

# Moderation

## Introduction to SEM with Lavaan



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# Outline

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Moderation Basics

Post Hoc Analysis

Latent Variable Interactions

- Products of Manifest Variables

- Products of Latent Variables

Multiple Moderation

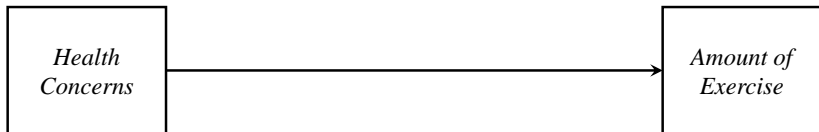
Categorical Moderators



# Refresher: Focal Effect Only

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The *healthConcerns* → *exerciseAmount* relation is our *focal effect*



- Mediation, moderation, and conditional process analysis all attempt to describe the focal effect in more detail.
- We always begin by hypothesizing a focal effect.

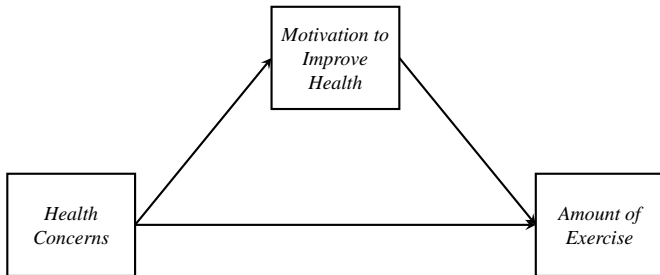


# Refresher: Mediation Hypothesis

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A mediation analysis will attempt to describe how health concerns affect amount of exercise.

- The *how* is operationalized in terms of intermediary variables.
- Mediator: Motivation to improve health (*motivation*).

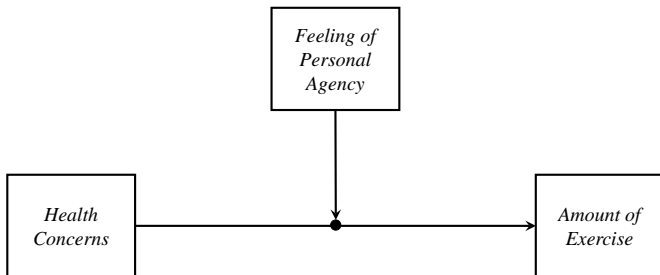


# Refresher: Moderation Hypothesis

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A moderation hypothesis will attempt to describe when health concerns affect amount of exercise.

- The *when* is operationalized in terms of interactions between the focal predictor and contextualizing variables
- Moderator: Sense of personal agency relating to physical health (*agency*).



# Equations

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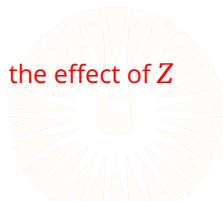
In additive MLR, we might have the following equation:

$$Y = \beta_0 + \beta_1 X + \beta_2 Z + \varepsilon$$

This additive equation assumes that  $X$  and  $Z$  are independent predictors of  $Y$ .

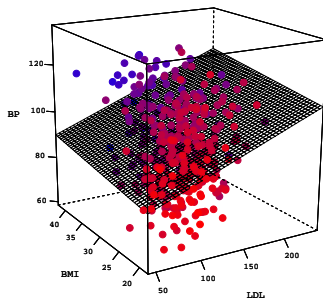
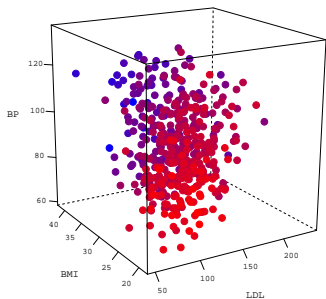
When  $X$  and  $Z$  are independent predictors, the following are true:

- $X$  and  $Z$  *can* be correlated.
- $\beta_1$  and  $\beta_2$  are *partial* regression coefficients.
- The effect of  $X$  on  $Y$  is the same at **all levels** of  $Z$ , and the effect of  $Z$  on  $Y$  is the same at **all levels** of  $X$ .



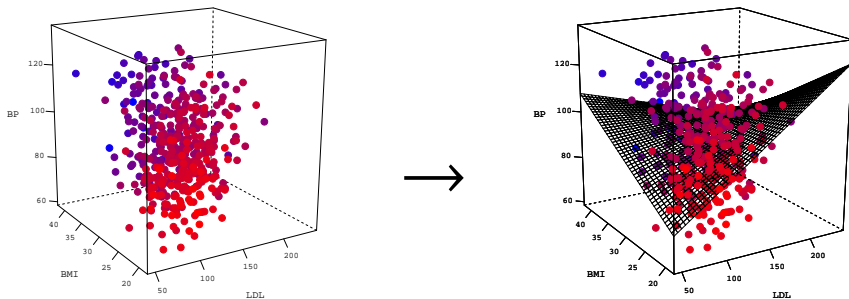
# Additive Regression

The effect of  $X$  on  $Y$  is the same at **all levels** of  $Z$ .



# Moderated Regression

The effect of  $X$  on  $Y$  varies **as a function** of  $Z$ .





# Equations

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The following derivation is adapted from ?.

- When testing moderation, we hypothesize that the effect of  $X$  on  $Y$  varies as a function of  $Z$ .
- We can represent this concept with the following equation:

$$Y = \beta_0 + f(Z)X + \beta_2Z + \varepsilon \quad (1)$$



# Equations

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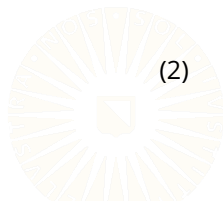
The following derivation is adapted from ?.

- When testing moderation, we hypothesize that the effect of  $X$  on  $Y$  varies as a function of  $Z$ .
- We can represent this concept with the following equation:

$$Y = \beta_0 + f(Z)X + \beta_2Z + \varepsilon \quad (1)$$

- If we assume that  $Z$  linearly (and deterministically) affects the relationship between  $X$  and  $Y$ , then we can take:

$$f(Z) = \beta_1 + \beta_3Z \quad (2)$$



# Equations

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- Substituting Equation 2 into Equation 1 leads to:

$$Y = \beta_0 + (\beta_1 + \beta_3 Z)X + \beta_2 Z + \varepsilon$$



# Equations

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- Substituting Equation 2 into Equation 1 leads to:

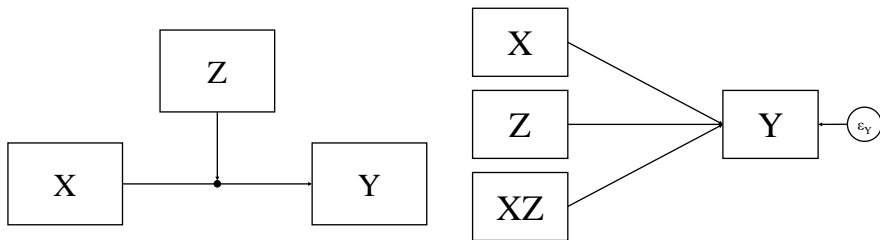
$$Y = \beta_0 + (\beta_1 + \beta_3 Z)X + \beta_2 Z + \varepsilon$$

- Which, after distributing  $X$  and reordering terms, becomes:

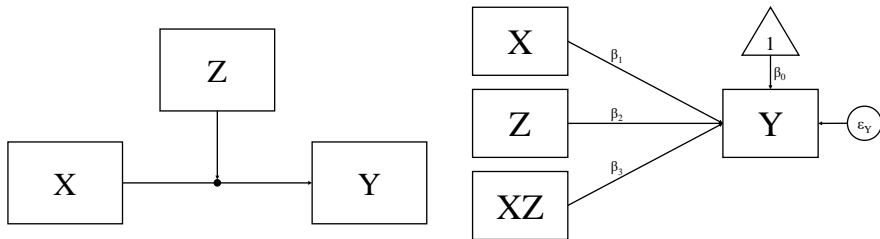
$$Y = \beta_0 + \beta_1 X + \beta_2 Z + \beta_3 XZ + \varepsilon$$



# Conceptual vs. Analytic Diagrams



# Conceptual vs. Analytic Diagrams



# Testing Moderation

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Now, we have an estimable regression model that quantifies the linear moderation we hypothesized.

$$Y = \beta_0 + \beta_1 X + \beta_2 Z + \beta_3 XZ + \varepsilon$$

- To test for significant moderation, we simply need to test the significance of the interaction term,  $XZ$ .
  - Check if  $\hat{\beta}_3$  is significantly different from zero.



# Interpretation

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Given the following equation:

$$Y = \hat{\beta}_0 + \hat{\beta}_1 X + \hat{\beta}_2 Z + \hat{\beta}_3 XZ + \hat{\varepsilon}$$

- $\hat{\beta}_3$  quantifies the effect of  $Z$  on the focal effect (the  $X \rightarrow Y$  effect).
  - For a unit change in  $Z$ ,  $\hat{\beta}_3$  is the expected change in the effect of  $X$  on  $Y$ .
- $\hat{\beta}_1$  and  $\hat{\beta}_2$  are *conditional effects*.
  - Interpreted where the other predictor is zero.
  - For a unit change in  $X$ ,  $\hat{\beta}_1$  is the expected change in  $Y$ , when  $Z = 0$ .
  - For a unit change in  $Z$ ,  $\hat{\beta}_2$  is the expected change in  $Y$ , when  $X = 0$ .



# Example

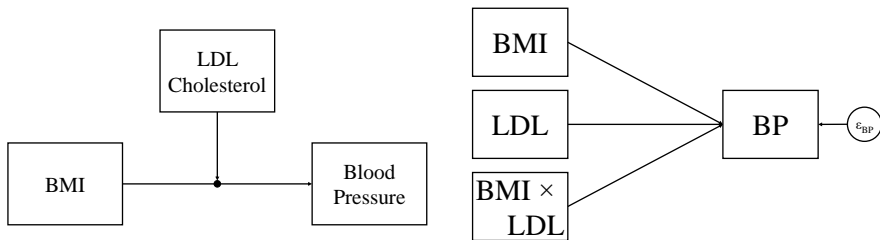
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Looking at the *diabetes* dataset.

- We suspect that patients' BMIs are predictive of their average blood pressure.
- We further suspect that this effect may be differentially expressed depending on the patients' LDL levels.



# Diagrams



# Example

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```
dDat <- readRDS("../data/diabetes.rds")
```

```
## Focal Effect:
```

```
out0 <- lm(bp ~ bmi, data = dDat)
```

```
partSummary(out0, -c(1, 2))
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	61.9973	3.6659	16.91	<2e-16
bmi	1.2379	0.1371	9.03	<2e-16

Residual standard error: 12.72 on 440 degrees of freedom

Multiple R-squared: 0.1563, Adjusted R-squared: 0.1544

F-statistic: 81.54 on 1 and 440 DF, p-value: < 2.2e-16

# Example

---

```
## Additive Model:
```

```
out1 <- lm(bp ~ bmi + ldl, data = dDat)  
partSummary(out1, -c(1, 2))
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	59.26577	3.91281	15.147	< 2e-16
bmi	1.16567	0.14156	8.235	2.08e-15
ldl	0.04016	0.02056	1.953	0.0515

Residual standard error: 12.68 on 439 degrees of freedom

Multiple R-squared: 0.1636, Adjusted R-squared: 0.1598

F-statistic: 42.94 on 2 and 439 DF, p-value: < 2.2e-16

# Example

---

```
## Moderated Model:
```

```
out2 <- lm(bp ~ bmi * ldl, data = dDat)  
partSummary(out2, -c(1, 2))
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	14.480616	14.291677	1.013	0.311514
bmi	2.867825	0.541312	5.298	1.86e-07
ldl	0.448771	0.127160	3.529	0.000461
bmi:ldl	-0.015352	0.004716	-3.255	0.001221

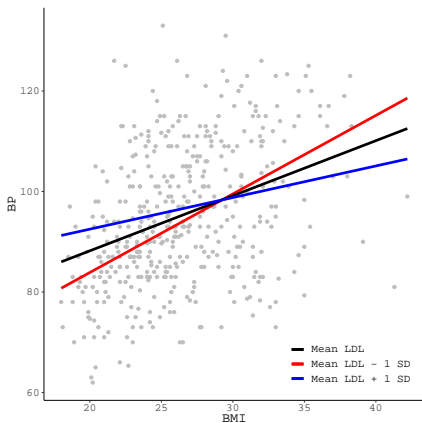
Residual standard error: 12.54 on 438 degrees of freedom

Multiple R-squared: 0.1834, Adjusted R-squared: 0.1778

F-statistic: 32.78 on 3 and 438 DF, p-value: < 2.2e-16

# Visualizing the Interaction

We can get a better idea of the patterns of moderation by plotting the focal effect at conditional values of the moderator.



# Example

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Of course, we can fit the same model in **lavaan**.

```
library(lavaan)

## Specify the model:
mod <- 'bp ~ 1 + bmi + ldl + bmi:ldl'

## Use a dplyr pipeline to create the product term and estimate the model:
lavOut <- sem(mod, data = dDat)
```

# Example

```
partSummary(lavOut, 7:9)
```

Regressions:

	Estimate	Std.Err	z-value	P(> z )
bp ~				
bmi	2.868	0.539	5.322	0.000
ldl	0.449	0.127	3.545	0.000
bmi:ldl	-0.015	0.005	-3.270	0.001

Intercepts:

	Estimate	Std.Err	z-value	P(> z )
.bp	14.481	14.227	1.018	0.309

Variances:

	Estimate	Std.Err	z-value	P(> z )
.bp	155.871	10.485	14.866	0.000



# POST HOC ANALYSIS

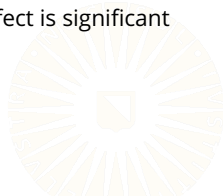


# Probing the Interaction

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A significant estimate of  $\beta_3$  tells us that the effect of  $X$  on  $Y$  depends on the level of  $Z$ , but nothing more.

- The plot above gives a descriptive illustration of the pattern, but does not support statistical inference.
  - The three conditional effects we plotted look different, but we cannot say much about how they differ with only the plot and  $\hat{\beta}_3$ .
- This is the purpose of *probing* the interaction.
  - Try to isolate areas of  $Z$ 's distribution in which  $X \rightarrow Y$  effect is significant and areas where it is not.



# Probing the Interaction

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The most popular method of probing interactions is to do a so-called *simple slopes* analysis.

- Pick-a-point approach
- Spotlight analysis

In simple slopes analysis, we test if the slopes of the conditional effects plotted above are significantly different from zero.

- To do so, we test the significance of *simple slopes*.



# Simple Slopes

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Recall the derivation of our moderated equation:

$$Y = \beta_0 + \beta_1 X + \beta_2 Z + \beta_3 XZ + \varepsilon$$

We can reverse the process by factoring out  $X$  and reordering terms:

$$Y = \beta_0 + (\beta_1 + \beta_3 Z)X + \beta_2 Z + \varepsilon$$

Where  $f(Z) = \beta_1 + \beta_3 Z$  is the linear function that shows how the relationship between  $X$  and  $Y$  changes as a function of  $Z$ .

$f(Z)$  is the *simple slope*.

- By plugging different values of  $Z$  into  $f(Z)$ , we get the value of the conditional effect of  $X$  on  $Y$  at the chosen level of  $Z$ .

# Significance Testing of Simple Slopes

The values of  $Z$  used to define the simple slopes are arbitrary.

- The most common choice is:  $\{(\bar{Z} - SD_Z), \bar{Z}, (\bar{Z} + SD_Z)\}$
- You could also use interesting percentiles of  $Z$ 's distribution.

The standard error of a simple slope is given by:

$$SE_{f(Z)} = \sqrt{SE_{\beta_1}^2 + 2Z \cdot \text{COV}(\beta_1, \beta_3) + Z^2 SE_{\beta_3}^2}$$

So, you can test the significance of a simple slope by constructing a Wald statistic or confidence interval using  $\hat{f}(Z)$  and  $SE_{f(Z)}$ :

$$t = \frac{\hat{f}(Z)}{SE_{f(Z)}}, \quad CI = \hat{f}(Z) \pm t_{crit} \times SE_{f(Z)}$$

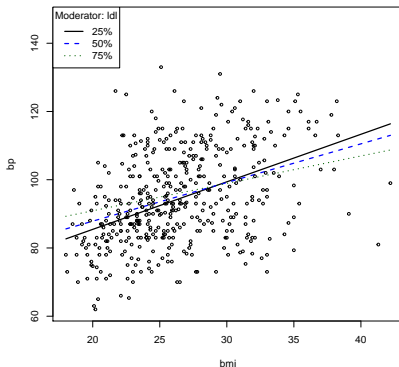


# Example

```
library(rockchalk)
```

```
## Prepare the metadata with rockchalk::plotSlopes():
```

```
psOut <- plotSlopes(out2, plotx = "bmi", modx = "ldl")
```



# Example

---

```
## Test the simple slopes with rockchalk::testSlopes():  
tsOut <- testSlopes(psOut)
```

Values of ldl OUTSIDE this interval:

	lo	hi
	154.7983	305.9235

cause the slope of  $(b1 + b2 * ldl) \text{bmi}$  to be statistically significant

tsOut\$hypotests

	"ldl"	slope	Std. Error	t value	Pr(> t )
25%	96.05	1.3932882	0.1565225	8.901520	1.471778e-17
50%	113.00	1.1330757	0.1403937	8.070700	6.794806e-15
75%	134.50	0.8030128	0.1789442	4.487505	9.222263e-06

# Example

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We can use **semTools** routines to probe interaction in **lavaan** models.

- `probe2WayMC()`: simple slopes/intercepts analysis
- `plotProbe()`: simple slopes plots

```
library(semTools)

## Estimate and test simple slopes and simple intercepts:
ssOut <- probe2WayMC(lavOut,
  nameX = c("bmi", "ldl", "bmi:ldl"),
  nameY = "bp",
  modVar = "ldl",
  valProbe = quantile(dDat$ldl, c(0.25, 0.50, 0.75))
)
```



# Example

---

```
## View the results:
```

```
ssOut
```

```
$SimpleIntcept
```

	ldl	est	se	z	pvalue
25%	96.05	57.585	4.017	14.334	0
50%	113.00	65.192	3.736	17.449	0
75%	134.50	74.840	4.944	15.139	0

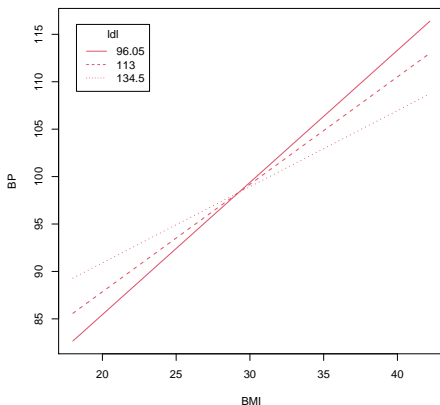
```
$SimpleSlope
```

	ldl	est	se	z	pvalue
25%	96.05	1.393	0.156	8.942	0
50%	113.00	1.133	0.140	8.107	0
75%	134.50	0.803	0.178	4.508	0

# Example

```
## Plot the simple slopes:
```

```
plotProbe(ssOut, xlim = range(dDat$bmi), xlab = "BMI", ylab = "BP")
```



# LATENT VARIABLE INTERACTIONS



# Latent Variable Interactions

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When we have two observed variables interacting to predict a latent variable, our job is easy:

1. Construct the product term of the observed focal and moderator variables
2. Use the observed focal, moderator, and interaction variables to predict the latent DV

If we want to model moderation when at least one of the predictors is latent, things get more difficult.

- If the moderator is observed and discrete, we can use multiple group modeling
- If the moderator is continuous and/or latent, then we need fancier methods

Two basic approaches:

1. Methods based on products of manifest variables
2. Methods based on directly estimating the products of latent variables

# Computing Interaction Indicators

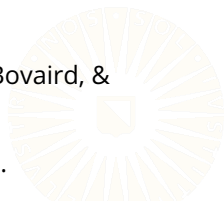
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The simplest approach is to create observed product terms and directly use those terms as indicators of the interaction construct.

- Naively indicating an interaction construct with the raw product terms is probably sub-optimal
- Collinearity among the interaction indicators and the raw items can cause estimation problems
- From a modeling perspective, we'd like to interpret our final model holistically

Two recommended approaches:

1. Orthogonalization through residual centering (Little, Bovaird, & Widaman, 2006).
2. Double mean centering (Lin, Wen, Marsh, & Lin, 2010).



# Orthogonalization

Say we want to estimate the moderated effect of  $Z$  on the  $X \rightarrow Y$  effect, where  $X$ ,  $Y$ , and  $Z$  are latent variables indicated by  $\{x_1, x_2, x_3\}$ ,  $\{y_1, y_2, y_3\}$ , and  $\{z_1, z_2, z_3\}$ , respectively.

Orthogonalization is performed by:

1. Construct all possible product terms:  
 $\{x_1z_1, x_1z_2, x_1z_3, x_2z_1, x_2z_2, x_2z_3, x_3z_1, x_3z_2, x_3z_3\}$ .
2. Regress each product term onto all observed indicators of  $X$  and  $Z$ :

$$\widehat{x_1z_1} = \alpha + \beta_1x_1 + \beta_2x_2 + \beta_3x_3 + \beta_4z_1 + \beta_5z_2 + \beta_6z_3$$

$$\widehat{x_2z_1} = \alpha + \beta_1x_1 + \beta_2x_2 + \beta_3x_3 + \beta_4z_1 + \beta_5z_2 + \beta_6z_3$$

$$\vdots$$

$$\widehat{x_3z_3} = \alpha + \beta_1x_1 + \beta_2x_2 + \beta_3x_3 + \beta_4z_1 + \beta_5z_2 + \beta_6z_3$$

# Orthogonalization

---

3. Calculate each product term's residual:

$$\delta_{x_1z_1} = x_1z_1 - \widehat{x_1z_1}$$

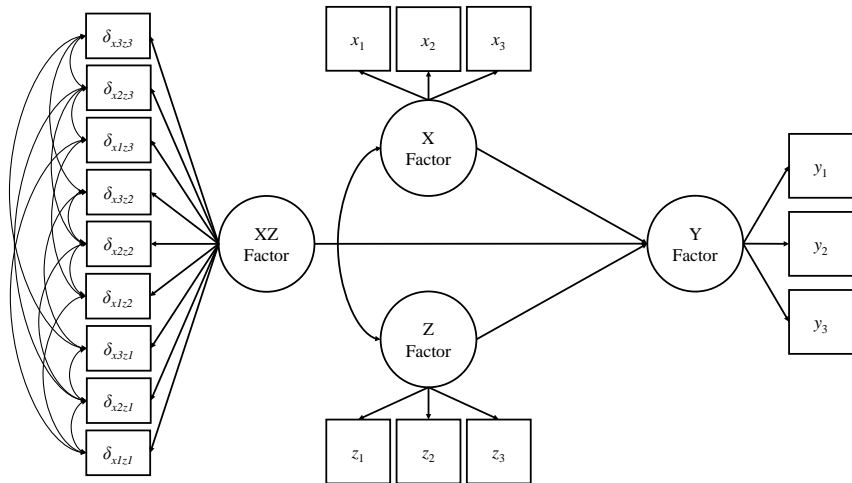
$$\delta_{x_2z_1} = x_2z_1 - \widehat{x_2z_1}$$

$$\vdots$$

$$\delta_{x_3z_3} = x_3z_3 - \widehat{x_3z_3}$$

4. Use these residuals to indicate a latent interaction construct.

# Orthogonalization





# Example

---

```
dat1 <- readRDS("../data/lecture12Data.rds")

mod1 <- '
fX =~ x1 + x2 + x3
fZ =~ z1 + z2 + z3
fY =~ y1 + y2 + y3
'

out1 <- cfa(mod1, data = dat1, std.lv = TRUE)
```

# Example

---

```
partSummary(out1, 1:6)
```

```
lavaan 0.6-12.1708 ended normally after 17 iterations
```

Estimator	ML
Optimization method	NLMINB
Number of model parameters	21
Number of observations	500

```
Model Test User Model:
```

Test statistic	41.021
Degrees of freedom	24
P-value (Chi-square)	0.017

```
Parameter Estimates:
```

Standard errors	Standard
Information	Expected
Information saturated (h1) model	Structured

# Example

```
partSummary(out1, 7)
```

Latent Variables:

	Estimate	Std.Err	z-value	P(> z )
fX =~				
x1	0.671	0.044	15.407	0.000
x2	0.661	0.043	15.226	0.000
x3	0.702	0.045	15.481	0.000
fZ =~				
z1	0.738	0.048	15.343	0.000
z2	0.734	0.048	15.157	0.000
z3	0.718	0.046	15.601	0.000
fY =~				
y1	0.787	0.045	17.614	0.000
y2	0.729	0.045	16.325	0.000
y3	0.761	0.043	17.797	0.000

# Example

---

```
partSummary(out1, 8)
```

Covariances:

	Estimate	Std.Err	z-value	P(> z )
fX ~~				
fZ	0.232	0.058	3.987	0.000
fY	0.827	0.033	25.310	0.000
fZ ~~				
fY	0.156	0.057	2.739	0.006

# Example

```
partSummary(out1, 9)
```

Variances:

	Estimate	Std.Err	z-value	P(> z )
.x1	0.510	0.042	11.998	0.000
.x2	0.514	0.042	12.141	0.000
.x3	0.550	0.046	11.938	0.000
.z1	0.523	0.052	10.141	0.000
.z2	0.546	0.052	10.443	0.000
.z3	0.461	0.048	9.706	0.000
.y1	0.492	0.044	11.185	0.000
.y2	0.545	0.044	12.253	0.000
.y3	0.444	0.040	11.007	0.000
fX	1.000			
fZ	1.000			
fY	1.000			

# Example

---

```
fitMeasures(out1, c("chisq", "df", "pvalue", "cfi", "tli", "rmsea", "srmr"))
```

chisq	df	pvalue	cfi	tli	rmsea	srmr
41.021	24.000	0.017	0.987	0.981	0.038	0.026

# Example

---

Now, we'll fit the additive model as an SEM.

```
mod2 <- '  
fX =~ x1 + x2 + x3  
fZ =~ z1 + z2 + z3  
fY =~ y1 + y2 + y3  
  
fY ~ fX + fZ  
'  
  
out2 <- sem(mod2, data = dat1, std.lv = TRUE)
```

# Example

```
partSummary(out2, 1:6)
```

```
lavaan 0.6-12.1708 ended normally after 22 iterations
```

Estimator	ML
Optimization method	NLMINB
Number of model parameters	21
Number of observations	500

```
Model Test User Model:
```

Test statistic	41.021
Degrees of freedom	24
P-value (Chi-square)	0.017

```
Parameter Estimates:
```

Standard errors	Standard
Information	Expected
Information saturated (h1) model	Structured



# Example

```
partSummary(out2, 7)
```

Latent Variables:

	Estimate	Std.Err	z-value	P(> z )
fX =~				
x1	0.671	0.044	15.407	0.000
x2	0.661	0.043	15.226	0.000
x3	0.702	0.045	15.481	0.000
fZ =~				
z1	0.738	0.048	15.343	0.000
z2	0.734	0.048	15.157	0.000
z3	0.718	0.046	15.601	0.000
fY =~				
y1	0.442	0.044	10.079	0.000
y2	0.409	0.041	9.877	0.000
y3	0.427	0.042	10.099	0.000

# Example

---

```
partSummary(out2, 8:9)
```

Regressions:

	Estimate	Std.Err	z-value	P(> z )
fY ~				
fX	1.488	0.190	7.820	0.000
fZ	-0.066	0.090	-0.732	0.464

Covariances:

	Estimate	Std.Err	z-value	P(> z )
fX ~~				
fZ	0.232	0.058	3.987	0.000

# Example

---

```
partSummary(out2, 10)
```

Variances:

	Estimate	Std.Err	z-value	P(> z )
.x1	0.510	0.042	11.998	0.000
.x2	0.514	0.042	12.141	0.000
.x3	0.550	0.046	11.938	0.000
.z1	0.523	0.052	10.141	0.000
.z2	0.546	0.052	10.443	0.000
.z3	0.461	0.048	9.706	0.000
.y1	0.492	0.044	11.185	0.000
.y2	0.545	0.044	12.253	0.000
.y3	0.444	0.040	11.007	0.000
fX	1.000			
fZ	1.000			
.fY	1.000			

# Example

---

```
fitMeasures(out2, c("chisq", "df", "pvalue", "cfi", "tli", "rmsea", "srmr"))
```

chisq	df	pvalue	cfi	tli	rmsea	srmr
41.021	24.000	0.017	0.987	0.981	0.038	0.026

# Example

---

```
library(dplyr)

## Set aside a copy of the predictor data for later use:
preds <- select(dat1, matches("x\\d|z\\d")) %>% as.matrix()

## Construct product terms:
products <- mutate(dat1,
  x1z1 = x1 * z1,
  x1z2 = x1 * z2,
  x1z3 = x1 * z3,

  x2z1 = x2 * z1,
  x2z2 = x2 * z2,
  x2z3 = x2 * z3,

  x3z1 = x3 * z1,
  x3z2 = x3 * z2,
  x3z3 = x3 * z3,
  .keep = "none")
```

# Example

---

```
## Residualize the product terms:  
products <- sapply(products,  
                    function(y, x) lm(y ~ x)$resid,  
                    x = preds)  
  
## Join data pieces:  
dat2 <- data.frame(dat1, products)
```

# Example

```
mod3 <- '  
fX  =~ x1 + x2 + x3  
fZ  =~ z1 + z2 + z3  
fY  =~ y1 + y2 + y3  
fXZ =~ x1z1 + x1z2 + x1z3 + x2z1 + x2z2 + x2z3 + x3z1 + x3z2 + x3z3  
  
fY ~ fX + fZ + fXZ  
  
fX ~~ 0*fXZ  
fZ ~~ 0*fXZ  
  
x1z1 ~~ x1z2 + x1z3 + x2z1 + x3z1  
x1z2 ~~ x1z3 + x2z2 + x3z2  
x1z3 ~~ x2z3 + x3z3  
  
x2z1 ~~ x2z2 + x2z3 + x3z1  
x2z2 ~~ x2z3 + x3z2  
x2z3 ~~ x3z3  
  
x3z1 ~~ x3z2 + x3z3  
x3z2 ~~ x3z3  
'
```

# Example

```
out3 <- sem(mod3, data = dat2, std.lv = TRUE, meanstructure = TRUE)
```

```
partSummary(out3, 7, 1:14)
```

Latent Variables:

	Estimate	Std.Err	z-value	P(> z )
fX =~				
x1	0.670	0.043	15.424	0.000
x2	0.660	0.043	15.256	0.000
x3	0.704	0.045	15.569	0.000
fZ =~				
z1	0.738	0.048	15.342	0.000
z2	0.734	0.048	15.156	0.000
z3	0.718	0.046	15.602	0.000
fY =~				
y1	0.396	0.046	8.545	0.000
y2	0.369	0.044	8.441	0.000
y3	0.383	0.045	8.558	0.000



# Example

---

```
partSummary(out3, 7, c(1, 2, 15:24))
```

Latent Variables:

	Estimate	Std.Err	z-value	P(> z )
fxZ =~				
x1z1	0.361	0.053	6.833	0.000
x1z2	0.427	0.056	7.615	0.000
x1z3	0.432	0.053	8.190	0.000
x2z1	0.558	0.056	9.914	0.000
x2z2	0.616	0.062	10.008	0.000
x2z3	0.520	0.057	9.153	0.000
x3z1	0.516	0.059	8.805	0.000
x3z2	0.626	0.063	10.007	0.000
x3z3	0.521	0.058	8.936	0.000

# Example

```
partSummary(out3, 8:9, -(14:39))
```

Regressions:

	Estimate	Std.Err	z-value	P(> z )
fY ~				
fX	1.658	0.239	6.930	0.000
fZ	-0.074	0.099	-0.750	0.453
fXZ	0.488	0.120	4.049	0.000

Covariances:

	Estimate	Std.Err	z-value	P(> z )
fX ~~				
fXZ	0.000			
fZ ~~				
fXZ	0.000			
fX ~~				
fZ	0.232	0.058	3.987	0.000

# Example

```
fitMeasures(out3, c("chisq", "df", "pvalue", "cfi", "tli", "rmsea", "srmr"))
```

chisq	df	pvalue	cfi	tli	rmsea	srmr
74.899	113.000	0.998	1.000	1.015	0.000	0.019

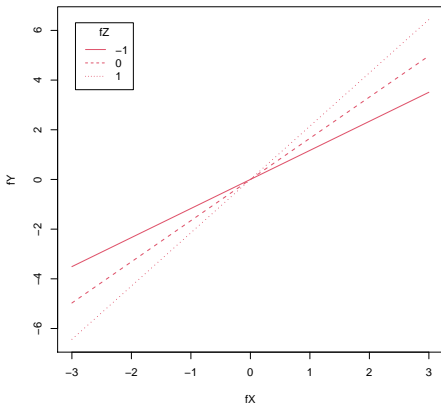
```
probeOut3 <- probe2WayRC(fit      = out3,  
                          nameX    = c("fX", "fZ", "fXZ"),  
                          nameY    = "fY",  
                          modVar   = "fZ",  
                          valProbe = c(-1, 0, 1)  
                          )
```

```
probeOut3$SimpleSlope
```

	fZ	est	se	z	pvalue
1	-1	1.170	0.207	5.653	0
2	0	1.658	0.238	6.974	0
3	1	2.145	0.310	6.923	0

# Example

```
plotProbe(probeOut3, xlim = c(-3, 3), xlab = "fX", ylab = "fY")
```



# Double Mean Centering

---

We could also specify the interaction factor using double mean centering.

1. Mean center every indicator of  $X$  and  $Z$ :

$$x_1^c = x_1 - \bar{x}_1$$

$$\vdots$$

$$z_1^c = z_1 - \bar{z}_1$$

$$\vdots$$

2. Use the centered indicators to construct all possible product terms:  
 $\{x_1^c z_1^c, x_1^c z_2^c, x_1^c z_3^c, x_2^c z_1^c, x_2^c z_2^c, x_2^c z_3^c, x_3^c z_1^c, x_3^c z_2^c, x_3^c z_3^c\}.$

# Double Mean Centering

---

3. Mean center each product term:

$$(x_1z_1)^c = x_1^c z_1^c - \overline{x_1^c z_1^c}$$

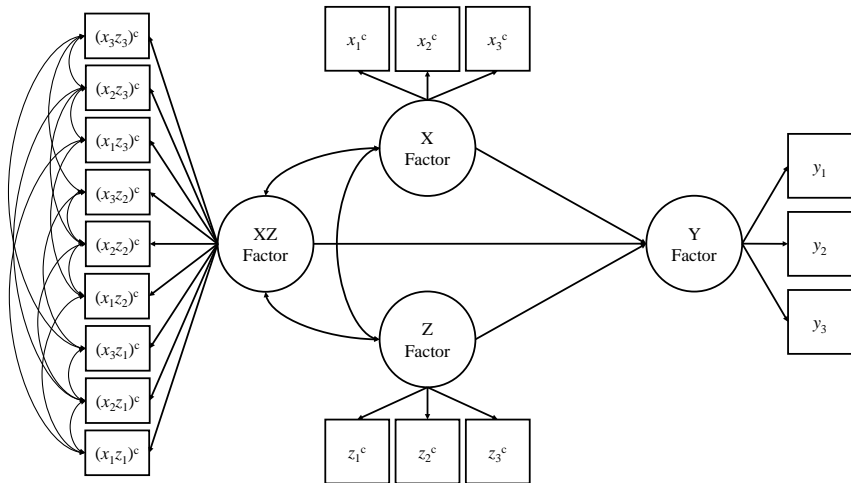
$$(x_1z_2)^c = x_1^c z_2^c - \overline{x_1^c z_2^c}$$

$\vdots$

$$(x_3z_3)^c = x_3^c z_3^c - \overline{x_3^c z_3^c}$$

4. Use the mean centered indicators of  $X$  and  $Z$ , and the “double mean centered” product terms to specify the latent interaction model.

# Double Mean Centering



# Example

---

```
## Mean-center the predictor variables:
```

```
preds <- scale(preds, scale = FALSE) %>% as.data.frame()
```

```
## Construct and mean-center the product terms:
```

```
products <- mutate(preds,  
  x1z1 = x1 * z1,  
  x1z2 = x1 * z2,  
  x1z3 = x1 * z3,  
  
  x2z1 = x2 * z1,  
  x2z2 = x2 * z2,  
  x2z3 = x2 * z3,  
  
  x3z1 = x3 * z1,  
  x3z2 = x3 * z2,  
  x3z3 = x3 * z3,  
  .keep = "none") %>%  
  scale(scale = FALSE)
```

```
## Join the data pieces:
```

```
dat3 <- select(dat1, matches("y\\d")) %>% data.frame(preds, products)
```



# Example

```
mod4 <- '  
fX =~ x1 + x2 + x3  
fZ =~ z1 + z2 + z3  
fY =~ y1 + y2 + y3  
fXZ =~ x1z1 + x1z2 + x1z3 + x2z1 + x2z2 + x2z3 + x3z1 + x3z2 + x3z3  
  
fY ~ fX + fZ + fXZ  
  
x1z1 ~~ x1z2 + x1z3 + x2z1 + x3z1  
x1z2 ~~ x1z3 + x2z2 + x3z2  
x1z3 ~~ x2z3 + x3z3  
  
x2z1 ~~ x2z2 + x2z3 + x3z1  
x2z2 ~~ x2z3 + x3z2  
x2z3 ~~ x3z3  
  
x3z1 ~~ x3z2 + x3z3  
x3z2 ~~ x3z3  
'
```

# Example

```
## Estimate the model:
out4 <- sem(mod4, data = dat3, std.lv = TRUE)

partSummary(out4, 7, 1:14)
```

Latent Variables:

	Estimate	Std.Err	z-value	P(> z )
fX =~				
x1	0.673	0.043	15.555	0.000
x2	0.659	0.043	15.260	0.000
x3	0.702	0.045	15.569	0.000
fZ =~				
z1	0.738	0.048	15.360	0.000
z2	0.734	0.048	15.154	0.000
z3	0.718	0.046	15.597	0.000
fY =~				
y1	0.386	0.048	8.009	0.000
y2	0.359	0.045	7.925	0.000
y3	0.373	0.047	8.018	0.000

# Example

---

```
partSummary(out4, 7, c(1, 2, 15:24))
```

Latent Variables:

	Estimate	Std.Err	z-value	P(> z )
fxZ =~				
x1z1	0.367	0.053	6.902	0.000
x1z2	0.434	0.056	7.715	0.000
x1z3	0.441	0.053	8.300	0.000
x2z1	0.550	0.056	9.788	0.000
x2z2	0.616	0.062	9.970	0.000
x2z3	0.519	0.057	9.115	0.000
x3z1	0.504	0.059	8.604	0.000
x3z2	0.628	0.063	10.039	0.000
x3z3	0.535	0.059	9.128	0.000

# Example

```
partSummary(out4, 8:9, -(10:35))
```

Regressions:

	Estimate	Std.Err	z-value	P(> z )
fY ~				
fX	1.757	0.270	6.515	0.000
fZ	-0.111	0.105	-1.062	0.288
fXZ	0.557	0.141	3.962	0.000

Covariances:

	Estimate	Std.Err	z-value	P(> z )
fX ~~				
fZ	0.232	0.058	3.987	0.000
fXZ	-0.087	0.067	-1.297	0.195
fZ ~~				
fXZ	0.040	0.066	0.613	0.540

# Example

```
fitMeasures(out4, c("chisq", "df", "pvalue", "cfi", "tli", "rmsea", "srmr"))
```

chisq	df	pvalue	cfi	tli	rmsea	srmr
134.186	111.000	0.066	0.993	0.991	0.020	0.030

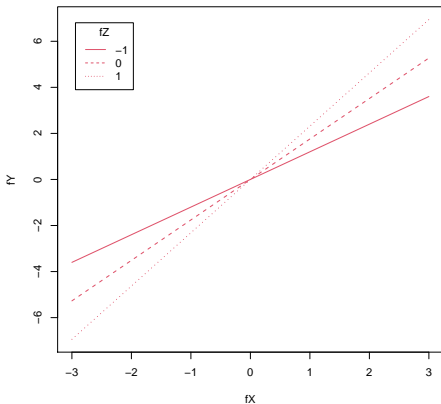
```
probeOut4 <- probe2WayMC(fit      = out4,  
                          nameX    = c("fX", "fZ", "fXZ"),  
                          nameY    = "fY",  
                          modVar    = "fZ",  
                          valProbe = c(-1, 0, 1)  
                          )
```

```
probeOut4$SimpleSlope
```

	fZ	est	se	z	pvalue
1	-1	1.200	0.210	5.722	0
2	0	1.757	0.270	6.515	0
3	1	2.314	0.376	6.163	0

# Example

```
plotProbe(probeOut4, xlim = c(-3, 3), xlab = "fX", ylab = "fY")
```



# Orthogonalization vs. Double Mean Centering

Orthogonalization and double mean centering tend to behave comparably, but each has its own strengths:

- When  $X$  and  $Z$  are bivariate normally distributed, both methods produce the same results.
- As  $X$  and/or  $Z$  stray from normality, orthogonalization produces biased estimates of the interaction effect, but double mean centering does not.
- Orthogonalization ensures that the latent  $XZ$  is perfectly independent of  $X$  and  $Z$ .
  - The  $X$  and  $Z$  parameters can be directly interpreted, without any conditioning

# Example

We can also use the `indProd()` function from **semTools** to create the product indicators.

```
## Use semTools to orthogonalize:
dat2.2 <- indProd(data      = dat1,
                  var1      = c("x1", "x2", "x3"),
                  var2      = c("z1", "z2", "z3"),
                  match     = FALSE,
                  meanC     = FALSE,
                  doubleMC  = FALSE,
                  residualC = TRUE,
                  namesProd = colnames(products)
                  )
```

```
## Compare to our manual results:
all.equal(dat2[colnames(products)],
          dat2.2[colnames(products)],
          check.attributes = FALSE)
```

```
[1] TRUE
```



# Example

---

```
## Use semTools to double mean center:
dat3.2 <- indProd(data      = dat1,
                  var1      = c("x1", "x2", "x3"),
                  var2      = c("z1", "z2", "z3"),
                  match     = FALSE,
                  meanC     = TRUE,
                  doubleMC  = TRUE,
                  residualC = FALSE,
                  namesProd = colnames(products)
                  )

all.equal(dat3[colnames(products)],
         dat3.2[colnames(products)],
         check.attributes = FALSE)

[1] TRUE
```

# Estimating Products of Latent Variables

---

In theory, we can directly estimate a latent variable defined as the product of two (or more) other latent variables.

- We cannot use ordinary ML estimation methods.

Three approaches seem sensible.

1. Latent moderated structural equations (LMS; Klein & Moosbrugger, 2000; Klein, Moosbrugger, Schermelleh-Engel, & Frank, 1997).
2. Structural-after-measurement (SAM) estimation (Rosseel & Loh, in press).
3. Bayesian SEM.

None of the above is currently implemented in **lavaan**.

- The SAM approach should be available soon.



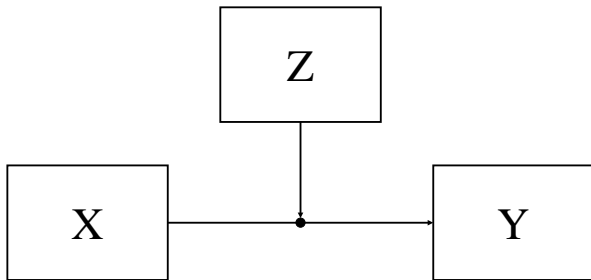
# MULTIPLE MODERATION



# Starting Point

---

So far, we've been looking at this type of model:



We've had one focal variable and one moderator.

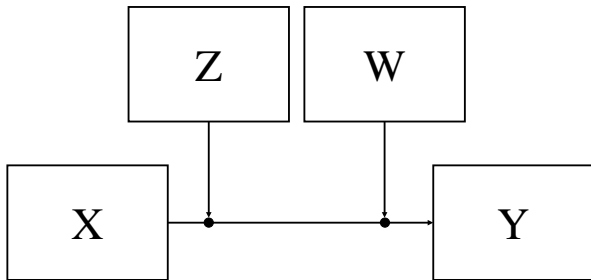
- We've been asking questions about how the focal effect changes as a function of the moderator.
- There's no reason we need to restrict ourselves to a single moderator.

# Multiple Moderation

---

Maybe we suspect that the focal effect changes as a function of two other variables.

- We could fit this type of model:



Now, the focal effect of  $X$  on  $Y$  changes as a function of both  $Z$  and  $W$ .

# Multiple Moderation

---

The preceding diagram implies the following formula:

$$Y = \alpha + f(Z, W)X + \beta_2Z + \beta_3W + e,$$

Taking  $f(Z, W)$  to be the following simple slope:

$$f(Z, W) = \beta_1 + \beta_4Z + \beta_5W$$

Produces the following analytic equation:

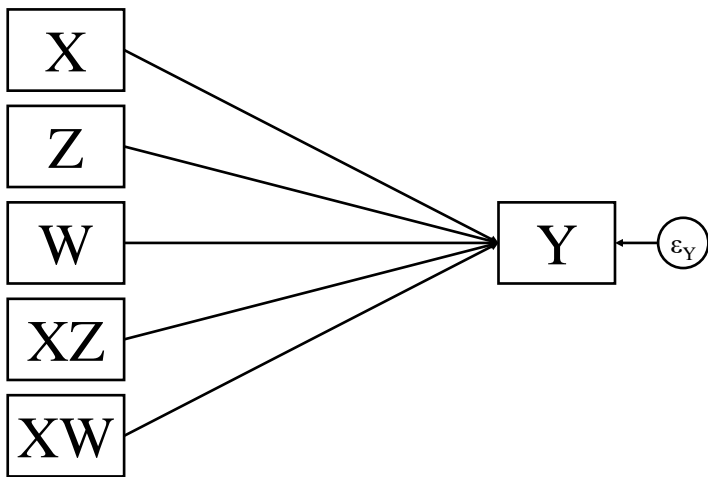
$$Y = \alpha + \beta_1X + \beta_2Z + \beta_3W + \beta_4XZ + \beta_5XW + e$$

We can easily fit this model in any regression (or path modeling) software.

- We can test for significant moderating effects of  $Z$  and  $W$  by testing for non-zero  $\beta_4$  and  $\beta_5$ , respectively.

# Multiple Moderation

Our analytic diagram is predictably extended:



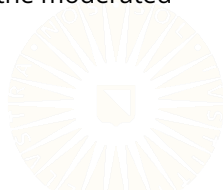
# Moderated Moderation

---

The additive two-way interaction model is more flexible than the simple single-moderator model, but it still imposes constraints.

- The moderating effect of  $Z$  (or  $W$ ) on the  $X \rightarrow Y$  relation is assumed to be constant across levels of  $W$  (or  $Z$ ).
- I.e., the moderation is not moderated

We can relax this constraint by modeling moderation of the moderated effect using a three-way interaction.

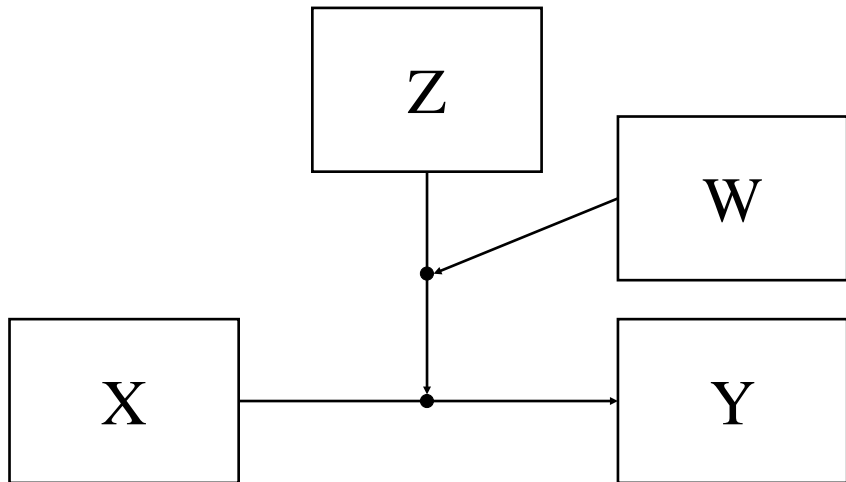




# Moderated Moderation

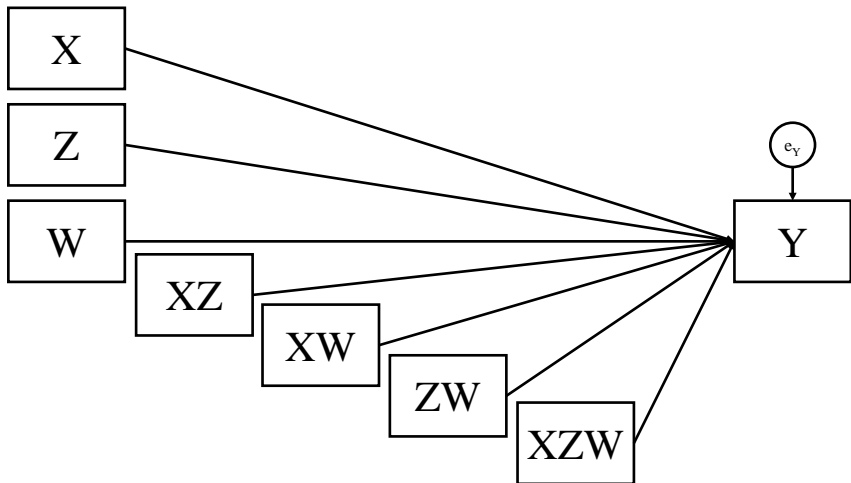
---

Moderated moderation implies the following conceptual diagram:



# Moderated Moderation

The preceding conceptual diagram implies this analytic diagram:



# Moderated Moderation

---

The preceding diagram represents the following equation:

$$Y = \alpha + \beta_1 X + \beta_2 Z + \beta_3 W + \beta_4 XZ + \beta_5 XW + \beta_6 ZW + \beta_7 XZW + e$$

Which can be restructured into:

$$\begin{aligned} Y &= \alpha + (\beta_1 + \beta_4 Z + \beta_5 W + \beta_7 ZW)X + \beta_2 Z + \beta_3 W + \beta_6 ZW + e \\ &= \alpha + g(Z, W)X + \beta_2 Z + \beta_3 W + \beta_6 ZW + e \end{aligned}$$

With moderated moderation, the simple slope is given by:

$$g(Z, W) = \beta_1 + \beta_4 Z + \beta_5 W + \beta_7 ZW$$

Which has the same structure as a single moderator model.

# Example

---

```
## Read in the BFI data:
dat1 <- readRDS("../data/bfiData1.rds")

## Three-way interaction model:
mod <- '
agree ~ 1 + open + conc + neuro + open:conc + open:neuro + conc:neuro + ocn
'

## Create the 3-way interaction via a pipeline and estimate the model:
out <- dat1 %>%
  mutate(ocn = open * conc * neuro) %>%
  sem(mod, data = .)
```

# Example

```
partSummary(out, 7:9)
```

Regressions:

	Estimate	Std.Err	z-value	P(> z )
agree ~				
open	1.279	0.257	4.975	0.000
conc	1.208	0.265	4.557	0.000
neuro	0.738	0.322	2.292	0.022
open:conc	-0.297	0.069	-4.292	0.000
open:neuro	-0.216	0.081	-2.676	0.007
conc:neuro	-0.256	0.082	-3.114	0.002
ocn	0.065	0.020	3.230	0.001

Intercepts:

	Estimate	Std.Err	z-value	P(> z )
.agree	-0.587	0.965	-0.609	0.543

Variances:

	Estimate	Std.Err	z-value	P(> z )
.agree	0.481	0.013	35.721	0.000

# Example

---

```
## Compute simple slopes by conditioning on both moderators:
ssOut <- probe3WayMC(out,
  nameX = c("open", "conc", "neuro",
            "open:conc", "open:neuro", "conc:neuro",
            "ocn"),
  nameY = "agree",
  modVar = c("conc", "neuro"),
  valProbe1 = quantile(dat1$conc, c(0.25, 0.5, 0.75)),
  valProbe2 = quantile(dat1$neuro, c(0.25, 0.5, 0.75))
)
```

# Example

---

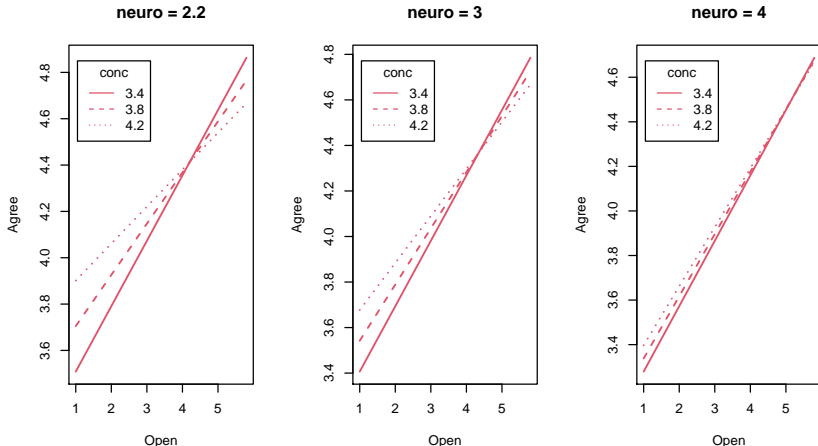
```
## View simple slopes:
```

```
ssOut$SimpleSlope
```

	conc	neuro	est	se	z	pvalue
1	3.4	2.2	0.282	0.034	8.316	0
2	3.8	2.2	0.221	0.035	6.400	0
3	4.2	2.2	0.160	0.042	3.802	0
4	3.4	3.0	0.287	0.031	9.346	0
5	3.8	3.0	0.247	0.027	8.980	0
6	4.2	3.0	0.206	0.032	6.379	0
7	3.4	4.0	0.293	0.041	7.179	0
8	3.8	4.0	0.279	0.032	8.607	0
9	4.2	4.0	0.265	0.033	8.032	0

# Example

```
plotProbe(ssOut, xlim = range(dat1$open), xlab = "Open", ylab = "Agree")
```





# CATEGORICAL MODERATORS



# Categorical Moderators

---

Categorical moderators encode *group-specific* effects.

- E.g., if we include sex as a moderator, we are modeling separate focal effects for males and females.

Given a set of codes representing our moderator, we specify the interactions as before:

$$Y_{total} = \beta_0 + \beta_1 X_{inten} + \beta_2 Z_{male} + \beta_3 X_{inten} Z_{male} + \varepsilon$$

$$Y_{total} = \beta_0 + \beta_1 X_{inten} + \beta_2 Z_{lo} + \beta_3 Z_{mid} + \beta_4 Z_{hi} \\ + \beta_5 X_{inten} Z_{lo} + \beta_6 X_{inten} Z_{mid} + \beta_7 X_{inten} Z_{hi} + \varepsilon$$

# Example

```
## Load data:
socSup <- readRDS("../data/social_support.rds")

## Focal effect model:
mod <- 'bdi ~ 1 + tanSat'

## Fit the model and summarize the results:
sem(mod, data = socSup) %>% partSummary(7:9)
```

## Regressions:

	Estimate	Std.Err	z-value	P(> z )
bdi ~				
tanSat	-0.810	0.309	-2.621	0.009

## Intercepts:

	Estimate	Std.Err	z-value	P(> z )
.bdi	24.409	5.294	4.611	0.000

## Variances:

	Estimate	Std.Err	z-value	P(> z )
.bdi	84.261	12.226	6.892	0.000

# Example

---

```
## Moderated model:
mod <- 'bdi ~ 1 + tanSat + male + tanSat:male'

## Dummy code sex in a pipeline and estimate the model:
out <- socSup %>%
  mutate(male = as.numeric(sex == "male")) %>%
  sem(mod, data = .)
```

# Example

```
partSummary(out, 7:9)
```

Regressions:

	Estimate	Std.Err	z-value	P(> z )
bdi ~				
tanSat	-0.577	0.354	-1.632	0.103
male	14.367	11.946	1.203	0.229
tanSat:male	-0.948	0.702	-1.350	0.177

Intercepts:

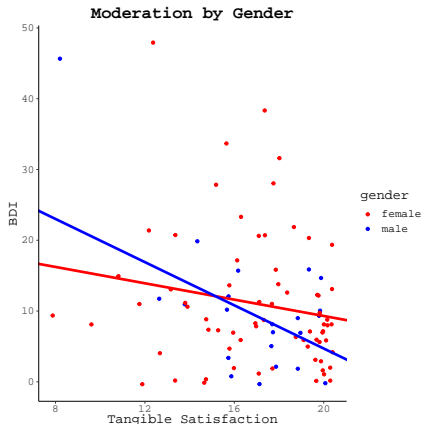
	Estimate	Std.Err	z-value	P(> z )
.bdi	20.848	6.079	3.429	0.001

Variances:

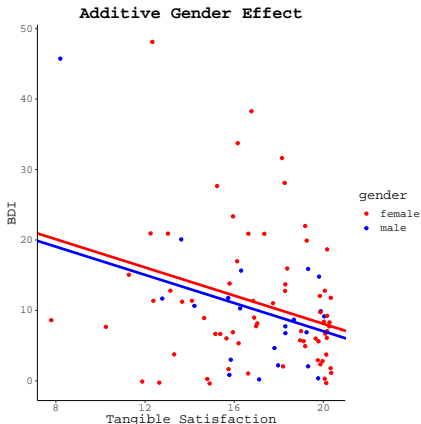
	Estimate	Std.Err	z-value	P(> z )
.bdi	82.261	11.936	6.892	0.000

# Visualizing Categorical Moderation

$$\hat{Y}_{BDI} = 20.85 - 0.58X_{tsat} + 14.37Z_{male} - 0.95X_{tsat}Z_{male}$$



$$\hat{Y}_{BDI} = 28.10 - 1.00X_{tsat} - 1.05Z_{male}$$

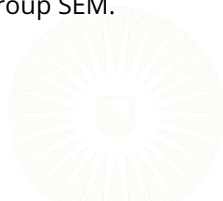


# Moderation via Multiple Group SEM

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When our moderator is a categorical variable, we can use multiple group CFA/SEM to test for moderation.

- Categorical moderators define groups.
- Significant moderation with categorical moderators implies between-group differences in the focal effect.
- We can directly test these hypotheses with multiple group SEM.



# Example

---

```
## Read the data and subset to only high school and college graduates:
dat2 <- readRDS("../data/bfiData2.rds") %>%
  filter(educ %in% c("highSchool", "college"))

## Specify the (configurally invariance) measurement model:
mod0 <- '
agree =~ A1 + A2 + A3 + A4 + A5
open  =~ O1 + O2 + O3 + O4 + O5
'

## Estimate the unrestricted model:
out0 <- cfa(mod0, data = dat2, std.lv = TRUE, group = "educ")
```



# Example

---

```
## Define the weakly invariant model:
mod1 <- measEq.syntax(configural.model = out0,
                      group = "educ",
                      group.equal = "loadings") %>%
  as.character()

## Define the strongly invariant model:
mod2 <- measEq.syntax(configural.model = out0,
                      group = "educ",
                      group.equal = c("loadings", "intercepts")
                      ) %>%
  as.character()

## Estimate the models:
out1 <- cfa(mod1, data = dat2, group = "educ")
out2 <- cfa(mod2, data = dat2, group = "educ")

## Test measurement invariance:
compareFit(out0, out1, out2) %>% summary()
```

# Example

```
##### Nested Model Comparison #####  
Chi-Squared Difference Test
```

	Df	AIC	BIC	Chisq	Chisq diff	Df diff	Pr(>Chisq)
out0	68	75336	75694	418.25			
out1	76	75358	75669	455.70	37.451	8	9.505e-06 ***
out2	84	75461	75726	575.15	119.446	8	< 2.2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
##### Model Fit Indices #####
```

	chisq	df	pvalue	rmsea	cfi	tli	srmr	aic	bic
out0	418.253†	68	.000	.066	.906†	.875	.046†	75336.292†	75693.810
out1	455.705	76	.000	.065†	.898	.879†	.050	75357.744	75669.130†
out2	575.151	84	.000	.070	.868	.858	.056	75461.190	75726.445

```
##### Differences in Fit Indices #####
```

	df	rmsea	cfi	tli	srmr	aic	bic
out1 - out0	8	-0.001	-0.008	0.004	0.004	21.451	-24.680
out2 - out1	8	0.005	-0.030	-0.021	0.006	103.446	57.315

# Example

---

```
## Specify a structural model:
mod3 <- '
agree =~ A1 + A2 + A3 + A4 + A5
open  =~ O1 + O2 + O3 + O4 + O5

agree ~ open
'

## Estimate the model with strong invariance constraints:
out3 <- sem(mod3,
  dat = dat2,
  std.lv = TRUE,
  group = "educ",
  group.equal = c("loadings", "intercepts")
)
```

# Example

---

```
## Check the group-specific slopes:
```

```
partSummary(out3, c(8, 10, 14, 16))
```

Group 1 [highSchool]:

Regressions:

	Estimate	Std.Err	z-value	P(> z )
agree ~				
open	-0.321	0.040	-7.957	0.000

Group 2 [college]:

Regressions:

	Estimate	Std.Err	z-value	P(> z )
agree ~				
open	-0.203	0.051	-3.972	0.000

# Example

---

```
## Specify the restricted model:
mod4 <- '
agree =~ A1 + A2 + A3 + A4 + A5
open  =~ O1 + O2 + O3 + O4 + O5

agree ~ c(beta, beta) * open
'

## Estimate the model:
out4 <- sem(mod4,
            dat = dat2,
            std.lv = TRUE,
            group = "educ",
            group.equal = c("loadings", "intercepts")
            )
```

# Example

---

```
## Check the slopes:
```

```
partSummary(out4, c(8, 10, 14, 16))
```

Group 1 [highSchool]:

Regressions:

		Estimate	Std.Err	z-value	P(> z )
agree ~					
open	(beta)	-0.278	0.032	-8.621	0.000

Group 2 [college]:

Regressions:

		Estimate	Std.Err	z-value	P(> z )
agree ~					
open	(beta)	-0.278	0.032	-8.621	0.000

# Example

---

```
## Do a chi-squared difference test for moderation:
```

```
anova(out3, out4)
```

Chi-Squared Difference Test

	Df	AIC	BIC	Chisq	Chisq diff	Df diff	Pr(>Chisq)
out3	84	75461	75726	575.15			
out4	85	75463	75722	578.59	3.435	1	0.06383 .

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# Example

```
## Do a similar test via OLS regression:
```

```
dat1 %>%  
  filter(educ %in% c("highSchool", "college")) %$%  
  lm(agree ~ open * educ) %>%  
  partSummary(-(1:2))
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.24965	0.12321	26.376	<2e-16
open	0.27115	0.03134	8.652	<2e-16
educcollege	0.03975	0.22849	0.174	0.862
open:educcollege	-0.05654	0.05856	-0.965	0.334

Residual standard error: 0.6972 on 2356 degrees of freedom

Multiple R-squared: 0.05314, Adjusted R-squared: 0.05194

F-statistic: 44.08 on 3 and 2356 DF, p-value: < 2.2e-16



# Probing Multiple Group Moderation

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Testing moderation with multiple group SEM has several advantages.

- Remove measurement error from the estimates
- Test for factorial invariance
- All simple effects are directly estimated in the unrestricted model



# Simple Slopes & Intercepts

Group 1 [highSchool]:

Regressions:

	Estimate	Std.Err	z-value	P(> z )
agree ~ open	-0.321	0.040	-7.957	0.000

Intercepts:

	Estimate	Std.Err	z-value	P(> z )
.agree	0.000			

Group 2 [college]:

Regressions:

	Estimate	Std.Err	z-value	P(> z )
agree ~ open	-0.203	0.051	-3.972	0.000

Intercepts:

	Estimate	Std.Err	z-value	P(> z )
.agree	0.170	0.056	3.058	0.002

# Simple Slopes Visualized

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We can visualize the simple slopes by plotting the factor scores.

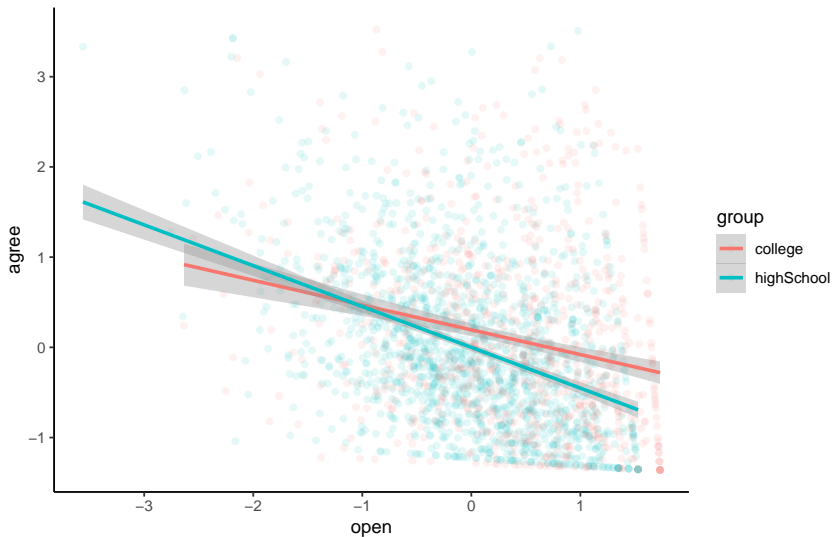
```
library(ggplot2)

## Generate factor scores:
tmp <- predict(out3)

## Stack factor scores into a "tidy" dataset:
pData <- data.frame(do.call(rbind, tmp),
                    group = rep(names(tmp), sapply(tmp, nrow))
                    )

## Create a simple slopes plot:
ssPlot <- ggplot(pData, aes(open, agree, color = group)) +
  geom_point(alpha = 0.1) +
  geom_smooth(method = "lm") +
  theme_classic()
```

# Simple Slopes Visualized



# References

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- Klein, A., & Moosbrugger, H. (2000). Maximum likelihood estimation of latent interaction effects with the LMS method. *Psychometrika*, 65(4), 457–474.
- Klein, A., Moosbrugger, H., Schermelleh-Engel, K., & Frank, D. (1997). A new approach to the estimation of latent interaction effects in structural equation models. *SoftStat*, 97, 479–486.
- Lin, G.-C., Wen, Z., Marsh, H. W., & Lin, H.-S. (2010). Structural equation models of latent interactions: Clarification of orthogonalizing and double-mean-centering strategies. *Structural Equation Modeling*, 17(3), 374–391.
- Little, T. D., Bovaird, J. A., & Widaman, K. F. (2006). On the merits of orthogonalizing powered and product terms: Implications for modeling interactions among latent variables. *Structural Equation Modeling*, 13(4), 497–519.

# References

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Rosseel, Y., & Loh, W. W. (in press). A structural-after-measurement (SAM) approach to structural equation modeling. *Psychological Methods*. Retrieved from <https://osf.io/pekbm/>

