Introduction to Likelihood Methods for SEM

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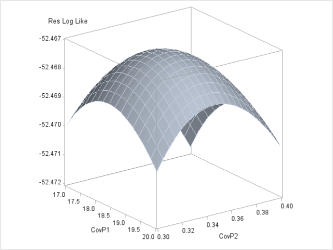


$$\Sigma = \Sigma(\Theta)$$

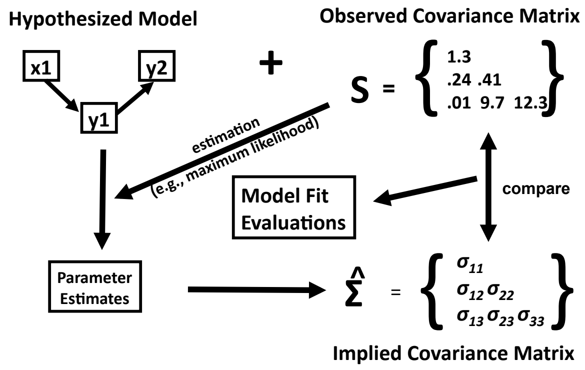
Why the Likelihood Approach?

- Piecewise fitting is flexible, but, does not accommodate full range of SEM complexity
- No latent variables
- No non-recursive relationships
- Cannot compare wide range of competing models simply

A Likely Outline

1. What is different about fitting using likelihood and covariance matrices?
2. Identifiability
3. Introduction to lavaan

How does ML Estimation Work?


Hypothesized Model
x1
y2
y1
+
Observed Covariance Matrix
S = { 1.3 / .24 .41 / .01 9.7 12.3 }
estimation
(e.g., maximum likelihood)
Model Fit Evaluations
compare
Parameter Estimates
Σ̂ = { σ11 / σ12 σ22 / σ13 σ23 σ33 }
Implied Covariance Matrix

The Maximum Likelihood Fitting Function

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

S = Sample covariance matrix
Σ = Fit covariance matrix
p = endogenous variables
q = exogenous variables

When S and Σ are equal, terms 1 and 3 = 0 and terms 2 and 4 = 0.
Thus, perfect model fit yields a value of F_{ML} of 0.

Assumptions Behind F_{ml}

- Multivariate normality
  - Test with multivariate Shapiro-Wilk's Test (library mvnormtest)
  - In particular, no skew
  - Violations biases parameter error and tests of model fit
- No missing data in calculation of S
  - Will bias your estimates
- No redundant variables
  - S must be positive definite
- Sample size is large
  - Advice varies – take home, get as much data as possible
  - 10-20 samples per param, n=p^3/2, etc…

Why FML? Alternatives?

F_{ML} is unbiased, scale invariant, best estimator

F_{GLS}=0.5*tr[(S- Σ(Θ))^2]

- A.K.A. the ULS criterion
- Least squares!
- Sensitive to scale of variables

F_{WLS}=0.5*tr[{(S- Σ(Θ))W^{-1}}^{2})]

- A.K.A. the ADF criterion – no normality assumption
- Weighted: flexible
- Scale free
- Asymptotically χ^2 distributed
- Sensitive to fat or thin tailed data
- Sensitive to sample size (n>1000)

A Likely Outline

1. What is different about fitting using likelihood and covariance matrices?
2. Identifiability
3. Introduction to lavaan

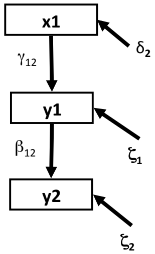
Identifiability Revisited

1. For the model parameters to be estimated with unique values, they must be <u>identified</u>. We need as many known pieces of information as we do unknown parameters.

2. Several factors can prevent identification, including:
   a. too many paths
   b. certain kinds of model specifications can make parameters unidentified
   c. multicollinearity
   d. combination of a complex model and a small sample

3. Some software checks for identification (in something called the information matrix) and lets you know which parameters are not identified.

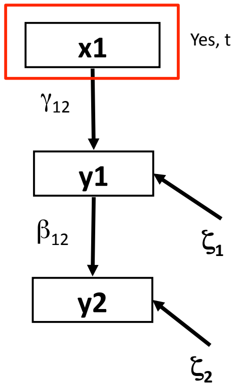
Whither the T-Rule
of Parameters v. Covariance Matrix



$$\text{Cov(x,y1,y2)=}\quad \begin{array}{cccc} & x1 & y1 & y2 \\ x1 & 0.5 & & \\ y1 & 0.7 & 0.5 & \\ y2 & 0.2 & 0.8 & 0.3 \end{array}$$

- # Parameters ≤ # Unique Entries in a Covariance Matrix
- **Necessary** condition for identification
- T-rule: $t \leq (p+q)(p+q+1)/2$
- t=# params, p=# endogenous variables, q=# exogenous variables
- Model DF=t_{max}-t

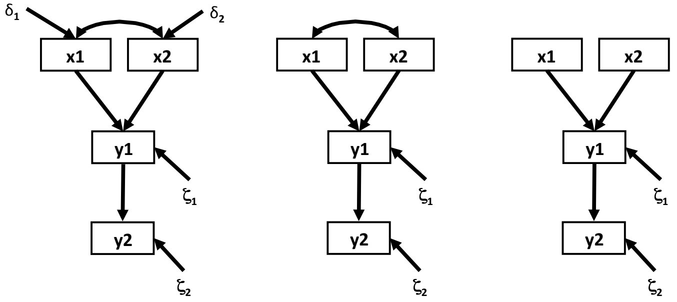
How Do I Count the Number of Parameters?



Yes, there is a variance here

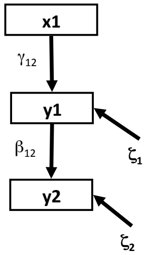
If variance and covariances among exogenous variables is not shown
T-rule: $t \leq (p+q)(p+q+1)/2-q(q+1)/2$

You will see path diagrams drawn many ways…



Check what researcher is doing with exogenous variables!
DF of all of these models = 4*5/2 – 8 = 2

Identification in SEM
of Parameters v. Covariance Matrix



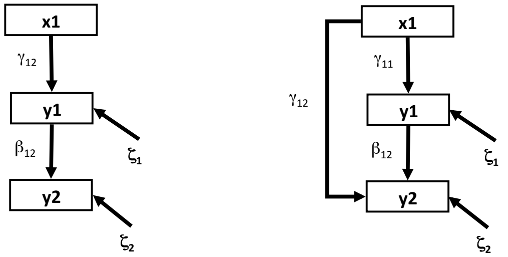
		x1	y1	y2
	x1	0.5		
Cov(x,y1,y2)=	y1	0.7	0.5	
	y2	0.2	0.8	0.3

Estimating 5 parameters from 6 variance/covariance relationships

DF=1

Model Is Overidentified

Identification in SEM
of Parameters v. Covariance Matrix

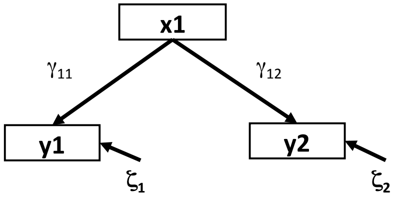


Overidentified

Just Identified

Just Identified models have no DF to evaluate fit

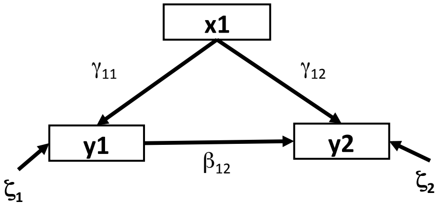
Identification in SEM
Is this model identified?



Yes: There are no relationships between endogenous variables

SUFFICIENT CONDITION

Identification in SEM
Is this model identified?

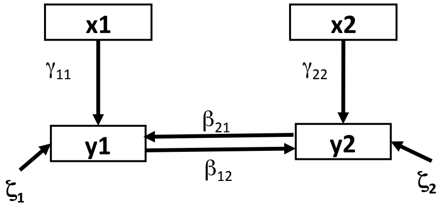


Yes: Model is Recursive

SUFFICIENT CONDITION

Identification in SEM

Is this model identified?

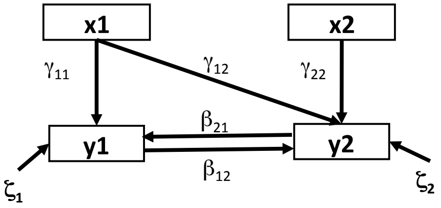


YES: Model is Non-recursive, but y's have unique information

NECESSARY CONDITION

Identification in SEM

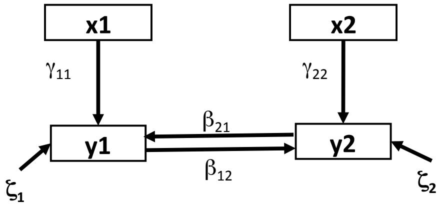
Is this model identified?



NO! Model is Non-recursive
AND not enough information for unique solution

Identification in SEM

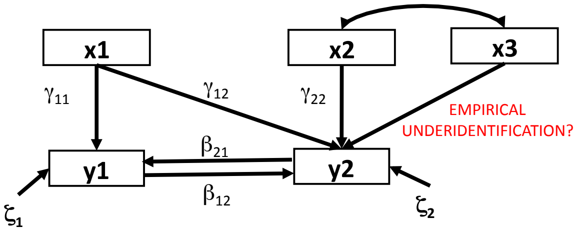
The Order Condition



- G = # incoming paths
- H = # of exogenous vars+ # indirectly connected endogenous vars
- G ≤ H
- **NECESSARY CONDITION**

Identification in SEM

Is this model identified?



NO! Everything that affects y2 affects y1 – Fails *Rank Test*

SUFFICIENT CONDITION

Rules of Identification

- t ≤ (p+q)(p+q+1)/2
  - p= # of y variables, q=# of x variables
  - necessary
- No paths between endogenous variables
  - sufficient
- Model is recursive
  - sufficient
- Order: G ≤ H
  - necessary
- Rank: see Kline 2005 or Bollen 1989
  - Endogenous vars must be affected uniquely
  - sufficient

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Packages for Fitting an SEM in R

- lavaan – http://www.lavaan.org
  - Initially based on Mplus
  - Similar to R linear model syntax

- sem – http://socserv.socsci.mcmaster.ca/jfox/Misc/sem/
  - RAM & equation syntax
  - good documentation
  - restricted, not always able to fit models

- openMx - http://openmx.psyc.virginia.edu/
  - Based off of Mx
  - Incredibly flexible, powerful

- REQS - http://www.mvsoft.com/
  - Interface for commercial EQS software
  - Flexible, developed by SEM statisticians

Extensions off of lavaan

- lavaan.survey – http://www.lavaan.org
  - corrects tests based on complex survey design
  - Accounts for clustering/nesting using `survey` package

- semTools - https://github.com/simsem/semTools/wiki
  - grab bag of additional tools
  - imputation and fit index tools
  - multivariate skew and kurtosis indices
  - Creation of new variables
  - and more! Constantly growing!

- semPlot - https://github.com/SachaEpskamp/semPlot/
  - plots fit models
  - can also be used to plot a piecewise SEM
  - works using `qgraph`

Lavaan: A Package for Fitting SEMs in R Using Covariance Matrix Methods

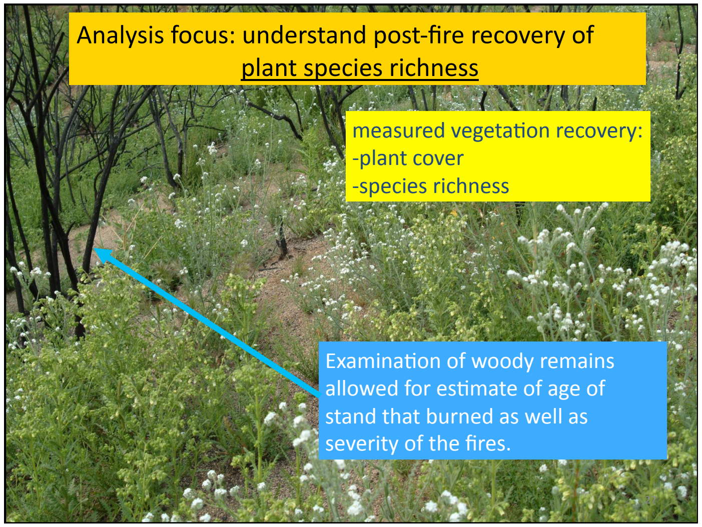
1. SOFTWARE IS A TOOL

2. IT IS NOT PERFECT

3. ALWAYS MAKE SURE IT IS DOING WHAT YOU THINK IT IS DOING!

Mediation in Analysis of Post-Fire Recovery of Plant Communities in California Shrublands*

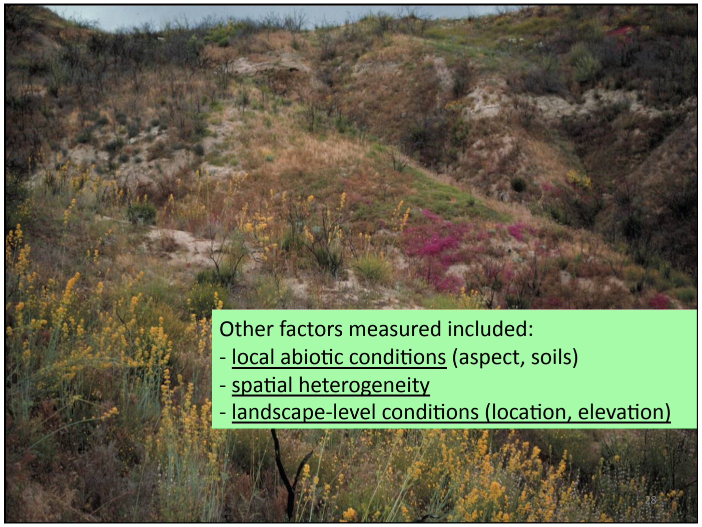
*Five year study of wildfires in Southern California in 1993. 90 plots (20 x 50m), (data from Jon Keeley et al.)



Analysis focus: understand post-fire recovery of plant species richness

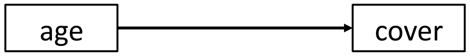
measured vegetation recovery:
-plant cover
-species richness

Examination of woody remains allowed for estimate of age of stand that burned as well as severity of the fires.



Other factors measured included:
- local abiotic conditions (aspect, soils)
- spatial heterogeneity
- landscape-level conditions (location, elevation)

Coding a Regression versus SEM



```
#regression
aLM<-lm(cover ~ age, data=keeley)

#sem
library(lavaan)
aSEM<-sem('cover ~ age', data=keeley)
```

summary(aSEM)

The model converged!

```
lavaan (0.4-11) converged normally after 15 iterations

  Number of observations                            90

  Estimator                                         ML
  Minimum Function Chi-square                    0.000
  Degrees of freedom                                 0
  P-value                                        1.000

Parameter estimates:

  Information                                 Expected
  Standard Errors                             Standard

                   Estimate  Std.err  Z-value  P(>|z|)
Regressions:
  cover ~
    age              -0.009    0.002   -3.549    0.000

Variances:
    cover             0.087    0.013
```

Model is saturated so, χ^2 test has no df

Compare to Regression

```
                   Estimate  Std.err  Z-value  P(>|z|)
Regressions:
  cover ~
    age              -0.009    0.002   -3.549    0.000

Variances:
    cover             0.087    0.013

> summary(aLM)

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.917395   0.071726   12.79  < 2e-16 ***
age         -0.008846   0.002520   -3.51  0.00071 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.2988 on 88 degrees of freedom
```

Compare to Residual SE
sqrt(0.087)=0.295

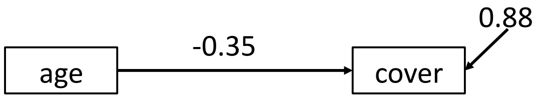
But what about the intercept?

Intercepts Estimated with Mean Structure

```
> aMeanSEM<-sem('cover ~ age',
  data=keeley, meanstructure=T)

> summary(aMeanSEM)
...
 Estimate  Std.err  Z-value  P(>|z|)
Regressions:
  cover ~
    age              -0.009    0.002   -3.549    0.000

Intercepts:
    cover             0.917    0.071   12.935    0.000

Variances:
    cover             0.087    0.013
```

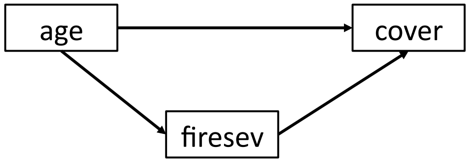
Standardized Coefficients

```
    lhs op   rhs  est.std    se      z  pvalue
1 cover  ~   age   -0.350 0.099 -3.549       0
2 cover ~~ cover    0.877 0.131  6.708       0
3   age ~~   age    1.000    NA     NA      NA
```



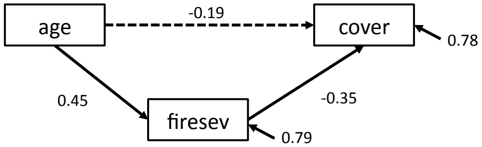
Also: `summary(aSEM, standardized=T, rsq=T)`

Bringing Back Fire



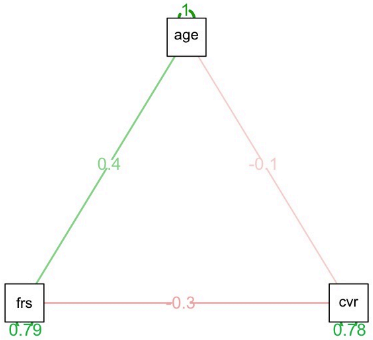
```
partialMedModel<-' firesev ~ age
                   cover ~ firesev + age'

partialMedSEM<-sem(partialMedModel,
                data=keeley)
```

summary(partialMedSEM, rsquare=T, standardized=T)



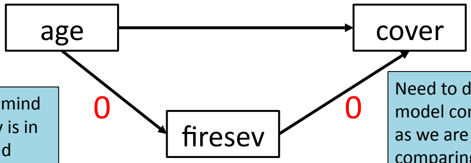
```
                   Estimate  Std.err  Z-value  P(>|z|)   Std.lv  Std.all
Regressions:
  firesev ~
    age               0.060    0.012    4.832    0.000    0.060    0.454
  cover ~
    firesev          -0.067    0.020   -3.353    0.001   -0.067   -0.350
    age              -0.005    0.003   -1.833    0.067   -0.005   -0.191

Variances:
    firesev           2.144    0.320                      2.144    0.794
    cover             0.078    0.012                      0.078    0.780

R-Square:

    firesev           0.206
    cover             0.220
```

semPlot



```
#plot
library(semPlot)
semPaths(partialMedSEM, "std")
```

What if we know better?

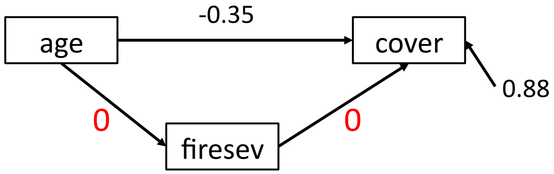


Fill in 0's to remind us that firesev is in the model, and fixed to 0

Need to do this for model comparison, as we are comparing covariance matrices

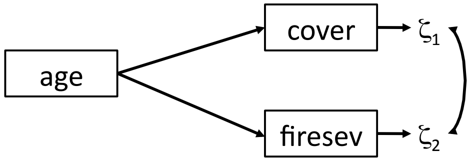
```
zeroMedModel<-' firesev ~ 0*age
                cover ~ 0*firesev + age'

zeroMedFit<-sem(zeroMedModel,
               data=keeley)
```

standardizedSolution(zeroMedFit)



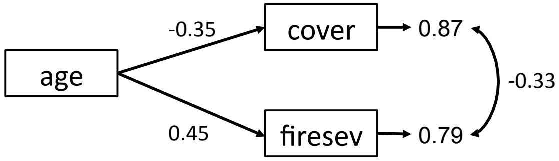
```
      lhs op      rhs est.std    se      z pvalue
1 firesev  ~      age   0.000    NA     NA     NA
2   cover  ~ firesev   0.000    NA     NA     NA
3   cover  ~      age  -0.350 0.099 -3.549      0
4 firesev ~~ firesev   1.000 0.149  6.708      0
5   cover ~~    cover   0.877 0.131  6.708      0
6     age ~~      age   1.000    NA     NA     NA
```

What about Correlated Error?



```
#what about correlations
corModel <-'firesev ~ age
            cover ~ age
            cover ~~ firesev'

corFit <- sem(corModel, data=keeley)
```

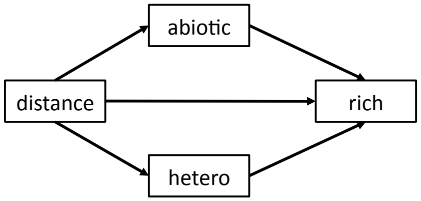
What about Correlated Error?



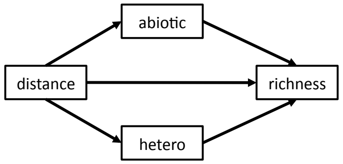
```
> standardizedSolution(corFit)
      lhs op      rhs est.std    se      z pvalue
1 firesev  ~      age   0.454 0.094  4.832      0
2   cover  ~      age  -0.350 0.099 -3.549      0
3 firesev ~~    cover  -0.333 0.094 -3.556      0
4 firesev ~~ firesev   0.794 0.118  6.708      0
5   cover ~~    cover   0.877 0.131  6.708      0
6     age ~~      age   1.000    NA     NA     NA
```

Morning Exercise

1. Fill in Standardized Coefficients and R^2 for this model
2. Refit is assuming that there is a 1:1 relationship between hetero and richness

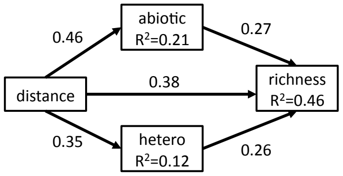


Solution 1: The Model



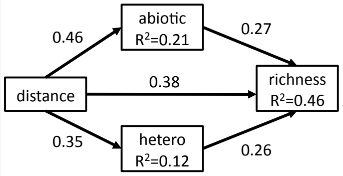
```
#The Richness Partial Mediation Model
distModel <- 'rich ~ distance + abiotic + hetero
              hetero ~ distance
              abiotic ~ distance'

distFit <- sem(distModel, data=keeley)
```

Solution 1: The Model

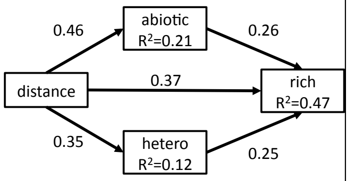


```
       lhs op      rhs est.std    se     z pvalue
1     rich  ~ distance   0.377 0.092 4.117  0.000
2     rich  ~  abiotic   0.268 0.087 3.079  0.002
3     rich  ~   hetero   0.256 0.082 3.104  0.002
4   hetero  ~ distance   0.346 0.099 3.498  0.000
5  abiotic  ~ distance   0.460 0.094 4.911  0.000
6     rich ~~     rich   0.539 0.080 6.708  0.000
7   hetero ~~   hetero   0.880 0.131 6.708  0.000
8  abiotic ~~  abiotic   0.789 0.118 6.708  0.000
9 distance ~~ distance   1.000    NA    NA     NA
```

Compare with Piecewise Fit

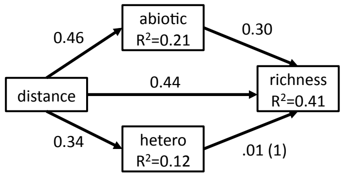


Likelihood



Piecewise

Solution 2: The Model



```
oneDistModel <- 'rich ~ distance + abiotic + 1*hetero
                hetero ~ distance
                abiotic ~ distance'
oneFit<-sem(oneDistModel, data=keeley)
summary(oneFit, stdandardized=T, rsquare=T)
```

Estimating Direct and Indirect Effects with Named Coefficients

```
totDistModel <- '
     rich ~ a*distance + b*abiotic + c*hetero
     hetero ~ b1*distance
     abiotic ~ c1*distance

     direct:=  a
     indirect:= b1*b + c1*c
     total:= b1*b + c1*c + a
'
```

summary(totDistFit, standardized=T, rsquare=T)

```
                   Estimate   Std.err   Z-value   P(>|z|)    Std.lv   Std.all
...

Defined parameters:
    direct            0.640     0.156     4.117     0.000     0.640     0.377
    indirect         13.357     5.090     2.624     0.009    13.357     0.210
    total            13.997     5.051     2.771     0.006    13.997     0.588
```

standardizedSolution(totDistFit)

```
        lhs op         rhs est.std    se     z pvalue
1      rich  ~    distance   0.377 0.092 4.117  0.000
2      rich  ~     abiotic   0.268 0.087 3.079  0.002
3      rich  ~      hetero   0.256 0.082 3.104  0.002
4    hetero  ~    distance   0.346 0.099 3.498  0.000
5   abiotic  ~    distance   0.460 0.094 4.911  0.000
6      rich ~~        rich   0.539 0.080 6.708  0.000
7    hetero ~~      hetero   0.880 0.131 6.708  0.000
8   abiotic ~~     abiotic   0.789 0.118 6.708  0.000
9  distance ~~    distance   1.000    NA    NA     NA
10   direct :=           a   0.377    NA    NA     NA
11 indirect :=   b1*b+c1*c   0.210    NA    NA     NA
12    total := b1*b+c1*c+a   0.588    NA    NA     NA
```