

# Mediation comparison v2

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## get libraries

```
library(lavaan)

## This is lavaan 0.6-5
## lavaan is BETA software! Please report any bugs.
#library(QuantPsyc)
```

## load data

```
df = read.csv('/Users/kelly/cueexp/data/q_demo_data/data__200603.csv')
```

## pull out and scale variables of interest

```
# re-code group index to be 0=control and 1=patient
df$gi[df$gi>0] <- 1

FA <- scale(df$inf_NAcc_fa)
BIS <- scale(df$BIS)
dx <- df$gi
age <- scale(df$age)
dwimotion <- scale(df$dwimotion)
```

## total effect of fa on diagnosis

```
# total effect path c controlling for age and motion
modc = glm(dx ~ FA + age + dwimotion)
summary(modc)
```

```
##
## Call:
## glm(formula = dx ~ FA + age + dwimotion)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.9481  -0.3835   0.1425   0.3718   0.6395
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.61165    0.04331  14.122 < 2e-16 ***
## FA          -0.13649    0.04596  -2.970  0.00374 **
## age          0.13811    0.04484   3.080  0.00268 **
## dwimotion   -0.04742    0.04464  -1.062  0.29076
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.1932178)
##
## Null deviance: 24.466  on 102  degrees of freedom
## Residual deviance: 19.129  on  99  degrees of freedom
## AIC: 128.9
##
## Number of Fisher Scoring iterations: 2
```

## set up SEM mediation model

```
require(lavaan)

med_cv.model <- '# mediator paths (a and b path)
                M ~ a*X + age + dwimotion
                Y ~ b*M
                # c prime path
                Y ~ cprime*X + age + dwimotion
                # indirect and total effects
                ab := a*b
                total := cprime + ab
                '
```

## mediation model: MFB FA > BIS > dx, controlling age and motion

```
set.seed(1234)
X <- FA
M <- BIS
Y <- dx
data <- data.frame(X = X, Y = Y, M = M, age=age,dwimotion=dwimotion)
#med.fit <- sem(med_cv.model, data = data)
med.fit <- sem(med_cv.model, data = data, se = 'bootstrap', bootstrap = 10000)
summary(med.fit, fit.measures=TRUE)
```

```
## lavaan 0.6-5 ended normally after 20 iterations
##
## Estimator ML
## Optimization method NLMINB
## Number of free parameters 9
##
## Number of observations 103
##
```

```

## Model Test User Model:
##
##   Test statistic           0.000
##   Degrees of freedom       0
##
## Model Test Baseline Model:
##
##   Test statistic           52.838
##   Degrees of freedom       7
##   P-value                   0.000
##
## User Model versus Baseline Model:
##
##   Comparative Fit Index (CFI)           1.000
##   Tucker-Lewis Index (TLI)             1.000
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)          -191.351
##   Loglikelihood unrestricted model (H1)    -191.351
##
##   Akaike (AIC)                          400.703
##   Bayesian (BIC)                        424.415
##   Sample-size adjusted Bayesian (BIC)     395.986
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                0.000
##   90 Percent confidence interval - lower  0.000
##   90 Percent confidence interval - upper  0.000
##   P-value RMSEA <= 0.05                  NA
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                0.000
##
## Parameter Estimates:
##
##   Standard errors                      Bootstrap
##   Number of requested bootstrap draws    10000
##   Number of successful bootstrap draws    10000
##
## Regressions:
##           Estimate  Std.Err  z-value  P(>|z|)
## M ~
##   X      (a)    -0.195    0.098   -1.990    0.047
##   age              0.078    0.108    0.723    0.470
##   dwimotn         -0.060    0.085   -0.707    0.479
## Y ~
##   M      (b)     0.192    0.036    5.281    0.000
##   X      (cprm)  -0.099    0.040   -2.477    0.013
##   age              0.123    0.042    2.932    0.003
##   dwimotn         -0.036    0.041   -0.879    0.379
##

```

```
## Variances:
##           Estimate Std.Err z-value P(>|z|)
##      .M           0.930   0.109   8.498   0.000
##      .Y           0.151   0.016   9.223   0.000
##
## Defined Parameters:
##           Estimate Std.Err z-value P(>|z|)
##      ab          -0.037   0.021  -1.776   0.076
##      total        -0.136   0.041  -3.294   0.001
```

`AIC`(med.fit)

```
## [1] 400.7028
```

`BIC`(med.fit)

```
## [1] 424.4154
```