

Structural Models

PSY9140

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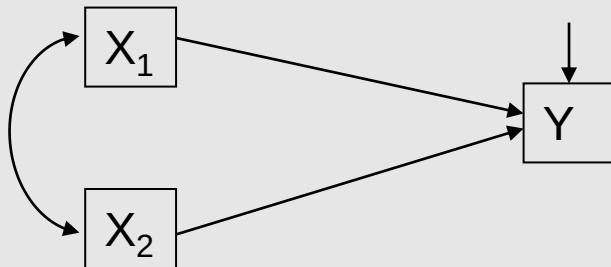
Overview

- Path models
 - Identification, multiple regressions, mediation
- Structural models
 - Identification, recursive models
- Mediation analysis
- Equivalent models
- Moderation analysis
- Multi-group analysis
- Some practical issues
 - Importing files from SPSS into Mplus

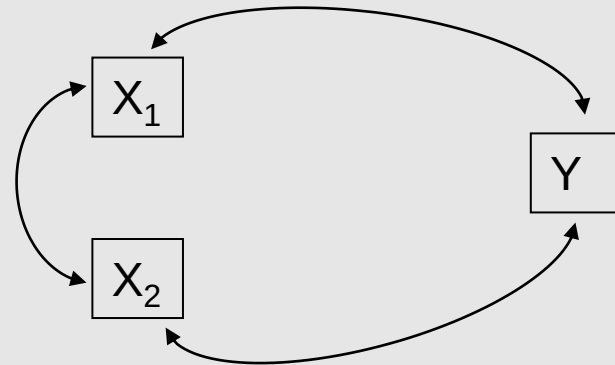
Path Models

Path model example

Multiple regression



Correlation



Variance-covariance matrix

	x_1	x_2	y
x_1	VAR_{x_1}		
x_2	$\text{COV}_{x_1x_2}$	VAR_{x_2}	
y	COV_{x_1y}	COV_{x_2y}	VAR_y

Number of variances and covariances

$$= p(p+1)/2$$

$$= 3(3+1)/2 = 6$$

Model Identification

- *Overidentified*: Fewer free parameters than variances and covariances
- *Just identified*: The same number of free parameters as variances and covariances
- *Underidentified*: More free parameters than variances and covariances
- «Standard» regression models are just identified

lavaan ~ operator

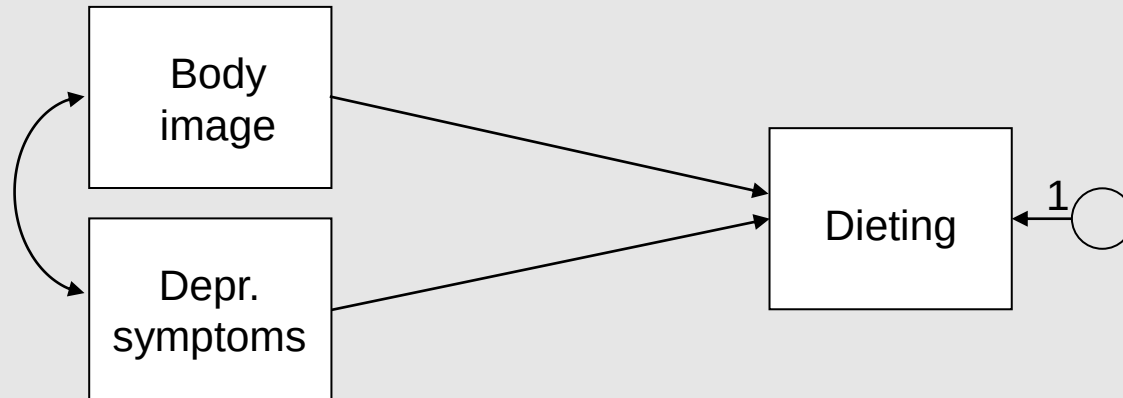
Y ~ X;

Y ←———— X

(Y regressed on X)

Path Model Example: Multiple Regression

Multiple regression analysis



```
model <- "diet ~ dep  
         diet ~ body  
         body ~~ dep"
```

```
model <- "diet ~ body + dep  
         body ~~ dep"
```

lavaan script

```
# load the datafile "data1.csv" as a dataframe with the name "df1" by using the "read.csv" command
df1 <- read.csv("https://www.sv.uio.no/psi/personer/vit/tilmanns/psy9140/data1.csv")

# descriptive statistics for all variables in "df1" by using "describe" from the "psych" package
describe(df1)

# Model specification
model <- "diet ~ dep
         diet ~ body
         body ~ dep"

# Running the model
fit <- sem(model, missing = "ML", meanstructure = TRUE, data = df1)

# Providing output for the model
summary(fit, fit.measures = TRUE, standardized=TRUE)
```

```
> fit <- sem(model, missing = "ML", meanstructure = TRUE, data = df1)
warning message:
In lav_data_full(data = data, group = group, cluster = cluster, :
lavaan WARNING: some cases are empty and will be ignored:
845
```

lavaan output

lavaan 0.6-3 ended normally after 23 iterations

Optimization method	NLMINB
Number of free parameters	9
	Used
Number of observations	2441
Number of missing patterns	6
Estimator	ML
Model Fit Test Statistic	0.000
Degrees of freedom	0

Model test baseline model:

Minimum Function Test Statistic	625.006
Degrees of freedom	3
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)	-6406.229
Loglikelihood unrestricted model (H1)	-6406.229
Number of free parameters	9
Akaike (AIC)	12830.457
Bayesian (BIC)	12882.659
Sample-size adjusted Bayesian (BIC)	12854.064

Root Mean Square Error of Approximation:

RMSEA	0.000
90 Percent Confidence Interval	0.000 0.000
P-value RMSEA <= 0.05	NA

Standardized Root Mean Square Residual:

SRMR	0.000
------	-------

Parameter Estimates

Regressions:

	Estimate	Std.Err	z-value	P(> z)	Std.lv	Std.all
diet ~						
dep	0.138	0.025	5.462	0.000	0.138	0.109
body	-0.394	0.022	-18.035	0.000	-0.394	-0.356

Covariances:

	Estimate	Std.Err	z-value	P(> z)	Std.lv	Std.all
dep ~						
body	-0.101	0.007	-13.673	0.000	-0.101	-0.293

Intercepts:

	Estimate	Std.Err	z-value	P(> z)	Std.lv	Std.all
.diet	2.924	0.098	29.863	0.000	2.924	4.213
dep	1.709	0.011	151.606	0.000	1.709	3.107
body	3.430	0.013	268.260	0.000	3.430	5.477

Variances:

	Estimate	Std.Err	z-value	P(> z)	Std.lv	Std.all
.diet	0.404	0.012	34.370	0.000	0.404	0.838
dep	0.303	0.009	34.471	0.000	0.303	1.000
body	0.392	0.011	34.605	0.000	0.392	1.000

DAY 3, EXERCISE 1 (*use the script 'day3.R', Exercise 1*)

- (1) Specify a multiple regression model with body image (*body*), depressive symptoms (*dep*) and body mass index (*bmi*) as independent variable and dieting (*diet*) as dependent variable.
- (2) Which independent variable is the strongest predictor of dieting?
- (3) How much variance is explained by all three independent variables together? (in *lavaan*, the option "rsquare = TRUE" in the "summary" command can be used to obtain R^2 , but try first to obtain this information without using the rsquare command)
- (4) Estimate the model *with* and *without* correlations among the independent variables. In which way do the results differ?

Variances of independent (exogeneous) variables

- By default, variances of independent variables are not estimated. Instead, their variances are fixed to their sample values and not displayed in the output).
- This also implies that covariances (correlations) between independent variables are not estimated.
- To estimate variances and covariances, they have to be explicitly specified in the model.
- Alternatively, the *fixed.x = FALSE* option can be used (default: *fixed.x = TRUE*).

Variances of independent (exogeneous) variables

```
# Model specification
model <- "diet ~ dep
         diet ~ body"

# Running the model
fit <- sem(model, missing = "ML",
           meanstructure = TRUE, data = df1)

# Providing output for the model
summary(fit, fit.measures = TRUE,
        standardized=TRUE)
```

Regressions:	
	Estimate
diet ~	
dep	0.137
body	-0.394
Intercepts:	
	Estimate
.diet	2.926
Variances:	
	Estimate
.diet	0.401

```
# Model specification
model <- "diet ~ dep
         diet ~ body"

# Running the model
fit <- sem(model, missing = "ML",
           meanstructure = TRUE,
           fixed.x = FALSE, data = df1)

# Providing output for the model
summary(fit, fit.measures = TRUE,
        standardized=TRUE)
```

Regressions:	
	Estimate
diet ~	
dep	0.138
body	-0.394
Covariances:	
	Estimate
dep ~~	
body	-0.101
Intercepts:	
	Estimate
.diet	2.924
dep	1.709
body	3.430
Variances:	
	Estimate
.diet	0.404
dep	0.303
body	0.392

Variances of independent (exogeneous) variables

```
# Model specification
model <- "diet ~ dep
         diet ~ body"

# Running the model
fit <- sem(model, missing = "ML",
           meanstructure = TRUE, data = df1)

# Providing output for the model
summary(fit, fit.measures = TRUE,
        standardized=TRUE)
```

```
warning message:
In lav_data_full(data = data, group =
group, cluster = cluster, :
lavaan WARNING: 114 cases were delet
ed due to missing values in
exogenous variable
(s), while fixed.x = TRUE.
```

```
# Model specification
model <- "diet ~ dep
         diet ~ body"

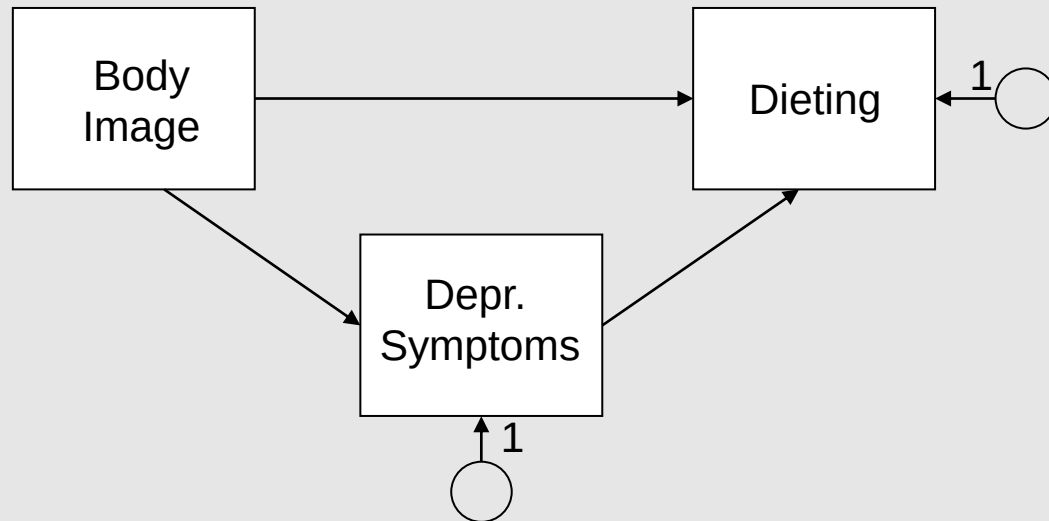
# Running the model
fit <- sem(model, missing = "ML",
           meanstructure = TRUE,
           fixed.x = FALSE, data = df1)

# Providing output for the model
summary(fit, fit.measures = TRUE,
        standardized=TRUE)
```

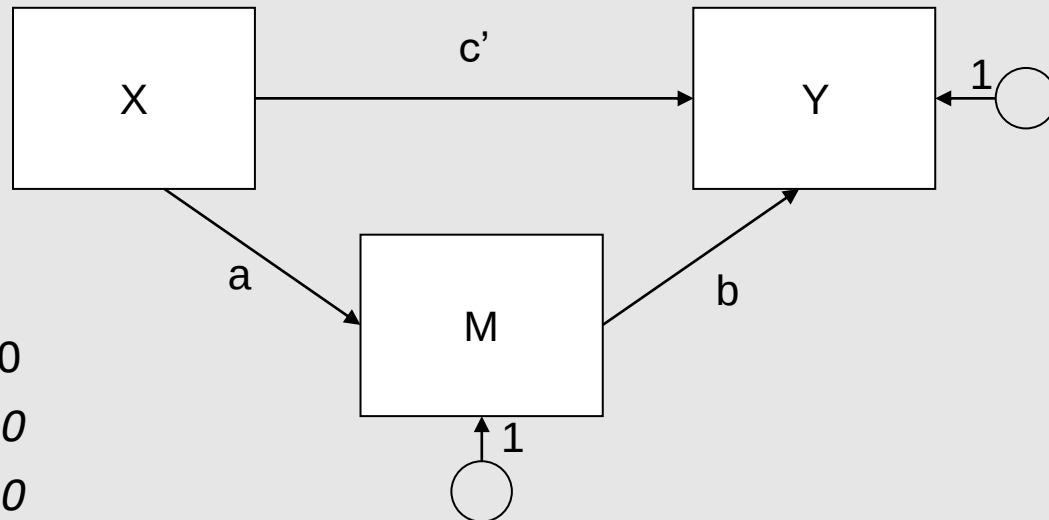
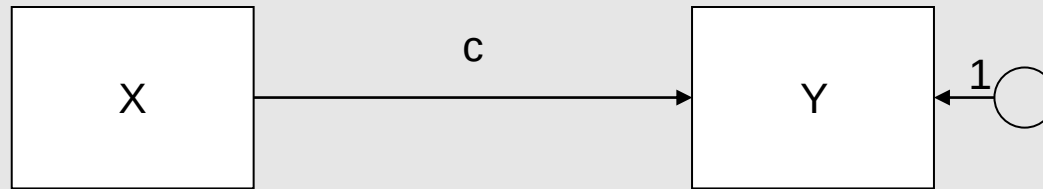
```
warning message:
In lav_data_full(data = data, group =
group, cluster = cluster, :
lavaan WARNING: some cases are empty
and will be ignored:
845
```

Path Model Example: Mediation

Mediation analysis



Mediation



1) $c \neq 0$

2) $a \neq 0$

3) $b \neq 0$

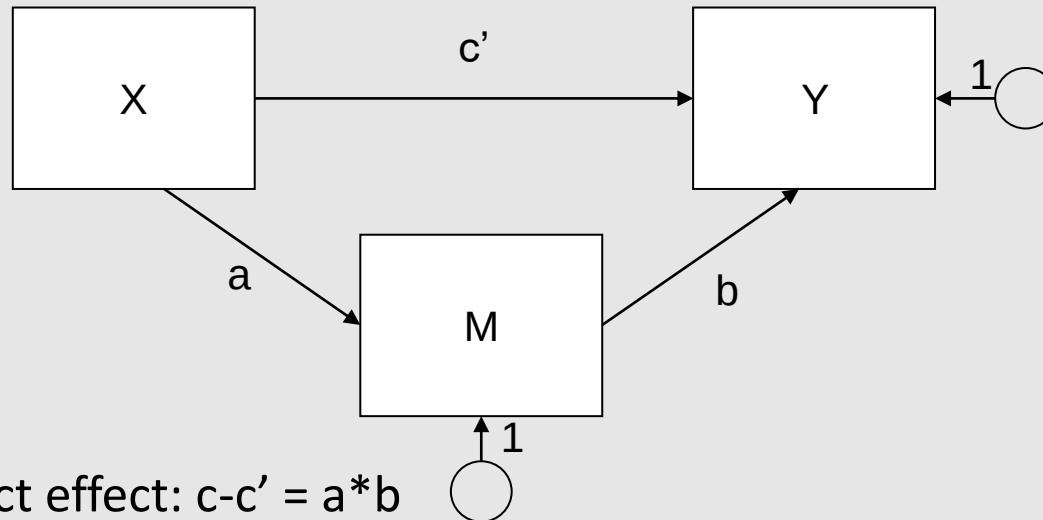
4) $c' < c$ (partial mediation); $c' = 0$ (full mediation)

Baron, R. M., & Kenny, D. A. (1986). The moderator-mediator variable distinction in social psychological research: Conceptual, strategic, and statistical considerations. *Journal of Personality and Social Psychology*, 51, 1173-1182.

Mediation models

- Mediation models are causal models
- Statistical models of mediation do not «prove» causality
- Problems with cross-sectional designs and causality

Newer Thoughts on Mediation



Indirect effect: $c - c' = a * b$

Sobel's test: $SE = \sqrt{b^2 SE_a^2 + a^2 SE_b^2}$

Bootstrapping as an alternative (Bias corrected bootstrap)

Hayes, A. F. (2009). Beyond Baron and Kenny: Statistical mediation analysis in the new millenium. *Communication Monographs*, 76, 408-420.

Hayes, A. F. (2013). *Introduction to mediation, moderation, and conditional process analysis: A regression-based approach* NY: Guilford.

Shrout, P. E., & Bolger, N. (2002). Mediation in experimental and nonexperimental studies: New procedures and recommendations. *Psychological Methods*, 7, 422-445.

Muthén, B. O., Muthén, L. K., & Asparouhov, T. (2017). Regression and mediation analysis using Mplus. Muthen & Muthen.

Effect decomposition

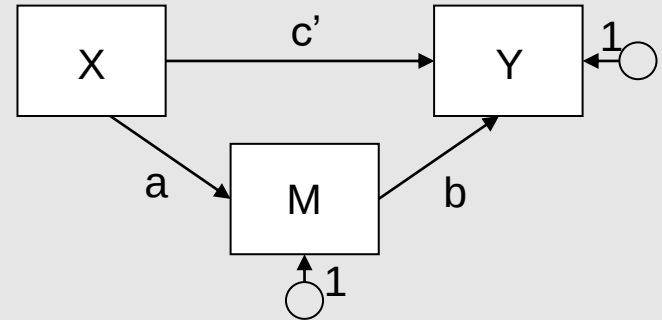
Total effect = direct effect + indirect effect

$$c = c' + a*b$$

Effect decomposition in by labelling parameters and using the “:=” operator

The := operator defines new parameters

```
model <- ' # direct effect
           Y ~ c*X
           # mediator
           M ~ a*X
           Y ~ b*M
           # indirect effect (a*b)
           ab := a*b
           # total effect
           total := c + (a*b) '
```

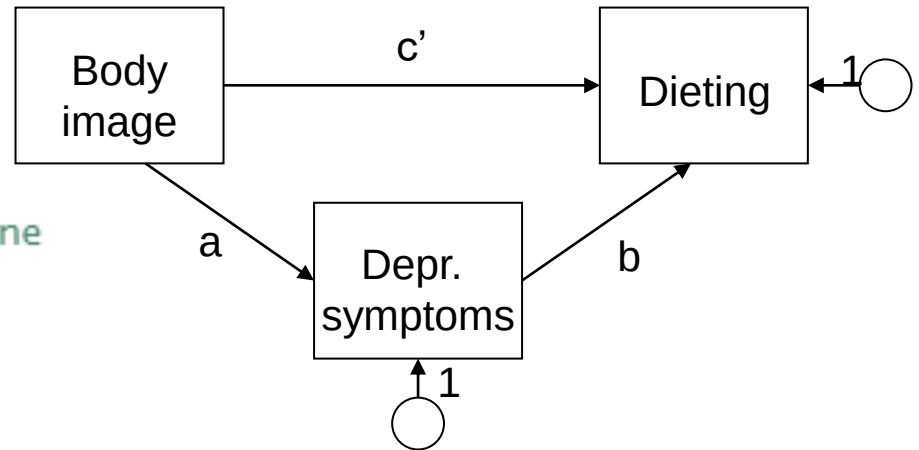


lavaan script

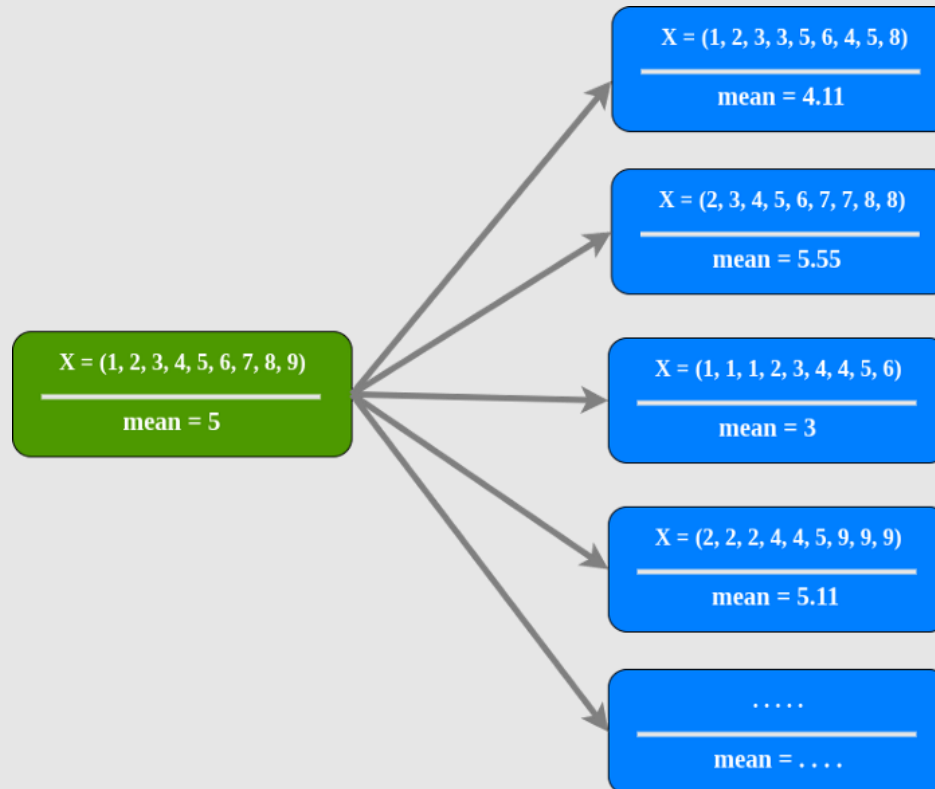
```
# Specify the model in the next line
model <- "# Mediation model
diet ~ b*dep + c*body
dep ~ a*body
# Indirect effect
ab := a*b
# Total effect
total := c + a*b"
```

```
# Running the model
fit <- sem(model, missing = "ML", meanstructure = TRUE, data = df1)

# Providing output for the model
summary(fit, fit.measures = TRUE, standardized=TRUE)
```



Bootstrapping



Bootstrapping

```
# Running the model with bootstrapping with 5,000 draws
fit <- sem(model, missing = "ML", meanstructure = TRUE,
          se = "bootstrap", bootstrap = 5000, data = df)

# Providing output for the model
summary(fit, fit.measures = TRUE, standardized=TRUE, ci = TRUE)

# Providing bias corrected standard errors from the bootstrap
parameterestimates(fit, boot.ci.type = "bca.simple")
```

lavaan output 1

Parameter Estimates:

Standard Errors	Bootstrap
Number of requested bootstrap draws	5000
Number of successful bootstrap draws	5000

Regressions:

		Estimate	Std.Err	z-value	P(> z)	ci.lower	ci.upper	std.lv	std.all
diet ~									
dep	(b)	0.138	0.028	4.848	0.000	0.084	0.195	0.138	0.109
body	(c)	-0.395	0.024	-16.583	0.000	-0.441	-0.348	-0.395	-0.356
dep ~									
body	(a)	-0.257	0.020	-13.143	0.000	-0.296	-0.220	-0.257	-0.293

Intercepts:

	Estimate	Std.Err	z-value	P(> z)	ci.lower	ci.upper	std.lv	std.all
.diet	2.926	0.109	26.875	0.000	2.714	3.135	2.926	4.214
.dep	2.590	0.070	36.842	0.000	2.457	2.732	2.590	4.714

Variances:

	Estimate	Std.Err	z-value	P(> z)	ci.lower	ci.upper	std.lv	std.all
.diet	0.404	0.012	33.642	0.000	0.380	0.427	0.404	0.839
.dep	0.276	0.010	26.555	0.000	0.256	0.296	0.276	0.914

Defined Parameters:

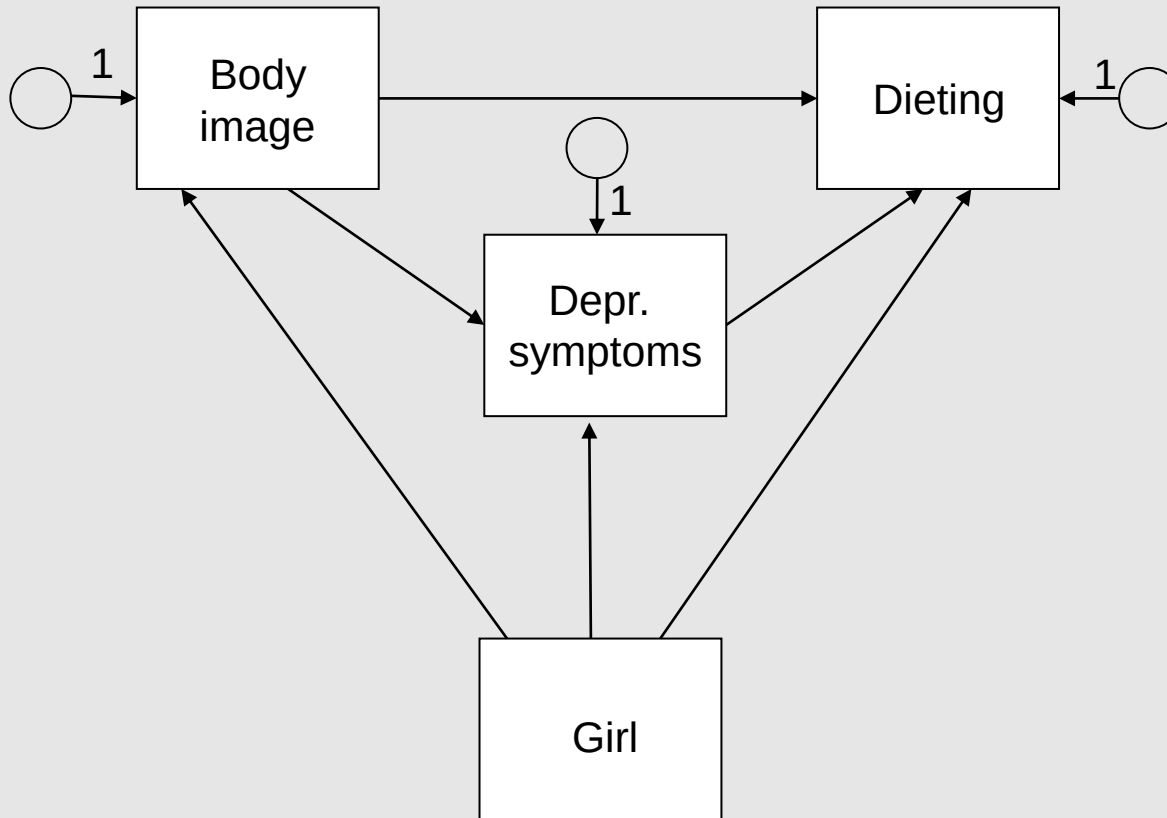
	Estimate	Std.Err	z-value	P(> z)	ci.lower	ci.upper	std.lv	std.all
ab	-0.035	0.008	-4.574	0.000	-0.051	-0.021	-0.035	-0.032
total	-0.430	0.023	-18.871	0.000	-0.475	-0.385	-0.430	-0.388

lavaan output 2

```
> # Providing bias corrected standard errors from the bootstrap
> parameterestimates(fit, boot.ci.type = "bca.simple")
```

	lhs	op	rhs	label	est	se	z	pvalue	ci.lower	ci.upper
1	diet	~	dep	b	0.138	0.028	4.848	0	0.082	0.194
2	diet	~	body	c	-0.395	0.024	-16.583	0	-0.441	-0.348
3	dep	~	body	a	-0.257	0.020	-13.143	0	-0.295	-0.219
4	diet	~~	diet		0.404	0.012	33.642	0	0.381	0.428
5	dep	~~	dep		0.276	0.010	26.555	0	0.256	0.296
6	body	~~	body		0.392	0.000	NA	NA	0.392	0.392
7	diet	~1			2.926	0.109	26.875	0	2.718	3.137
8	dep	~1			2.590	0.070	36.842	0	2.454	2.730
9	body	~1			3.430	0.000	NA	NA	3.430	3.430
10	ab	:=	a*b	ab	-0.035	0.008	-4.574	0	-0.052	-0.021
11	total	:=	c+a*b	total	-0.430	0.023	-18.871	0	-0.476	-0.386

Multiple mediation model



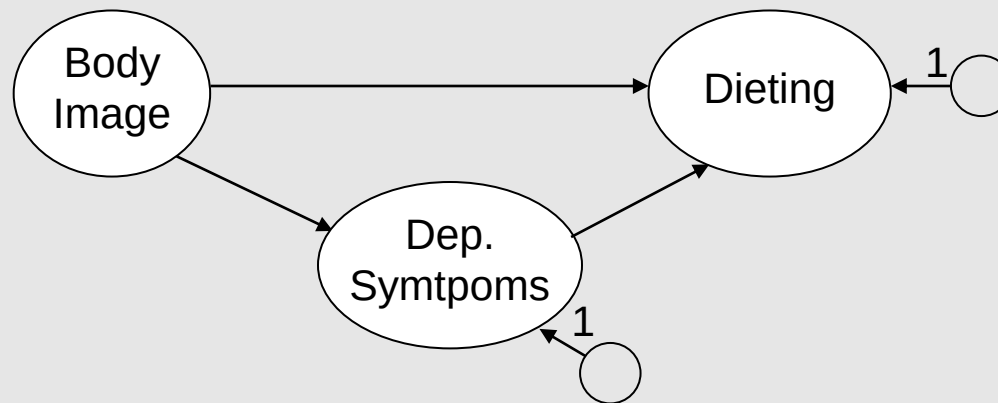
DAY3, EXERCISE 2 *(use the script 'day3.R', Exercise 2)*

- (1) Specify the multiple mediation model as depicted in the previous slide.
- (2) Point out the different mediational processes that can be estimated in the model.
- (3) Test one (or several) of them by using the `:=` operator command.
- (4) Use Sobel's test and/or bootstrapping (with 100 draws) to test for mediation.
- (5) Are there possible alternative mediation models with different causal directions? Specify and estimate one of them. Is the alternative model substantially plausible?

Structural Models

Combination of Factor Models and Path Analysis

Example: Mediation Model



Steps in constructing structural models

0) Test factor models by conducting EFA

1) Test each factor model separately with CFA

2) Test all factor models in one combined model where all factors are correlated

3) Test the full model (structural and measurement part combined)

4) Modify the model at each step, if necessary

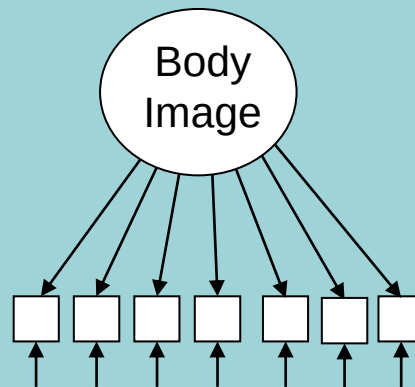
Body Image – Body Area Satisfaction Scale (BASS)

How dissatisfied or satisfied are you with each of the following aspects of your body?

	Very Dissatisfied	Mostly Dissatisfied	Neither Or	Mostly Satisfied	Very Satisfied
	1	2	3	4	5
<i>body1</i> : Face (facial features, complexion)	☐	☐	☐	☐	☐
<i>body2</i> : Lower torso (buttocks, hips, thighs, legs)...	☐	☐	☐	☐	☐
<i>body3</i> : Mid torso (waist, stomach).....	☐	☐	☐	☐	☐
<i>body4</i> : Upper torso (chest or breasts, shoulders, arms) ..	☐	☐	☐	☐	☐
<i>body5</i> : Muscle tone	☐	☐	☐	☐	☐
<i>body6</i> : Weight.....	☐	☐	☐	☐	☐
<i>body7</i> : Height.....	☐	☐	☐	☐	☐

DAY 3, EXERCISE 3 - Step 1 (*use the script 'day3.R'*)

1. Test the measure of Body Image by conducting a CFA
2. Modify the measurement model, if necessary. Use both results from the analyses (for instance modification indices and factor loadings) and substantive considerations when modifying the model.



Dieting (Dieting factor of Eating Attitude Test 12)

Below are some statements about food and eating habits.

	Never	Rarely	Often	Always
	1	2	3	4
<i>diet1</i> : I am preoccupied with the desire to be thinner.....	☐	☐	☐	☐
<i>diet2</i> : I engage in dieting behavior	☐	☐	☐	☐
<i>diet3</i> : I feel uncomfortable after eating sweets.....	☐	☐	☐	☐
<i>diet4</i> : I think about burning up calories when I exercise	☐	☐	☐	☐

Depressive Symptoms (Version of HSCL)

Indicate whether you have been bothered by the following troubles the last two weeks:

Not bothered
at all

A little bit
bothered

Quite a bit
bothered

Extremely
bothered

1

2

3

4

dep1: Felt too tired to do things.....

☐
☐
☐
☐

dep2: Had trouble sleeping

☐
☐
☐
☐

dep3: Felt unhappy, sad, or depressed.....

☐
☐
☐
☐

dep4: Felt hopeless about the future

☐
☐
☐
☐

dep5: Felt tense or keyed up.....

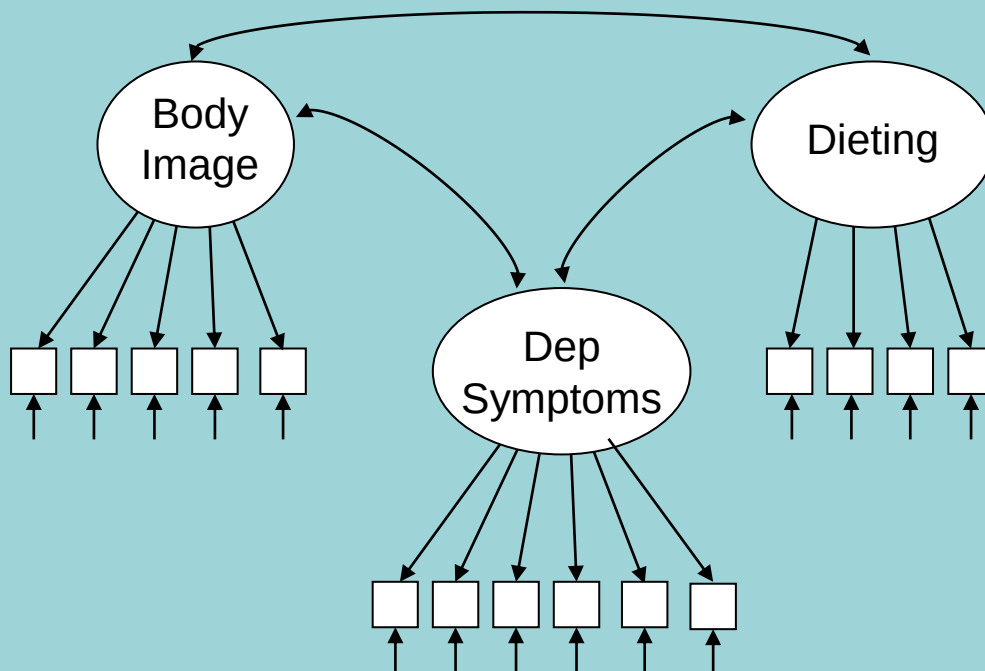
☐
☐
☐
☐

dep6: Worried too much about things.....

☐
☐
☐
☐

DAY 3, EXERCISE 3 - Step 2

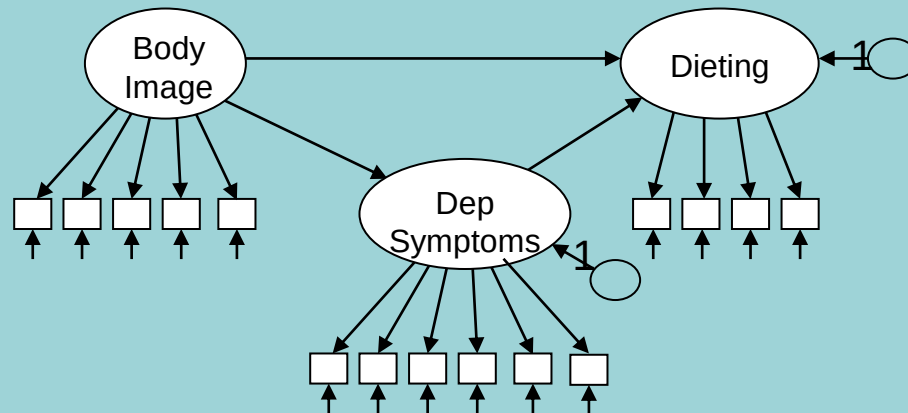
3. Combine all factors in one model with correlations among latent factors
4. Examine model fit. Does the model fit the data well?



DAY 3, EXERCISE 4 - Step 1

use the script in day3.R, Exercise 4 or your own script from the previous exercise

1. Specify and estimate the combined measurement and structural model depicted below.
2. Assess mediation by using the “:=” operator. Do the results differ from the mediation model based on mean scores?

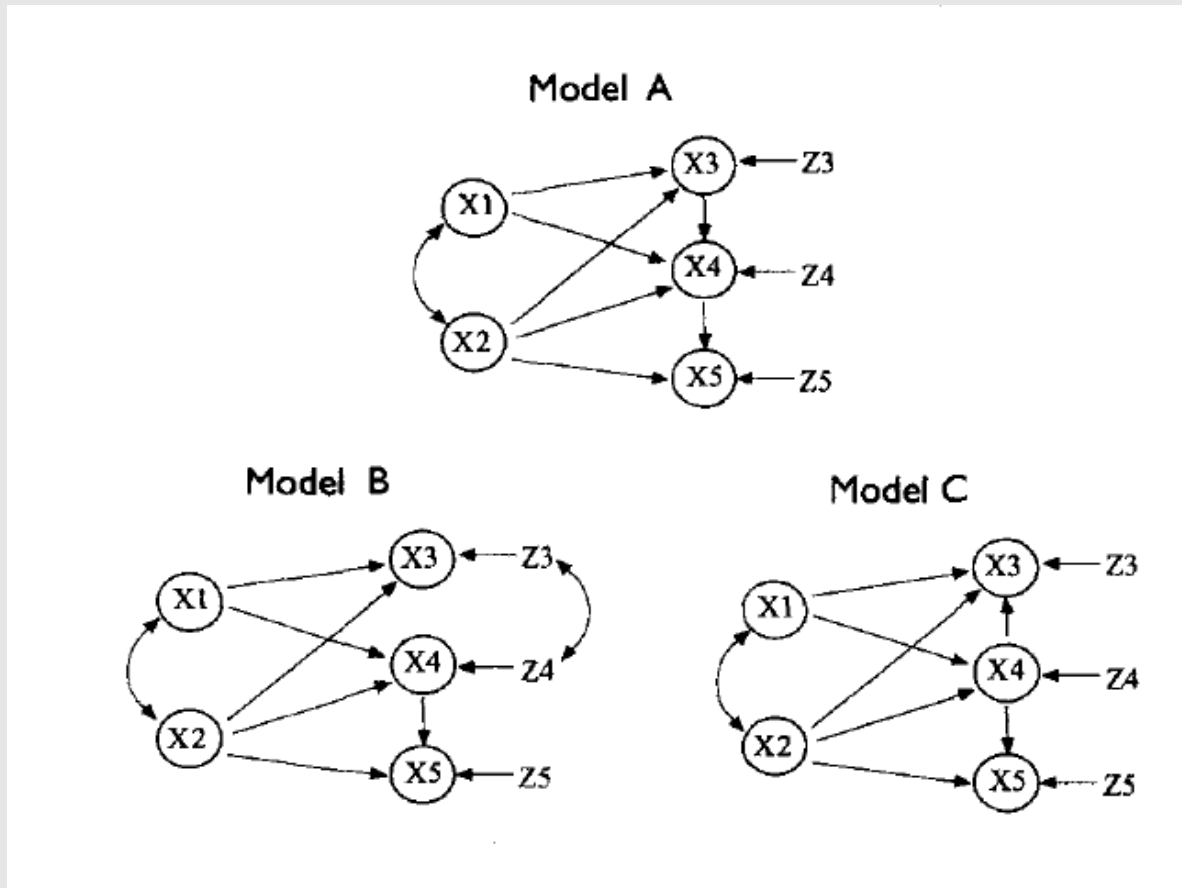


Model Equivalence

- Even though a causal model fits the data, it does not mean that it is the correct model
- There are always competing models which fit the data equally well → Model equivalence.
 - All just identified models are equivalent
 - In many cases, a regression path can be replaced by a regression path in the opposite direction or a correlation among residuals

MacCallum, R. C., Wegener, D. T., Uchino, B. N., & Fabrigar, L. R. (1993). The problem of equivalent models in applications of covariance structure analysis. *Psychological Bulletin*, 114, 185-199.

Example of Model Equivalence – Replacing Rule



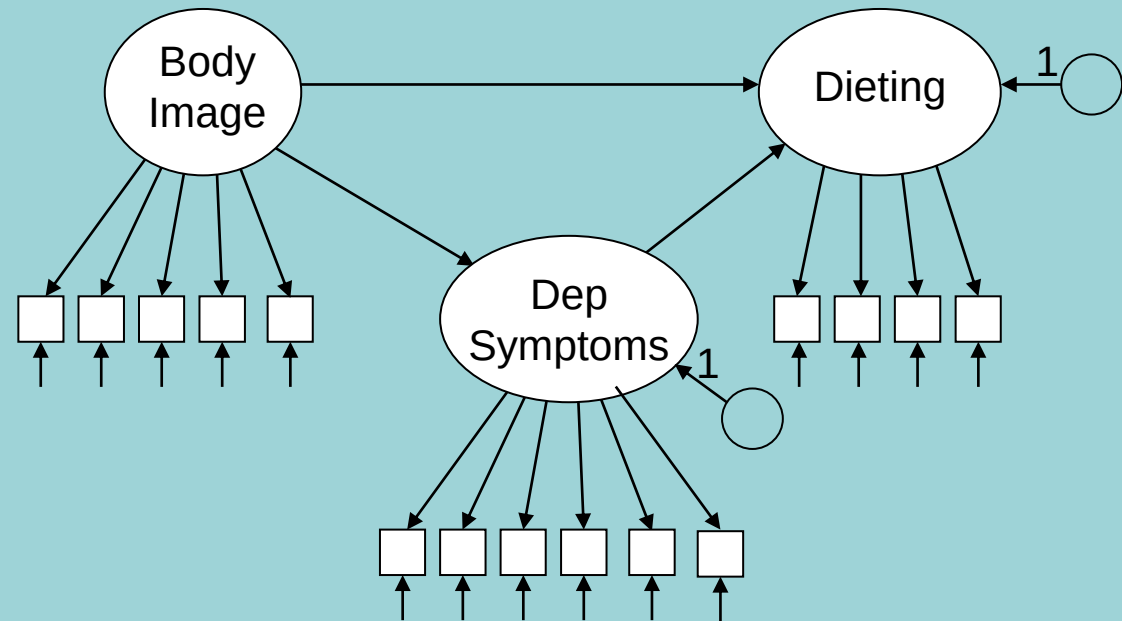
from:
MacCallum
et al. (1993)

Because X3 and X4 are predicted by the same variables (X1 and X2),
Models B and C are equivalent with Model A

DAY3, EXERCISE 4, Step 2

3. Specify and estimate alternative mediation models (with other causal directions) and check for equivalence in model fit.

Original model:



Multi-group analysis and moderation

Are there differences between groups?

- Level: Means
- Variation: Variances
- Relationships: Regression coefficients, correlations
- Structure: Factor loadings

Disadvantages of conducting separate analyses for each group

- Difficult to test differences for significance
- Parameters cannot be constraint to be equal
- CFA means cannot be compared

Option in the *sem* function:

```
sem(group = "grouping_var ")
```

Example:

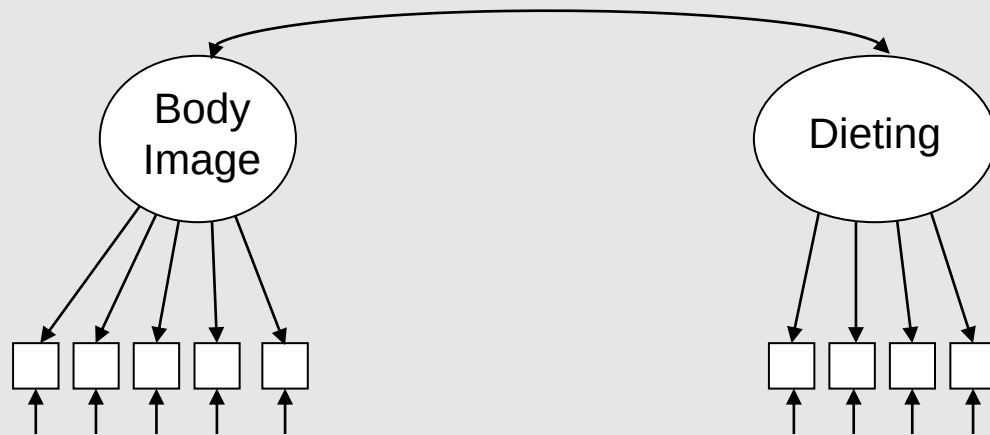
```
sem(model, data = df2, group = "girl")
```

Using multi-group analysis

```
model <- "# CFA
  body =~ body1 + body2 + body3 + body4 + body6
  diet =~ diet1 + diet2 + diet3 + diet4
# Covariances
  diet =~ body"

fit1 <- sem(model, missing = "ML", meanstructure = TRUE, data = df2, group = "girl")

# Providing output for model 1
summary(fit1, fit.measures = TRUE, standardized=TRUE)
```



Constraining different parameters one by one

factor loadings:

factor =~ indicator1 + c(l2, l2)* indicator2 + c(l3, l3)* indicator3

factor =~ c(NA,NA)*indicator1 + c(1,1)*indicator2 + indicator3

regression coefficients:

y ~ c(b1, b1)*x1 + c(b2, b2)*x2

covariances:

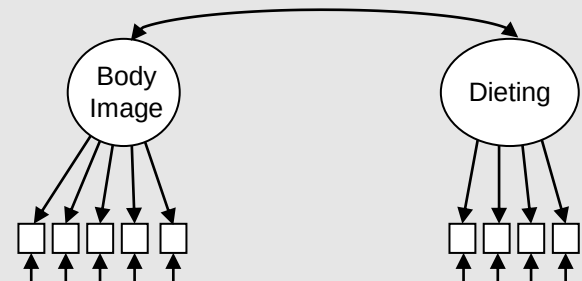
x1 ~~ c(cov12, cov12)*x2

variances

x1 ~~ c(var1, var1)*x1

Is the correlation between body image and dieting significantly different for boys and girls?

- Use parameter constraints
- Compare models with and without parameter constraints
- Use ML



```
model <- "body =~ body1 + body2 + body3 + body4 + body6  
diet =~ diet1 + diet2 + diet3 + diet4  
diet ~~ c(a,a)*body"
```

Using multi-group analysis

```
model <- "# CFA
  body =~ body1 + body2 + body3 + body4 + body6
  diet =~ diet1 + diet2 + diet3 + diet4
  # Covariances
  diet ~~ body"

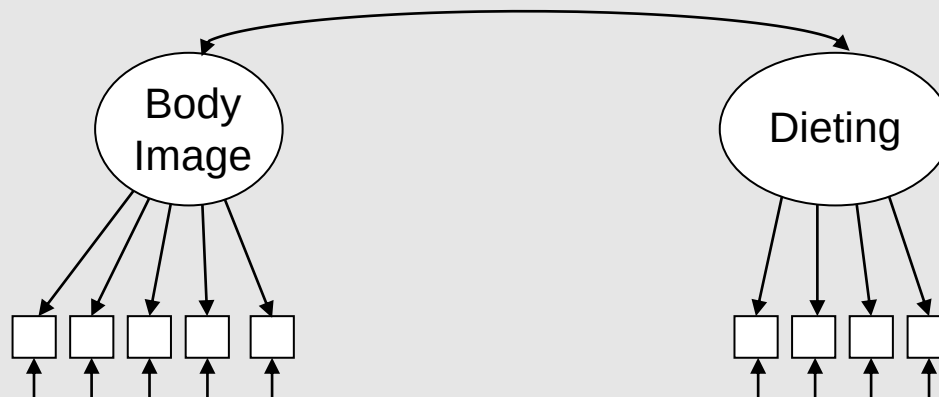
fit1 <- sem(model, missing = "ML", meanstructure = TRUE, data = df2, group = "girl")

# Providing output for the model
summary(fit1, fit.measures = TRUE, standardized=TRUE)

model <- "# CFA
  body =~ body1 + body2 + body3 + body4 + body6
  diet =~ diet1 + diet2 + diet3 + diet4
  # Covariances
  diet ~~ c(cov,cov)*body"

fit2 <- sem(model, missing = "ML", meanstructure = TRUE, data = df2, group = "girl")

# Providing output for the model
summary(fit2, fit.measures = TRUE, standardized=TRUE)
```



WITHOUT CONSTRAINTS

lavaan 0.6-7 ended normally after 71 iterations

Estimator	ML	
Optimization method	NLMINB	
Number of free parameters	56	
Number of observations per group:	Used	Total
0	1012	1026
1	1386	1416
Number of missing patterns per group:		
0	19	
1	15	

Model Test User Model:

Test statistic	494.293
Degrees of freedom	52
P-value (Chi-square)	0.000
Test statistic for each group:	
0	200.053
1	294.240

WITH CONSTRAINTS

lavaan 0.6-7 ended normally after 65 iterations

Estimator	ML	
Optimization method	NLMINB	
Number of free parameters	56	
Number of equality constraints	1	
Number of observations per group:	Used	Total
0	1012	1026
1	1386	1416
Number of missing patterns per group:		
0	19	
1	15	

Model Test User Model:

Test statistic	494.530
Degrees of freedom	53
P-value (Chi-square)	0.000
Test statistic for each group:	
0	200.173
1	294.357

Group 1 [0]:

Latent Variables:

	Estimate
body =~	
body1	1.000
body2	1.806
body3	2.456
body4	1.620
body6	2.009
diet =~	
diet1	1.000
diet2	0.483
diet3	0.356
diet4	0.787

Covariances:

	Estimate
body ~ diet	
(cov)	-0.135

Intercepts:

	Estimate
.body1	3.698
.body2	3.677
.body3	3.548
.body4	3.632
.body6	3.591
.diet1	1.623
.diet2	1.365
.diet3	1.615
.diet4	1.541
body	0.000
diet	0.000

Group 2 [1]:

Latent Variables:

	Estimate
body =~	
body1	1.000
body2	2.757
body3	2.941
body4	1.240
body6	3.215
diet =~	
diet1	1.000
diet2	0.742
diet3	0.604
diet4	0.805

Covariances:

	Estimate
body ~ diet	
(cov)	-0.135

Intercepts:

	Estimate
.body1	3.424
.body2	3.076
.body3	3.085
.body4	3.197
.body6	3.140
.diet1	2.186
.diet2	1.803
.diet3	2.049
.diet4	1.967
body	0.000
diet	0.000

Chi-square Distribution Table

d.f.	.995	.99	.975	.95	.9	.1	.05	.025	.01
1	0.00	0.00	0.00	0.00	0.02	2.71	3.84	5.02	6.63
2	0.01	0.02	0.05	0.10	0.21	4.61	5.99	7.38	9.21
3	0.07	0.11	0.22	0.35	0.58	6.25	7.81	9.35	11.34
4	0.21	0.30	0.48	0.71	1.06	7.78	9.49	11.14	13.28
5	0.41	0.55	0.83	1.15	1.61	9.24	11.07	12.83	15.09
6	0.68	0.87	1.24	1.64	2.20	10.64	12.59	14.45	16.81
7	0.99	1.24	1.69	2.17	2.83	12.02	14.07	16.01	18.48
8	1.34	1.65	2.18	2.73	3.49	13.36	15.51	17.53	20.09
9	1.73	2.09	2.70	3.33	4.17	14.68	16.92	19.02	21.67
10	2.16	2.56	3.25	3.94	4.87	15.99	18.31	20.48	23.21

Comparing nested models

lavaan:

`anova(fit_model1, fit_model2)`

`lavTestLRT(fit_model1, fit_model2)`

semTools:

`measEq.syntax()`

```
> anova(fit1, fit2)
Chi-Squared Difference Test
```

	Df	AIC	BIC	Chisq	Chisq diff	Df diff	Pr(>Chisq)
fit1	52	48189	48513	494.29			
fit2	53	48187	48505	494.53	0.23659	1	0.6267

```
> lavTestLRT(fit1, fit2)
Chi-Squared Difference Test
```

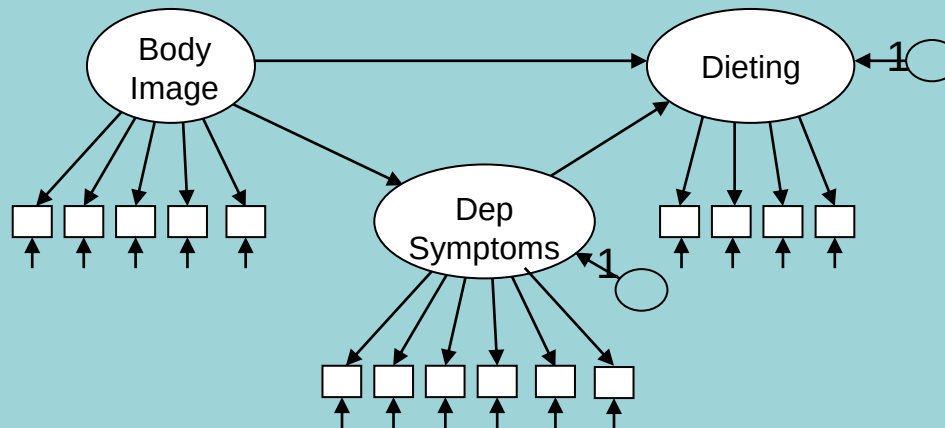
	Df	AIC	BIC	Chisq	Chisq diff	Df diff	Pr(>Chisq)
fit1	52	48189	48513	494.29			
fit2	53	48187	48505	494.53	0.23659	1	0.6267

DAY 3, EXERCISE 5

use the script in day3.R, Exercise 5 or your own script from the previous exercise

Use the structural model you worked on in Exercise 4 and estimate a multiple group model with gender as the grouping variable.

- 1) Use parameter constraints to examine whether the relationships between the variables are moderated by gender.
- 2) Which paths show significant gender differences?



Constraining groups of parameters

```
sem(group.equal = c("...", "...", "..."))
```

Most often used: *loadings*. Other commands:

- `intercepts`: the intercepts of the observed variables
- `means`: the intercepts/means of the latent variables
- `residuals`: the residual variances of the observed variables
- `residual.covariances`: the residual covariances of the observed variables
- `lv.variances`: the (residual) variances of the latent variables
- `lv.covariances`: the (residual) covariances of the latent variables
- `regressions`: all regression coefficients in the model

Example:

```
sem(model, data = df2, group = "girl", group.equal = c("loadings"))
```

Measurement invariance

```
model <- "# CFA
  body =~ body1 + body2 + body3 + body4 + body6
  diet =~ diet1 + diet2 + diet3 + diet4
# Covariances
  diet ~~ body"

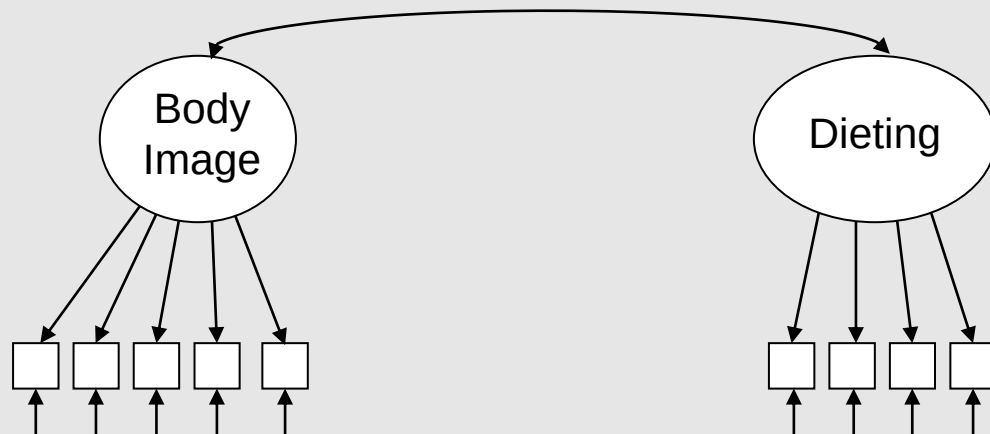
fit1 <- sem(model, missing = "ML", meanstructure = TRUE, data = df2, group = "girl")

# Providing output for model 1
summary(fit1, fit.measures = TRUE, standardized=TRUE)

fit2 <- sem(model, missing = "ML", meanstructure = TRUE, data = df2, group = "girl", group.equal = c("loadings"))

# Providing output for model 2
summary(fit2, fit.measures = TRUE, standardized=TRUE)

anova(fit1, fit2)
lavTestLRT(fit1, fit2)
```



WITHOUT CONSTRAINTS

lavaan 0.6-7 ended normally after 71 iterations

Estimator	ML	
Optimization method	NLMINB	
Number of free parameters	56	
Number of observations per group:	Used	Total
0	1012	1026
1	1386	1416
Number of missing patterns per group:		
0	19	
1	15	

Model Test User Model:

Test statistic	494.293
Degrees of freedom	52
P-value (Chi-square)	0.000
Test statistic for each group:	
0	200.053
1	294.240

WITH CONSTRAINTS

lavaan 0.6-7 ended normally after 54 iterations

Estimator	ML	
Optimization method	NLMINB	
Number of free parameters	56	
Number of equality constraints	7	
Number of observations per group:	Used	Total
0	1012	1026
1	1386	1416
Number of missing patterns per group:		
0	19	
1	15	

Model Test User Model:

Test statistic	635.128
Degrees of freedom	59
P-value (Chi-square)	0.000
Test statistic for each group:	
0	278.251
1	356.878

Group 1 [0]:

Latent Variables:

	Estimate
body =~	
body1	1.000
body2 (.p2.)	2.260
body3 (.p3.)	2.682
body4 (.p4.)	1.472
body6 (.p5.)	2.570
diet =~	
diet1	1.000
diet2 (.p7.)	0.627
diet3 (.p8.)	0.503
diet4 (.p9.)	0.801

Covariances:

	Estimate
body ~ diet	-0.108

Intercepts:

	Estimate
.body1	3.698
.body2	3.677
.body3	3.548
.body4	3.633
.body6	3.591
.diet1	1.623
.diet2	1.366
.diet3	1.616
.diet4	1.541
body	0.000
diet	0.000

Group 2 [1]:

Latent Variables:

	Estimate
body =~	
body1	1.000
body2 (.p2.)	2.260
body3 (.p3.)	2.682
body4 (.p4.)	1.472
body6 (.p5.)	2.570
diet =~	
diet1	1.000
diet2 (.p7.)	0.627
diet3 (.p8.)	0.503
diet4 (.p9.)	0.801

Covariances:

	Estimate
body ~ diet	-0.161

Intercepts:

	Estimate
.body1	3.424
.body2	3.076
.body3	3.085
.body4	3.197
.body6	3.140
.diet1	2.186
.diet2	1.804
.diet3	2.049
.diet4	1.966
body	0.000
diet	0.000

```

> anova(fit1, fit2)
Chi-Squared Difference Test

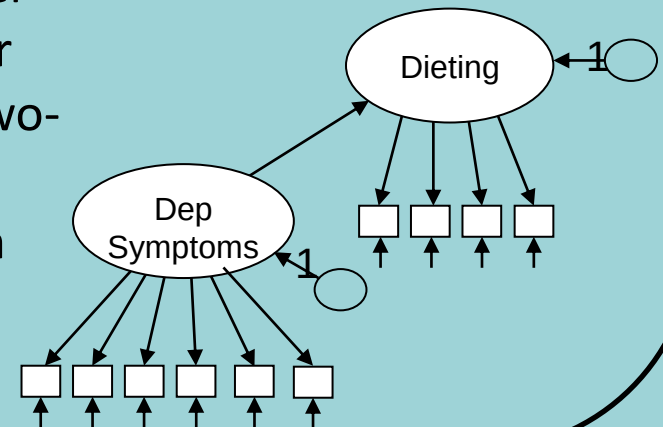
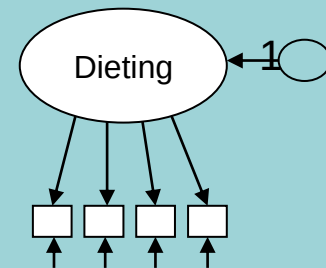
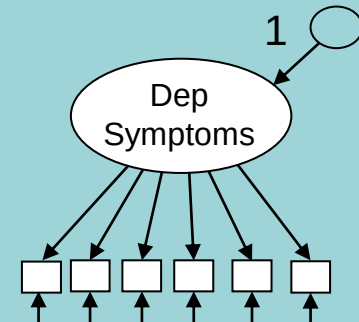
      Df    AIC    BIC  Chisq Chisq diff Df diff Pr(>Chisq)
fit1  52 48189 48513 494.29
fit2  59 48316 48599 635.13      140.84      7 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> lavTestLRT(fit1, fit2)
Chi-Squared Difference Test

      Df    AIC    BIC  Chisq Chisq diff Df diff Pr(>Chisq)
fit1  52 48189 48513 494.29
fit2  59 48316 48599 635.13      140.84      7 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

DAY 3, EXERCISE 6

- 1) Conduct a multi-group analysis for a CFA for depressive symptoms. Do you find measurement invariance (equal factor loadings) across gender?
- 2) Examine measurement invariance across gender for dieting. Which factor loadings have to be freed to improve model fit?
- 3) Estimate the following structural model with depressive symptoms as predictor and dieting as outcome variable in a two-group analysis with measurement invariance. Is the relationship between depressive symptoms and dieting moderated by gender?



Freeing up parameters one by one (partial variance)

```
fit <- sem(model, data = df2, group = "grouping_var", group.equal =  
c("loadings"), group.partial = "factor=~indicator2")
```

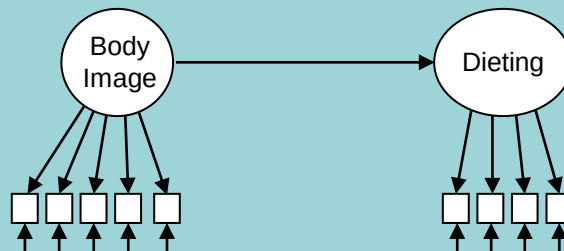
Modification indices for constraint parameters

Function: `lavTestScore(fit)`

DAY 3, EXERCISE 7

Estimate the structural model presented below by using the script file *day3, Exercise 7*.

- 1) Use the *anova* or *lavTestLRT* function to compare the estimated model with a model without measurement invariance.
- 2) Use the *lavTestScore()* function to obtain information about constraint parameters that may be freed.
- 3) Use the *group.partial =* function to free one or several parameters (e.g., factor loadings).



Data transfer from SPSS to R

Transfer data from SPSS to R

Use package *foreign*

```
# install package foreign. Has just to be done once
install.packages("foreign")

# load foreign
library(foreign)

# set working directory to the directory where the data file is stored
# (use "/" and not "\\")
setwd("c:/")

# Load SPSS file as data frame
df <- read.spss("data.sav", use.value.labels=FALSE, to.data.frame = TRUE)
```

DAY 3, EXERCISE 8

1) Transfer data from SPSS to R

- You can do so by using the code in day3.R, Exercise 8
- Alternative, download the SPSS file “cosmetics.sav” from <https://www.sv.uio.no/psi/personer/vit/tilmanns/psy9140/>
- Use the foreign package in R and the read.spss() function

2) Specify and estimate the following model:

