

Step 1: Specification

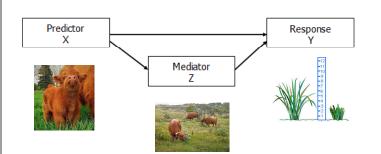
Formally define your hypothesized relationships

Define variables

• Define relationships between all variables

→ Strength of inference directly dependent on strength of confirmatory nature of analysis

Step 1: Specification



Step 2: Identification

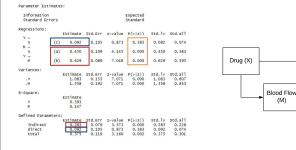
Check that your dataset is sufficient to answer your hypothesized network.

Rules of thumb:

- 1) Residuals are normally distributed
- 2) More observations than variables
- 3) Directional nature constant within each variable
- 4) No error in measurement
- 5) No loops between variables

Step 4: Evaluation

Gauge degree of agreement between hypothesized relationship and actual results



Step 5: Re-specification

Step 3: Estimation

Run calculations and analysis

i.e. lavaan package

If results are a poor fit, go back to Step 1 and adjust hypothesis relationship

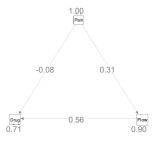
nodel <- 'Y ~ c*X #direct effect: DRUG has direct effect on Pain# M ~ a*X #mediator DRUG has on effect on FLOW # Y ~ b*M #mediator: FLOW has an effect on PAIN# indirect := a*b #indirect effect#

direct :=c total:= c +(a*b)'#total effect = sum of direct and indirect #

Information Standard Errors		Expected Standard					D 00	v	D-1-00	
tegressions								Drug (X)	∧►	Pain (Y
-		Estimate	Std. Err	z-value	P(> z)	Std. lv	Std.all			
Y ~										
X M~	(c)	0.092	0.105	0.873	0.383	0.092	0.074			T
×	(a)	0.450	0.109	4.145	0.000	0.450	0.383		Blood Flow	
Y~ M										
M	(b)	0.629	0.089	7.048	0.000	0.629	0.595		「 (M) 「	

Step 6: Visualization and Interpretation

- Graphically present results
- Infer relationships
 semPlot package



Pain (Y)

Questions?



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