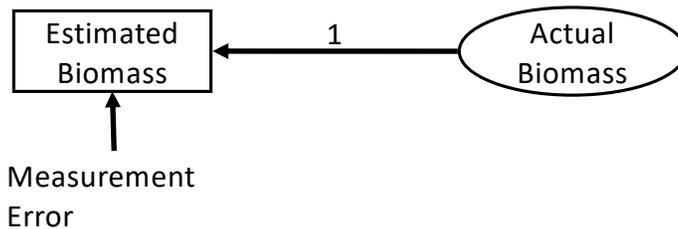


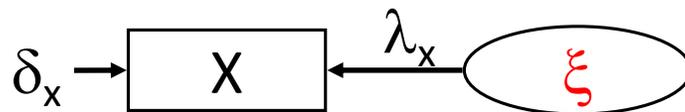
## Latent Variables



## Latent Variables

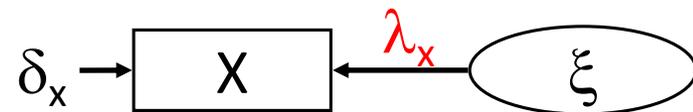
1. What is a latent variable?
2. Latent variables with multiple indicators
3. Fitting a latent variable
4. Factor Analysis
5. Latent Variables as a Response
6. Coping with measurement error

## What is a latent variable?



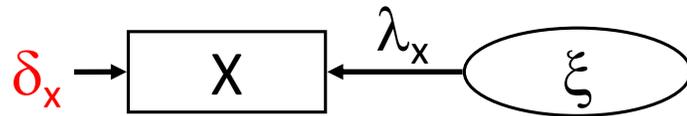
$\xi$  : A latent variable is a variable that is unmeasured, but is hypothesized to exist

## What is a latent variable?



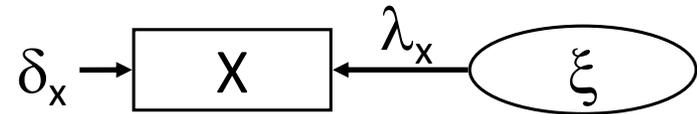
$\lambda_x$  : The relationship between a latent variable and its observed counterpart

What is a latent variable?



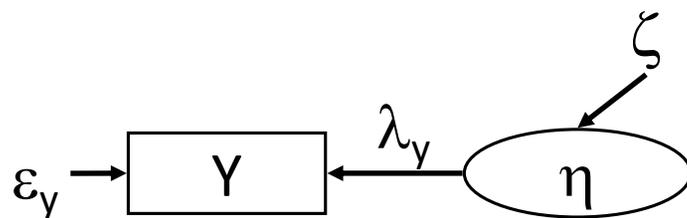
$\delta_x$ : The error in the measurement of  $x$  by  $\xi$

Latent Exogenous Variables



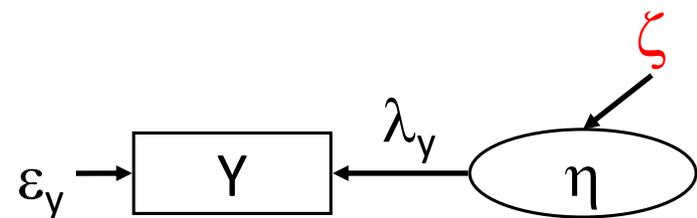
$$X = \lambda_x \xi + \delta_x$$

Latent Endogenous Variables



$$y = \lambda_y \eta + \epsilon_y$$

Latent Endogenous Variables

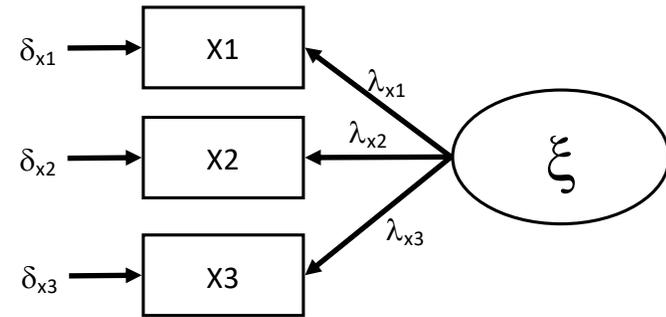


$\zeta$ : Variance in response to predictors

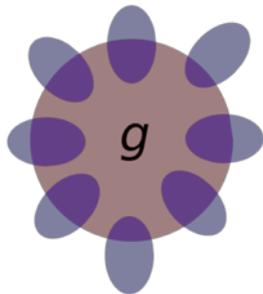
## Latent Variables

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## Latent Variables with Multiple Indicators

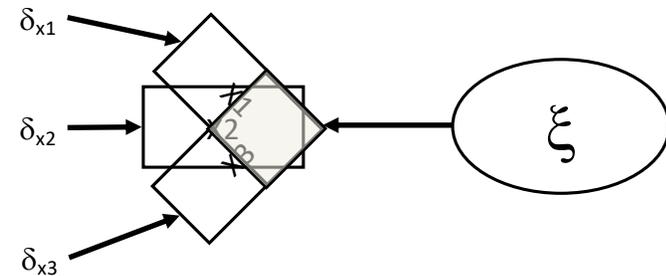


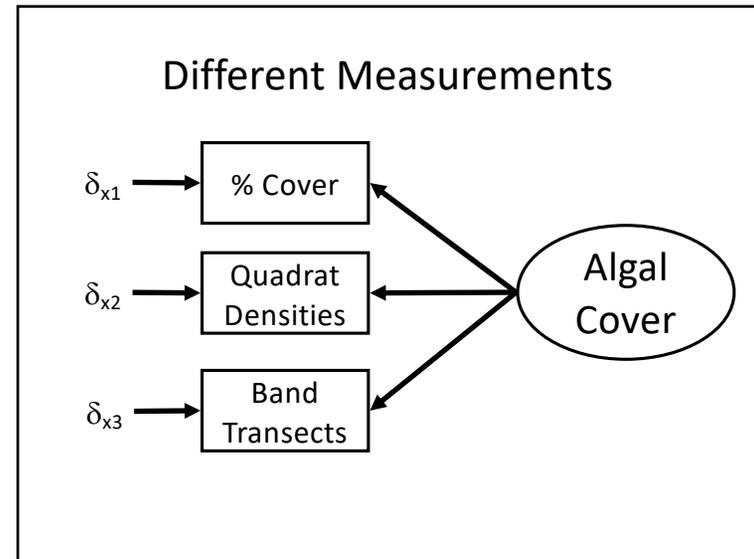
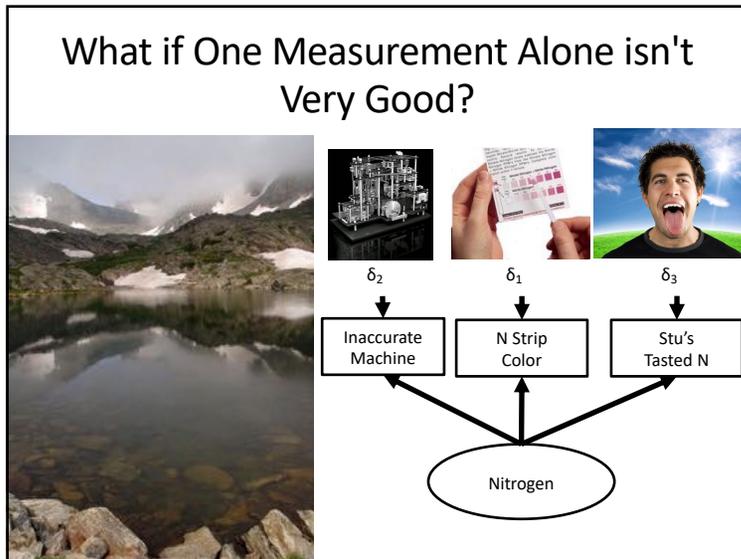
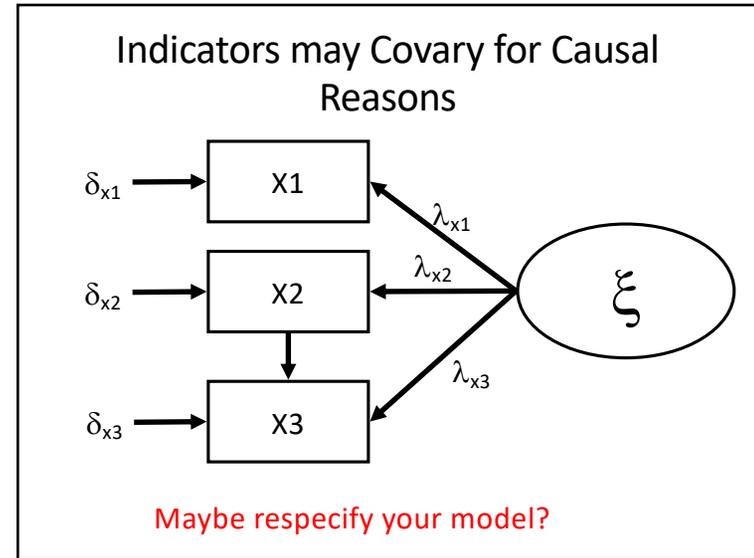
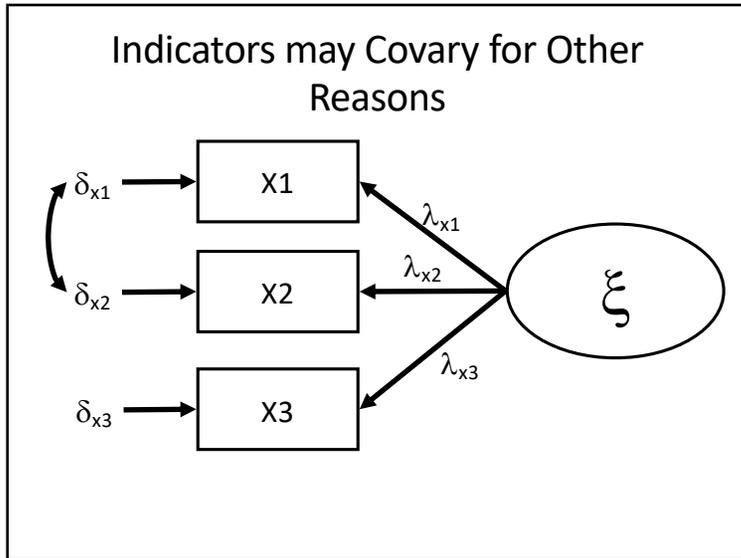
Latent variables represents shared information of indicators

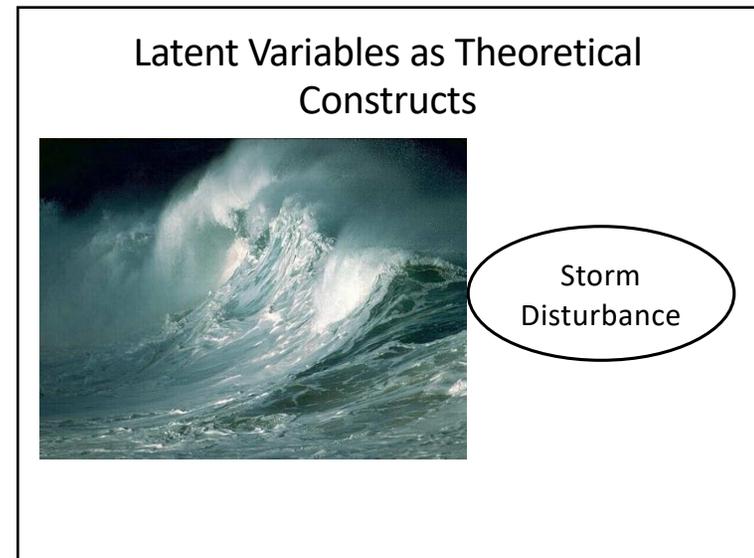
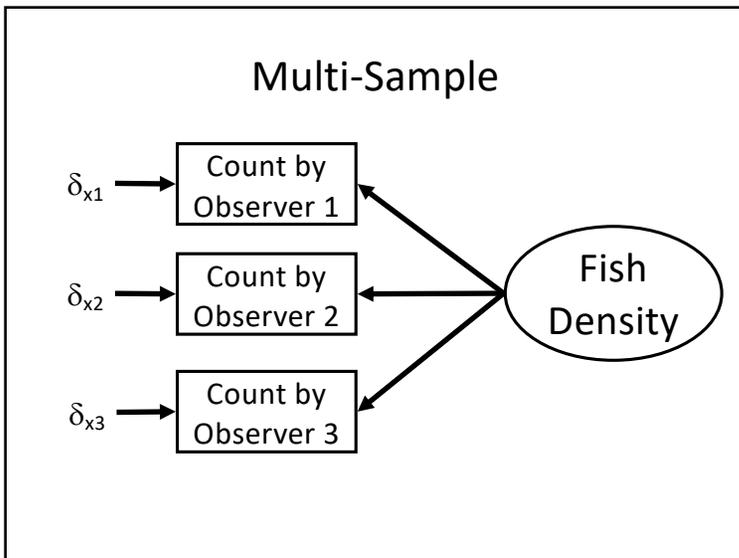
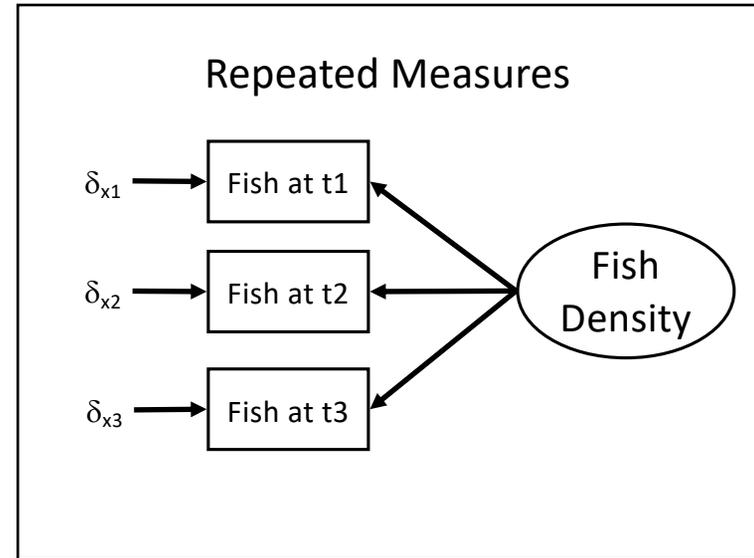
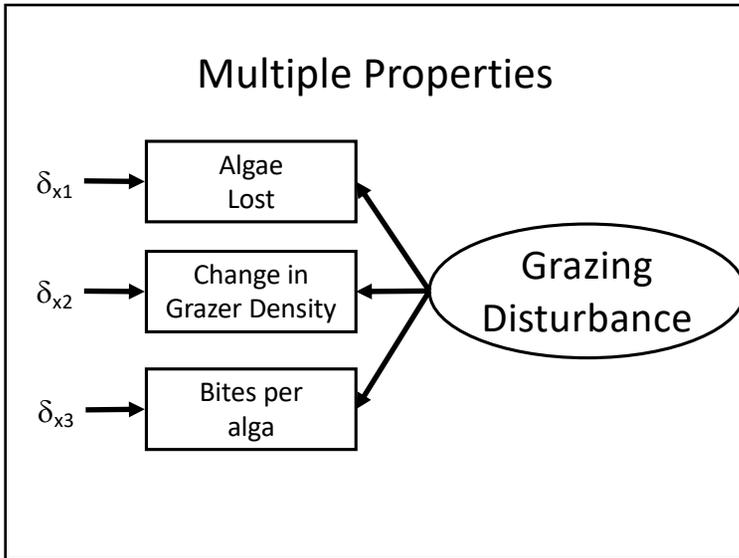


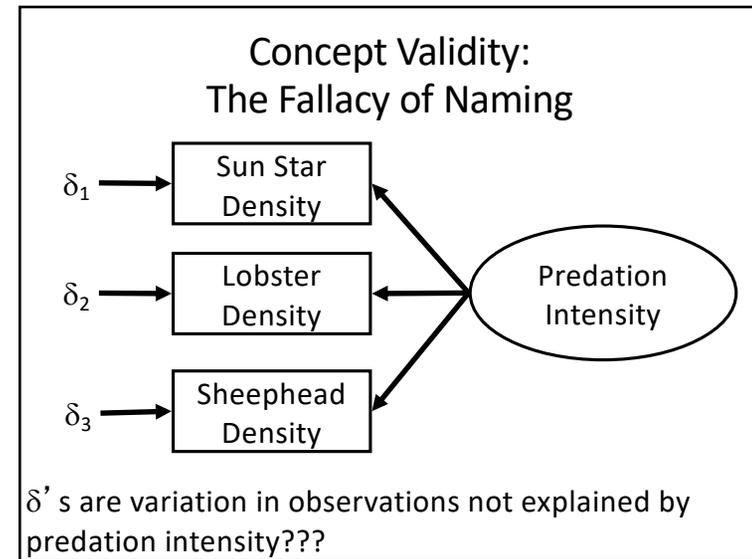
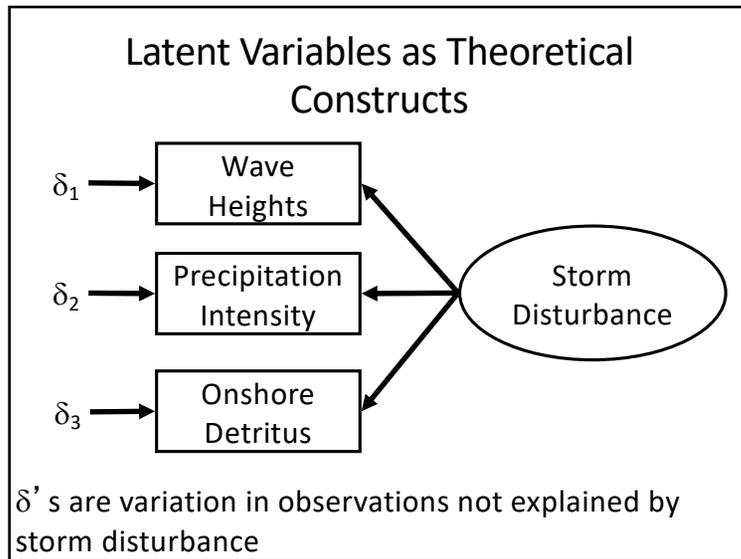
Common conceptual diagram of Spearman's analysis of "G-Theory," the idea of a generalized intelligence factor underlying test performance. Note shared variance of tests indicate "g."

Latent variables represents shared information of indicators









“The skepticism regarding 'latent variables' among many statisticians can probably be attributed to the metaphysical status of hypothetical constructs. On the other hand ... the concept of a 'good statistician' is not real, but nevertheless useful ...”

- Skrondal and Rabe-Hesketh

### Why Use Latent Variables with Multiple Indicators?

1. Better accuracy in measurement of relationships due to shared variation between indicators.
2. You cannot measure a theoretical construct!

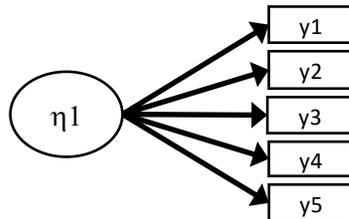
### Latent Variables

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### Evaluating Whether Indicators Will Make a Good Latent Variable

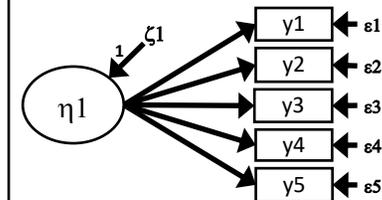
Observed Correlations:					
	y1	y2	y3	y4	y5
y1	1.000				
y2	0.933	1.000			
y3	0.813	0.834	1.000		
y4	0.773	0.728	0.693	1.000	
y5	0.730	0.646	0.603	0.969	1.000

- (1) Correlations among candidate indicators tell us whether data is consistent with what is implied by our model.
- (2) Note correlations are all strong, but not all equally strong. This shows us that these are not redundant indicators that are completely interchangeable.
- (3) In particular, variables y4 and y5 are more strongly correlated with each other than with the other vars.



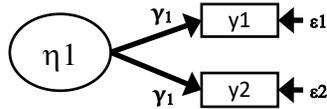
### Fixing Parameters for Identifiability

- (1) We need to "fix" some parameters (specify their values) for identifiability.
- (2) In this case, I chose to set variance of latent variable = 1.0.
- (3) The other choice would be to fix one of the path coefficients to 1.0.
- (4) Fixing a loading to 1 puts the latent variable on the scale of that indicator.
- (5) Test model with different paths fixed to 1 to ensure that your latent variable is good



### Latent Variable with Two Indicators

1. Problem - we have only one piece of information about  $y_1$  and  $y_2$  - their correlation (= 0.933).
2. Model has two path coefficients, plus the variance of our latent variable.
3. We can fix the value of our LV to 1, but that still leaves us with one known and two unknowns.



**One Solution:** when there are only two indicators, they have equal weight in the estimation of the LV (absent other information).  
**So, we can standardize the two measures, and only estimate a single parameter for both paths.**

NOT IDENTIFIED.

### Example: Aposematism in Poison Dart Frogs



Santos, J.C. & Cannatella, D.C. (2011). Phenotypic integration emerges from aposematism and scale in poison frogs. *Proc. Natl. Acad. Sci. U.S.A.*, 108, 6175–6180.

### What drives the evolution of warning coloration?

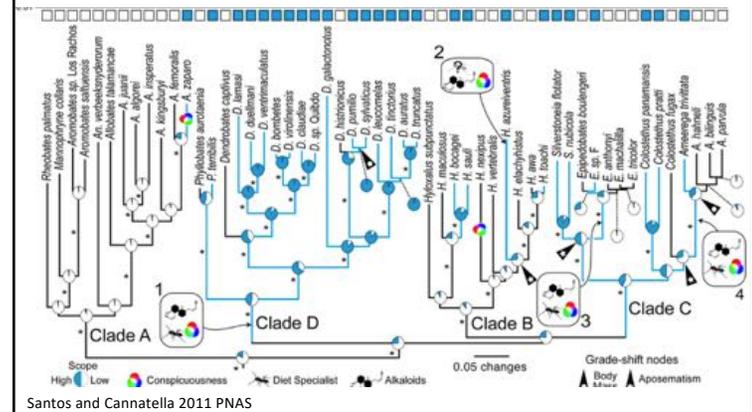


Toxicity?

Diet?

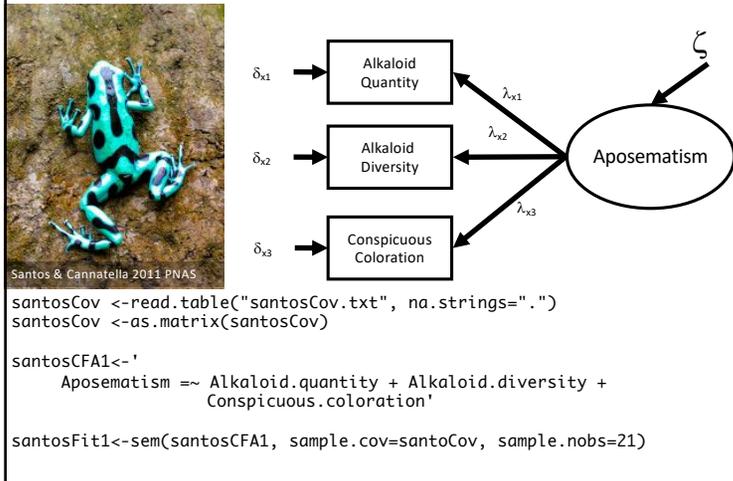
Body condition?

### A Phylogenetic Approach to SEM using Independent Contrasts

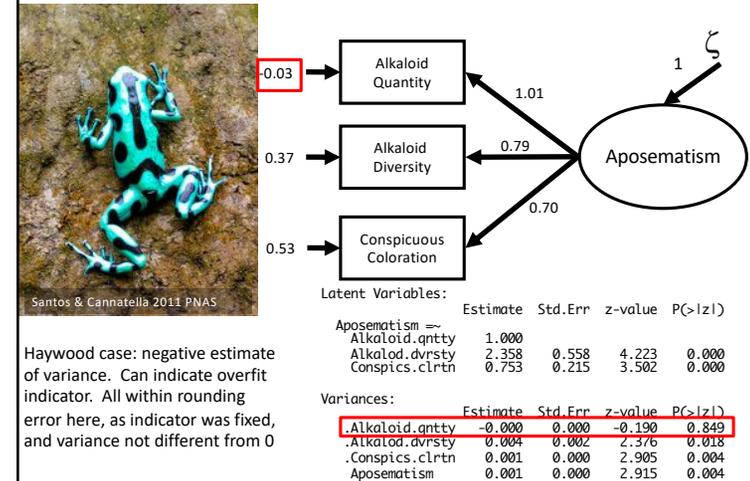


Santos and Cannatella 2011 PNAS

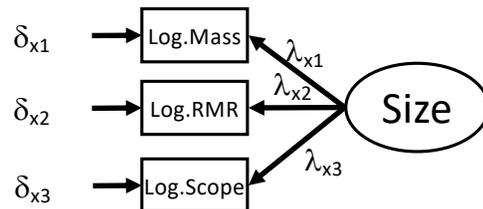
## Aposematism as a Latent Variable



## Aposematism as a Latent Variable

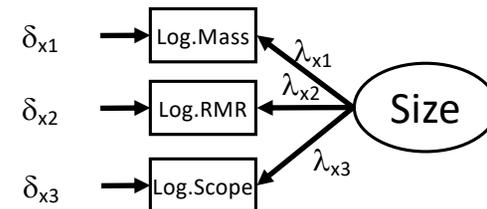


## Exercise: Fitting Latent Variables



- The Santos covariance matrix has many other variables related to frog diet and frog size – try out 'body size' as a latent variable

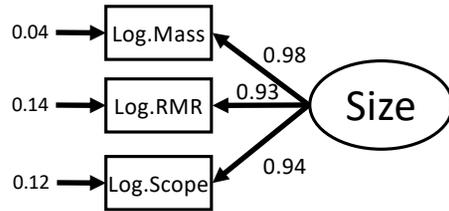
## Exercise: Fitting Latent Variables



```
santosSize<-'
Size =~ Log.Mass + Log.RMR + Log.Scope'

santosSizeFit<-sem(santosSize,
sample.cov=santosCov, sample.nobs=21)
```

### Exercise: Fitting Latent Variables



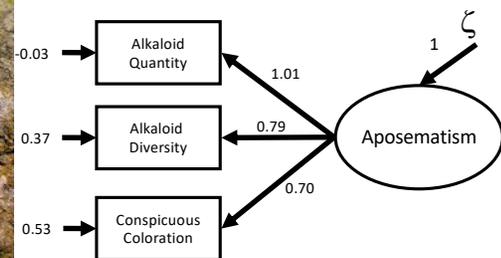
	Estimate	Std.err	z-value	P(> z )	Std.lv	Std.all
Latent variables:						
Size =~						
Log.Mass	1.000				0.096	0.981
Log.RMR	0.815	0.083	9.771	0.000	0.078	0.930
Log.Scope	0.861	0.084	10.228	0.000	0.082	0.938

Questions?

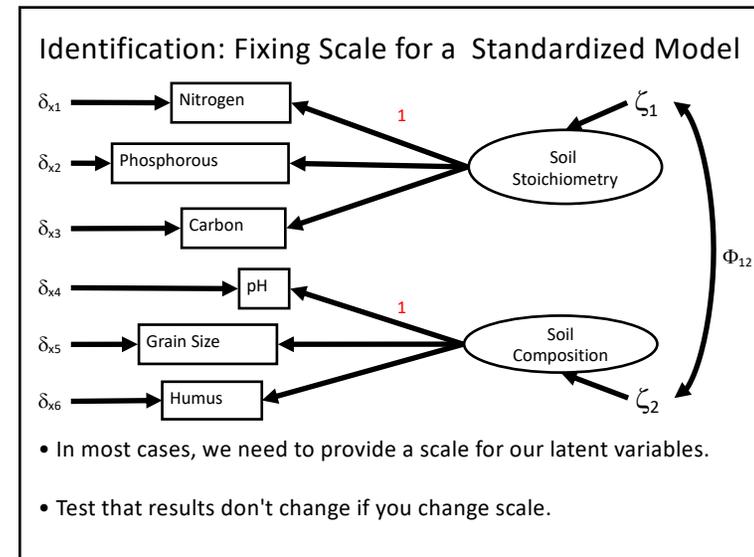
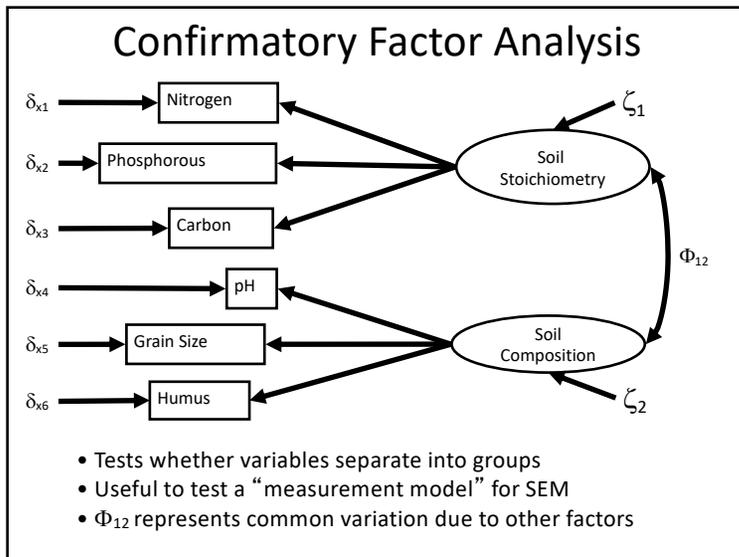
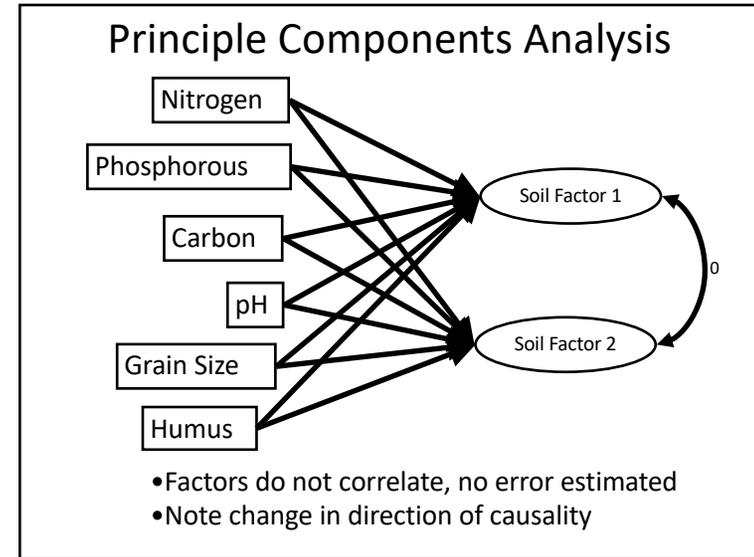
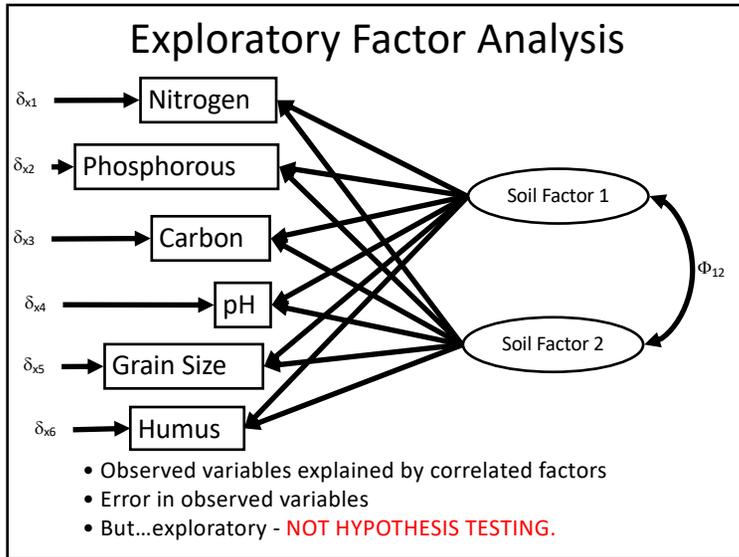
### Latent Variables

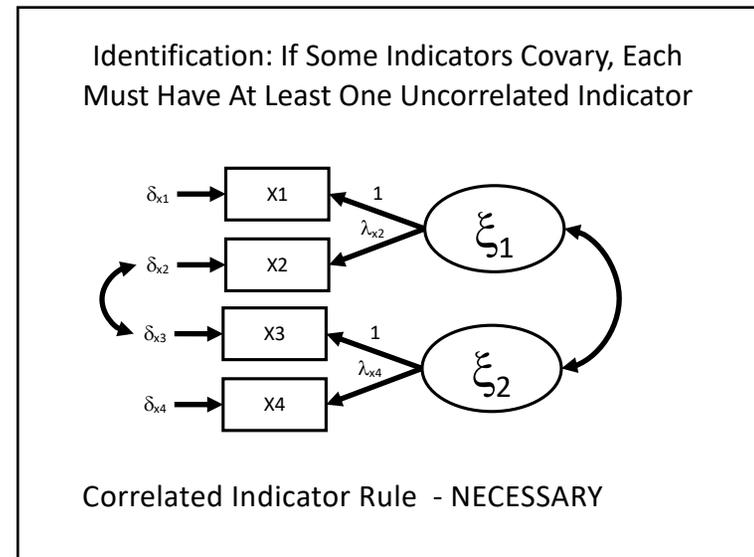
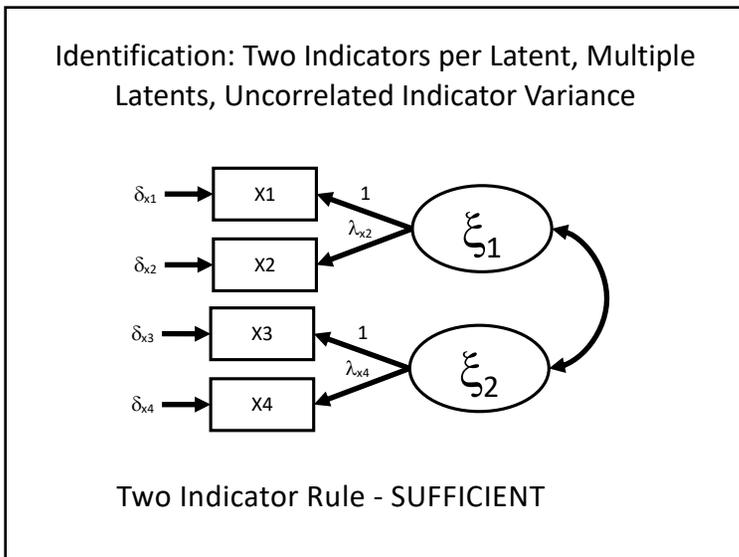
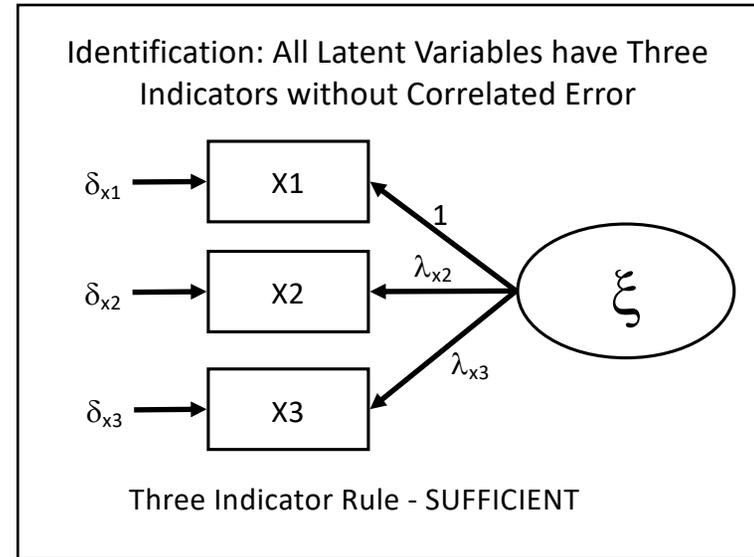
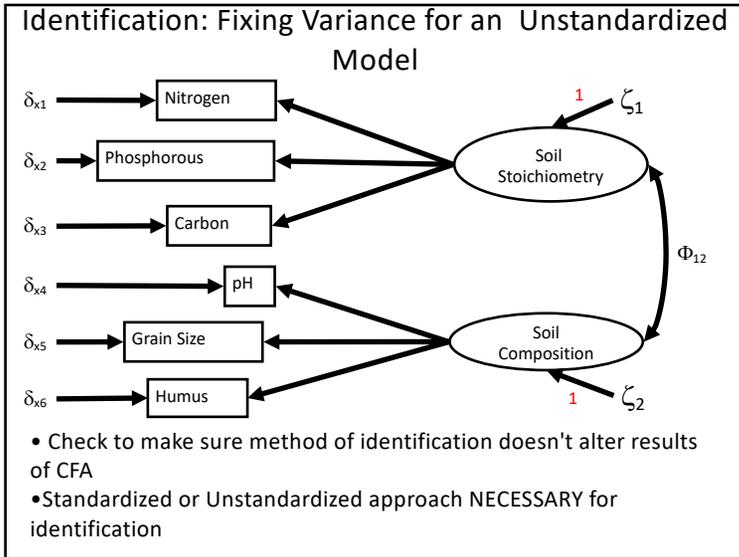
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### Example: Phylogenetic CFA!

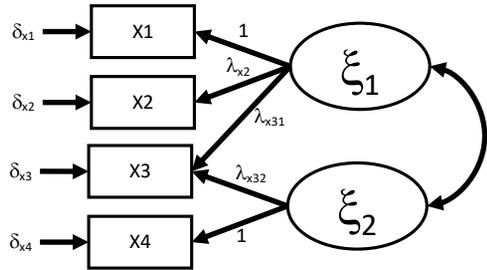


(Confirmatory Factor Analysis)



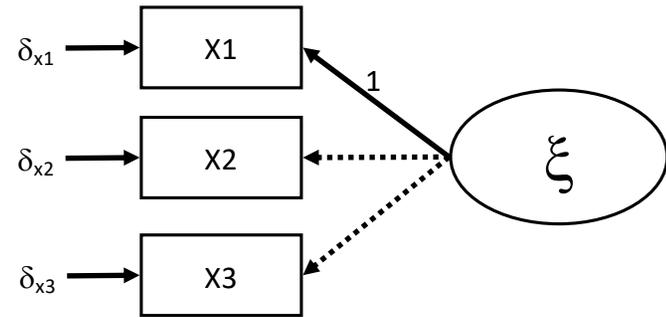


Identification: If Indicators Shared, Each Latent Needs One Unique Indicator



Shared Indicator Rule - NECESSARY

Empirical Underidentification Still Possible

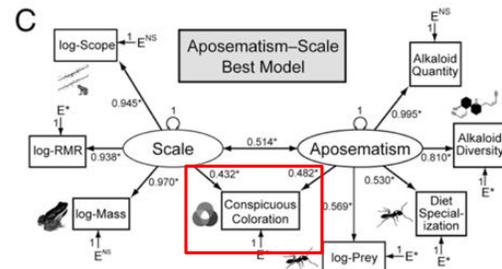


### General Rules for Identification

1. T-rule still holds – necessary
2. Standardization - necessary
3. Three indicator rule – sufficient
4. Two Indicator rule – sufficient
5. Correlated Indicator rule – necessary
6. Shared Indicator Rule - necessary

**N.B. None of these are both necessary and sufficient!**

### Exercise: Phylogenetic CFA!



$\chi^2 = 16.242$ ,  $df = 18$ ,  $P_{10} = 0.576^{NS}$   
 $AIC = -502.361$ ,  $BIC = -484.438$   
 $CFI = 1.000$ ,  $TLI = 1.022$ ,  $SRMR = 0.096$

```
santosCFA2 <- paste(santosCFA1,
```

```
  Aposematism =~ Ant.Mite.Specialization+log.Prey
```

```
  Scale =~ Log.Mass+Log.RMR+Log.Scope+Conspicuous.coloration',
```

```
  sep="\n")
```

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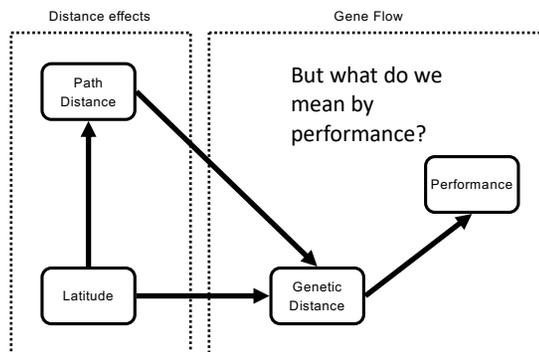
**The Example: The general performance of transplanted plants as a function of their genetic dissimilarity to local populations.**

from:

Travis, S.E. and Grace, J.B. 2010. Predicting performance for ecological restoration: a case study using *Spartina alterniflora*. *Ecological Applications* 20:192-204.

## The Theory Driving the Modeling

Theory suggests following for transplanted *Spartina*.



## Performance as a latent construct

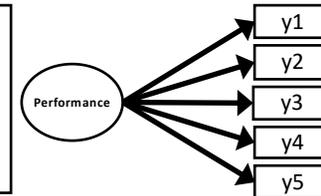
Performance implies complex, intercorrelated response by many traits reflecting some underlying, unmeasured cause or causes.

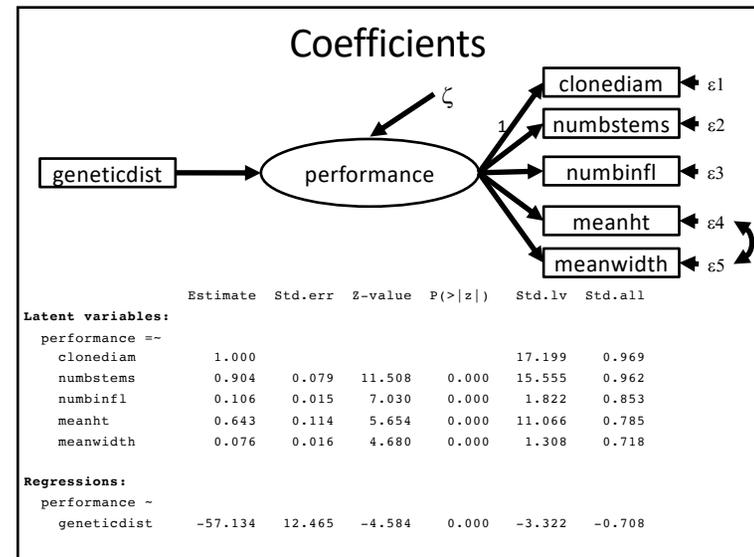
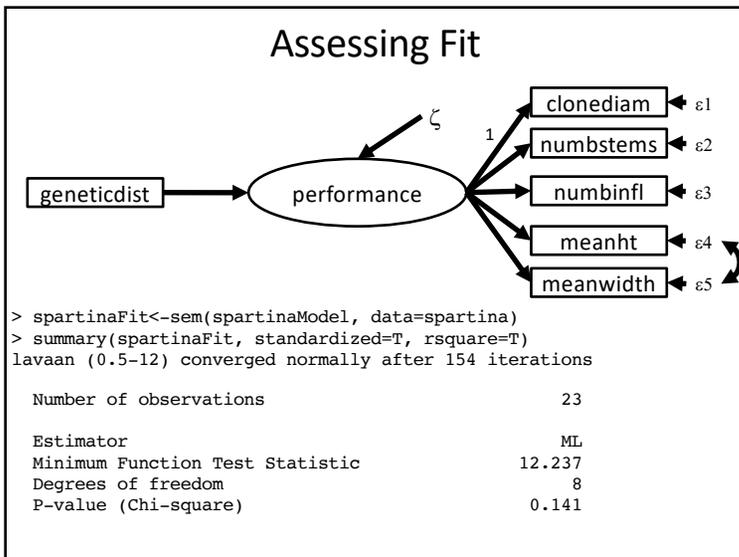
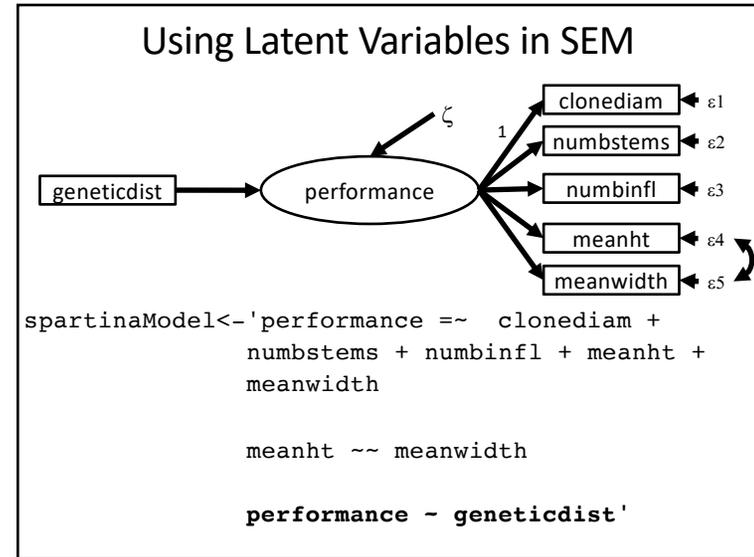
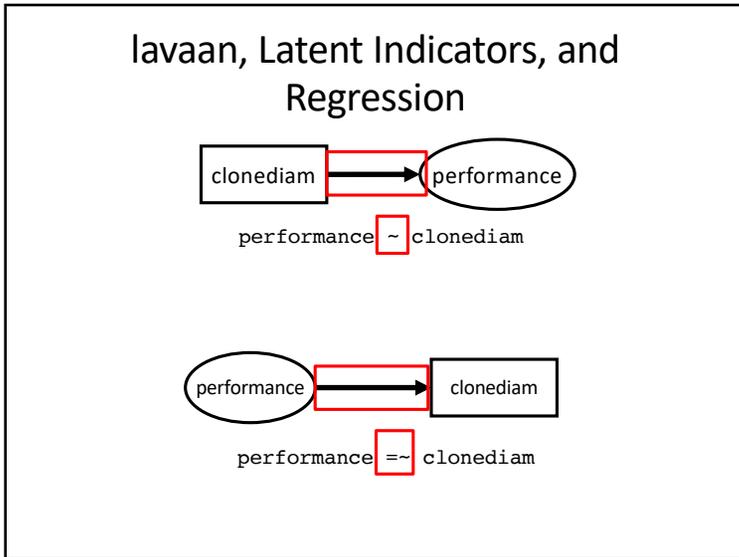
Simply linking a bunch of measures to a latent variable does not mean you have correctly specified the model.

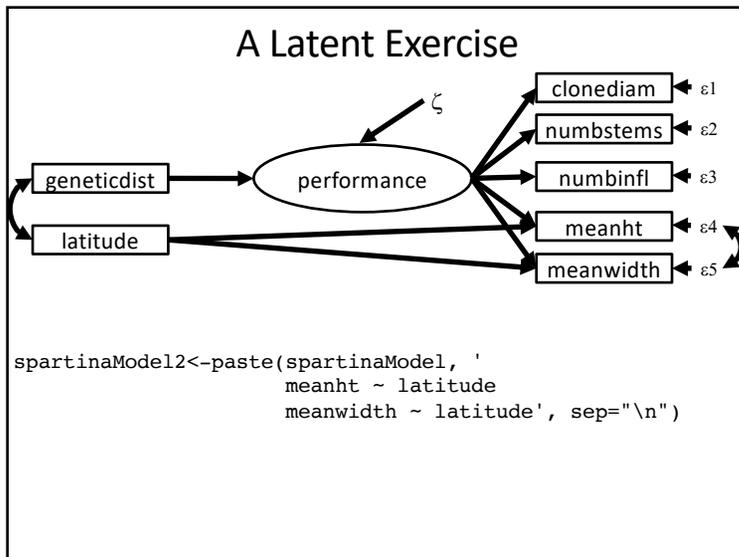
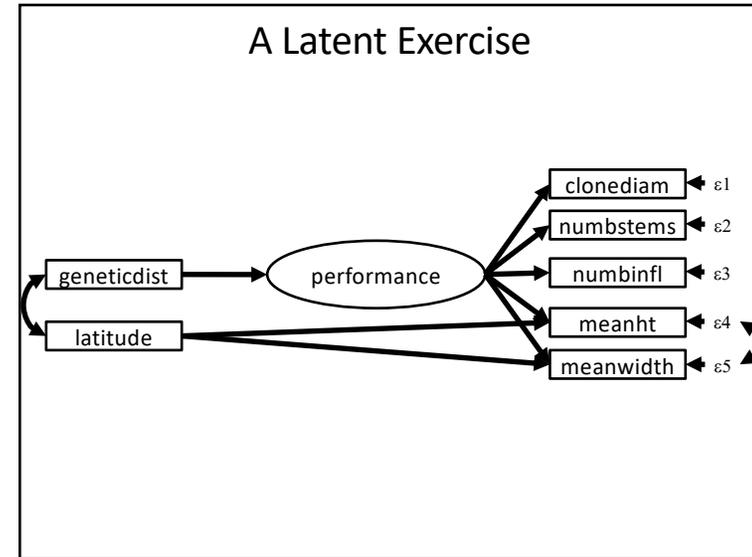
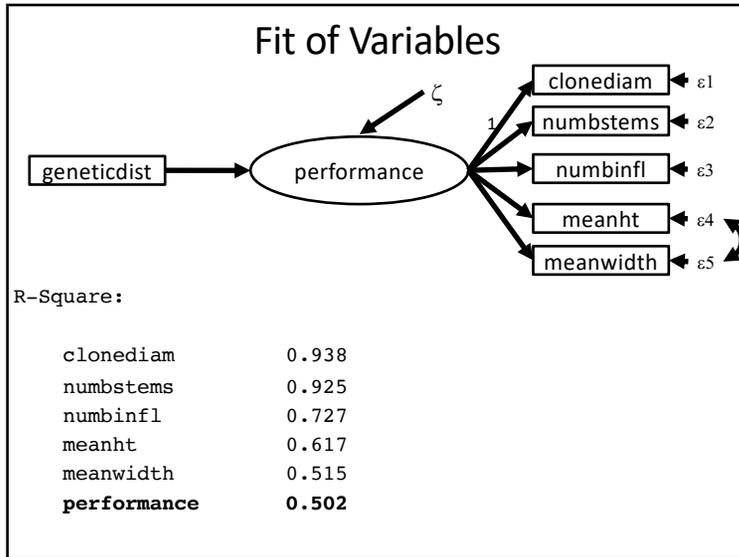
Stay focused on the **causes** of an indicator to aid latent variable model specification

Model hypothesizes five observed responses whose intercorrelations are consistent with a single underlying cause.

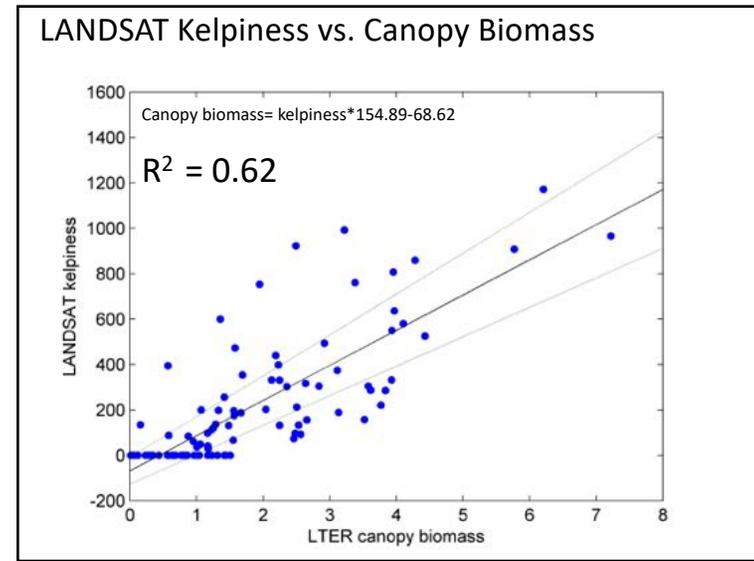
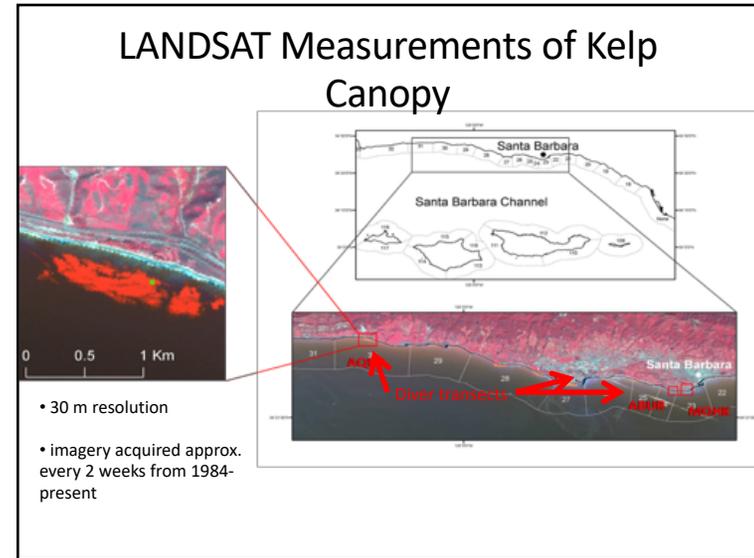
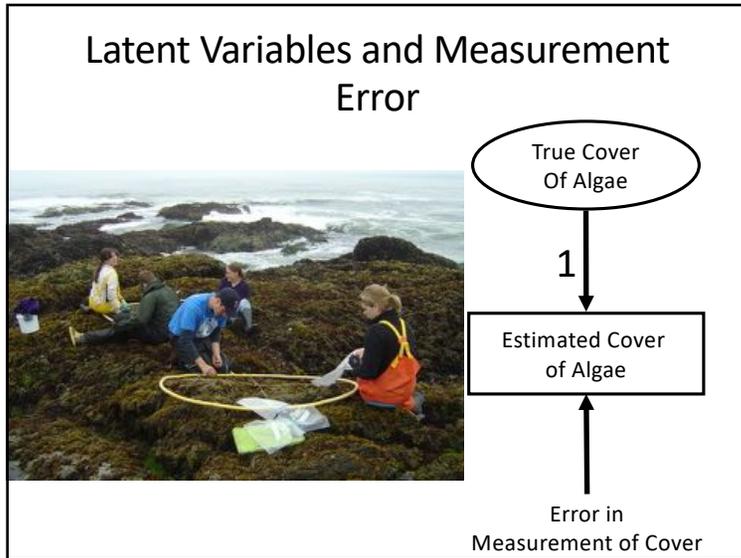
There may be other things that influence y1-y5 and affect their observed intercorrelations.







- ### Latent Variables
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### LANDSAT Kelpiness vs. Canopy Biomass

We can transform satellite data to canopy biomass, and fix the unstandardized loading to 1.

$\delta_x$  → Measured Canopy Biomass ← (1) True Canopy Biomass

**But what about error?**

We know that  $R^2 = 1 - \text{estimated var}/\text{observed var}$

$\delta_x = (1 - R^2)$

Unstandardized Measurement Error =  $\delta_x * \text{var}(\text{Measured Canopy Biomass})$

### Let's Look at the LTER data: Data Prep

```

library(lavaan)
lter<-read.csv("./lter_kelp.csv")

#1) Calculate fitted values for spring biomass
#landsat observations to biomass
lter$landsat_spring_biomass<-154.89*lter$spring_canopy+68.62

#2) Calculate fitted values for summer biomass
#summer kelp counts to biomass y=0.08x+0.01 r^2=0.79
lter$summer_kelp_biomass<-0.08*lter$kelp+0.01

#3) Transform fitted values for easier fitting
#transformation for easier fitting
lter$summer_kelp_biomass<-log(lter$summer_kelp_biomass+1)
lter$landsat_spring_biomass <-log(lter$landsat_spring_biomass +1)
    
```

### LANDSAT Kelpiness vs. Canopy Biomass

Fit this Model!

LANDSAT Spring Canopy Biomass → 0.50 (0.26) → Measured Summer Kelp Biomass ← 0.75

`noerror<- 'summer_kelp_biomass ~ landsat_spring_biomass'`

(unstandardized coefficients)

### LANDSAT Kelpiness vs. Canopy Biomass

True Spring Kelp Biomass → Measured Summer Kelp Biomass ←  $\epsilon$

True Spring Kelp Biomass → (1) → Measured Spring Canopy Biomass → 0.38 → Measured Summer Kelp Biomass

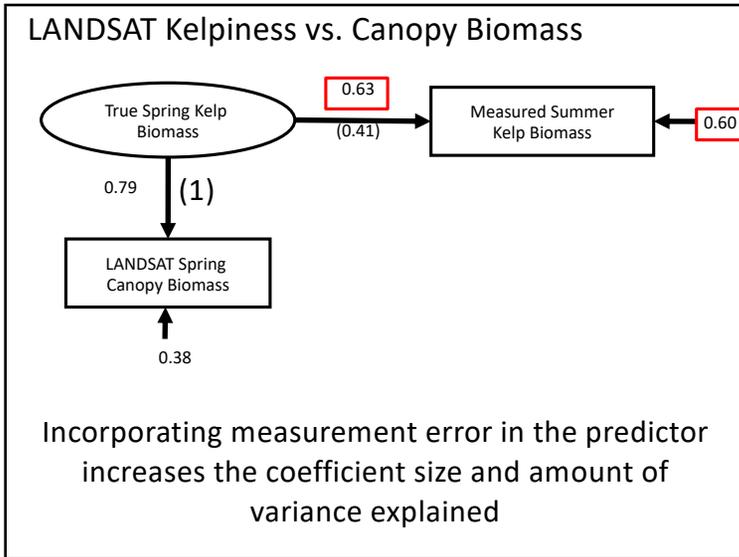
$R^2=0.62, 1-0.62=0.38$

```

var(lter$landsat_spring_biomass, na.rm=T)*(0.38)
[1] 3.762301

errorCanopy<- '
true_spring_biomass =~ 1 landsat_spring_biomass
summer_kelp_biomass ~ true_spring_biomass

#error
landsat_spring_biomass =~ 3.762301 landsat_spring_biomass
    
```



### Exercise: Code this model!

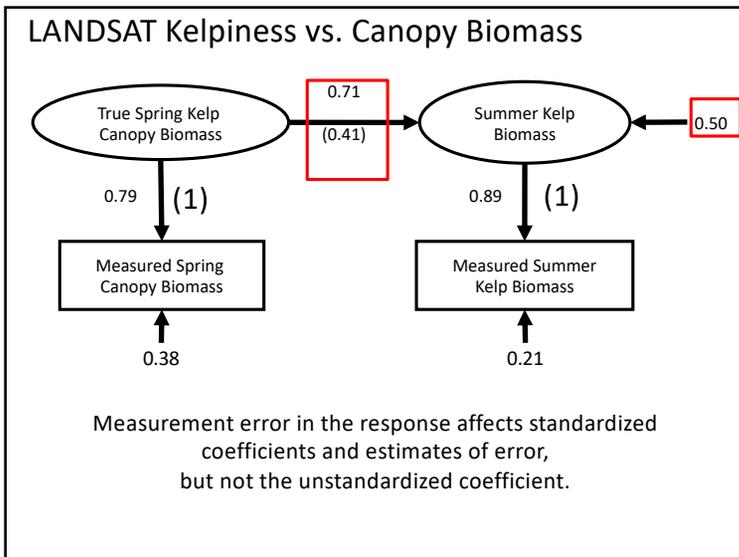
```

var(lter$summer_kelp_biomass, na.rm=T)*(0.21)
[1] 0.5495345

error_both<-'
true_spring_biomass =~ 1*landsat_spring_biomass
true_summer_biomass =~ 1*summer_kelp_biomass

true_summer_biomass ~ true_spring_biomass

#error
landsat_spring_biomass ~ 3.762301*landsat_spring_biomass
summer_kelp_biomass ~ 0.5495345* summer_kelp_biomass
    
```



- ### Reasons to Think about Measurement Error
1. We know our measurements are not perfect!
  2. Increased accuracy in estimating relationships between variables.
  3. Increasing explanatory power of your hard-earned measurements.

