

Extending ANOVA and ANCOVA Analyses using SEM

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1

In this module I consider an example where randomized experiments were used to study effects. Here I try to show how SEM permits additional understanding to be developed.

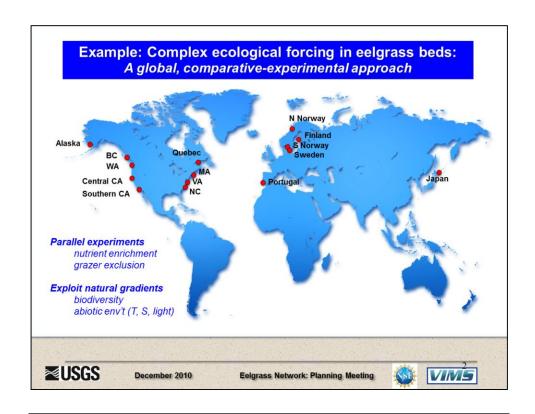
An appropriate citation for this material is

Whalen, M.A., Duffy, J.E. and Grace, J.B. 2013. Temporal shifts in top-down versus bottom-up control of epiphytic algae in a seagrass ecosystem. *Ecology* 94:510-520.

Notes: IP-056512; Support provided by the USGS Climate & Land Use R&D and Ecosystems Programs. I would like to acknowledge formal review of this material by Jesse Miller and Phil Hahn, University of Wisconsin. Many helpful informal comments have contributed to the final version of this presentation. The use of trade names is for descriptive purposes only and does not imply endorsement by the U.S. Government.

Last revised 17.02.05.

Source: https://www.usgs.gov/centers/wetland-and-aquatic-research-center/science/quantitative-analysis-using-structural-equation



These data come from a global experiment being conducted on seagrasses.

Data from:

Field-based Experimental Study of the Importance of Small Herbivores in a Seagrass Ecosystem:

Matthew A Whalen and J Emmett Duffy

Whalen, Duffy, and Grace, 2013. *Ecology* 94:510-520. (http://www.esajournals.org/doi/abs/10.1890/12-0156.1)

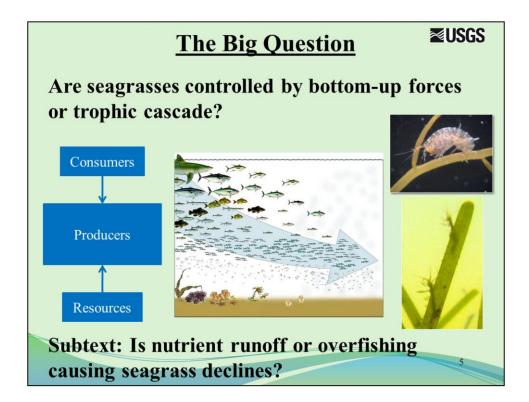


More specifically, these are from a study in Virginia.

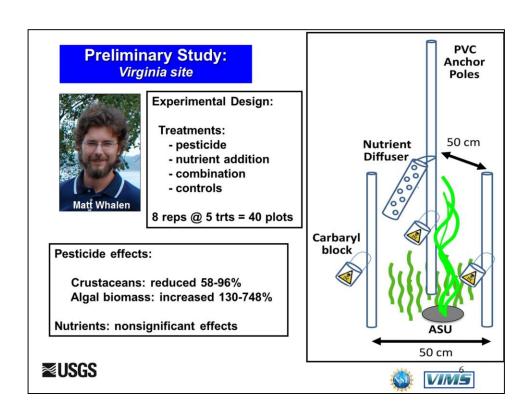


It is all about microcrustaceans grazing on the epiphytes that live on eelgrasses, a particularly important seagrass.

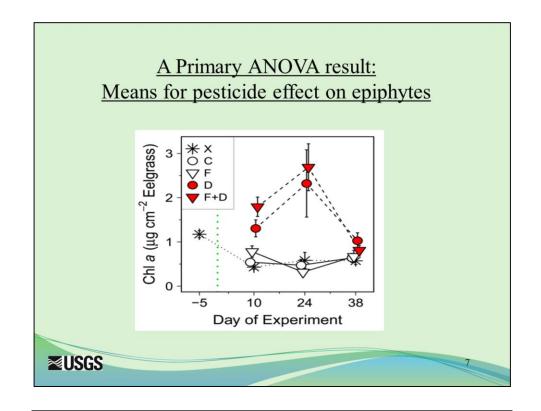
If grazers don't keep epiphytes grazed down, they lead to the death of the seagrasses, causing the base of the ecosystem to collapse.



Part of the big deal is a question of what may be causing eelgrass declines worldwide and the broader implications of this issue.



Here is the part of the experimental study discussed in this example.



Anova results provide limited information.

Illustration of ANOVA-type model # Read Whalen Seagrass Data w.dat <- read.csv("WhalenData.csv") # ANOVA Model anovaModel <- 'epiphytes ~ pesticides' Pesticide We are using slightly different notation here. 8

An anova, in its most basic form, is a very simple model. The simplicity is created by the physical control in combination with randomization.

Illustration of ANOVA-type model (cont.)

```
# Fit ANOVA Model
anovaFit <- sem(anovaModel, data=w.dat)
# Get Results
summary(anovaFit, standardized=T, rsq=T)</pre>
```

```
Est SE Z P Std.all

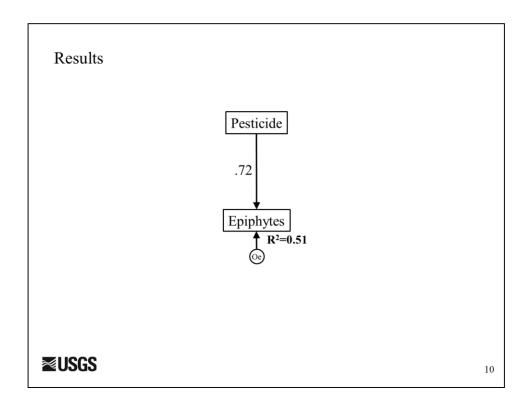
Regressions:
    epiphytes ~
        pesticides 0.998 0.154 6.48 0.000 0.716

Variances:
        epiphytes 0.227 0.051 0.488

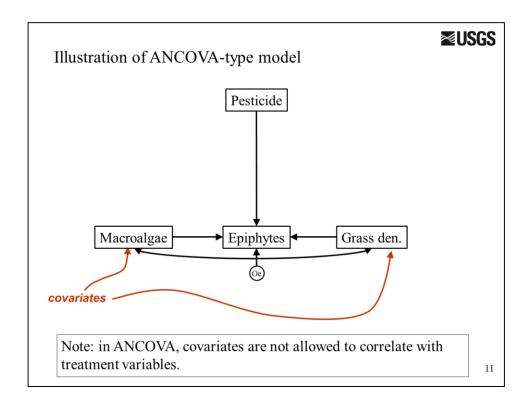
R-Square:
        epiphytes 0.512
```

Here are the net-effect results. Note that the information extracted is similar to that obtained from an ANOVA. The main difference is that we are now treating treatment levels as points on a continuum (regression perspective) instead of simply testing for whether treatment means differ.

9



And shown graphically.

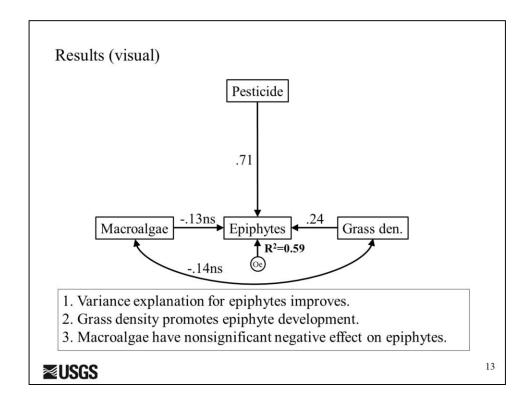


There are two covariates in this study, a macro alga and the density of eelgrass. We have not anticipation about what the macroalgae might do, but we expect greater eelgrass density to promote epiphytes by buffering water movement and physical damage to epiphytes.

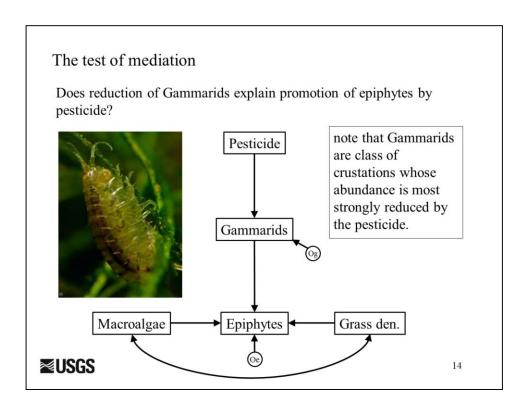
In ANCOVA, the covariates are supposed to be uncorrelated with the treatment, which holds true in this case.

Simple ANCOVA Model ancovaModel <- 'epiphytes ~ pesticides + macroalgae + grass' Pesticides Pesticides Grass den. 12

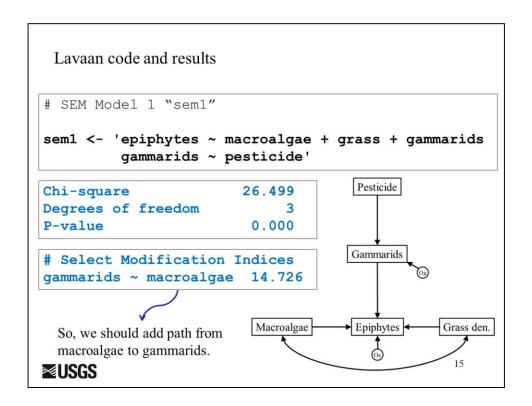
A simple ANCOVA here.



And the results



Here we perform the test of mediation with one of the microcrustaceans, the Gammarids.



Results suggest something missing from model.

Modifying our model: adding needed linkages Pesticide Gammarids Gammarids Festicide Festicide Festicide Grass den. # New Model - SEM Model 2 "sem2" sem2 <- 'epiphytes ~ macroalgae + grass + gammarids gammarids ~ pesticide + macroalgae'

An important discovery is an effect of macroalgae on Gammarids.

Results

```
Chi-square 8.136
Degrees of freedom 2
P-value 0.017
```

```
# Chi-square difference test
anova(sem1.fit, sem2.fit)

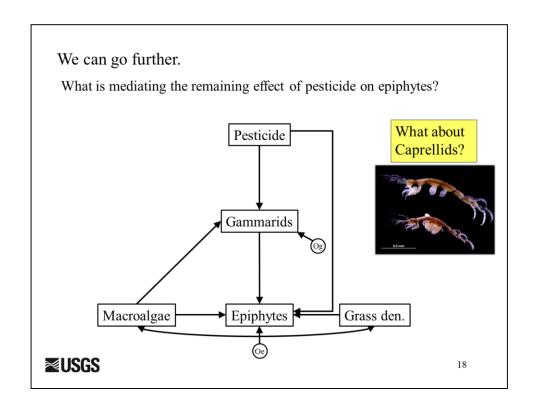
Chisq-diff = 18.363,
df-dif = 1
p = < 0.001</pre>
```

```
# Select Modification Indices
gammarids ~ grass 3.319
epiphytes ~ pesticide 4.205
```

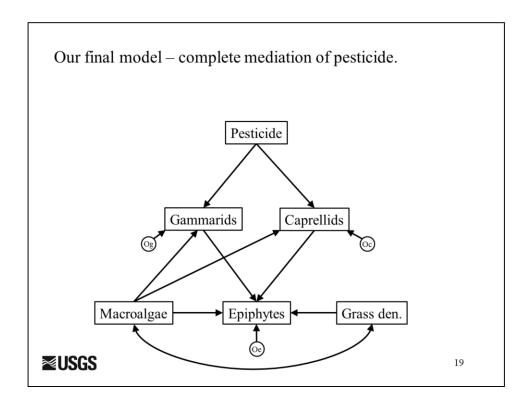


17

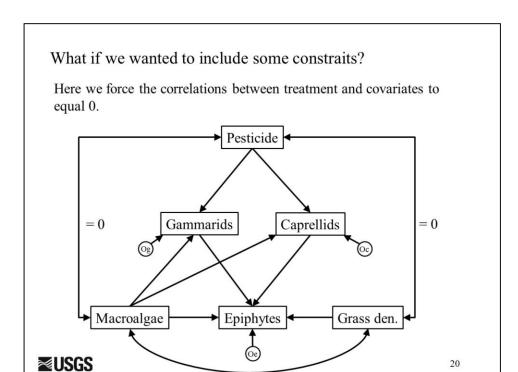
Model still missing another link, though the link added in model 2 definitely improved model fit dramatically. Modification indices suggest a remaining direct path from pesticide to epiphytes.



Now we bring in the second most abundant type of micrograzer.



Finally, a fully-mediate model.		
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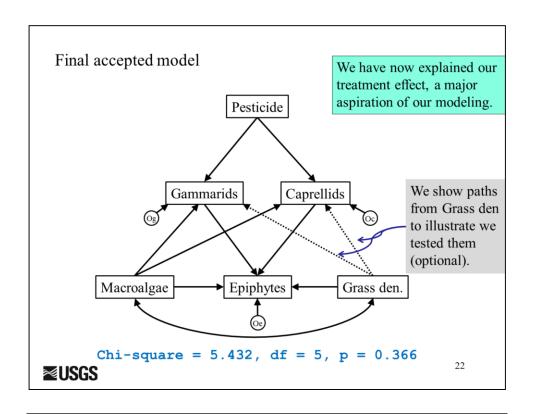
Here we simple demonstrate setting exogenous correlations to zero. this permits more pure causal attribution (if it holds).

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"sem5" model and results

```
# SEM Model 5 "sem5"
sem5 <- 'epiphytes ~ macroalgae + grass + gammarids</pre>
                   + caprellids
         gammarids ~ pesticide + macroalgae
         caprellids ~ pesticide + macroalgae
         pesticide ~~ 0*macroalgae
         pesticide ~~ 0*grass'
sem5.fit <- sem(sem5, data=w.dat, fixed.x=F)</pre>
# Chi-square difference test
                                   # note we must
                                   declare
anova(sem4.fit, sem5.fit)
                                   "fixed.x=FALSE"
                                   to work with
Chisq-diff = 1.363
                                   exogenous
df-dif
        = 3
                                   {\tt correlations.}^{21}
          = highly ns
p
```

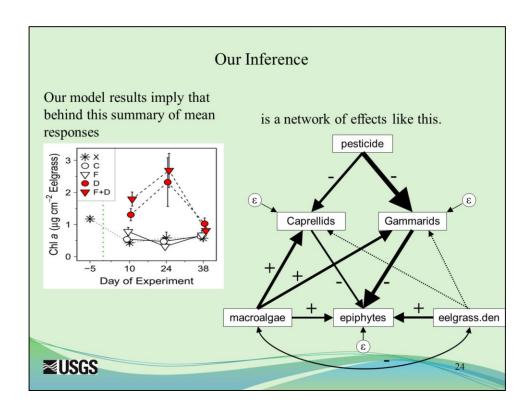
Code in red shows how we set correlations to zero.



Final model.	

■USGS Results Est. Std.err Z-val P(>|z|) Std.all Regressions: epiphytes ~ macroalgae 0.105 0.040 2.612 0.009 0.290 0.405 0.100 4.034 0.000 0.389 grass -0.663 -0.329 0.057 -5.828 0.000 gammarids caprellids -0.240 0.085 -2.834 0.005 -0.335gammarids ~ -2.053 0.215 -9.570 0.000 -0.748pesticide 0.304 0.057 5.347 macroalgae 0.000 0.418 0.315 0.164 1.922 0.055 0.150 grass caprellids ~ pesticide -0.7480.231 -3.239 0.001 -0.393 0.243 0.061 3.965 0.000 0.481 macroalgae 0.231 0.176 1.311 0.190 0.159 grass R-Square: epiphytes 0.645 gammarids 0.756 23 0.411 caprellids

Here are the details of the estimates. Shown are raw parameter estimates (Est.), their standard errors (Std.err), associated Z-values (which are like likelihood-based t-values, the probabilities associated with the Z-values ($P(>\z\rangle)$, and the standardized parameter estimates (Std.all).



So, behind the standard anova result (on the left), lies a network of relationships going on.

Note that there is an exercise tutorial in which you may work through the mechanics of this analysis is you like. Consult

"SEM_5_Ex1_Test_of_Mediation_Exercise.pdf" and the associated code and data.

Lessons about using SEM with experimental data

- 1. Test of mediation is neglected concept in biometrics.
- 2. Careful with classic ANCOVA; if we used mediating variables as covariates, results would indicate no significant treatment effect!
- SEM easy to implement with simple experimental designs. With blocking, nested designs, etc., more work required for SEM analyses.
- 4. Recommend performing classic analyses along with SEM analyses and reporting both. Classical analyses can more easily detect interactions and in SEM you have to work to examine them (more on that later).



Just a few summary points.