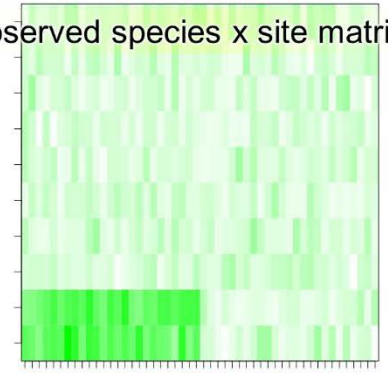
Inferring species associations from co-occurrence data

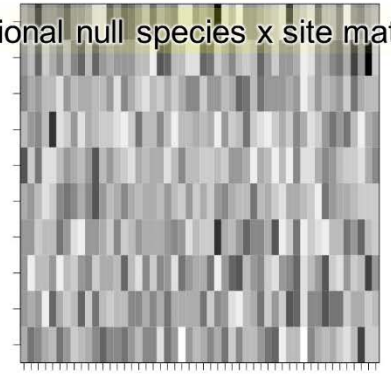
- Combining BIEN plots and occurrences

Step 1. Obtain observed and expected community data

Observed species x site matrix **O**

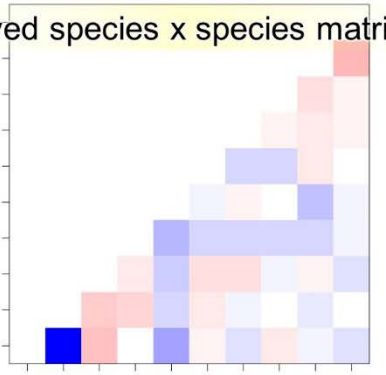


Regional null species x site matrix **N**

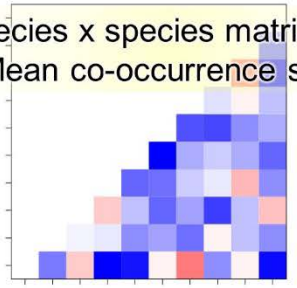


Step 2. Calculate observed and null co-occurrence scores

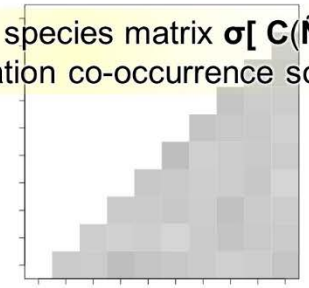
Observed species x species matrix **C(O)**



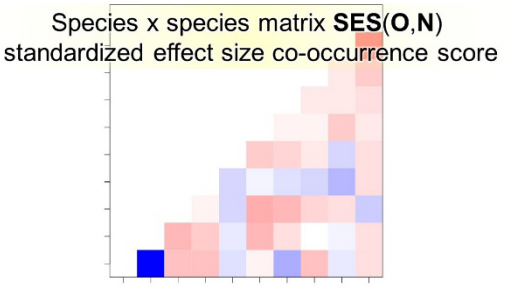
Null species x species matrix **μ[C(O)]**
Mean co-occurrence score



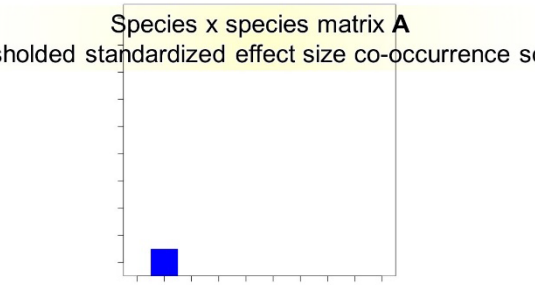
Null species x species matrix **σ[C(Ñ)]**
standard deviation co-occurrence score



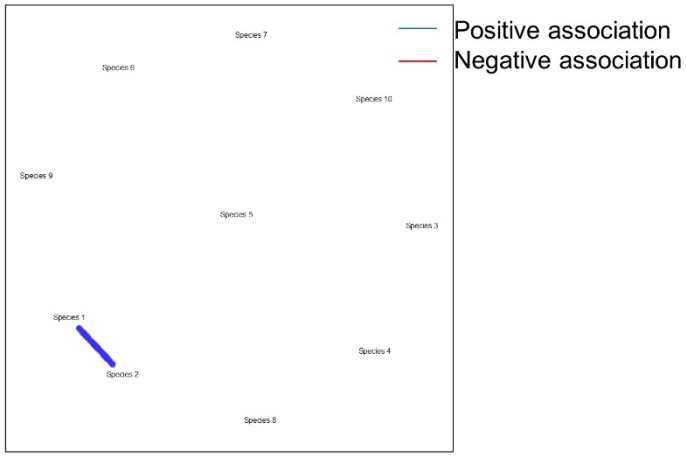
Step 3. Calculate strength and direction of each association

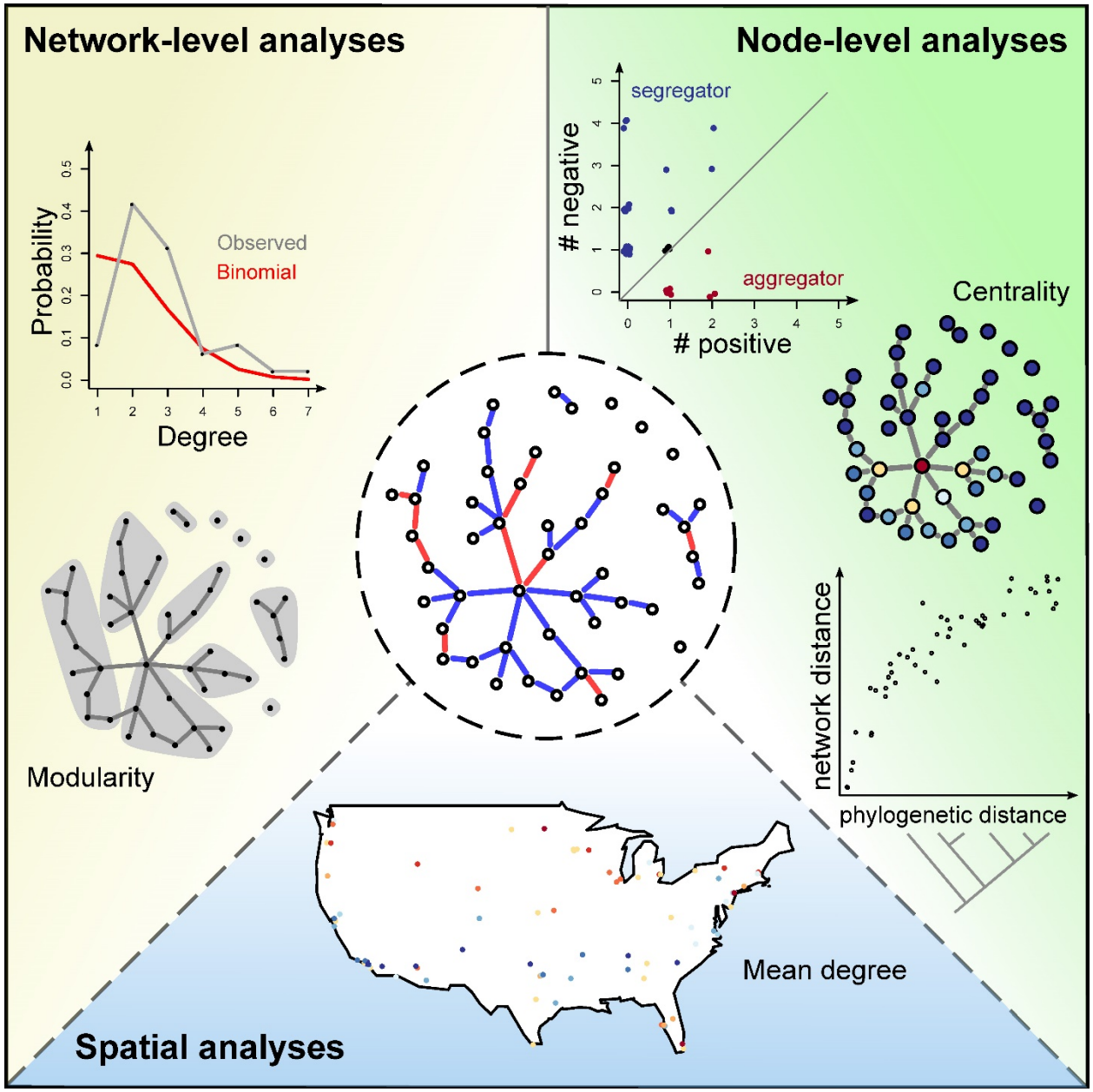


Step 4. Threshold values to detect significant associations



Step 5. Represent association matrix as weighted network




Network-level analyses
Node-level analyses
Probability
Degree
Observed
Binomial
negative
positive
segregator
aggregator
Centrality
Modularity
network distance
phylogenetic distance
Mean degree
Spatial analyses

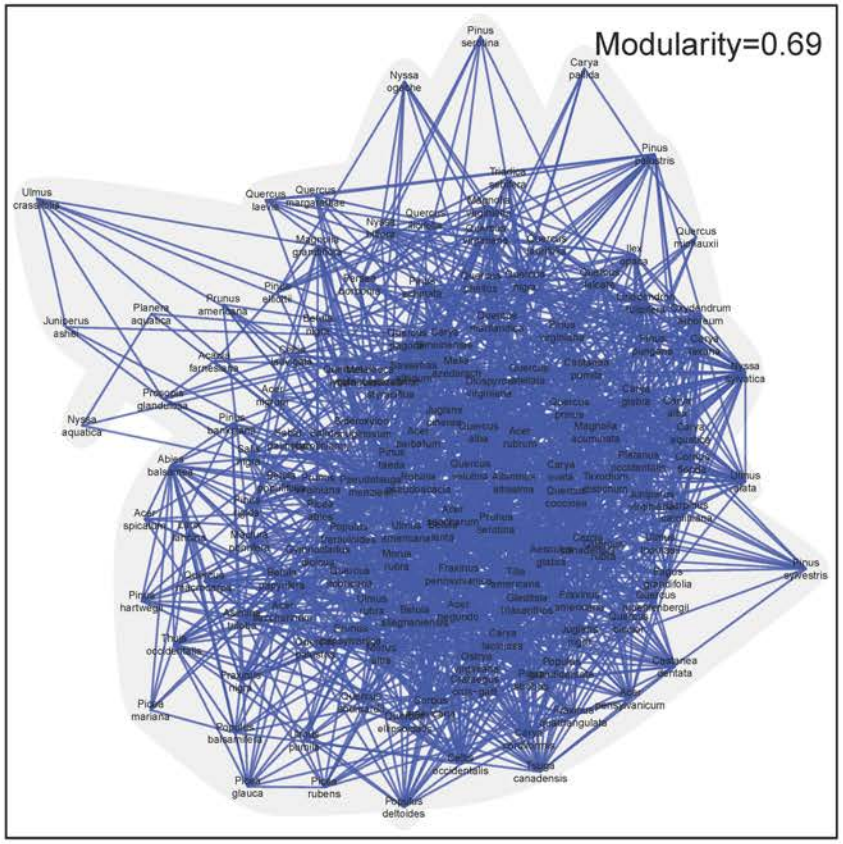
Combining plots and occurrences

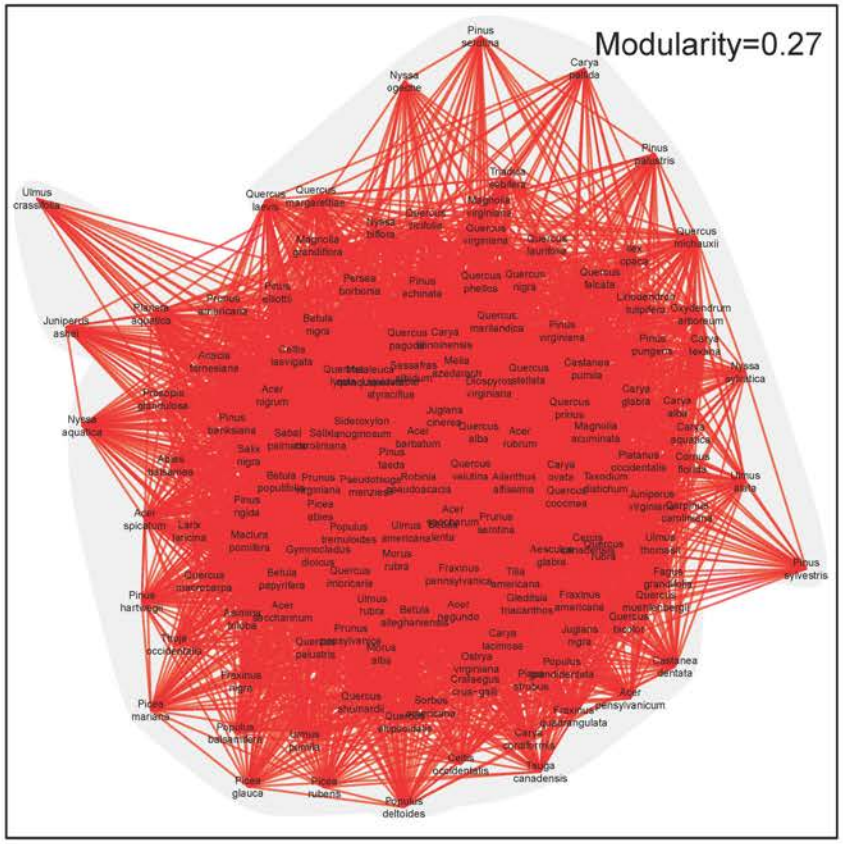
- 1009 FIA plots (abundance data)
- 139 tree species

- MaxEnt modelling for null:
  - BIEN occurrence data
  - “Standard” approach

- LOESS regression for null:
  - 5132 FIA plots

Random swap

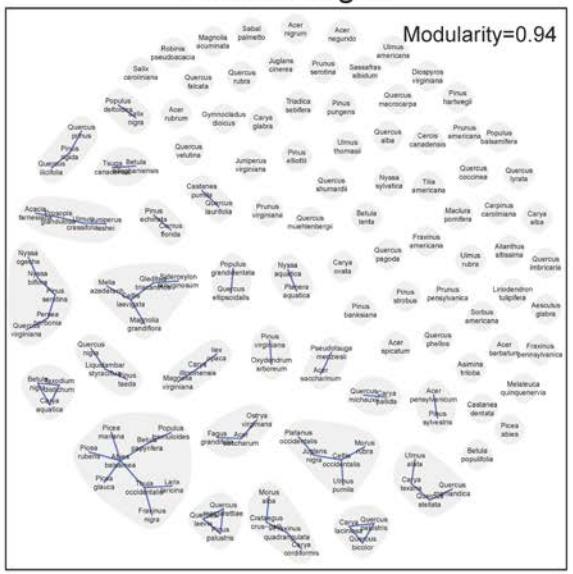


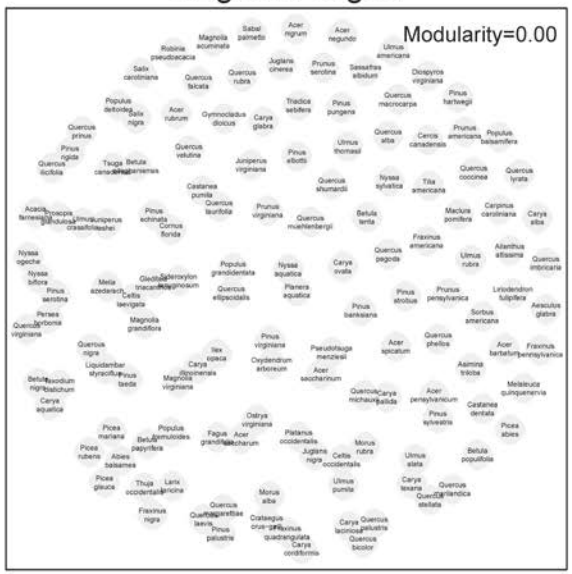


Positive edges

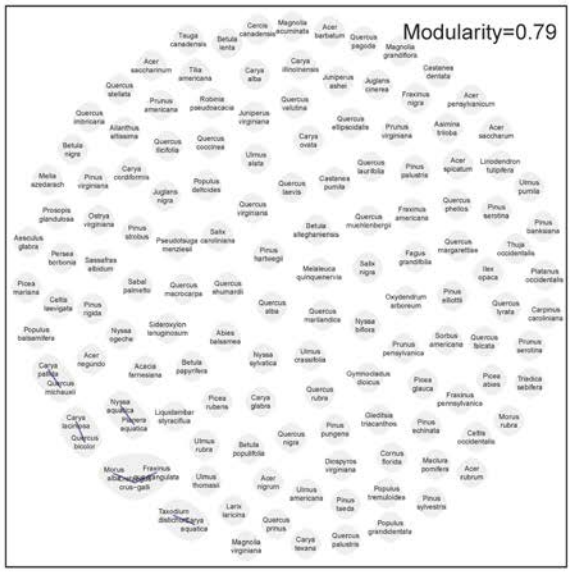
Negative edges

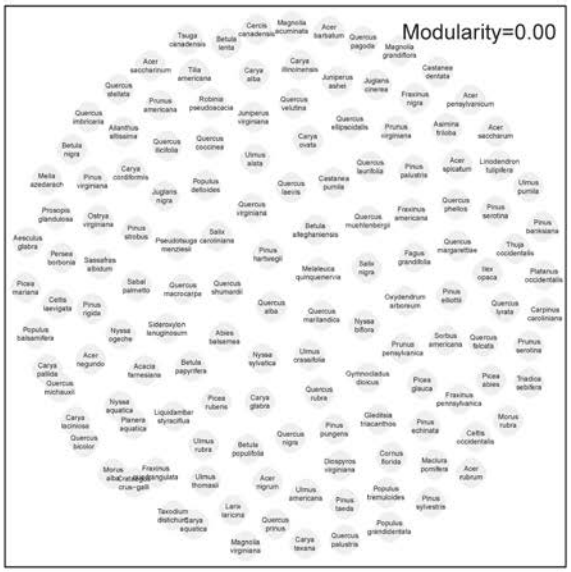
MaxEnt



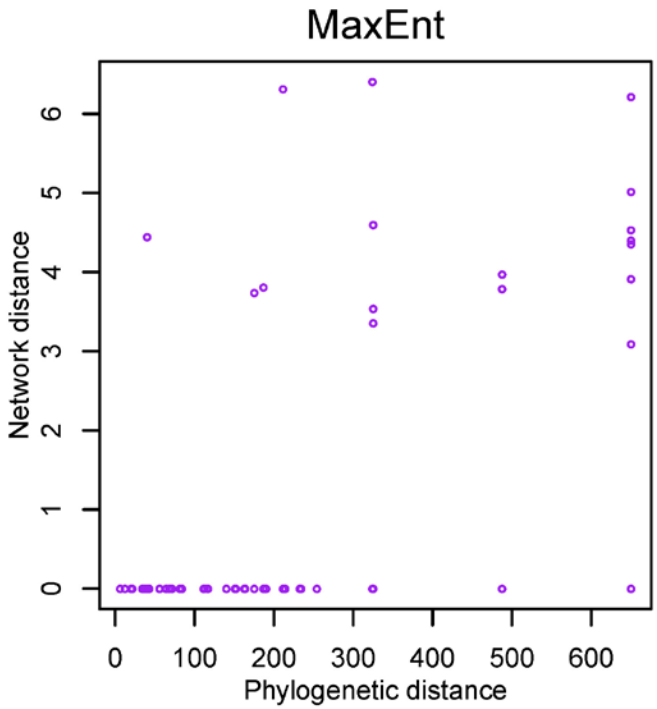


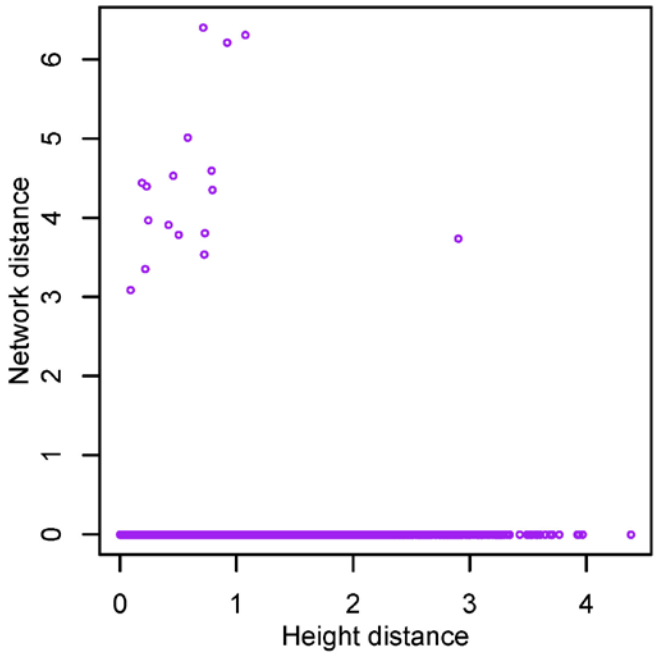
LOESS



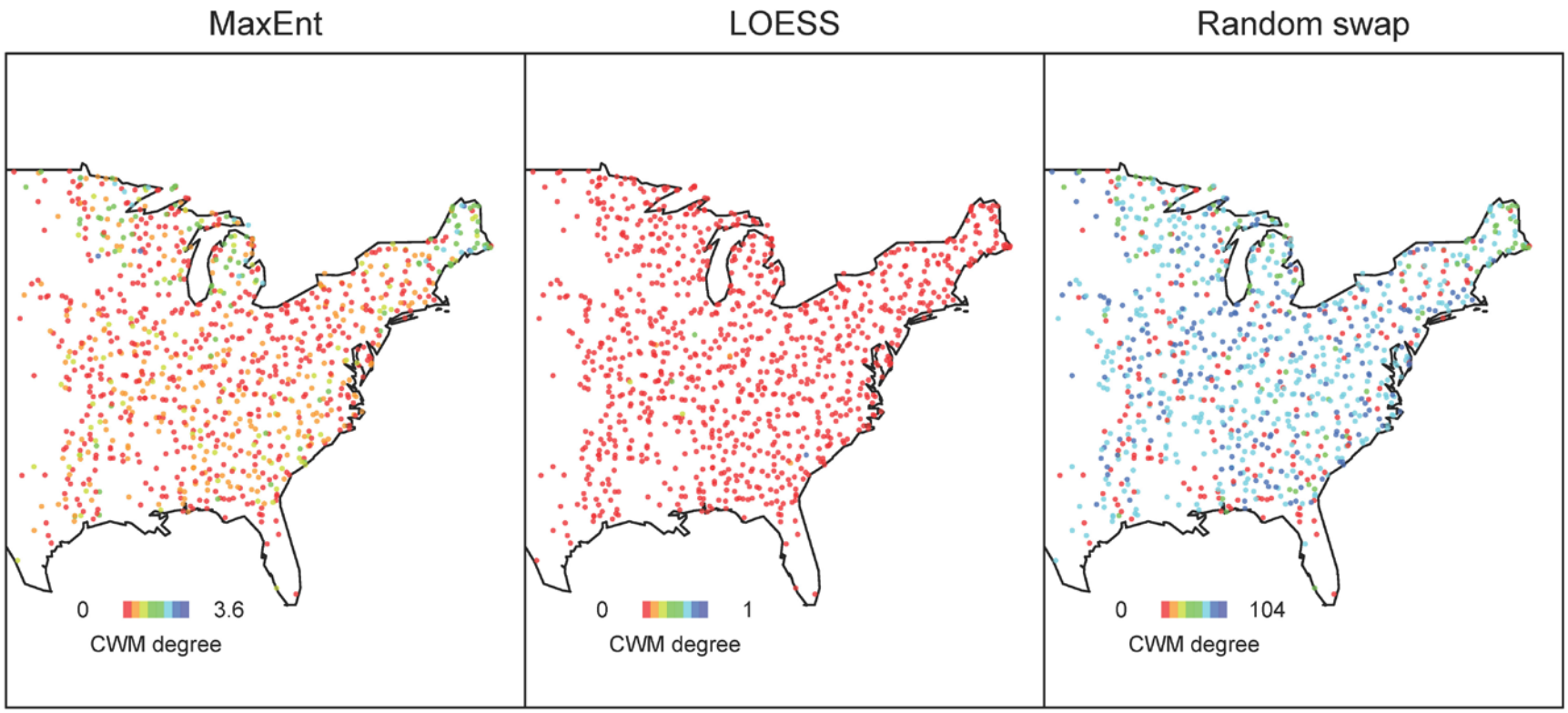


Testing for drivers of associations





Testing for drivers of associations

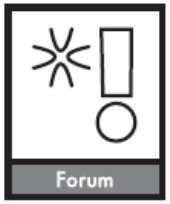


Main advantages of approach

- Spatially explicit null model:
  - Autocorrelation
  - Test deviations from a priori null expectation (e.g. broad scale drivers) based on independent
- Takes into account indirect species associations

- With network metrics, can test for drivers

To learn more…



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A network approach for inferring species associations from co-occurrence data

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