How repeatable are communities in Fomes polypores?

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To cite this version:

Agnès Ardanuy-Gabarra, Olivier Rose, Antoine Brin, Christophe Bouget, F. Laroche. How repeatable are communities in Fomes polypores?. SFE2 GfÖ EEF - International Conference on Ecological Sciences, Nov 2022, Metz, France. 24p. hal-03931425

HAL Id: hal-03931425
https://hal.inrae.fr/hal-03931425v1

Submitted on 9 Jan 2023


M. Roy

How repeatable are communities in *Fomes* polypores?

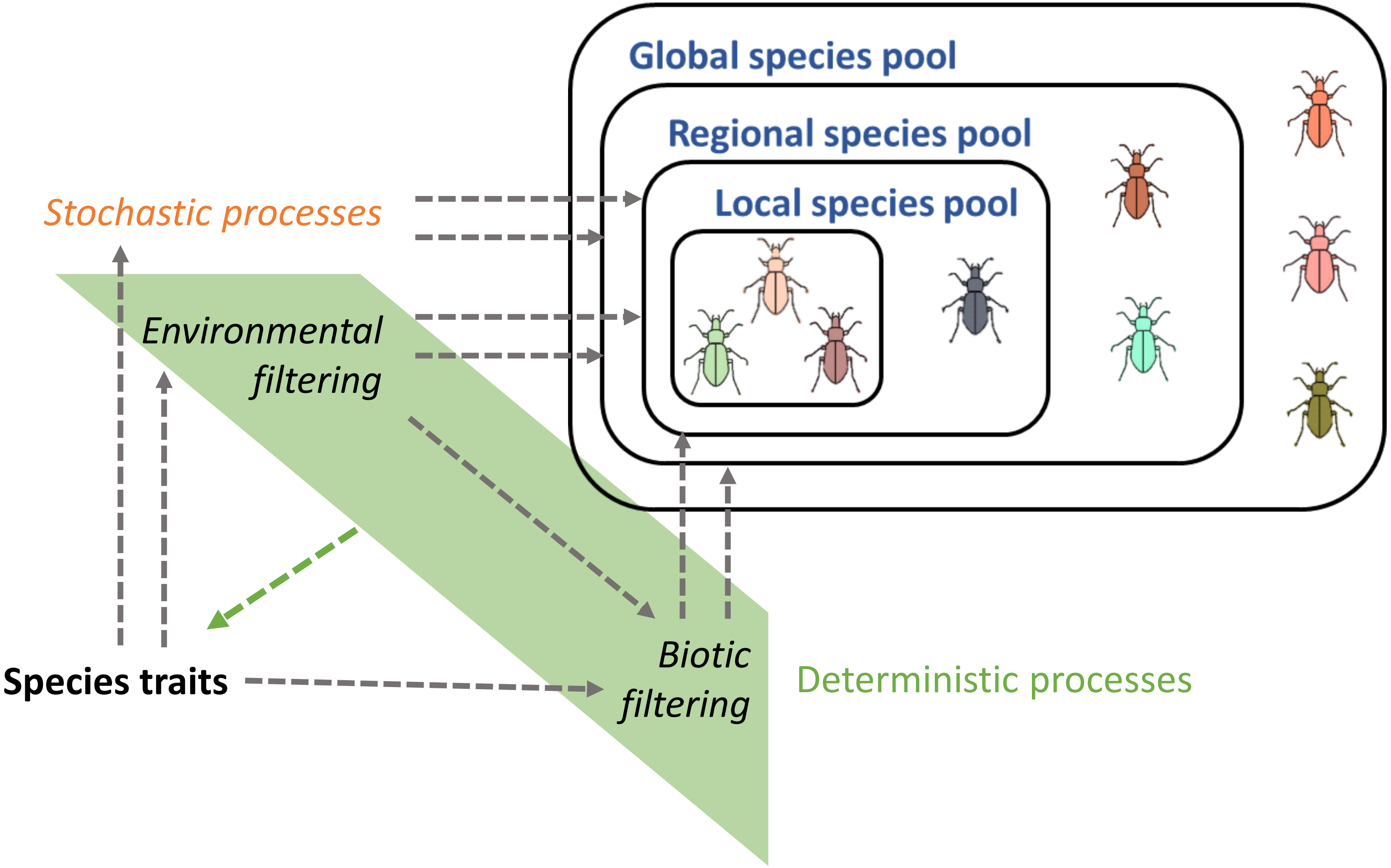
SFE² GfÖ EEF - International Conference on Ecological Sciences

Metz, 23 November 2022

Agnès Ardanuy, Olivier Rose, Antoine Brin, Christophe Bouget, Fabien Laroche

1. Community assembly
2. Diversity patterns
3. Study system and methods
4. Hypotheses and predictions
5. Results
6. Conclusions and way forward

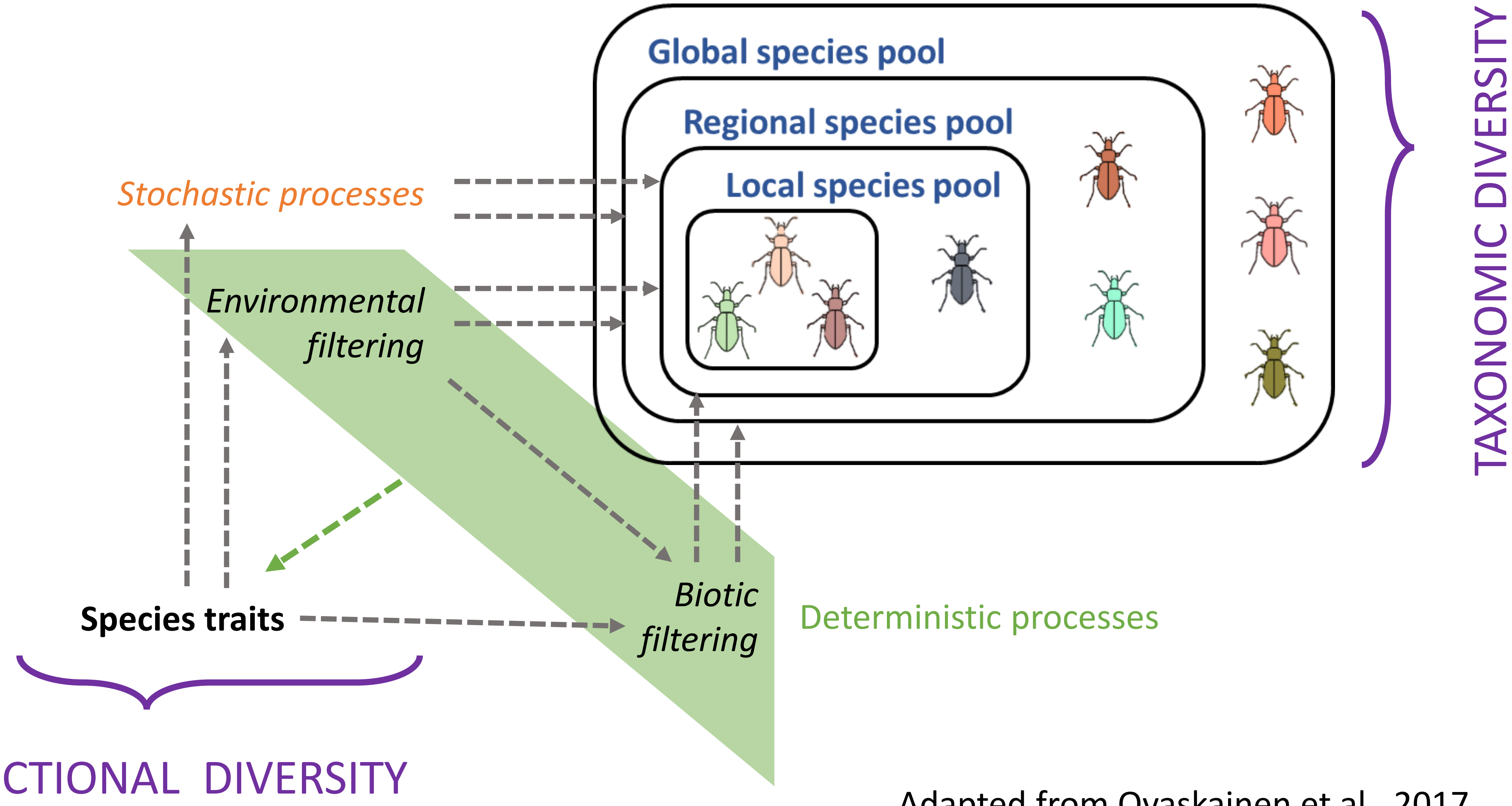
1. Community assembly: patterns and processes



Adapted from Ovaskainen et al., 2017

e.g. Weiher and Keddy 1995; Wobel 1997, Chase et al., 2011; HilleRisLambers et al., 2012; Kraft et al., 2015

1. Community assembly: patterns and processes



Global species pool

Regional species pool

Local species pool

TAXONOMIC DIVERSITY

Stochastic processes

Environmental filtering

Biotic filtering

Deterministic processes

Species traits

FUNCTIONAL DIVERSITY

Adapted from Ovaskainen et al., 2017

e.g. Weiher and Keddy 1995; Wobel 1997, Chase et al., 2011; HilleRisLambers et al., 2012; Kraft et al., 2015

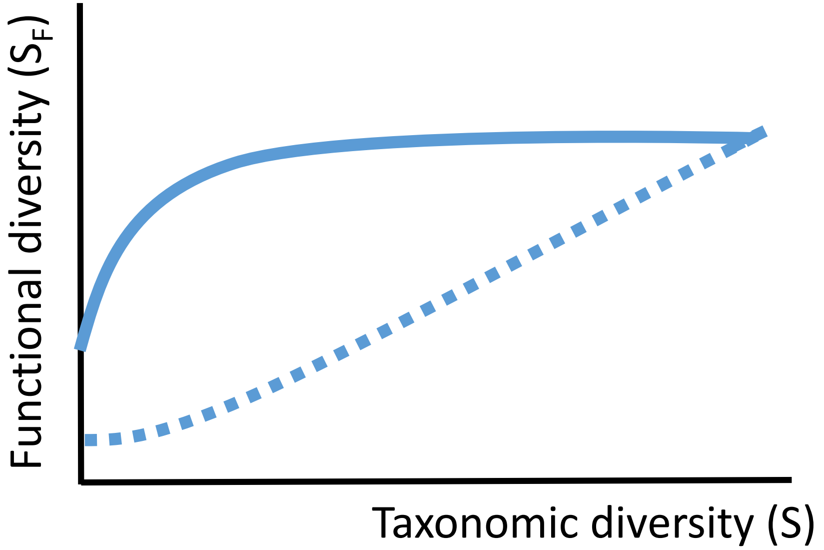
2. Diversity patterns and functional redundancy

PATTERNS can be studied with elements of diversity in communities

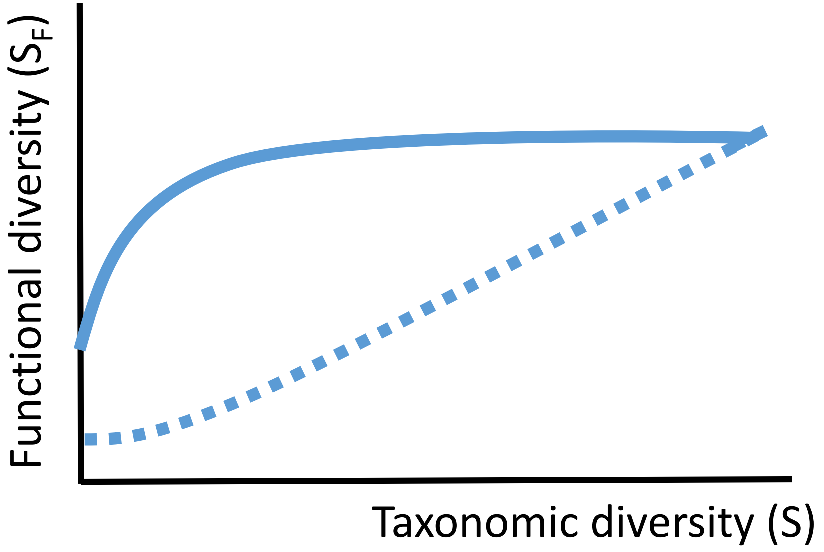
- **α diversity** metrics
- **β diversity** metrics (& decomposition)

For all organisational facets **taxonomic, functional & phylogenetic**

The link between the facets across scales provides information on whether communities are “**repeatable”.**



2. Diversity patterns and functional redundancy



PATTERNS can be studied with elements of diversity in communities

- **α diversity** metrics
- **β diversity** metrics (& decomposition)

For all organisational facets **taxonomic, functional & phylogenetic**

The link between the facets across scales provides information on whether communities are **"repeatable".**

A "**repeatable community**"
is a community that presents
functional redundancy

→

(β) differences between taxonomic and functional diversity

e.g De Bello 2007; Ricotta et al., 2016; Graco-Roza et al., 2022

To evaluate when and how these patterns differ from random assembly we will use **constrained null models** at diferent scales

3. Study system & methods: *Fomes* polypores, Vosges

Work by Olivier Rose

Coleopteran community in *Fomes* polypores- 196 *spp* from 35 families.

- Sampling July 2007 October 2008 in Vosges (NE, France)

- 5 sites
- 5 plots per site
- 8 polypores per plot

- Plots of 30m radius – 100 m distance between plots

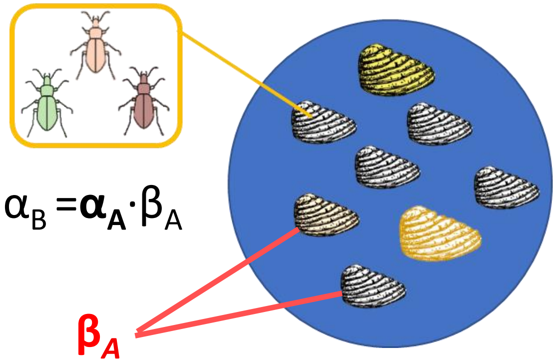
- **Trophic guilds = Functional groups**

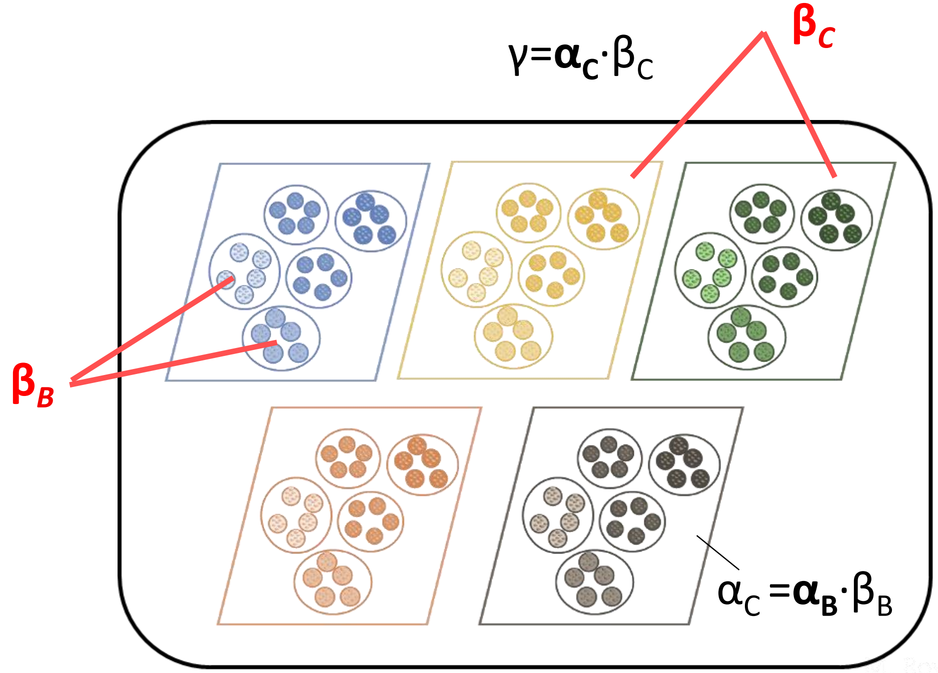
6 Mycetophagus(=Fungivorous), Zoophagus, Xylophagus, Saprofagous, Saproxylophagus, Non-saproxylic

Defined by boundaries (=polypore) and not convention

4. Study system & methods: null communities by constrained permutation

We modified **α diversity** at one scale (A,B,C) and kept other αs invariable





OBS.	α_{obs}	β_{obs}
NULL	α_{null}	β_{null}

Calculation of standardized effect size (SES)

2 comparisons

Taxonomic vs. Functional group (FG)
Fungivorous vs. Zoophagous

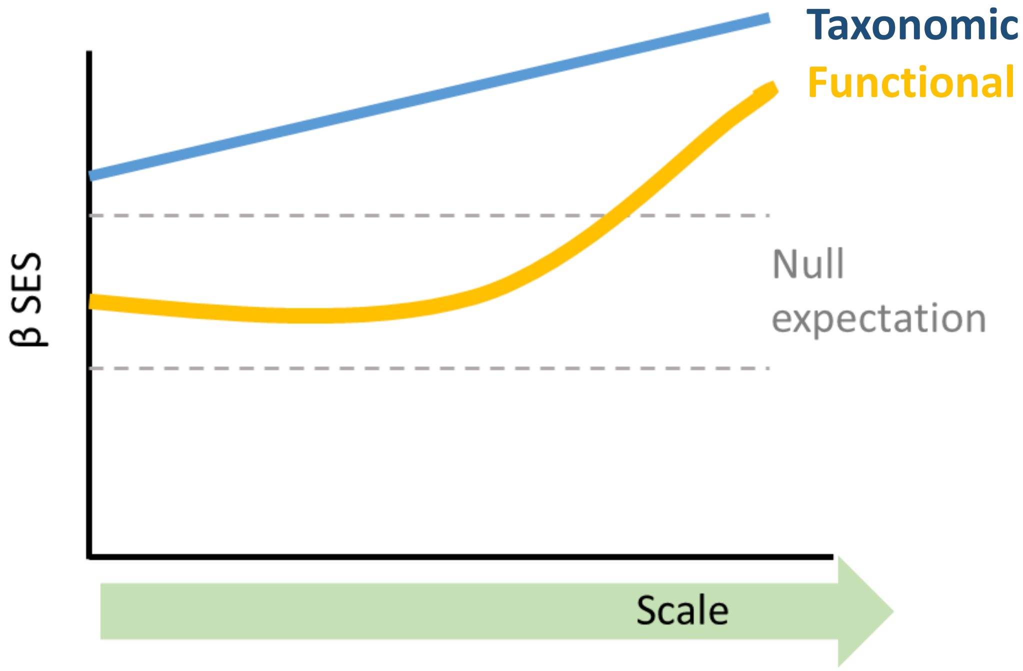
Computation of: α (multipart, package vegan) – *abundance data* and partition of β (Baselga, package betapart; Podani & Schmera, package BAT) – *ocurrence data*.

4. Hypothesis and predictions

H1/ Coleopteran communities within polypores are trophically redundant.

Functional group β diversity will not differ from random generated communities while taxonomic β diversity will be larger.

This will show that spp are **redundant** within spp of the same feeding guild



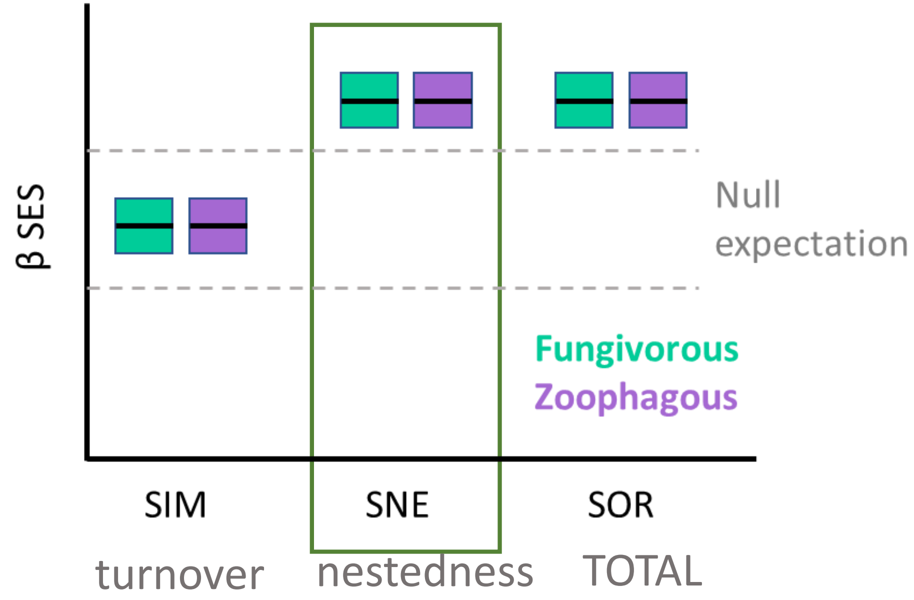
4. Hypothesis and predictions

H1/ Coleopteran communities within polypores are trophically redundant.

H2/ Species within a functional group will present a nested pattern.

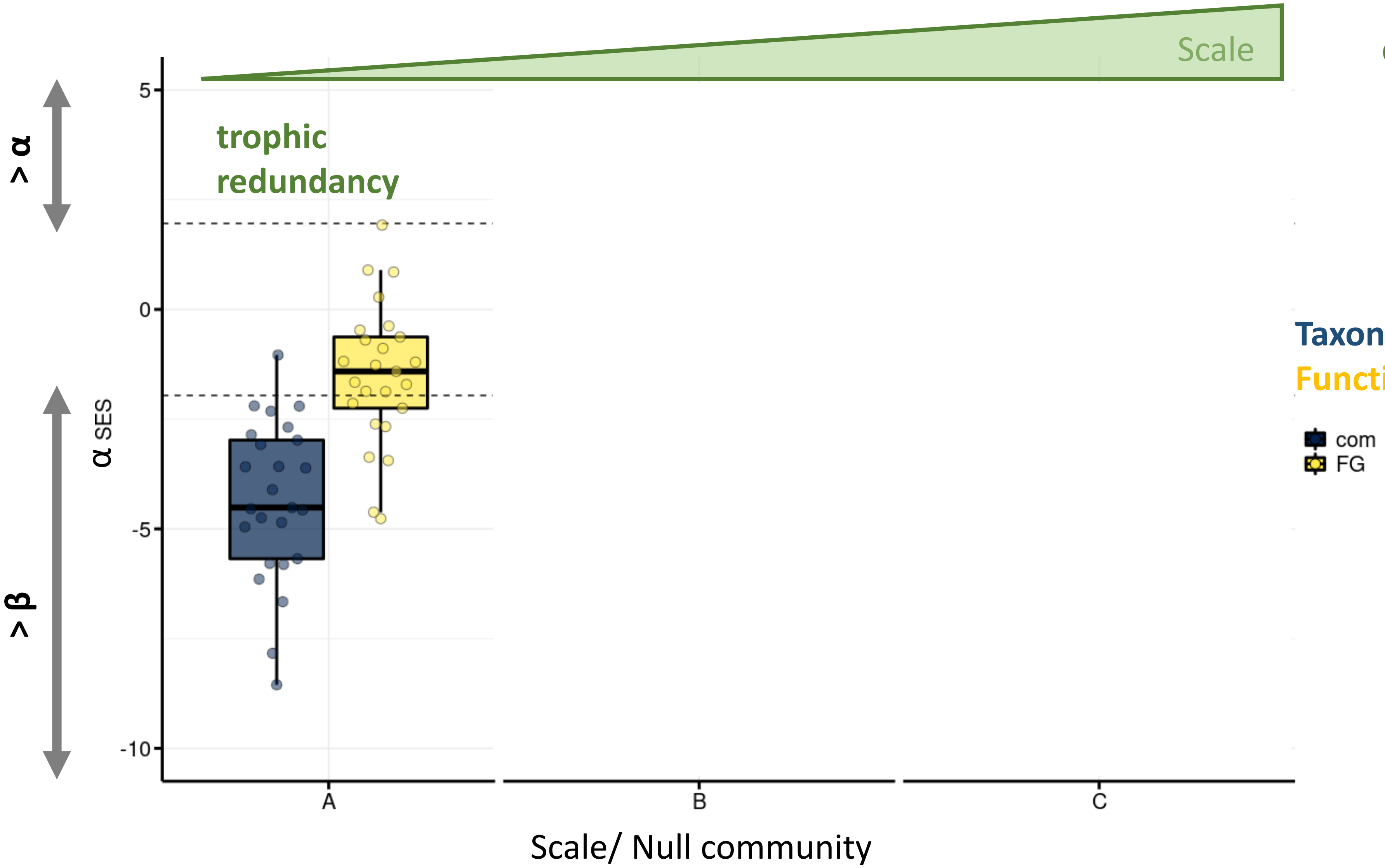
The nestedness component of **β diversity within FG will be larger than that of random generated communities**

This would show that FG classification is a « sufficient » descriptor of functional groups



At which scale? Spatial aggregation (Thuiller et al., 2015)

5. Results: Are Coleopteran communities within polypores trophically redundant?



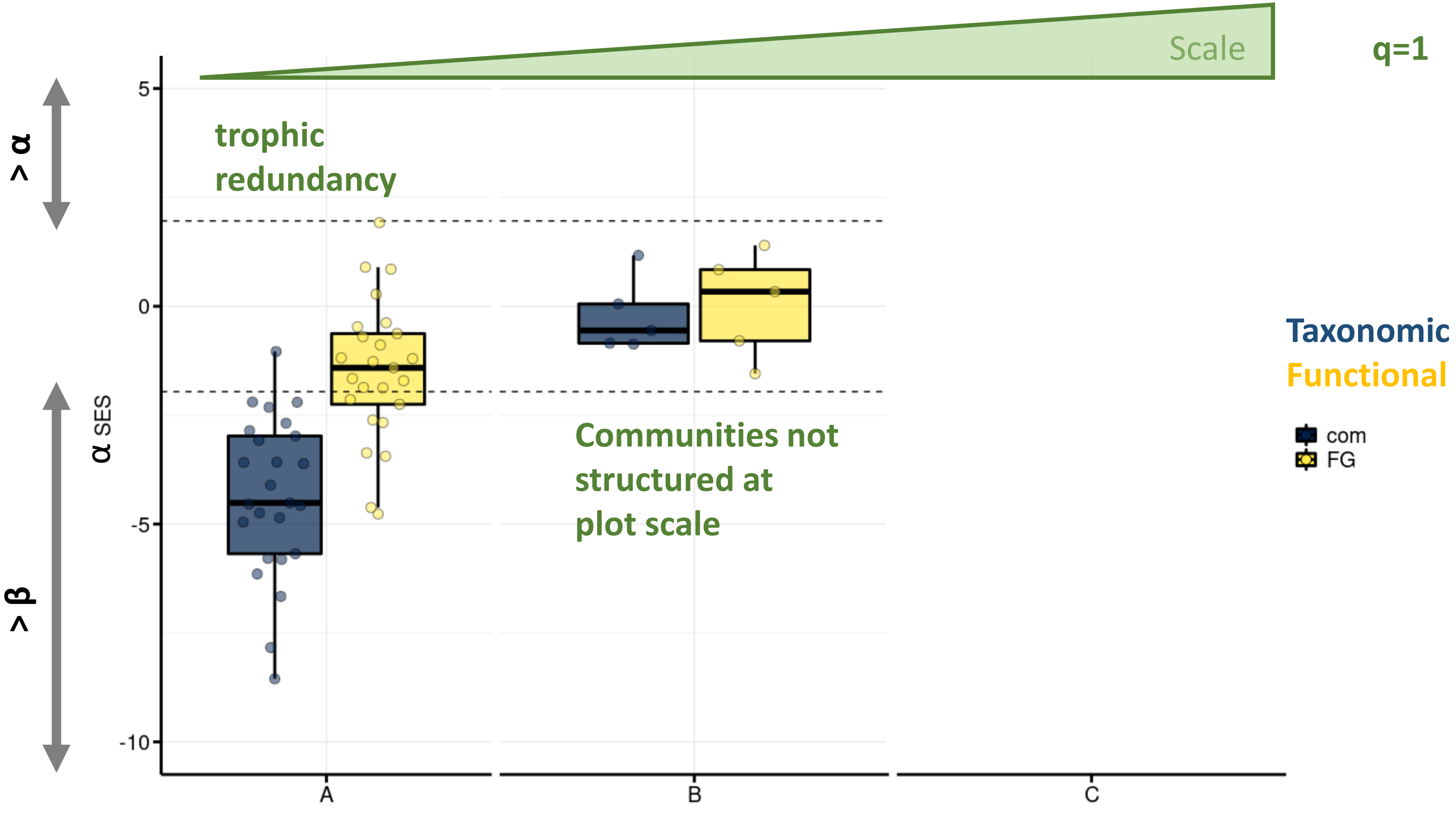
q=1

Taxonomic

Functional

Hill number q0- species richness; q1- eq to Shannon index, q2- eq to Simpson index

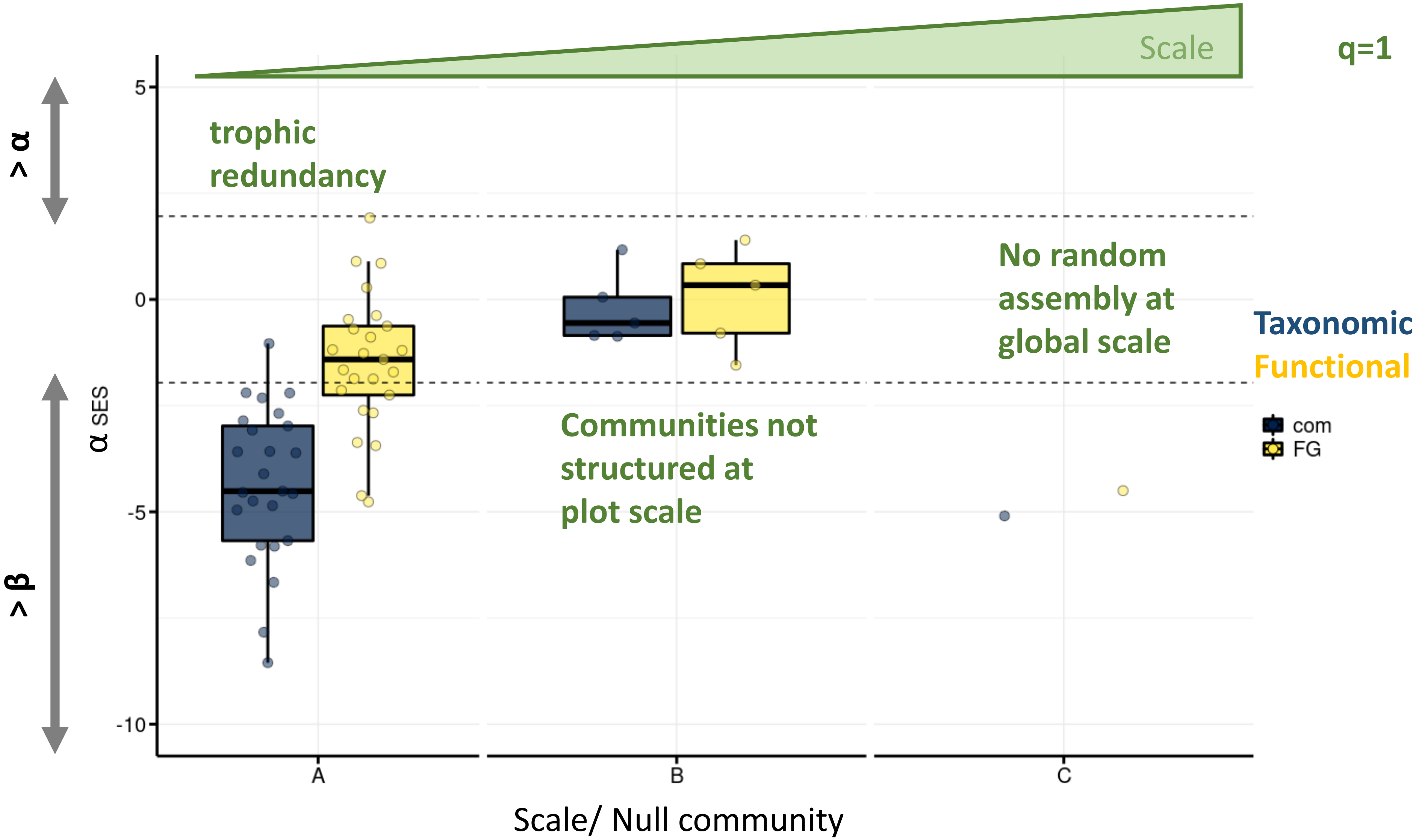
5. Results: Are Coleopteran communities within polypores trophically redundant?



Scale/ Null community

Hill number q0- species richness; q1- eq to Shannon index, q2- eq to Simpson index

5. Results: Are Coleopteran communities within polypores trophically redundant?



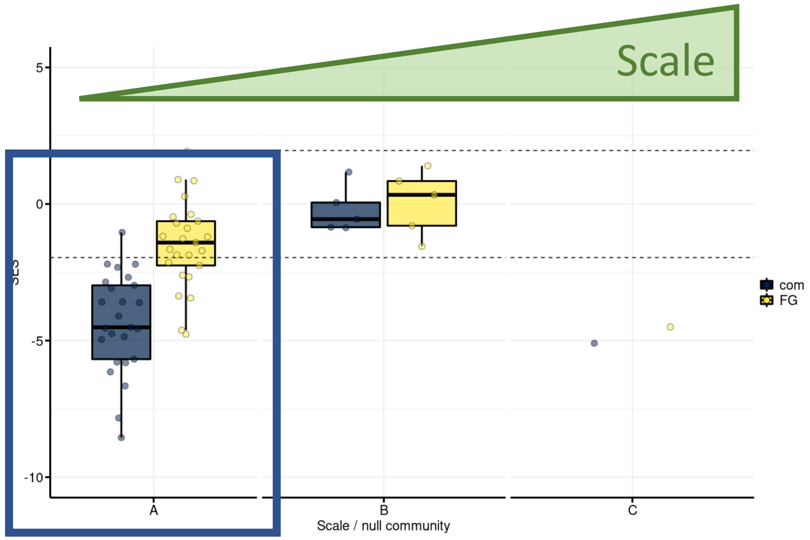
trophic redundancy

No random assembly at global scale

Communities not structured at plot scale

Hill number q0- species richness; q1- eq to Shannon index, q2- eq to Simpson index

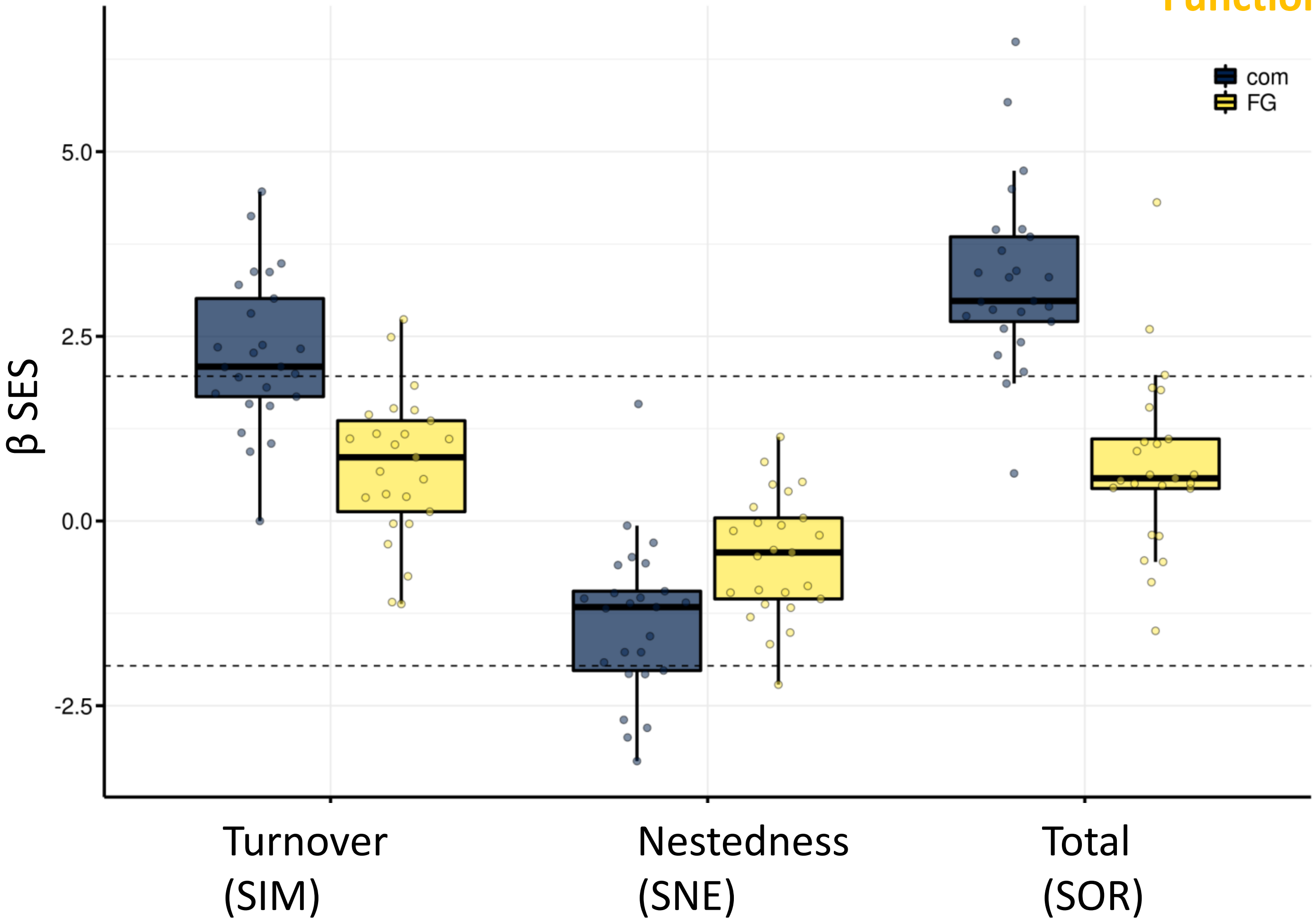
6. Results: Are Coleopteran communities within polypores are trophically redundant?



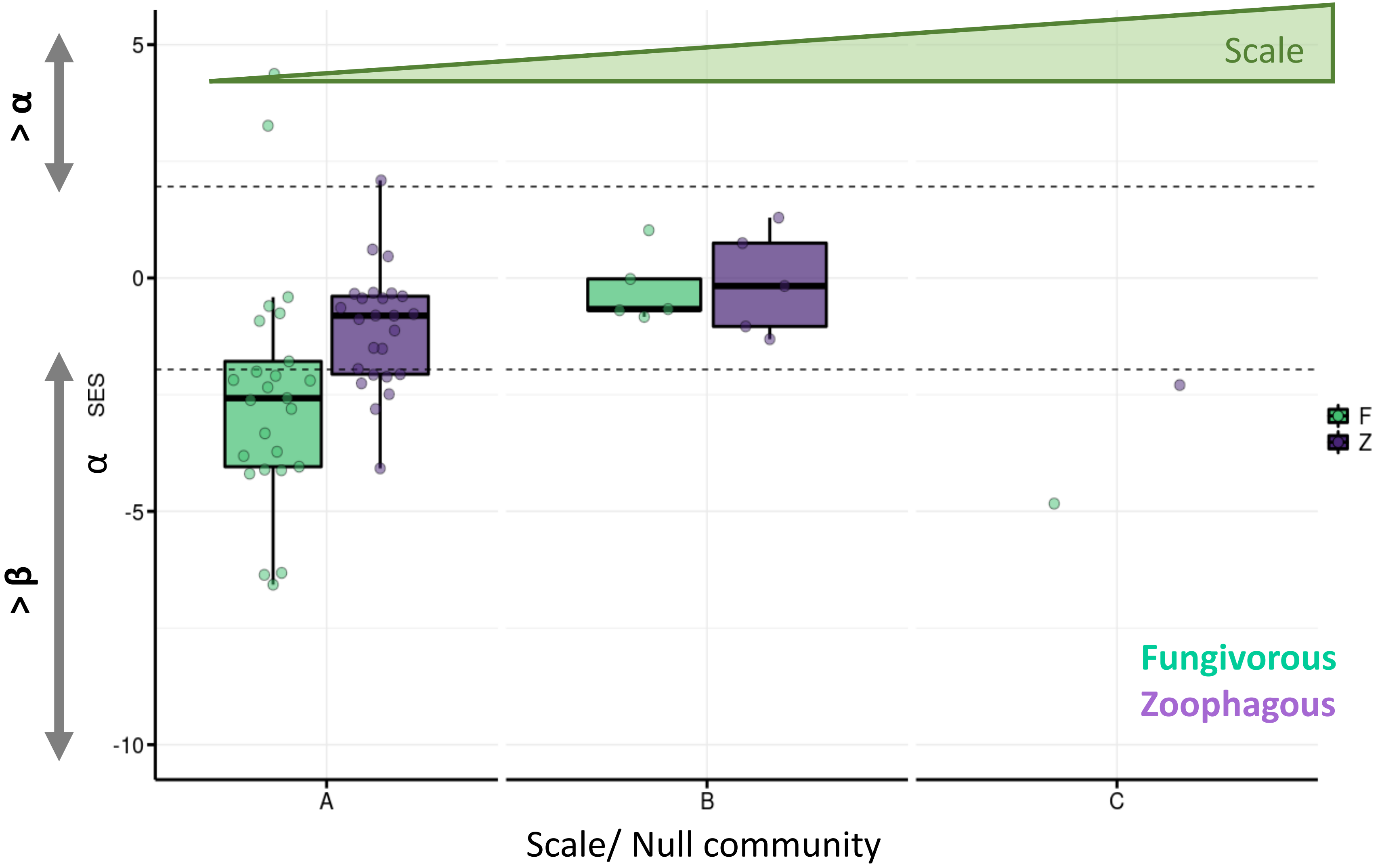
Trophic redundancy – random subsampling of *spp.* pool

Turnover component/replacement (not due to nestedness or richness*)

Taxonomic
Functional



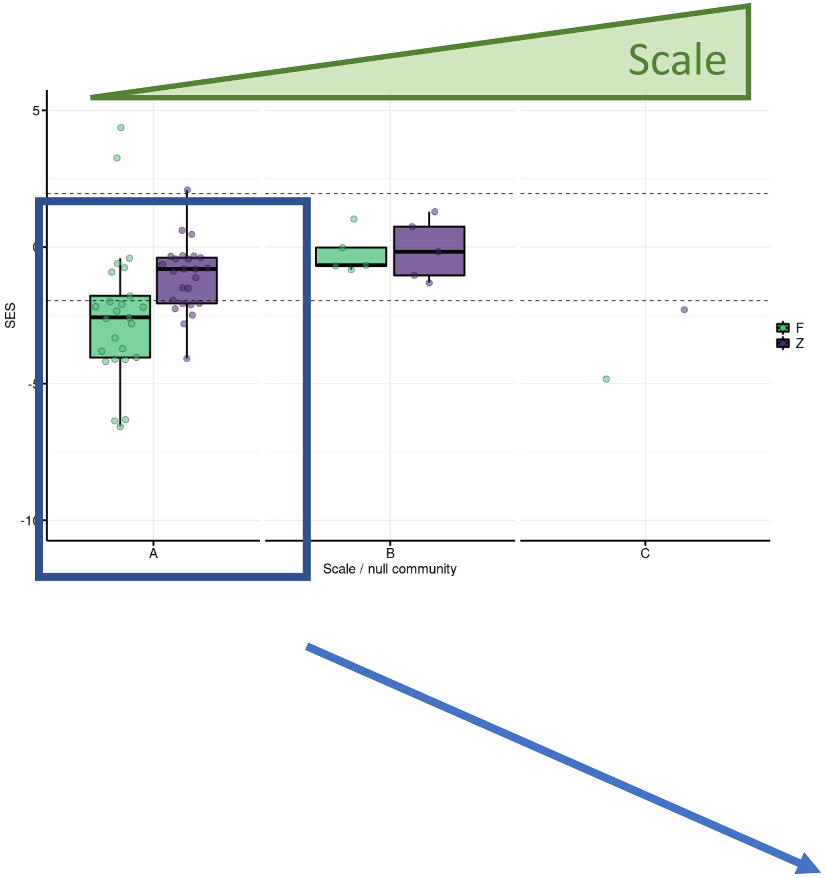
5. Results: Do species within a functional group present a nested pattern?

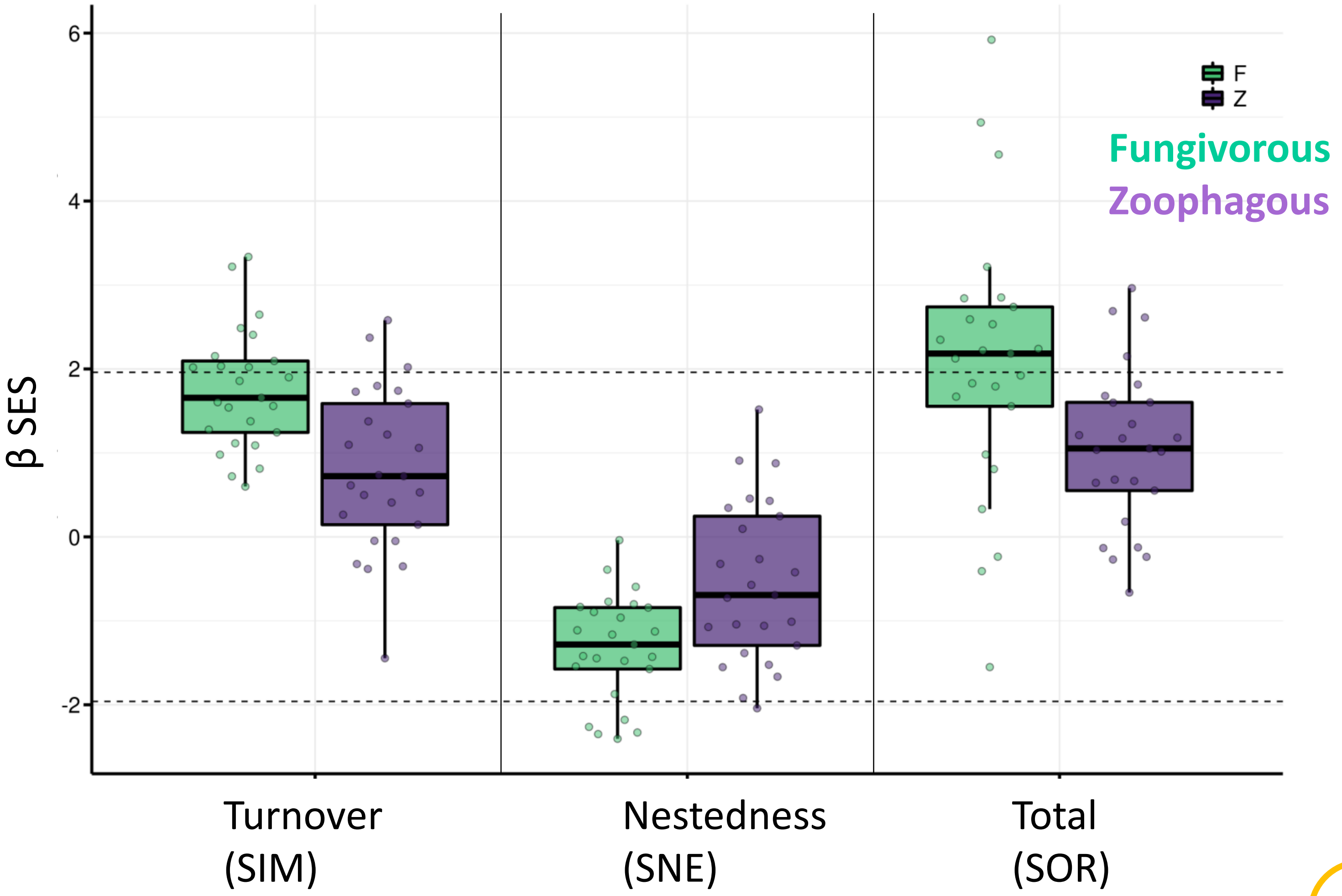


q=1

Fungivorous group show similar trend than taxonomic diversity

5. Results: Do species within a functional group present a nested pattern?





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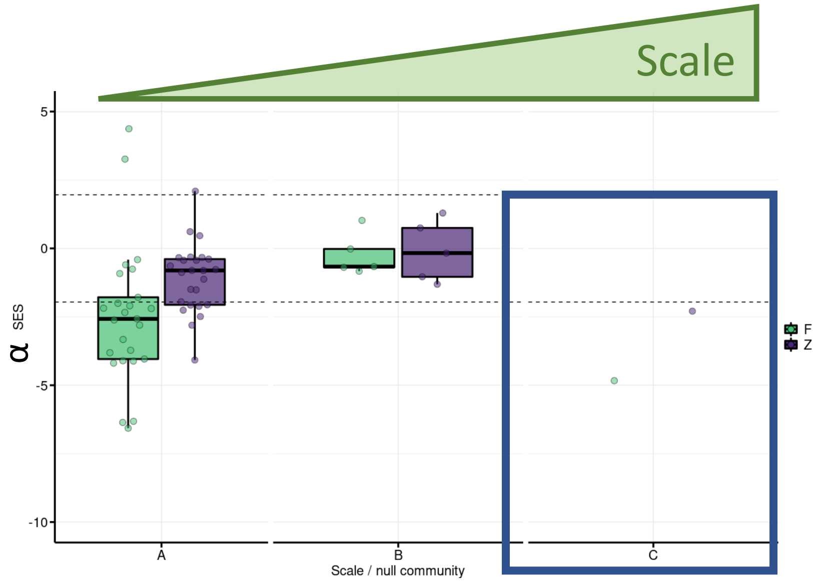
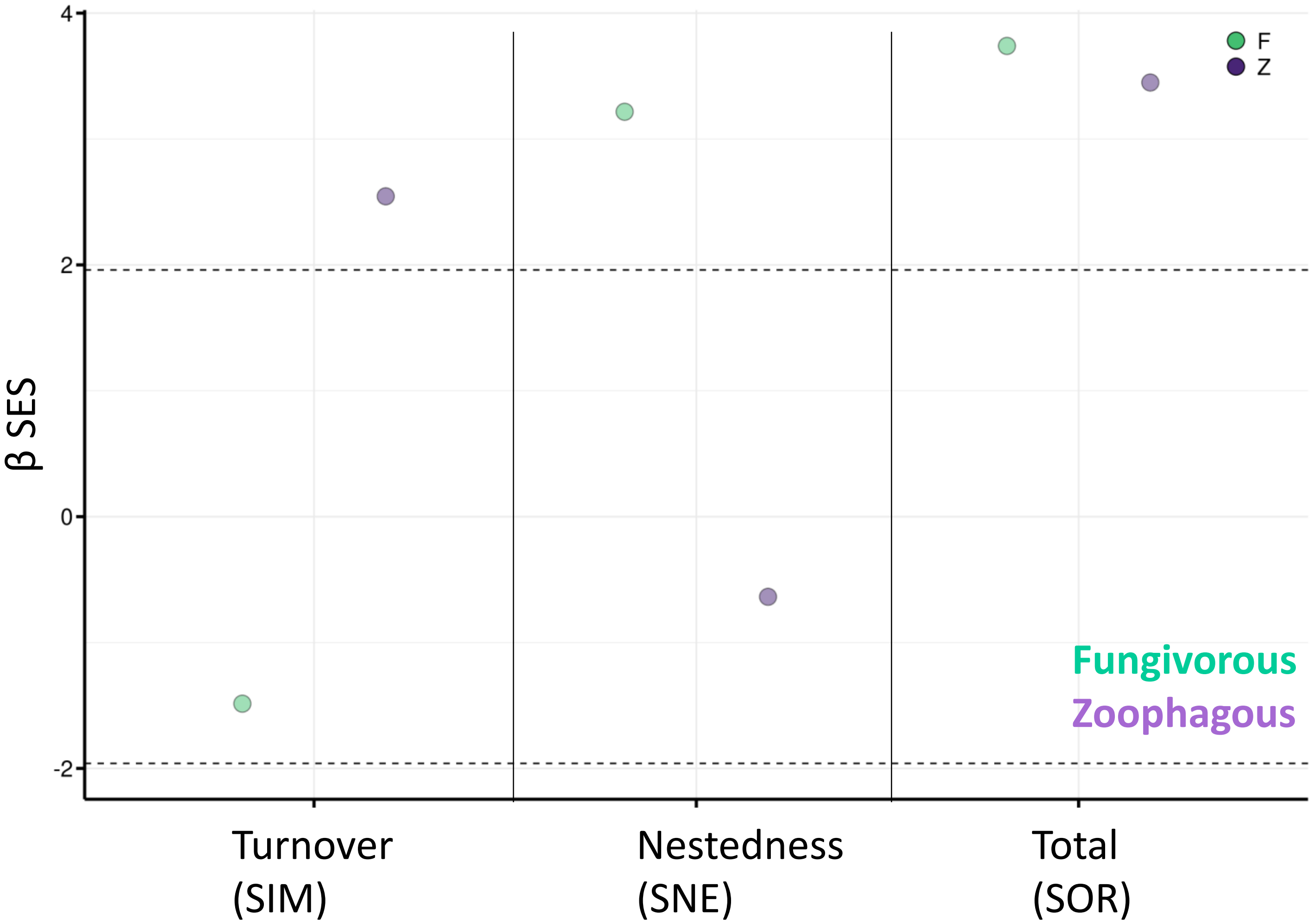


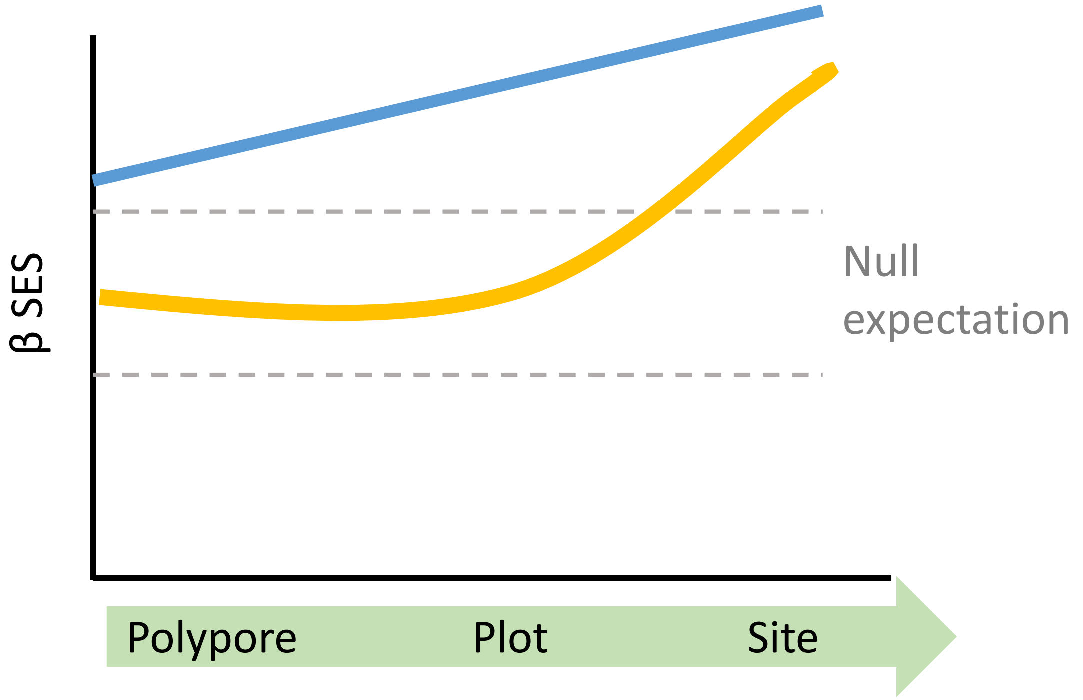
Zoophagous communities present a non-random turnover component

Fungivorous communities present a non-random nested component



Conclusions and way forward

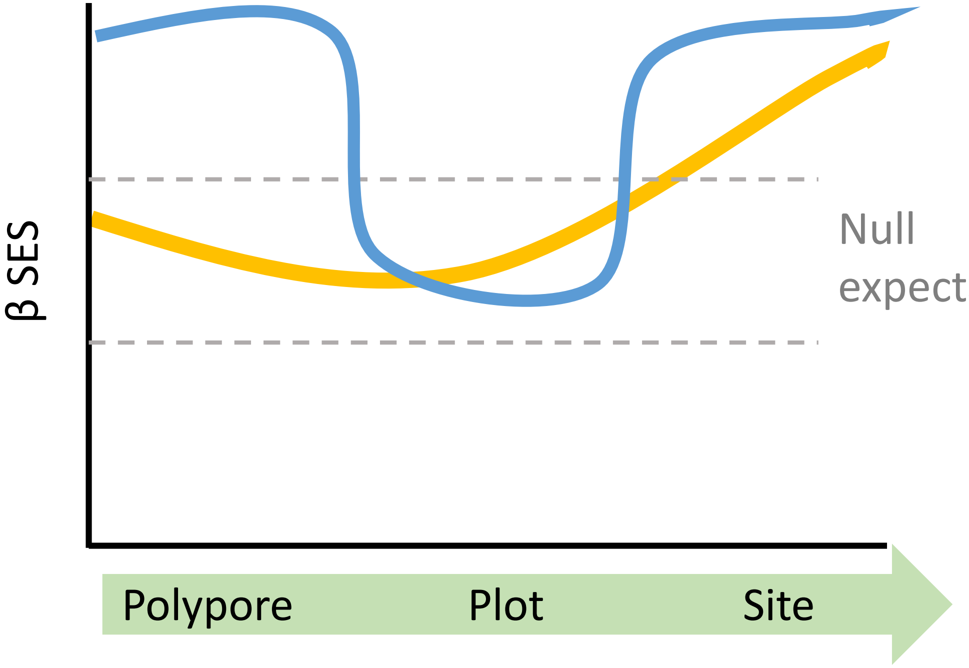
H1/ Coleopteran communities within polypores are trophically redundant.



Conclusions and way forward

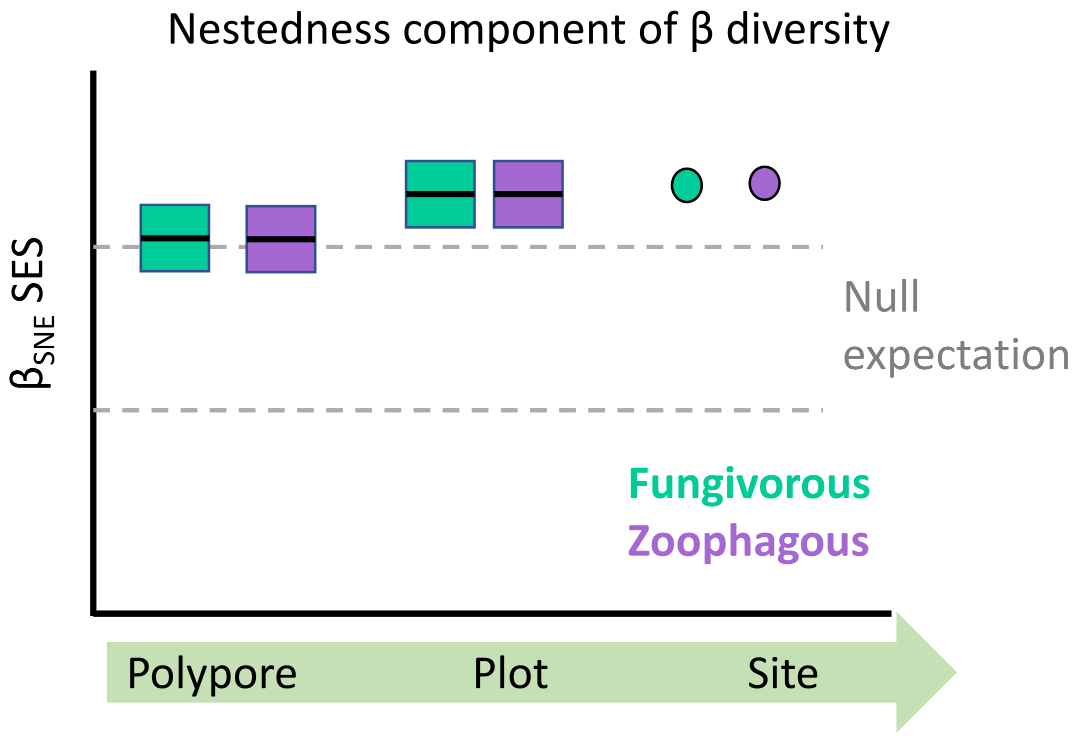
H1/ Coleopteran communities within polypores are trophically redundant.

- ✓ Yes, at the polypore scale.
- ✓ Plot structure not relevant for communities (or any FG)
- ✓ Next step would be the study of species sorting al site scale



Conclusions and way forward

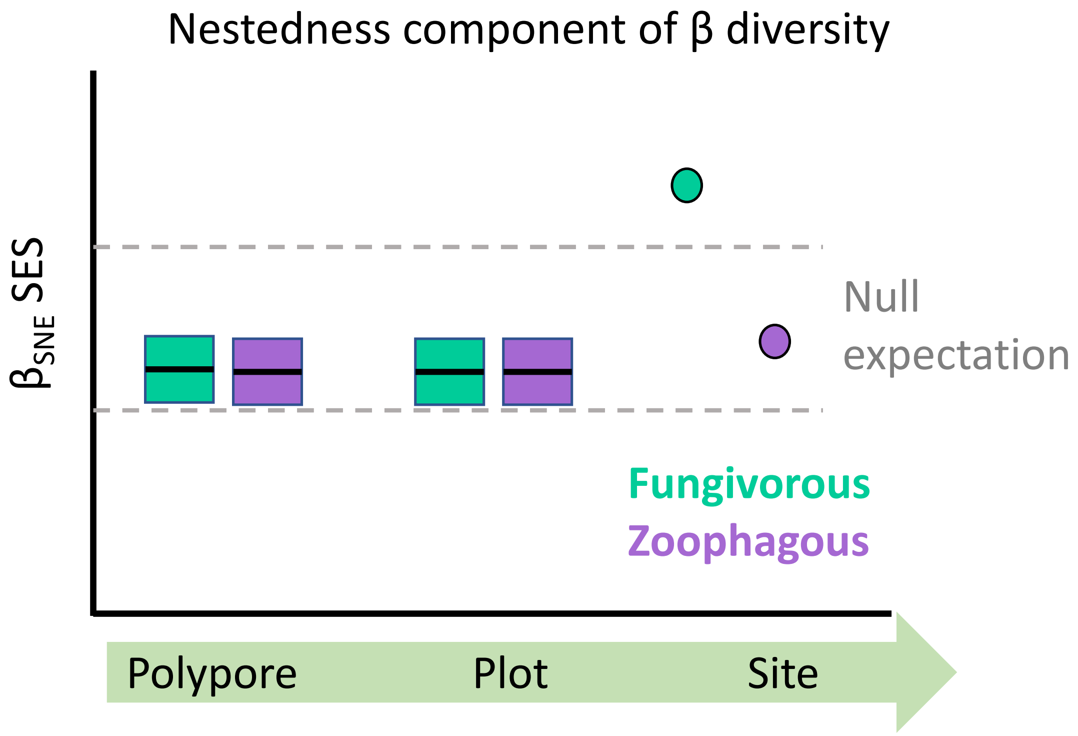
H2/ Species within a functional group will present a nested pattern.



Conclusions and way forward

H2/ Species within a functional group will show a nested pattern.

- ✓ Only for the fungivorous group at the large scale. Is there a gradient in polypore availability or quality?
- ✓ For Zoophagus, species sorting, (dispersal), or sampling effect? Would a finer definition of this FG group be enough?

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Thank you

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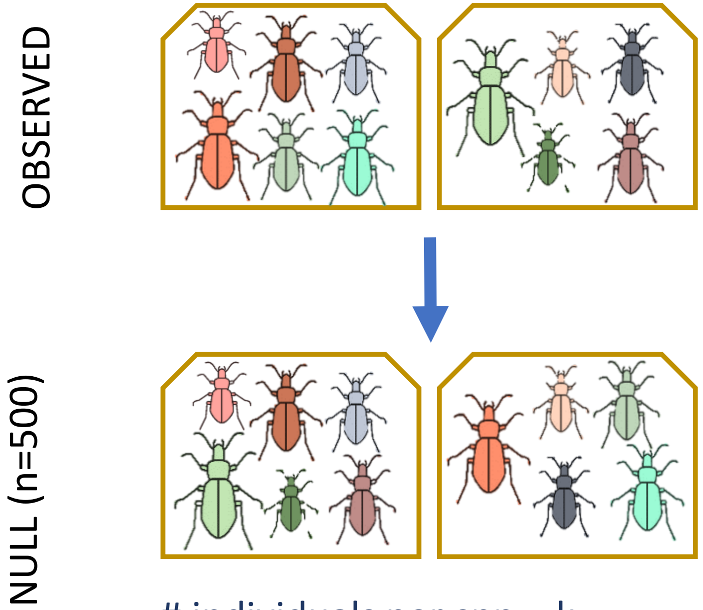
NULL COMMUNITIES- by constrained permutation

A. «permutation of species among polypores **within plots** » 

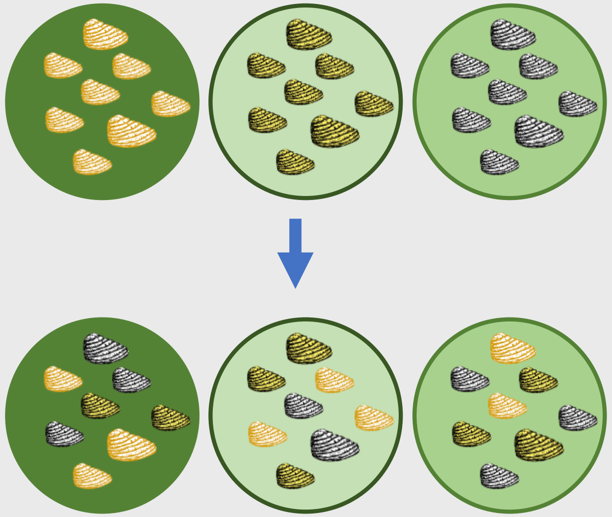


individuals per spp = k
individuals per polypore= k

alpha a

We test if spp are exchangeable – importance of spp identity

B. « permutation of polypores among plots **within sites** »



alpha b

We test whether plot scale structures the communities

C. « permutation of plots among sites »

alpha c

We test whether site scale structures the communities