# Introduction to structural equation modelling

# Basic modelling

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# Quick introduction of participants

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- Why do you want to learn about SEM?

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- · Who are you?
- · Why do you want to learn about SEM?
- What is your research question for day 3?

General information

· Dr. Frank Pennekamp (main instructor)



- · Dr. Frank Pennekamp (main instructor)
- Dr. James Grace (advanced topics and model clinic)



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- · Dr. Rachel Korn (course development)



- Dr. Frank Pennekamp (main instructor)
- Dr. James Grace (advanced topics and model clinic)
- Dr. Rachel Korn (course development)
- Dr. Noémie Pichon, Dr. Fletcher Halliday, Dr. Eliane Meier, Dr. Hugo Saiz, Dr. Debra Zuppinger-Dingley, Rebecca Oester, Annabelle Constance, Fabienne Wiederkehr (course development)



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  - $\boldsymbol{\cdot}$  General introduction to SEM to model ecological systems

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- Day 3:
  - Self-study with possibility to meet with instructor(s)

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- · What will not be covered
  - · Local estimation of SEMs (with piecewiseSEM)
  - Advanced topics like incorporating random effects, feedbacks, temporal autocorrelation

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 Participants understand the advantages and limits of SEMs to draw inferences from data

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- Participants are able to fit, interpret and visualize a SEM with lavaan.
- · Participants are able to apply SEM to their own dataset

Getting started with Structural
Equation Modeling



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## Research questions



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- We often have ideas how things could be connected in ecological systems.
- To test hypotheses, we need a way to dissect when they occur for a reason versus randomness.
- We use statistics to understand what is signal and what is noise.
- Research questions are often about cause and effect.

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- SEM unites multiple variables in a single causal network: simultaneous tests of multiple hypotheses.
- · Causality is central:
  - SEM assumes that the specified relationships among variables represent causal links.



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- Everything else being equal, seeing variation in X leading to variation in Y.
- · Experiments to isolate effect of X on Y.
- Experiments not always feasible, hence development of SEM.

9

Differences and similarities between

SEM and regression models

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- · We want to test and evaluate multivariate causal relationship.
- Test direct and indirect effects on assumed causal relationships.
- Incorporate observed and latent variables.

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- 1) Understand the underlying causal network driving the correlation/covariance among a set of variables.
- 2) Explain as much of their variance as possible with the model specified.

## Thinking about the model

A SEM is usually specified based on theory to determine and validify a proposed causal process and/or model.

Which variables to include?

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Which variables to include?

- · Supported by theory.
- · Ecologically meaningful.
- Garbage in garbage out (both data quality and ecologically meaningful).

## SEM modelling philosophy

• Continuum between theory (hypothesis-driven) to exploratory (data-driven) modelling.

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- Continuum between theory (hypothesis-driven) to exploratory (data-driven) modelling.
- · Important to be explicit about the approach taken.



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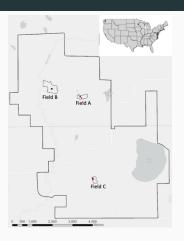
- Disturbance
- Nitrogen deposition
- · Changes in precipitation

## Research questions:

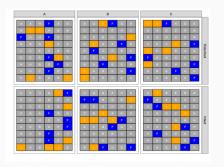
1) How has aboveground biomass changed as a function of disturbance (disking) and nutrient addition?

### Research questions:

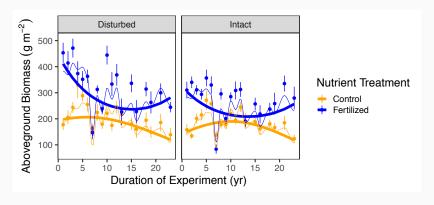
- How has aboveground biomass changed as a function of disturbance (disking) and nutrient addition?
- 2) How are these effects mediated by diversity?



Location of the study site (Cedar Creek Ecosystem Science Reserve), the location of the three study fields within the reserve, and location of the 35 x 55 m intact (black) and disturbed (red) plots within each field.

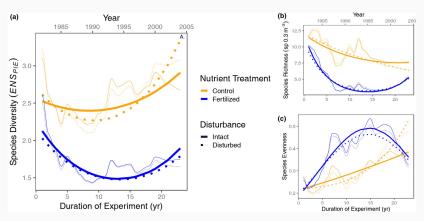


Location of the 4  $\times$  4 m nutrient treatment plots within each 35  $\times$  55 m Intact or Disturbed plot within each of three fields (A, B, and C). Letters indicate the nutrient treatments.



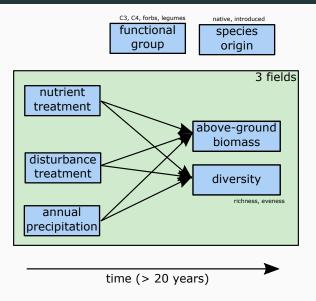
Effect of soil disturbance (disking) and nutrient enrichment on live, aboveground plant biomass. Colors indicate nutrient addition treatment:

Control and NPK+ (all nutrients plus 9.5 g N m-2 yr-1).

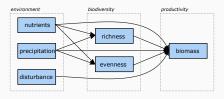


Effect of soil disturbance (disking) and nutrient enrichment on (a) diversity (ENSPIE), (b) richness (S, species 0.3 m-2), and (c) evenness (ENSPIE S-1).

### Question of interest: what is the effect of richness on biomass?



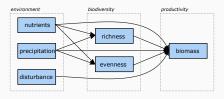
#### Meta-model



Meta-model are conceptual models that allow to link data with theory.

 Productivity (biomass) is directly influenced by the environment (nutrients, disturbance and precipitation)

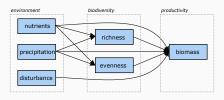
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- Productivity (biomass) is directly influenced by the environment (nutrients, disturbance and precipitation)
- 2) Productivity (biomass) is directly influenced by biodiversity (richness and evenness).
- 3) The environment also influences biodiversity and thus, have an indirect effect on productivity via biodiversity.

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- Edges (one-headed arrows) are causal relationships such as X affects Y.
- Edges (two-headed arrows) are non-causal relationships such as X and Y are correlated.

# Exercise:

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• Draw a meta-model of the dataset you will work with on Thursday.

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- · Make a table with putative causal relationships.

## A simple bivariate model.



· Linear regression

## A simple bivariate model.



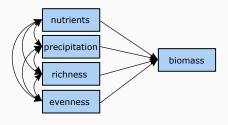
- · Linear regression
- $\boldsymbol{\cdot}$  Regression coefficient quantifies the strength of relationship

#### A simple bivariate model.



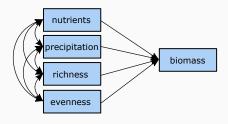
#### lm(biomass ~ precipitation)

- · Linear regression
- · Regression coefficient quantifies the strength of relationship
- · Change in Y for one unit change in X



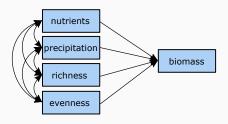
```
lm(biomass ~ precipitation + nutrients + ...)
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- Often more than one independent variable important  $\rightarrow$  multiple regression
- Estimates partial regression coefficients (i.e. effect of precipitation on biomass when nutrient addition is fixed)
- Only direct effects.

From regression models to SEM

#### SEM: variance-covariance matrix

```
## [,1] [,2] [,3]
## [1,] 1875.3209 429.8712 462.4775
## [2,] 429.8712 1306.9817 -262.8231
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Comparison of specified SEM to observed variance-covariance matrix

#### SEM: variance-covariance matrix

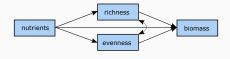
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- · Comparison of specified SEM to observed variance-covariance matrix
- The variances appear along the diagonal and covariances appear in the off-diagonal elements

#### SEM: correlation matrix

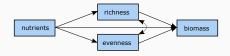
```
## [,1] [,2] [,3]
## [1,] 1.0000000 0.2745780 0.3885349
## [2,] 0.2745780 1.0000000 -0.2644881
## [3,] 0.3885349 -0.2644881 1.0000000
```

· Correlation matrix is standardized variance-covariance matrix



```
lm(richness ~ nutrients)
lm(evenness ~ nutrients)
lm(biomass ~ richness + evenness)
```

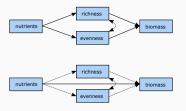
 Indirect effect is the effect of an independent variable on a dependent variable through one or more intervening or mediating variables.



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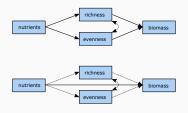
- Indirect effect is the effect of an independent variable on a dependent variable through one or more intervening or mediating variables.
- Indirect effects can be quantified by the product of the compound path.

#### Mediation



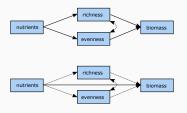
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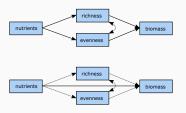


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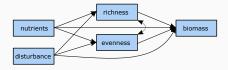


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- · Possibilities: complete mediation, partial mediation, no mediation.

## System level approach



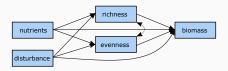
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- Exogenous variables only have paths emanating from them (i.e., do not have arrows going into them).
- Endogenous variables have paths directed into them.
- An endogenous variable can also have arrows directing out of it, but the sole condition is that they must be predicted.

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- 4) When variables are connected by more than one pathway, each pathway is the 'partial' regression coefficient.

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- 8) The total effect (including undirected paths) is equivalent to the total correlation.

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- Root-mean squared error of approximation (RMSEA): statistic penalizes models based on sample size. A value < 0.10 is acceptable, and anything < 0.08 is good.</li>
- Standardized root-mean squared residual (SRMR): the standardized difference between the observed and predicted correlations. A value
   0.08 is considered good.

 $\cdot$  (Multivariate) normality of endogenous variables

34

- (Multivariate) normality of endogenous variables
- · Global estimation based on variance-covariance matrix<sup>1</sup>

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- · (Multivariate) normality of endogenous variables
- Global estimation based on variance-covariance matrix<sup>1</sup>
- · Directed (acyclic) relationships<sup>2</sup>
- Linear relationships<sup>3</sup>

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- Over-identified: parameters can be uniquely identified and positive dfs to test model goodness-of-fit (df > 0).

"t-rule" to quickly gauge whether a model is under-, just, or overidentified:

$$t \le \frac{n(n+1)}{2}$$

*t* = number of unknowns (parameters to be estimated, i.e. variances & covariances)

n = number of knowns (observed variables).

The LHS is how many pieces of information we want to know.

RHS: information we have (number of unique cells in the observed variance-covariance matrix).

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- Ideally, replication is 5-20x the number of estimated parameters.
- The larger the sample size, the more precise (unbiased) the estimates.

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- 4) Select measures for the variables represented in the model
- 5) Collect data
- 6) Conduct preliminary descriptive statistical analysis (e.g., scaling, missing data, collinearity issues, outlier detection)
- 7) Estimate parameters in the model
- 8) Assess model goodness-of-fit
- 9) Check for missing or unnecessary links

- Review the relevant theory and research literature to support model specification
- 2) Specify a model (e.g., diagram)
- 3) Determine model identification
- 4) Select measures for the variables represented in the model
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- 6) Conduct preliminary descriptive statistical analysis (e.g., scaling, missing data, collinearity issues, outlier detection)
- 7) Estimate parameters in the model
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- 9) Check for missing or unnecessary links
- 10) Interpret and present results visually

Lavaan syntax

#### Lavaan syntax

```
Define model:
```

```
simple <-
"mass.above ~ nadd + rich + even + precip.mm + disk
rich ~ nadd + precip.mm
even ~ nadd + precip.mm"</pre>
```

#### Fit model:

```
fit.simple <- sem(simple, data = seabloom)</pre>
```

## Lavaan syntax

| Formula type | R   | Meaning                    | Example                 |
|--------------|-----|----------------------------|-------------------------|
| regression   | ~   | is regressed on            | y ~ x                   |
| correlation  | ~~  | correlate errors for       | y1 ~~ y2                |
| latent       | =~  | set reflective indicators  | Height =~ y1 + y2 + y3  |
| composite    | <~  | set formative indicators   | Comp1 <~ 1*x1 + x2 + x3 |
| intercept    | ~ 1 | estimate mean for <b>y</b> | y ~ 1                   |
| labelling    | *   | name coefficients          | y ~ b1*x1 + b2*x2       |
| defining     | :=  | define quantity            | Total := b1*b3 + b2     |

# Questions?

Live coding session

Your turn: working with the
Seabloom dataset

• Exploration of dataset (variables and treatments)

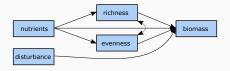
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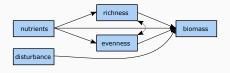
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  - · Multiple regression (direct effects of predictors on AGB)

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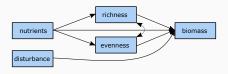
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- Check collinearity and normality
- Fitting linear models to estimate coefficients
  - Multiple regression (direct effects of predictors on AGB)
  - · Multiple regression (indirect effects on richness and evenness)
  - · What can you conclude?



• Fitting of above SEM to Seabloom data:



- Fitting of above SEM to Seabloom data:
  - · Assess model goodness of fit.



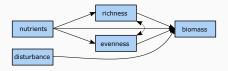
- · Fitting of above SEM to Seabloom data:
  - · Assess model goodness of fit.
  - Investigate the modification indices. Are there paths to add that are reasonable?



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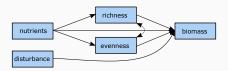
After finding a model with good fit:

Model analysis:



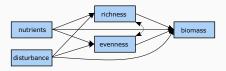
After finding a model with good fit:

- · Model analysis:
  - · Calculate the standardized coefficients.

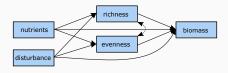


After finding a model with good fit:

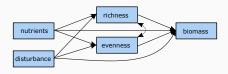
- · Model analysis:
  - · Calculate the standardized coefficients.
  - Add derived quantities (direct and indirect effects of nutrients and disturbance).



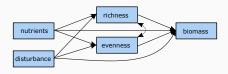
· Saturated model:



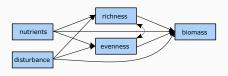
- · Saturated model:
  - · Model comparison with simpler models used previously.



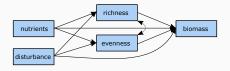
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  - · Perform model pruning.



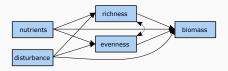
- · Saturated model:
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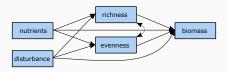
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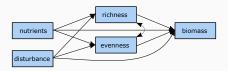
• Perform mediation analysis:



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  - Compare model fit to simple model. What do you conclude?