

Using motifs and to analyse (multiple) bipartite networks

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Outline

Bipartite networks and motifs

A null model

Motif distribution

Network embedding

Goodness-of-fit and network comparison

Distance-based network comparison

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Bipartite network

Two types of actors.

- ▶ Mutualistic: plant-pollinator
- ▶ Antagonistic: host-parasite

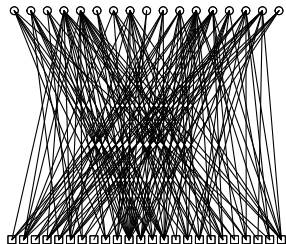
Topological analysis:

understanding the network organisation

Local: node or edge properties (degree, betweenness)

Global: density, connected components, nestedness

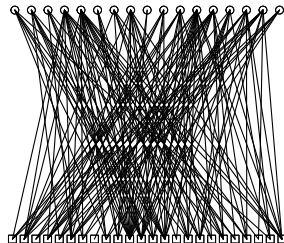
Zackenberg network: [SROB16]



Bipartite network: notations

Species.

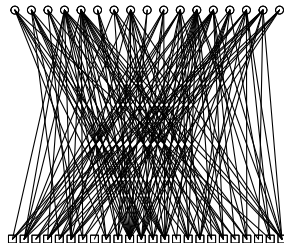
- ▶ $i = 1, \dots, m$ pollinators = rows = bottom nodes
- ▶ $j = 1, \dots, n$ plants = columns = top nodes



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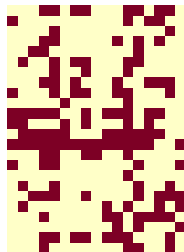
Interactions.

- ▶ $A_{ij} = 1$ if pollinator i interacts with plant j ,
0 otherwise

$$A_{ij} = 1 \Leftrightarrow i \sim j$$

- ▶ adjacency matrix : $m \times n$

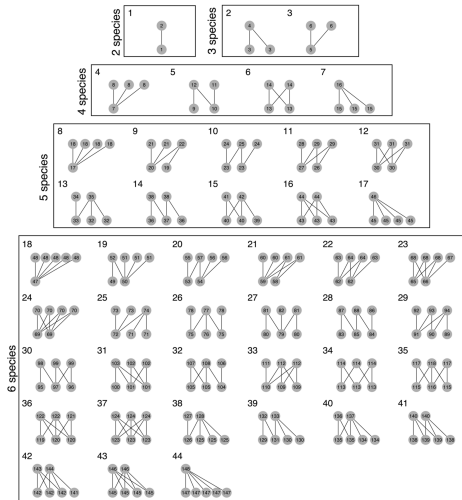
$$A = [A_{ij}]_{1 \leq i \leq m, 1 \leq j \leq n}$$



Bipartite motifs

'Meso-scale' analysis. [SCB⁺19]

- Motifs = 'building-blocks'
- between local (several nodes) and global (sub-graph)



Bipartite motifs

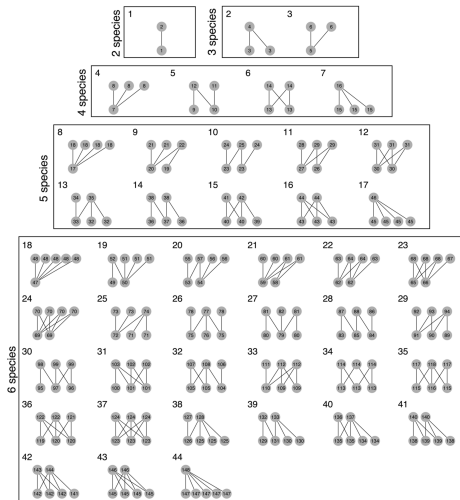
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Interest.

- ▶ Generic description of a network
- ▶ Enables network comparison
- ▶ Even when the nodes are different

(+ 'species-role': out of the scope here)



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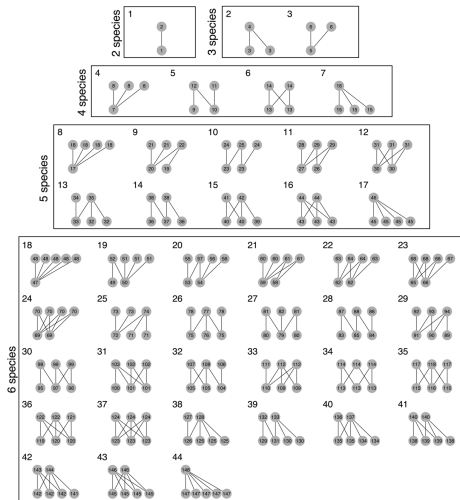
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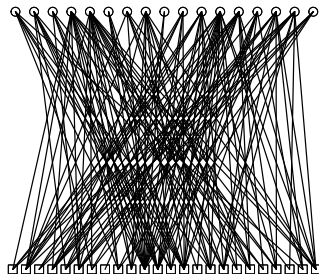
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Existing tool. `bmotif` package [SSS⁺19]:
counts motif occurrences



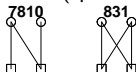
Example

Plant-pollinator network [SROB16]

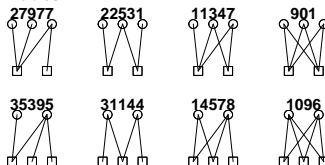


Motif counts.

4 nodes (species)

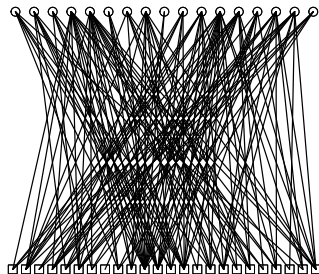


5 nodes



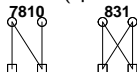
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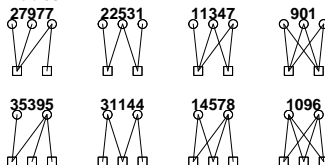


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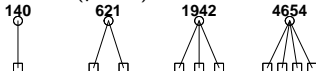
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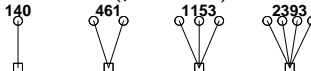
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top 'stars' (plants)



bottom 'stars' (pollinators)



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Need for a null model

Motif counts obviously depend on

- ▶ the size of the network: $n \times m$
- ▶ the density of the network
- ▶ the imbalance between bottom-node degrees (specialist vs generalist pollinators)
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Bipartite expected degree distribution (BEDD) model: (in words)

- ▶ Consider m pollinators ($i = 1, \dots, m$):
each plant i has a specific propensity to interact (degree of generalism)
- ▶ Consider n plants ($j = 1, \dots, n$):
each plant j has a specific propensity to interact (idem)
- ▶ The probability for pollinator i and plant j to interact is proportional to the product of their respective propensities.

BEDD model

Bipartite expected degree distribution (BEDD) model: (formaly)

- ▶ ρ = network density
- ▶ g = top node degree imbalance ($\int g = 1$)
- ▶ h = bottom node degree imbalance ($\int h = 1$)

$$\{U_i\}_{i=1,\dots,m} \text{ iid } \sim \mathcal{U}[0, 1] \qquad \{V_j\}_{j=1,\dots,n} \text{ iid } \sim \mathcal{U}[0, 1]$$

$$\mathbb{P}\{i \sim j \mid U_i, V_j\} = \rho \, g(U_i) \, h(V_j)$$

(Bipartite version of the EDD model [CL02])

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Model parameters:

$$\theta = (\rho, g, h).$$

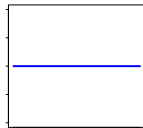
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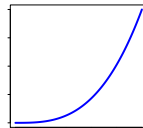
$$\mathbb{E}(D_i \mid U_i) = n \rho g(U_i)$$

$$\mathbb{E}(D_j \mid V_j) = m \rho g(V_j)$$

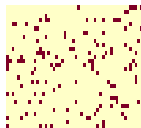
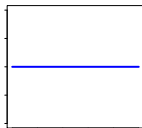
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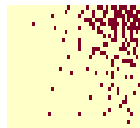
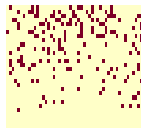
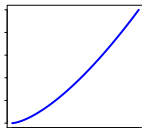
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$$g(u) =$$



Properties of the BEDD model

Assumptions.

- ▶ No preferred or avoided specific connexion
- ▶ **Graph-exchangeable** model: pollinators can be permuted and plants can be permuted

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- ▶ 'Nested' structure by construction

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Sufficient statistics to fit BEDD:

- ▶ Pollinator degrees + plant degrees
- ▶ or, equivalently, star (single edge, top, bottom) frequencies

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Counting motifs

Number of 'positions'.

- ▶ Choose p nodes among m
- ▶ Choose q nodes among n
- ▶ Try all *automorphisms*

$$c_s := \binom{m}{p} \times \binom{n}{q} \times r_s$$

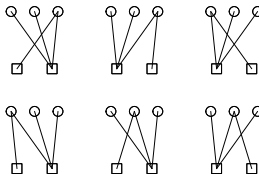
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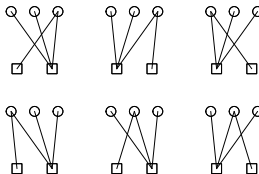
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Motif count. Try all positions $\alpha = 1, \dots, c_s$, define

$$Y_{s\alpha} = 1 \text{ if match, } 0 \text{ otherwise,}$$

then count the number of matches:

$$N_s = \sum_{\alpha} Y_{s\alpha}$$

→ **Motif frequency:** $F_s := N_s / c_s$

Motif probability

Occurrence probability $\overline{\phi}_s = \mathbb{P}\{Y_{s\alpha} = 1\}$. Under the B-EDD model [OLR22]:

$$\left(\begin{array}{c} \circ \\ \circ \\ \circ \\ \square \\ \square \end{array} \right) = \underline{\hspace{10cm}}$$

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Estimated probability \bar{F}_s .

$$\bar{\phi}_s := \frac{\phi_2 \phi_4}{\phi_1} \quad \rightarrow \quad \bar{F}_s := \frac{F_2 F_4}{F_1}$$

where F_1, F_2, F_4 = observed frequencies of edges, top stars and bottom stars.

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- ▶ Number of positions: c_s
- ▶ Mean: $\mathbb{E}_{BEDD}(N_s) = c_s \times \overline{\phi}_s$

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 → Need to account for overlap between positions (*super-motifs*: [PDK⁺08] [\[#32\]](#))



→ Compute the respective expected count in the way as for regular motifs

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► **Asymptotic normality:** [#33] [#34] $(F_s - \bar{F}_s) / \sqrt{\widehat{\mathbb{V}}(F_s)} \xrightarrow{m, n \rightarrow \infty} \mathcal{N}(0, 1)$

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Using motifs. K networks

$$(\text{Network})_k \rightarrow (N_1^k, \dots, N_S^k) \in \mathbb{R}^S$$

but need to correct for: network sizes, correlation between motif frequencies, etc...

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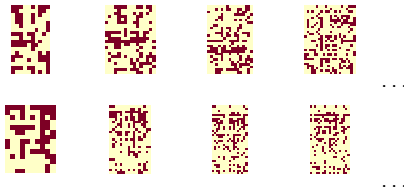
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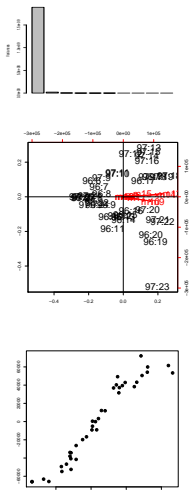
Zackenberg dataset. $K = 46$ networks

- ▶ 2 years
- ▶ 1 network observed every few days



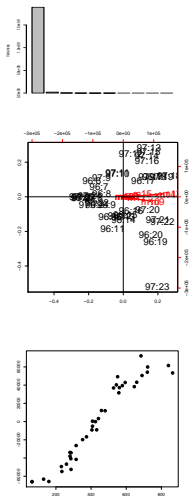
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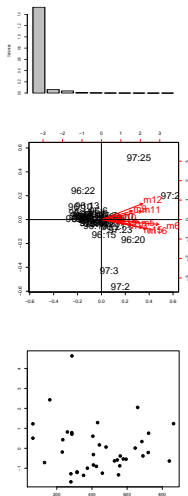


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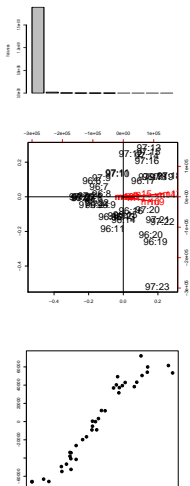


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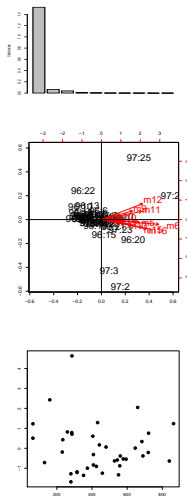


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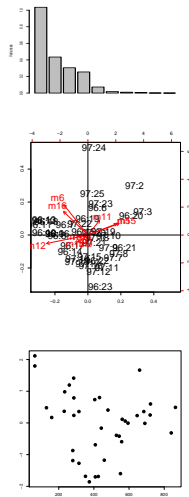
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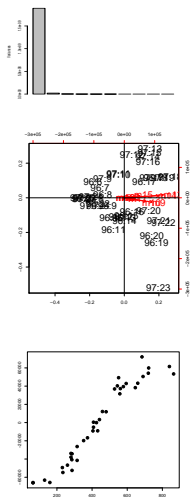


Choleski [#36].

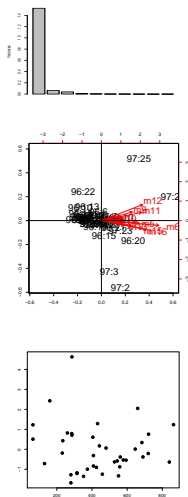


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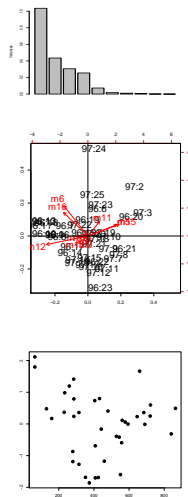
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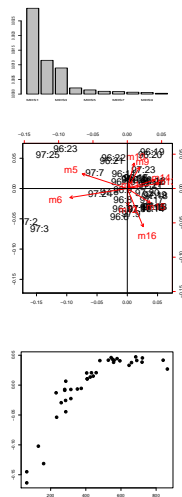
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Bray-Curtis MDS



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A null model

Motif distribution

Network embedding

Goodness-of-fit and network comparison

Distance-based network comparison

Goodness-of-fit (GOF)

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Example.

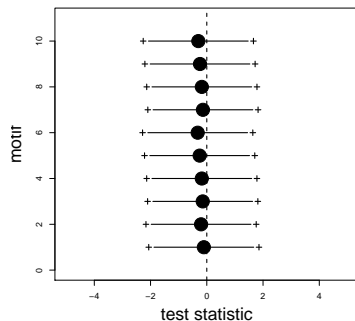
1. Data = observed plant-pollinator network
2. Statistic T = motif count N_5
3. Model = BEDD

Goodness-of-fit (GOF) of the BEDD model

Zackenberg network.

Raw statistic:

$$T_s = \frac{N_s - \hat{\mathbb{E}}N_s}{\sqrt{\hat{\mathbb{V}}N_s}}$$



Goodness-of-fit (GOF) of the BEDD model

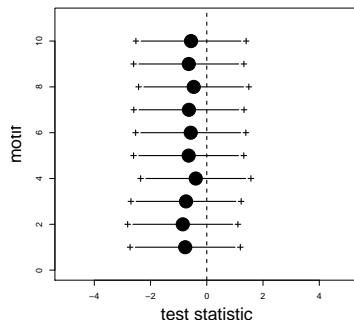
Zackenberg network.

Raw statistic:

$$T_s = \frac{N_s - \hat{\mathbb{E}}N_s}{\sqrt{\hat{\mathbb{V}}N_s}}$$

Corrected stat.: accounts for the estimation error in $\hat{\mathbb{E}}N$ [#37]

$$T'_s = \frac{N_s - (\hat{\mathbb{E}}N_s - \hat{\mathbb{B}}(\hat{\mathbb{E}}N_s))}{\sqrt{\hat{\mathbb{V}}(N_s - \hat{\mathbb{E}}N_s)}}$$



Testing degree imbalance

Question. Is there some degree imbalance between plants?

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Statistical test.

- Assume $A \sim BEDD(\rho, g, h)$,

$$H_0 = \{h = 1\}$$

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$$W_s = (N_s - \widehat{\mathbb{E}}_0(N_s)) / \sqrt{\widehat{\mathbb{V}}_0(N_s)}$$

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Example. (only one significant difference)

plant-pollinator					
s	5	6	10	15	16
W_s	$-6.45 \cdot 10^{-2}$	$9.96 \cdot 10^{-1}$	$-6.63 \cdot 10^{-2}$	$7.52 \cdot 10^{-1}$	2.43

seed dispersal					
s	5	6	10	15	16
W_s	$-2.14 \cdot 10^{-1}$	$-2.14 \cdot 10^{-1}$	$-2.93 \cdot 10^{-1}$	$-2.95 \cdot 10^{-1}$	$-3.56 \cdot 10^{-1}$

Comparing network imbalances

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- Assume $A \sim BEDD(\rho^A, g^A, h^A)$ and $B \sim BEDD(\rho^B, g^B, h^B)$

$$H_0 = \{g^A = g^B\}$$

- For motif s , evaluate $\hat{\mathbb{E}}_{\hat{\rho}^A, \hat{g}^B, \hat{g}^A}(N_s^A)$ and $\hat{\mathbb{E}}_{\hat{\rho}^B, \hat{g}^A, \hat{g}^B}(N_s^B)$ and compare

$$W_s^{(g)}(A, B) = \frac{(N_s^A - \hat{\mathbb{E}}_0(N_s^A)) - (N_s^B - \hat{\mathbb{E}}_0(N_s^B))}{\sqrt{\hat{\mathbb{V}}_0(N_s^A) + \hat{\mathbb{V}}_0(N_s^B)}}$$

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with $\mathcal{N}(0, 1)$

Example. (no significant difference)

s	5	6	10	15	16
F_s^A	$9.21 \cdot 10^{-5}$	$1.00 \cdot 10^{-5}$	$8.12 \cdot 10^{-6}$	$3.32 \cdot 10^{-7}$	$4.47 \cdot 10^{-8}$
$\hat{\mathbb{E}}_0 F_s^A$	$1.96 \cdot 10^{-4}$	$3.75 \cdot 10^{-5}$	$1.74 \cdot 10^{-5}$	$4.25 \cdot 10^{-6}$	$1.33 \cdot 10^{-6}$
F_s^B	$5.13 \cdot 10^{-4}$	$1.15 \cdot 10^{-4}$	$5.07 \cdot 10^{-5}$	$1.79 \cdot 10^{-5}$	$5.96 \cdot 10^{-6}$
$\hat{\mathbb{E}}_0 F_s^B$	$2.66 \cdot 10^{-4}$	$2.92 \cdot 10^{-5}$	$2.85 \cdot 10^{-5}$	$1.50 \cdot 10^{-6}$	$1.69 \cdot 10^{-7}$
W_s	-1.56	-1.56	-0.97	-1.28	-0.96

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Plant-pollinator networks in space & time

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- ▶ along the environmental gradient?
- ▶ across sites within the season?

¹Joint work with Natasha de Manincor & François Massol + Sarah Ouadah & Pierre Latouche

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Dataset.

- ▶ 6 sites: 3 regions \times 2 sites per region
 - ▶ 2 years
 - ▶ 7 months (April to October) per year
- $n = 82$ networks, [4, 39] plants, [8, 80] insects

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Approach. Define a motif-based distance between each pair of networks.

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Distance-based network comparison

Network distance. For a pair of networks (A, B)

- ▶ for a given comparison (insect imbalance):

$$H_0^{(g)} = \{g^A = g^B\},$$

- ▶ for a given motif s : test statistic $W_s^{(g)}$,
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$$D^{(g)}(A, B) = \sqrt{\sum_s \left(W_s^{(g)}\right)^2}$$

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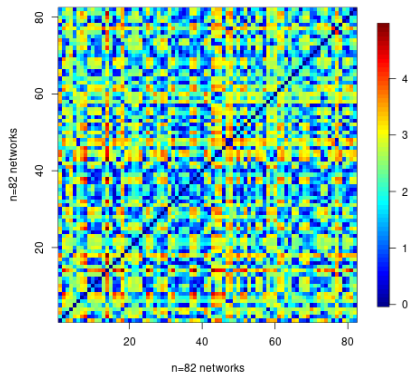
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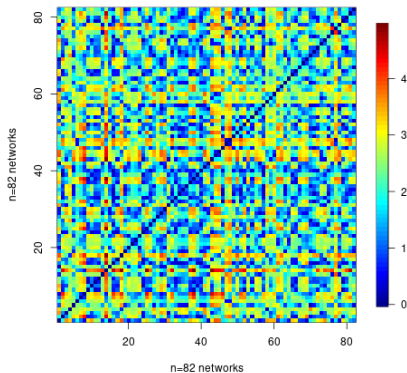
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The same for

- ▶ plant imbalance: $H_0^{(h)} = \{h^A = h^B\} \rightarrow W_s^{(h)} \rightarrow D^{(h)}(A, B)$
- ▶ both imbalance: $H_0^{(gh)} = \{g^A = g^B, h^A = h^B\} \rightarrow W_s^{(gh)} \rightarrow D^{(gh)}(A, B)$

Distance matrix:



Distance-based analysis of variance ('Adonis')

Data at hand. n networks ($A = 1, \dots, n$)

- ▶ network covariates: e.g. region, year, month, ...
- ▶ distance matrix $D = [D(A, B)]$ for all pairs of networks

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Analysis of variance for distance matrices [And01]. Briefly speaking:

- ▶ Think of the regular linear model (regression, analysis of variance)
- ▶ Do as if the distance was computed on pseudo variable rules by a linear model
- ▶ 'Model':

$$D(A, B) = f(\text{region}_A, \text{region}_B, \text{month}_A, \text{month}_B, \\ (\text{region*month})_A, (\text{region*month})_B, \dots)$$

- ▶ Compute a pseudo F statistics for each effect of interest
- ▶ Assess significance using permutation tests.

(see [MA01, ZS06] [#38], `vegan` R package `-adonis2-`)

Results

Insect imbalance $D^{(g)}$.

	Df	Sum Of Sqs	R^2	F	Pr(F)
insectNb	1	69.9	0.2595	42.69	1e-05
plantNb	1	31.17	0.1157	19.04	1e-05
Year	1	2.66	0.0099	1.62	0.22212
Month	6	24.8	0.092	2.52	0.00959
Region	2	8.67	0.0322	2.65	0.04531
Year:Month	6	4.81	0.0179	0.49	0.88756
Year:Region	2	5.51	0.0204	1.68	0.1787
Month:Region	12	32.41	0.1203	1.65	0.06346
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- ▶ No effect is found for the plant imbalance distance $D^{(h)}$ [#40]

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Super-motifs

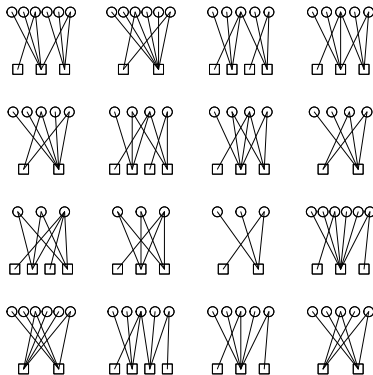
Motif:



Variance:

$$\begin{aligned}
 N_s^2 &= \left(\sum_{\alpha} Y_{s\alpha} \right)^2 \\
 &= \sum_{\alpha, \beta: \alpha \cap \beta = \emptyset} Y_{s\alpha} Y_{s\beta} \\
 &\quad + \underbrace{\sum_{\alpha, \beta: \alpha \cap \beta \neq \emptyset} Y_{s\alpha} Y_{s\beta}}_{\text{occurrence of a super-motif}}
 \end{aligned}$$

Some super-motifs:



... 396 super-motifs

Covariance: same game, for $Y_{s\alpha} Y_{s'\beta}$ with $s \neq s'$ [#16]

Asymptotic distribution of the count

Estimated probability.

$$\bar{\phi}_s := \phi_2 \phi_4 / \phi_1 \quad \rightarrow \quad \bar{F}_s := F_2 F_4 / F_1$$

where F_1, F_2, F_4 = observed frequencies of top stars, bottom stars and edges.

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Asymptotic normality for non-star motifs. Under BEDD (and sparsity conditions):

$$(F_s - \bar{F}_s) / \sqrt{\hat{V}(F_s)} \xrightarrow{m, n \rightarrow \infty} \mathcal{N}(0, 1)$$

Proof:

► decompose

$$F_s - \bar{F}_s = \underbrace{(F_s - \phi_s)}_{\text{random fluctuations}} + \underbrace{(\phi_s - \bar{\phi}_s)}_{\text{null under BEDD}} + \underbrace{(\bar{\phi}_s - \bar{F}_s)}_{\text{estimation error} \rightarrow 0},$$

► construct a counting martingale [GL17] for $F_s - \phi_s$

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Test statistic. Under BEDD:

$$N_s \approx \mathcal{N}(\hat{\mathbb{E}}(N_s), \hat{V}(N_s)) \quad \Leftrightarrow \quad (N_s - \hat{\mathbb{E}}(N_s)) / \sqrt{\hat{V}(N_s)} \approx \mathcal{N}(0, 1)$$

[#16]

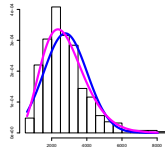
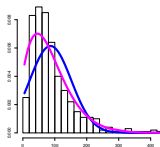
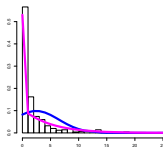
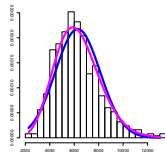
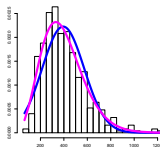
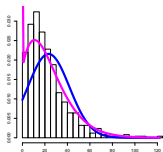
In practice: Asymptotic normality

$$(n = 2m/3)$$

$$m = 50$$

$$m = 100$$

$$m = 200$$



Normal distribution, Poisson-geometric distribution with same mean and variance [Sta01, PDK⁺08] [#16]

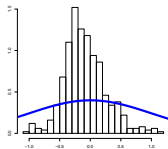
In practice: Test statistic

Need to account for the estimation error of $\hat{\mathbb{E}}N$

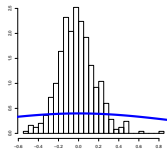
Regular stat.:

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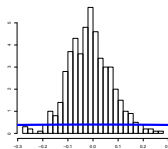
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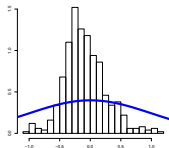
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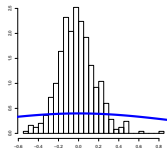
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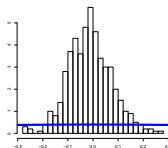
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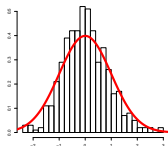
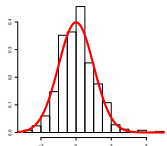
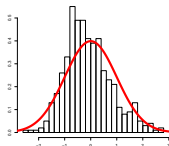


$m = 200$



Correction:

$$\frac{N - (\hat{\mathbb{E}}N - \hat{\mathbb{B}}(\hat{\mathbb{E}}N))}{\sqrt{\hat{\mathbb{V}}(N - \hat{\mathbb{E}}N)}}$$



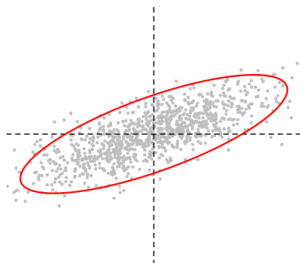
- Need to evaluate $\mathbb{V}(N - \hat{\mathbb{E}}(N))$ and $\mathbb{B}(\hat{\mathbb{E}}N)$: resort to Taylor expansion (Δ -method) [\[#22\]](#)

Choleski transform

Aim: 'Remove' correlation and variance heterogeneity

Covariance matrix of (X_1, X_2) :

$$\Sigma_{X_1, X_2} = \begin{bmatrix} \sigma_1^2 & \sigma_{12} \\ \sigma_{12} & \sigma_2^2 \end{bmatrix}$$



Diagonalization: $\Sigma = P\Lambda P^{-1}$

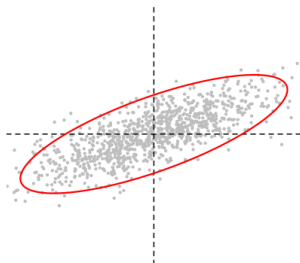
Choleski matrix: $\Sigma^{-1/2} = P\Lambda^{-1/2}P^{-1}$

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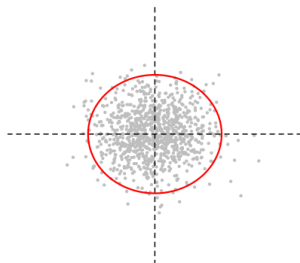


Diagonalization: $\Sigma = P\Lambda P^{-1}$

Choleski matrix: $\Sigma^{-1/2} = P\Lambda^{-1/2}P^{-1}$

Choleski transform:

$$\begin{bmatrix} X'_1 \\ X'_2 \end{bmatrix} = \Sigma^{-1/2} \begin{bmatrix} X_1 \\ X_2 \end{bmatrix}$$



$$\Sigma_{X'_1, X'_2} = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$$

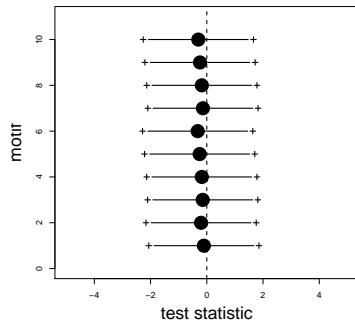
[#19]

Goodness-of-fit (GOF) of the BEDD model

Raw statistic:

$$T_s = \frac{N_s - \hat{\mathbb{E}}N_s}{\sqrt{\hat{\mathbb{V}}N_s}}$$

Zackenberg network.



[#22]

$${}^2\Sigma = P\Lambda P^\top, \Sigma = P\Lambda^{-1/2}P^\top$$

Goodness-of-fit (GOF) of the BEDD model

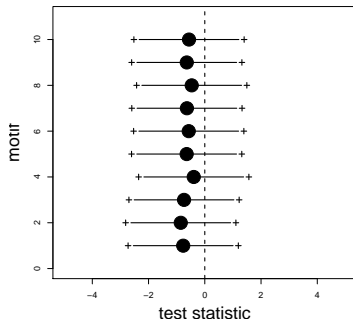
Raw statistic:

$$T_s = \frac{N_s - \hat{\mathbb{E}}N_s}{\sqrt{\hat{\mathbb{V}}N_s}}$$

Corrected stat.: accounts for the estimation error in $\hat{\mathbb{E}}N$

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Zackenberg network.



[#22]

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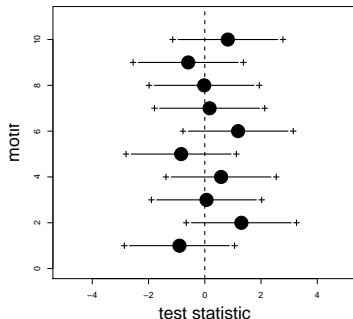
$$T'_s = \frac{N_s - (\hat{\mathbb{E}}N_s - \hat{\mathbb{B}}(\hat{\mathbb{E}}N_s))}{\sqrt{\hat{\mathbb{V}}(N_s - \hat{\mathbb{E}}N_s)}}$$

Cholevski² transformation: accounts for the correlation between the counts

$$\Sigma_{s,s'} = \text{Cov}(N_s - \hat{\mathbb{E}}N_s, N_{s'} - \hat{\mathbb{E}}N_{s'})$$

$$T'' = \hat{\Sigma}^{-1/2} \left[N_s - (\hat{\mathbb{E}}N_s - \hat{\mathbb{B}}(\hat{\mathbb{E}}N_s)) \right]$$

Zackenberg network.



[#22]

An intuition for Adonis

Variance. Remind that $\sum_{i=1}^n (y_i - \bar{y})^2 = \frac{1}{2n} \sum_{i=1}^n \sum_{i'=1}^n (y_i - y_{i'})^2$

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Analysis of variance. Remind that, for g groups, with r replicates ($n = r g$),

$$\underbrace{\sum_{i=1}^g \sum_{j=1}^r (y_{ij} - \bar{y})^2}_{\text{Total}} = \underbrace{\sum_{i=1}^g r (\bar{y}_i - \bar{\bar{y}})^2}_{\text{Between}} + \underbrace{\sum_{i=1}^g \sum_{j=1}^r (y_{ij} - \bar{y}_i)^2}_{\text{Within}}$$

Anova test statistic $F \propto \text{Between/Within}$

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Distance. p variables $y_{ij} = (y_{ijk})_{k=1\dots p}$: $D^2(y_{ij}, y_{i'j'}) = \sum_{k=1}^p (y_{ijk} - y_{i'j'k})^2$

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Adonis. Define Between = Total - Within, where

$$\text{Total} = \frac{1}{2n} \sum_{i=1}^g \sum_{i'=1}^g \sum_{j'=1}^r D^2(y_{ij}, y_{i'j'}), \quad \text{Within} = \frac{1}{2} \sum_{i=1}^g \sum_{j=1}^r \sum_{j'=1}^r D^2(y_{ij}, y_{ij'}),$$

and determine the p -value for $F = \text{Between/Within}$ by permutation. [#28]

Null simulations

100 sets of 83 synthetic networks, with dimensions as the original ones and fixed ρ , g , and h

Without correction.

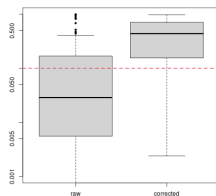
	Df	SumOfSqs	R^2	F	Pr(F)
Year	1	1.5	0.0114	0.94	0.443
Month	6	25.17	0.1914	2.61	0.012
Region	2	0.69	0.0052	0.21	0.845
Year:Month	6	7.46	0.0568	0.77	0.653
Year:Region	2	2.52	0.0191	0.78	0.543
Month:Region	12	12.55	0.0954	0.65	0.831
Year:Month:Region	12	17.39	0.1322	0.9	0.578
Residual	40	64.23	0.4884		
Total	81	131.51	1		

With correction.

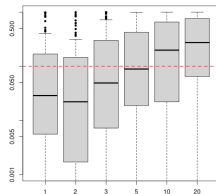
	Df	SumOfSqs	R^2	F	Pr(F)
insectNb	1	10.55	0.0803	7.17	0.003
plantNb	1	7.32	0.0556	4.97	0.015
Year	1	0.77	0.0059	0.53	0.622
Month	6	8.96	0.0681	1.01	0.458
Region	2	4.39	0.0334	1.49	0.241
Year:Month	6	8.54	0.0649	0.97	0.496
Year:Region	2	2.17	0.0165	0.74	0.569
Month:Region	12	13.99	0.1064	0.79	0.699
Year:Month:Region	12	18.9	0.1437	1.07	0.421
Residual	38	55.93	0.4253		
Total	81	131.51	1		

[#29]

Over 100 networks.



Increasing the networks' size.



Results for other motif distances

Plant imbalance $D^{(h)}$.

	Df	Sum Of Sqs	R^2	F	Pr(F)
insectNb	1	9.81	0.1935	19.53	1e-05
plantNb	1	1.42	0.028	2.83	0.06594
Year	1	0.67	0.0133	1.34	0.27518
Month	6	4.14	0.0818	1.38	0.20713
Region	2	0.99	0.0196	0.99	0.43126
Year:Month	6	2.61	0.0514	0.86	0.58258
Year:Region	2	1.87	0.037	1.87	0.1283
Month:Region	12	4.33	0.0854	0.72	0.8062
Year:Month:Region	12	5.75	0.1135	0.95	0.53039
Residual	38	19.09	0.3766		
Total	81	50.69	1		

Both imbalance $D^{(gh)}$.

	Df	Sum Of Sqs	R^2	F	Pr(F)
insectNb	1	56.21	0.265	48.58	1e-05
plantNb	1	16.44	0.0775	14.21	1e-05
Year	1	0.83	0.0039	0.71	0.56559
Month	6	24.41	0.1151	3.52	0.00012
Region	2	8.83	0.0417	3.82	0.00321
Year:Month	6	10.09	0.0476	1.45	0.14299
Year:Region	2	3.15	0.0149	1.36	0.25071
Month:Region	12	29.92	0.1411	2.16	0.0028
Year:Month:Region	12	18.24	0.086	1.31	0.16496
Residual	38	43.96	0.2073		
Total	81	212.09	1		

[#29]