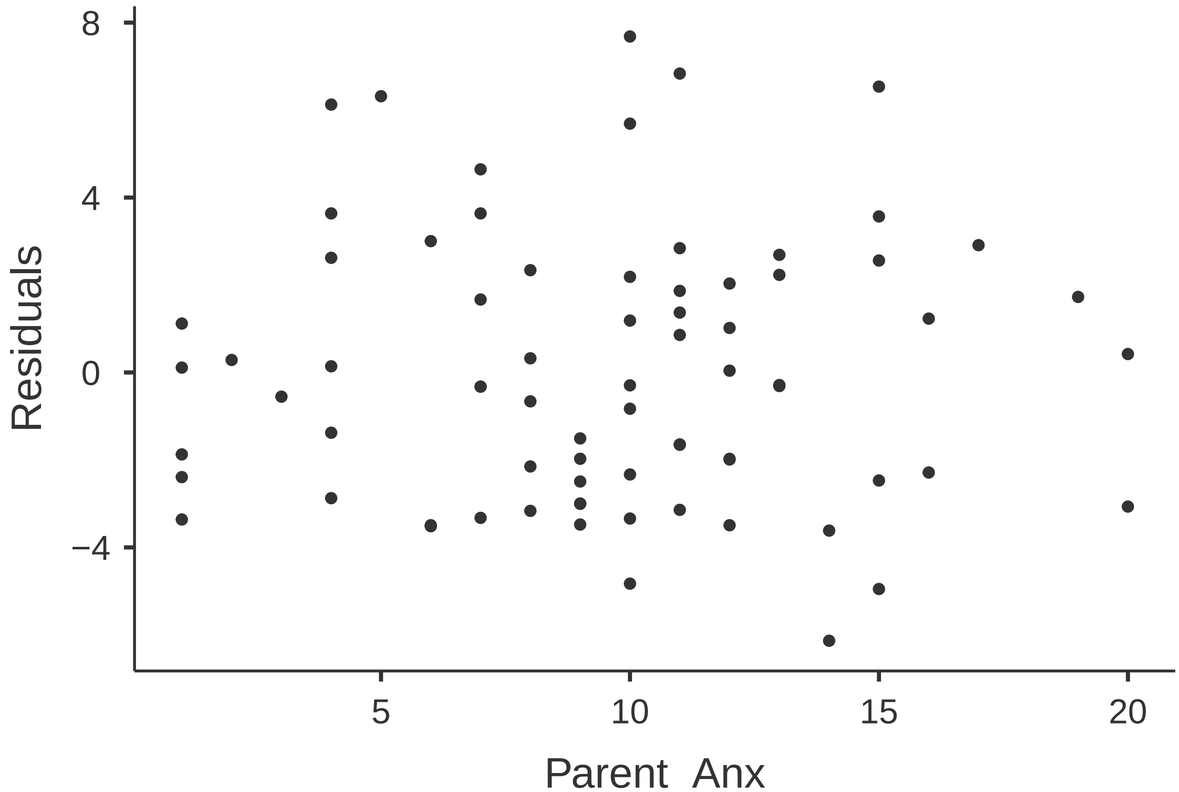


Standardized Residuals
2
1
0
−1
−2
−2
−1
0
1
2
Theoretical Quantiles

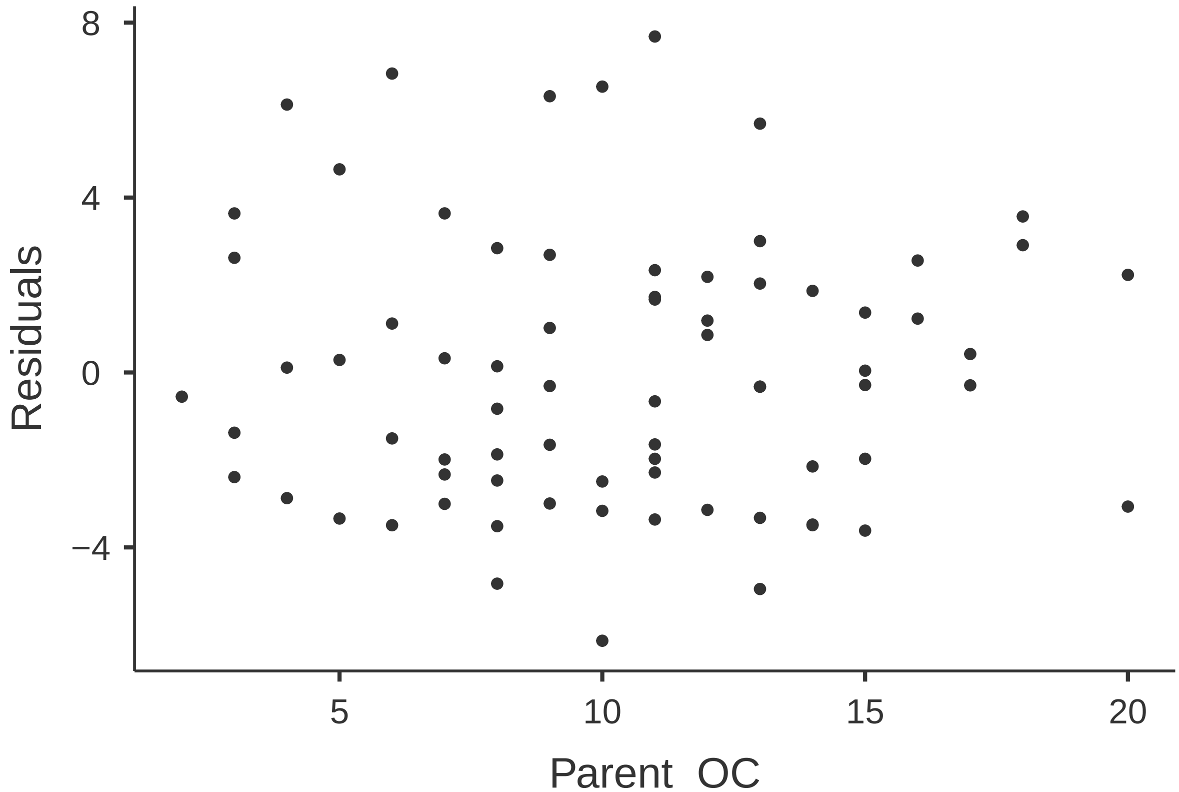

8
4
0
−4
4
8
12
16
Residuals
Fitted



8
4
0
−4
Residuals
5
10
15
20
Child_Anx



8
4
0
−4
Residuals
5
10
15
20
Parent_Anx




```
#Alternate not using jvm library
#model <- lm(model, data)
#plot(model)
```

3b. Multivariate Outliers

```
#Check and remove multivariate outliers based on Cook's distance (CD)
#for Mahalanobis' Distance (leverage only), see /Regression/Regression_Diagnostics.Rmd for how-to
#CD = Influence = Leverage + Discrepancy (Discrepancy = how much an observation deviates from the overa

#create model
model.cook <- lm(datboot$Child_Anx ~ datboot$Parent_Anx + datboot$Parent_OC)
model.cook
```

```
##
## Call:
## lm(formula = datboot$Child_Anx ~ datboot$Parent_Anx + datboot$Parent_OC)
##
## Coefficients:
##        (Intercept)  datboot$Parent_Anx   datboot$Parent_OC
##             2.5754              0.3284              0.4962
```

```
summary(model.cook)
```

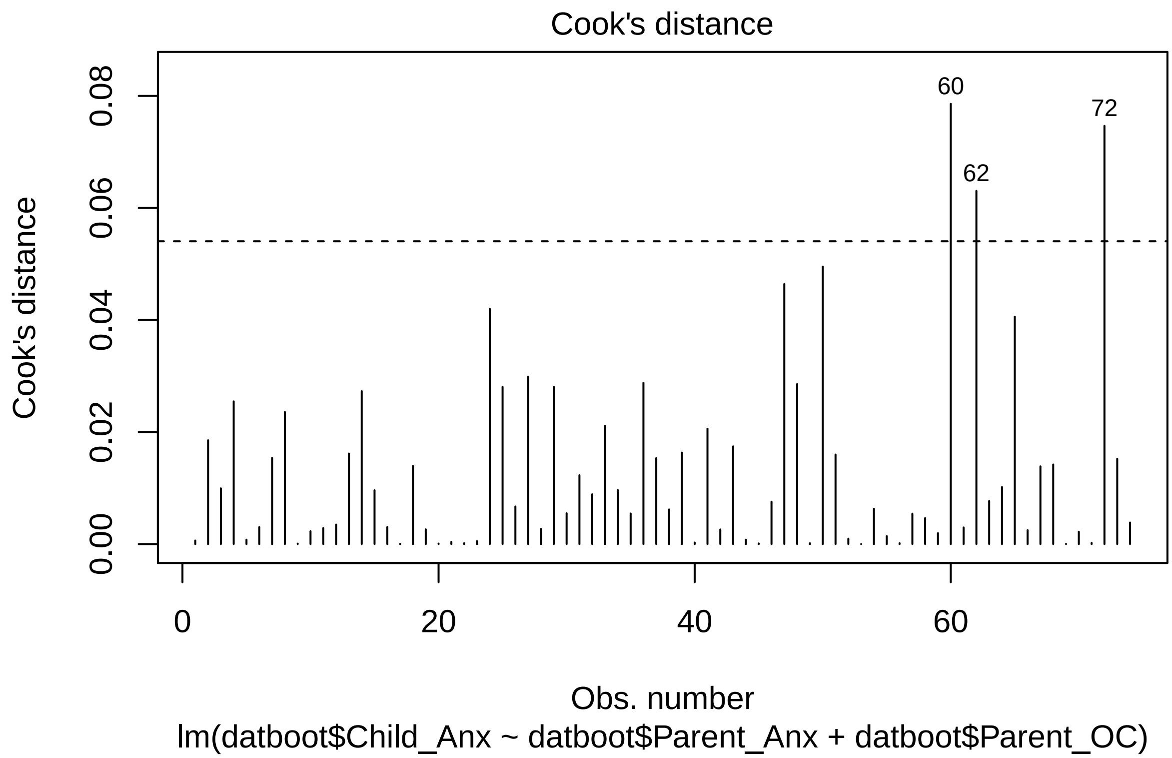
```
##
## Call:
## lm(formula = datboot$Child_Anx ~ datboot$Parent_Anx + datboot$Parent_OC)
##
```

```
## Residuals:
##    Min     1Q Median     3Q    Max
## -6.134 -2.451 -0.302  2.148  7.683
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)           2.5754     0.9978   2.581  0.01192 *
## datboot$Parent_Anx    0.3284     0.1015   3.236  0.00184 **
## datboot$Parent_OC     0.4962     0.1067   4.650  1.5e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.137 on 71 degrees of freedom
## Multiple R-squared:  0.5258, Adjusted R-squared:  0.5124
## F-statistic: 39.36 on 2 and 71 DF,  p-value: 3.145e-12
```

```r
#find cook's distance for that model
datboot$cook <- cooks.distance(model.cook)

#create the cutoff [> 4/N]
cook.cutoff <- 4/nrow(datboot)
print(paste("Our Cook cutoff =", round(cook.cutoff, 3), "- anything above this value will be removed"))
```

```
## [1] "Our Cook cutoff = 0.054 - anything above this value will be removed"
```

```r
#plot it out
plot(model.cook, which = 4, cook.levels = cook.cutoff)

#Add a cutoff line
abline(h = cook.cutoff, lty = 2)
```




```
#Show and remove all outliers above your cutoff line
datboot.no.outliers <- datboot[!(datboot$cook) > cook.cutoff, ]

print(paste("There were", nrow(datboot), "observations before removing multivariate outliers"))
```

```
## [1] "There were 74 observations before removing multivariate outliers"
```

```
print(paste("We removed outlier observation #:", datboot[(datboot$cook) > cook.cutoff, 1], "with a Cook
```

```
## [1] "We removed outlier observation #: 60 with a Cook's distance = 0.079"
## [2] "We removed outlier observation #: 62 with a Cook's distance = 0.063"
## [3] "We removed outlier observation #: 72 with a Cook's distance = 0.075"
```

```
print(paste("We now have", nrow(datboot.no.outliers), "total observations saved in the new dataset afte
```

```
## [1] "We now have 71 total observations saved in the new dataset after removing 3 outliers"
```

```
#N is now 39 after removing 1 multivariate outlier observation(s)
    #was 40 after removing 0 univariate outlier observation(s)
    #was 40 after removing 0 observation(s) with missing parameters
    #was 40 originally (total 1 observation(s) removed from orginal dataset - 3%)
```

4. Heteroscedasticity

```
p_load(car)
#Breusch-Pagan test
#H0 = no change in variance across residuals.
model.breusch_pagan <- lm(datboot.no.outliers$Child_Anx ~ datboot.no.outliers$Parent_Anx + datboot.no.ou
ncvTest(model.breusch_pagan)
```

```
## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 0.0003392379, Df = 1, p = 0.98531
```

```
#not significant = homoscedastic
#If violated use Box-cox transformation [boxcox(model)] in library MASS
```

5. Multi-collinearity

```
#Multicollinearity is expected in mediation

model.multicoll <- linReg(data = datboot.no.outliers,
                 dep = 'Child_Anx',
                 cov = c('Parent_Anx', 'Parent_OC'),
                 blocks = list(c('Parent_Anx', 'Parent_OC')),
                 modelTest = TRUE,
                 r2Adj = TRUE,
                 stdEst = TRUE,
                 ciStdEst = TRUE,
                 collin = TRUE) #this line does the thing
model.multicoll
```

```
##
##  LINEAR REGRESSION
##
##  Model Fit Measures
##  ---------------------------------------------------------------------------
##    Model    R        R²       Adjusted R²    F       df1    df2    p
##  ---------------------------------------------------------------------------
##        1    0.771    0.594          0.582    49.7      2     68    < .001
##  ---------------------------------------------------------------------------
##
##
##  MODEL SPECIFIC RESULTS
##
##  MODEL 1
##
##  Model Coefficients
##  ---------------------------------------------------------------------------------------------
##    Predictor     Estimate    SE        t        p         Stand. Estimate    Lower     Upper
##  ---------------------------------------------------------------------------------------------
##    Intercept        1.899    0.9375    2.03     0.047
##    Parent_Anx       0.263    0.0954    2.76     0.007               0.269    0.0747    0.464
##    Parent_OC        0.594    0.1004    5.92    < .001               0.576    0.3820    0.771
##  ---------------------------------------------------------------------------------------------
##
##
##  ASSUMPTION CHECKS
##
##  Collinearity Statistics
##  -----------------------------------
##                 VIF     Tolerance
##  -----------------------------------
##    Parent_Anx    1.59        0.629
##    Parent_OC     1.59        0.629
##  -----------------------------------
```

```r
#Tolerance for all variables indicates low/no multicollinearity
```

Mediation 1. Regression a. Y ~ X b. M ~ X c. Y ~ X + M

2. No bootstrapping

a. Model
b. Sobel Test

3. Bootstrapping

1. Regression a. Y ~ X

```r
model1 <- linReg(data = datboot.no.outliers,
                 dep = 'Child_Anx',
                 covs = 'Parent_Anx',
                 blocks = list(c('Parent_Anx')),
                 modelTest = TRUE,
                 stdEst = TRUE,
                 ci = TRUE,
                 ciWidth = 95)
model1
```

```
##
##  LINEAR REGRESSION
##
##  Model Fit Measures
##  -----------------------------------------------------------
##    Model    R        R²       F       df1    df2    p
##  -----------------------------------------------------------
##        1    0.620    0.385    43.2      1     69    < .001
##  -----------------------------------------------------------
##
##
##  MODEL SPECIFIC RESULTS
##
##  MODEL 1
##
##  Model Coefficients
##  ------------------------------------------------------------------------------------------
##    Predictor     Estimate    SE        Lower    Upper    t       p         Stand. Estimate
##  ------------------------------------------------------------------------------------------
##    Intercept        4.826    0.9730    2.885    6.767    4.96    < .001
##    Parent_Anx       0.607    0.0924    0.423    0.791    6.57    < .001              0.620
##  ------------------------------------------------------------------------------------------
```

b. M ~ X

```r
model2 <- linReg(data = datboot.no.outliers,
                 dep = 'Parent_OC',
                 covs = 'Child_Anx',
                 blocks = list(c('Child_Anx')),
                 modelTest = TRUE,
                 stdEst = TRUE,
                 ci = TRUE,
                 ciWidth = 95)
model2
```

```
##
## LINEAR REGRESSION
##
## Model Fit Measures
## -----------------------------------------------------------
##   Model    R        R²       F       df1    df2    p
## -----------------------------------------------------------
##       1    0.740    0.548    83.7      1     69    < .001
## -----------------------------------------------------------
##
##
## MODEL SPECIFIC RESULTS
##
## MODEL 1
##
## Model Coefficients
## -----------------------------------------------------------------------------------------------------
##   Predictor    Estimate    SE        Lower    Upper    t       p          Stand. Estimate
## -----------------------------------------------------------------------------------------------------
##   Intercept       2.814    0.9018    1.015    4.613    3.12     0.003
##   Child_Anx       0.719    0.0785    0.562    0.875    9.15    < .001               0.740
## -----------------------------------------------------------------------------------------------------
```

c. Y ~ X + M

```
model3 <- linReg(data = datboot.no.outliers,
                 dep = 'Child_Anx',
                 covs = c('Parent_Anx', 'Parent_OC'),
                 blocks = list(c('Parent_Anx', 'Parent_OC')),
                 modelTest = TRUE,
                 stdEst = TRUE,
                 ci = FALSE,
                 ciWidth = 95)
model3
```

```
##
## LINEAR REGRESSION
##
## Model Fit Measures
## -----------------------------------------------------------
##   Model    R        R²       F       df1    df2    p
## -----------------------------------------------------------
##       1    0.771    0.594    49.7      2     68    < .001
## -----------------------------------------------------------
##
##
## MODEL SPECIFIC RESULTS
##
## MODEL 1
##
## Model Coefficients
## ------------------------------------------------------------------------------
##   Predictor     Estimate    SE        t       p          Stand. Estimate
## ------------------------------------------------------------------------------
##   Intercept        1.899    0.9375    2.03     0.047
```

```
##    Parent_Anx       0.263     0.0954     2.76     0.007              0.269
##    Parent_OC        0.594     0.1004     5.92    < .001              0.576
##  -------------------------------------------------------------------------
```

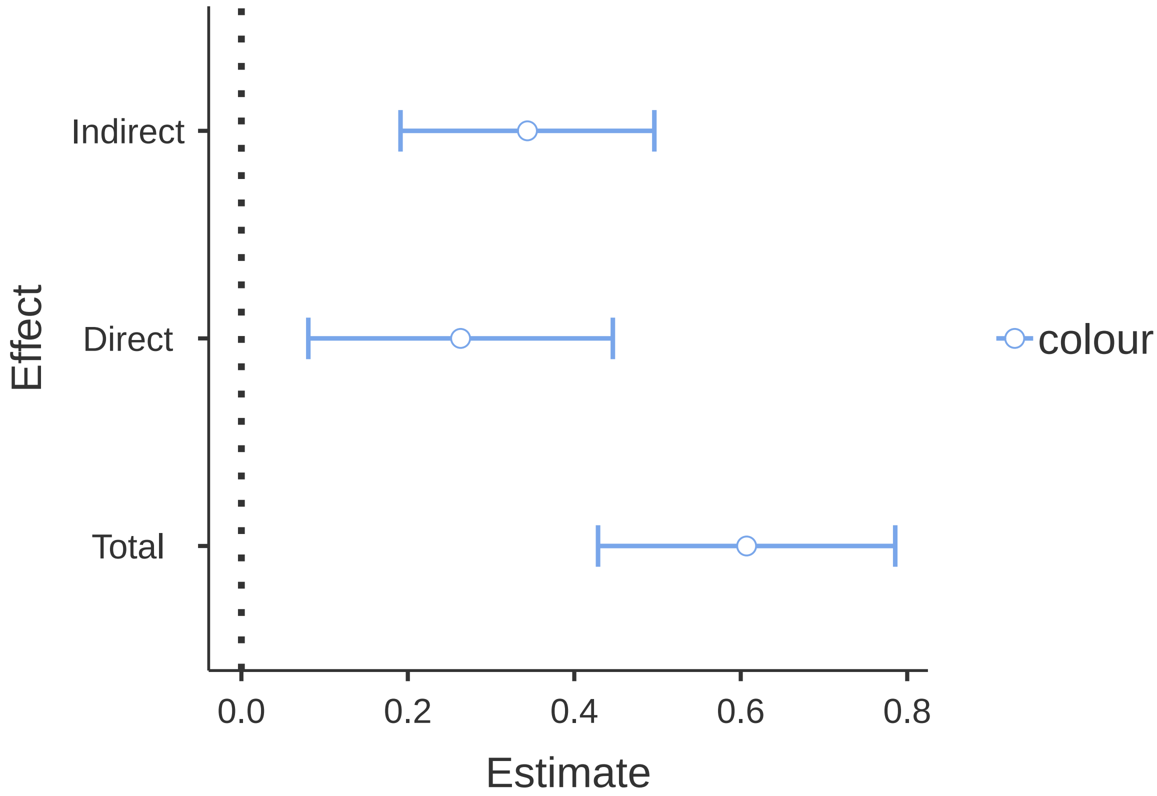
2. No bootstrapping

a. Model b. Sobel Test

```r
# (a * b) = (c - c') = Indirect Effect [i.e., amount of mediation]
# Z  = Sobel test
# a  = Path Estimate from X to M
# b  = Path Estimate from M to Y
# c  = Total Estimate (Direct Estimate + Indirect Estimate)
# c' = Direct Estimate

med <- medmod::med(datboot.no.outliers,
           dep = 'Child_Anx',
           pred = 'Parent_Anx',
           med = 'Parent_OC',
           pm = TRUE,
           ci = FALSE,
           paths = TRUE,
           label = TRUE,
           estPlot = TRUE)
med
```

```
##
##  MEDIATION
##
##  Mediation Estimates
##  --------------------------------------------------------------------------------
##    Effect      Label         Estimate    SE        Z       p          % Mediation
##  --------------------------------------------------------------------------------
##    Indirect    a × b            0.344    0.0778    4.42    < .001            56.6
##    Direct      c                0.263    0.0933    2.82     0.005            43.4
##    Total       c + a × b        0.607    0.0911    6.66    < .001           100.0
##  --------------------------------------------------------------------------------
##
##
##  Path Estimates
##  ---------------------------------------------------------------------------------
##                                    Label    Estimate    SE        Z       p
##  ---------------------------------------------------------------------------------
##    Parent_Anx    <U+2192>    Parent_OC    a           0.579    0.0894    6.47    < .001
##    Parent_OC     <U+2192>    Child_Anx    b           0.594    0.0983    6.04    < .001
##    Parent_Anx    <U+2192>    Child_Anx    c           0.263    0.0933    2.82     0.005
##  ---------------------------------------------------------------------------------
```

```
## Scale for 'colour' is already present. Adding another scale for
## 'colour', which will replace the existing scale.
```




```r
# Look at this in comparison to the indirect mediation estimate.
# sobel(X, M, Y)
cat("\n")
```

```r
sobel(datboot.no.outliers$Parent_Anx, datboot.no.outliers$Parent_OC, datboot.no.outliers$Child_Anx)
```

```
## $`Mod1: Y~X`
##             Estimate Std. Error  t value     Pr(>|t|)
## (Intercept) 4.825577 0.97296433 4.959665 4.863136e-06
## pred        0.607077 0.09240246 6.569922 7.931925e-09
##
## $`Mod2: Y~X+M`
##              Estimate Std. Error  t value     Pr(>|t|)
## (Intercept) 1.8994837 0.93752054 2.026072 4.668296e-02
## pred        0.2633798 0.09537577 2.761496 7.391486e-03
## med         0.5939162 0.10040604 5.915144 1.195656e-07
##
## $`Mod3: M~X`
##              Estimate Std. Error  t value     Pr(>|t|)
## (Intercept) 4.9267776 0.95486459 5.159661 2.264567e-06
## pred        0.5786964 0.09068353 6.381494 1.723080e-08
##
## $Indirect.Effect
## [1] 0.3436972
##
## $SE
## [1] 0.07922674
```

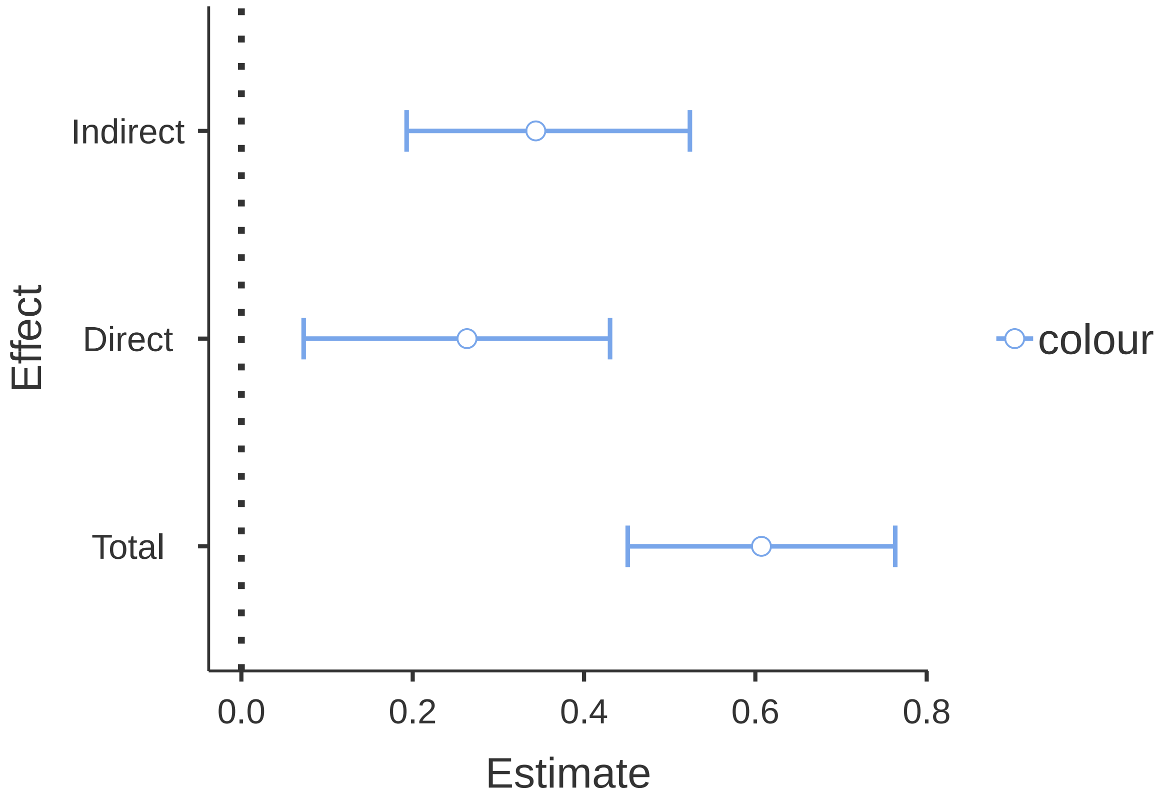
```
##
## $z.value
## [1] 4.338146
##
## $N
## [1] 71
```

3. Bootstrapping

```
boot <- medmod::med(datboot.no.outliers,
            dep = 'Child_Anx',
            pred = 'Parent_Anx',
            med = 'Parent_OC',
            estMethod = 'bootstrap',
            bootstrap = 1000,
            pm = TRUE,
            ci = TRUE,
            paths = TRUE,
            label = TRUE,
            estPlot = TRUE)

boot
```

```
##
##  MEDIATION
##
##  Mediation Estimates
##  ----------------------------------------------------------------------------------------------------
##    Effect      Label         Estimate    SE        Lower     Upper    Z       p         % Mediation
##  ----------------------------------------------------------------------------------------------------
##    Indirect    a × b            0.344    0.0829    0.1929    0.524    4.15    < .001           56.6
##    Direct      c                0.263    0.0911    0.0727    0.430    2.89     0.004           43.4
##    Total       c + a × b        0.607    0.0795    0.4510    0.763    7.64    < .001          100.0
##  ----------------------------------------------------------------------------------------------------
##
##
##  Path Estimates
##  ----------------------------------------------------------------------------------------------------
##                                  Label    Estimate    SE        Lower     Upper    Z       p
##  ----------------------------------------------------------------------------------------------------
##    Parent_Anx    <U+2192>    Parent_OC    a           0.579    0.0873    0.4035    0.735    6.63
##    Parent_OC     <U+2192>    Child_Anx    b           0.594    0.0957    0.4112    0.782    6.20
##    Parent_Anx    <U+2192>    Child_Anx    c           0.263    0.0911    0.0727    0.430    2.89
##  ----------------------------------------------------------------------------------------------------
```

```
## Scale for 'colour' is already present. Adding another scale for
## 'colour', which will replace the existing scale.
```




```
# Check the z-values, SE, and p-values for pathways to see differences (X -> Y for this one).
```