



HAL
open science

How repeatable are communities in Fomes polypores?

Agnès Ardanuy-Gabarra, Olivier Rose, Antoine Brin, Christophe Bouget, F. Laroche

► **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-03931425>

Submitted on 9 Jan 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



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

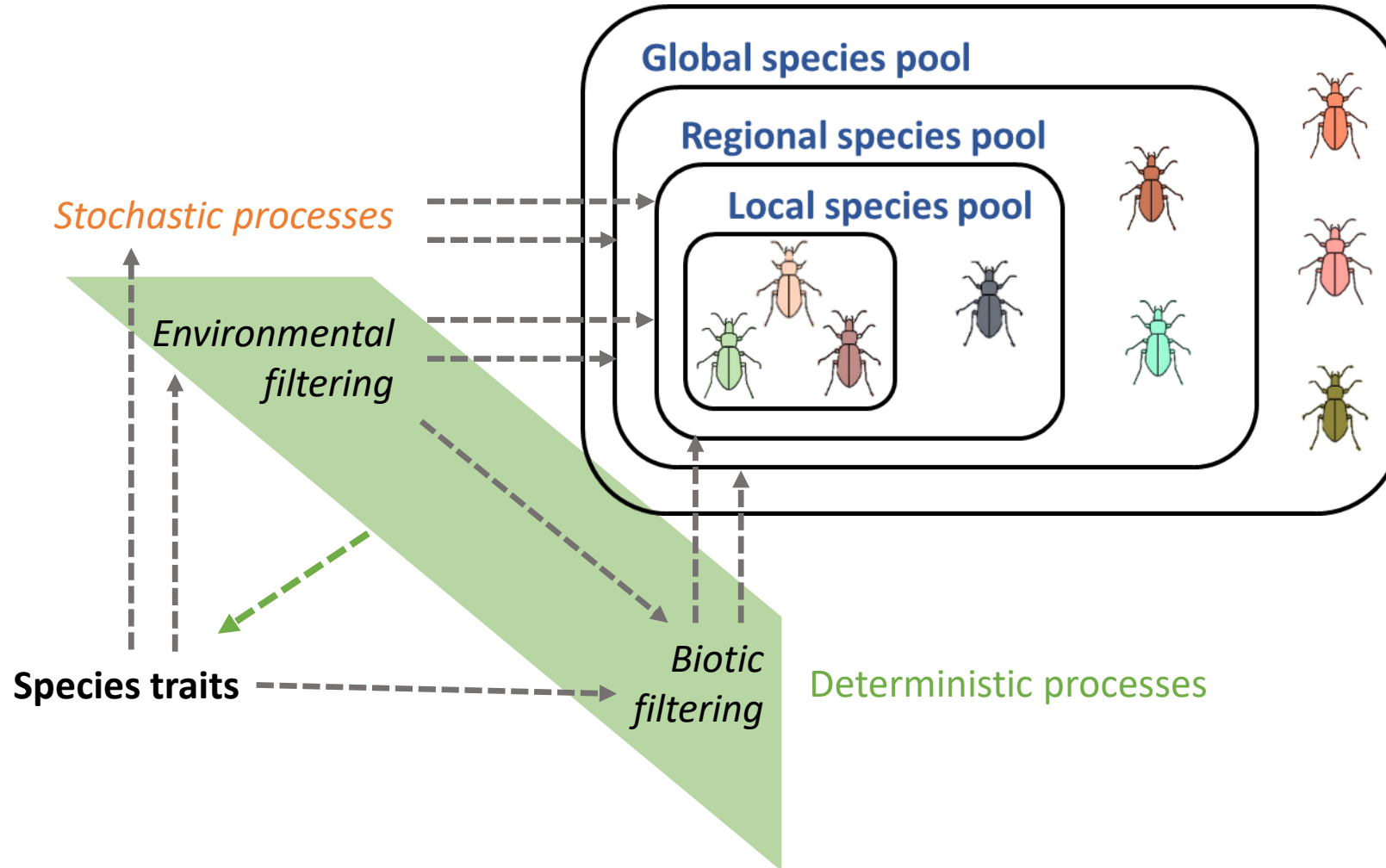
M. Roy

INRAE


DYNAFOR

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

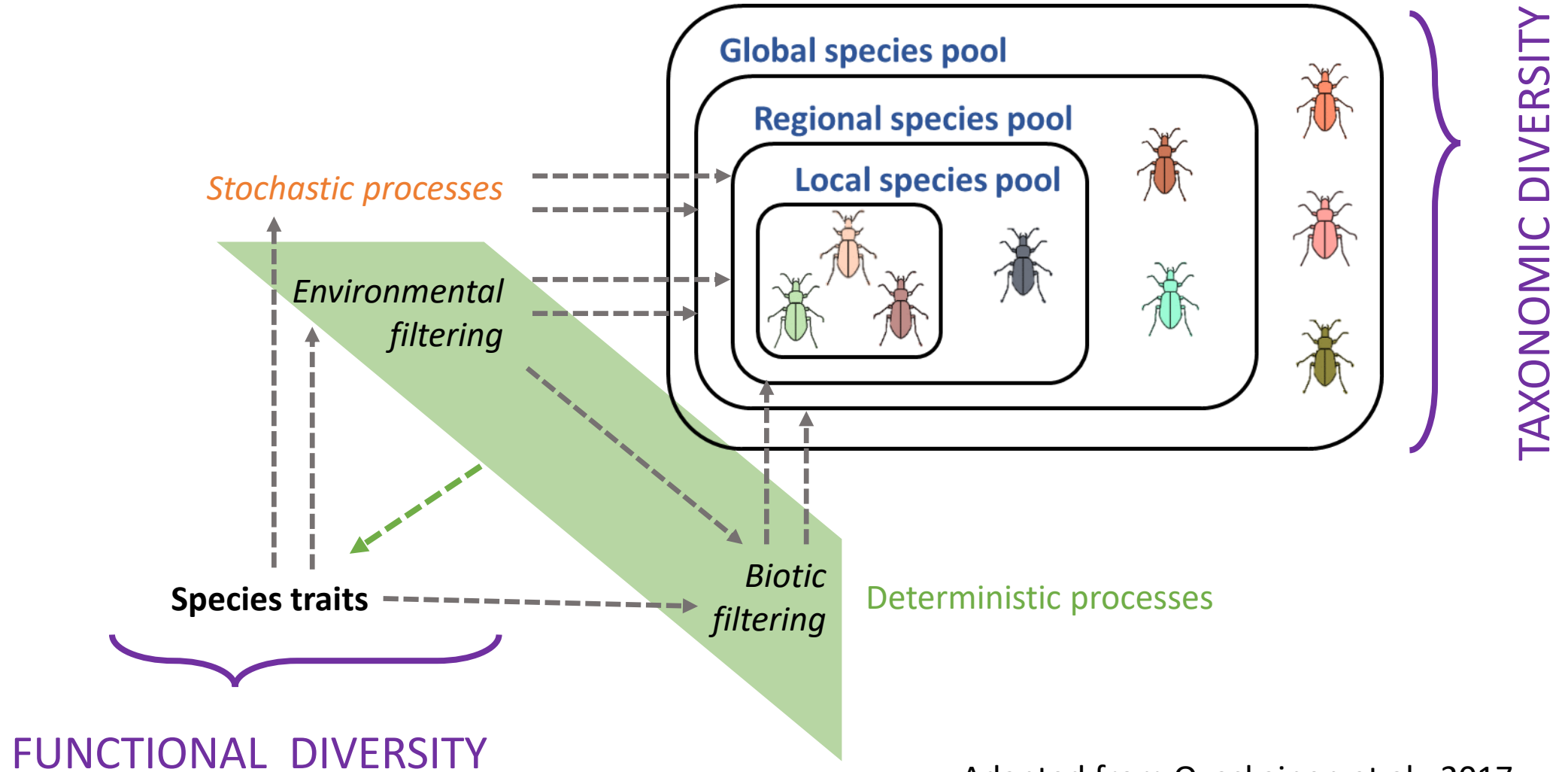
1. Community assembly: patterns and processes



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



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

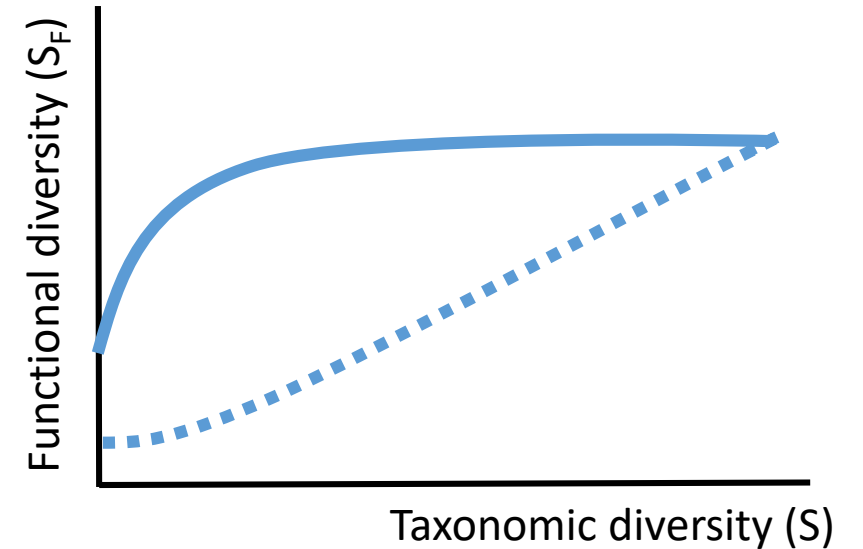
2. Diversity patterns and functional redundancy

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**

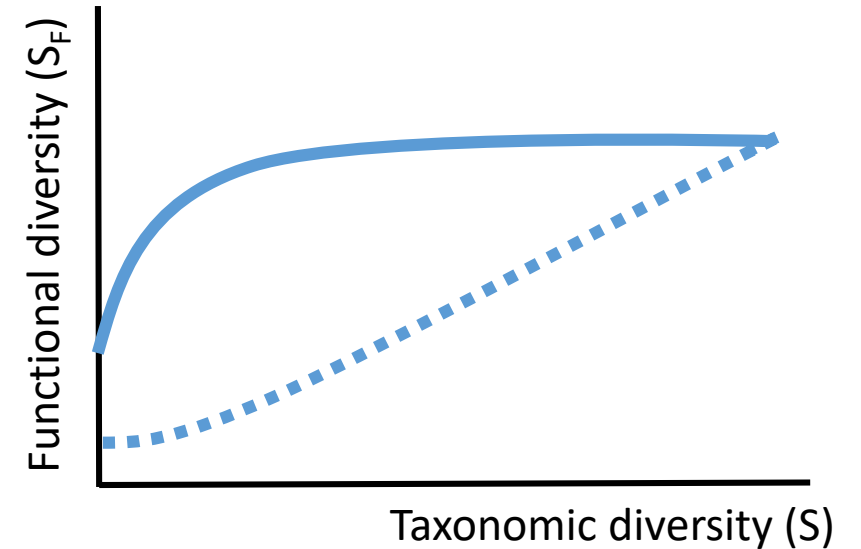
The link between the facets across scales provides information on whether communities are “**repeatable**”.

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 different scales

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

Work by Olivier Rose

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

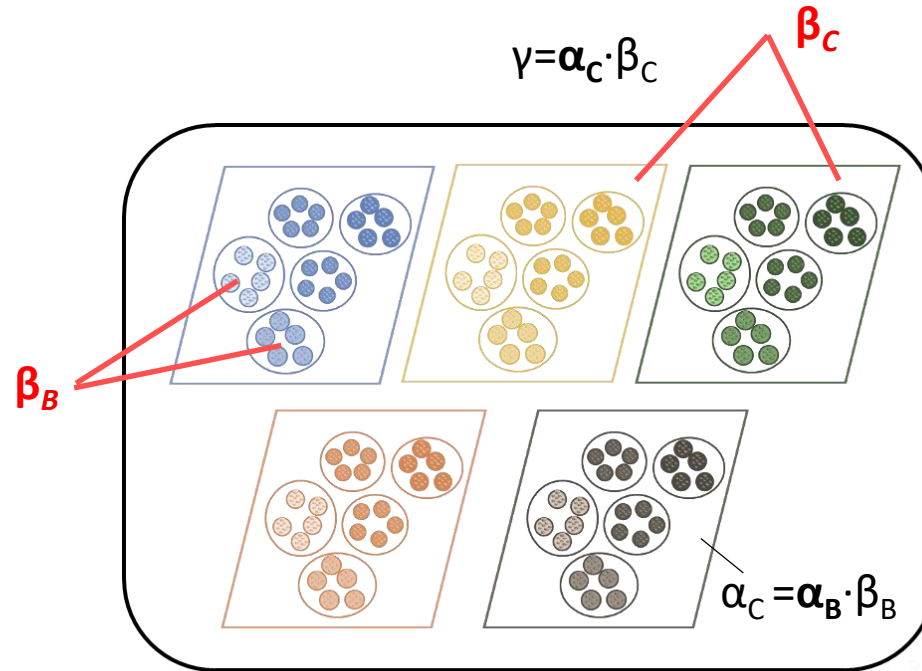
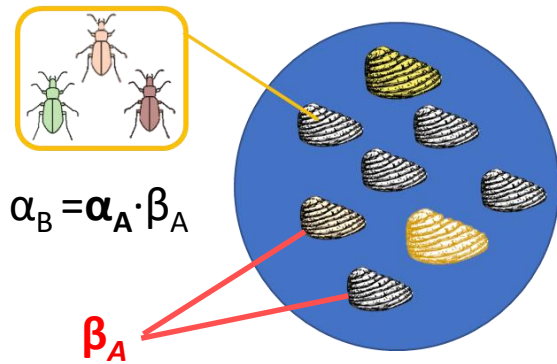
- Sampling July 2007 October 2008 in Vosges (NE, France)
- 5 sites
- 5 plots per site
- 8 polypores per plot
- Plots of 30m radius – 100 m distance between plots
- **Trophic guilds = Functional groups**
6 Mycetophagus(=Fungivorous), Zoophagus, Xylophagus, Saprofagous, Saproxylophagus, Non-saproxylic

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 α s 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

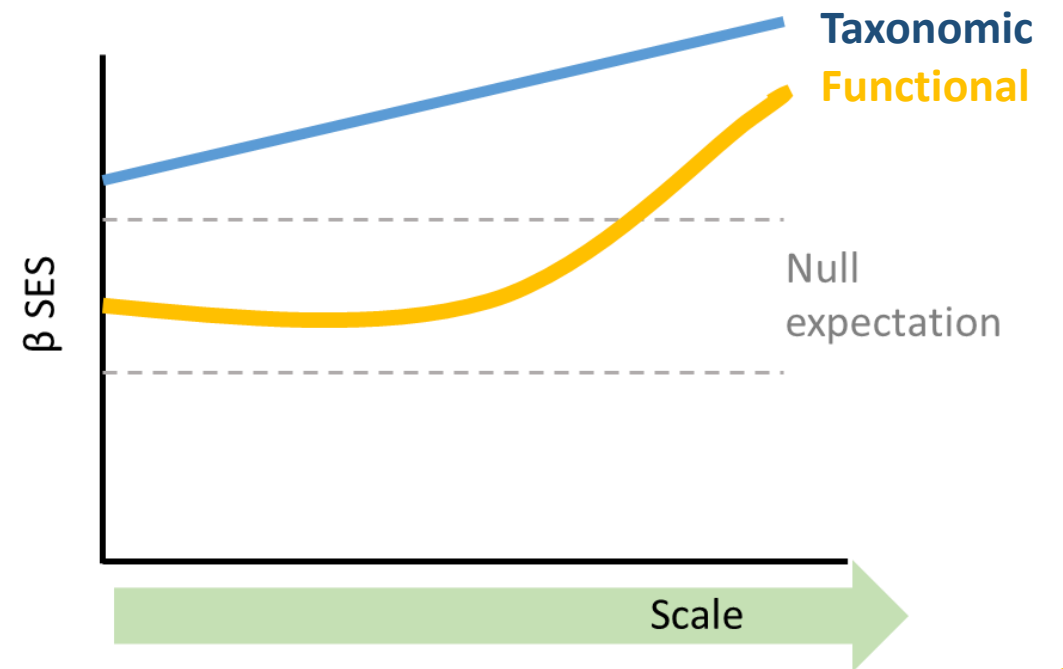
Computation of: α (multipart, package vegan) – *abundance data* and partition of β (Baselga, package betapart; Podani & Schmera, package BAT) – *ocurrence data*.

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



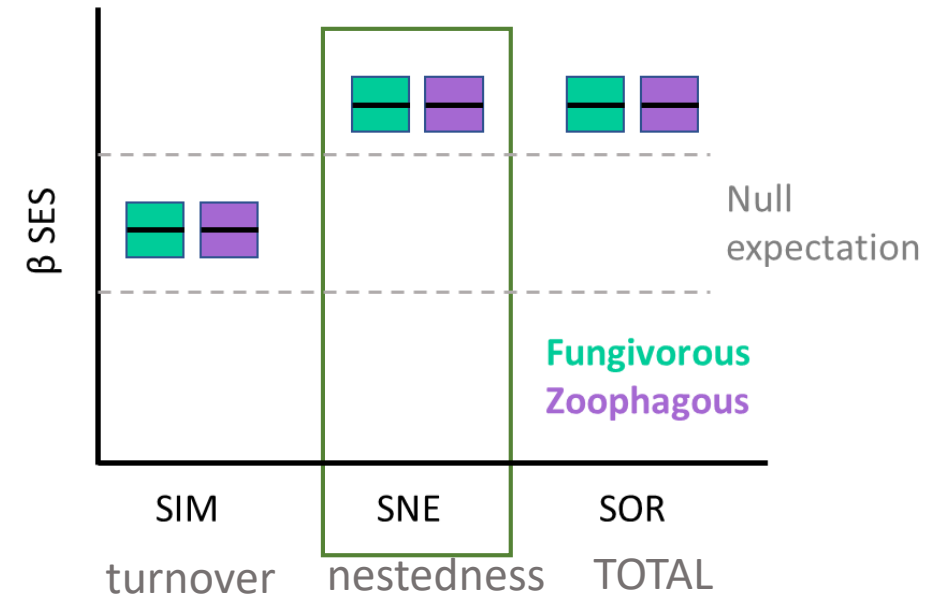
4. Hypothesis and predictions

H1/ Coleopteran communities within polypores are trophically redundant.

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

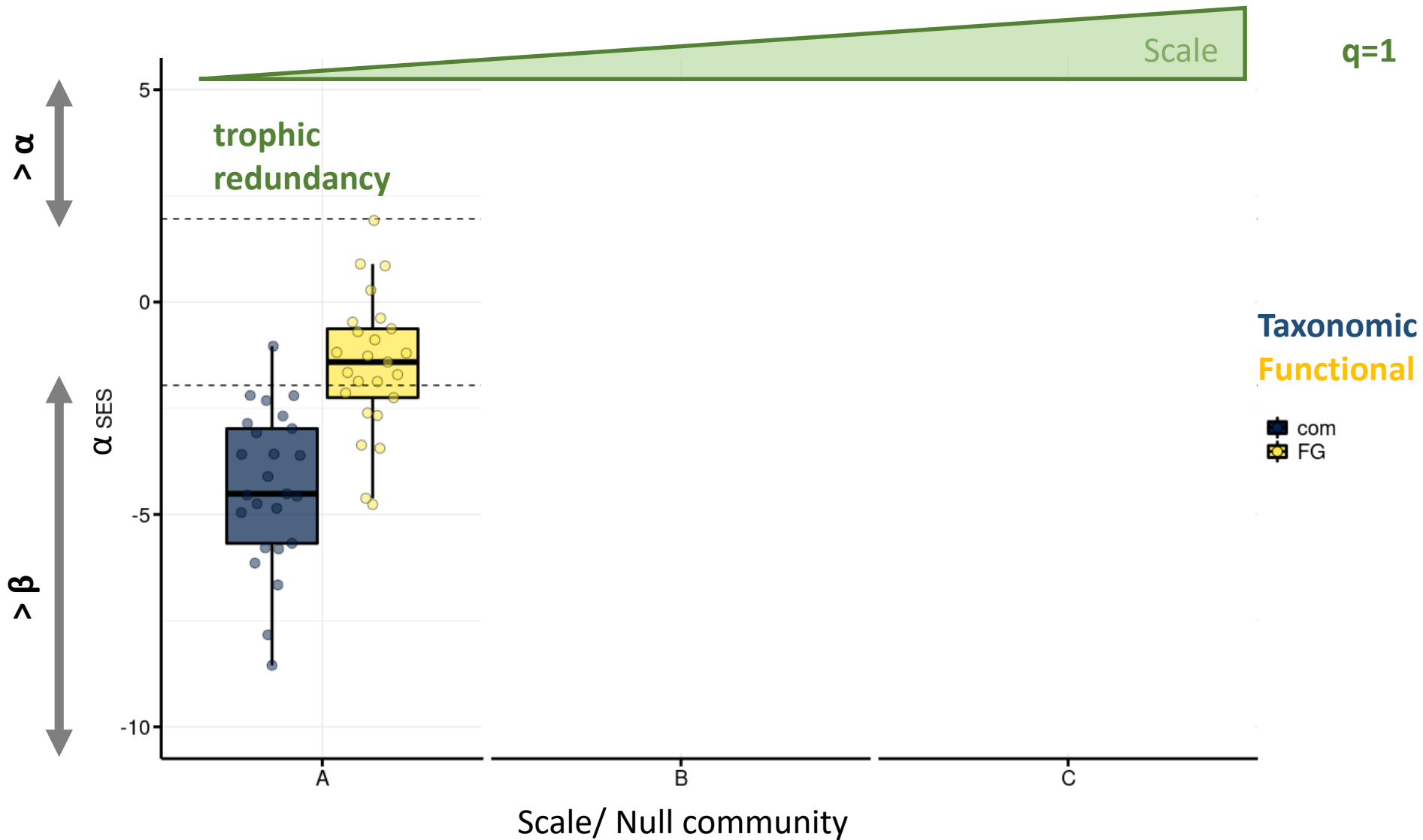
The nestedness component of β diversity within FG will be larger than that of random generated communities

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

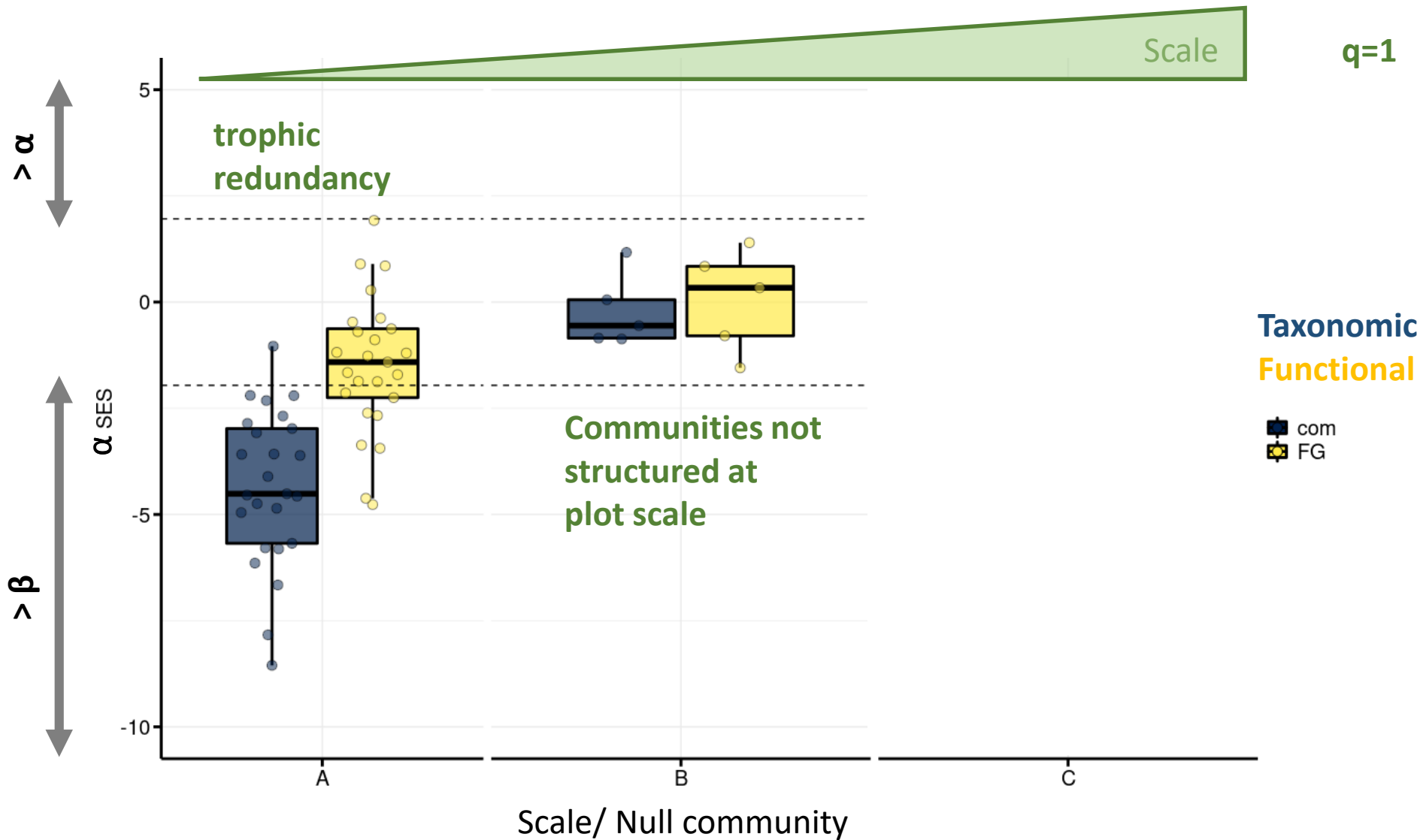


At which scale? Spatial aggregation (Thuiller et al., 2015)

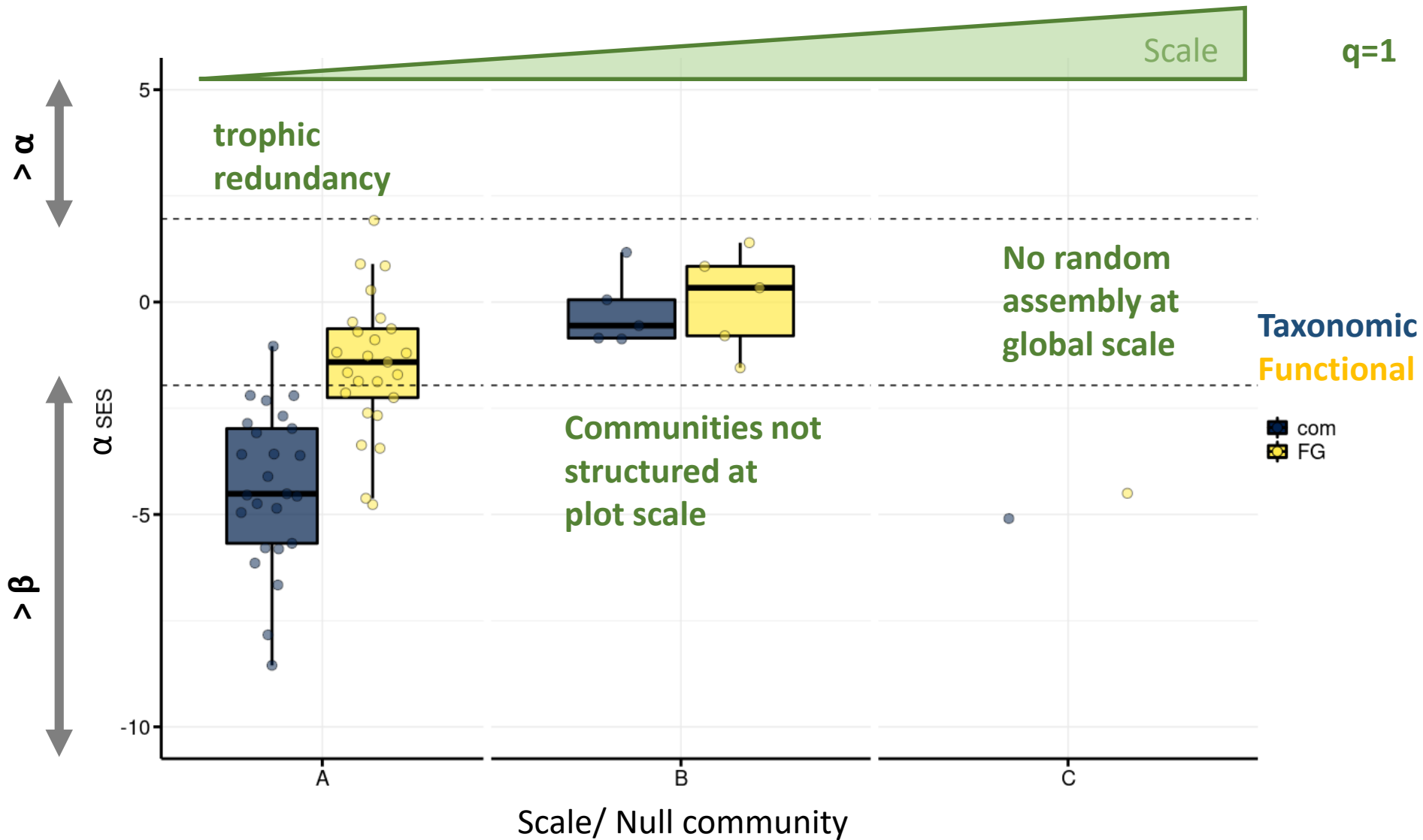
5. Results: Are Coleopteran communities within polypores trophically redundant?



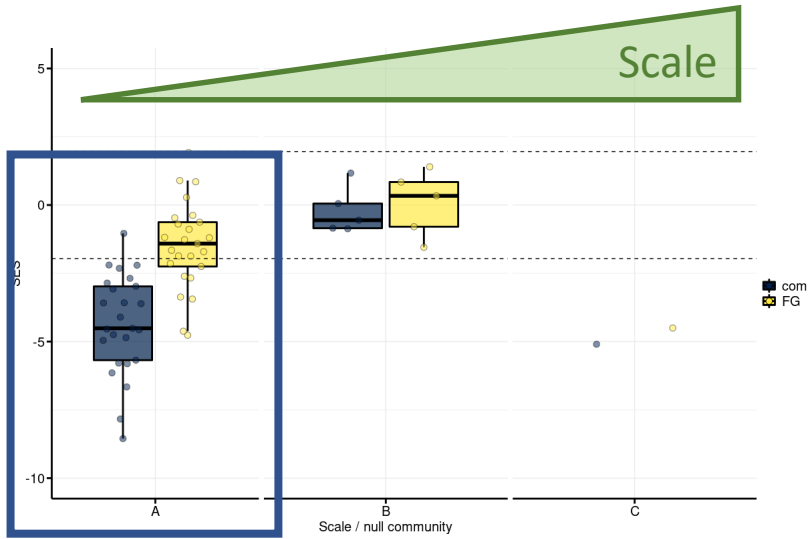
5. Results: Are Coleopteran communities within polypores trophically redundant?



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

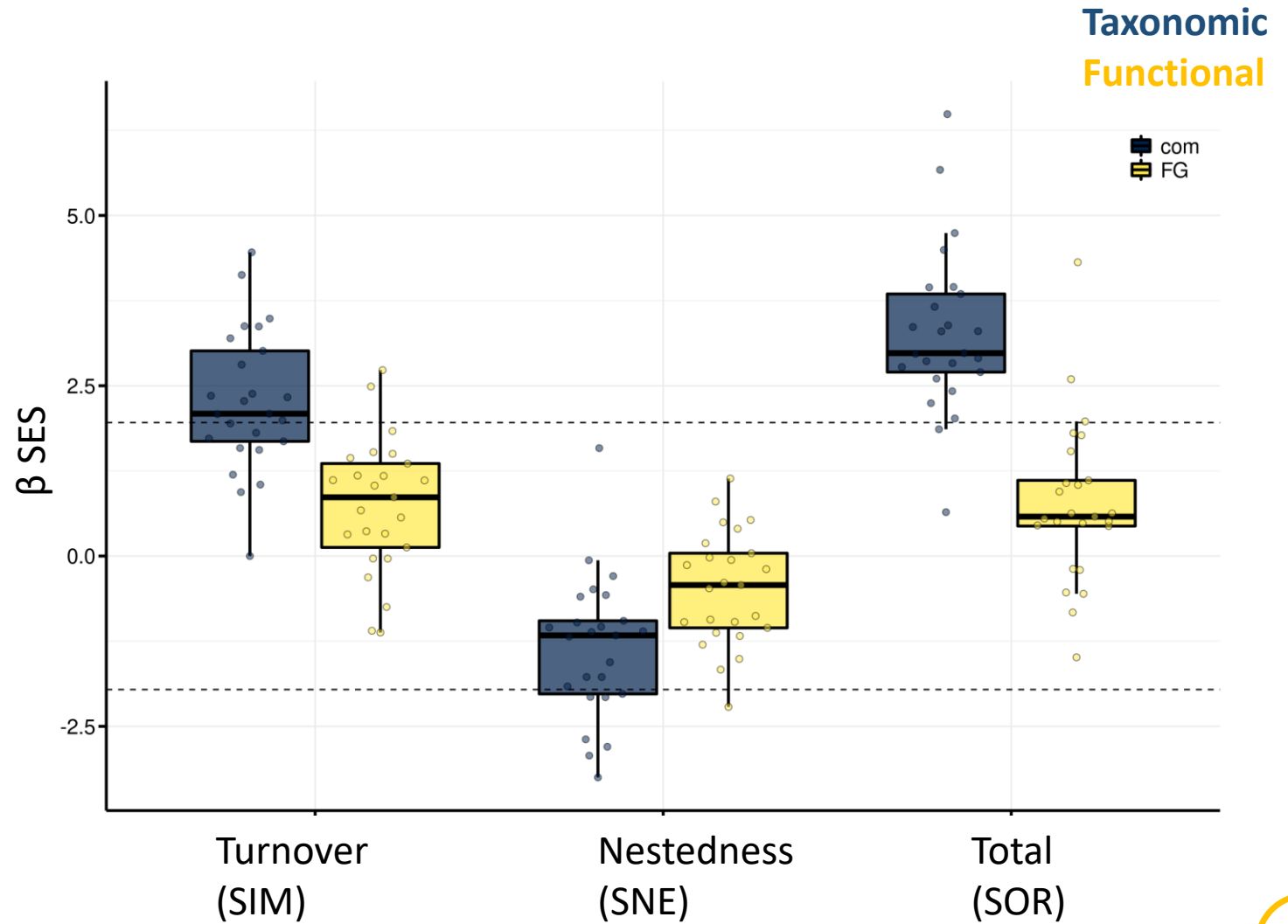


6. Results: Are Coleopteran communities within polypores are trophically redundant?

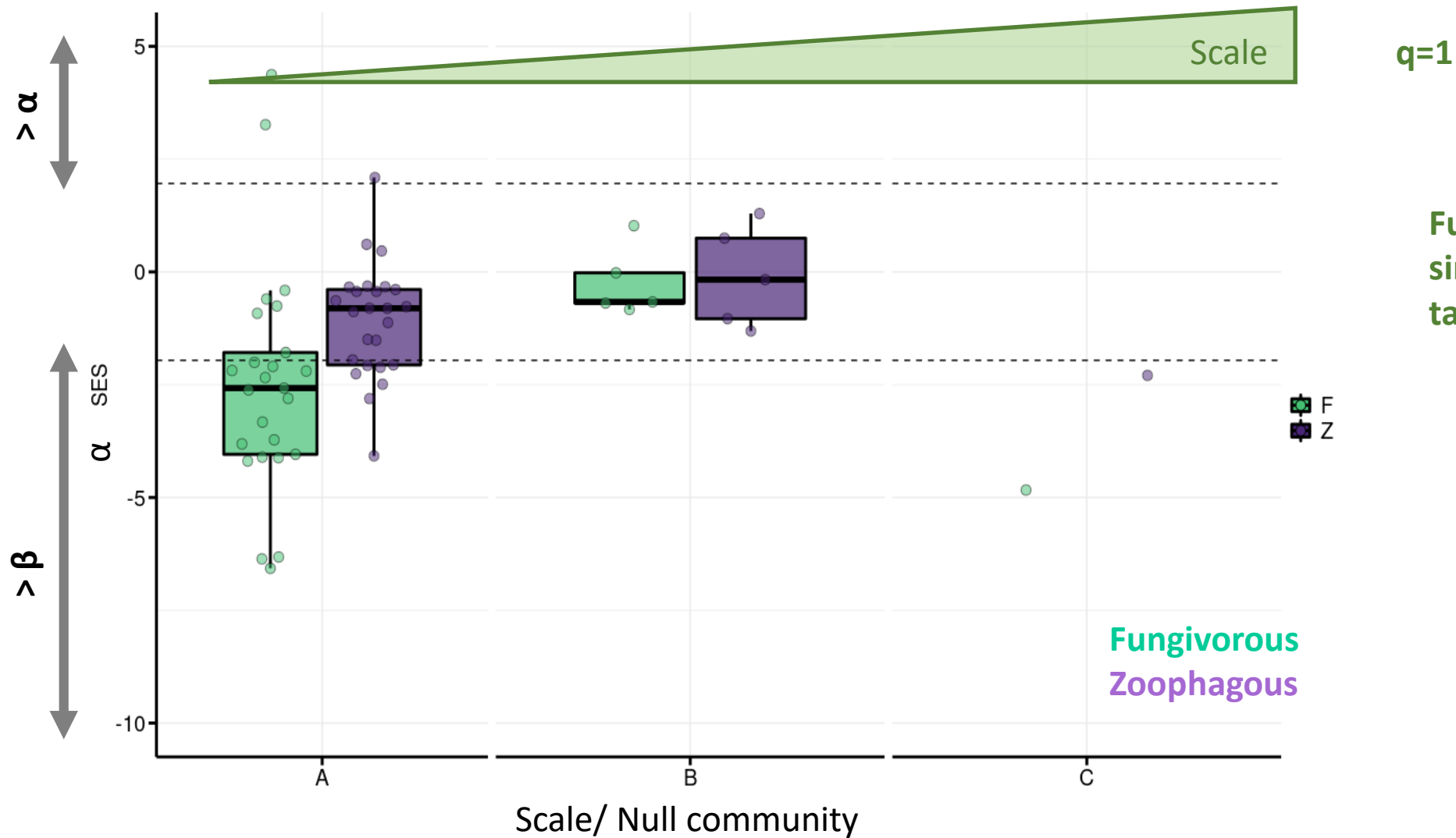


Trophic redundancy –
random subsampling of
spp. pool

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



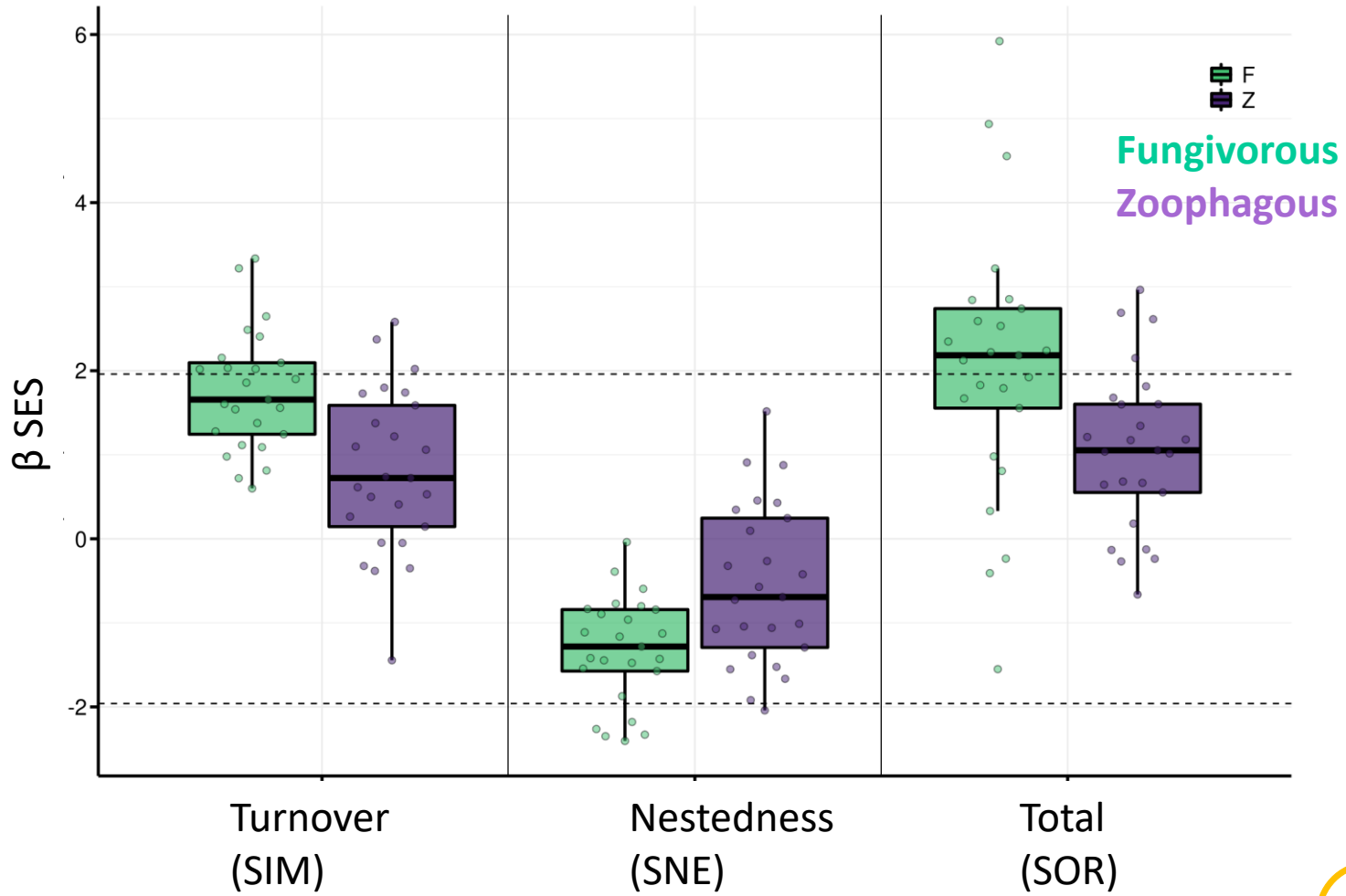
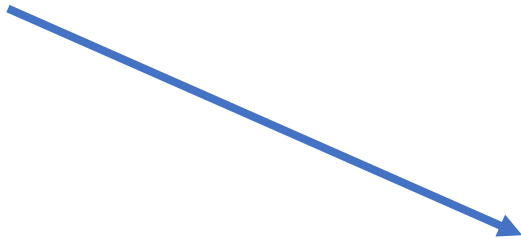
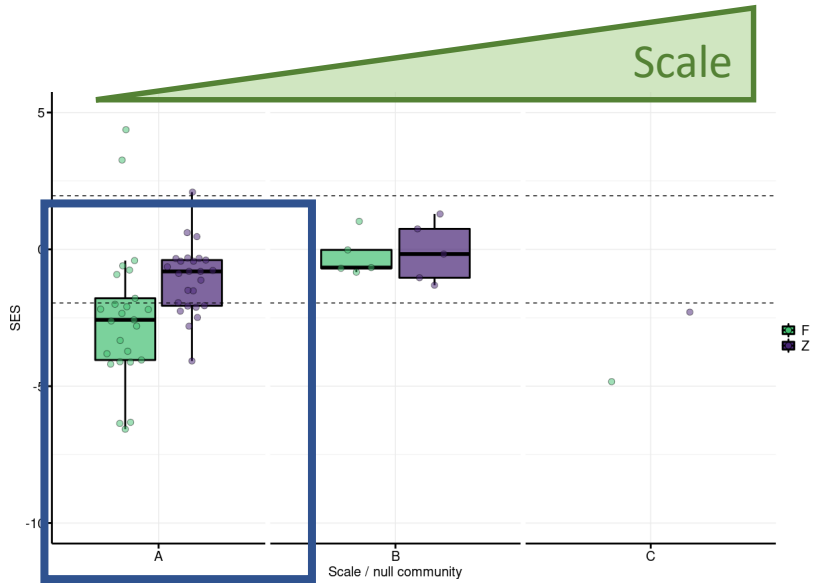
5. Results: Do species within a functional group present a nested pattern?



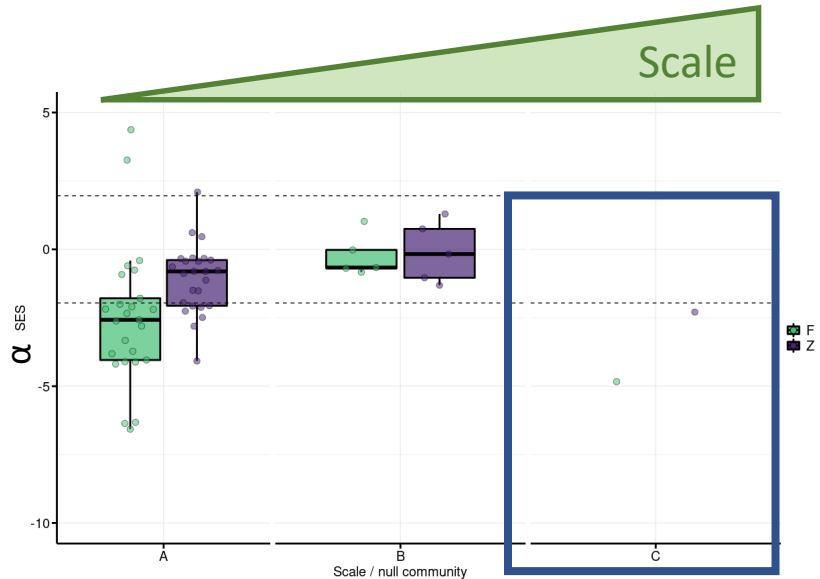
Fungivorous group show similar trend than taxonomic diversity

Fungivorous
Zoophagous

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

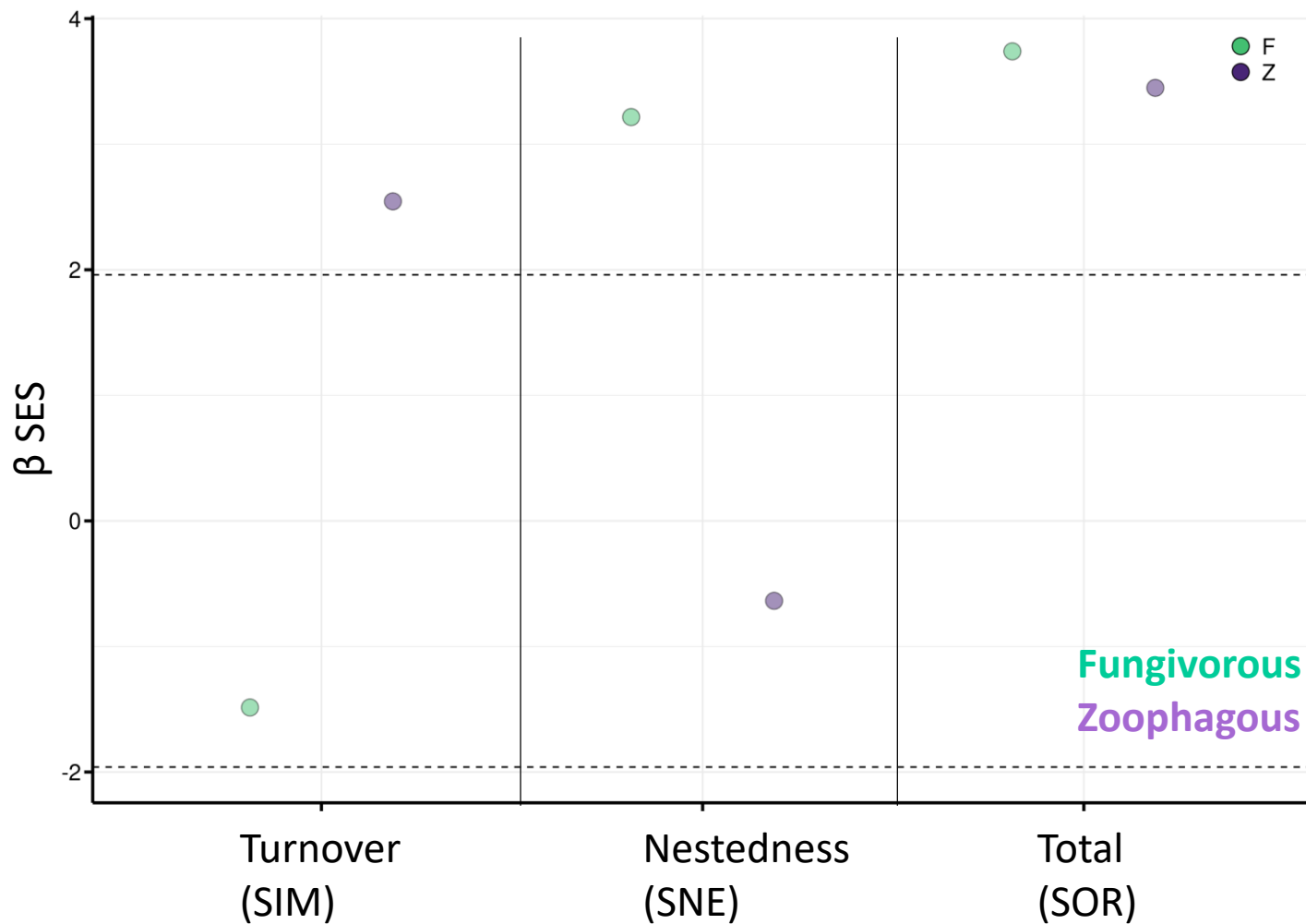


5. Results: Do species within a functional group present a nested pattern?

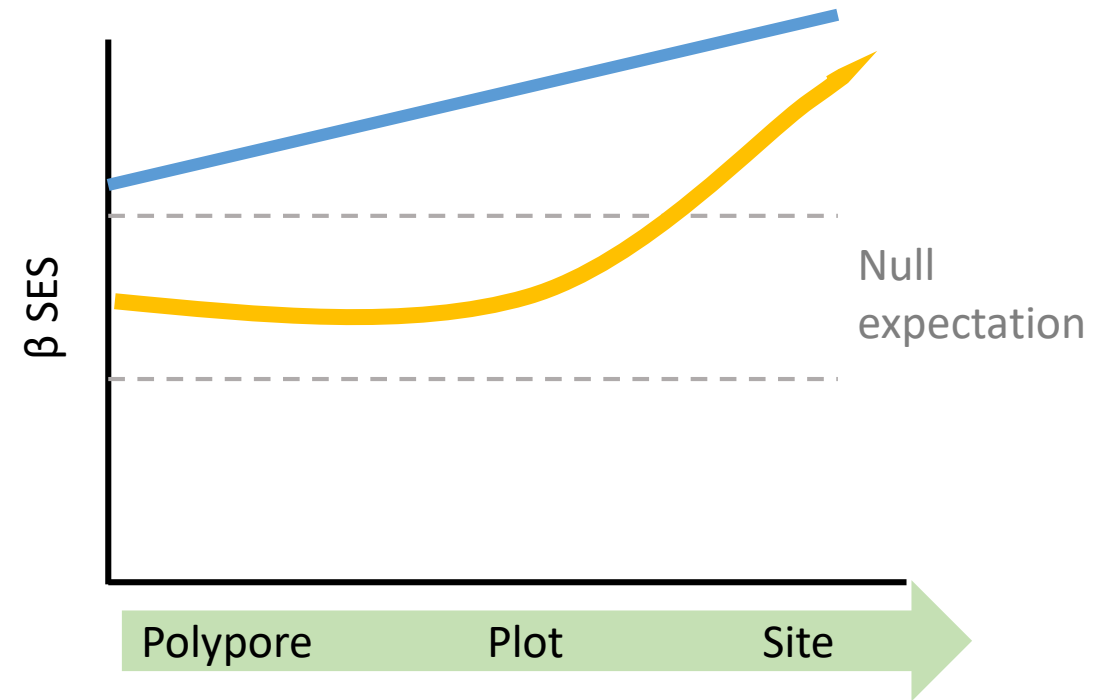


Zoophagous communities present a non-random turnover component

Fungivorous communities present a non-random nested component

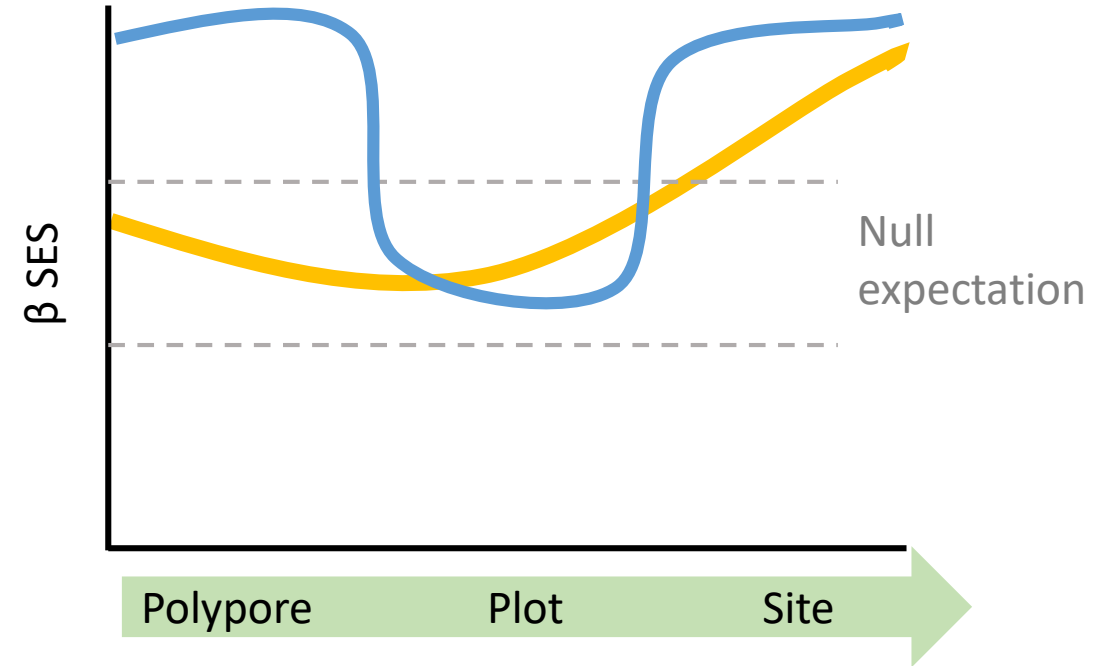


H1/ Coleopteran communities within polypores are trophically redundant.

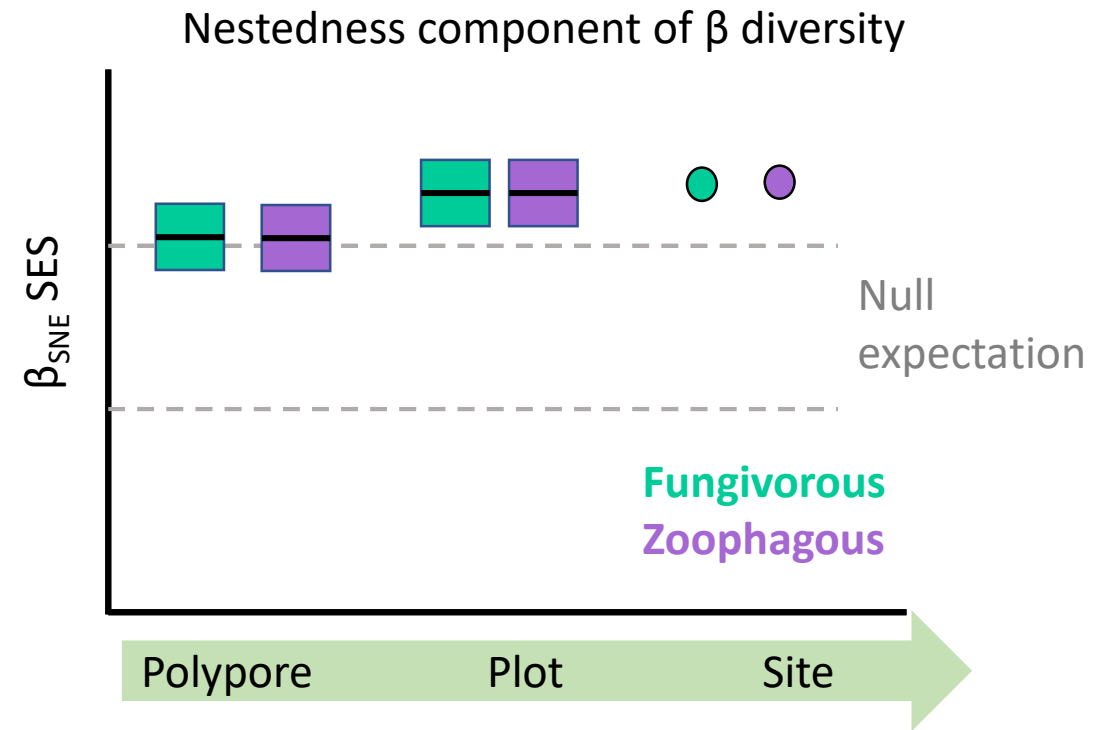


H1/ Coleopteran communities within polypores are trophically redundant.

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

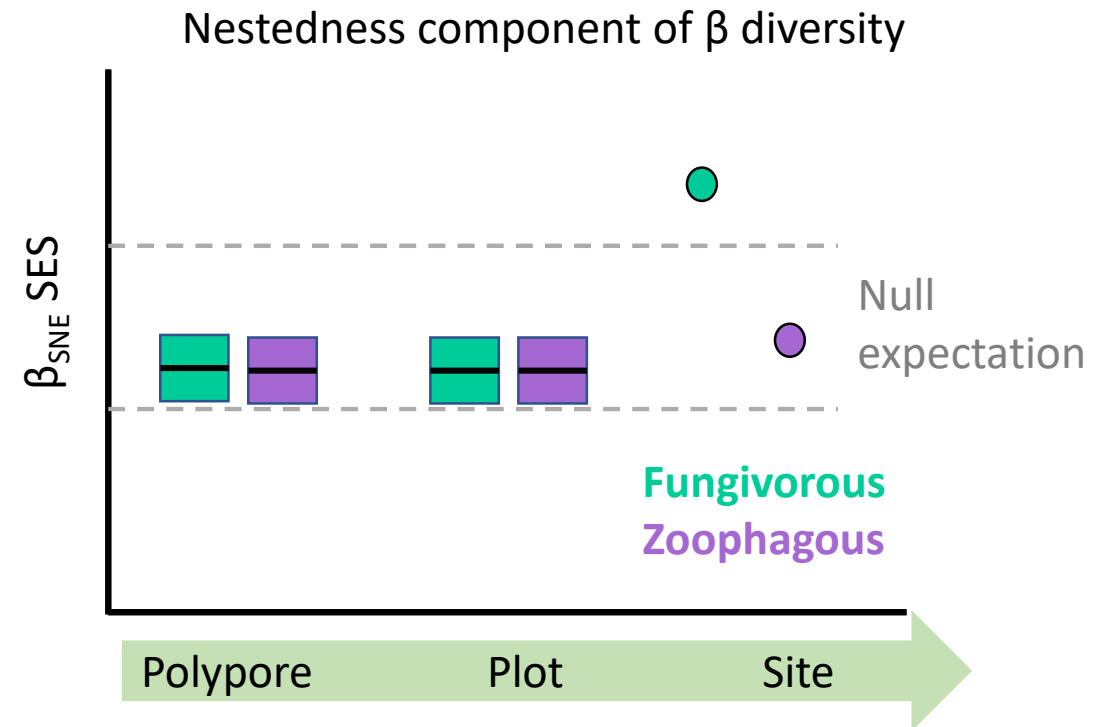


H2/ Species within a functional group will present a nested pattern.



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?





M. Roy

Thank you

**SFE² GfÖ EEF - International Conference
on Ecological Sciences**

Metz, 23 November 2022

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

INRAE

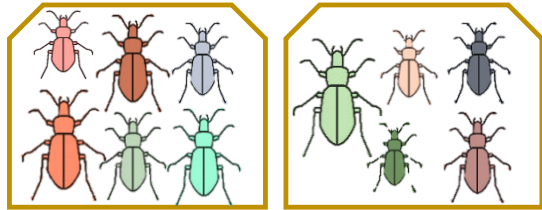


DYNAFOR

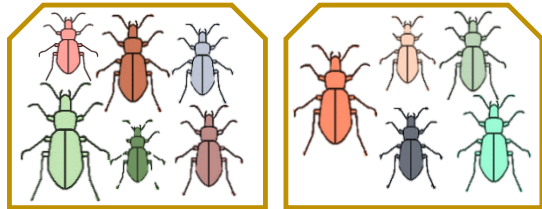
NULL COMMUNITIES- by constrained permutation

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

OBSERVED

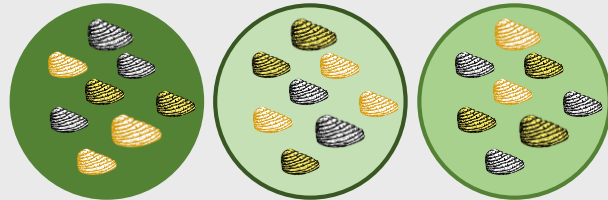
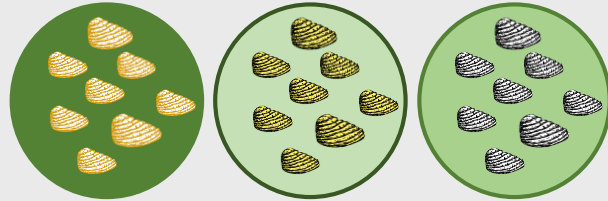


NULL (n=500)

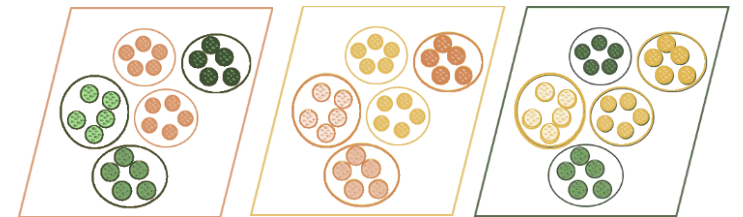
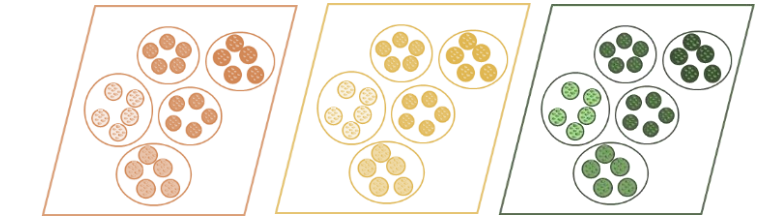


individuals per spp = k
individuals per polypore = k

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



C. « permutation of plots among sites »



alpha a

We test if spp are exchangeable – importance of spp identity

alpha b

We test whether plot scale structures the communities

alpha c

We test whether site scale structures the communities