Do morphological identification and DNA metabarcoding provide different perspectives of insect communities?

Nicole Remmel, Dominik Buchner, Julian Enss, Viktor Hartung, Florian Leese, Ellen Welti, James Sinclair, & Peter Haase

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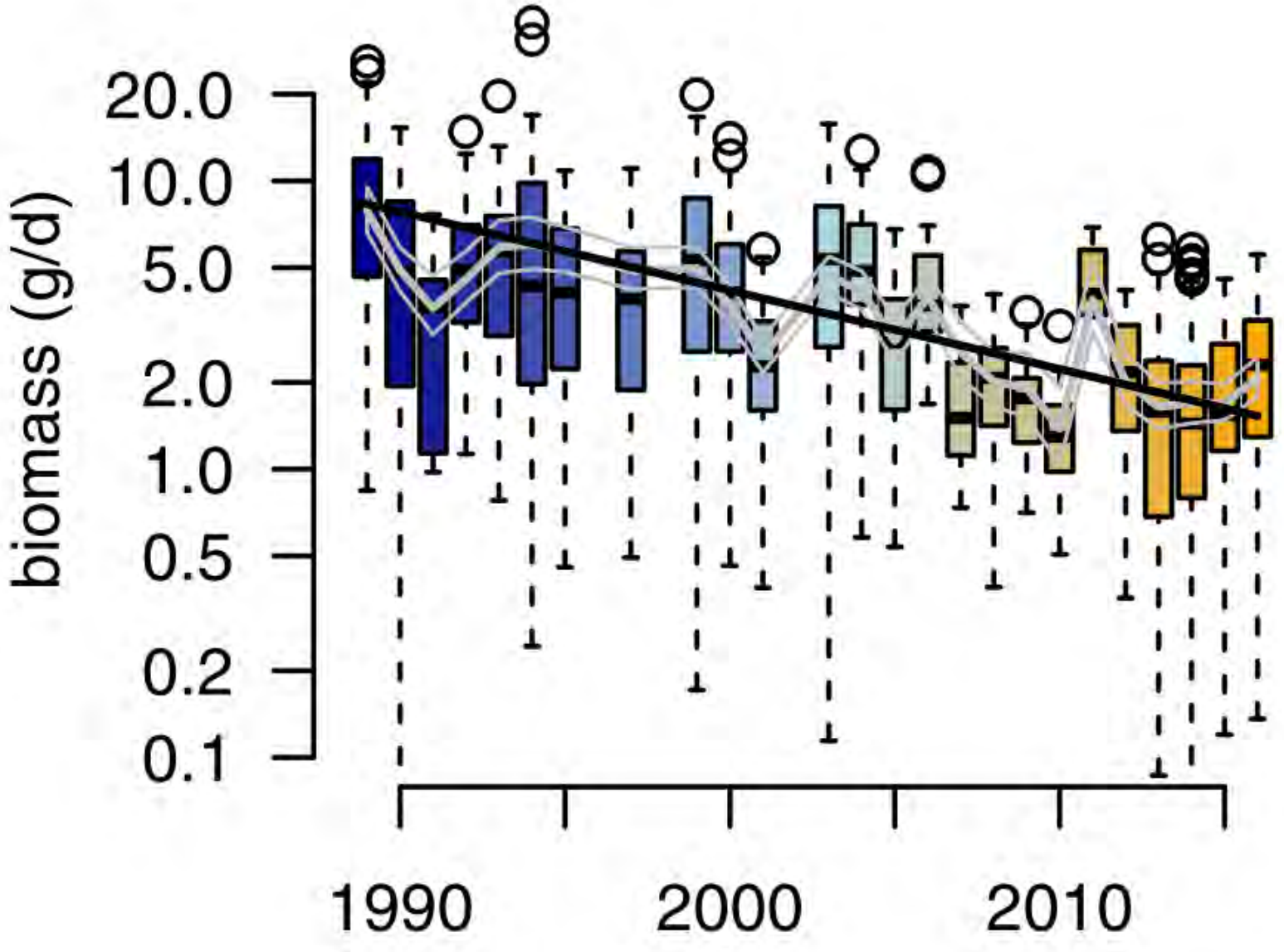
world of biodiversity

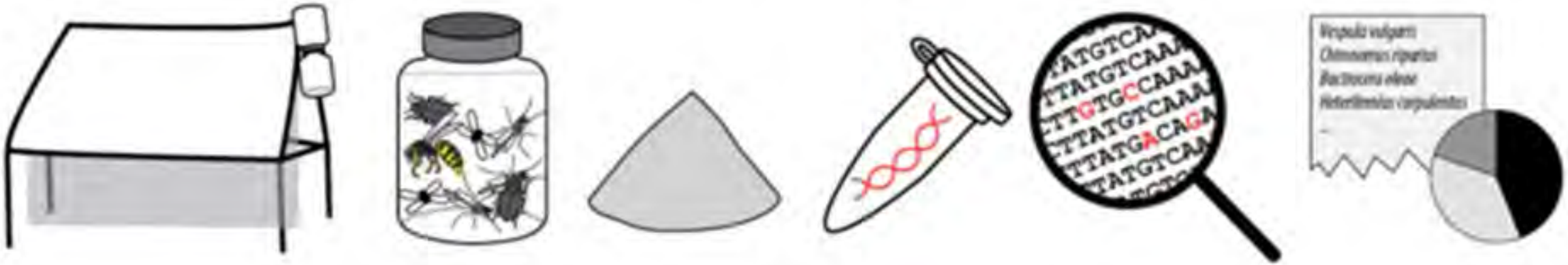
Leibniz
Leibniz Association

Reported declines in insects



Hallmann et al. 2017

Metabarcoding



Trapped

Preserved

Homogenized

DNA extraction & PCR

Sequencing

Matched

< 50€ per sample

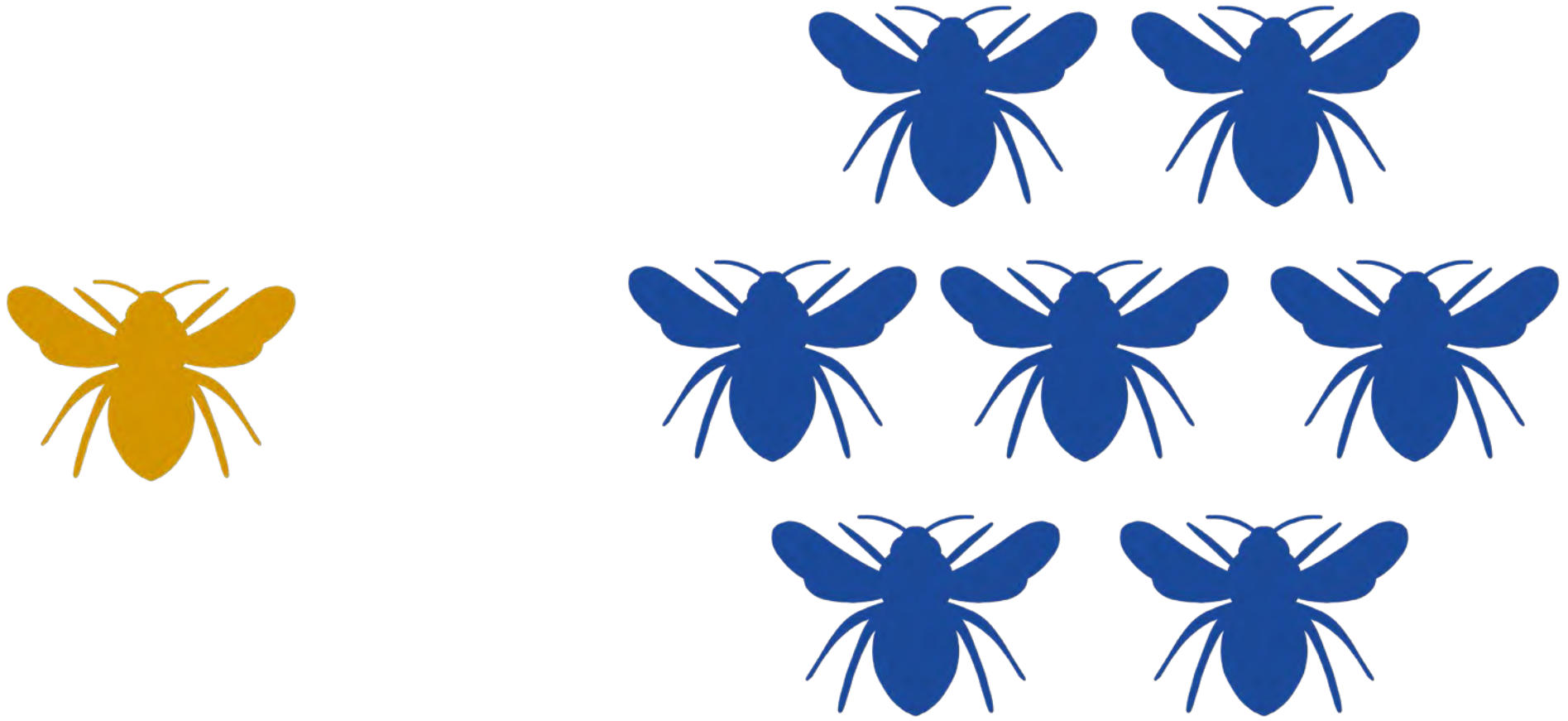
about 3 weeks / 1000 samples

Limitations

1. Presence/absence only

2. Potential biomass bias

Abundance



Body size

Limitations

1. Presence/absence only

2. Potential biomass bias

→Low-abundance species

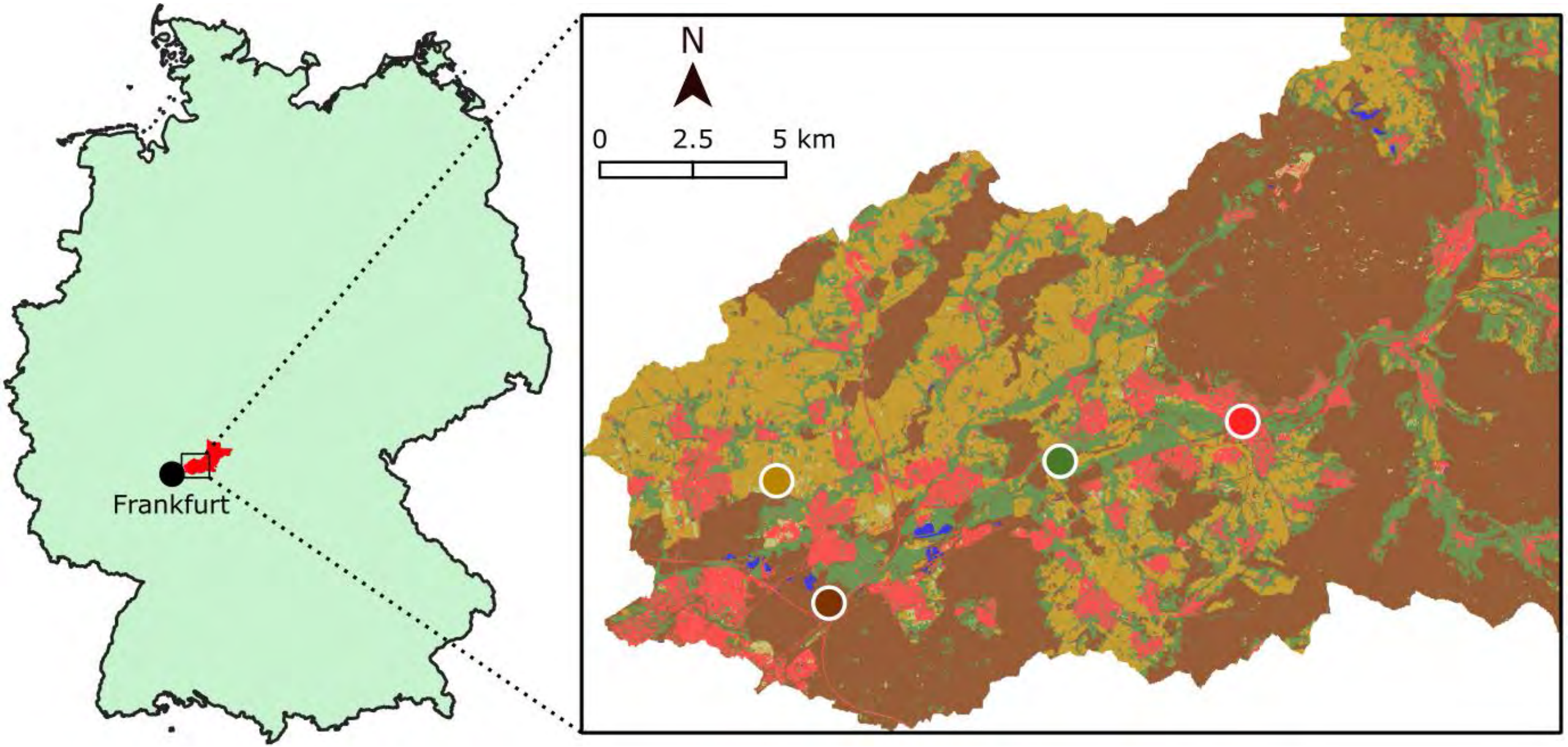
→Smaller-bodied species

Do morphological identification and DNA metabarcoding provide different perspectives of insect communities?

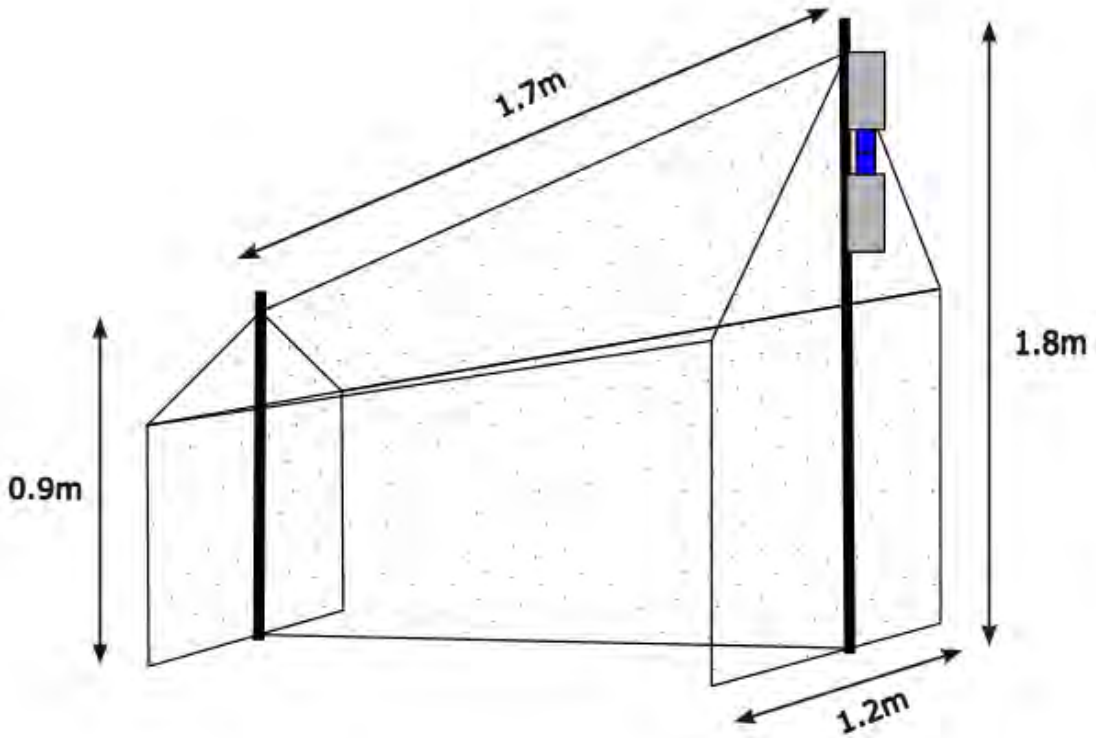
Morphological
(pick out and put back in)

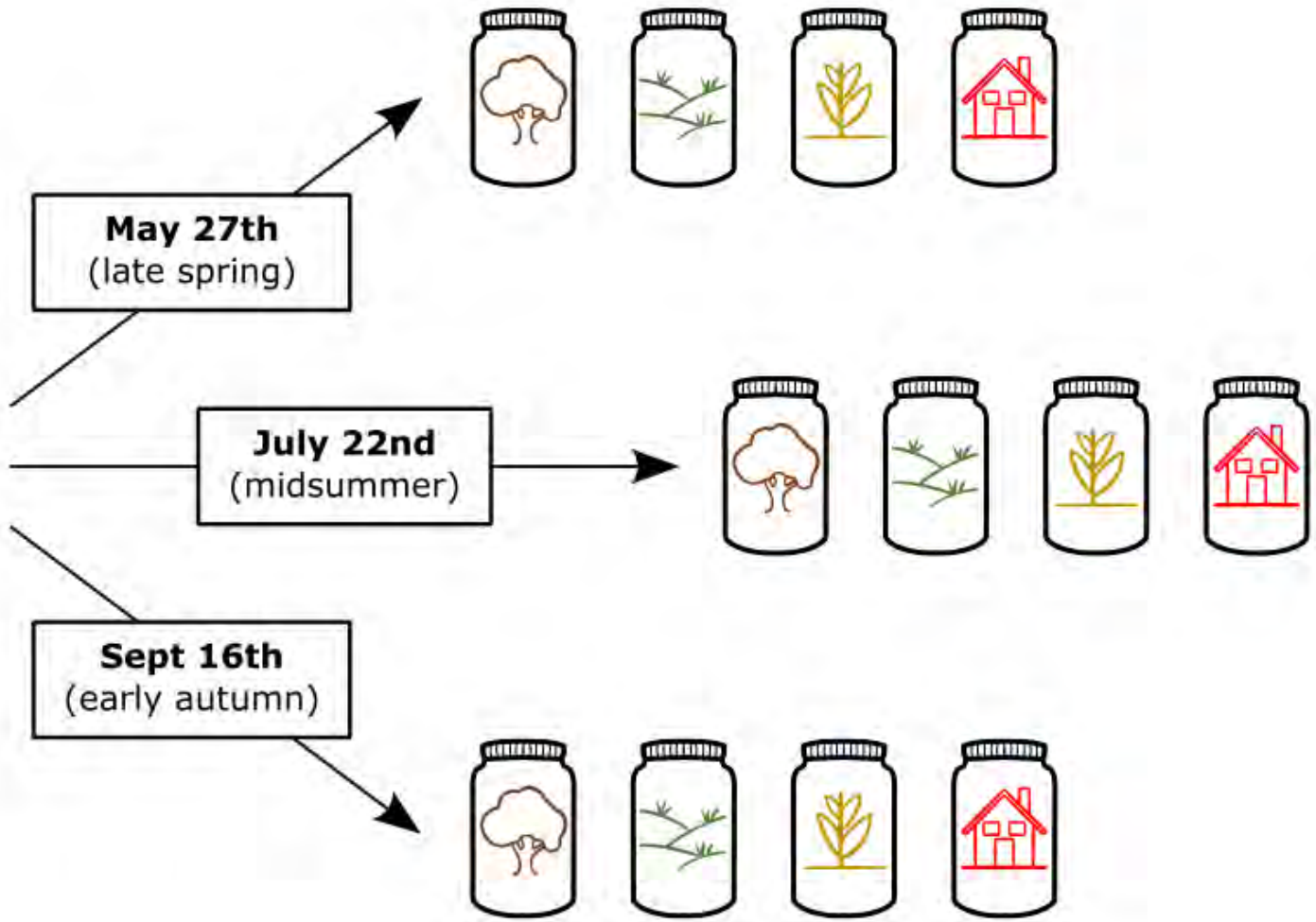
Metabarcoding
(same sample)

Methods

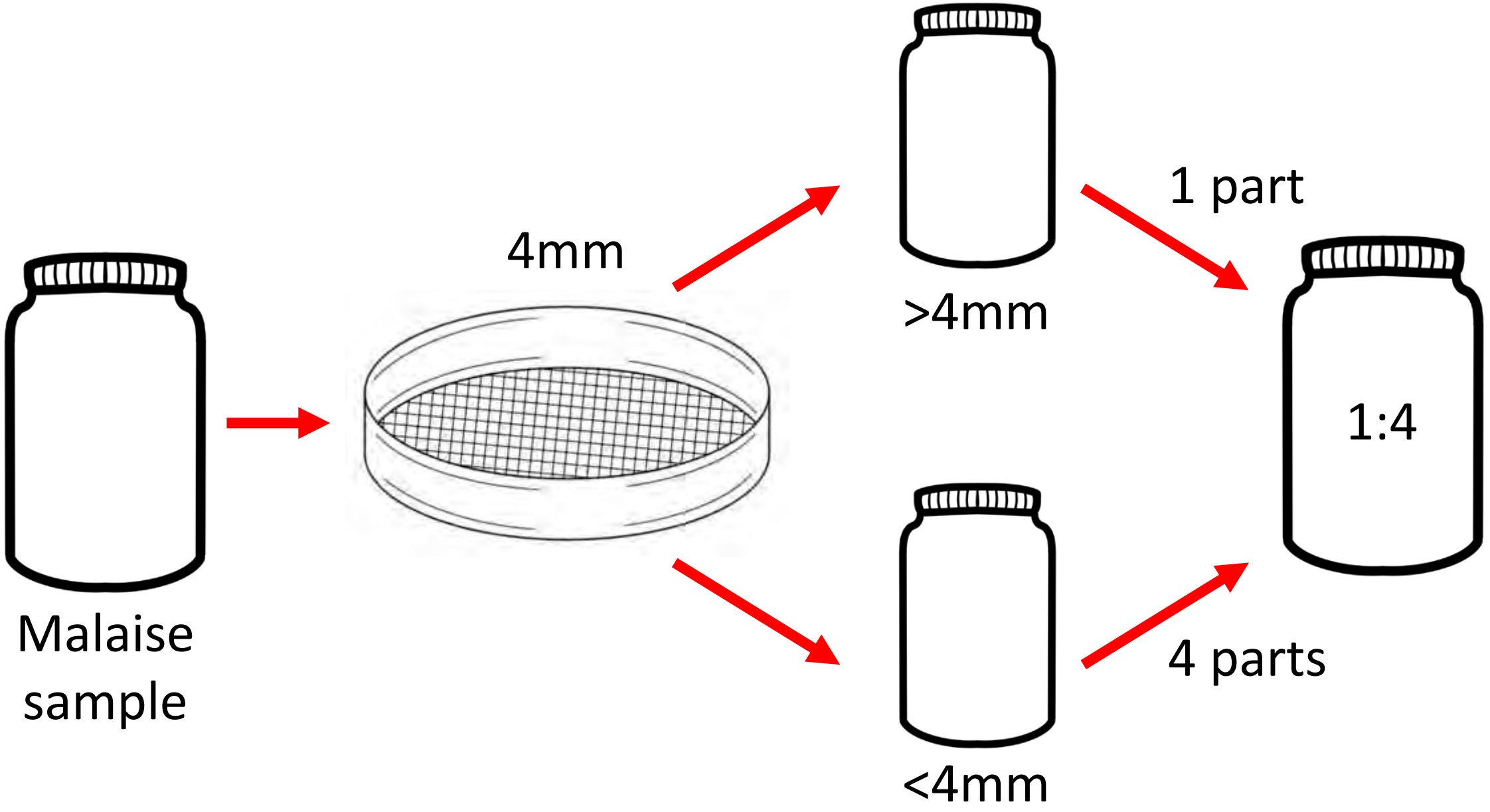


Methods


1.7m
0.9m
1.8m
1.2m


May 27th
(late spring)
July 22nd
(midsummer)
Sept 16th
(early autumn)

Methods



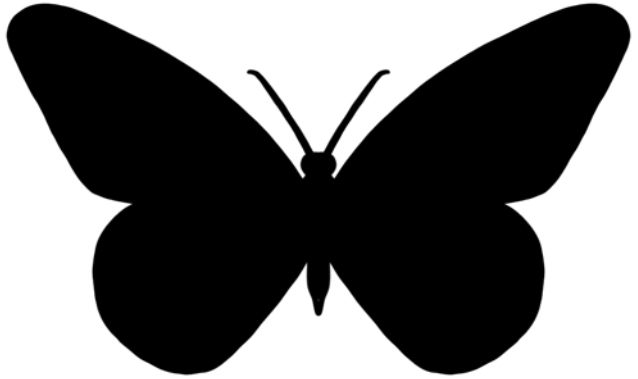
Metrics

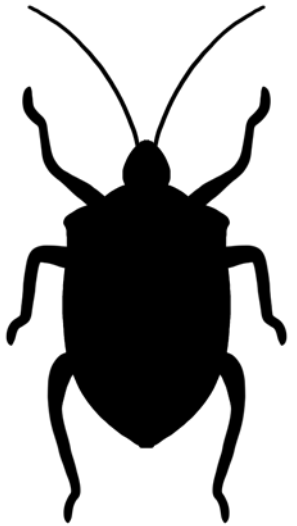
1. Total richness

→ Apiformes (bees), Heteroptera (true bugs), Syrphidae (hoverflies), Rhopalocera (butterflies), Trichoptera, Ephemeroptera, Plecoptera, Mecoptera

2. Richness of four taxonomic groups

Metrics





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2. Richness of four taxonomic groups

→ Bees, butterflies, hoverflies, and true bugs

3. Species detection (0/1)

Metrics

Morphology

Pieris rapae

Metabarcoding

Pieris rapae

Metrics

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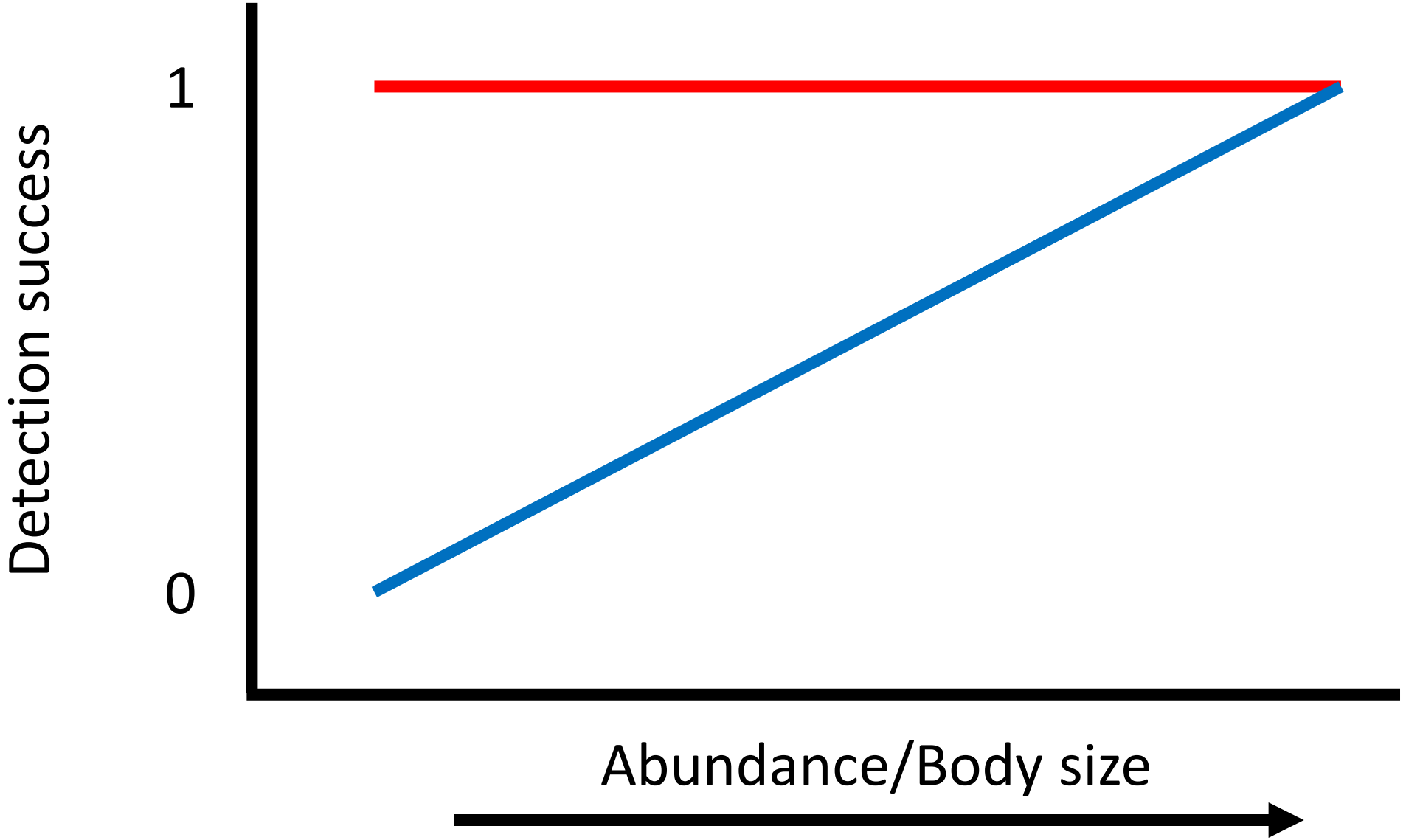
3. Species detection (0/1) ~ Abundance + Body size

Metrics



Metrics

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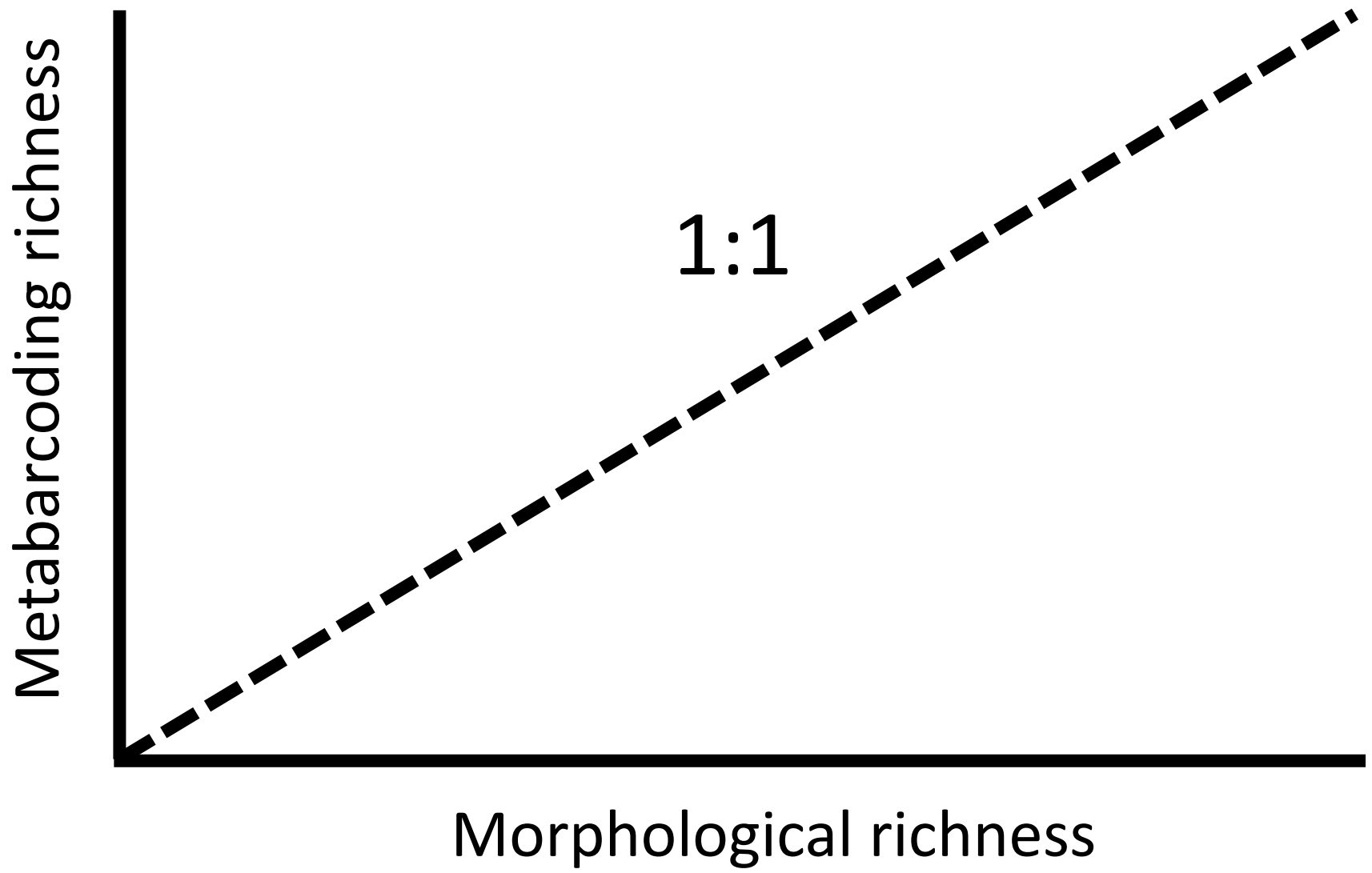
2. Richness of four taxonomic groups

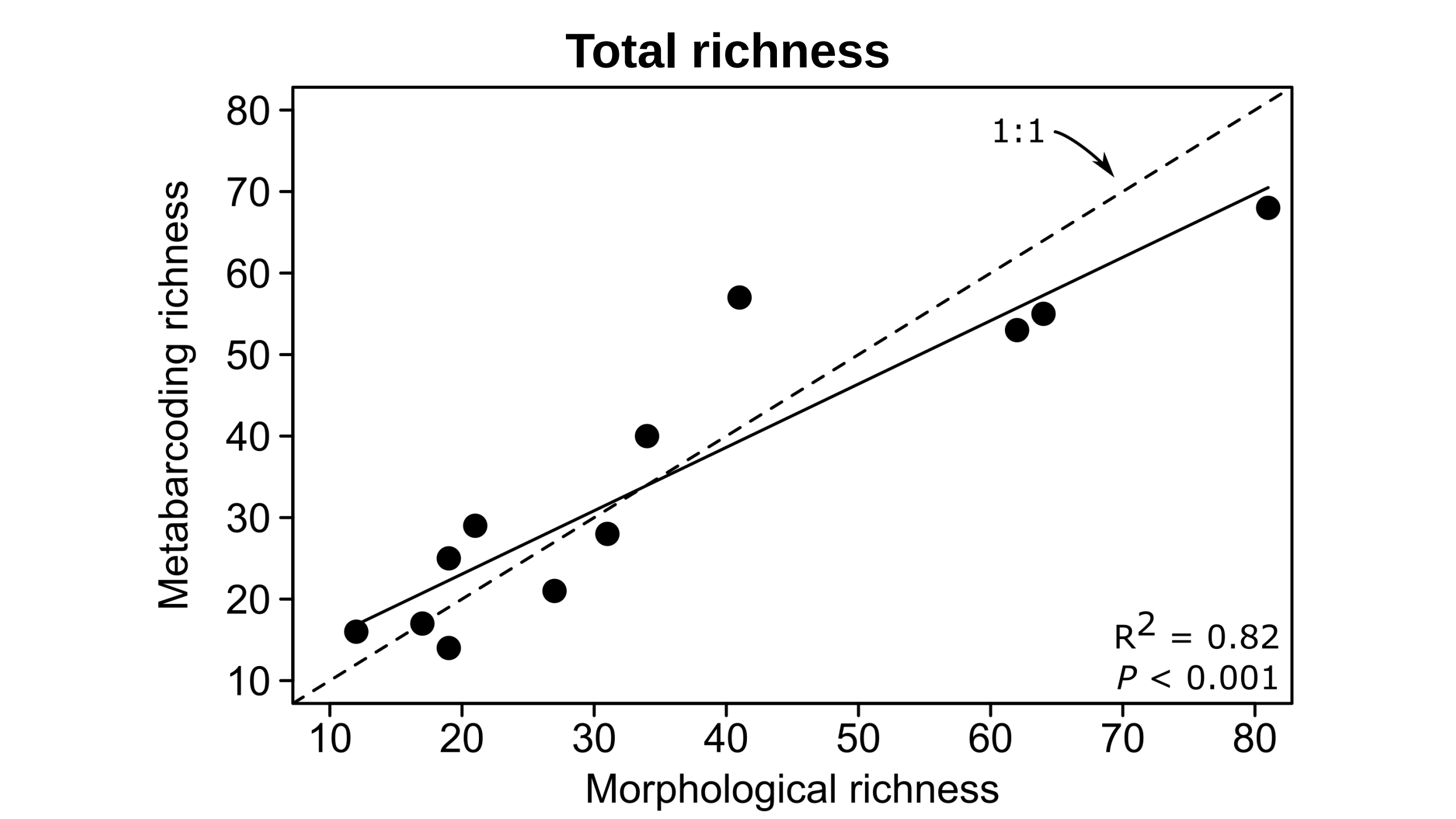
→ Bees, butterflies, hoverflies, and true bugs

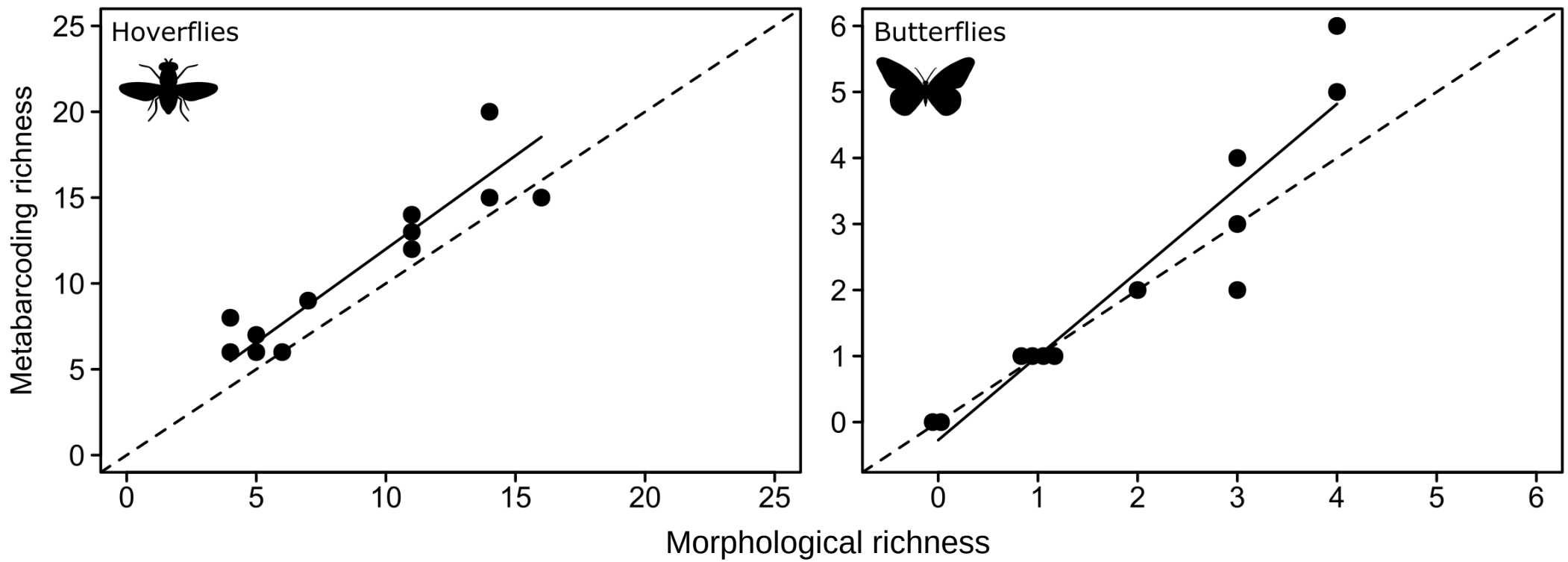
3. Species detection (0/1) ~ Abundance + Body size

4. Community composition (taxa and body size)

Total richness




Total richness
Metabarcoding richness
Morphological richness
1:1
R^2 = 0.82
P < 0.001
10
20
30
40
50
60
70
80

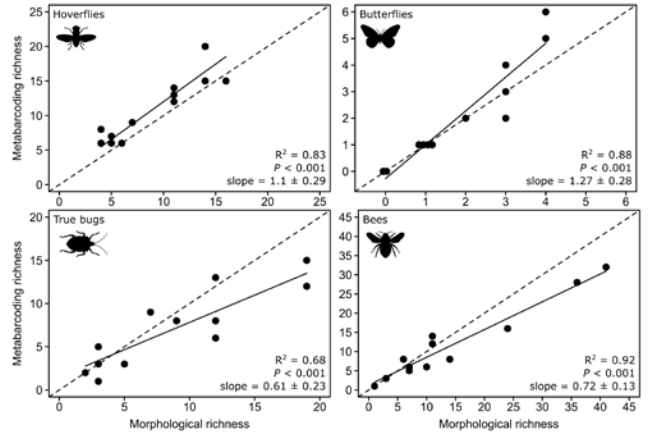

Hoverflies
Butterflies
Metabarcoding richness
Morphological richness
0
5
10
15
20
25
0
1
2
3
4
5
6

Summary

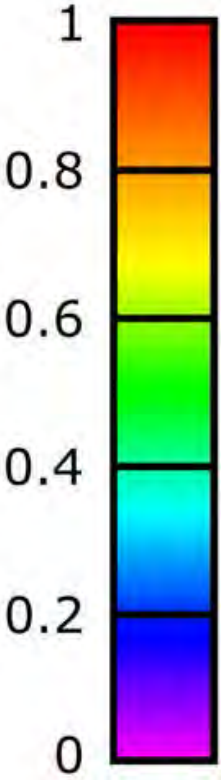
1. Richness

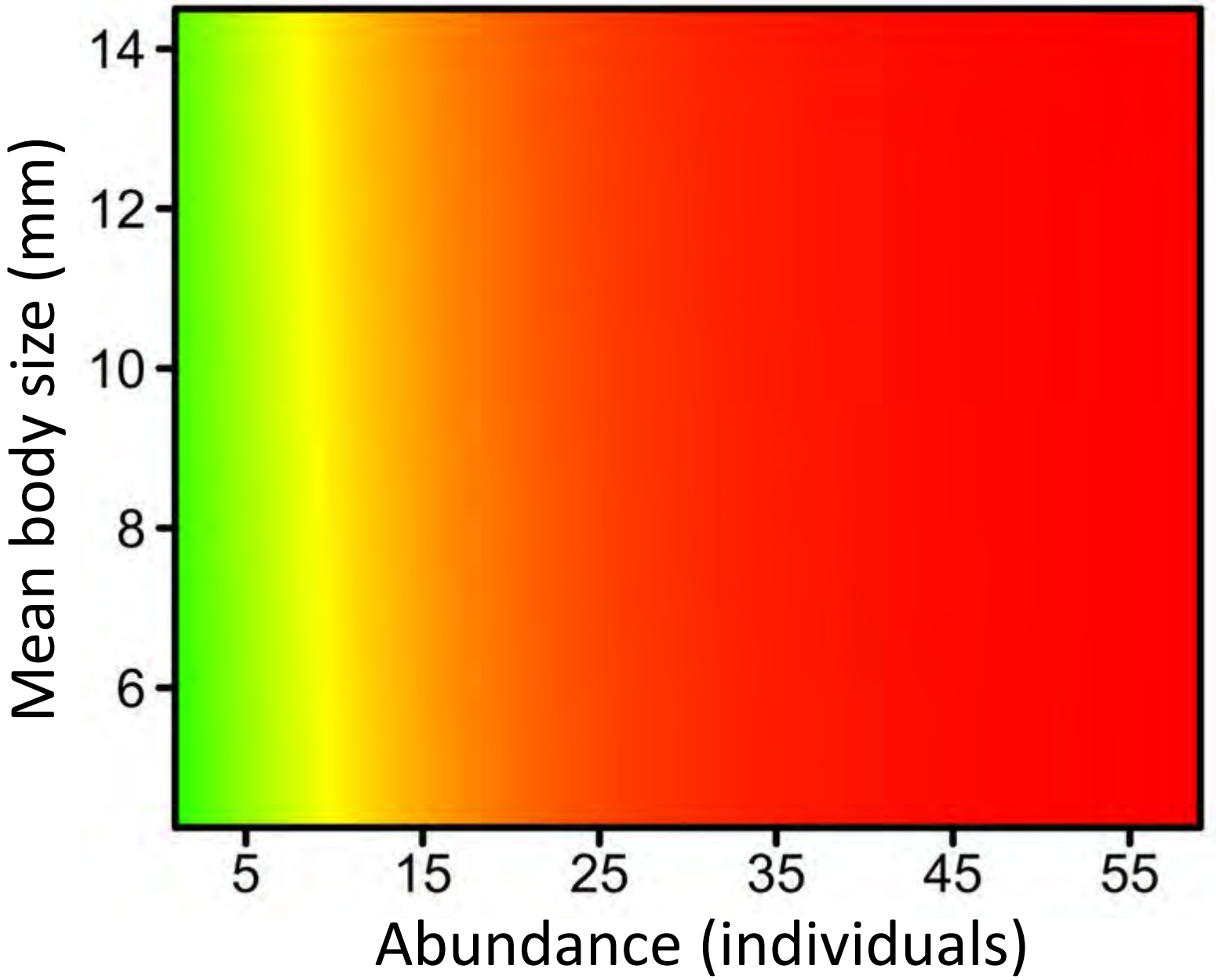
→ Missing species at higher diversity, driven by true bugs and bees

→ Can detect more hoverflies and butterflies

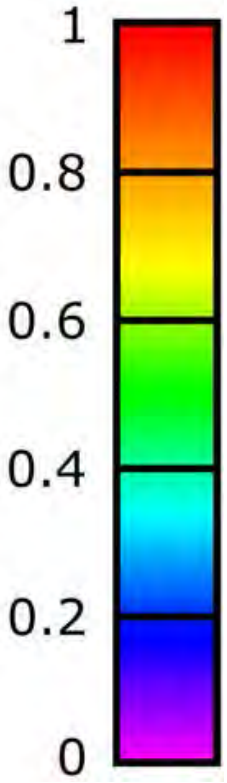


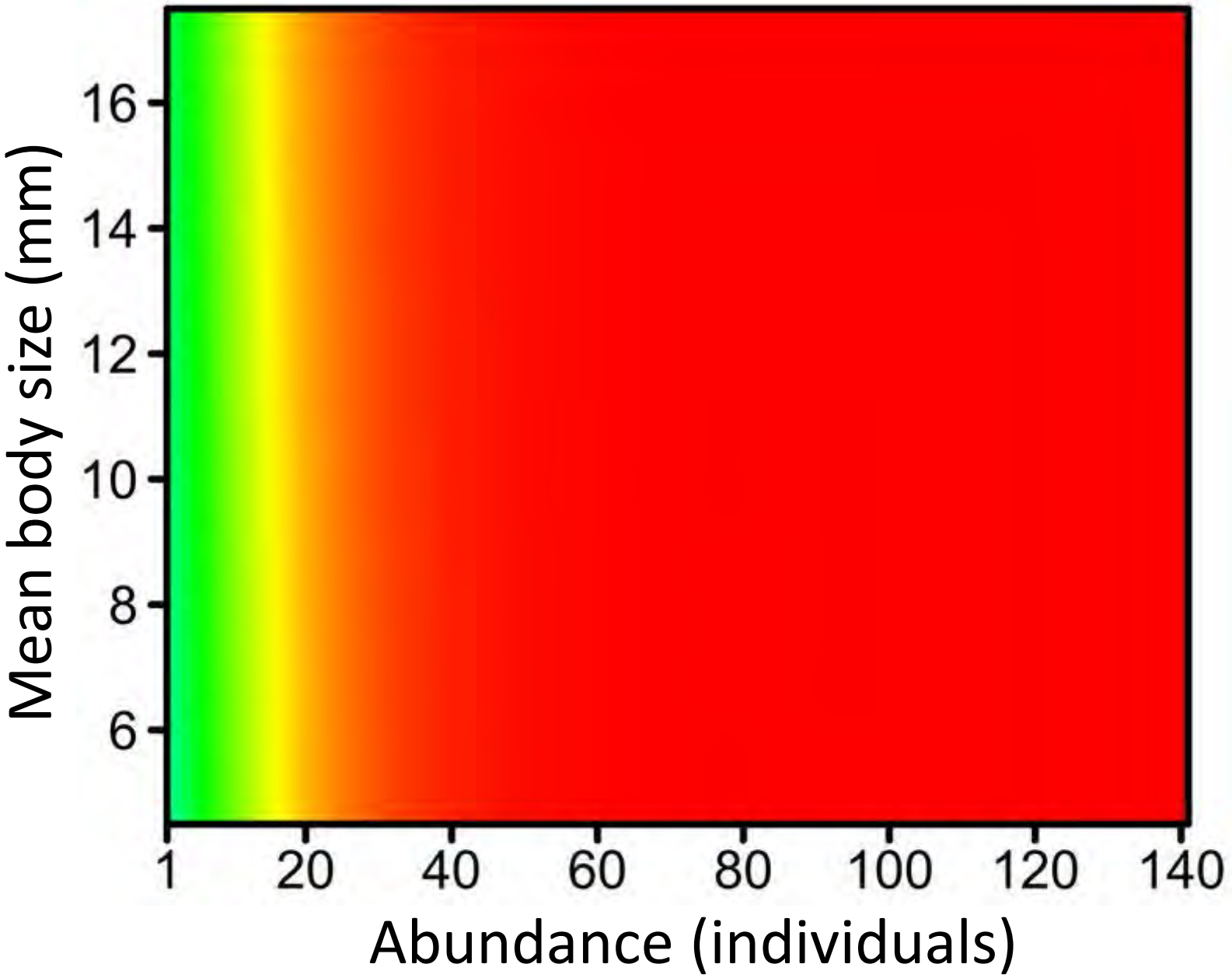
Detection success (0/1) ~ Abundance + Body size



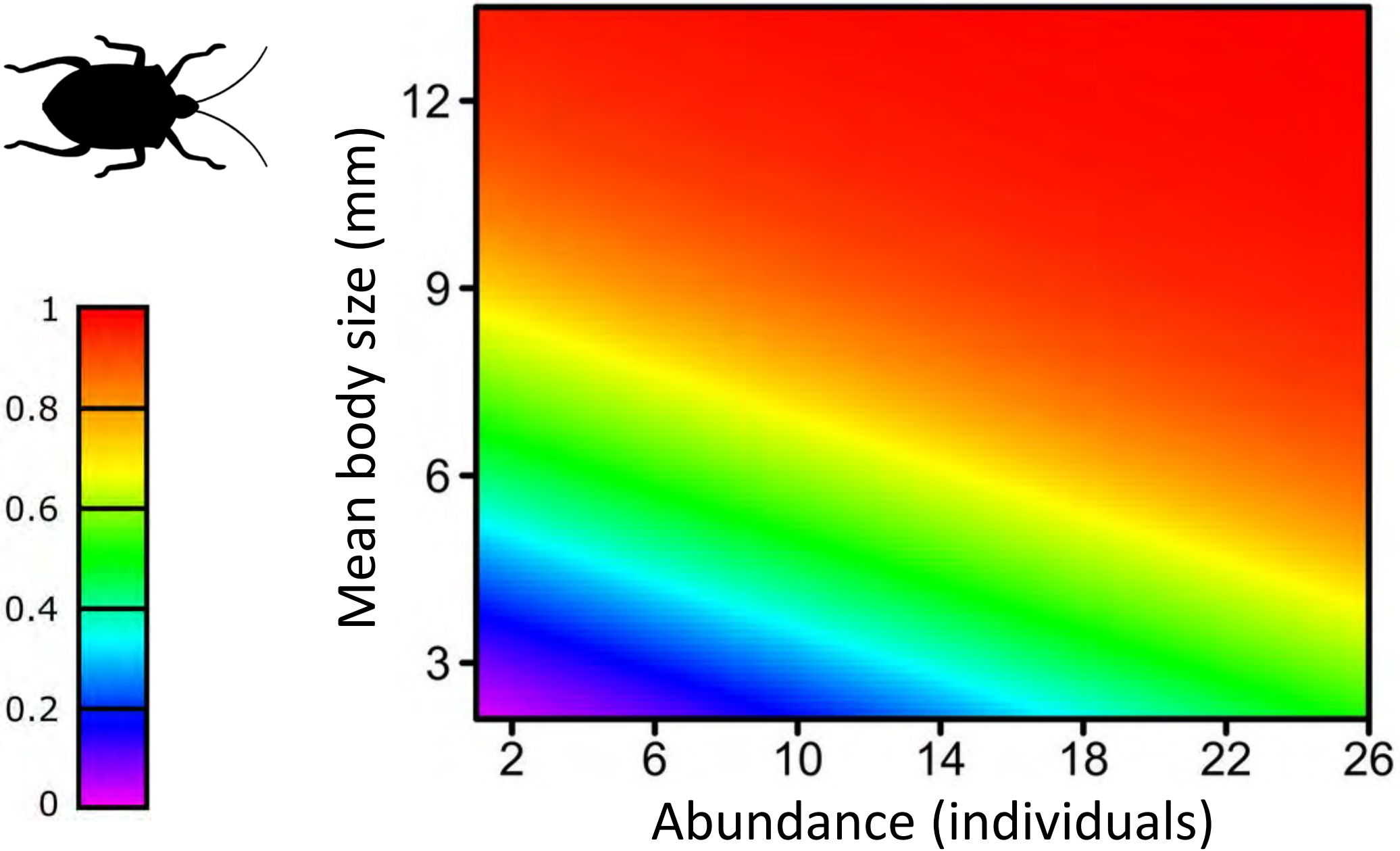


Detection success (0/1) ~ Abundance + Body size





Detection success (0/1) ~ Abundance + Body size



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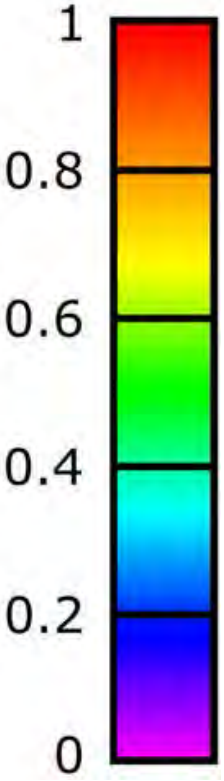
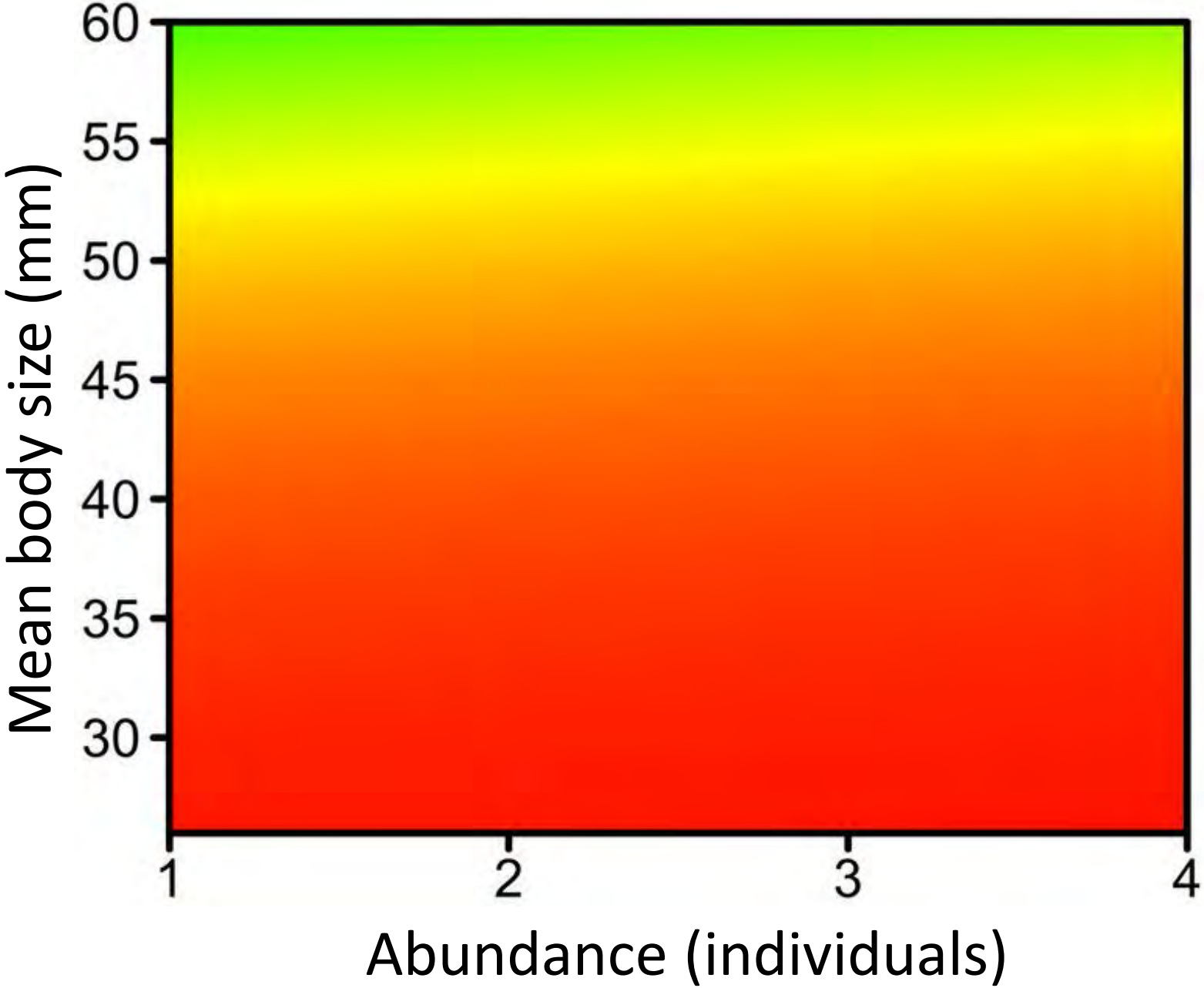
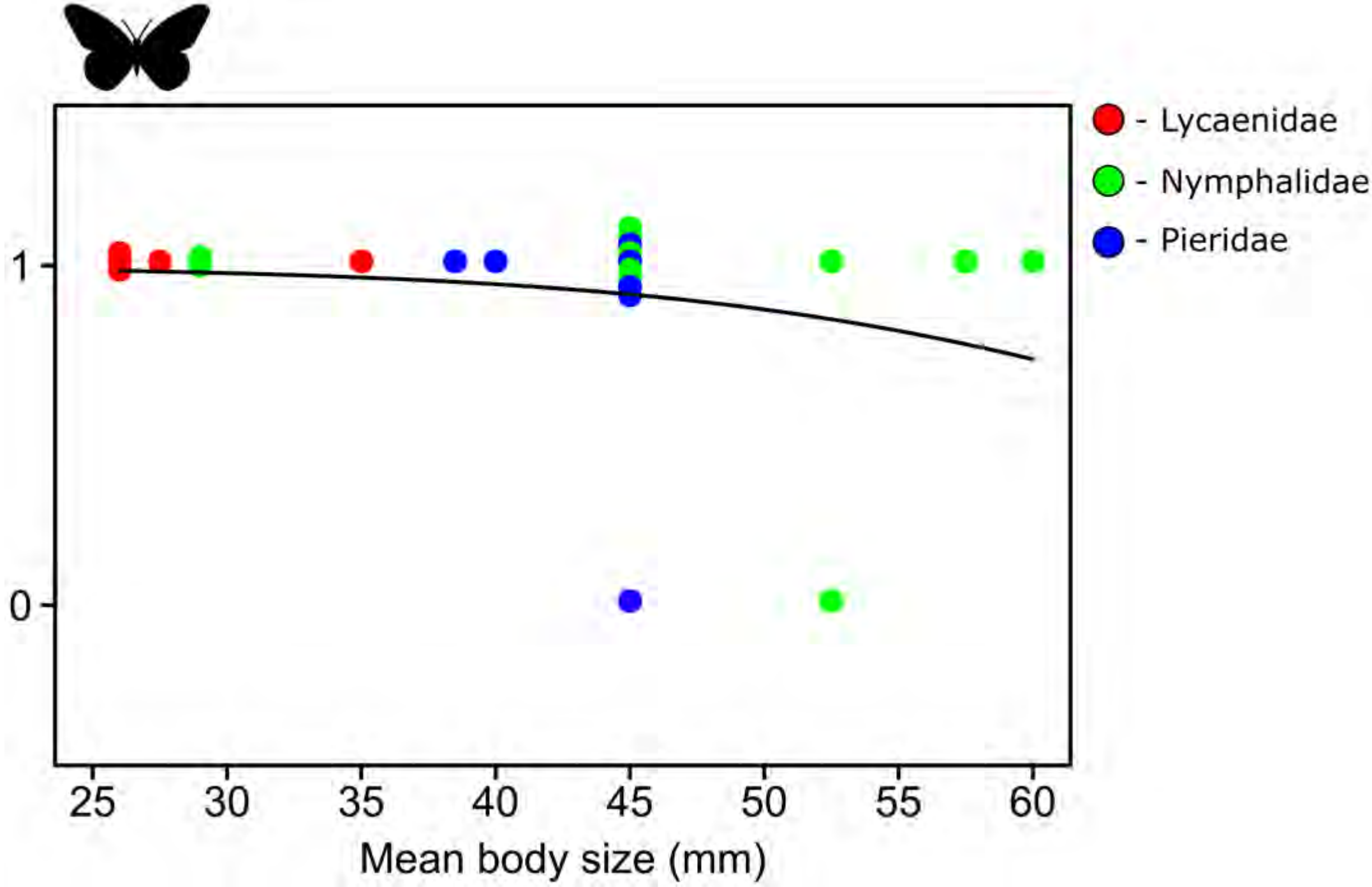





- Lycaenidae
- Nymphalidae
- Pieridae
1
0
25
30
35
40
45
50
55
60
Mean body size (mm)

Summary

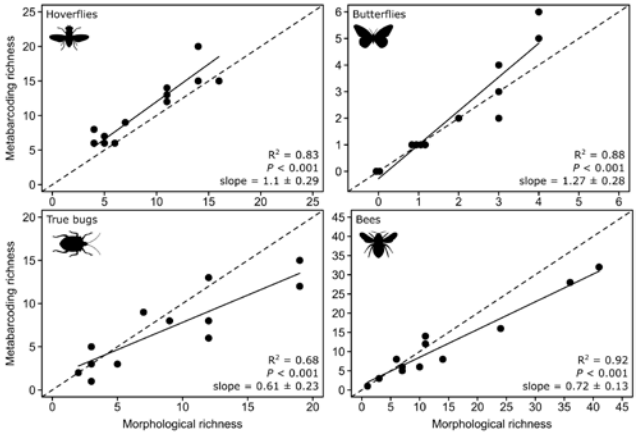
1. Richness

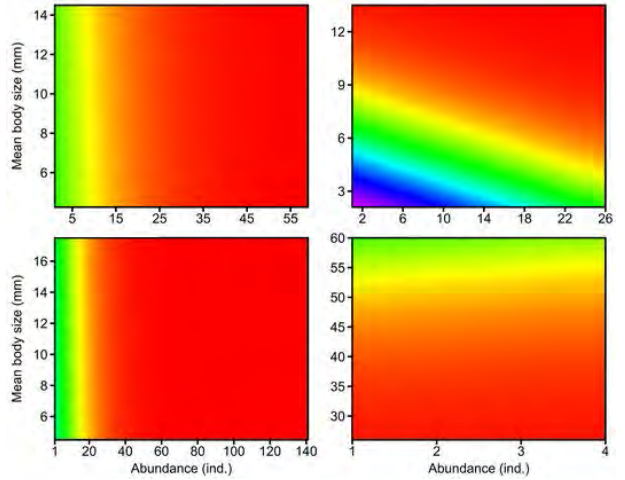
→ Missing species at higher diversity, driven by true bugs and bees

→ Can detect more hoverflies and butterflies

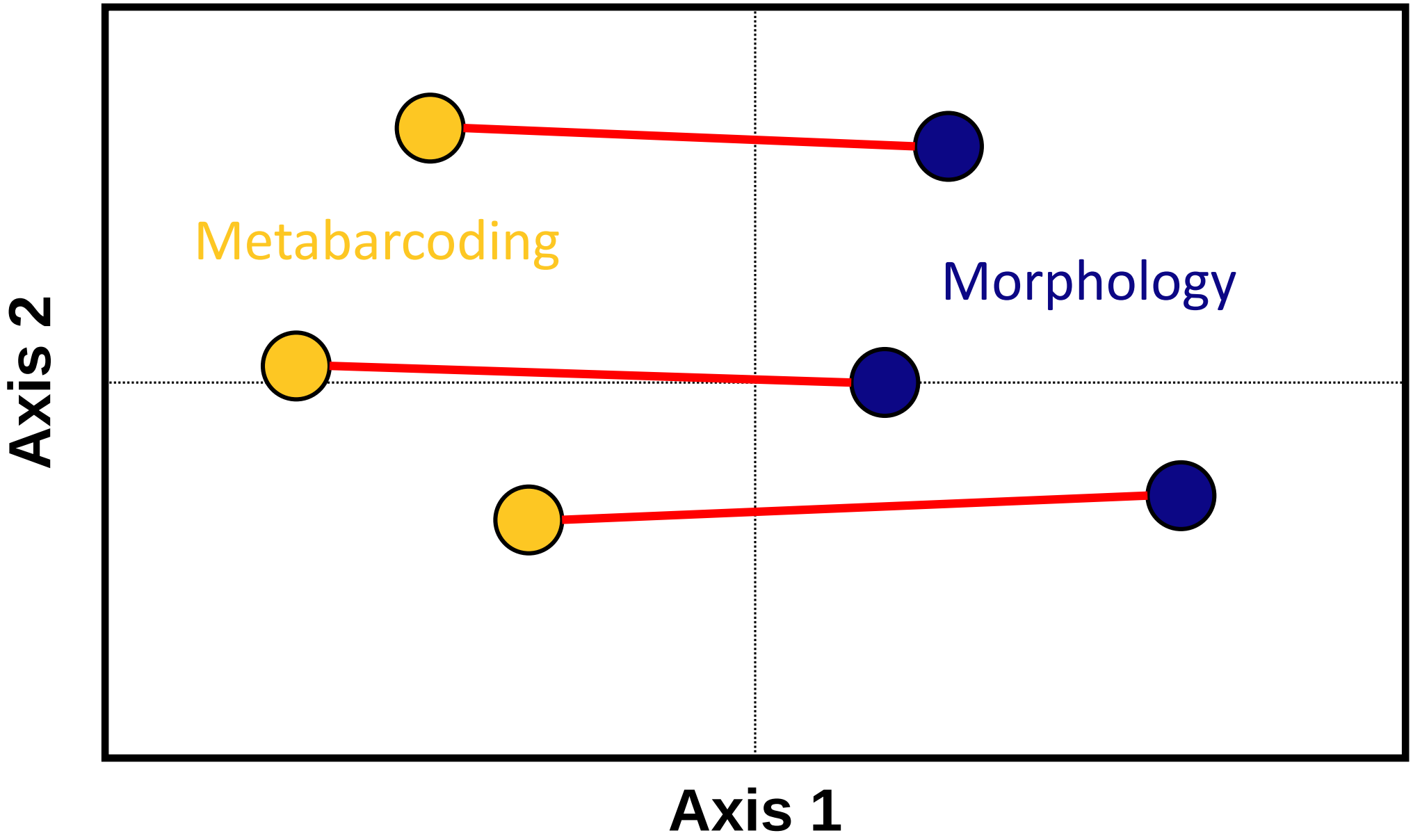
2. Species detection

→ Missing rarer hoverflies, bees, and true bugs, and smaller-bodied true bugs





Taxonomic composition



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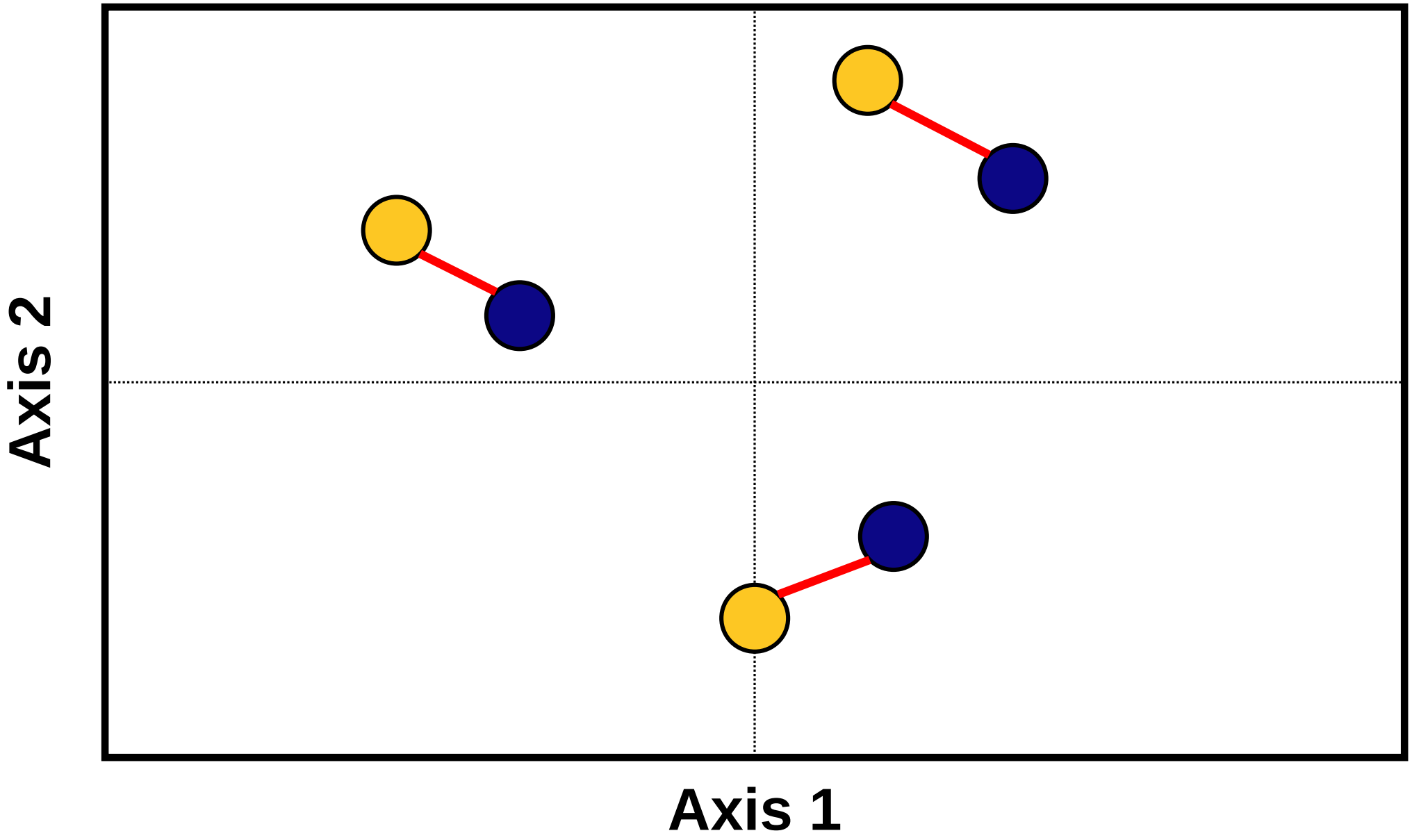
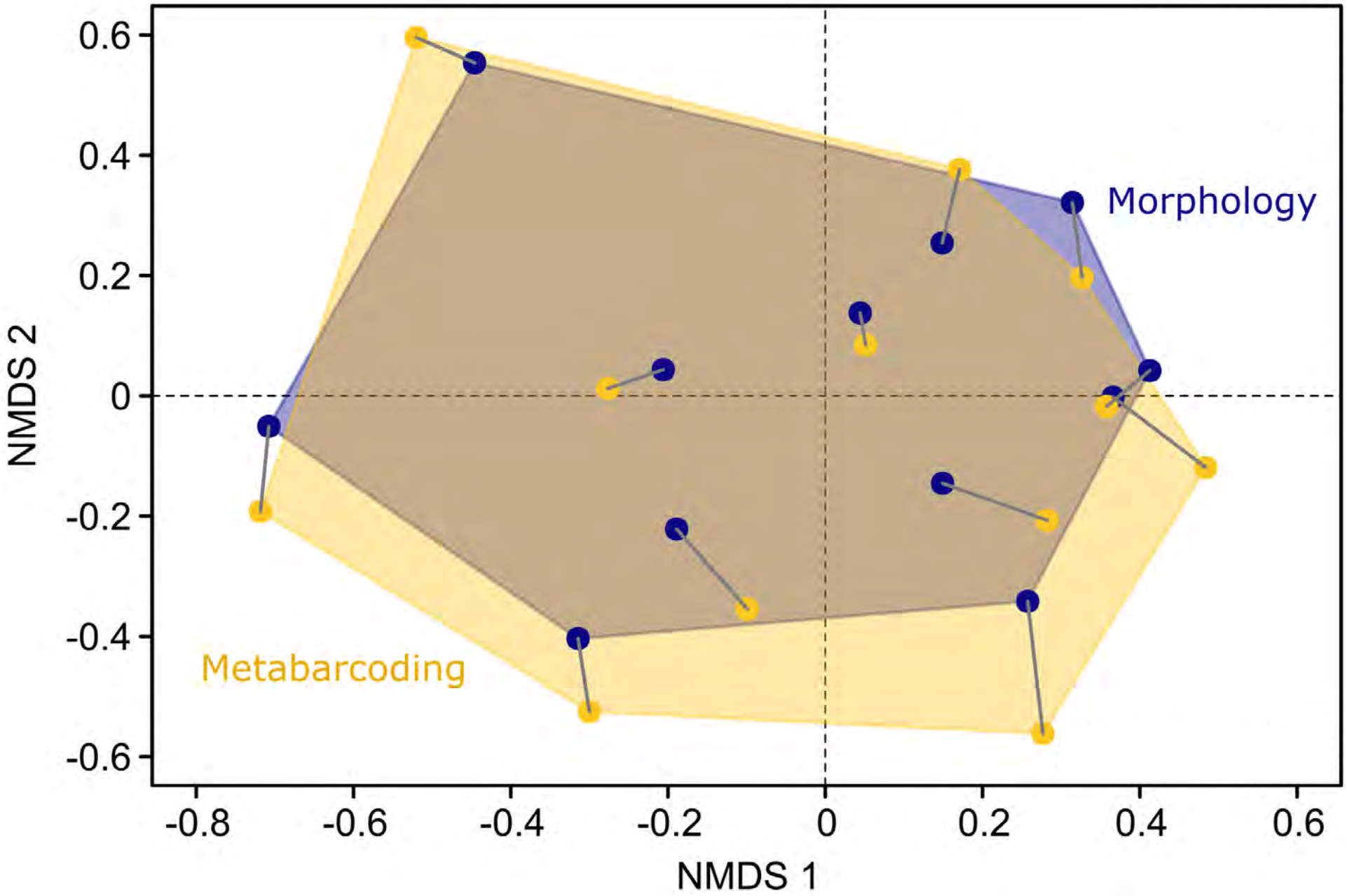
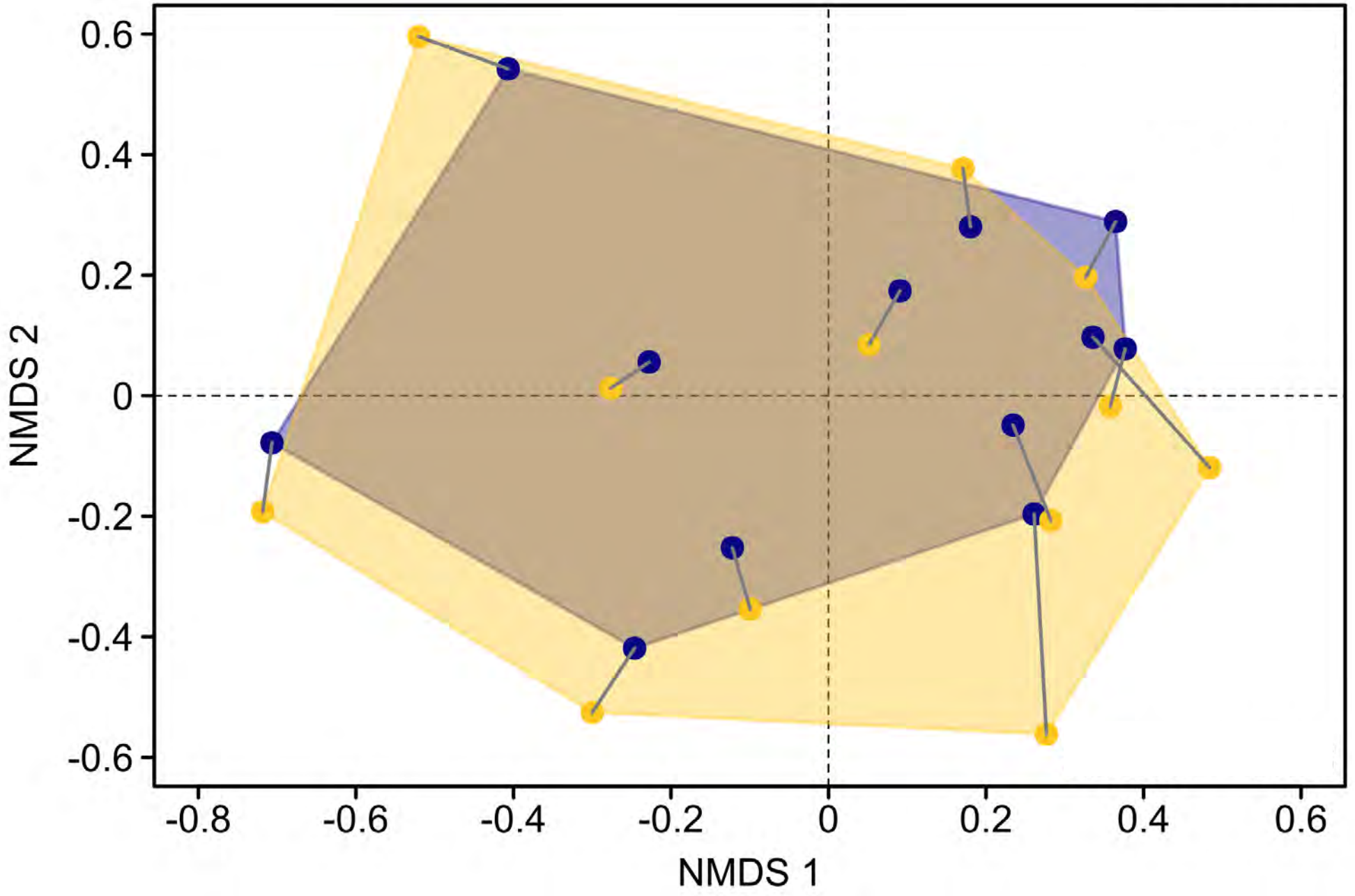


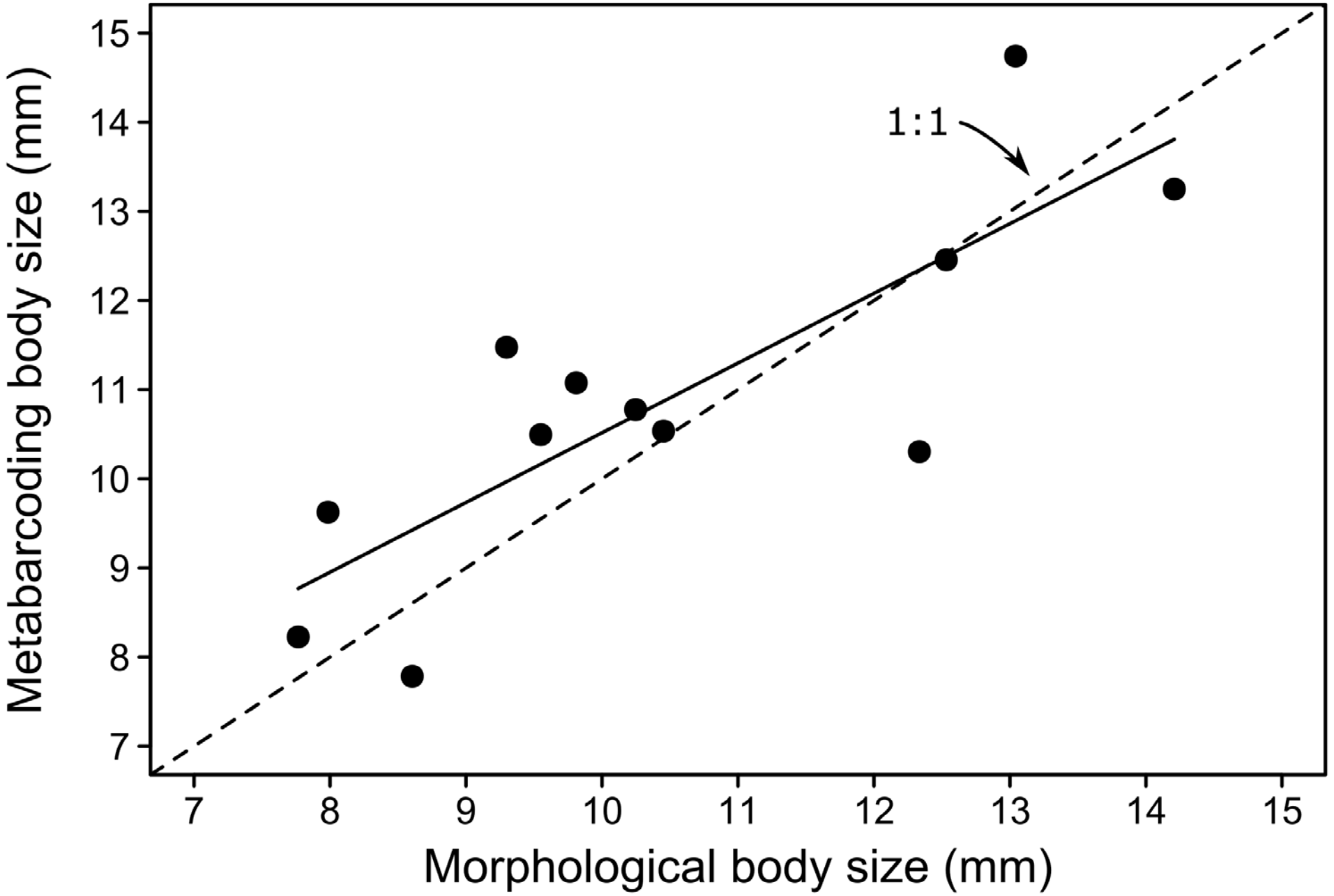
Taxonomic composition – Presence/absence



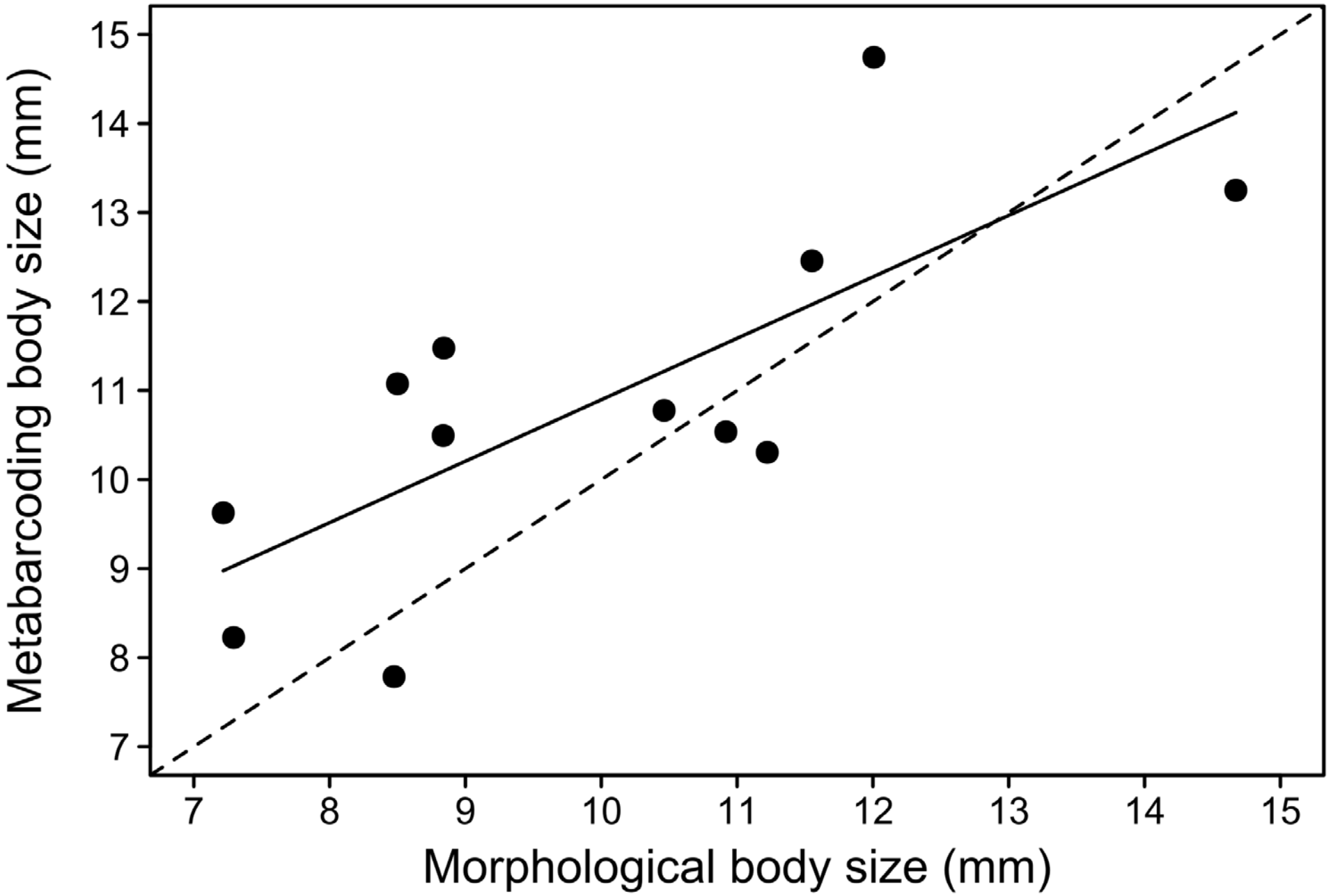
Taxonomic composition – Abundance weighted



Community body size – Presence/absence



Community body size – Abundance weighted



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→ Missing species at higher diversity, driven by true bugs and bees

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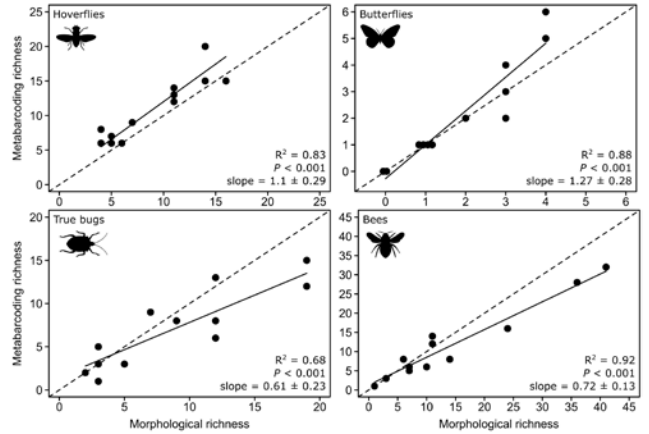
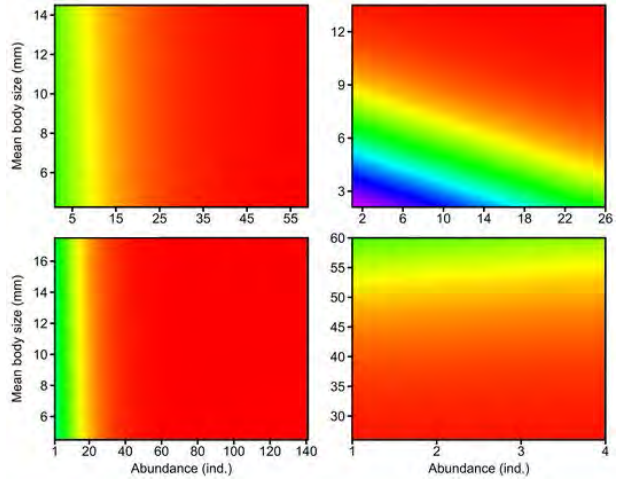


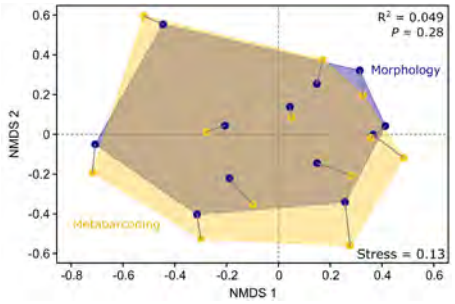
2. Species detection

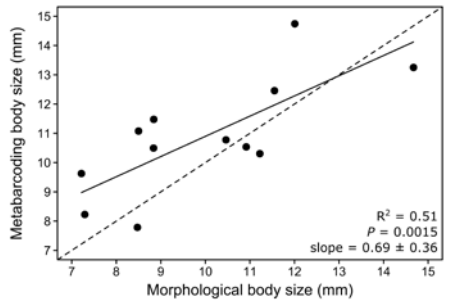
→ Missing rarer hoverflies, bees, and true bugs, and smaller-bodied true bugs



3. Composition

→ No strong differences in taxonomic composition, but traits may be affected by missing smaller-bodied species





Take-home messages

- Metabarcoding can provide an accurate overview of insect community differences in a way that is comparable to morphological identification

→ for potentially less time and cost

→ can better resolve some taxonomic groups to species level

- However, metabarcoding can miss some low-abundance and smaller-bodied species

→ These species can provide key functions

→ Can somewhat bias estimates of richness and trait composition

Questions?

Insect Conservation and Diversity
Royal Entomological Society

DNA metabarcoding and morphological identification reveal similar richness, taxonomic composition and body size patterns among flying insect communities

Nicole Remmel[1,2] | Dominik Buchner[2] | Julian Enss[2,3] | Viktor Hartung[4] | Florian Leese[2,3] | Ellen A. R. Welti[5] | James S. Sinclair[1] | Peter Haase[1,2,3]

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