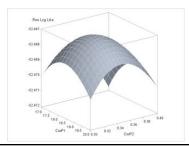
# Introduction to Likelihood Methods for SEM

Jarrett E. K. Byrnes
University of Massachusetts Boston



$$\Sigma = \Sigma(\Theta)$$

"There are no routine statistical questions, only questionable statistical routines"

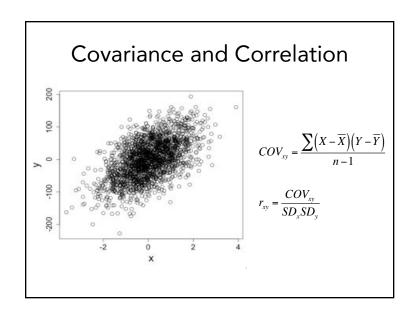
- Sir David Cox

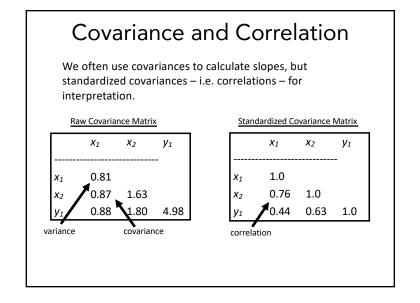
# What is Covariance-Based SEM Estimation with Likelihood?

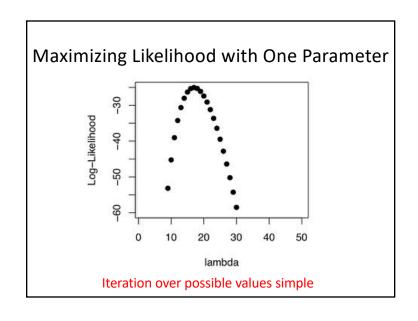
- Estimation of parameters given covariance of the data
- Equivalent to Linear Regressions, but...
- Estimation of each parameter influences the others
- Can accomodate unobserved (latent) variables and feedbacks

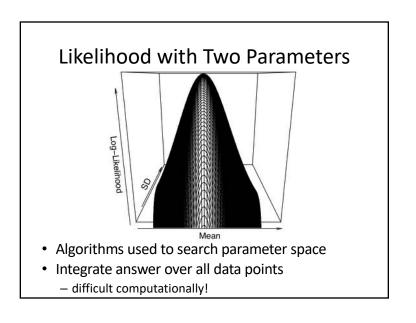
# A Likely Outline

- 1. What is SEM using likelihood and covariance matrices?
- 2. Model Identifiability
- 3. Sample Size for SEM
- 4. Standardized Coefficients
- 5. Introduction to lavaan

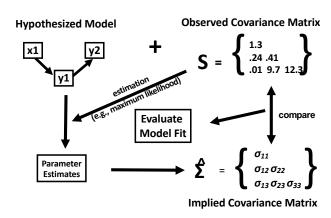








### How does ML Estimation Work?



### What we're used to with ML

Data Generation:  $\mu_i = a + bX_i$ 

Likelihood Function:  $F_r = Y_i \sim dnorm(\mu_i, \sigma)$ 

We minimize the likelihood function, Fr

# It's...More Complicated with SEM

Data Generation:

$$\Sigma = \begin{pmatrix} \Sigma_{yy} & \Sigma_{yx} \\ \Sigma_{xy} & \Sigma_{xx} \end{pmatrix} = \begin{pmatrix} \Lambda_y (I - B)^{-1} (\Gamma \Phi \Gamma' + \Psi) (I - B)^{-1'} \Lambda_y' + \theta_\varepsilon & \Lambda_y (I - B)^{-1} \Gamma \Phi \Lambda_x' \\ \Lambda_x \Phi \Gamma' (I - B)^{-1'} & \Lambda_x \Phi \Lambda_x' + \theta_\delta \end{pmatrix}$$

Likelihood Function:

$$F_{ML} = \log |\hat{\Sigma}| - \log |\mathbf{S}| + tr(\mathbf{S}\hat{\Sigma}^{-1}) - (p+q)$$

# The Maximum Likelihood Fitting Function

$$F_{ML} = \log \left| \hat{\Sigma} \right| - \log \left| \mathbf{S} \right| + tr \left( \mathbf{S} \hat{\Sigma}^{-1} \right) - \left( p + q \right)$$

S = Sample covariance matrix

Linear Algebra Review

S = Fit covariance matrix

Det(A) = scalar number

p = endogenous variablesq = exogenous variables

A\*A-1 = Diagonal matrix of ones

- If  $S = \Sigma$ , term 1 2 = 0 and terms 3 4 = 0.
- $F_{ML} = 0$  with perfect fit

# Assumptions Behind F<sub>ml</sub>

- Multivariate normality
  - Fairly robust (non-normality of residuals bigger problem)
  - Test with multivariate Shapiro-Wilk's Test (library mvnormtest)
  - In particular, no skew
  - Severe violations bias parameter error and tests of model fit
- No missing data in calculation of S
  - Biases your estimates with pairwise corrections
- No redundant variables
  - S must be positive definite
- Sample size is "large" (more soon)

# Identifiability

- 1. To fit a model, it must be identified
- 2. We need as much unique information as parameters
- 3. What can make a model non-identified?
  - Too many paths relative to # of variables
  - Certain model structures
  - High multicollinearity (r>0.9)
  - Complex model & small sample
- 4. How do I know if my model is identified?

# A Likely Outline

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## Identification: An Algebra-Eye View

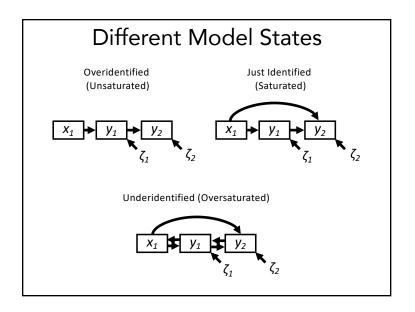
3 = a + b4 = 2a + b a and b have unique solutionsJust identified

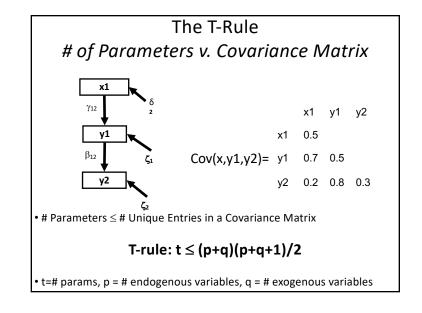
3 = a + b + c a, b, and c have no unique 4 = 2a + b + 3c solution Underidentified

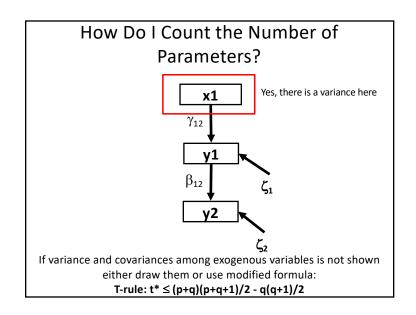
3 = a + b a and b have unique solutions,

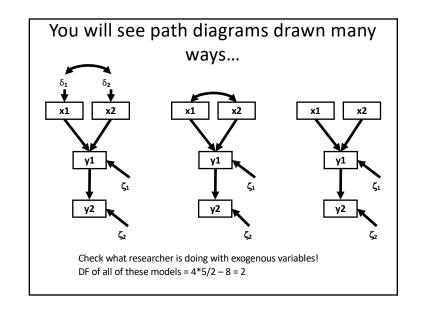
4 = 2a + b more knowns than **Overidentified** 

7 = 3b + a unknowns



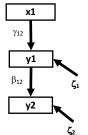






### Model Degrees of Freedom

$$DF = t_{max} - t$$



$$Cov(x,y1,y2)=$$
 y1 0.7 0.5

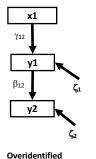
y2 0.2 0.8 0.3

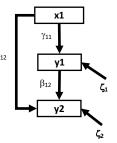
0.5

Estimating 5 parameters from 6 variance/covariance relationships

DF=1 Model Is <u>Overidentified</u>

# Identification in SEM # of Parameters v. Covariance Matrix

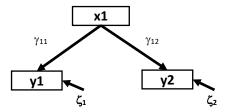




Just Identified

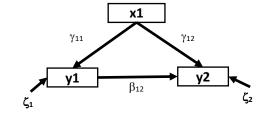
Just Identified models have no DF to evaluate fit

# Identification in SEM Many Regressions



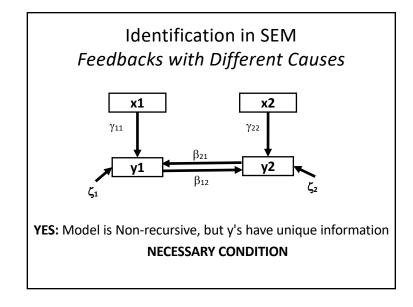
Yes: There are no relationships between endogenous variables
SUFFICIENT CONDITION

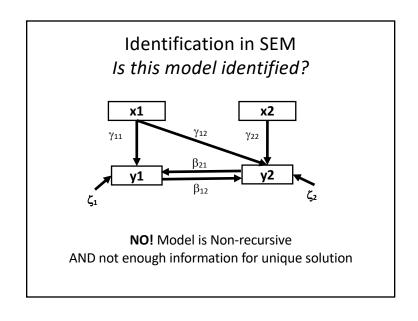
# Identification in SEM No Feedbacks

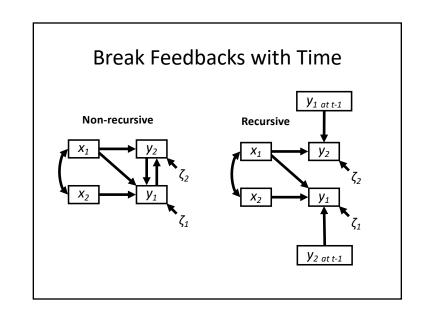


Yes: Model is Recursive SUFFICIENT CONDITION

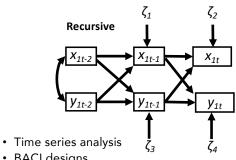
# Feedbacks and SEM Recursive Non-recursive $x_1$ $x_2$ $x_3$ Non-recursive = each item in a series is directly determined by the preceding item Non-recursive = there is bidirectionality (feedbacks) implicit in the model







### Cross-Lagged Panel Models to Solve Feedbacks!



- BACI designs
- Etc...

# A Likely Outline

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# Identification: Can I Fit My Model?

- **NECESSARY**: Fewer parameters than entries in covariance diagonal matrix (T-Rule)
- **SUFFICIENT**: And my model is recursive
- If you have feedbacks, then...
  - Break your model into time-lags (this is easy)
  - Or, ensure you have unique information for all variables (this can be hard!)

### Sample Size

- 1. The further you are in a model from an exogenous datagenerating, the weaker it's influence.
- 2. Our ability to detect these tapering effect sizes is proportional to our information (especially sample size) and the number of parameters being estimated.
- 3. Sample size sets an upper limit for the complexity of the model we can obtain.
- 4. Sample Size influences our ability to detect lack of model fit
  - This might not be a benefit...

# So...What's my Sample Size?

- 1. <u>Rules of thumb for sample size</u> at least 5 samples per estimated parameter
  - prefer 20 samples per parameter
  - Really, p<sup>3/2</sup>/n should approach 0 (Portnoy 1988)
- 2. Path coefficients add to our parameter list, not the variances

# Number of Estimated Parameters There are a total of 12 parameters shown. However, only 6 of these require unique information... Chi-sqr = 5.147; df = 3; p = .161 AIC = 29.147; NPAR = 12

### **Parameters Needing Unique Information** Variances & covariance of exogenous variables can be obtained from the data. For "pesticide", "Macroalgae", and "Grass", this removes 4 LNGammarids parameters. Error variances (and R2) for endogenous variables are calculated from other Grass Macroalgae Epiphytes parameters. This removes 2 parameters. Only 6 parameters require unique Chi-sqr = 5.147; df = 3; p = .161information. AIC = 29.147; NPAR = 12 Samples/parameters = 40/6 = 6.7.

### A Likely Outline

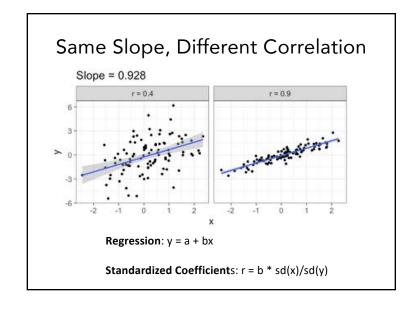
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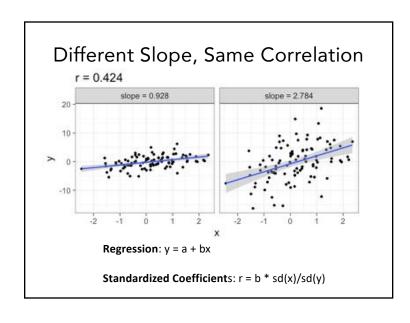
# Standardization

- Unstandardized coefficient = absolute strength of the pathway
  - "An 1 unit change in X results in some unit change in Y"

$$\beta_{xy \text{ std}} = b_{xy} * sd_x/sd_y$$

- Standardized coefficient = relative strength of the pathway
  - " A 1 standard deviation change in X results in some standard deviation change in Y"
  - Path Coefficient





Unstandardized	Standardized
Good for prediction: coefficients are in raw units	Good for ranking: coefficients are in equivalent units
Has direct real world meaning	Less clear real world meaning
Can be compared across pathways or models that have identical units	Can be compared across all pathways in all models

# A Likely Outline

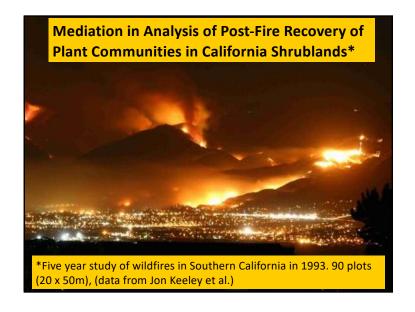
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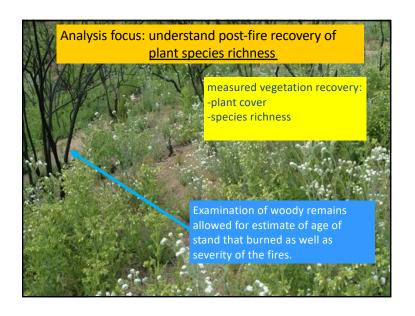
### What is lavaan?

- Stands for LAtent VAriable Analaysis
- Written by Yves Roseel in 2010
- Currently in version 5, but 6 coming soon
- Uses R lm syntax

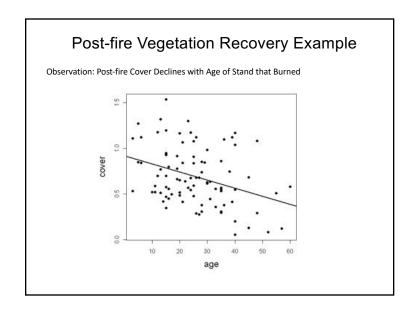
### A Reminder

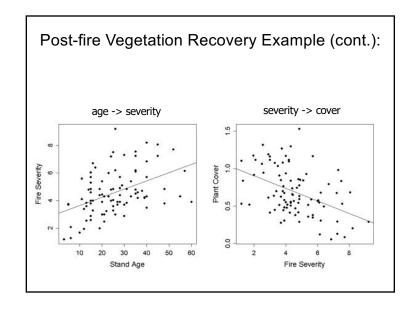
- 1. SOFTWARE IS A TOOL
- 2. IT IS NOT PERFECT
- 3. ALWAYS MAKE SURE IT IS DOING WHAT YOU THINK IT IS DOING!

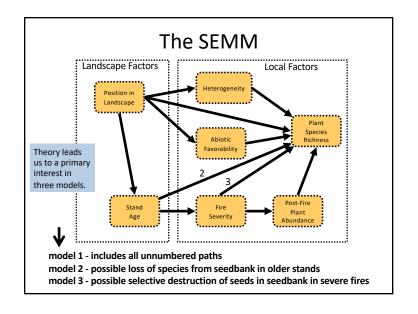


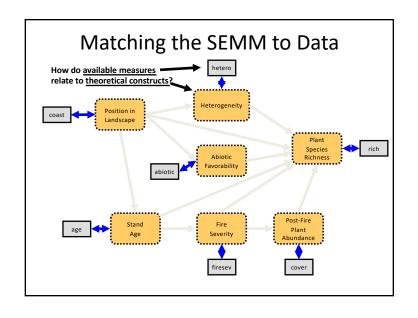


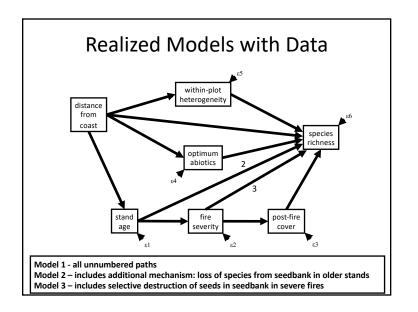


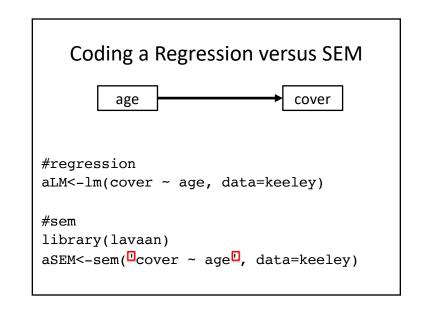


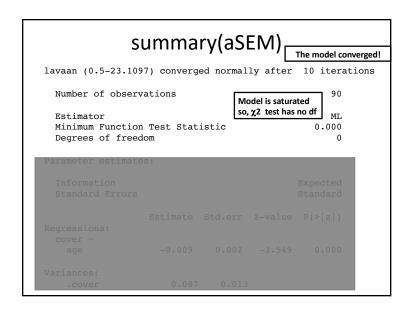


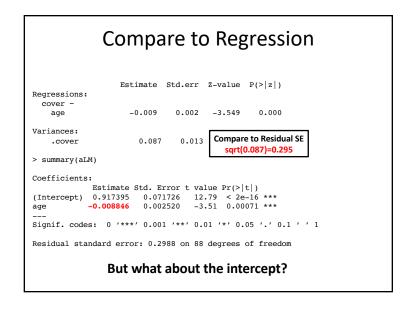




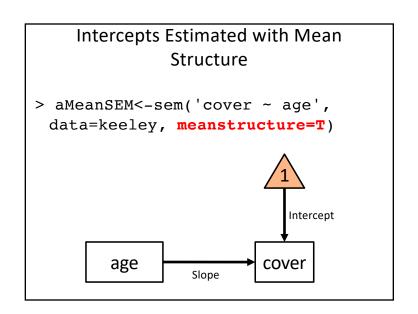






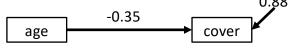


### Intercepts Estimated with Mean Structure > aMeanSEM<-sem('cover ~ age',</pre> data=keeley, meanstructure=T) > summary(aMeanSEM) Estimate Std.err Z-value P(>|z|)Regressions: cover ~ -0.009 0.002 -3.549 0.000 Intercepts: 0.917 0.071 12.935 0.000 Variances: 0.087 0.013 .cover



### **Standardized Coefficients**

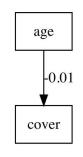
>standardizedSolution(aSEM)



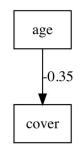
Also: summary(aSEM, standardized=T, rsq=T)

### Can I See It?

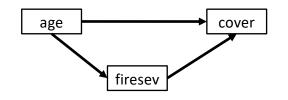
library(lavaanPlot)
lavaanPlot(model = aSEM, coefs = TRUE)

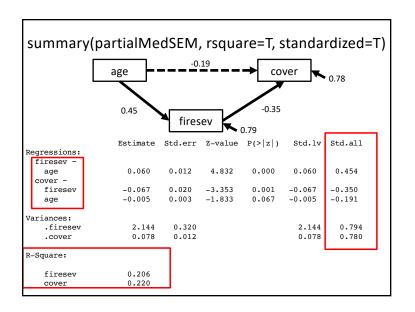


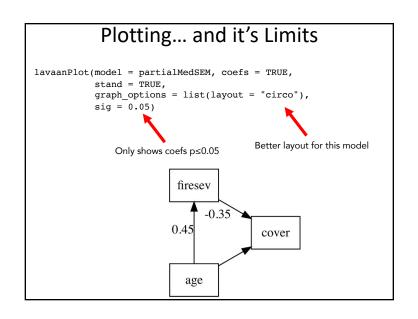
### Can I See It?

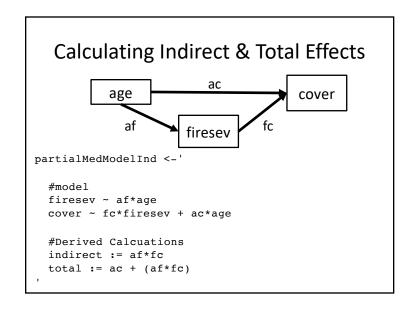


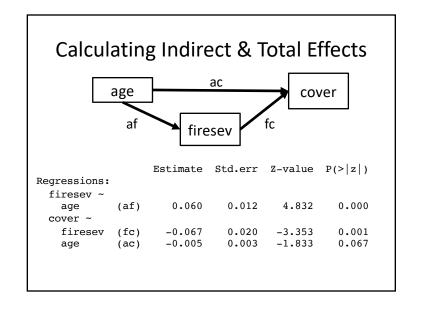
### **Indirect Effects and Fire**

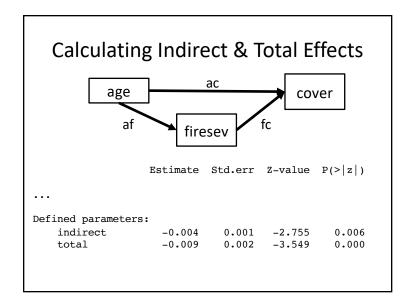


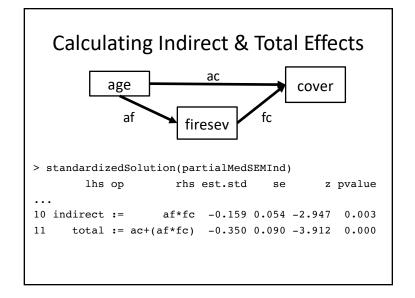






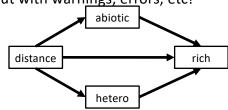






## Take Lavaan for a Spin!

- 1. Fit this model!
- 2. Fill in Standardized Coefficients and R<sup>2</sup> for this model
- 3. Calculate summed direct and indirect effects of distance on richness
- 4. Call out with warnings, errors, etc!



### The dreaded variance warning!

### Warning message:

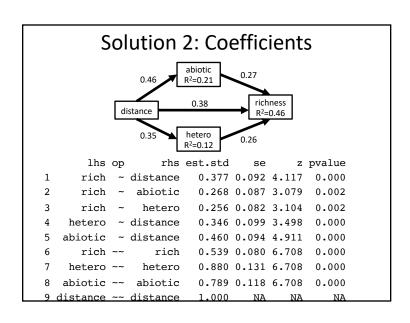
In lav\_data\_full(data = data, group =
group, cluster = cluster, :
 lavaan WARNING: some observed
variances are (at least) a factor
1000 times larger than others; use
varTable(fit) to investigate

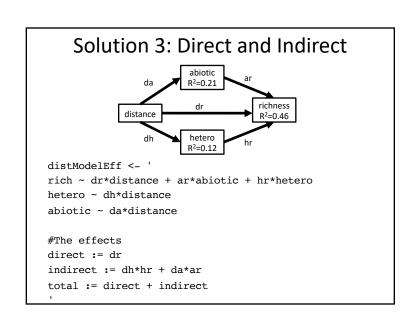
### **Diagnosing Error Issues**

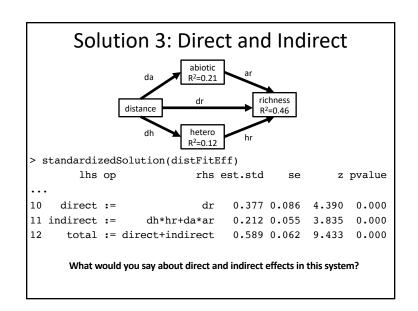
### Is this OK?

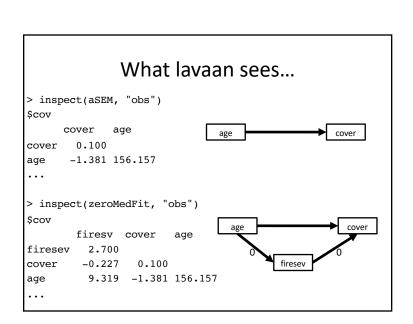
- 1. Does it indicate an outlier or data problem?
- 2. This is a likelihood algorithm problem can be fine!
- 3. If you are worried, rescale by 10s, see if answers change

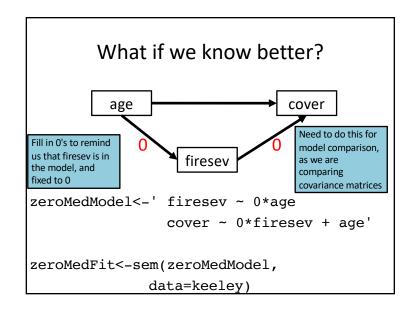
# #The Richness Partial Mediation Model distModel <- 'rich ~ distance + abiotic + hetero hetero ~ distance abiotic ~ distance' distFit <- sem(distModel, data=keeley) standardizedSolution(distFit)

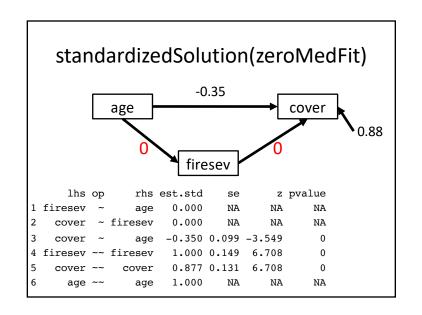


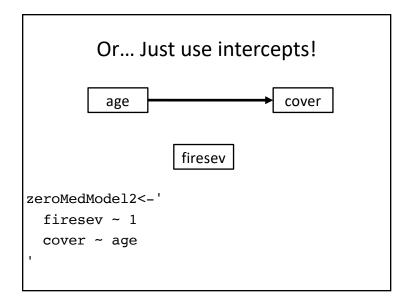


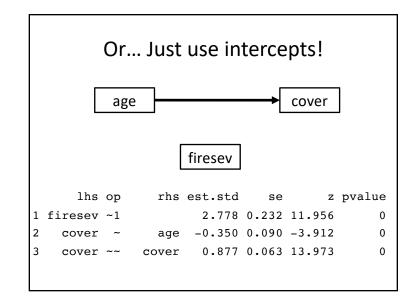


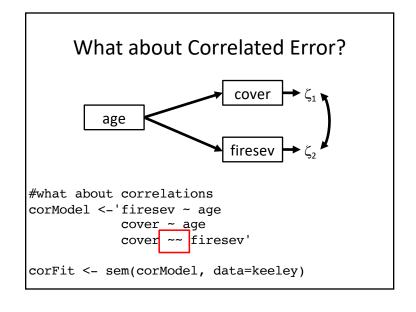


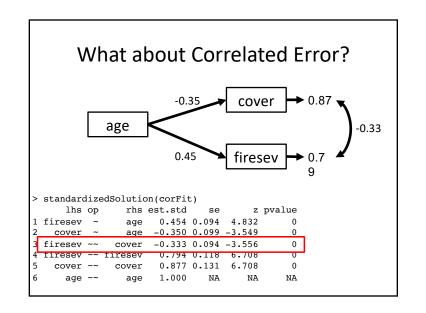






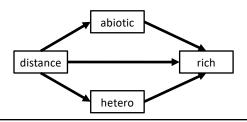






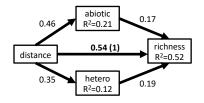
### **Final Exercise**

- 1. How does this model differ if the abiotic and hetero error correlate?
- 2. Fit assuming that there is a 1:1 (think 1 instead of 0) relationship between distance and richness
  - No error correlation please



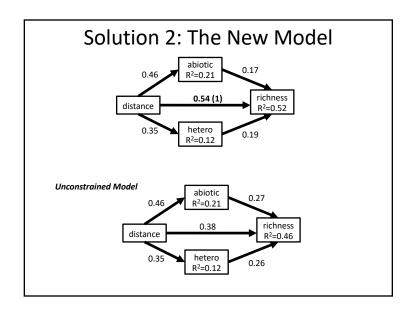
# Solution 1: Error Correlation 0.46 0.46 0.27 richness R²=0.21 0.26 corErrorModel <- ' rich ~ distance + abiotic + hetero hetero ~ distance abiotic ~ distance abiotic ~ hetero Coefficients unaffected

### Solution 2: The New Model



oneDistModel <- 'rich ~ 1\*distance + abiotic + hetero
 hetero ~ distance
 abiotic ~ distance'</pre>

oneFit<-sem(oneDistModel, data=keeley)
summary(oneFit, stdandardized=T, rsquare=T)</pre>



# Now that you're armed and dangerous...



ATOOLUSED BY PEOPLE WHO WANT TO MANIPULATE THOSE WHO DON'T UNDERSTAND MATH.

Fit your data to a **SIMPLE** model with lavaan