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How repeatable are communities in Fomes polypores?

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HAL Authorization



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

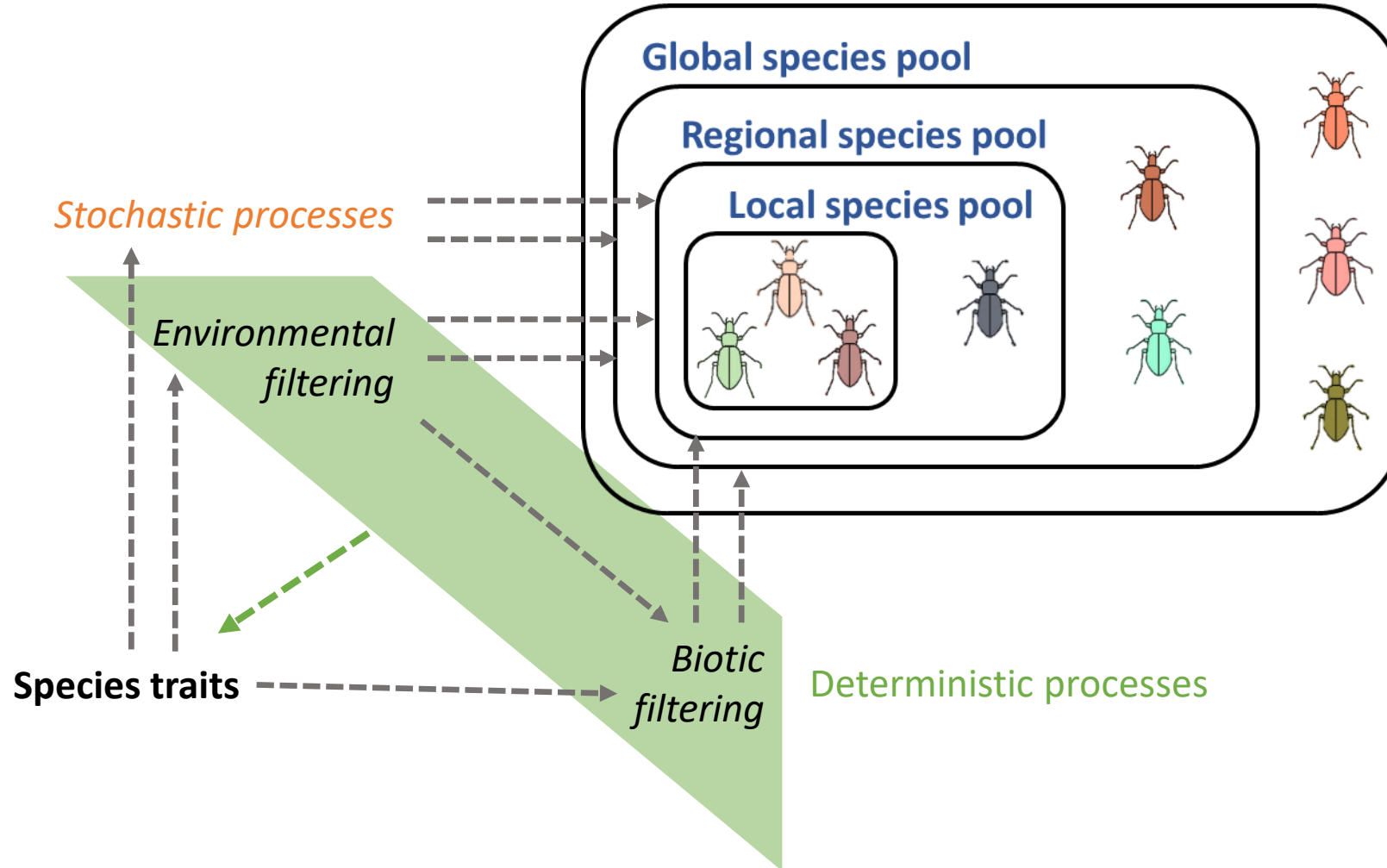
M. Roy

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DYNAFOR

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

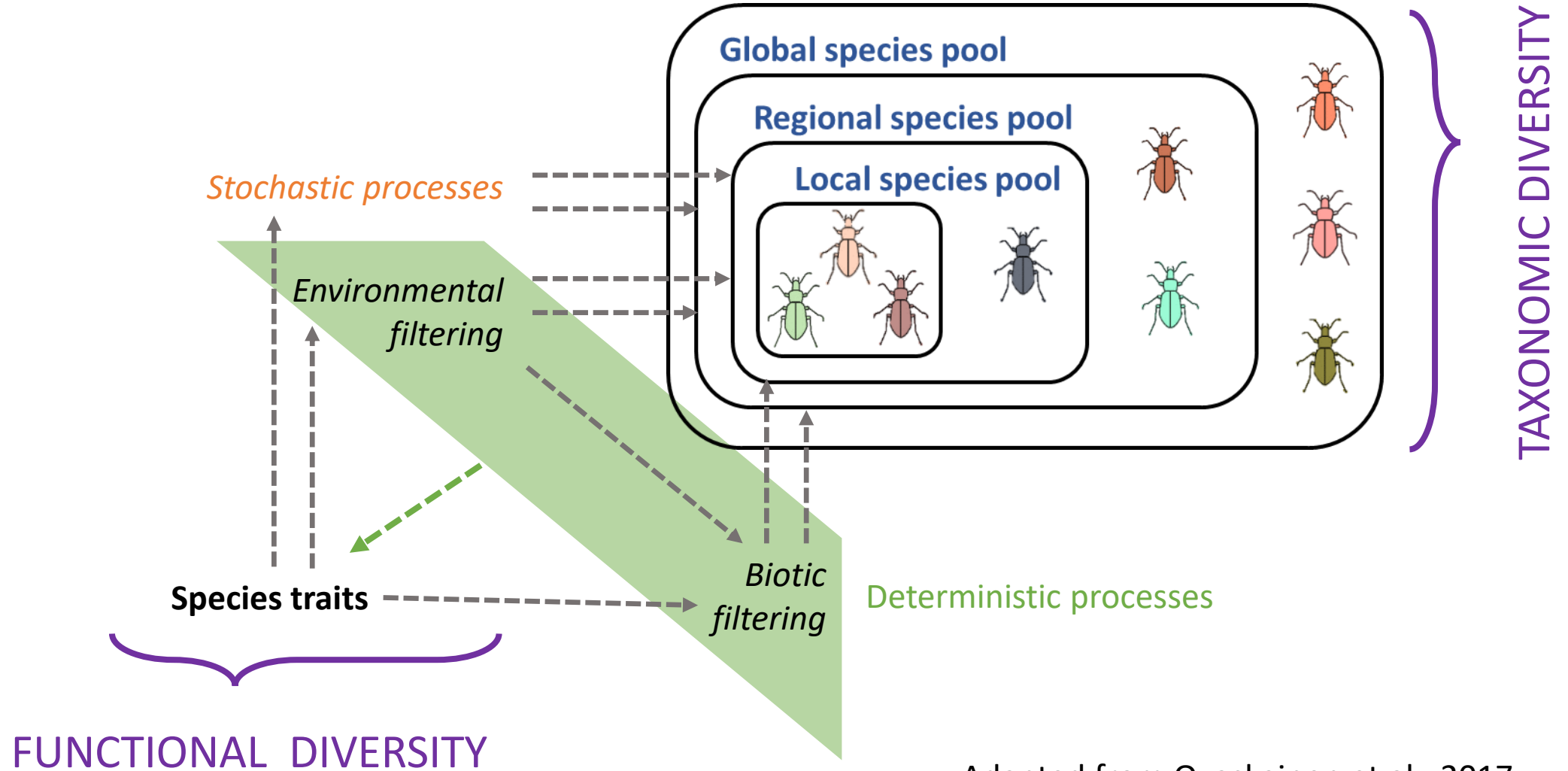
1. Community assembly: patterns and processes



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



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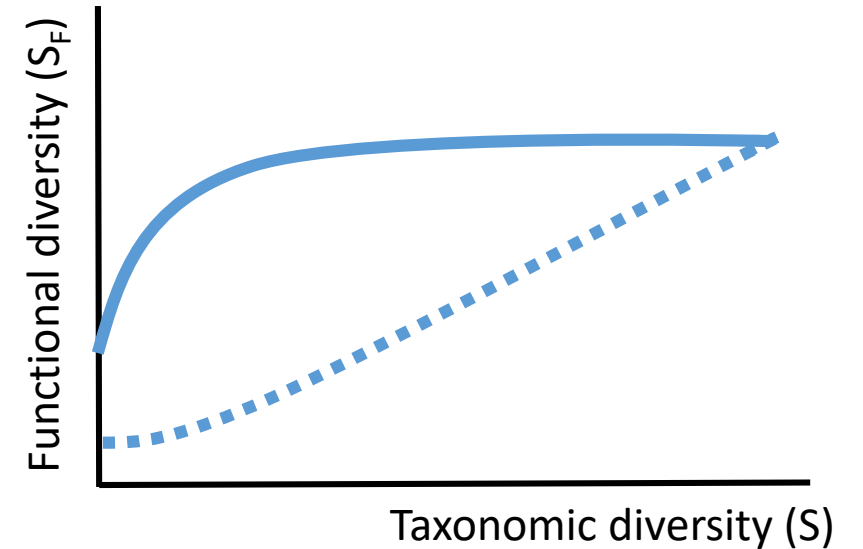
2. Diversity patterns and functional redundancy

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**”.



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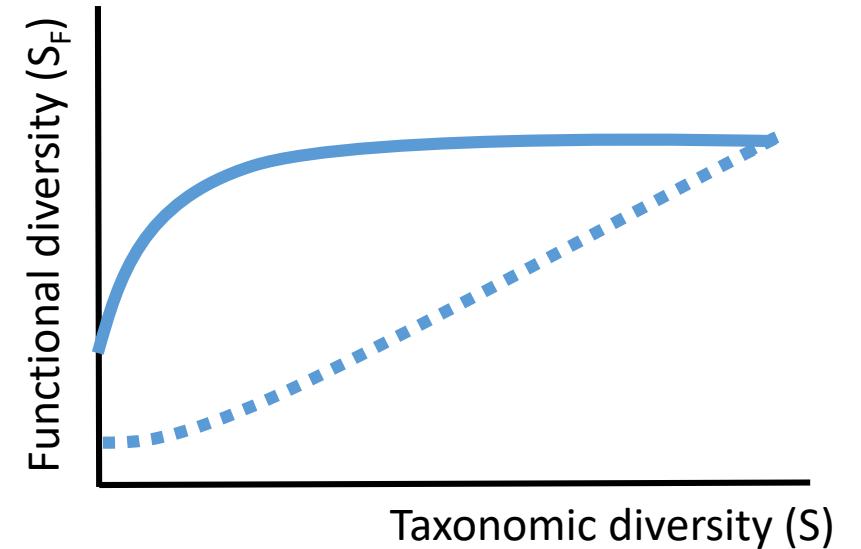
The link between the facets across scales provides information on whether communities are “**repeatable**”.

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.

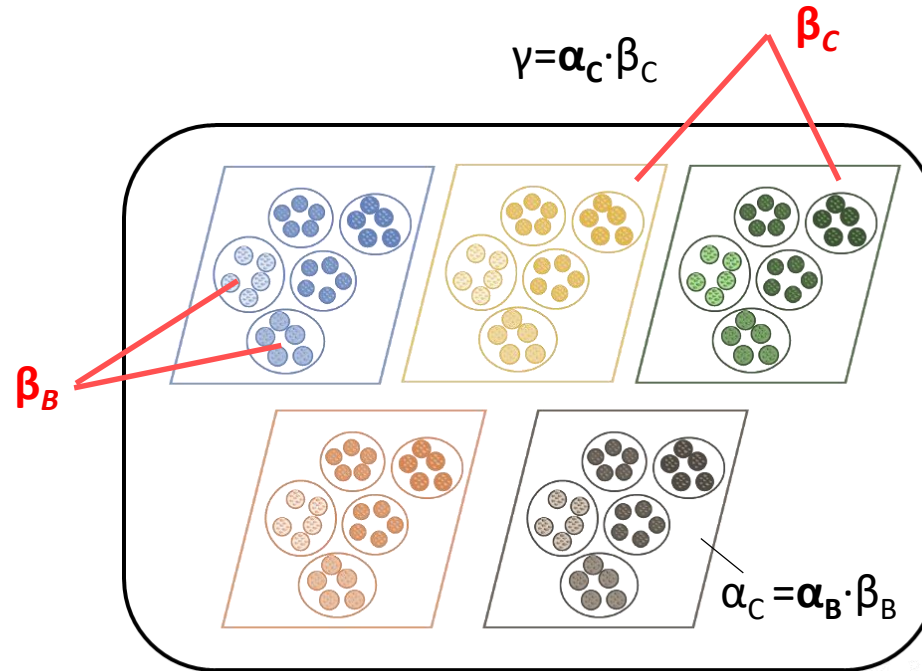
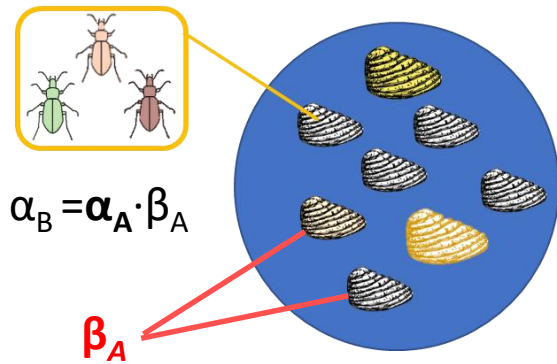
- Sampling July 2007 October 2008 in Vosges (NE, France)
- 5 sites
- 5 plots per site
- 8 polypores per plot
- Plots of 30m radius – 100 m distance between plots
- **Trophic guilds = Functional groups**
6 Mycetophagus(=Fungivorous), Zoophagus, Xylophagus, Saprofagous, Saproxylophagus, Non-saproxylic

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

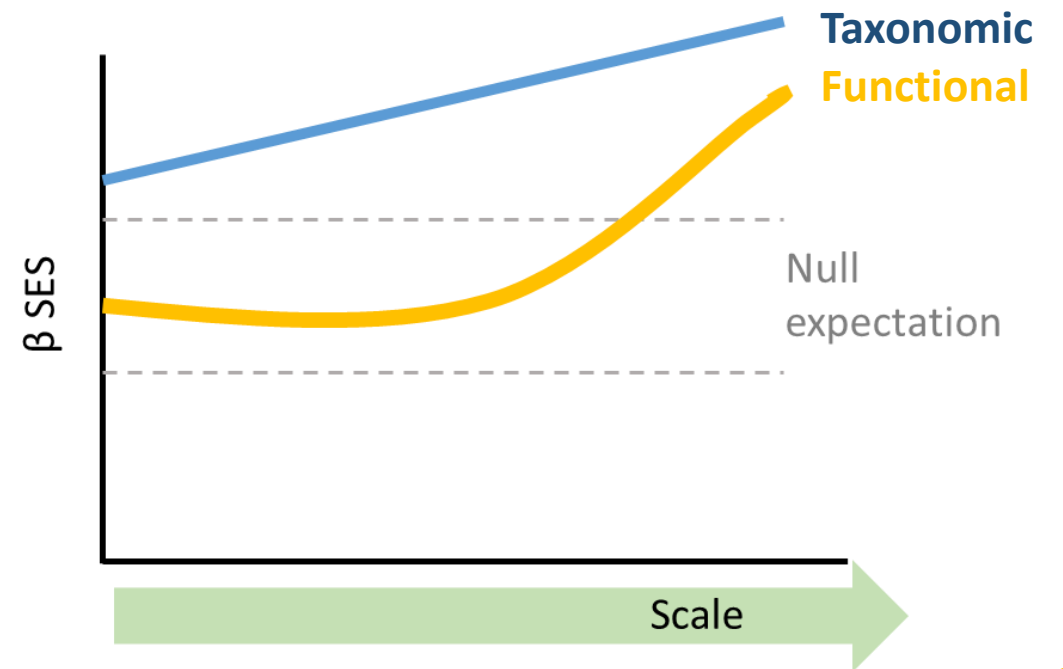
Computation of: α (multipart, package vegan) – *abundance data* and partition of β (Baselga, package betapart; Podani & Schmera, package BAT) – *ocurrence data*.

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



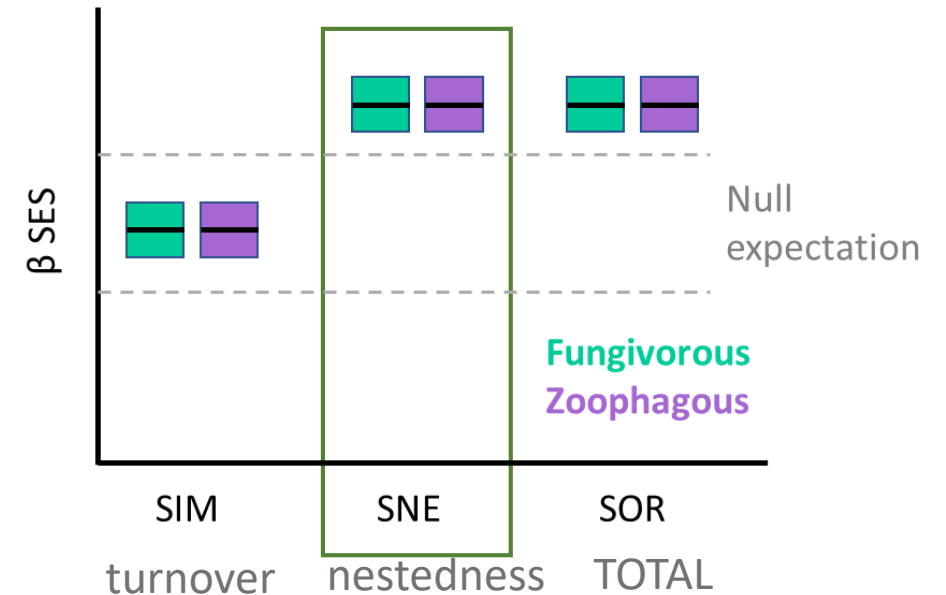
4. Hypothesis and predictions

H1/ Coleopteran communities within polypores are trophically redundant.

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

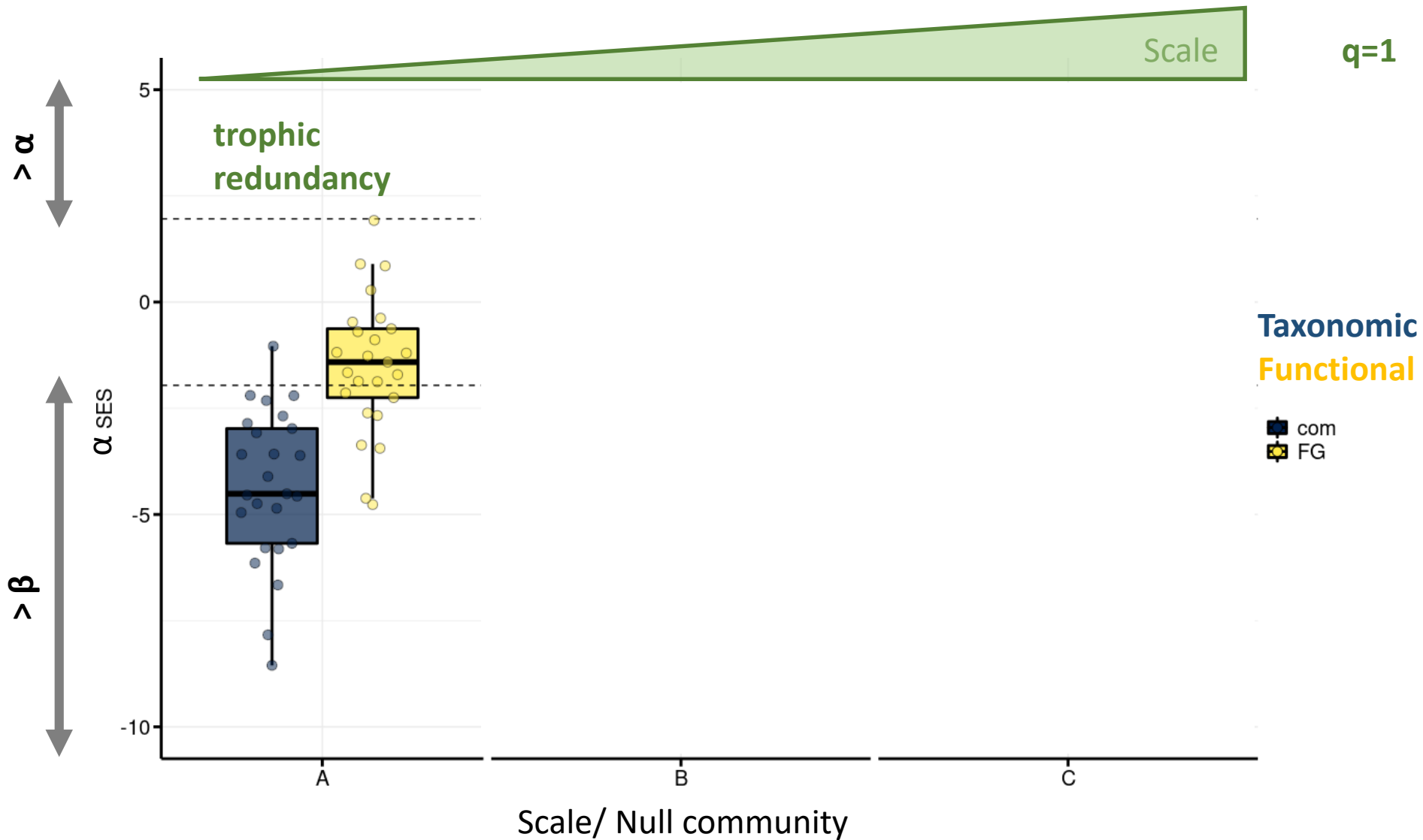
The nestedness component of β diversity within FG will be larger than that of random generated communities

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

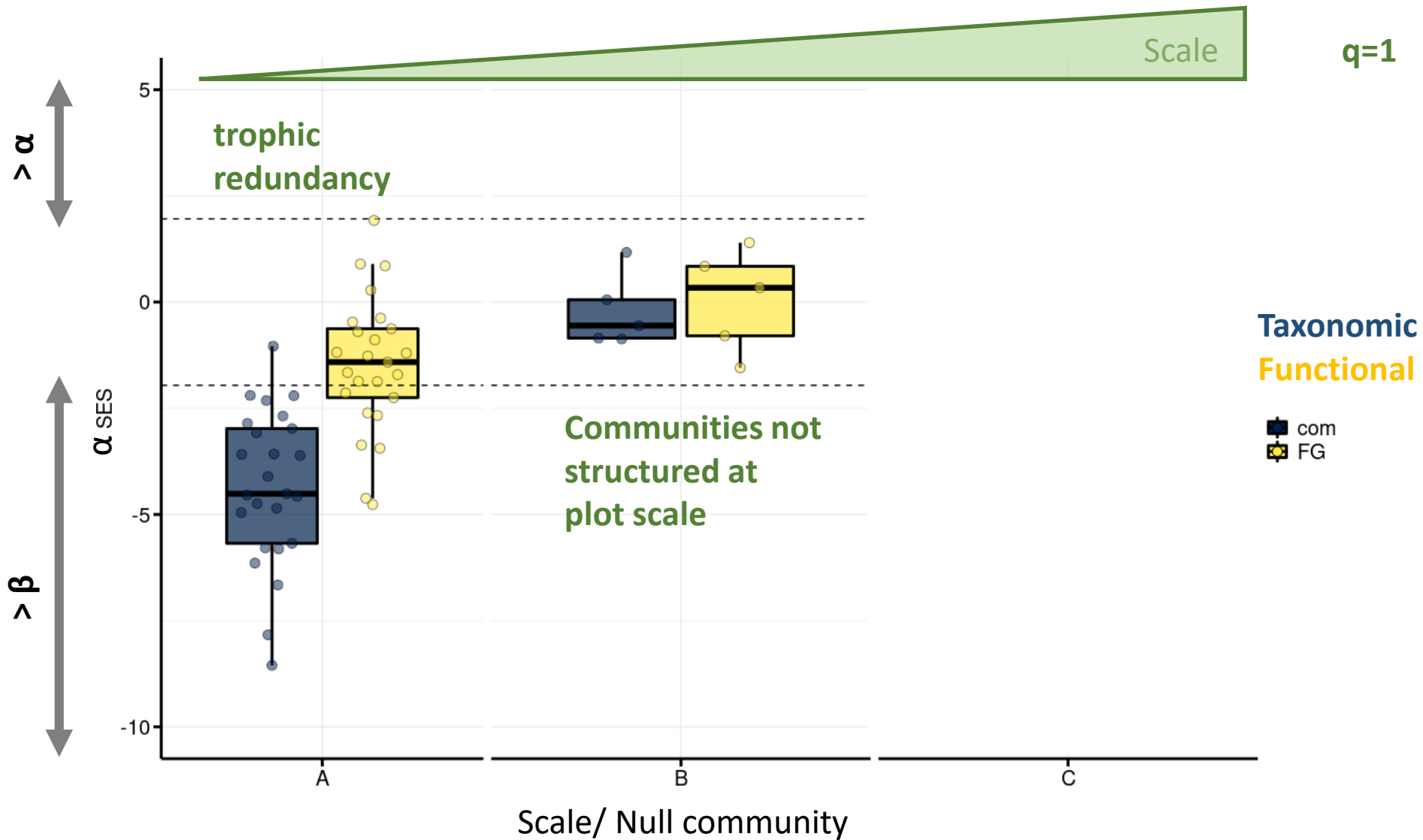


At which scale? Spatial aggregation (Thuiller et al., 2015)

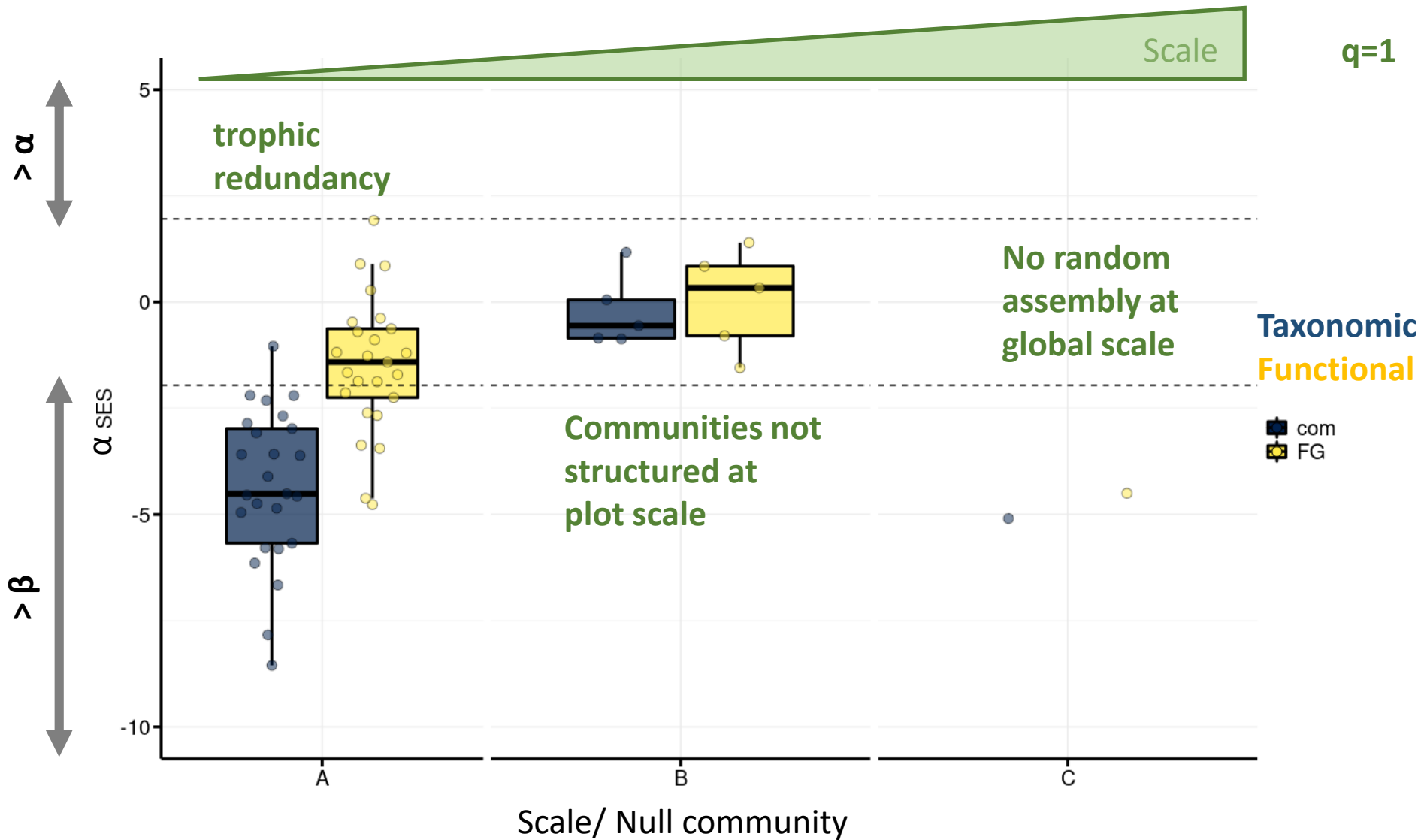
5. Results: Are Coleopteran communities within polypores trophically redundant?



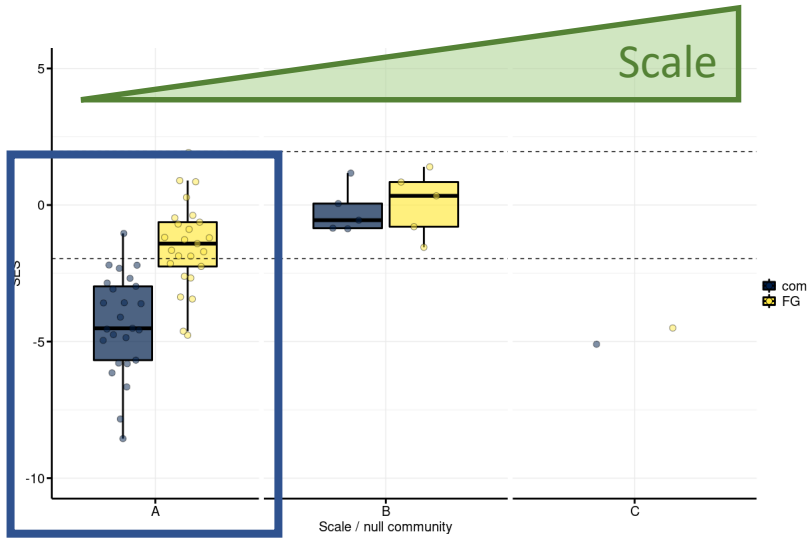
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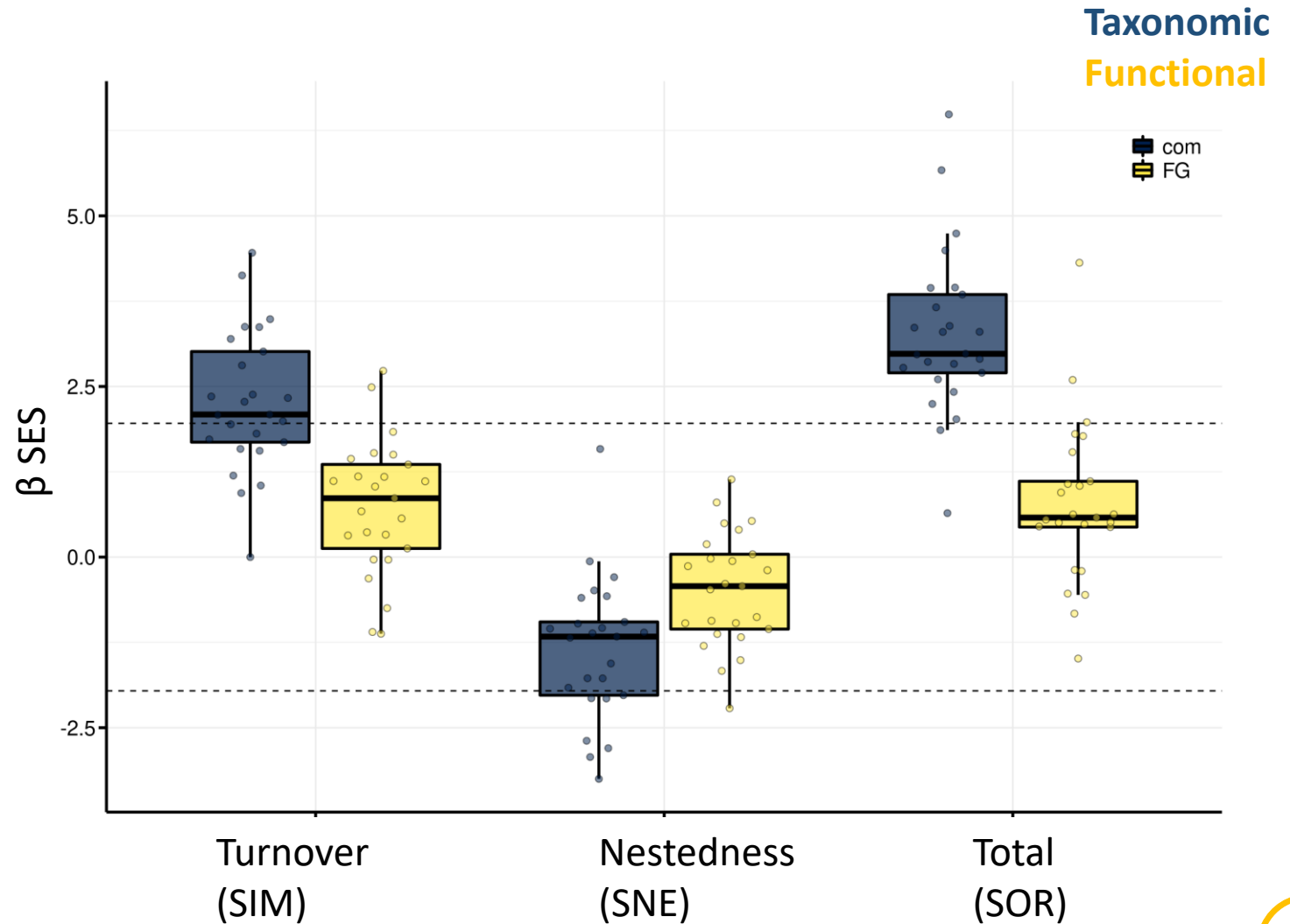


6. Results: Are Coleopteran communities within polypores are trophically redundant?

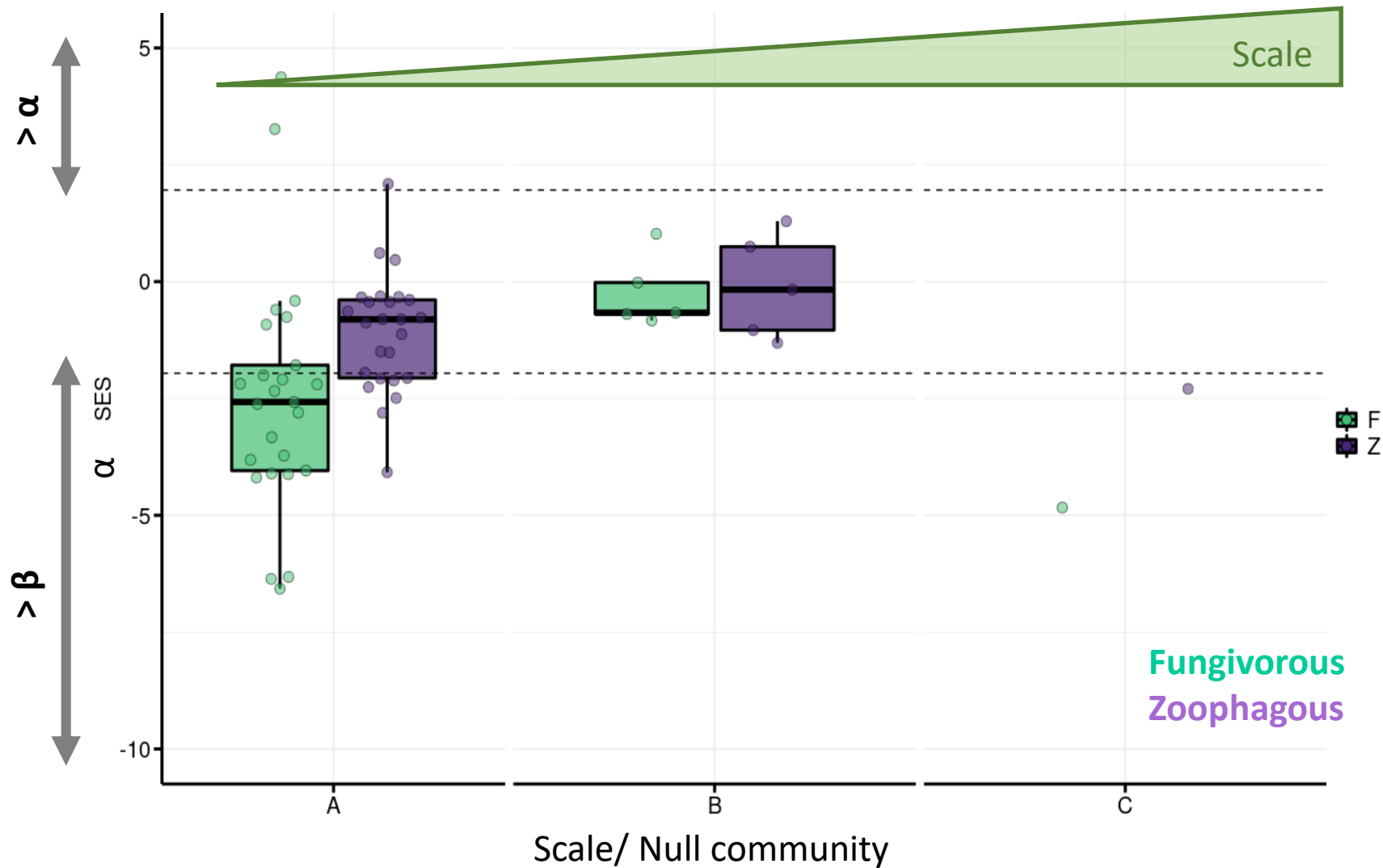


Trophic redundancy – random subsampling of *spp.* pool

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



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

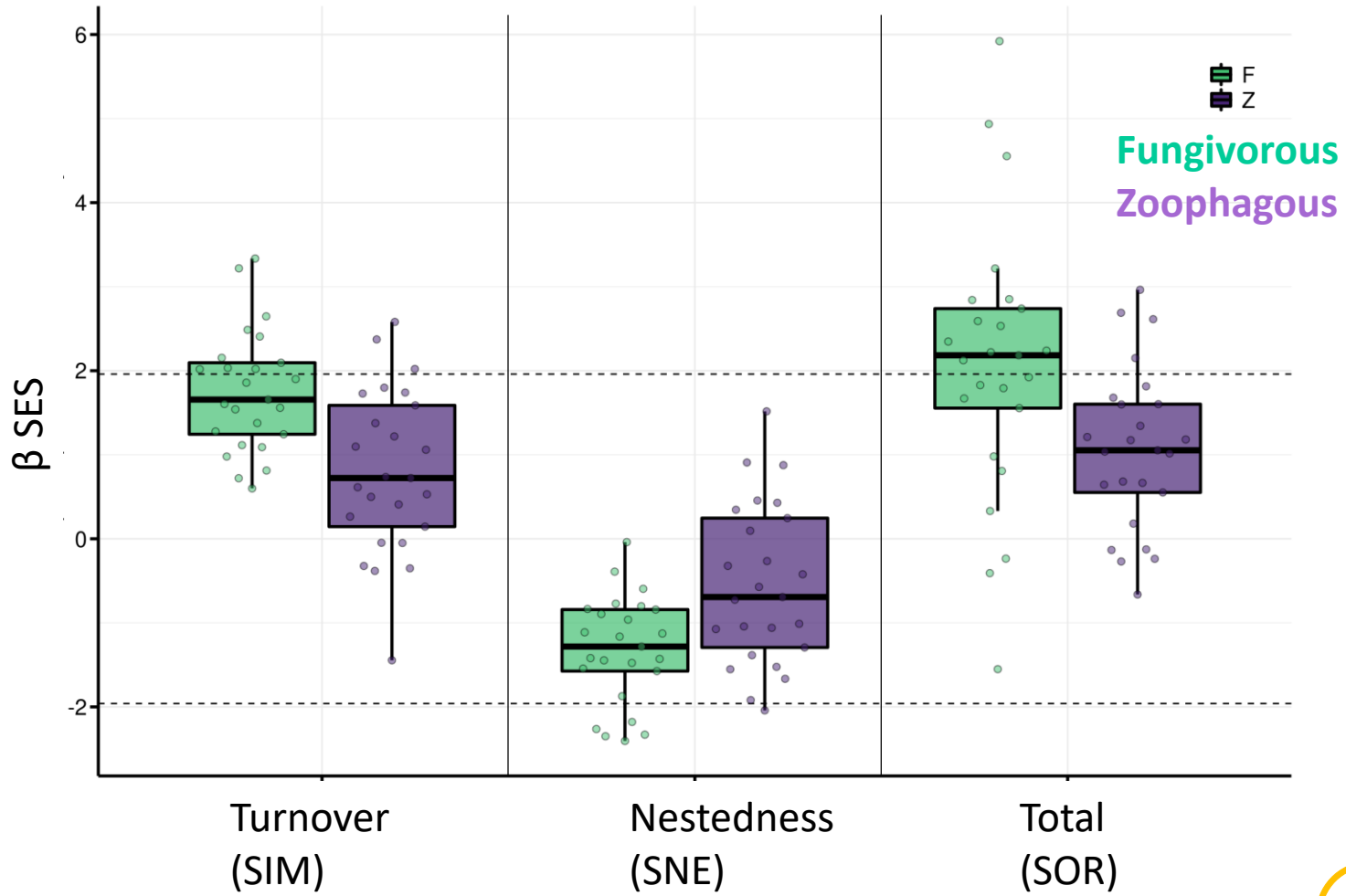
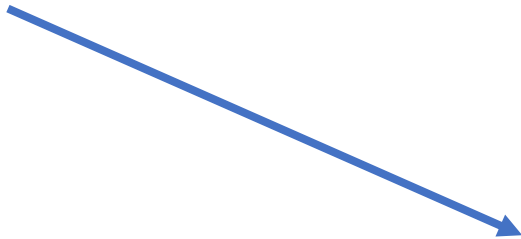
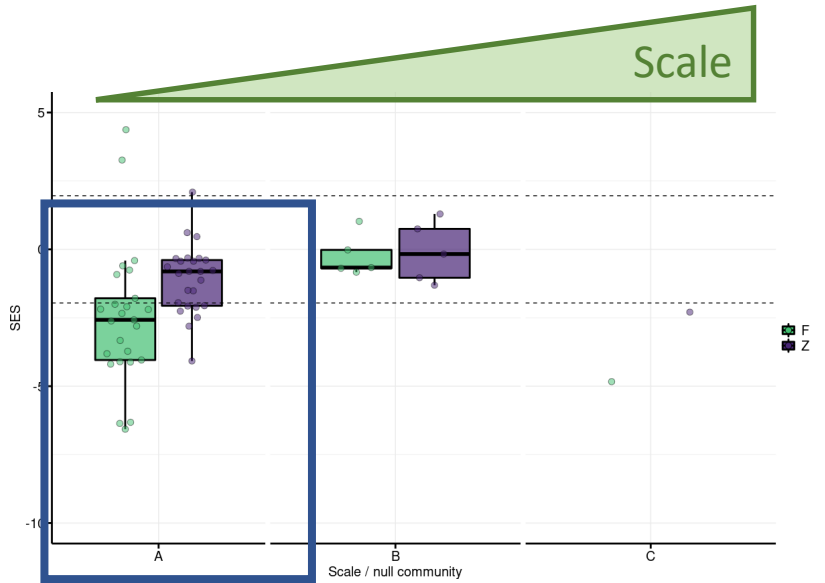


$q=1$

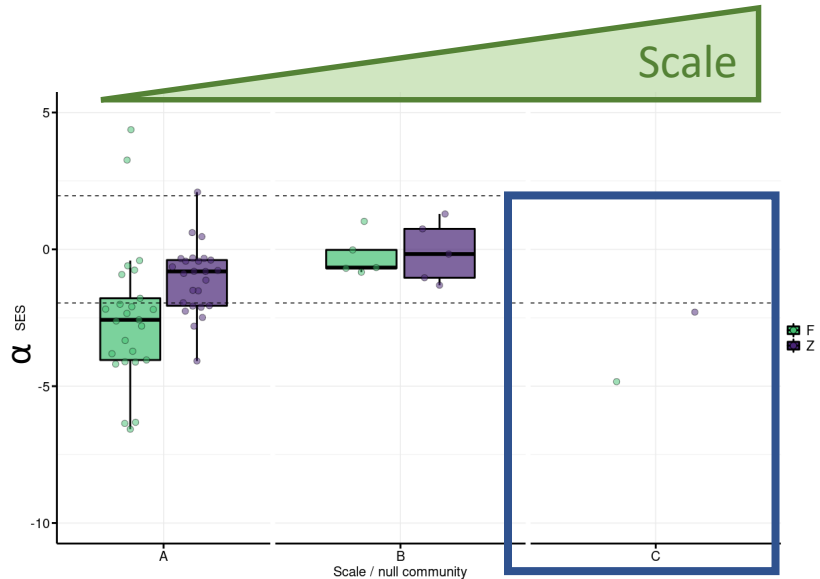
Fungivorous group show similar trend than taxonomic diversity

Fungivorous
Zoophagous

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

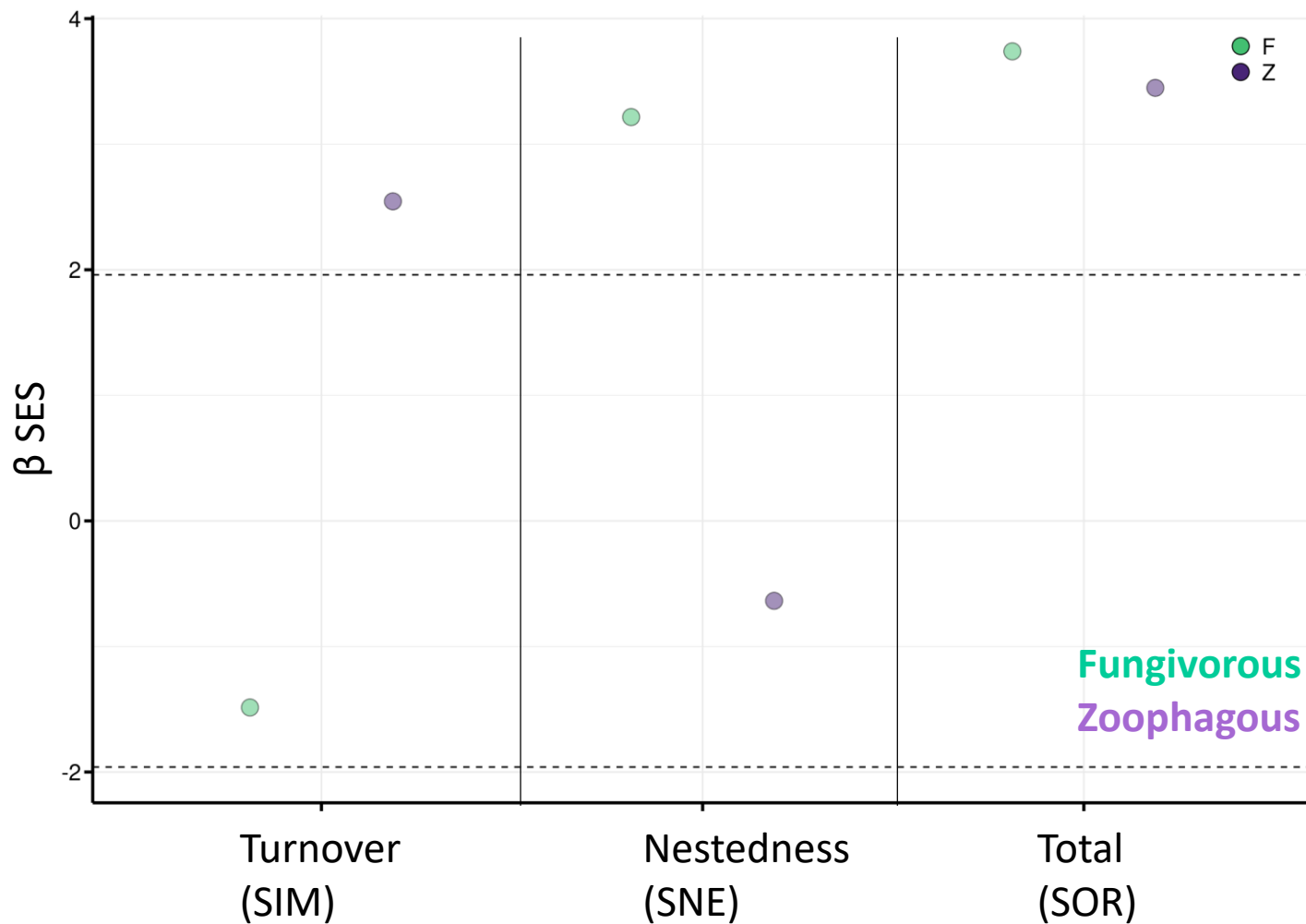


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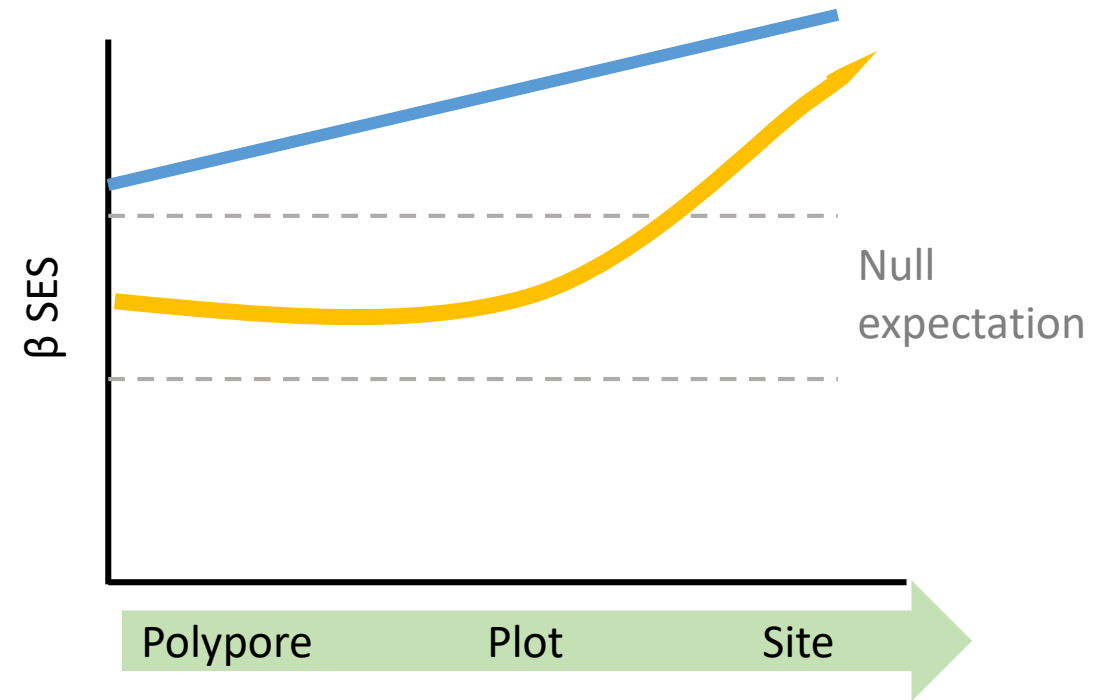


Zoophagous communities present a non-random turnover component

Fungivorous communities present a non-random nested component

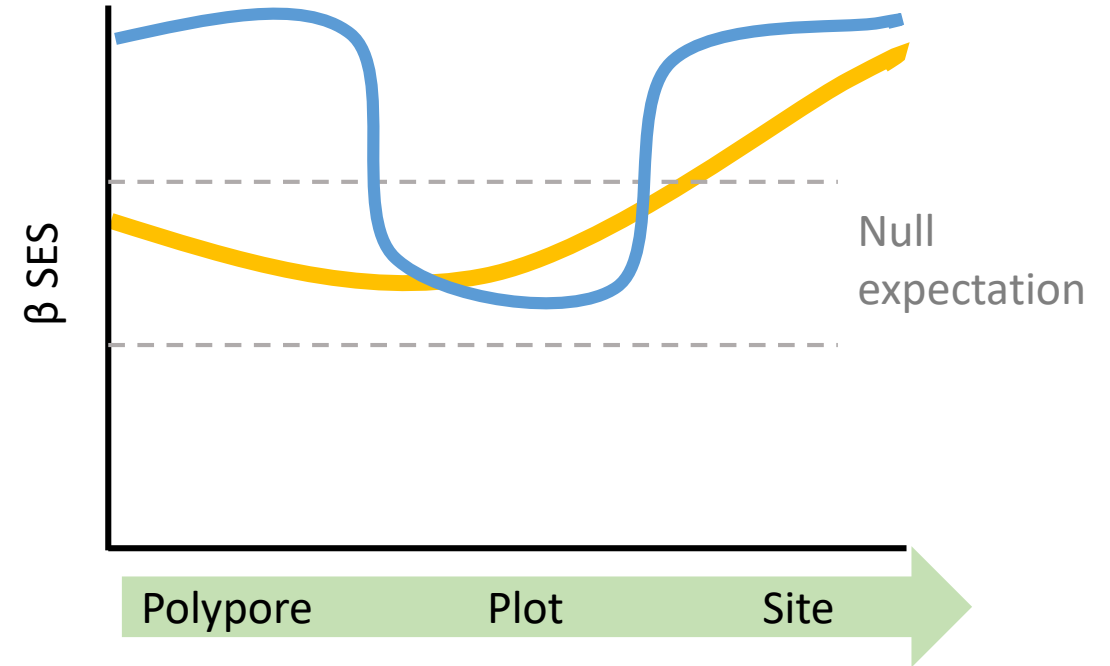


H1/ Coleopteran communities within polypores are trophically redundant.

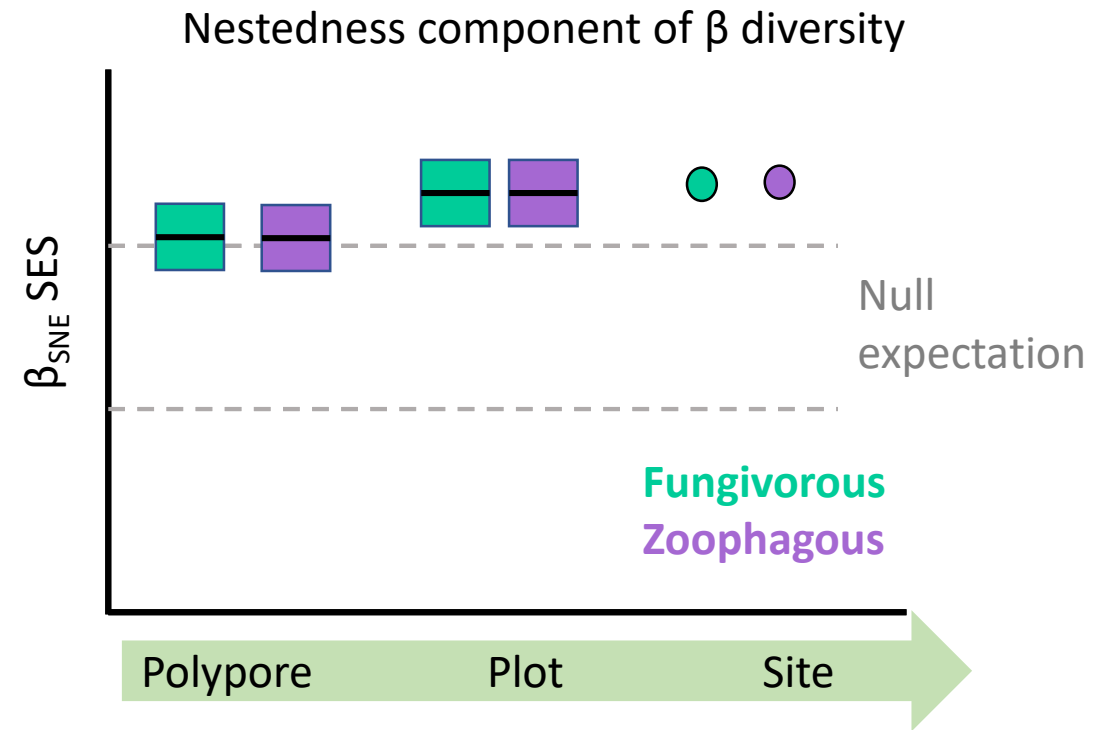


H1/ Coleopteran communities within polypores are trophically redundant.

- ✓ 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

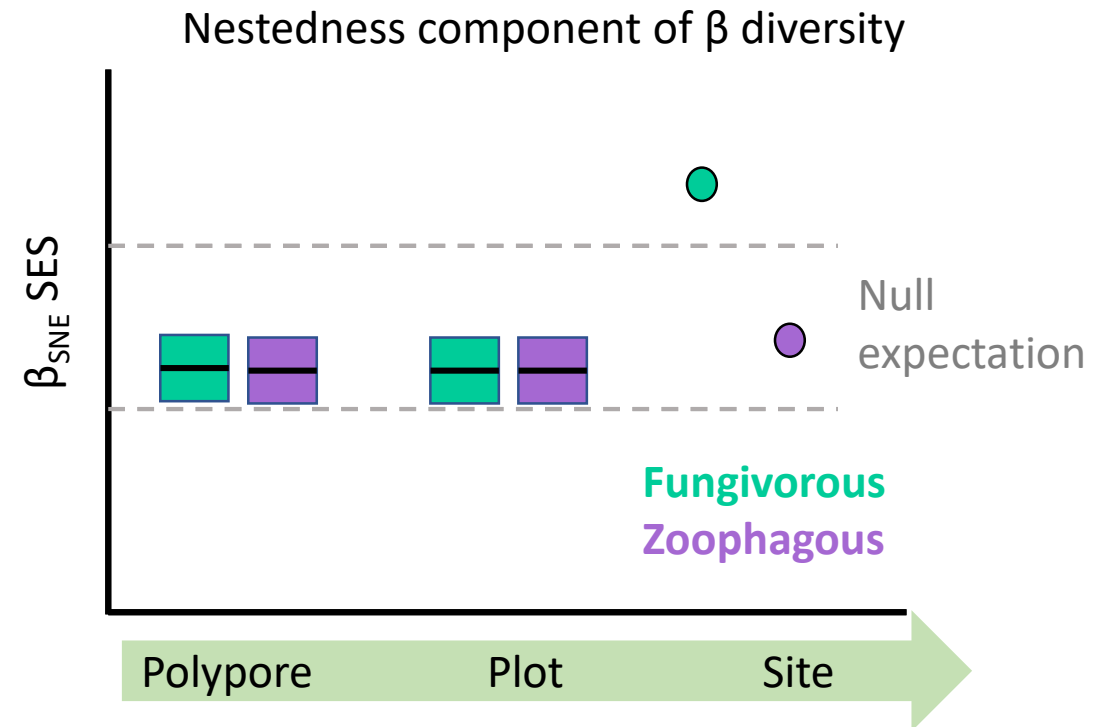


H2/ Species within a functional group will present a nested pattern.



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

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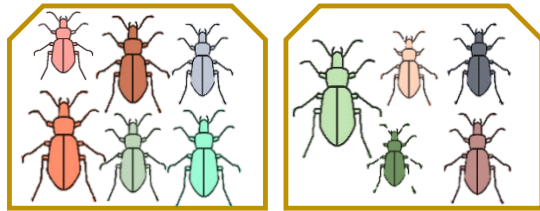
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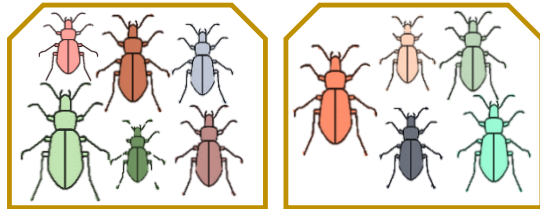
NULL COMMUNITIES- by constrained permutation

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

OBSERVED

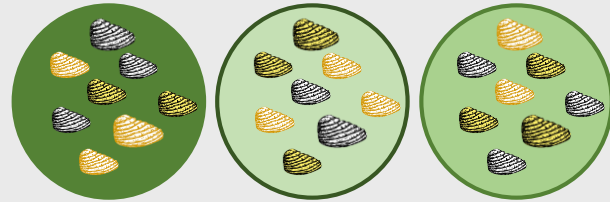
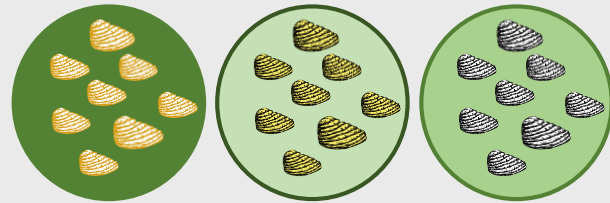


NULL (n=500)

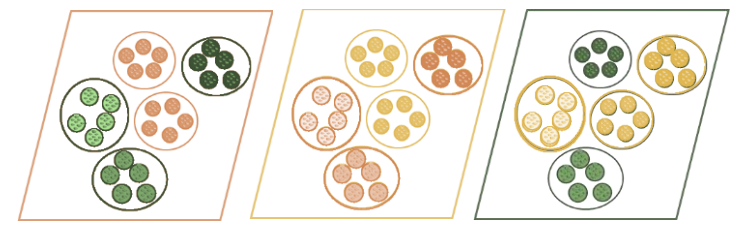
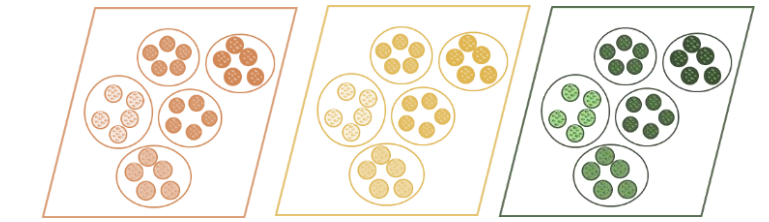


individuals per spp = k
individuals per polypore= k

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