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# Introduction to structural equation modeling and mixed models in

## **Day 4 – Part 2: SEM**

Oksana Buzhdygan

[oksana.buzh@fu-berlin.de](mailto:oksana.buzh@fu-berlin.de)

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- Model Comparison in SEM
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# The concept of Goodness of Fit

## 1) Are we ignoring important links?

Links = Processes

**When we are missing important paths:**

- our parameter estimates may be incorrect
- our model is misspecified

Does the model fit the data?

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Does the model  
represent the data well?

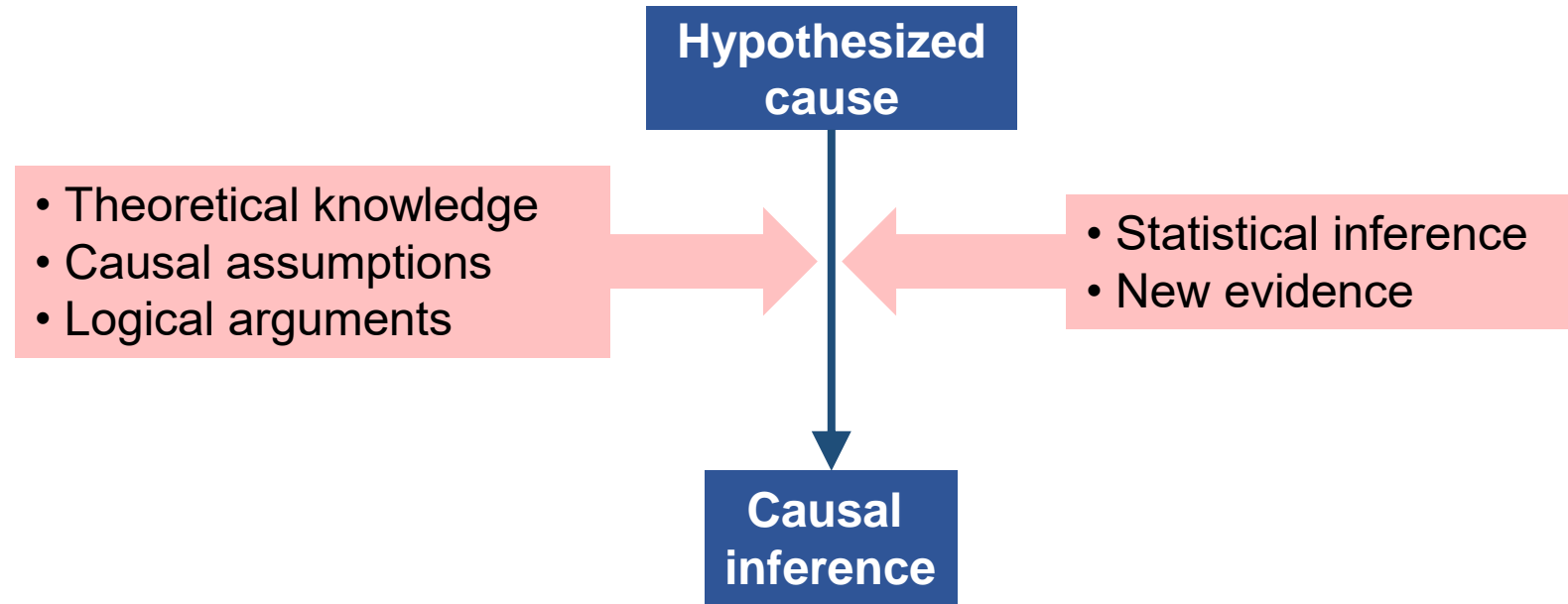
=

Are we missing important  
information?

## 2) Are all the included links supported by the data?

# Model Comparison

## Model selection is a “Decision Problem”



- SEM is not null hypothesis testing, but evaluating theory
- Decision should be based on
  - 1) a priory causal knowledge **and**
  - 2) the weight of data

# Model Comparison

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**Question 1. Are we ignoring important links?**

# Model Comparison



California, USA.

Photos credit: USFS, and Jon Keeley, USGS

[doi.org/10.1186/s42408-019-0041-0](https://doi.org/10.1186/s42408-019-0041-0)

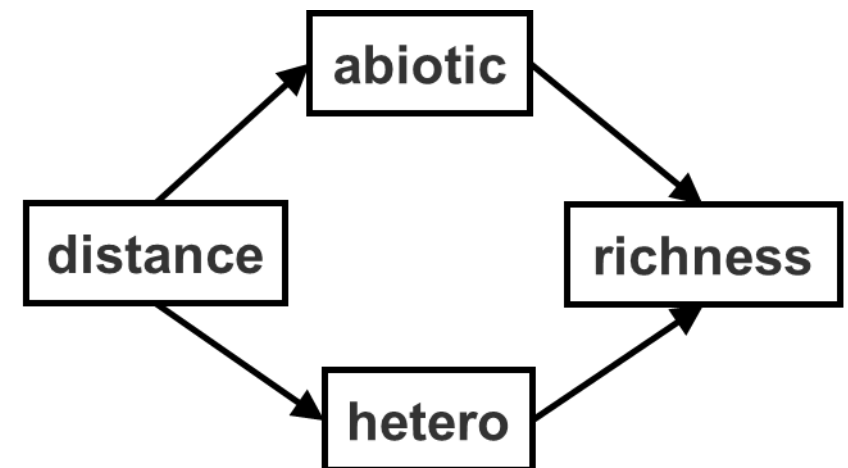
[doi.org/10.1071/WF07049](https://doi.org/10.1071/WF07049)

```
# Keeley data  
library(piecewiseSEM)  
data(keeley)
```

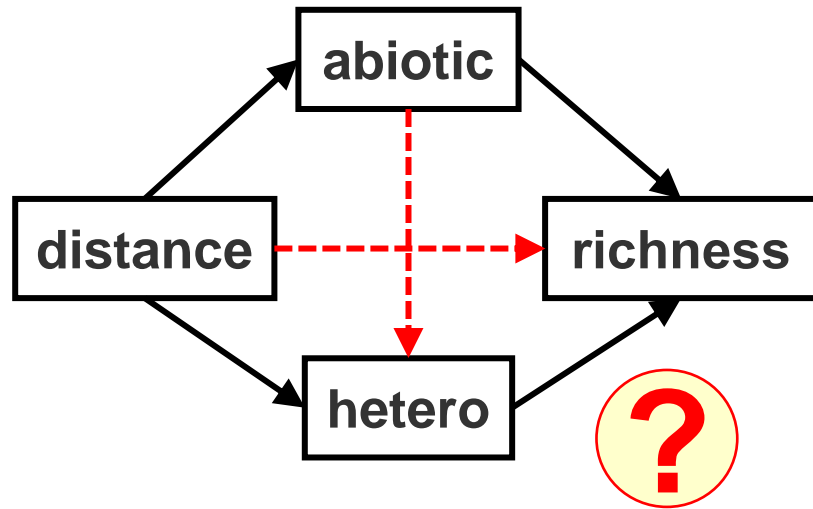
Data: Grace, J.B. and Keeley, J.E. 2006. Ecological Applications 16:503-514

## Postfire recovery of plant communities in California shrublands

- Vegetation species richness "**richness**"
- Local abiotic conditions (aspect, soils) "**abiotic**"
- Spatial heterogeneity "**hetero**"
- Distance from coast "**distance**"



# Model Comparison



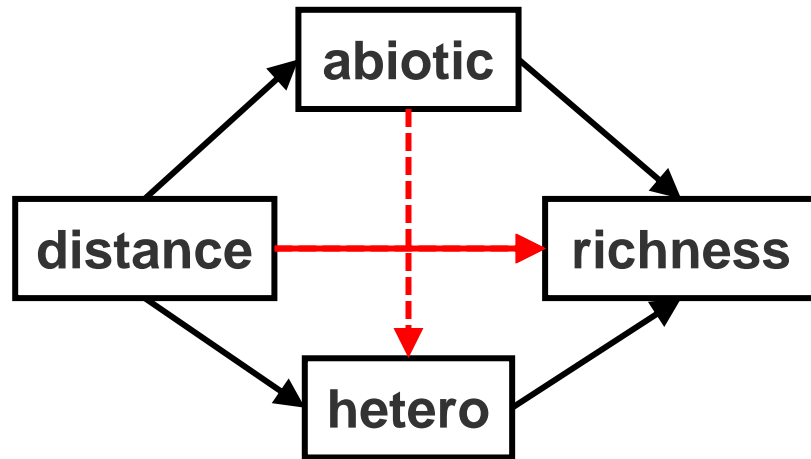
```
library(piecewiseSEM)
data(keeley)
# Specify the model in lavaan
sem_m1 <- '
  rich ~ abiotic + hetero
  hetero ~ distance
  abiotic ~ distance'

# Fit the model
sem_fit1 <- sem(sem_m1, data=keeley)
summary(sem_fit1, standardize = T)
```

```
>
...
Model Test User Model:
```

Test statistic	17.831
Degrees of freedom	2
P-value (Chi-square)	0.000

# Model Comparison

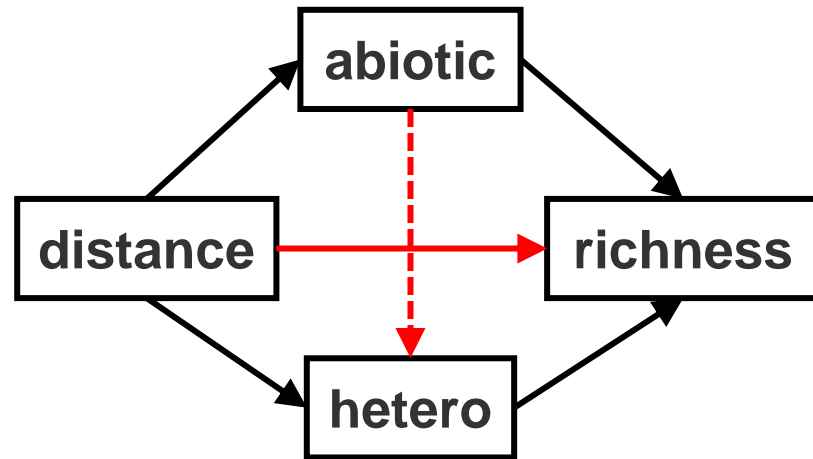


```
# residual correlation  
resid(sem_fit1, "cor")$cov  
  
>  
      rich  hetero abiotc distnc  
rich      0.000  
hetero    0.042 0.000  
abiotic   0.032 0.118 0.000  
distance 0.271 0.000 0.000 0.000
```

Large Residual Correlation for  
"distance" – "rich"



# Model Comparison



## Modification Indices (Lagrange Multipliers)

```
# Request modification indices
summary(sem_fit1, standardize = T,
        modindices=T)

# or
modificationIndices(sem_fit1, standardized=F)
```

- the (approximate) amount that  $\chi^2$  would decrease due to including a path.

# Model Comparison

Modification  
index

Expected  
parameter change

```
>
      lhs  op   rhs    mi    epc
8 distance ~~ distance 0.000  0.000
9   rich  ~~   hetero 15.181 -1.690
10  rich  ~~   abiotic 15.181 -76.202
11 hetero ~~   abiotic  1.792  0.103
12  rich  ~ distance 15.181  0.662
13 hetero ~    rich   1.141 -0.002
14 hetero ~   abiotic  1.792  0.002
15 abiotic ~    rich   3.811 -0.196
16 abiotic ~   hetero  1.792  8.933
17 distance ~    rich 14.728  0.347
18 distance ~   hetero  0.000  0.000
19 distance ~   abiotic  0.000  0.000
```

## Modification Indices (Lagrange Multipliers)

```
# Request modification indices
summary(sem_fit1, standardize = T,
        modindices=T)

# or
modificationIndices(sem_fit1, standardized=F)
```

- **mi** - the (approximate) amount that  $\chi^2$  would decrease due to including a path.
- Looking for 'mi' values > 3.84

The “single-degree-of-freedom chi-square criterion” = 3.84

# Model Comparison

## Modification Indices (Lagrange Multipliers)

```
>
      lhs op      rhs      mi      epc
9     rich ~~   hetero 15.181  -1.690
10    rich ~~   abiotic 15.181 -76.202
12    rich ~ distance 15.181   0.662
15  abiotic ~      rich   3.811  -0.196
17 distance ~      rich 14.728   0.347
```

```
# Look for indices  $\geq 3.84$ 
```

```
modificationIndices(sem_fit, standardized=F,
                    minimum.value=3.8)
```

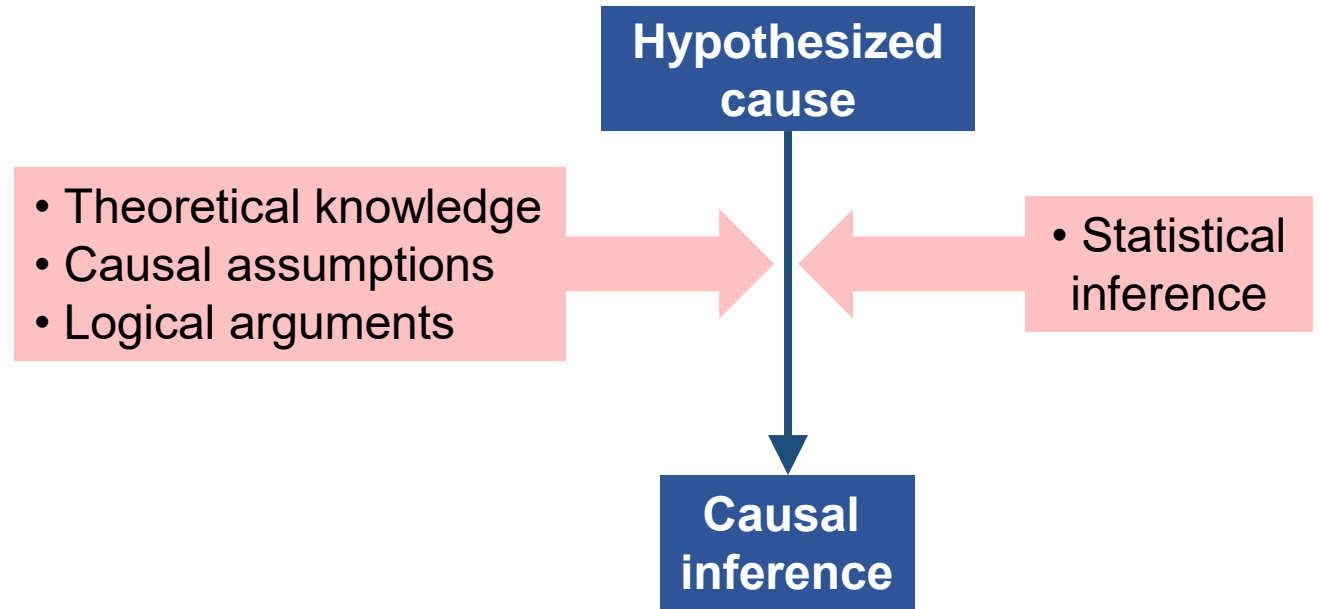
- **mi** - the (approximate) amount that  $\chi^2$  would decrease due to including a path.
- Looking for **mi** values  $> 3.84$
- **Be very careful here for data dredging.**

# Model Comparison

## Modification Indices (Lagrange Multipliers)

```
>
      lhs op      rhs      mi      epc
9     rich ~~   hetero 15.181  -1.690
10    rich ~~   abiotic 15.181 -76.202
12    rich ~ distance 15.181   0.662
15   abiotic ~      rich  3.811  -0.196
17 distance ~      rich 14.728   0.347
```

- Not a good practice for confirmatory modelling
- Ok for exploratory modelling

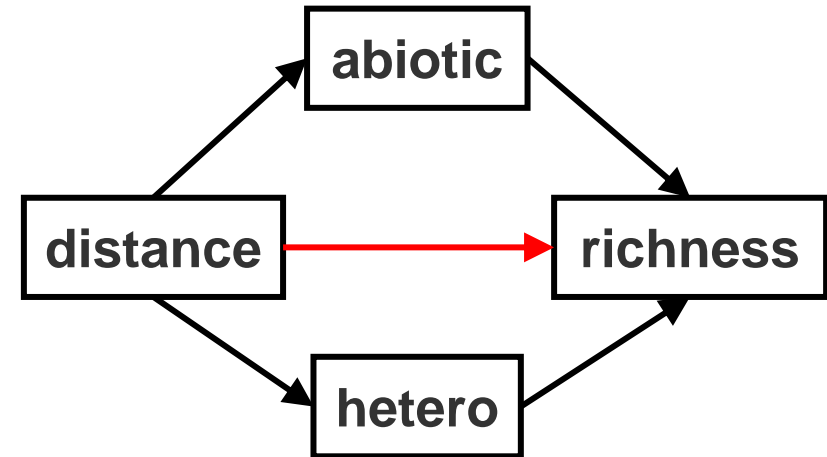


- Looking for **mi** values > 3.84
- Be very careful here for data dredging.

# Model Comparison

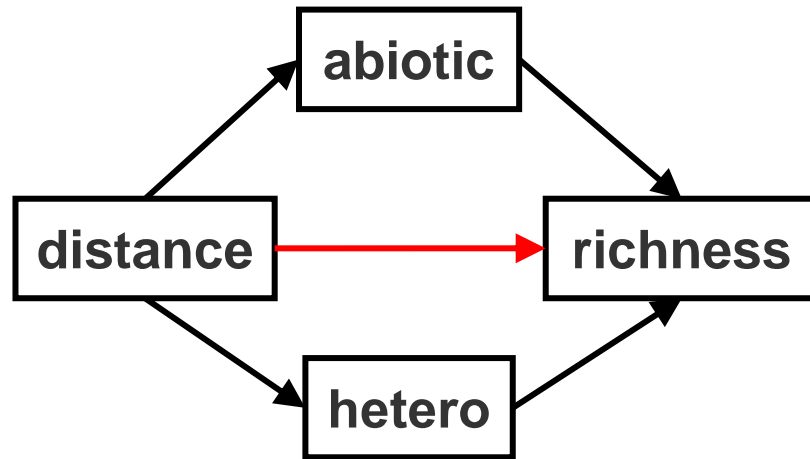
## Modification Indices (Lagrange Multipliers)

```
>
      lhs op      rhs      mi      epc
9    rich ~~ hetero 15.181 -1.690
10   rich ~~ abiotic 15.181 -76.202
12   rich ~ distance 15.181  0.662
15 abiotic ~      rich  3.811 -0.196
17 distance ~      rich 14.728  0.347
```



- **mi** - the (approximate) amount that  $\chi^2$  would decrease due to including a path.
- Looking for **mi** values  $> 3.84$
- Be very careful here for data dredging.

# Model Comparison



```
# Specify the model 2 in lavaan
sem_m2 <- '
  rich ~ abiotic + hetero + distance
  hetero ~ distance
  abiotic ~ distance`

# Fit the model
sem_fit2 <- sem(sem_m2, data=keeley)
summary(sem_fit2, standardize = T)
```

## # Model 2

Model Test User Model:

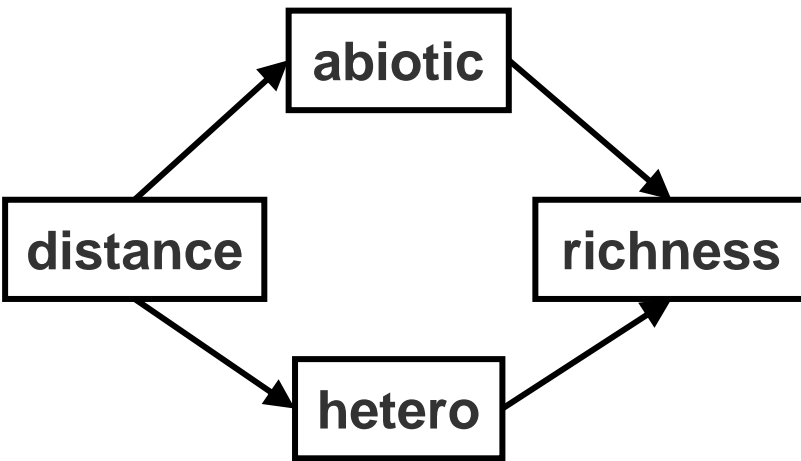
Test statistic	1.810
Degrees of freedom	1
P-value (Chi-square)	0.178

## # Model 1

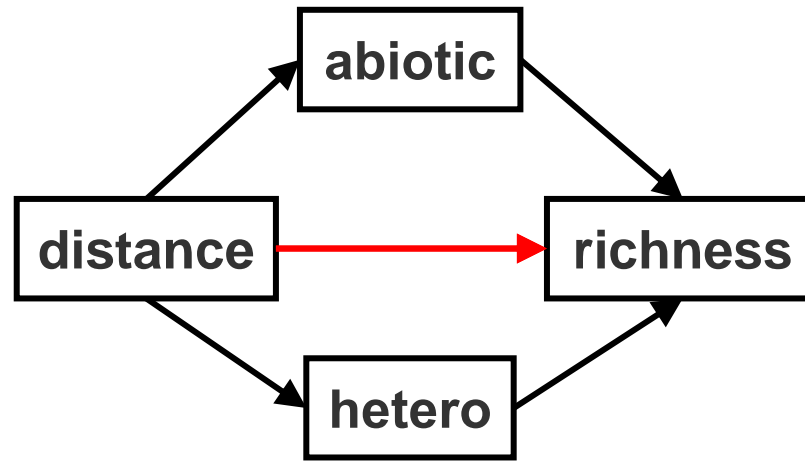
Test statistic	17.831
Degrees of freedom	2
P-value (Chi-square)	0.000

# Model Comparison

The likelihood-ratio test  
( $\chi^2$  – difference test)



Model 1



Model 2

```
# The likelihood-ratio test
```

```
anova(sem_fit1, sem_fit2)
```

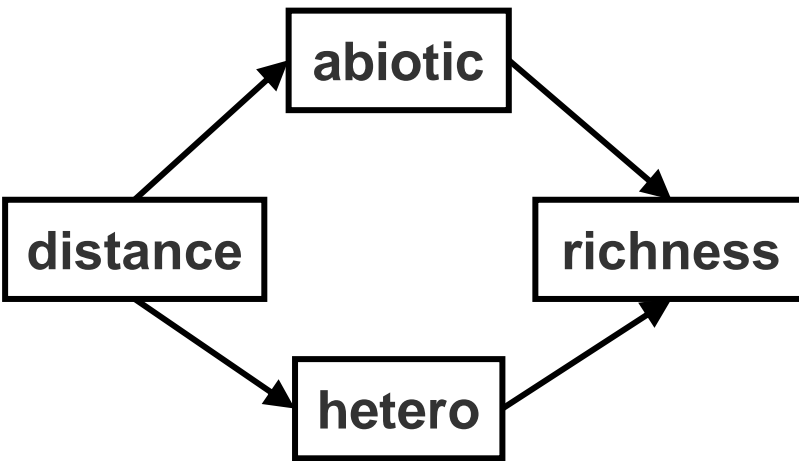
```
>
```

```
Chi-Squared Difference Test
```

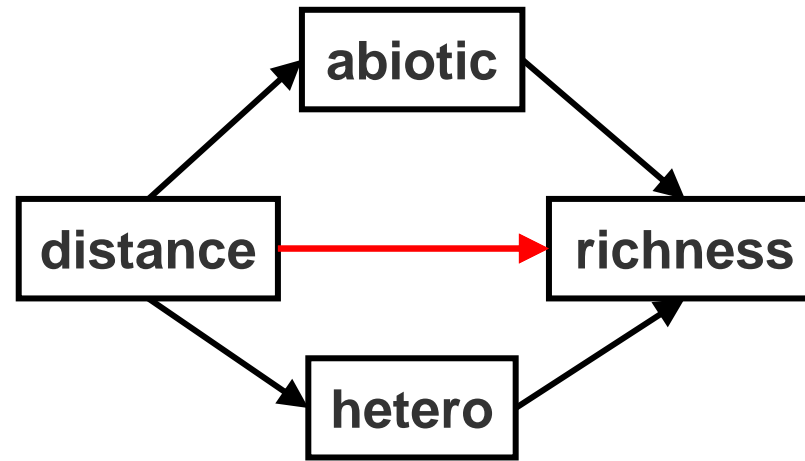
	Df	AIC	BIC	Chisq	Chisq diff	Df diff	Pr(>Chisq)
sem_fit2	1	1155.3	1175.3	1.8104			
sem_fit1	2	1169.3	1186.8	17.8307	16.02	1	6.267e-05 ***

# Model Comparison

The likelihood-ratio test  
( $\chi^2$  – difference test)



Model 1



Model 2

```
# The likelihood-ratio test
```

```
anova(sem_fit1, sem_fit2)
```

```
>
```

```
Chi-Squared Difference Test
```

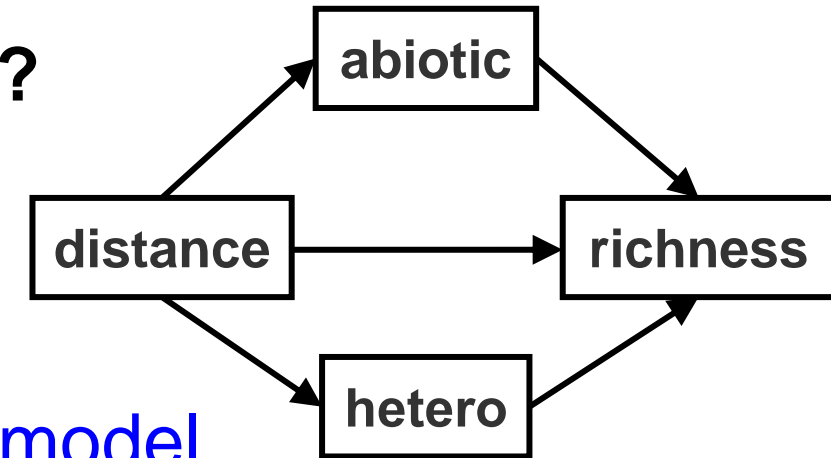
	Df	AIC	BIC	Chisq	Chisq diff	Df diff	Pr(>Chisq)
sem_fit2	1	1155.3	1175.3	1.8104			
sem_fit1	2	1169.3	1186.8	17.8307	16.02	1	6.267e-05 ***



# Model Comparison

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**Question 1. Are we ignoring important links?**



We are not missing major links in our model

**Question 2. Are all the included links supported by the data?**

# Model Comparison

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1. Does a simpler model still reproduce the more complex model's covariance matrix? Models are required to be nested.
  - Likelihood Ratio Testing (LR)
2. Compare the weight of evidence across multiple models (models are not required to be nested)
  - Information Theoretic Approaches (e.g. AIC)

The two can be used complementarily, however!

# Model Comparison

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How many parameters it takes to fit your model?



@RealFabianBerg

Remember the principle of **parsimony**

# Model Comparison

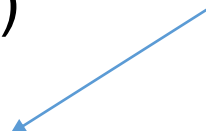
---

## Akaike information criterion (AIC)

- Based on model fit  $\chi^2$
- Parsimony adjusted for model complexity  $q$
- Models are not required to be nested (like in LR test)

$$AIC = \chi^2 + 2q$$

**$q$**  number of estimated parameters in a model



# Model Comparison

## Akaike information criterion (AIC)

- Based on model fit  $\chi^2$
- Parsimony adjusted for model complexity  $q$
- Models are not required to be nested (like in LR test)

$$AIC = \chi^2 + 2q$$

$q$  number of estimated parameters in a model

$$AIC_c = AIC + \left( \frac{2q(q+1)}{n-q-1} \right)$$

**AIC<sub>c</sub>**

- Small Sample-Size Adjusted
- More complex parsimony correction term

$n$  number of samples

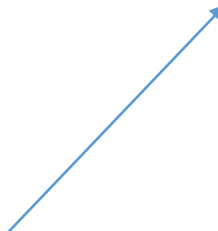
# Model Comparison

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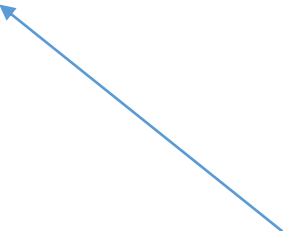
## Bayesian Information Criterion (BIC)

$$BIC = \chi^2 - DF \times \log(n)$$

***DF*** degrees of freedom



***n*** number of samples



# Model Comparison

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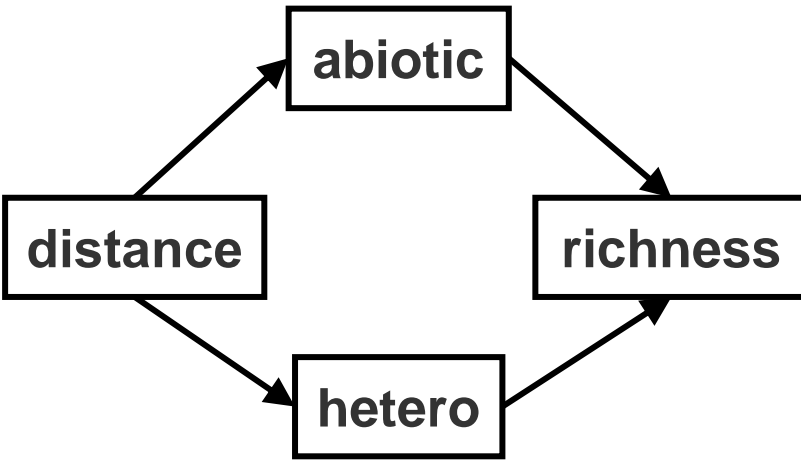
## AIC difference criteria

AIC difference	Support for equivalency of models
0-2	substantial
4-7	weak
> 10	none

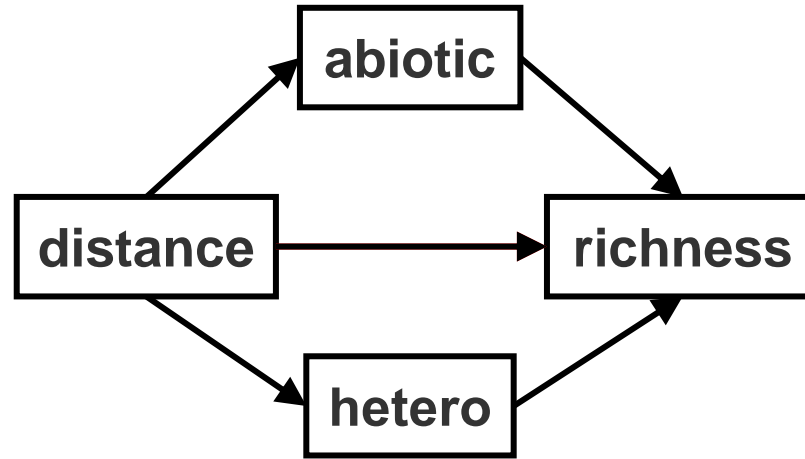
Burnham, K.P. and Anderson, D.R. 2002. Model Selection and Multimodel Inference. Springer Verlag. (second edition), p 70.

# Model Comparison

## Model Comparison with $AIC_c$



Model 1. Fully mediated

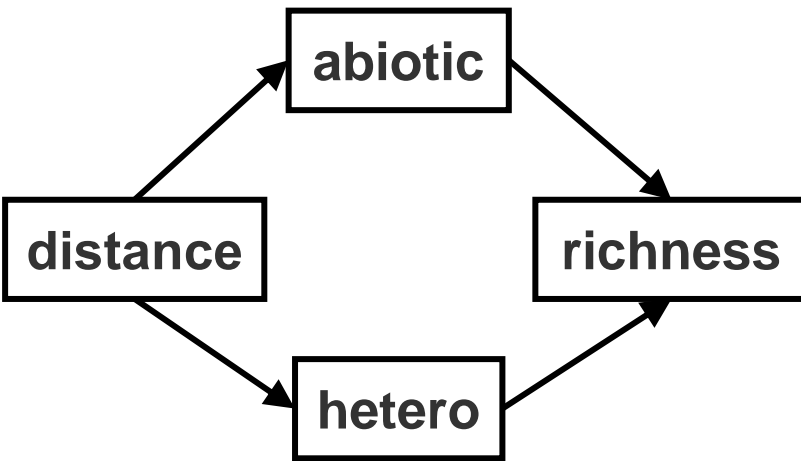


Model 2. Partially mediated

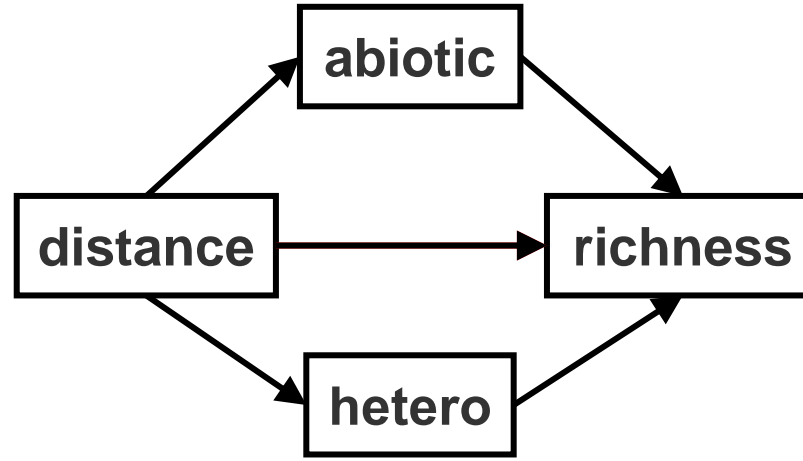


# Model Comparison

## Model Comparison with $AIC_c$



Model 1. Fully mediated



Model 2. Partially mediated

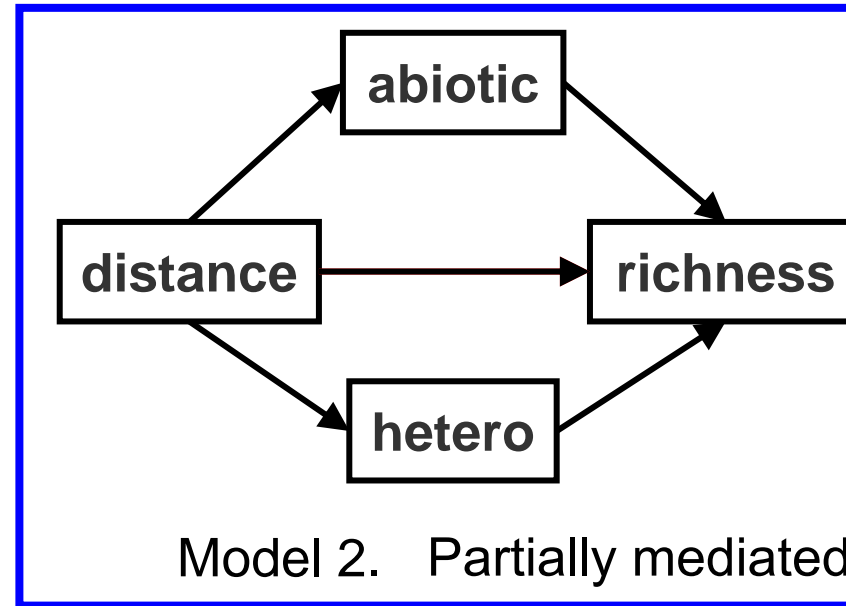
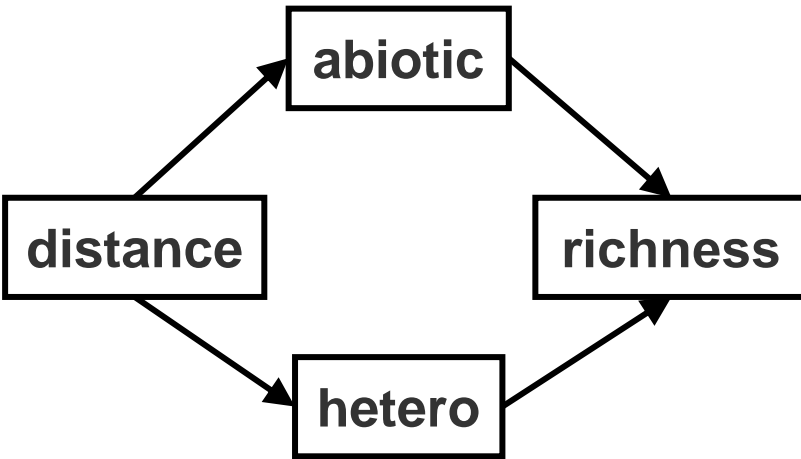
```
# Model selection based on AICc:  
library(AICcmodavg)  
aictab(cand.set = list(sem_fit1, sem_fit2),  
       modnames = c("Full", "Partial"))
```

```
> Model selection based on AICc:
```

	K	AICc	Delta_AICc	AICcWt	Cum.Wt	LL
Partial	8	1157.05	0.00	1	1	-569.63
Full	7	1170.66	13.61	0	1	-577.64

# Model Comparison

## Model Comparison with $AIC_c$



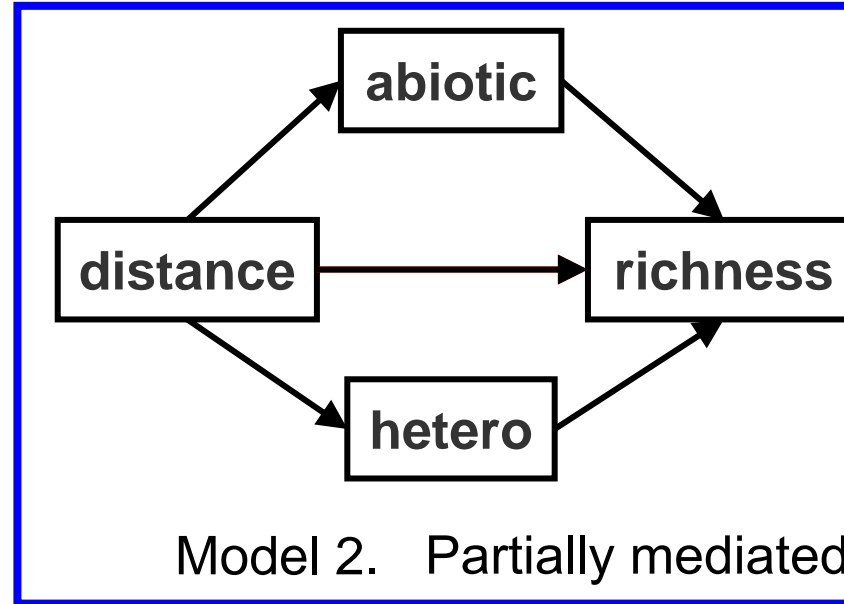
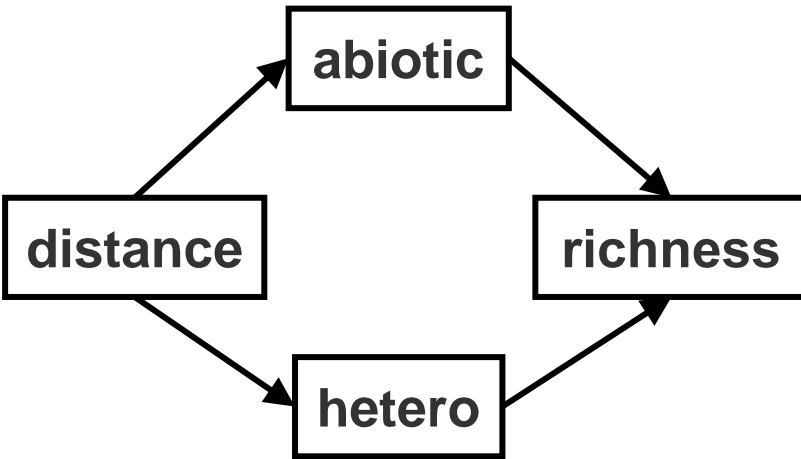
```
# Model selection based on AICc:  
library(AICcmodavg)  
aictab(cand.set = list(sem_fit1, sem_fit2),  
       modnames = c("Full", "Partial"))
```

> Model selection based on AICc:

	K	AICc	Delta_AICc	AICcWt	Cum.Wt	LL
Partial	8	1157.05	0.00	1	1	-569.63
Full	7	1170.66	13.61	0	1	-577.64

# Model Comparison

## Model Comparison with $AIC_c$



```
# Model selection based on AICc:  
library(AICcmodavg)  
aictab(cand.set = list(sem_fit1, sem_fit2),  
       modnames = c("Full", "Partial"))
```

> Model selection based on AICc:

	K	AICc	Delta_AICc	AICcWt	Cum.Wt	LL
Partial	8	1157.05	0.00	1	1	-569.63
Full	7	1170.66	13.61	0	1	-577.64

# Model Comparison

```
# Model Comparison with AIC
aic <- AIC(sem_fit1, sem_fit2)
> aic
      df      AIC
sem_fit1  7 1169.29
sem_fit2  8 1155.27

# Calculate delta AIC
d_aic <- aic[2] - min(aic[2])
>      AIC
sem_fit1 14.02032
sem_fit2  0.00000

# Rank delta AIC in ascending order
library(dplyr)
arrange(d_aic, +AIC)
      AIC
sem_fit2 0.00000
sem_fit1 14.02032
```

## Model Comparison with AIC

---

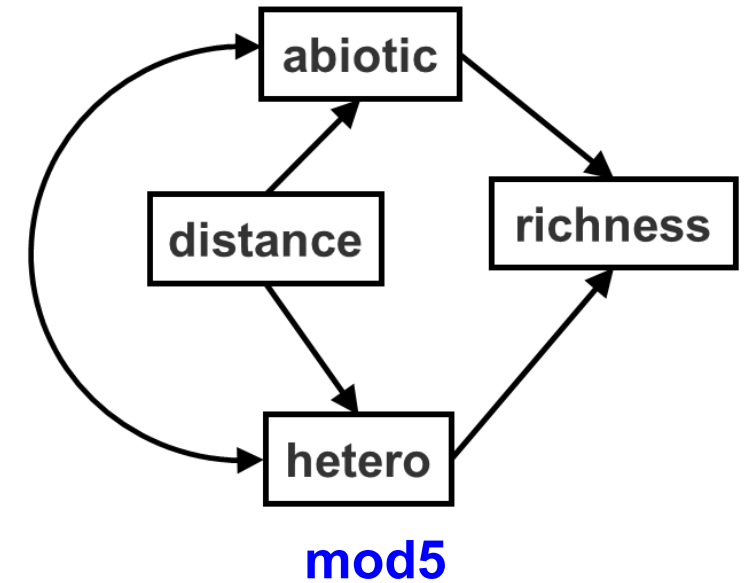
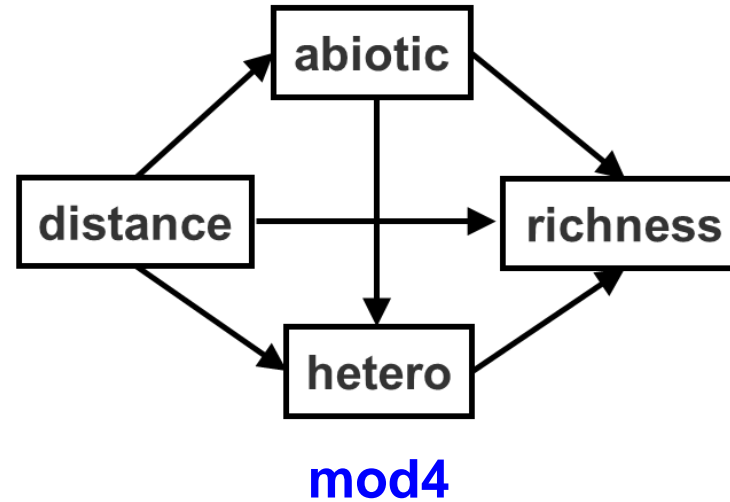
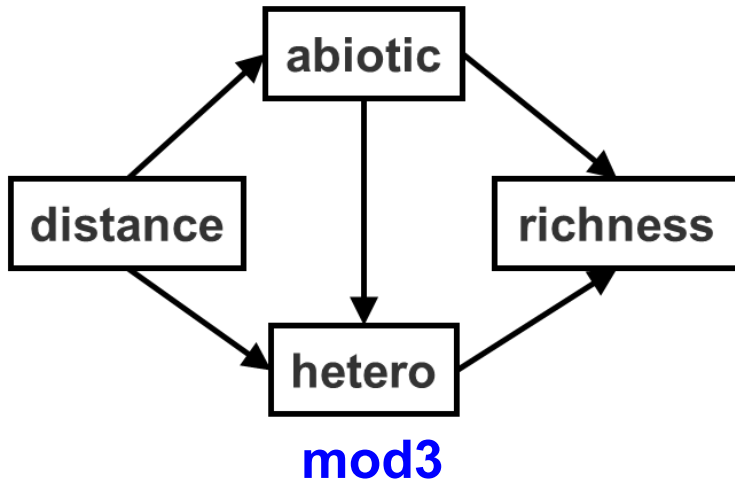
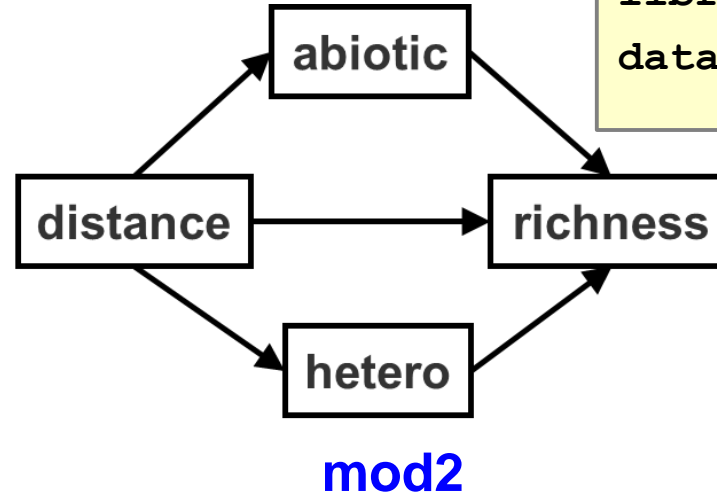
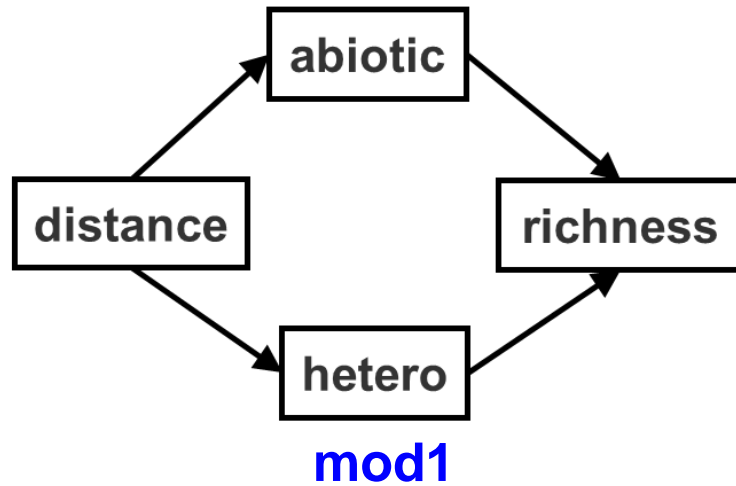
# Model Comparison

## Day 4 Task 2

# Day 4 Task 2

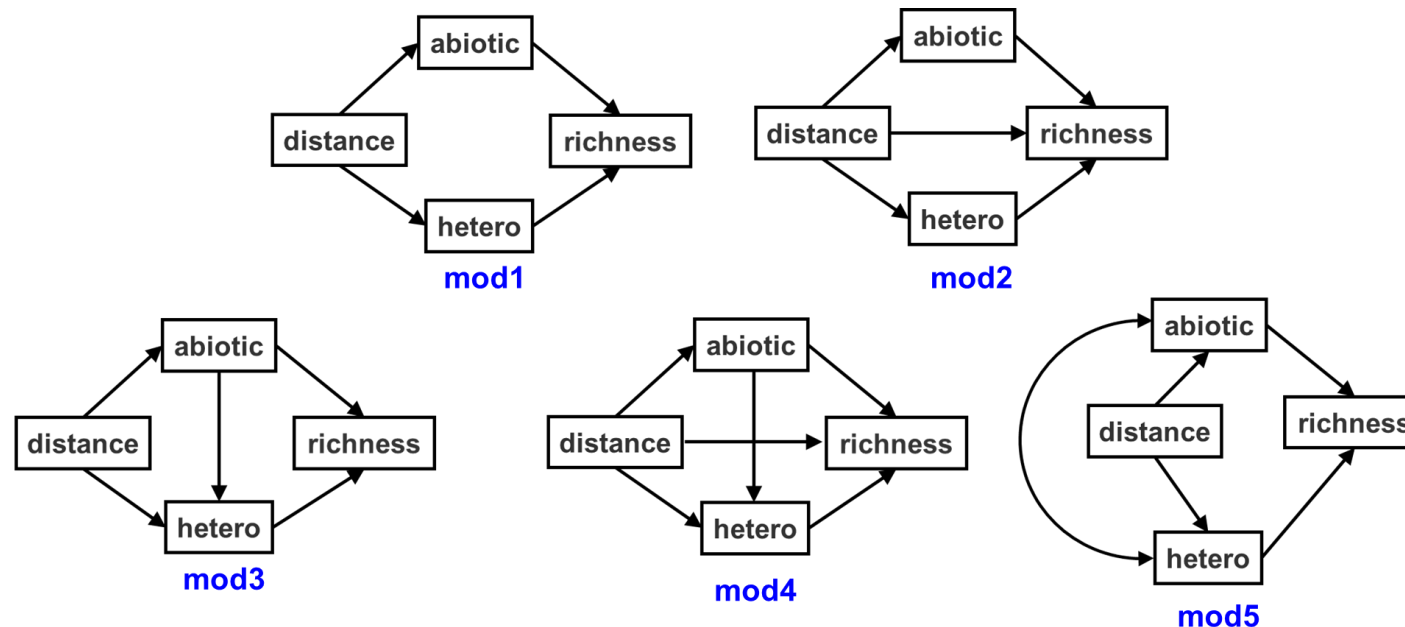
# Model Comparison

```
# Keeley data  
library(piecewiseSEM)  
data(keeley)
```



# Day 4 Task 2

1. Think about the scientific meaning when we include the correlations among “hetero” and “abiotic” (in model 5)
2. Specify each model in lavaan
3. Fit each model using data `data(keeley)`
4. Compare the models using AICc and select the best model



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# Test of Mediation

## Day 4 Task 3



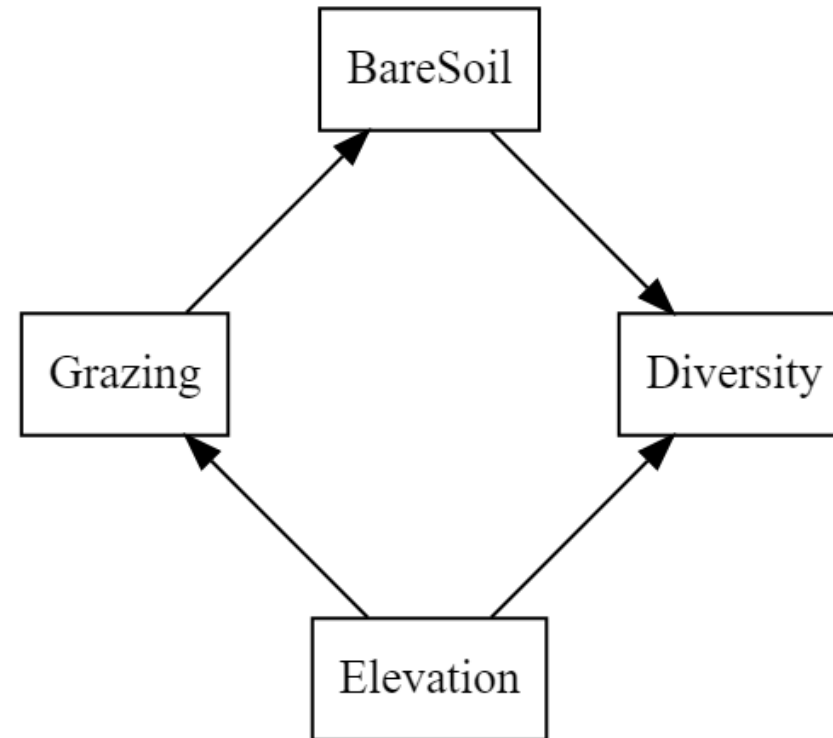
# Day 3 Task 3

## Test of mediation

### Effects of grazing on plant diversity along elevation gradient



```
# data  
data <- read.csv("Grass1_data_2.csv")
```



# Day 3 Task 3

For the model on Fig. 1:

1. For the variables on Fig 1 and data “Grassl\_data\_2.csv” check the assumptions of the covariance-based SEM
2. If there are any violations of the assumptions use the needed procedures to adjust for these violations (see slide 30 in part 1 Day 4) while you fit the model.
3. Get the fit indices.
4. Follow the procedures in this lecture (part 2) and test the following questions:
  - Are we ignoring important links?
  - Are all the included links supported by the data?

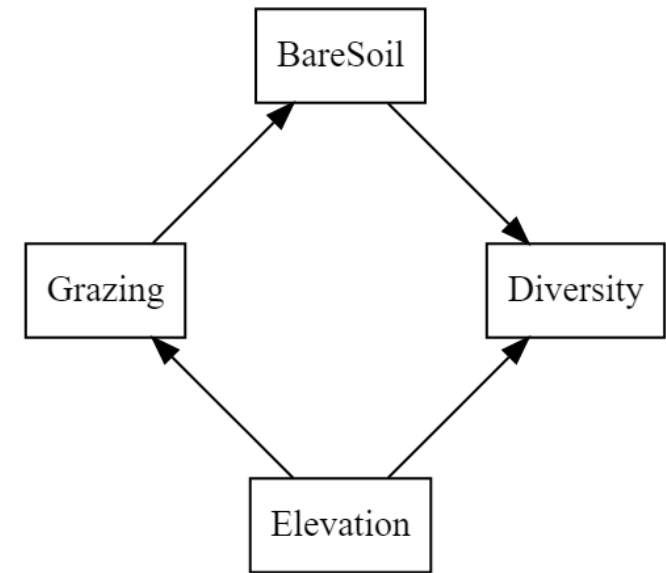


Fig. 1

# Day 4 Task 3

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For the model on Fig. 1:

1. For the variables on Fig 1 and data “Grassl\_data\_2.csv” check the assumptions of the covariance-based SEM
2. If there are any violations of the assumptions use the needed procedures to adjust for these violations (see slide 30 in part 1 Day 4) while you fit the model.
3. Get the fit indices.
4. Follow the procedures in this lecture (part 2) and test the following questions:
  - Are we ignoring important links?
  - Are all the included links supported by the data?

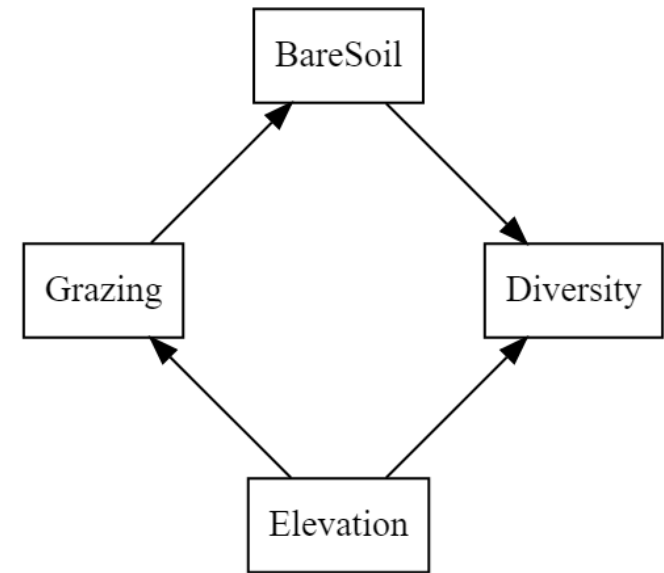


Fig. 1