

# Mesososcopic analysis of ecological networks using Hill numbers



OSUG

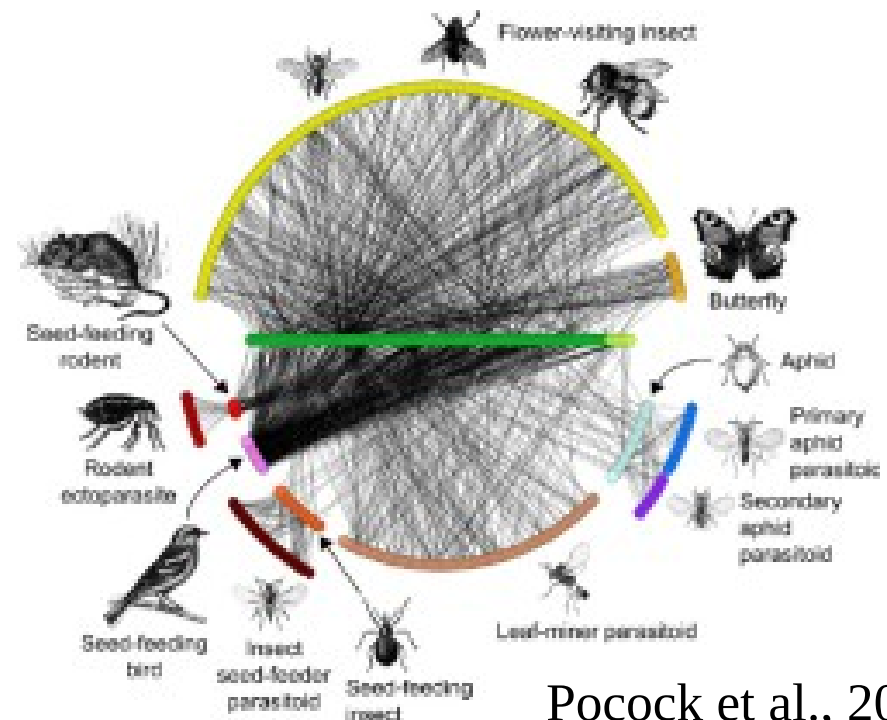
*Jump In*  
Jackson Pollock

**Aim : assess the diversity of one or several ecological communities that are interacting through an ecological network**

$\alpha$ -diversity : *richness of a community*

$\beta$ -diversity : *“the extent of change in community composition, or degree of community differentiation, in relation to a complex-gradient of environment, or a pattern of environments” Whittaker 1960*

Classic diversity index omit interactions



Pocock et al., 2012

Measuring diversity of a community ?

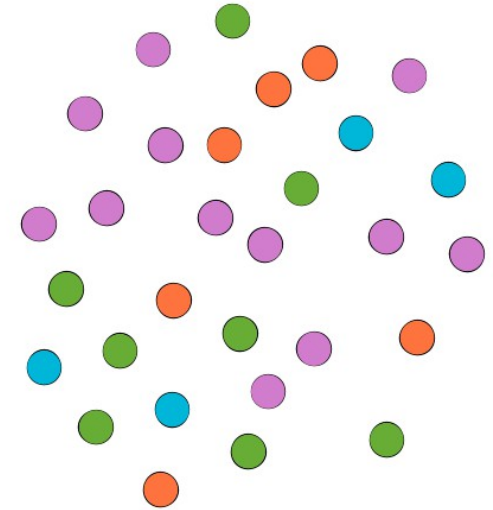
A diversity of metrics

Shannon entropy

Simpson index

Unifying framework : True diversity (Hill numbers, 1973)

*set of organisms  
colours are species*



Suppose that (E) is composed of N individuals, belonging to S distinct species, with relative abundances :  $(p_1, \dots, p_s)$

$$M_{q-1} = \sqrt[q-1]{\sum_{i=1}^S p_i p_i^{q-1}}$$

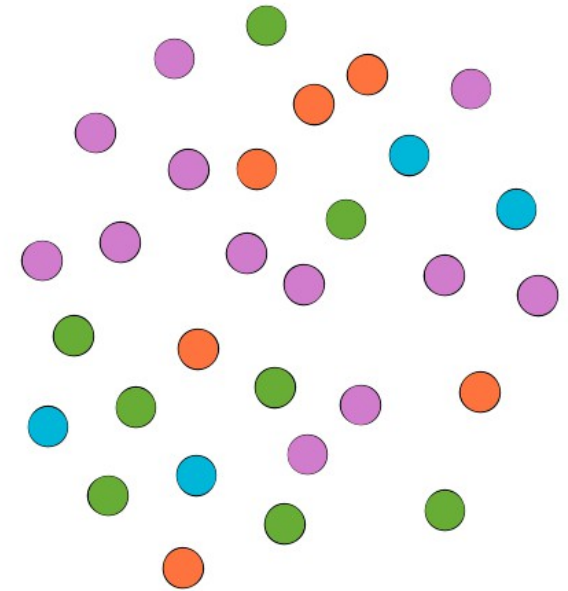
Generalized mean of order q-1

$$D_q = 1/M_{q-1} = \left( \sum_{i=1}^S p_i^q \right)^{1/(1-q)}$$

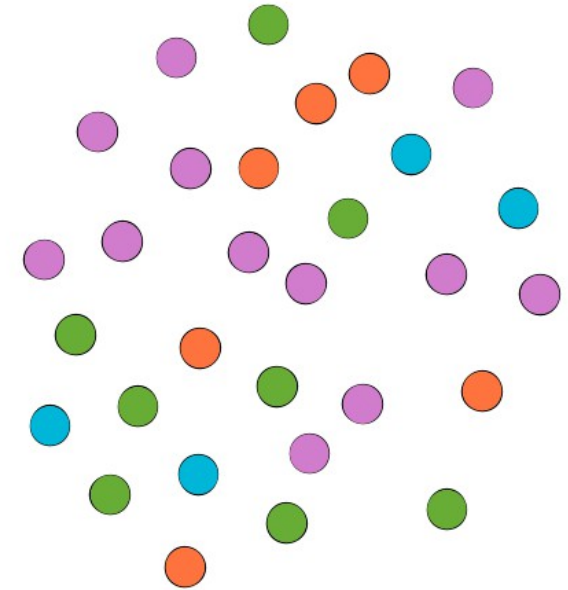
$$D_1 = \exp\left(-\sum_{i=1}^S p_i \log(p_i)\right)$$

$$D_q = 1/M_{q-1} = \left( \sum_{i=1}^S p_i^q \right)^{1/(1-q)}$$

Hill number of order  $q$



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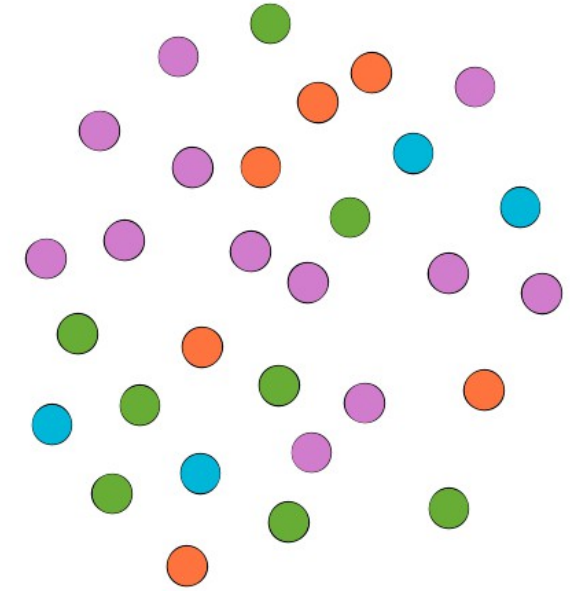
Hill number of order  $q$ 

$$D_0 = S \quad \text{Species richness}$$

$$D_1 = \exp\left(\sum_{i=1}^S p_i \log(p_i)\right) \quad \text{Shannon entropy (exp)}$$

$$D_2 = \frac{1}{\sum_{i=1}^S p_i^2} \quad \text{Inverse of Simpson index}$$

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Hill number of order  $q$ 

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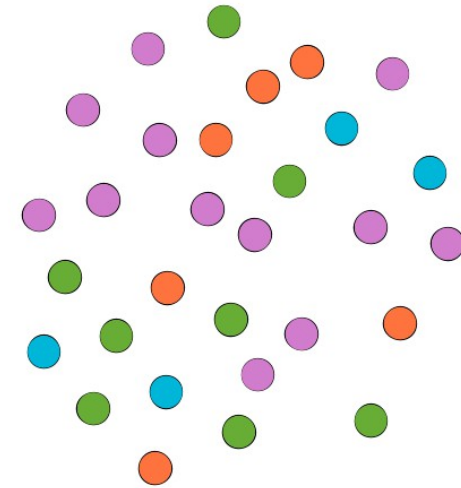
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 **$\alpha$ -diversity**

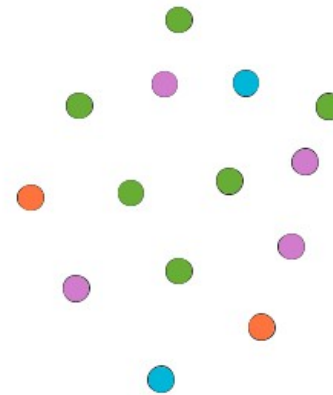
## Comparing two communities

 *$\beta$ -diversity concept :*

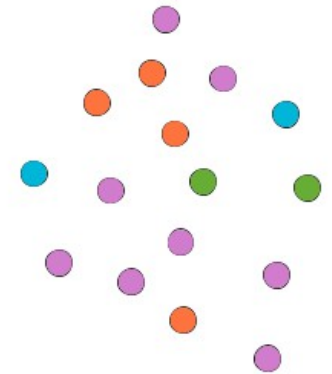
*“The extent of change in community composition, or degree of community differentiation, in relation to a complex-gradient of environment, or a pattern of environments’ Whittaker, 1960*



Meta-community



community 1

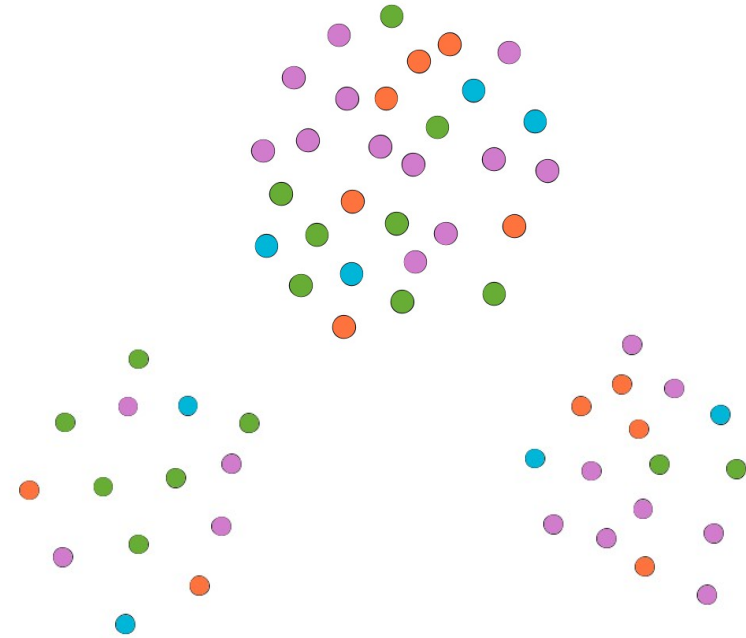


community 2

## Comparing two communities

 *$\beta$ -diversity concept :*

*“The extent of change in community composition, or degree of community differentiation, in relation to a complex-gradient of environment, or a pattern of environments’ Whittaker, 1960*



$$\beta(q) = \begin{cases} \frac{\gamma(q)}{(\omega(\alpha_1(q))^{1-q} + (1-\omega)(\alpha_2(q))^{1-q})^{\frac{1}{1-q}}} & q \neq 1 \\ \frac{\gamma(q)}{\exp(\omega \log(\alpha_1(q))) + (1-\omega) \log(\alpha_2(q))} & q = 1 \end{cases}$$

$$\omega = \frac{n_1}{n_1 + n_2}$$

$$1 \leq \beta(q) \leq 2$$

$$\beta(q) \leftarrow \beta(q) - 1$$

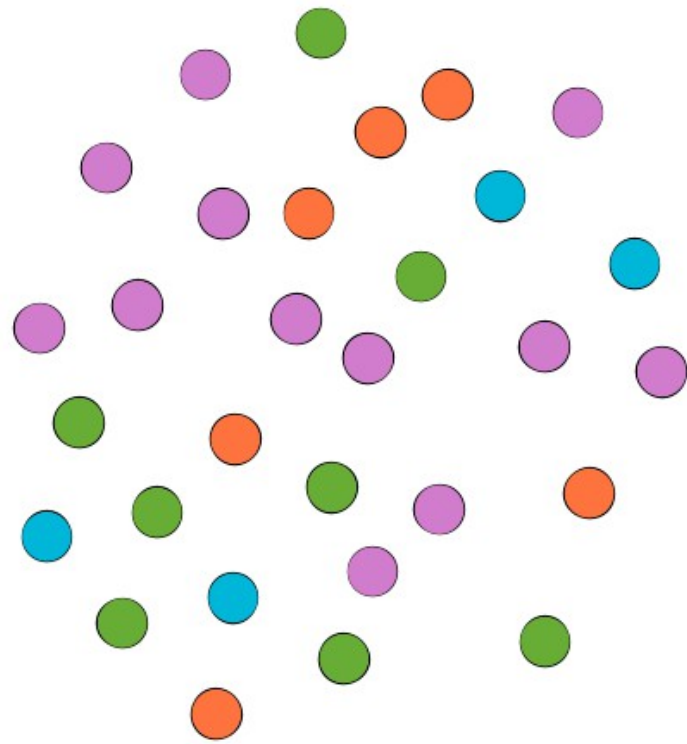
$$0 \leq \beta(q) \leq 1$$

ratio of generalised means in presence of two classifications (species and space)  
cf Tuomisto, 2010, Ecography

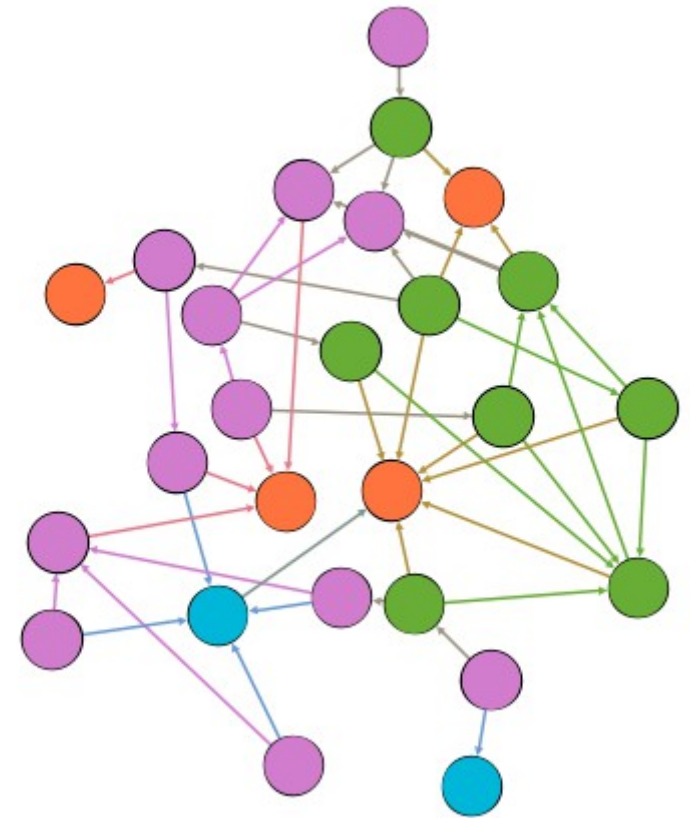
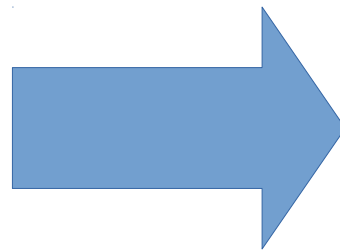


**$\beta$ -diversity**





Biotic interactions



Interaction network

$G$  a network,  $A$  its adjacency matrix,  
 $V(G)$  set of nodes,  $|V(G)| = n$   
 $E(G)$  set of edges,  $|E(G)| = L$   
 $Q$  set of classes (e.g. species, functional groups)

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### Connectance

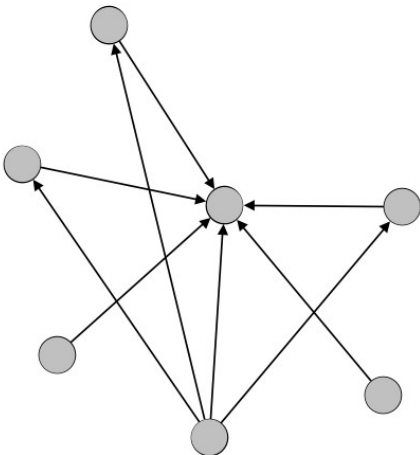
$$Q = \{q\}$$

$$\pi = Pr(i \rightarrow j | i, j \in q)$$

$$C = \hat{\pi} = L/S^2$$

Connectance does not  
take into account  
species identity

Not a measure of diversity,  
since there is only one group



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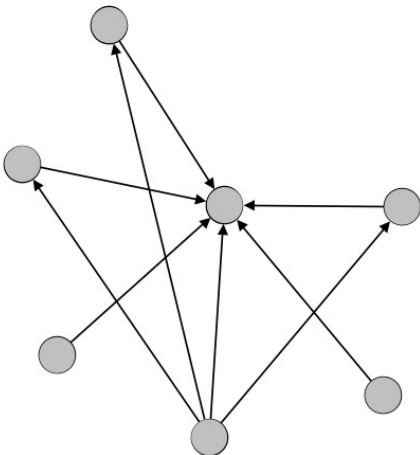
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### Link number

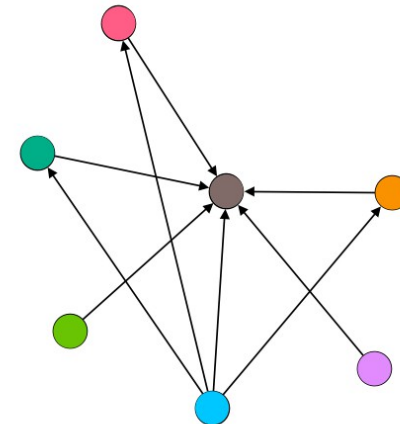
$$Q = \{S_1, \dots, S_n\}$$

$$\pi_{i,j} = Pr(i \rightarrow j | i \in S_i, j \in S_j)$$

$$\hat{\pi}_{i,j} = A_{i,j} \in \{0, 1\}$$

$$L = \sum_{1 \leq i, j \leq n} A_{i,j}$$

*Measure of  $\alpha$ -diversity*



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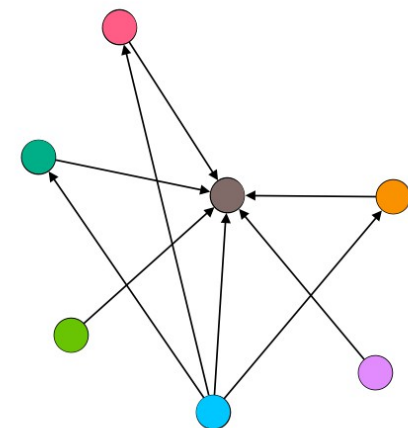
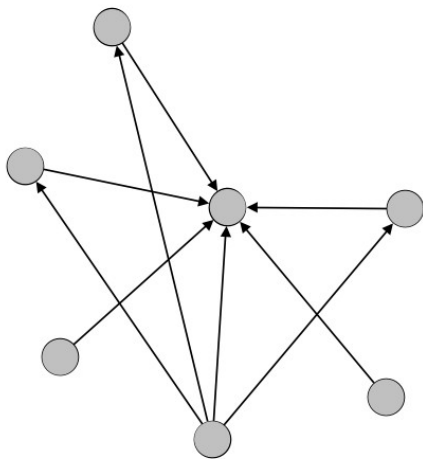
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scale (size of  $Q$ )

Macroscopic scale

Microscopic scale



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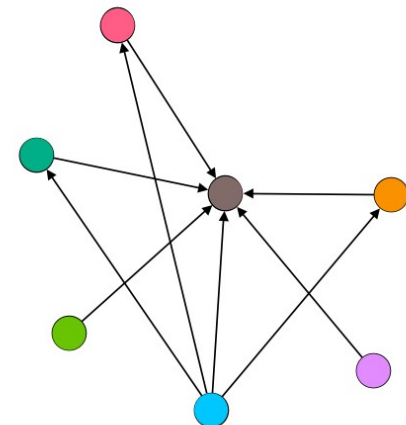
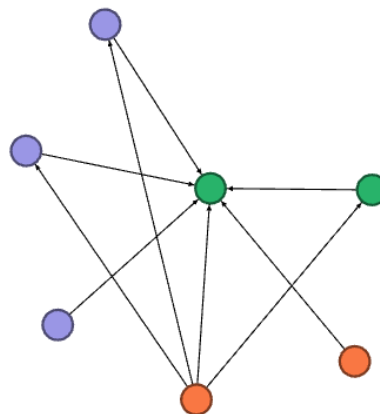
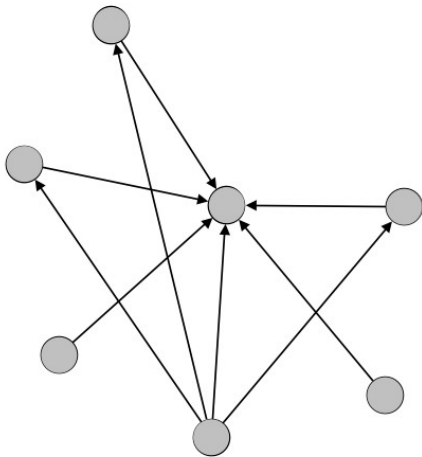
$$L = \sum_{1 \leq i, j \leq n} A_{i,j}$$

scale (size of  $Q$ )

Macroscopic scale

Microscopic scale

Mesoscopic scale ?



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 $Q = \{1, \dots, |Q|\}$   $1 \leq |Q| \leq n$

$$\alpha_k = \frac{\sum_{i=1}^n \mathbf{1}(i \in k)}{n}$$

→ group proportion

$$l_{k,l} = \frac{\sum_{i=1}^n \mathbf{1}(i \rightarrow j, i \in k, j \in l)}{L}$$

→ link proportion (connecting group  $k$  and  $l$ )

$$\pi_{k,l} = Pr(i \rightarrow j | i \in k, j \in l)$$

$$\hat{\pi}_{k,l} = \frac{\sum_{i=1}^n \mathbf{1}(i \rightarrow j, i \in k, j \in l)}{\sum_{i=1}^n \mathbf{1}(i \in k) \sum_{j=1}^n \mathbf{1}(j \in l)}$$

→ connectance between class  $k$  and  $l$

**If there is only one class, then it's a scalar equal to connectance**

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$$D_{q,\alpha} = \left( \sum_{k=1}^{|Q|} \alpha_k^q \right)^{\frac{1}{1-q}}$$

$$D_{q,l} = \left( \sum_{1 \leq k, l \leq |Q|} l_{k,l}^q \right)^{\frac{1}{1-q}}$$

$$D_{q,\pi} = \left( \sum_{1 \leq k, l \leq |Q|} \left( \frac{\pi_{k,l}}{\sum_{k,l} \pi_{k,l}} \right)^q \right)^{\frac{1}{1-q}}$$



Hill number on group proportion



Hill number on links proportion

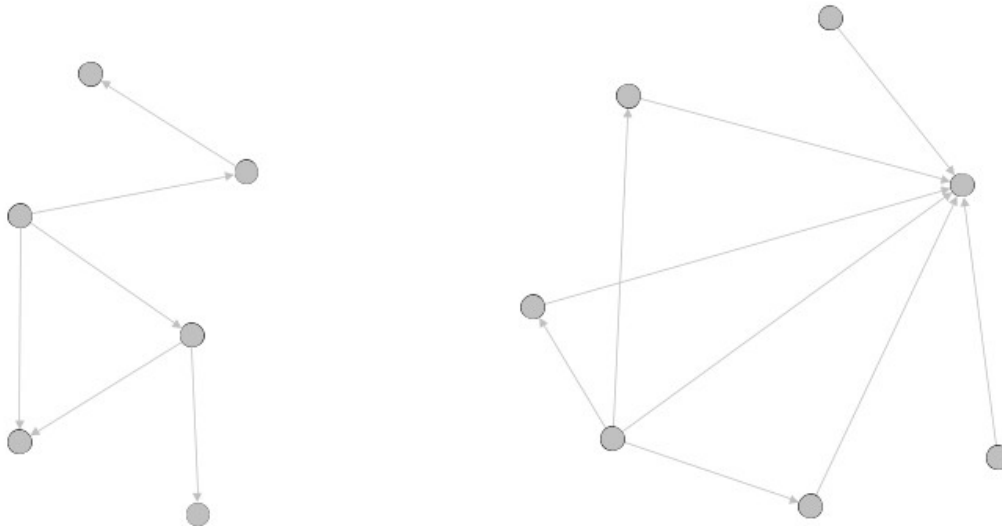


Hill number on connectance matrix



## The network dissimilarity problem

$G_1$  a network,  $A_1$  its adjacency matrix  
 $V(G_1)$  set of nodes,  $|V(G_1)| = n_1$   
 $E(G_1)$  set of edges,  $|E(G_1)| = L_1$



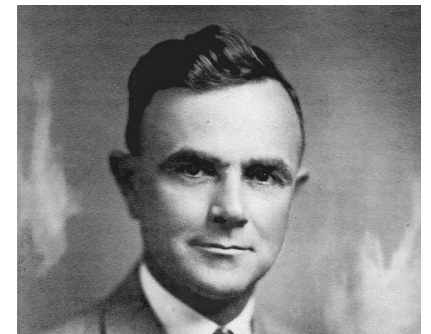
$G_2$  a network,  $A_2$  its adjacency matrix  
 $V(G_2)$  set of nodes,  $|V(G_2)| = n_2$   
 $E(G_2)$  set of edges,  $|E(G_2)| = L_2$

### Macroscopic comparison

$Q$  : set of groups of the metaweb  
**Elton niches= species that have a similar position in the network**

$Q = \{q\}$

Compare connectance of the two networks



Charles Elton (1900-1991)

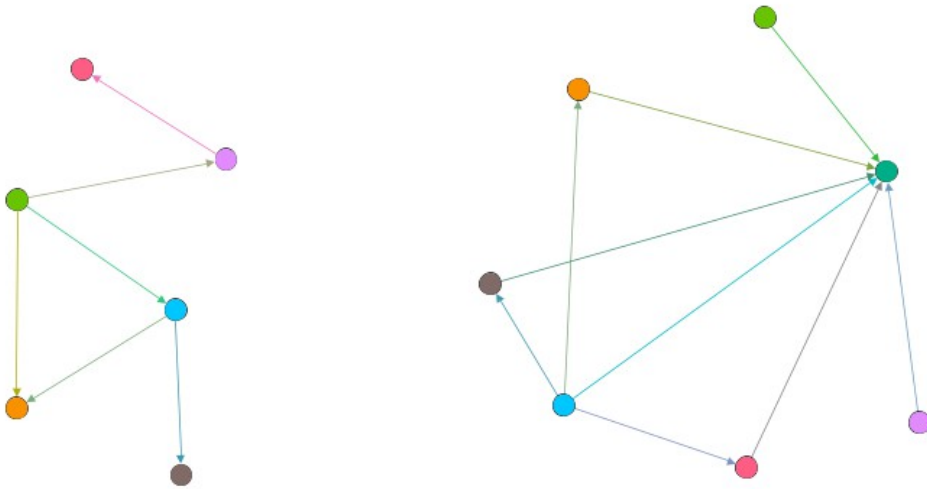
## Microscopic comparison

$$Q_1 = \{S_1, \dots, S_{n_1}\}$$

$$Q_2 = \{S_1, \dots, S_{n_2}\}$$

$$Q_{meta} = Q_1 \cup Q_2$$

$$Q_{inter} = Q_1 \cap Q_2$$



What already exists : Poisot, 2012

$$\beta_{WN} = 1 - \frac{A_1 \odot A_2}{(|A_1| + |A_2|)/2}$$

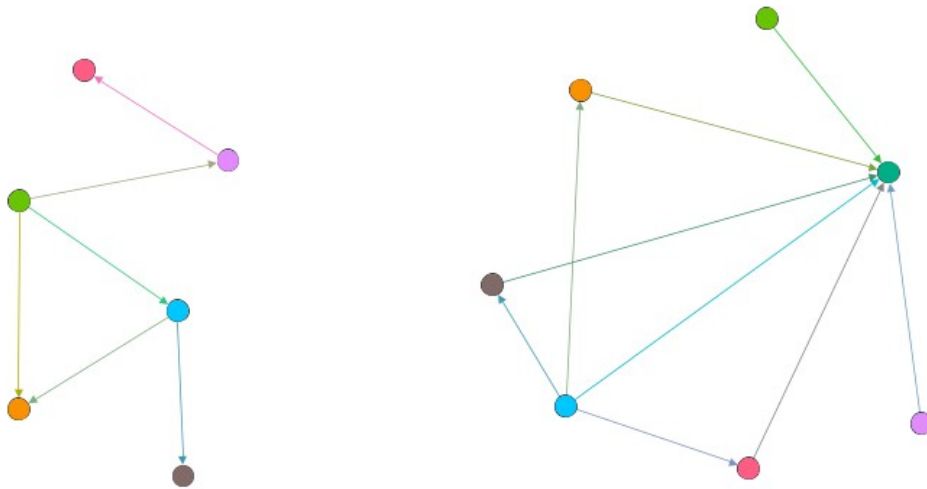
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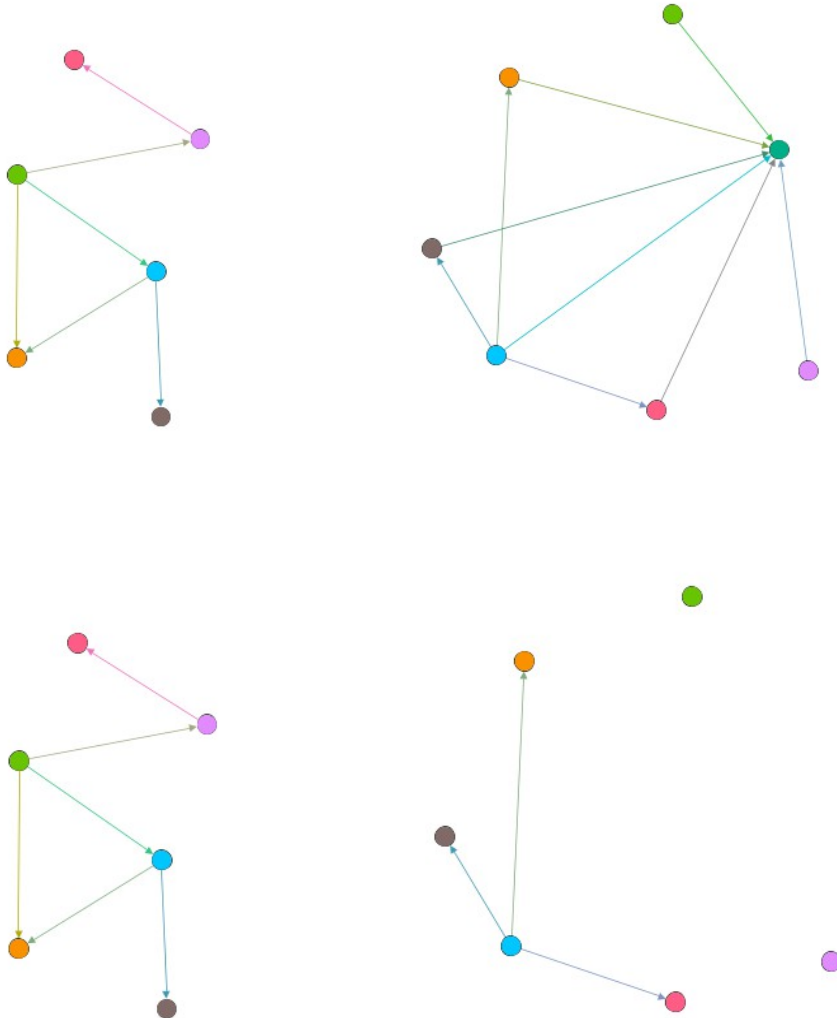
What already exists : Poisot, 2012

$$\beta_{WN} = 1 - \frac{A_1 \odot A_2}{(|A_1| + |A_2|)/2}$$

Both species turnover and plasticity of interactions (at a species level) contribute to  $\beta_{WN}$

**Aim** : separate these two effects

## Microscopic comparison



$$G_1^{inter} = induced.subgraph(G_1, Q_{inter})$$

$$A_1^{inter} : adjacency\ matrix$$

$$G_2^{inter} = induced.subgraph(G_2, Q_{inter})$$

$$A_2^{inter} : adjacency\ matrix$$

$$\beta_{WN} = 1 - \frac{A_1 \odot A_2}{(|A_1| + |A_2|)/2}$$

➔ Total  
dissimilarity

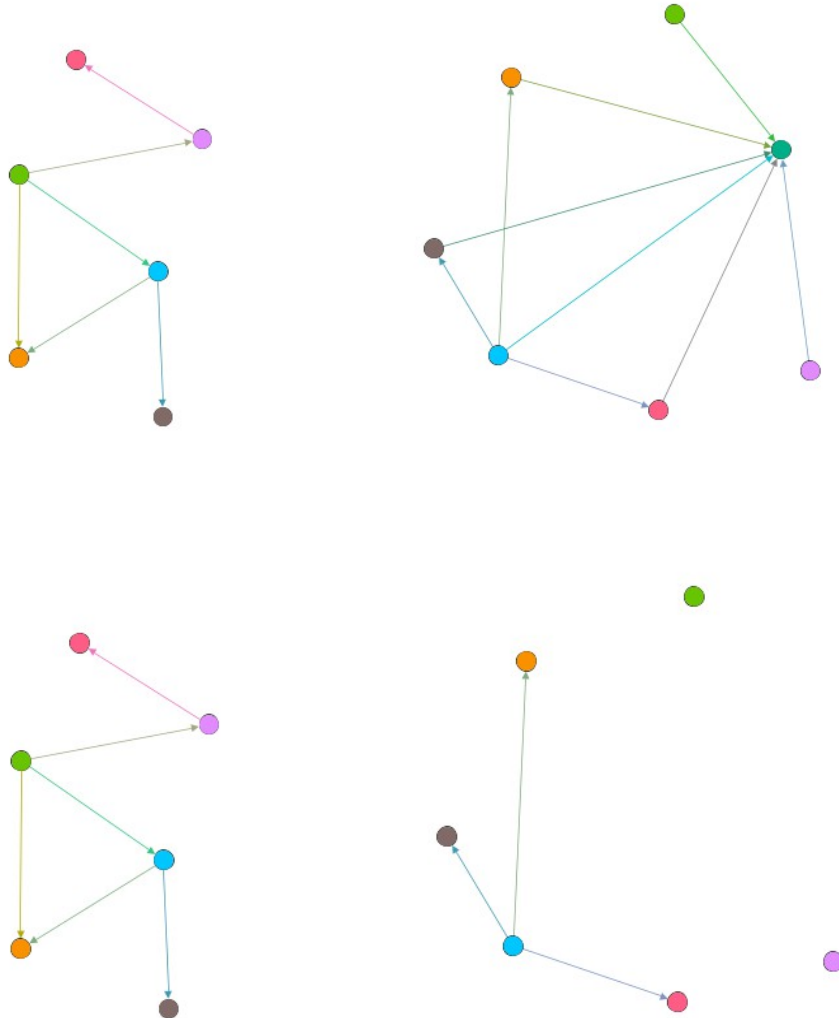
$$\beta_{OS} = 1 - \frac{A_1^{inter} \odot A_2^{inter}}{(|A_1^{inter}| + |A_2^{inter}|)/2}$$

➔ Dissimilarity  
due to  
**plasticity of  
interactions**

$$\beta_{ST} = \beta_{WN} - \beta_{OS}$$

➔ Dissimilarity  
due to  
**species  
turnover**

## Microscopic comparison



$$\beta_{WN} = 1 - \frac{A_1 \odot A_2}{(|A_1| + |A_2|)/2}$$

➔ **Total**  
dissimilarity

$$\beta_{OS} = 1 - \frac{A_1^{inter} \odot A_2^{inter}}{(|A_1^{inter}| + |A_2^{inter}|)/2}$$

➔ Dissimilarity  
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$$\beta_{ST} = \beta_{WN} - \beta_{OS}$$

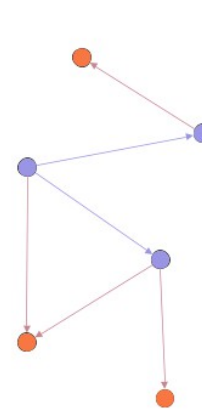
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**Mesososcopic comparison ?**

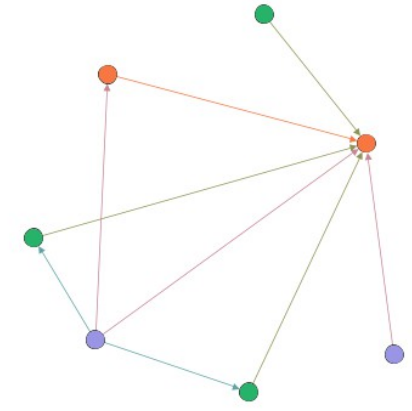
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 $Q_2 = \{1, \dots, |Q_2|\}$   $1 \leq |Q_2| \leq n$

$Q_{inter} = Q_1 \cap Q_2$



G1

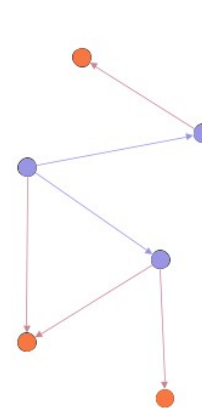


G2

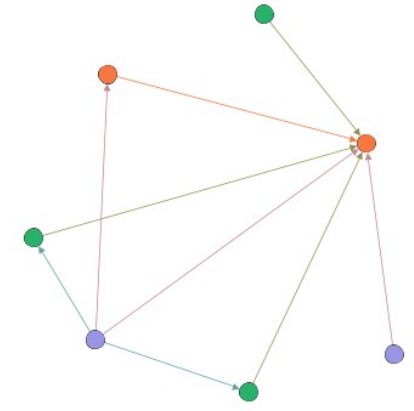
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$Q_{inter} = Q_1 \cap Q_2$



G1



G2

$$\alpha_{G_{meta},k} = \omega \alpha_{G_2,k} + (1 - \omega) \alpha_{G_1,k}$$

$$\omega = \frac{n_1}{n_1 + n_2}$$

$$l_{G_{meta},k} = \omega l_{G_2,k} + (1 - \omega) l_{G_1,k}$$

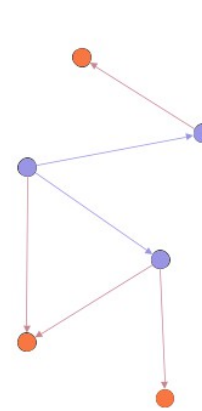
$$\omega = \frac{L_1}{L_1 + L_2}$$

$$\alpha_{G_{meta},k} = \omega \alpha_{G_2,k} + (1 - \omega) \alpha_{G_1,k}$$

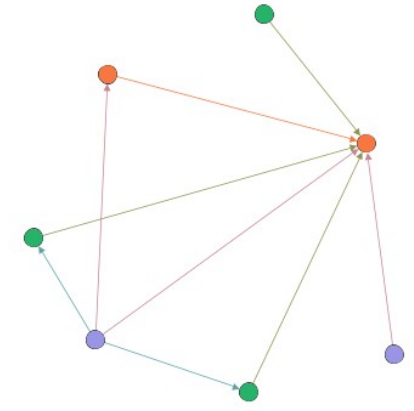
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$$\omega = \frac{L_1}{L_1 + L_2}$$



G1



G2

$$\beta_\alpha(q) = \frac{D_\alpha^{G_{meta}}(q)}{(\omega(D_\alpha^{G_1}(q))^{1-q} + (1-\omega)(D_\alpha^{G_2}(q))^{1-q})^{\frac{1}{1-q}}}$$

$$\beta_L(q) = \frac{D_L^{G_{meta}}(q)}{(\omega(D_L^{G_1}(q))^{1-q} + (1-\omega)(D_L^{G_2}(q))^{1-q})^{\frac{1}{1-q}}}$$



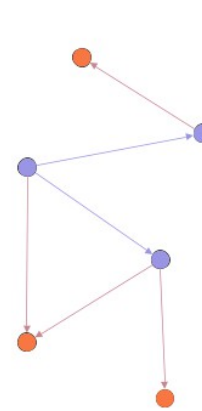
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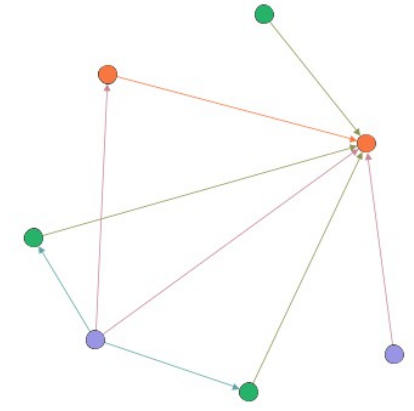
$$1 \leq \beta_{\alpha,L}(q) \leq 2$$

$$\beta_{\alpha,L}(q) \leftarrow \beta_{\alpha,L}(q) - 1$$

$$0 \leq \beta_{\alpha,L}(q) \leq 1$$



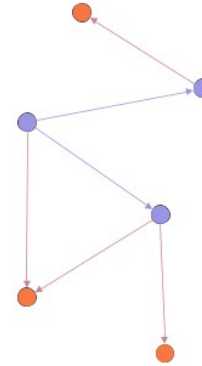
G1



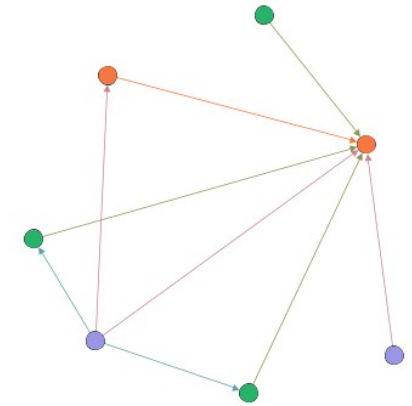
G2

$$\beta_{\alpha}(q) = \frac{D_{\alpha}^{G_{meta}}(q)}{(\omega(D_{\alpha}^{G_1}(q))^{1-q} + (1-\omega)(D_{\alpha}^{G_2}(q))^{1-q})^{\frac{1}{1-q}}}$$

$$\beta_L(q) = \frac{D_L^{G_{meta}}(q)}{(\omega(D_L^{G_1}(q))^{1-q} + (1-\omega)(D_L^{G_2}(q))^{1-q})^{\frac{1}{1-q}}}$$



G1



G2

**A particular case : Tim Poisot case** (microscopic turnover)

$$Q_1 = \{1, \dots, n_1\}$$

$$Q_2 = \{1, \dots, n_2\}$$

$$\omega = 1/2$$

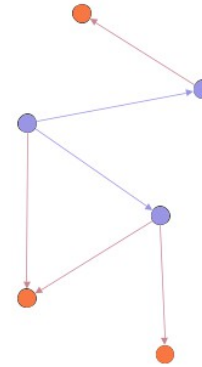
Easy to show that :

$$\beta_{\alpha}(0) = \beta_S$$

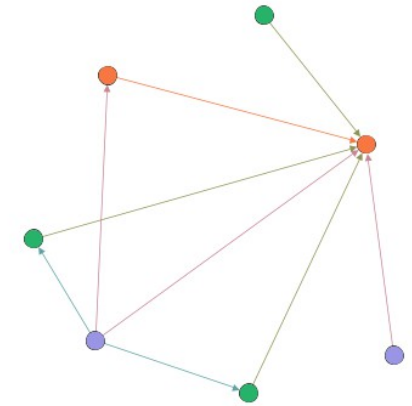
$$\beta_L(0) = \beta_{WN}$$

$$\beta_{\alpha}(q) = \frac{D_{\alpha}^{G_{meta}}(q)}{(\omega(D_{\alpha}^{G_1}(q))^{1-q} + (1-\omega)(D_{\alpha}^{G_2}(q))^{1-q})^{\frac{1}{1-q}}}$$

$$\beta_L(q) = \frac{D_L^{G_{meta}}(q)}{(\omega(D_L^{G_1}(q))^{1-q} + (1-\omega)(D_L^{G_2}(q))^{1-q})^{\frac{1}{1-q}}}$$



G1



G2

**A particular case : Tim Poisot case** (microscopic turnover)

$$Q_1 = \{1, \dots, n_1\}$$

$$Q_2 = \{1, \dots, n_2\}$$

$$\omega = 1/2$$

Easy to show that :

$$\beta_{\alpha}(0) = \beta_S$$

$$\beta_L(0) = \beta_{WN}$$

Do change of link diversity reflect  
change in connectivity ?

Yes, but there is a group size effect too !

Here, we work on :  $G_1^{inter}$   
 $G_2^{inter}$

$$\left( \pi_{k,l}^{G_1^{inter}} \right)_{1 \leq k,l \leq |Q_{inter}|}$$

$$\left( \pi_{k,l}^{G_2^{inter}} \right)_{1 \leq k,l \leq |Q_{inter}|}$$

$$\pi_{k,l}^{G_{meta}^{inter}} = \omega \pi_{k,l}^{G_1^{inter}} + (1 - \omega) \pi_{k,l}^{G_2^{inter}}$$

Here, we work on :  $G_1^{inter}$   
 $G_2^{inter}$

$$\left( \pi_{k,l}^{G_1^{inter}} \right)_{1 \leq k,l \leq |Q_{inter}|}$$

$$\left( \pi_{k,l}^{G_2^{inter}} \right)_{1 \leq k,l \leq |Q_{inter}|}$$

$$\pi_{k,l}^{G_{meta}^{inter}} = \omega \pi_{k,l}^{G_1^{inter}} + (1 - \omega) \pi_{k,l}^{G_2^{inter}}$$

$$\beta_\pi(q) = \frac{D_\pi^{G_{meta}^{inter}}(q)}{(\omega (D_\pi^{G_1^{inter}}(q))^{1-q} + (1-\omega) (D_\pi^{G_2^{inter}}(q))^{1-q})^{\frac{1}{1-q}}}$$

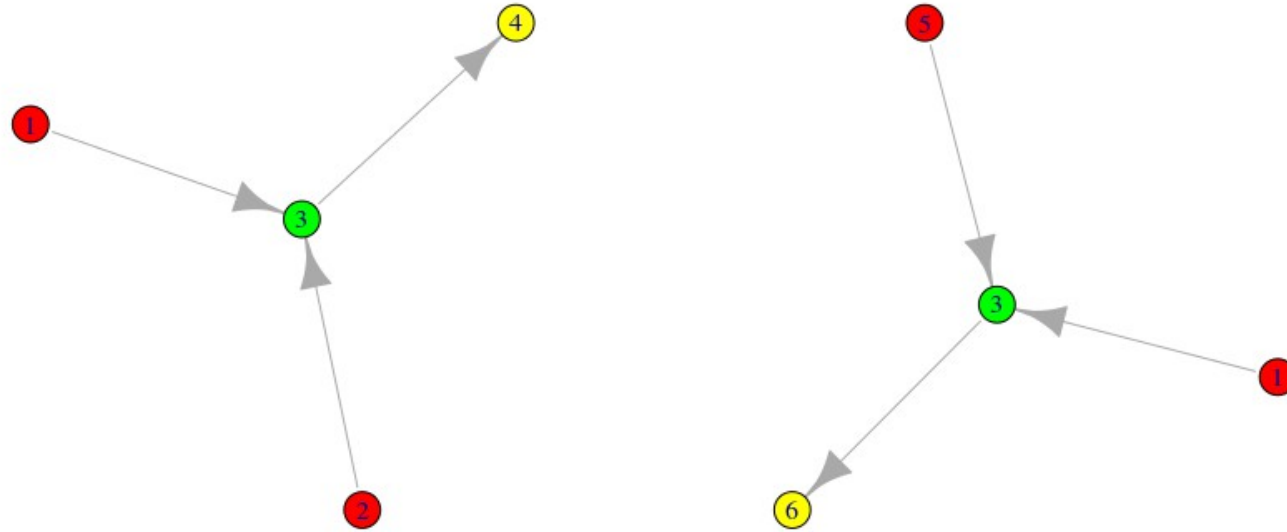
**A particular case : Tim Poisot case** (microscopic scale)

$$Q_1 = \{1, \dots, n_1\}$$

$$Q_2 = \{1, \dots, n_2\}$$

$$\omega = 1/2$$

$$\beta_\pi(0) = \beta_{OS}$$



*Macroscopic scale*

$$C=0.19$$

Mesoscopic scale

$$\beta_{\alpha}=0$$

$$\beta_L=0$$

$$\beta_{\pi}=0$$

*Microscopic scale*

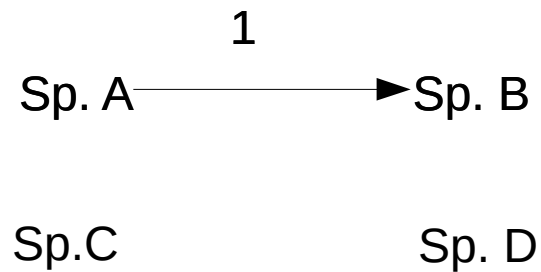
$$\beta_S=0.5$$

$$\beta_{WN}=2/3$$

$$\beta_{OS}=0$$

$$\beta_{ST}=2/3$$

Forbidden links between species ?

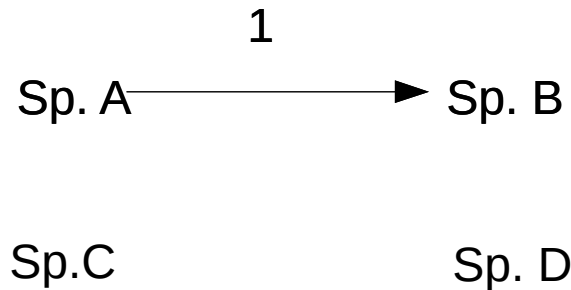


*At individual level :*

$$\Pr(i \rightarrow j | i \in A, j \in B) = 1$$

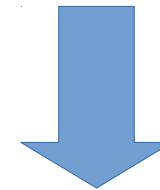
$$\Pr(i \rightarrow j | i \in C, j \in D) = 0$$

## Forbidden links between species ?



$$\Pr(i \rightarrow j | i \in A, j \in B) = 1$$

$$\Pr(i \rightarrow j | i \in C, j \in D) = 0$$



These binary relations neglect the intraspecific trait variability compared to interspecific trait variability

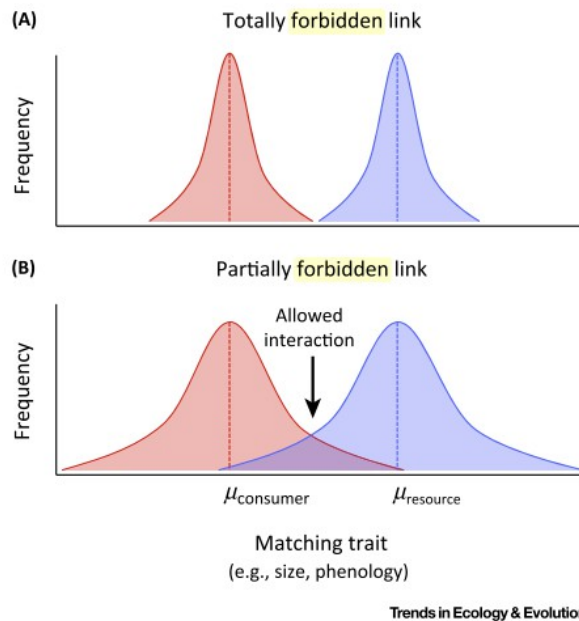
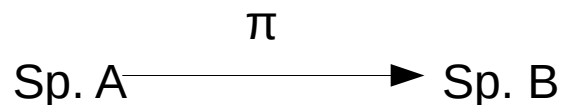


Figure 1. Frequency Distribution of Matching Traits (e.g., Body Size or Phenology) in a Consumer and a Resource Species. Interaction is possible whenever  $x_{\text{consumer}} \geq x_{\text{resource}}$ . (A) Mismatching between both trait means and intraspecific variability prevent interaction, leading to a **totally forbidden link**. (B) Mismatching occurs between trait means but intraspecific variability allows interaction, leading to a **partially forbidden link**. The difference between (A) and (B) – thus, our ability to infer interactions – may depend on how broadly intraspecific trait variability has been assessed in space and time (Box 1).

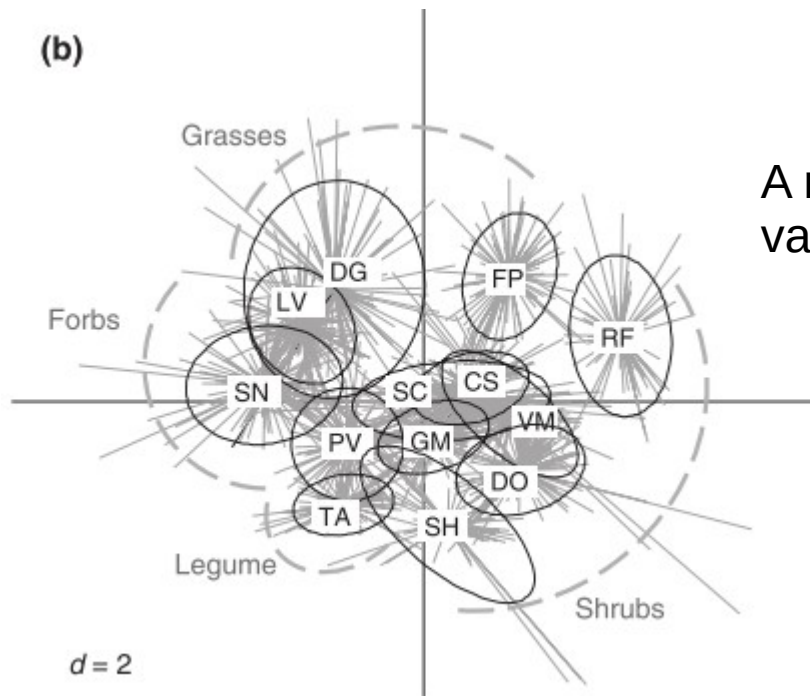
Taken from :  
*The labile limit of forbidden interactions*  
Gonzalez-Varo  
Trends in Ecology and Evolution, 2016



$$\Pr(i \rightarrow j | i \in A, j \in B) = \pi$$



Can we neglect intra-specific traits variability ?

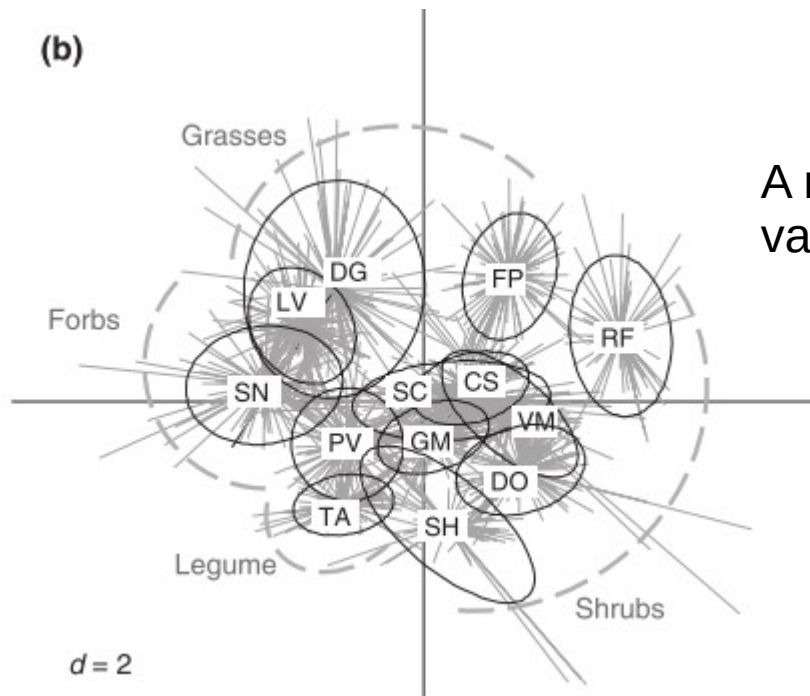


A mono-trophic view of traits intra/interspecific variability

Taken from :

*A multi-trait approach reveals the structure and the relative importance of intra- vs. interspecific variability in plant traits*  
Albert et al., *Functional Ecology*, 2010

Can we neglect intra-specific traits variability ?



A mono-trophic view of traits intra/interspecific variability

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*For trophic networks :*

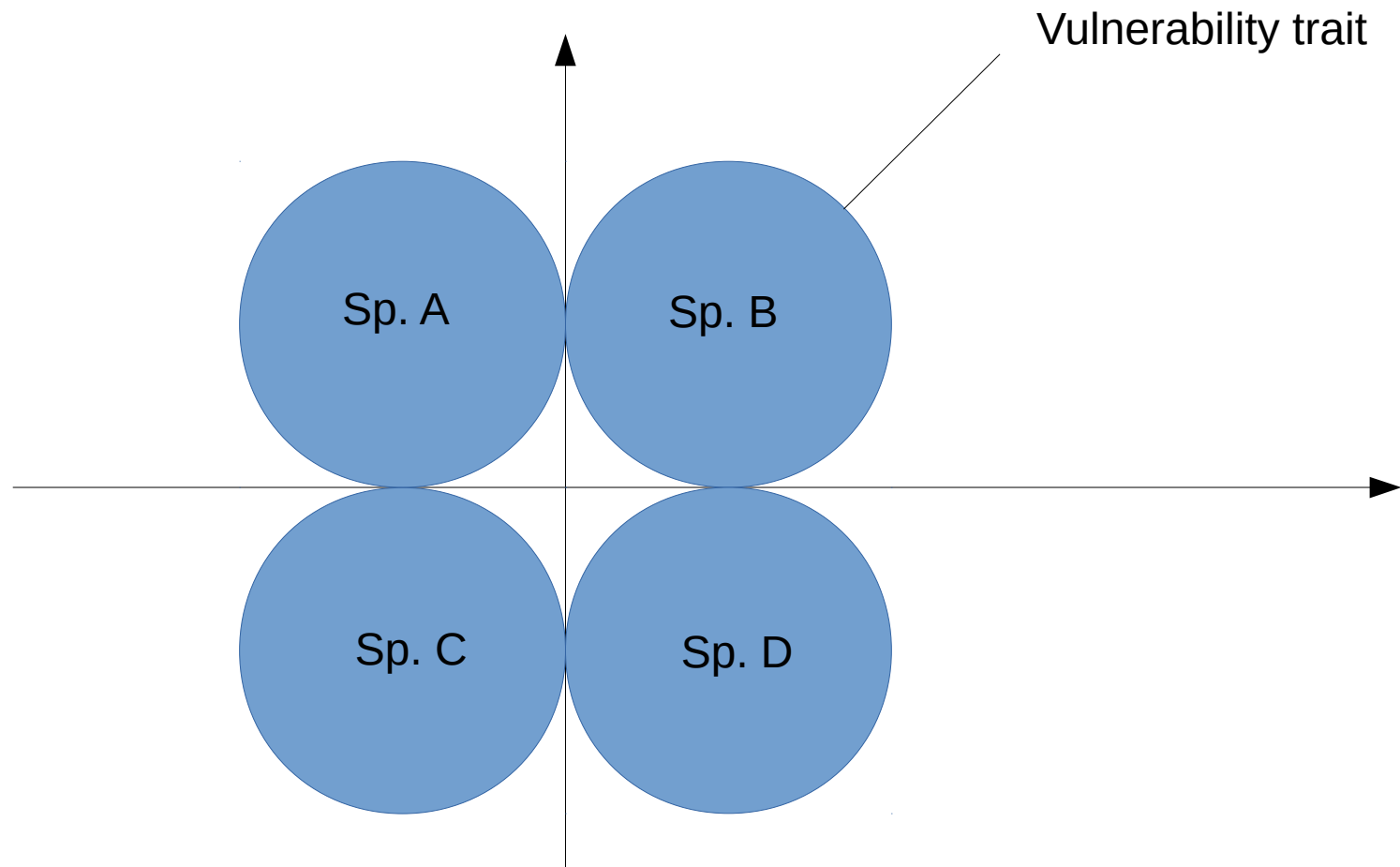
Interaction is the resultant of a match between a vulnerability trait (prey) and a foraging trait (predator)

see : Gravel et al., 2016

*For trophic networks :*

Interaction is the resultant of a match between a vulnerability trait (prey) and a foraging trait (predator)

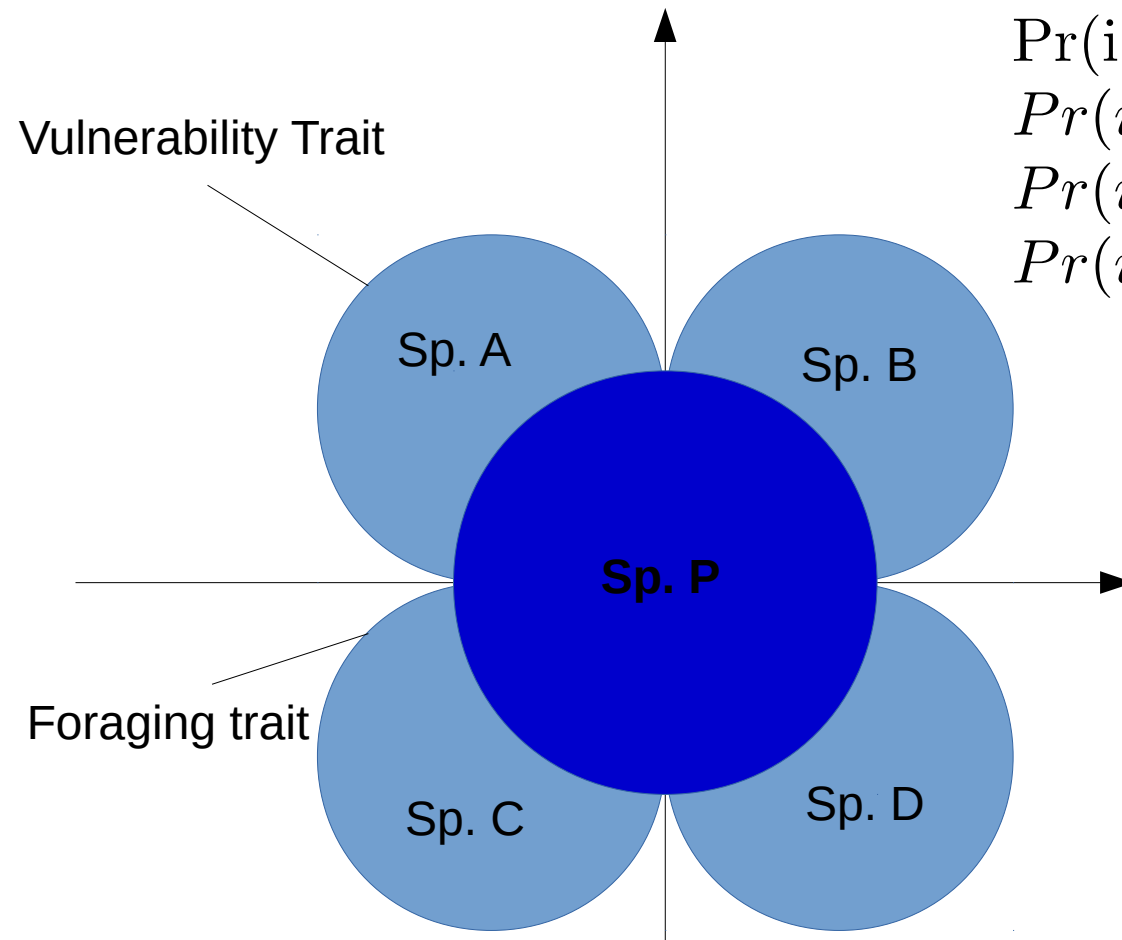
see : Gravel et al., 2016



*For trophic networks :*

Interaction is the resultant of a match between a vulnerability trait (prey) and a foraging trait (predator)

see : Gravel et al., 2016

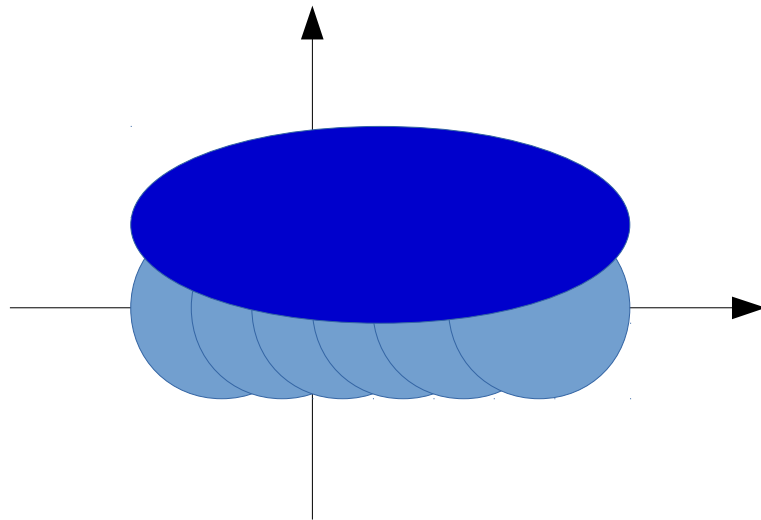


$$\Pr(i \rightarrow j | i \in A, j \in P) = \pi$$

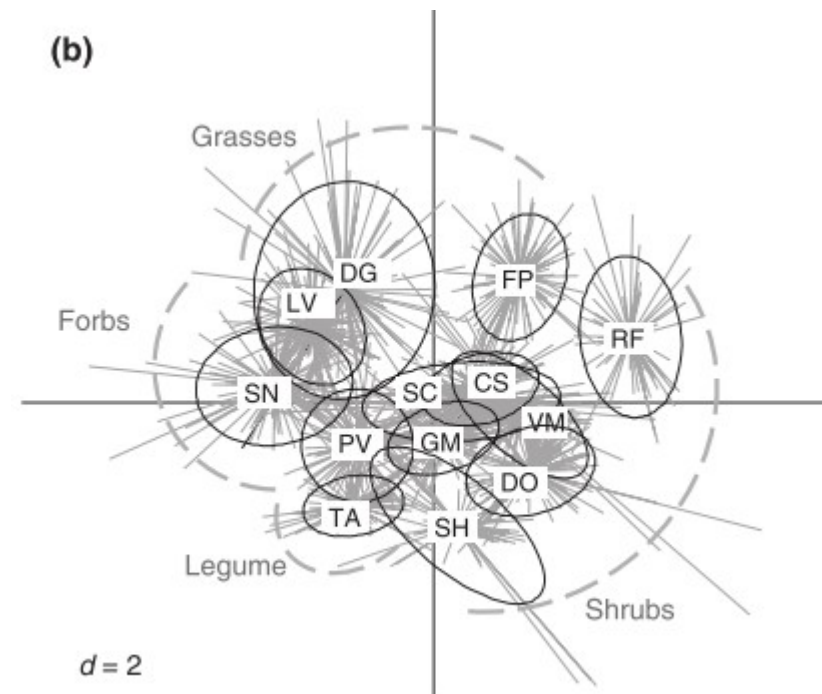
$$\Pr(i \rightarrow j | i \in B, j \in P) = \pi$$

$$\Pr(i \rightarrow j | i \in C, j \in P) = \pi$$

$$\Pr(i \rightarrow j | i \in D, j \in P) = \pi$$



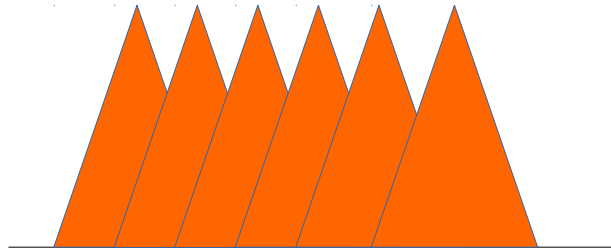
relevant in that case



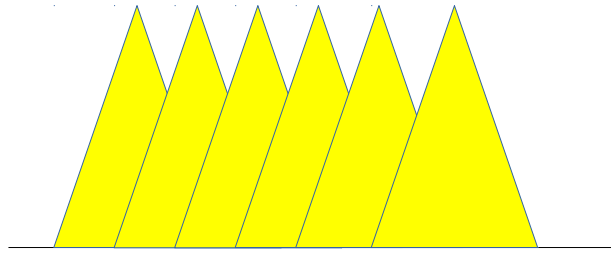
Taken from :

*A multi-trait approach reveals the structure and the relative importance of intra- vs. interspecific variability in plant traits*

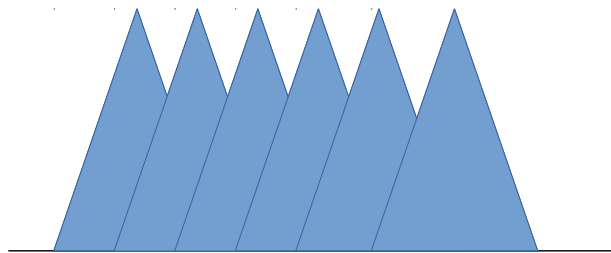
Albert et al., *Functional Ecology*, 2010



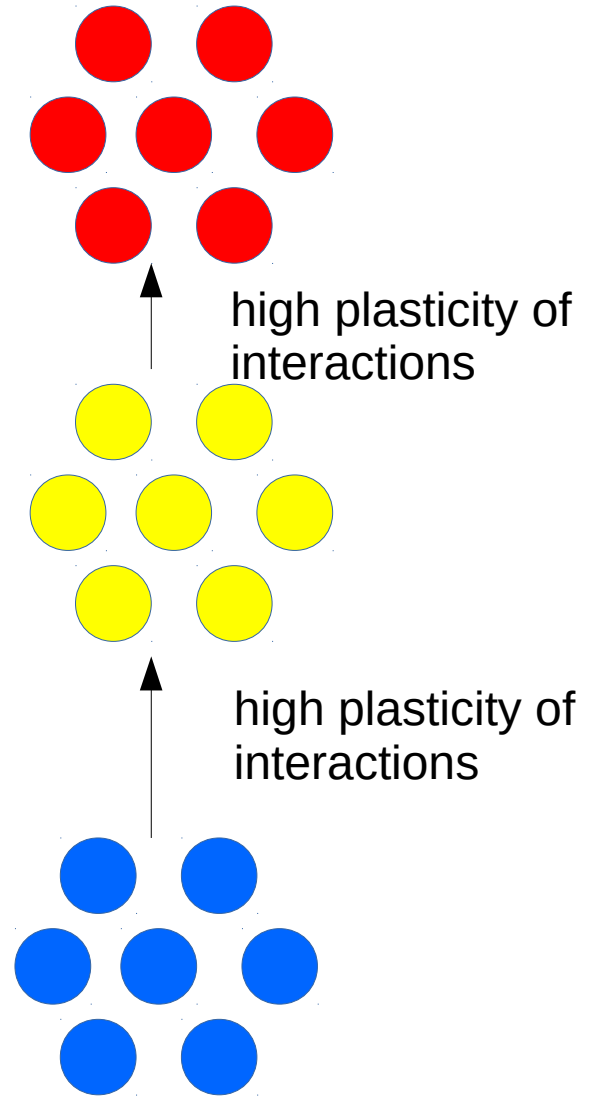
Traits group A

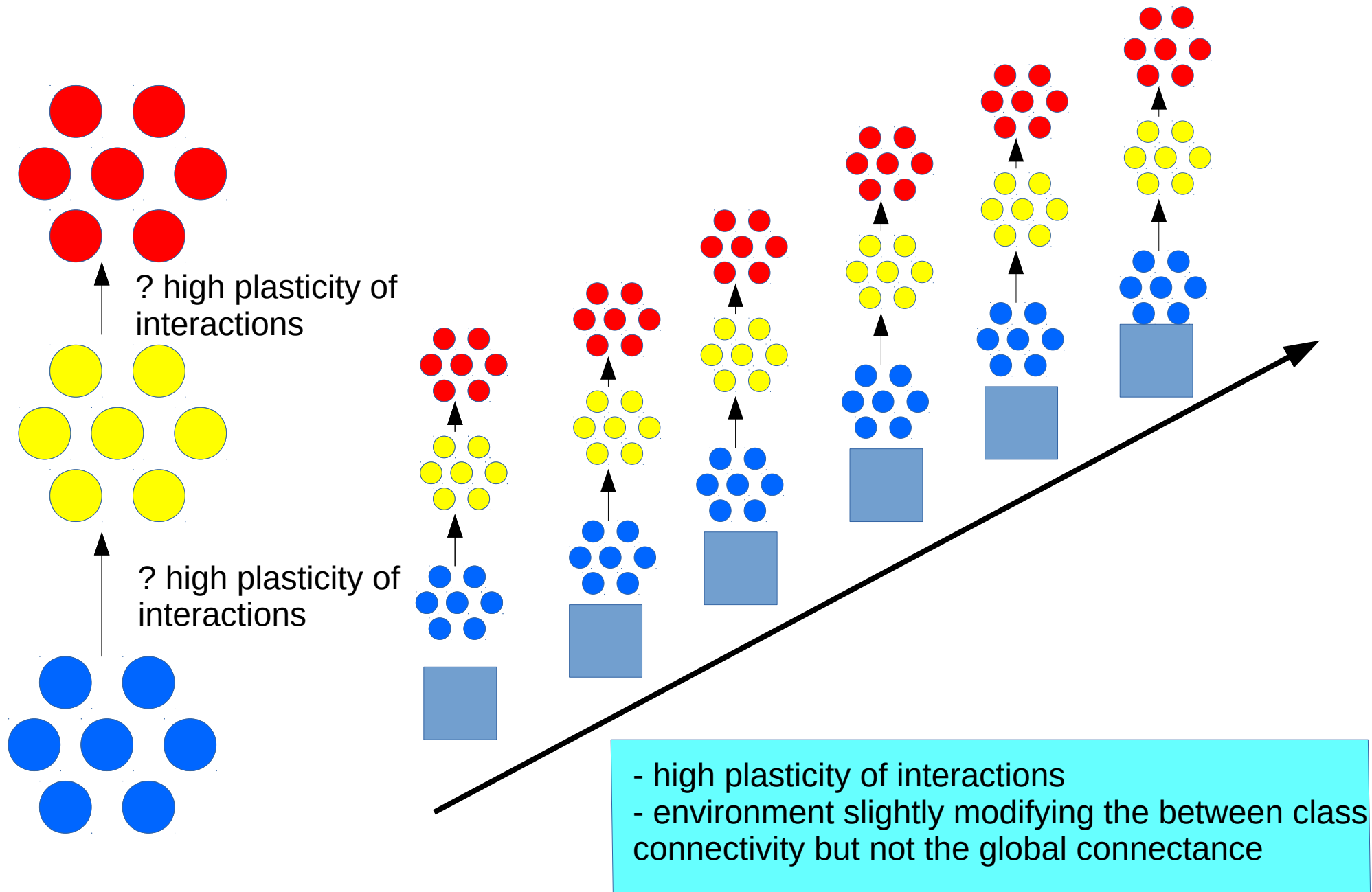


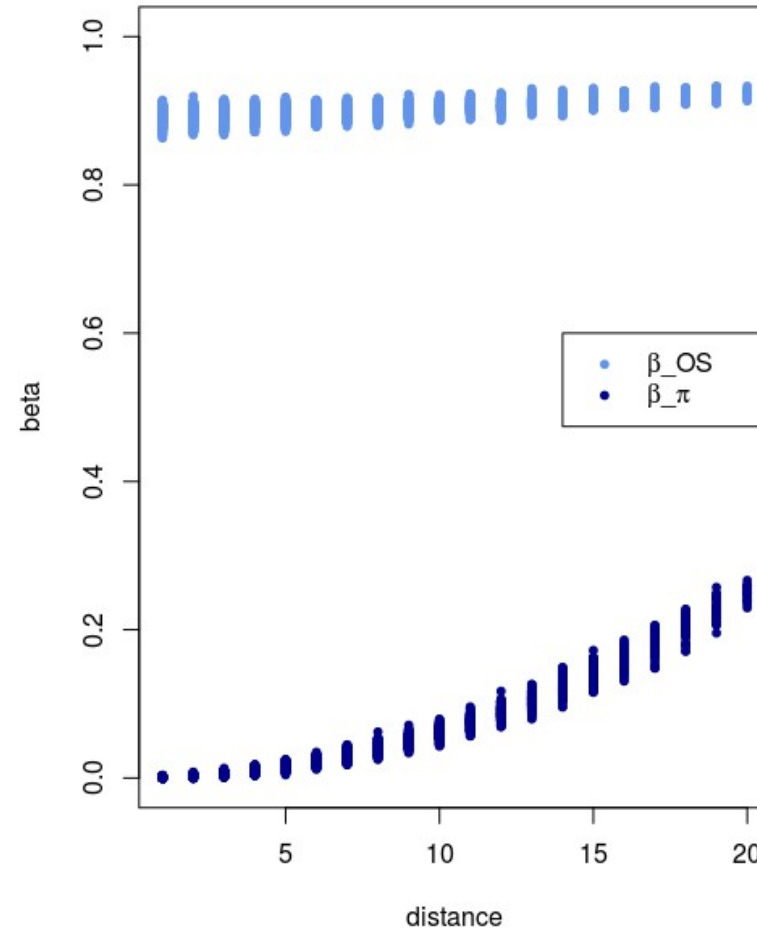
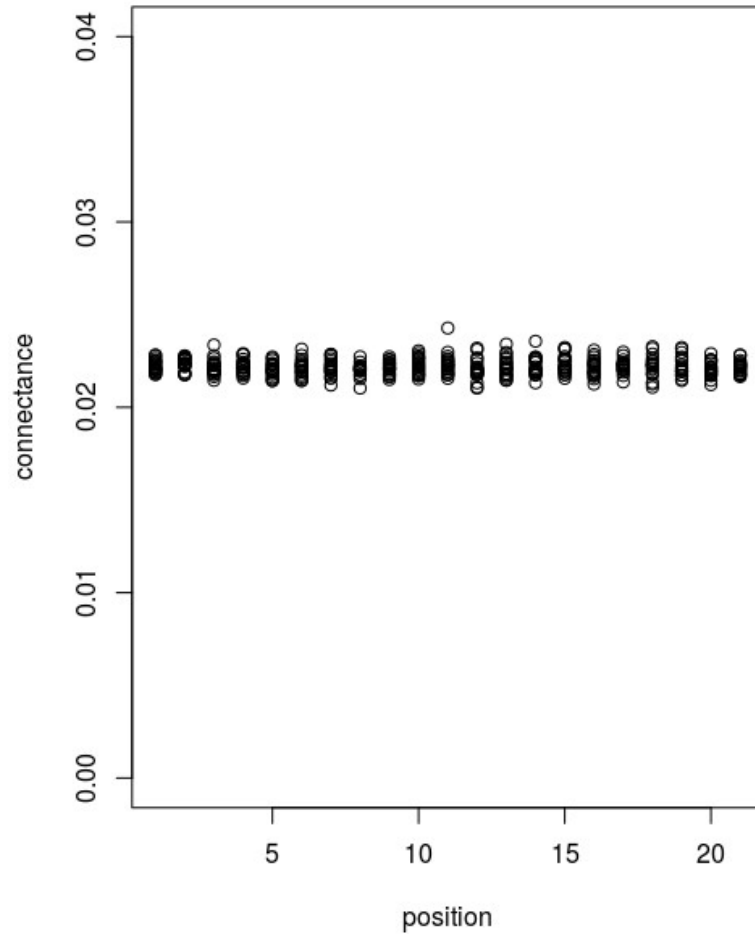
Traits group B



Traits group C







Macroscopic scale : no variations

Microscopic scale : too much variations

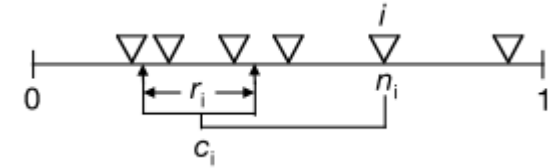
Mesoscopic scale : strong pattern



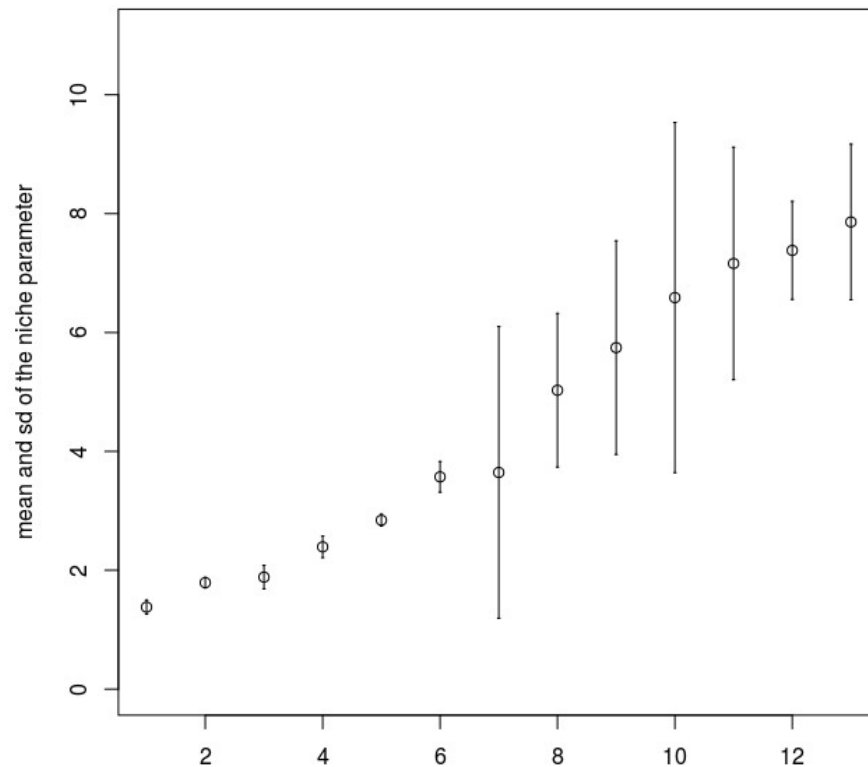
## Aim : Test the robustness of mesoscopic metrics to incomplete sampling

Using a model of food web :  
the niche model (Williams and Martinez, 2000)

Inferring classes of nodes using Stochastic Block Model  
( a model of community detection)

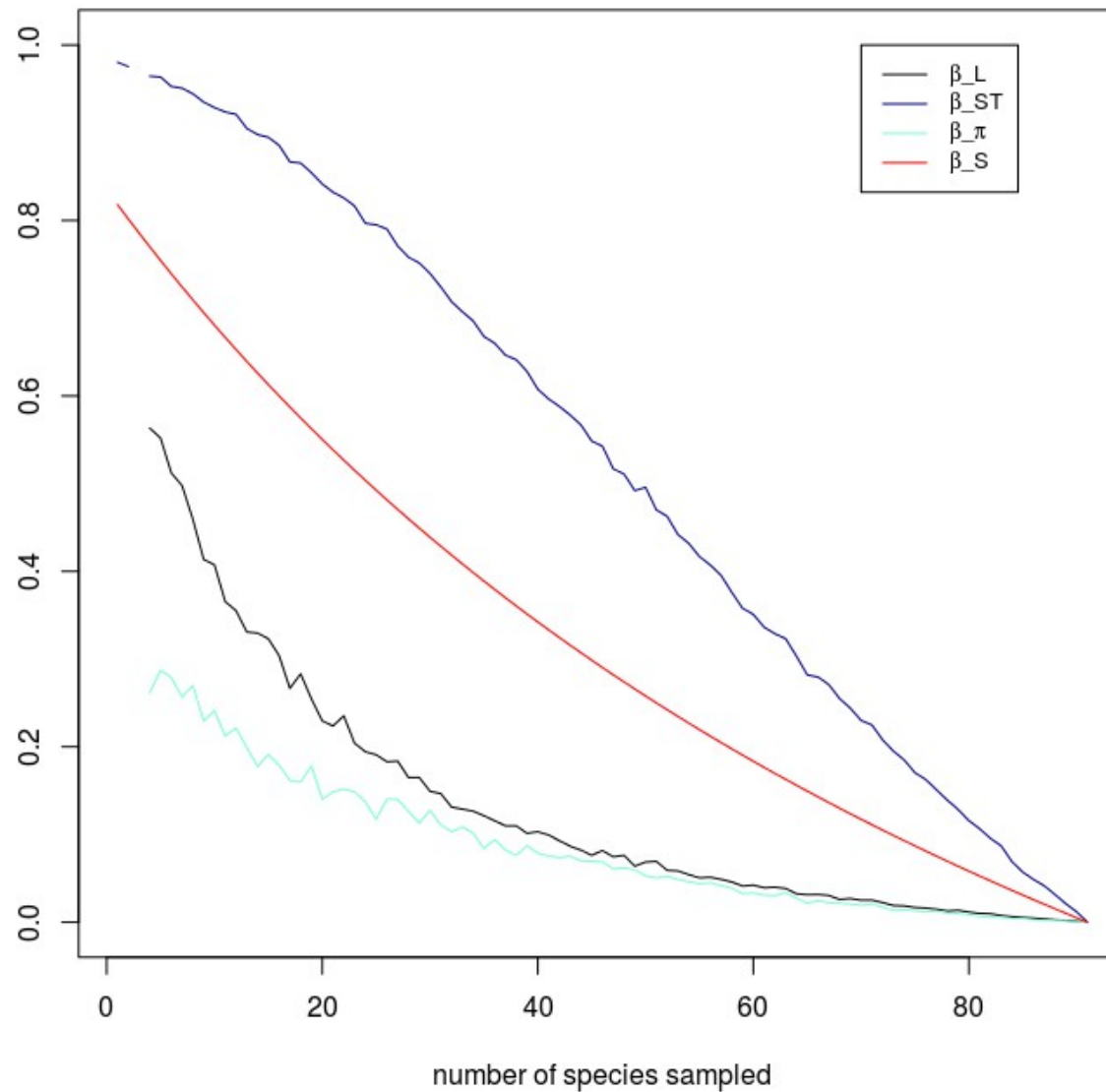


Taken from :  
*Simple rules yield complex food webs*,  
Williams and Martinez, 2000, Nature



**Groups inferred using SBM are  
almost functional groups**

Rarefaction curves : how robust are our metrics to incomplete species sampling ?



A framework using Hill numbers that allows network comparison at different scales, from macroscopic scale to microscopic scale

Ecological networks might evolve at different Elton niches scales, especially if you're interested in microbial/soil ecology

Mesoscopic analysis is more robust to incomplete sampling

Key question : *how to determine Elton niches ?*

Using network topology ?

Traits ?