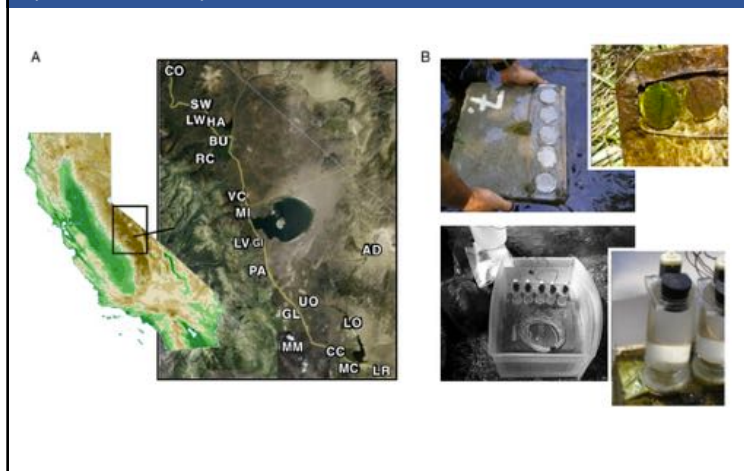


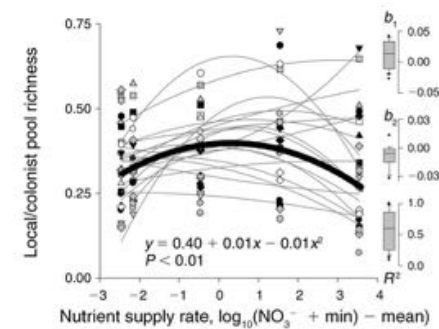
Non-linearities and More

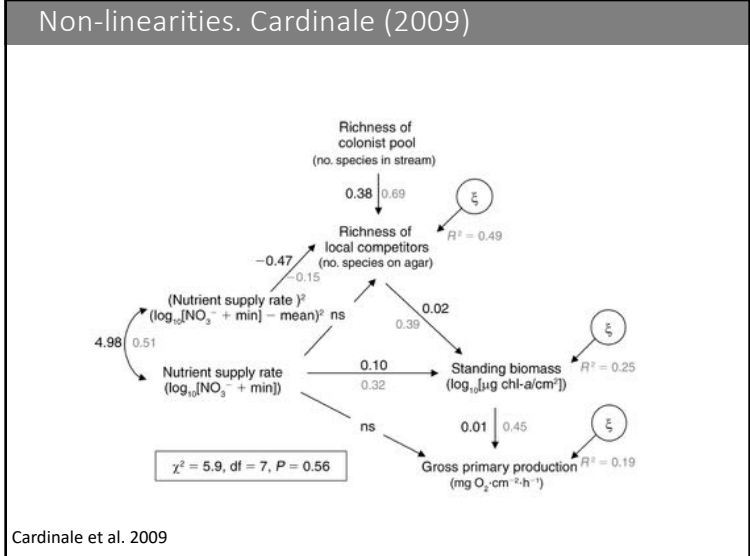
1. Non-linearities in models
 - Polynomial Terms
 - Interactions
2. Generalized Linear Models
3. Special Considerations for GLMs and Dsep
4. Standardized Nonlinear Coefficients

Cardinale et al. (2009) - Does diversity drive productivity or vice versa?

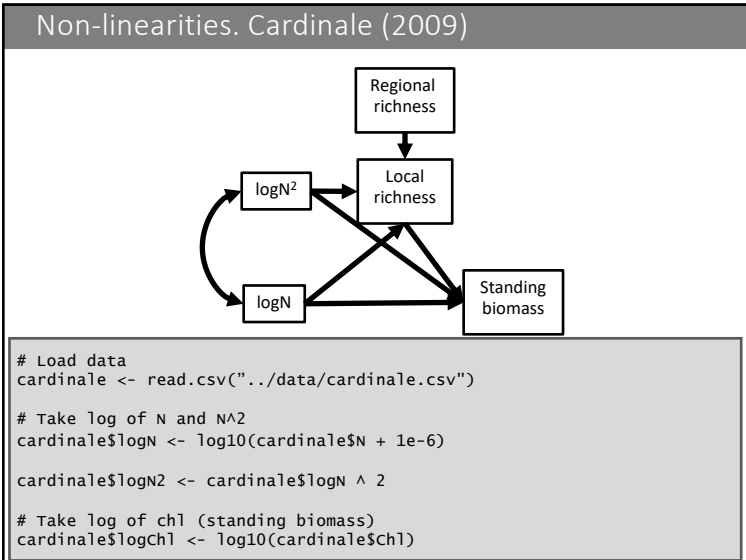
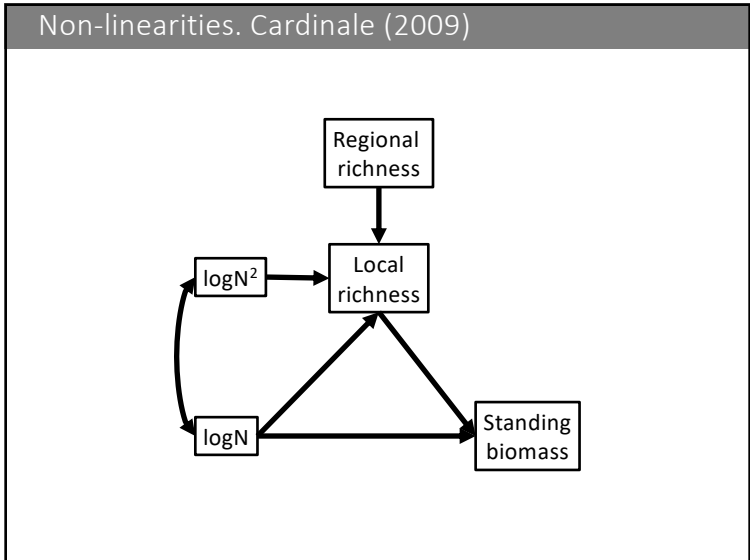


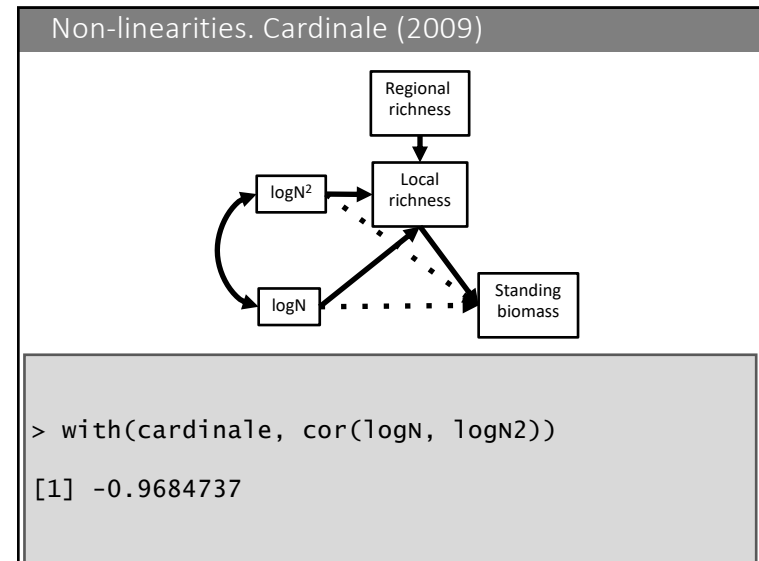
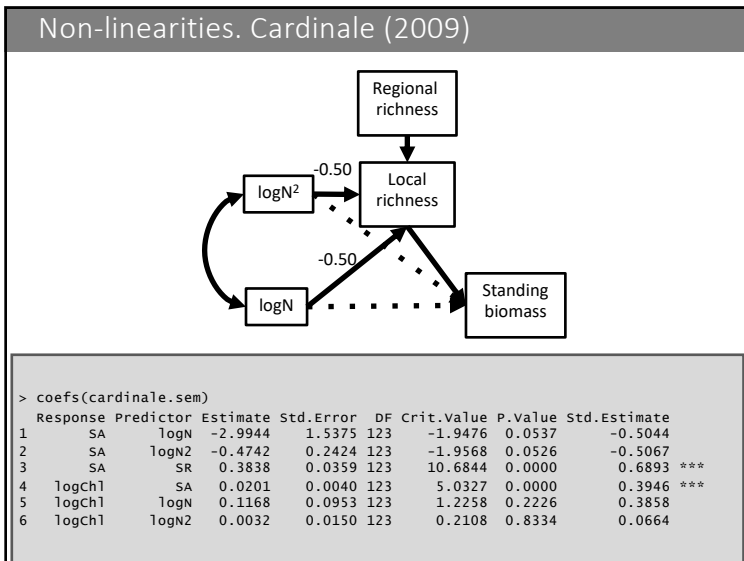
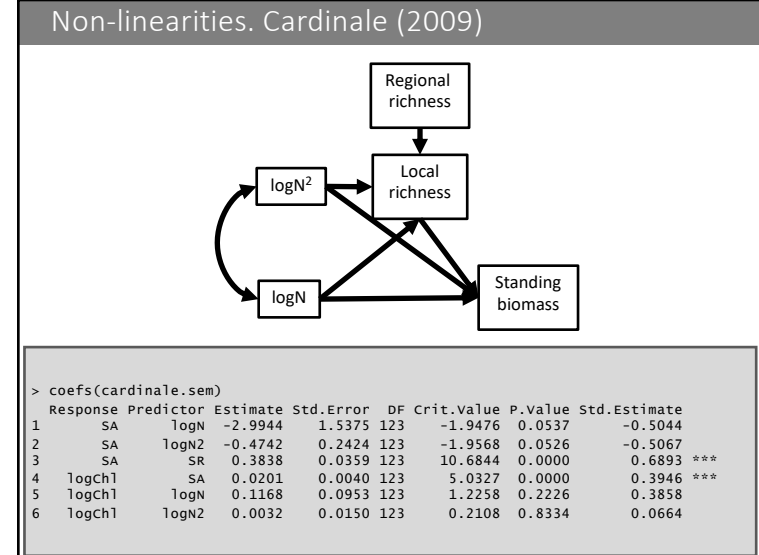
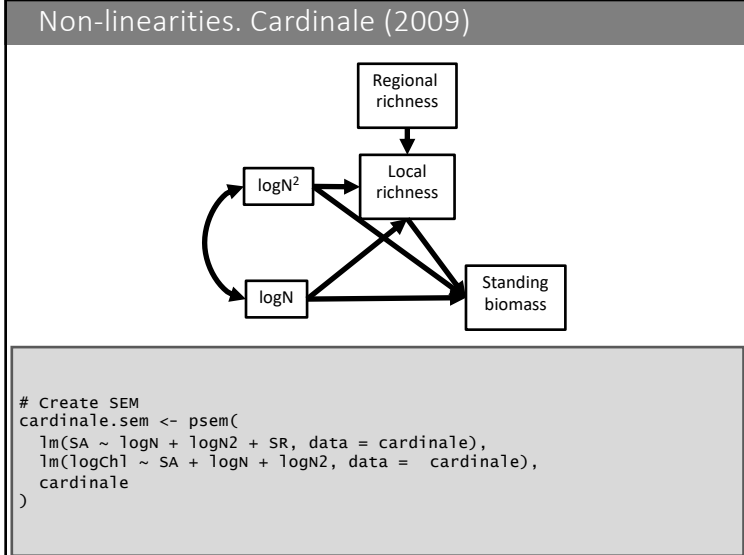
Non-linearities. Cardinale (2009)





- ### Non-linearities
- Code as independent linear and squared, cubed, etc. terms
 - Currently squirrely if transformed inside model formula, e.g., $\text{lm}(y \sim \text{poly}(x, 2))$, $\text{I}(x^2)$





Centering Reduces Correlation

Centering helps remove collinearities.

Warning: it does change interpretation of interaction effects.

```
# Center polynomial to reduce collinearity
cardinale$logN.cen = scale(cardinale$logN, scale = F)
cardinale$logN2.cen = scale(cardinale$logN, scale = F) ^ 2
```

Centering Reduces Correlation

```
> cor(cardinale$logN.cen, cardinale$logN2.cen)
      [,1]
[1,] 0.5126311
```

Centering Reduces Correlation

```
# Re-fit SEM using centered predictors
cardinale.sem2 <- psem(
  lm(SA ~ logN.cen + logN2.cen + SR, data = cardinale),
  lm(logCh1 ~ SA + logN.cen + logN2.cen, data = cardinale),
  cardinale
)
```

Centering Reduces Correlation

```
> coefs(cardinale.sem2)
Response Predictor Estimate Std.Error DF Crit.Value P.value Std.Estimate
1 SA logN.cen 0.3668 0.4460 123 0.8223 0.4125 0.0618
2 SA logN2.cen -0.4742 0.2424 123 -1.9568 0.0526 -0.1470
3 SA SR 0.3838 0.0359 123 10.6844 0.0000 0.6893 ***
4 logCh1 SA 0.0201 0.0040 123 5.0327 0.0000 0.3946 ***
5 logCh1 logN.cen 0.0944 0.0275 123 3.4320 0.0008 0.3116 ***
6 logCh1 logN2.cen 0.0032 0.0150 123 0.2108 0.8334 0.0193
```

Centering Reduces Correlation

```

> dsep(cardinale.sem2)
      Independ.Claim  Estimate  Std.Error  DF  Crit.Value  P.Value
1 logCh1 ~ SR + ...  0.002044185  0.003078878  122  0.6639384  0.5079826
  
```

With lavaan

```

cardinale_mod <- '
SA ~ logN.cen + logN2.cen + SR
logCh1 ~ SA + logN.cen + logN2.cen
logN.cen ~ logN2.cen
'

cardinale_fit <- sem(cardinale_mod, data=cardinale, fixed.x=F)
  
```

With lavaan...

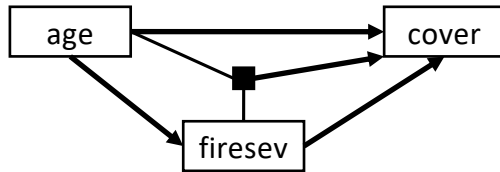
Regressions:	Estimate	Std.Err	z-value	P(> z)	Std.lv	Std.all
SA ~						
logN.cen	0.367	0.439	0.836	0.403	0.367	0.062
logN2.cen	-0.474	0.238	-1.989	0.047	-0.474	-0.147
SR	0.384	0.035	10.858	0.000	0.384	0.028
logCh1 ~						
SA	0.020	0.004	5.114	0.000	0.020	0.395
logN.cen	0.094	0.027	3.486	0.000	0.094	0.312
logN2.cen	0.003	0.015	0.214	0.831	0.003	0.019

Interaction Effects

```

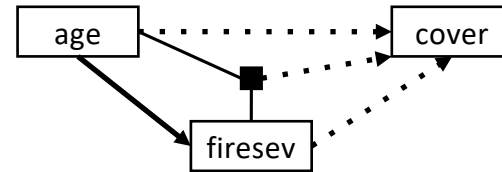
keeley_int <- psem(
  lm(cover ~ age*firesev, data = keeley),
  lm(firesev ~ age, data = keeley),
  data = keeley
)
  
```

Model is Saturated



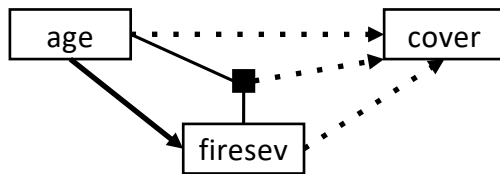
```
> fisherC(keeley_int)
Fisher.C df P.Value
1      0  0      1
```

Where did the firesev effect go?



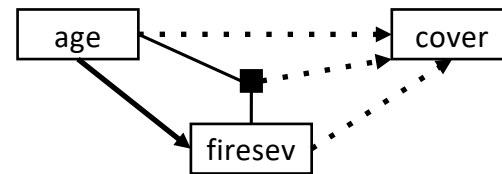
```
> coefs(keeley_int)
Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
1 cover age 0.0045 0.0067 86 0.6786 0.4992 0.1800
2 cover firesev -0.0149 0.0398 86 -0.3729 0.7101 -0.0774
3 cover age:firesev -0.0021 0.0014 86 -1.5263 0.1306 -0.5700
4 firesev age 0.0597 0.0125 88 4.7781 0.0000 0.4539 ***
```

Is this a problem?



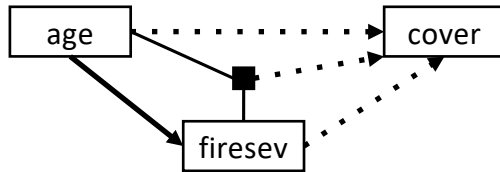
```
> with(keeley, cor(age, age*firesev))
[1] 0.8687952
```

Centering for Interactions



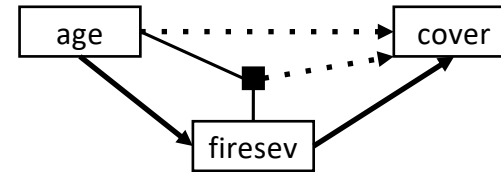
```
keeley$fire_cent <- scale(keeley$firesev, scale=FALSE)
keeley$age_cent <- scale(keeley$age, scale=FALSE)
```

Centering for Interactions



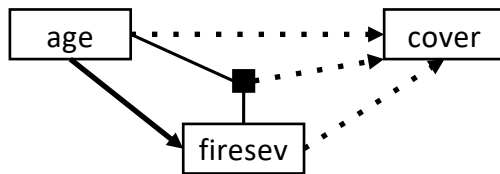
```
keeley_int_cent <- psem(
  lm(cover ~ age_cent * fire_cent, data = keeley),
  lm(fire_cent ~ age_cent, data = keeley),
  data = keeley
)
```

Additive Effect Recovered



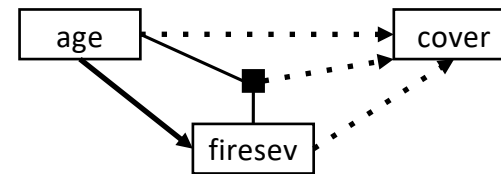
```
> coefs(keeley_int_cent)
Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
1 cover age_cent -0.0050 0.0027 86 -1.8810 0.0634 -0.1985
2 cover fire_cent -0.0684 0.0203 86 -3.3752 0.0011 -0.3561 **
3 cover age_cent:fire_cent -0.0021 0.0014 86 -1.5263 0.1306 -0.1438
4 fire_cent age_cent 0.0597 0.0125 88 4.7781 0.0000 0.4539 ***
```

In Lavaan Same Problem



```
partialMedModel_int<-' firesev ~ age
  cover ~ firesev + age + firesev:age'
```

Model Also Does Not Fit



```
lavaan (0.5-23.1097) converged normally after 24 iterations
Number of observations              90
Estimator                          ML
Minimum Function Test Statistic     121.892
Degrees of freedom                   1
P-value (Chi-square)                0.000
```

Collinearity Shows Up in Modification Indices

```

> modificationindices(partialMedFit_int)
      lhs      op      rhs      mi      epc sepc.lv sepc.all sepc.nox
...
11 firesev ~      cover 66.770 -14.162 -14.162  -2.673  -2.673
12 firesev ~ firesev:age 66.770  0.030  0.030   1.550  0.018
16 firesev:age ~ firesev 53.016 19.871 19.871  0.380  0.380
    
```

Same Solution

```

partialMedModel_int_scale<-'
fire_cent ~ age_cent
cover ~ fire_cent + age_cent + fire_cent:age_cent
'
    
```

Same Solution

```

lavaan (0.5-23.1097) converged normally after 31 iterations

Number of observations              90

Estimator                          ML
Minimum Function Test Statistic     0.121
Degrees of freedom                  1
P-value (Chi-square)                0.728
    
```

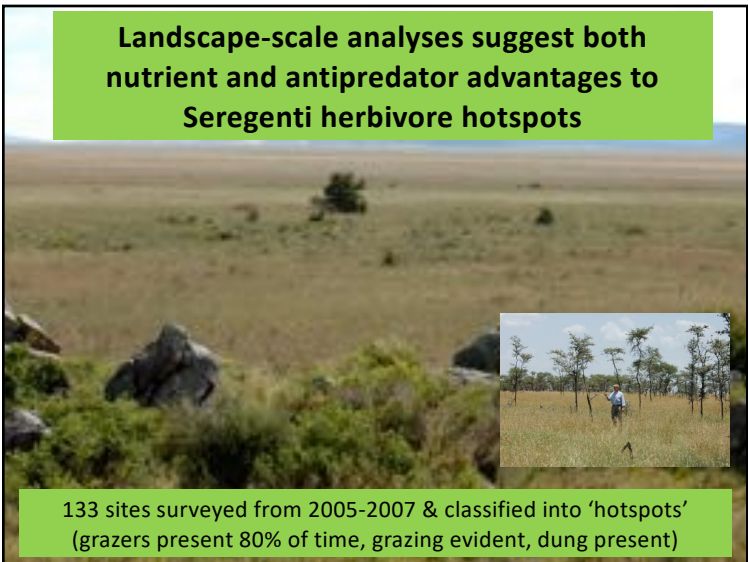
Final Notes on Centering

- In uncentered model, additive paths estimate the effect of one variable in the absence of the other.
- In centered model, additive paths estimate the effect of one variable at the average level of the other.
- E.g., fire severity has no effect when age = 0 **versus** fire severity has an effect at the mean level of age

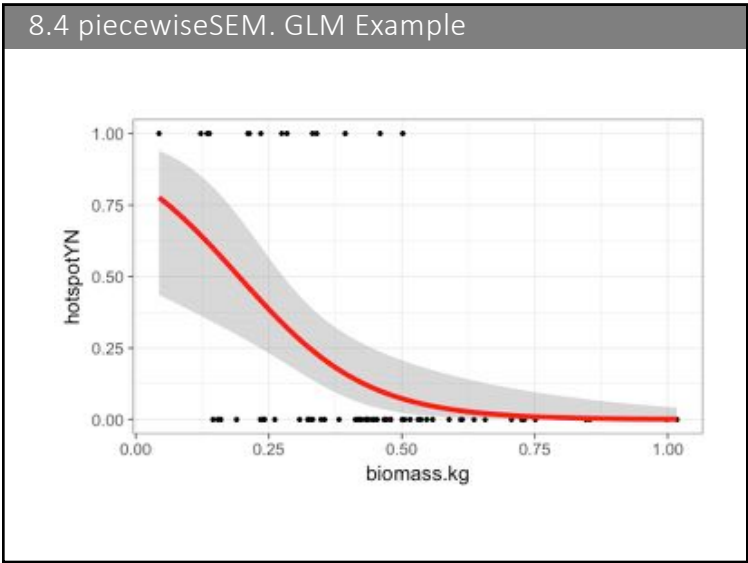
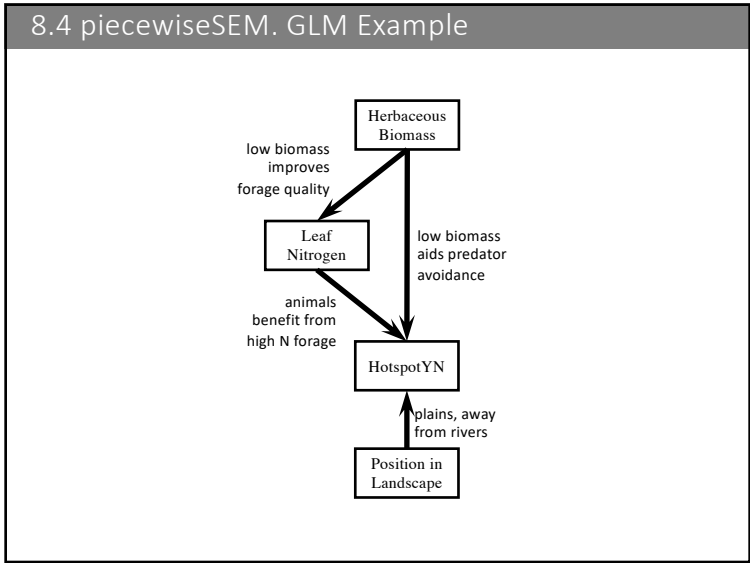
Non-linearities and More

1. Non-linearities in models
 - Polynomial Terms
 - Interactions
2. Generalized Linear Models
3. Special Considerations for GLMs
4. Standardized Nonlinear Coefficients

Landscape-scale analyses suggest both nutrient and antipredator advantages to Seregenti herbivore hotspots



133 sites surveyed from 2005-2007 & classified into 'hotspots' (grazers present 80% of time, grazing evident, dung present)

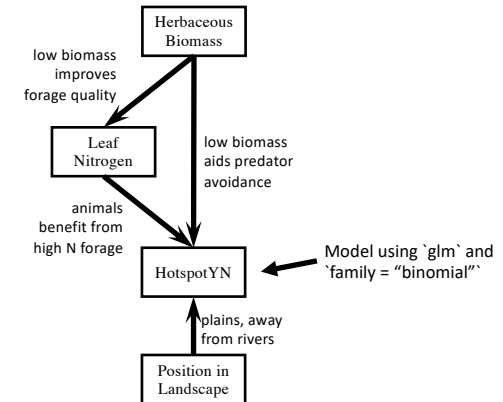


GLM. Components

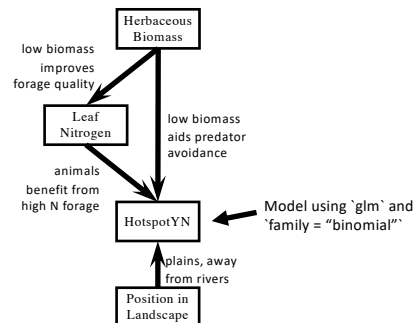
1. A likelihood: $y_i \sim \text{dbin}(\text{prob} = \mu_i, \text{size} = 1)$
 - Could also be poisson, Gamma, negative binomial, etc.
2. A link function: $g(\mu_i) = \eta_i$
 - Logit for binomial
 - Could be log, identity, inverse, etc. for others
3. A linear predictor: $\eta_i = \sum \beta X_i$

Other distributions possible – we are exploring other packages

8.4 piecewiseSEM. GLM Example

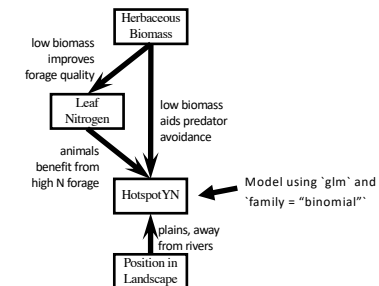


8.4 piecewiseSEM. GLM Example



```
# Load data and fit this model!
anderson <- read.csv("../data/anderson.csv")
```

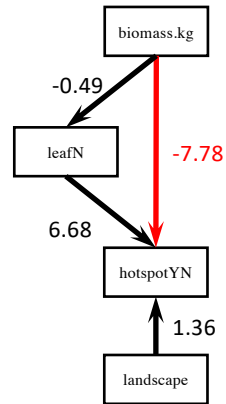
ACTIVITY. Anderson results



```
anderson.sem <- psem(
  lm(leafN ~ biomass.kg, anderson),
  glm(hotspotYN ~ leafN + biomass.kg + landscape,
      family = "binomial", data = anderson),
  data = anderson
)
```

ACTIVITY. Anderson results from coefs

UNSTANDARDIZED

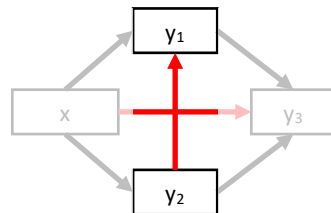


Non-linearities and More

1. Non-linearities in models
2. Generalized Linear Models
3. Special Considerations for GLMs and Dsep
4. Standardized Nonlinear Coefficients

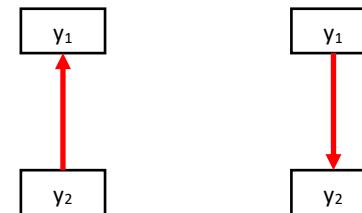
8.5 Directed Separation. A warning

- Intermediate non-normal endogenous variables pose a challenge



8.5 Directed Separation. A warning

- If normal, significance values are reciprocal



8.5 Directed Separation. A warning

```
# Show that y2 ~ y1 is the same as y2 ~ y1 for LM
mody1.y2 <- lm(y1 ~ y2 + x, data)

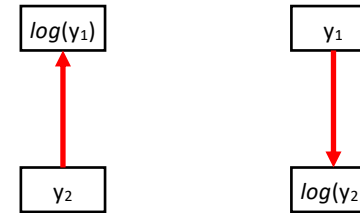
mody2.y1 <- lm(y2 ~ y1 + x, data)

summary(mody1.y2)$coefficients[2, 4]
[1] 0.5152512

summary(mody2.y1)$coefficients[2, 4]
[1] 0.5152512
```

8.5 Directed Separation. A warning

- If non-normal, significance values are *not* reciprocal because of transformation via link function



8.5 Directed Separation. A warning

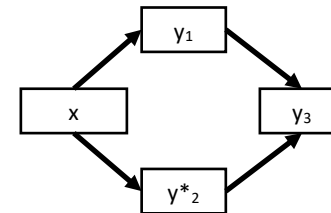
```
# Show that y2 ~ y1 is not the same as y2 ~ y1 for GLM
mody1.y2 <- lm(y1 ~ y2 + x, data)

mody2.y1.glm <- glm(y2 ~ y1 + x, "poisson", data)

summary(mody1.y2)$coefficients[2, 4]
[1] 0.5152512

summary(mody2.y1.glm)$coefficients[2, 4]
[1] 0.4792175
```

8.5 Directed Separation. A warning



```
# Create SEM with GLM
modelList <- psem(
  lm(y1 ~ x, data),
  glm(y2 ~ x, "poisson", data),
  lm(y3 ~ y1 + y2, data),
  data
)
```

8.5 Directed Separation. A warning

```
# Run summary
summary(modelList)

Error:
Non-linearities detected in the basis set where P-values are not symmetrical.
This can bias the outcome of the tests of directed separation.

Offending independence claims:
y2 <- y1 *OR* y2 -> y1

Option 1: Specify directionality using argument 'direction = c()'.

Option 2: Remove path from the basis set by specifying as a correlated error
using '%~%'.

Option 3: Use argument 'conserve = TRUE' to compute both tests, and return the
most conservative P-value.
```

8.5 Directed Separation. Options

1. Specify directionality
 - You know a priori which direction the claim should flow
2. Remove path from the basis set
 - Eh.....
3. Calculate both p-value and choose the *lower* one to be conservative
 - Often the most honest choice
 - piecewiseSEM's default

8.5 Directed Separation. A warning

```
# Address conflict using conserve = T
summary(modelList, conserve = T)

dSep(modelList, conserve = T)

  Independ.Claim  Estimate Std.Error DF  Crit.Value  P.Value
1 y3 ~ x + ... -0.2006020 0.1088444 96 -1.8430170 0.06841223
2 y2 ~ y1 + ... -0.2826168 0.3994236 97 -0.7075617 0.47921747

summary(mody1.y2)$coefficients[2, 4]

[1] 0.5152512

summary(mody2.y1.glm)$coefficients[2, 4]

[1] 0.4792175
```

8.5 Directed Separation. A warning

```
# Address conflict using direction = c()
dSep(modelList, direction = c("y2 <- y1"))

  Independ.Claim  Estimate Std.Error DF  Crit.Value  P.Value
1 y3 ~ x + ... -0.20060205 0.10884438 96 -1.8430170 0.06841223
2 y1 ~ y2 + ... -0.01818537 0.02784565 97 -0.6530776 0.51525122

dSep(modelList, direction = c("y1 <- y2"))

  Independ.Claim  Estimate Std.Error DF  Crit.Value  P.Value
1 y3 ~ x + ... -0.2006020 0.1088444 96 -1.8430170 0.06841223
2 y2 ~ y1 + ... -0.2826168 0.3994236 97 -0.7075617 0.47921747
```

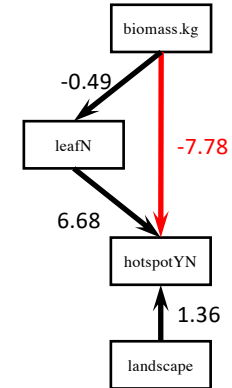
8.5 Directed Separation. A warning

```
# Address conflict using correlated errors
modelList2 <- update(modelList, y2 %~~% y1)

dSep(modelList2)

Independ.Claim Estimate Std.Error DF Crit.Value P.Value
1 y3 ~ x + ... -0.200602 0.1088444 96 -1.843017 0.06841223
```

ACTIVITY. Anderson results



```
> fisherC(anderson.sem, conserve=TRUE)
Fisher.C df P.Value
1 2.491 2 0.288
```

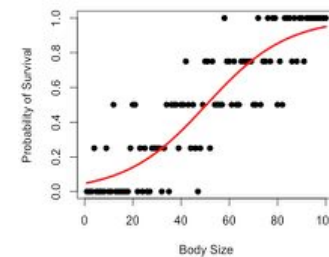
Non-linearities and More

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GLM. The problem

PROBLEM: the relationship between y and x is non-linear; the estimated Betas of the effect on η are on a linear scale

The standard deviation of y is different than the standard deviation of η . Must use sd of η to standardize Beta...how do we get it?



Grace et al. In Review

GLM Review

Expectation (some distribution is applied for likelihood):
 $E(y) = \mu$

Link Function (is the inverse) $x \rightarrow \eta \rightarrow \mu \rightarrow y$
 $g(\mu) = \eta$

Linear Relationship at the core
 $\eta = x\beta$

A Latent Theoretic Approach

- Assume that y is related to η via some unobserved variable y^*
 $x \rightarrow \eta \rightarrow y^* \rightarrow y$
- When $y^* > \text{some value}$, $y=1$, else $y = 0$
- Variance in $y^* = \text{variance in } \eta + \text{theoretical variance of the error distribution (sd}_\epsilon)$ – every error distribution has one!
 - E.g. 1 for probit link, $\pi^2/3$ for logit

$$\beta_j = b_j \text{sd}_x / (\text{sd}_\eta + \text{sd}_\epsilon)$$

Observed Variance Approach

Thinking about R^2 (more on that later):

$$R^2 = \sigma^2_{E(y)} / \sigma^2_y$$

So, $\text{sd}_y = \text{sd}_{E(y)} / R$

$$\beta_j = b_j \text{sd}_x / (\text{sd}_{E(y)} / R)$$

Anderson results with OE formulation

```

> coefs(anderson.sem, standardize.type = "Menard.OE")
  Response Predictor Estimate Std.Error DF Crit.Value P.Value Std.Estimate
1  leafN biomass.kg -0.4880  0.1050  65  -4.6486  0.0000  -0.4995 ***
2 hotspotYN leafN  6.6867  2.7818  63   2.4037  0.0162  0.2638 *
3 hotspotYN biomass.kg -7.7838  3.5694  63  -2.1807  0.0292  -0.3143 *
4 hotspotYN landscape  1.3600  0.4955  63   2.7449  0.0061  0.4913 **
    
```

