Designing

sampling campaigns for long-term soil biodiversity monitoring via metabarcoding
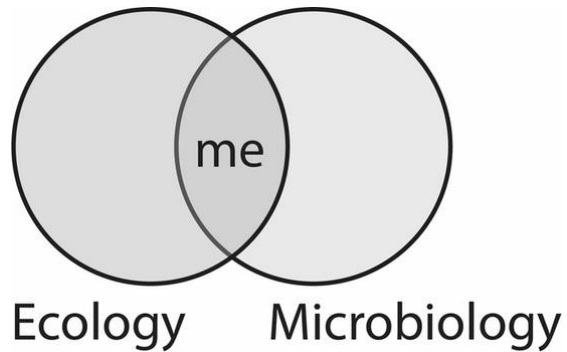
Stephanie Jurburg

s.d.jurburg@gmail.com

I am a soil microbial ecologist

- **Uncovering invisible ecology**
- **Tiny solutions for big problems.**
- **The overlooked microbial zoo**
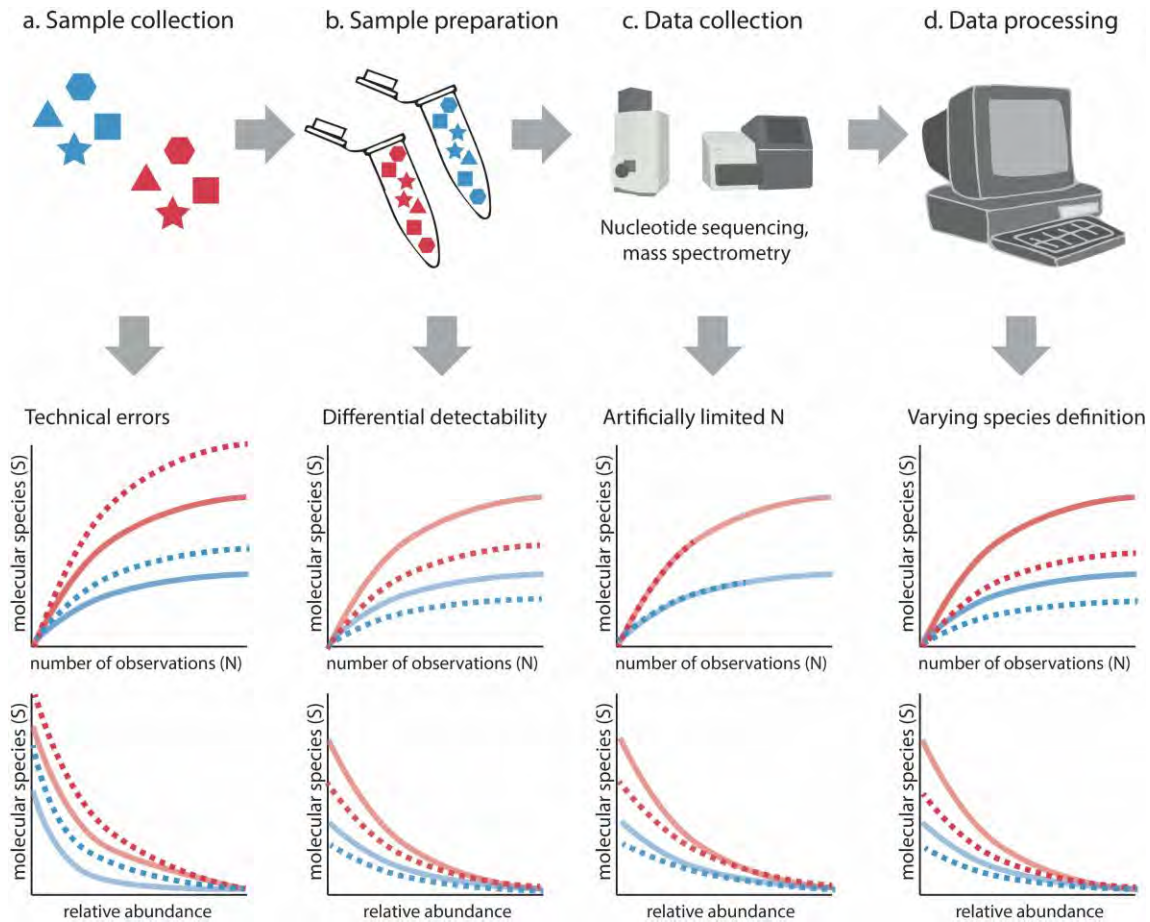

Ecology Microbiology

me

I am particularly interested in improving how we do ecology with *omics* data (especially metabarcoding)
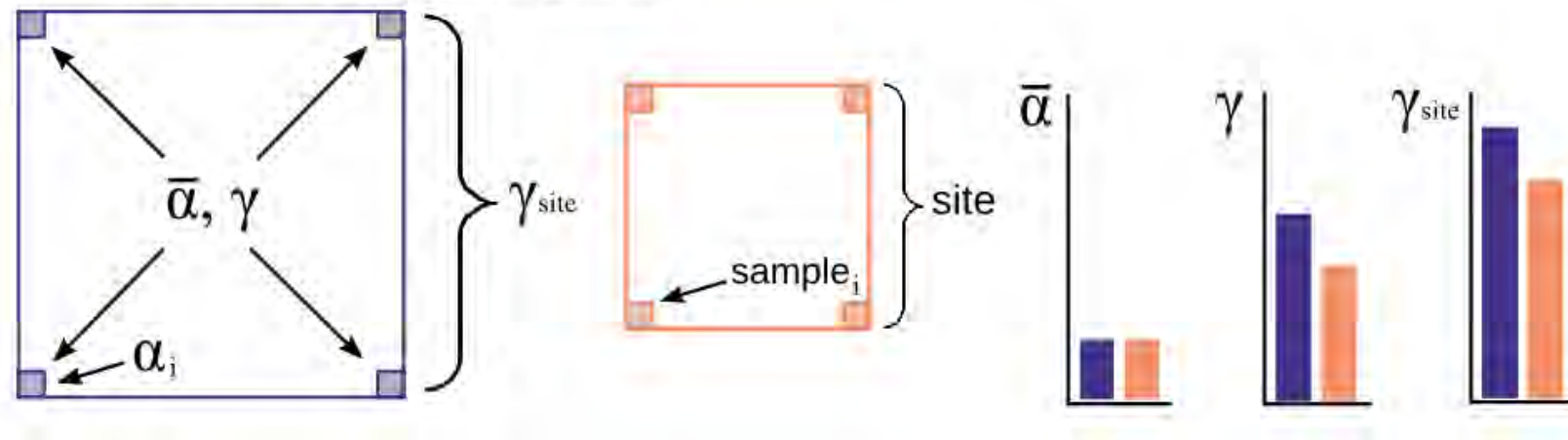
A more complete view of the belowground zoo

A better understanding of microbial interactions requires targeted sampling designs
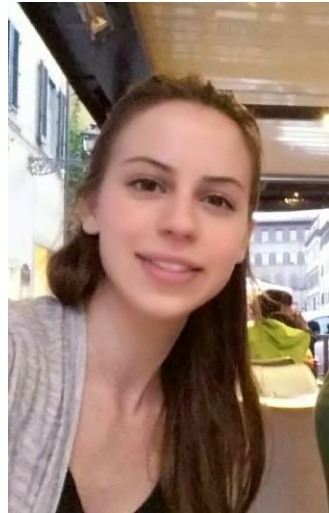

a constant site shape, varying area

Spatial assembly in soil microbial communities across scales, land cover, and land use
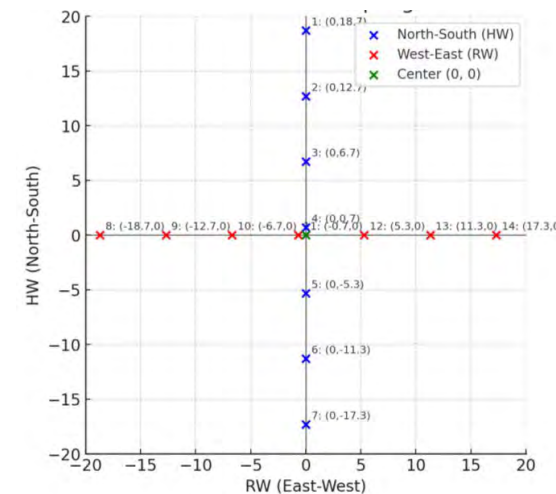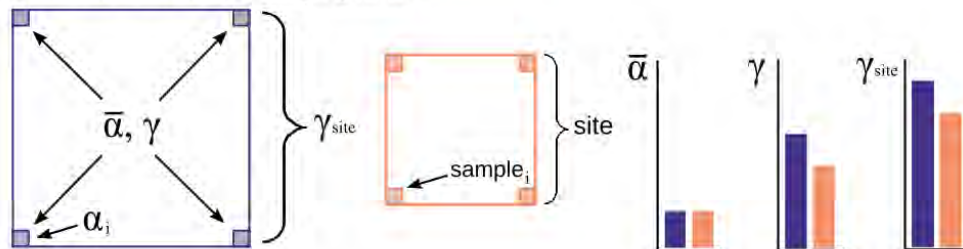

Ma. Jose Alvarez

Maria Kostakou

Niklas Neisse

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VIP plot

To what extent do the composite samples capture the diversity of individual soil cores?
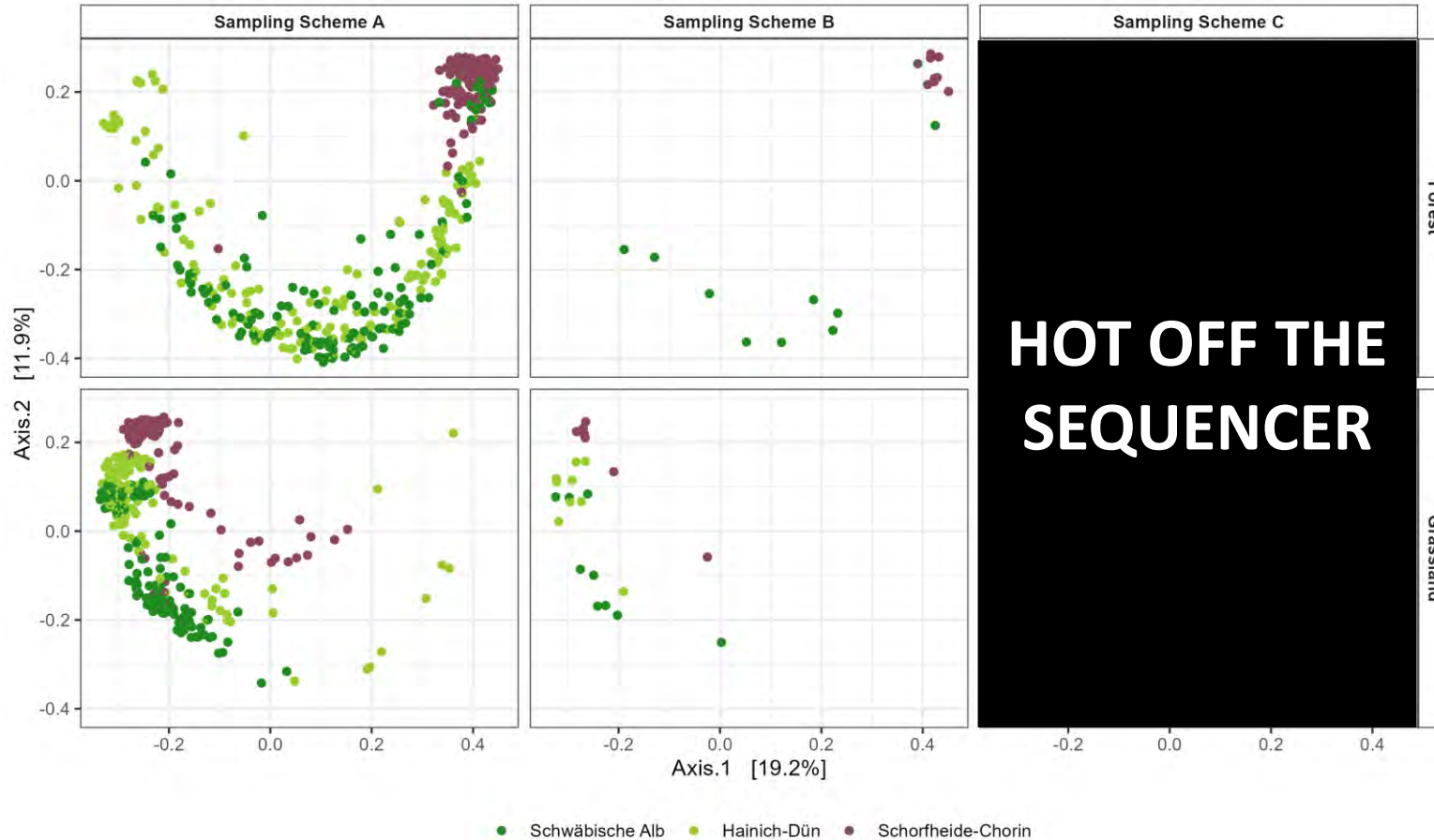

- Large scale sampling
- For each plot, 14 individual samples in a transect and 1 homogenized sample (~800 samples)
- DNA extraction
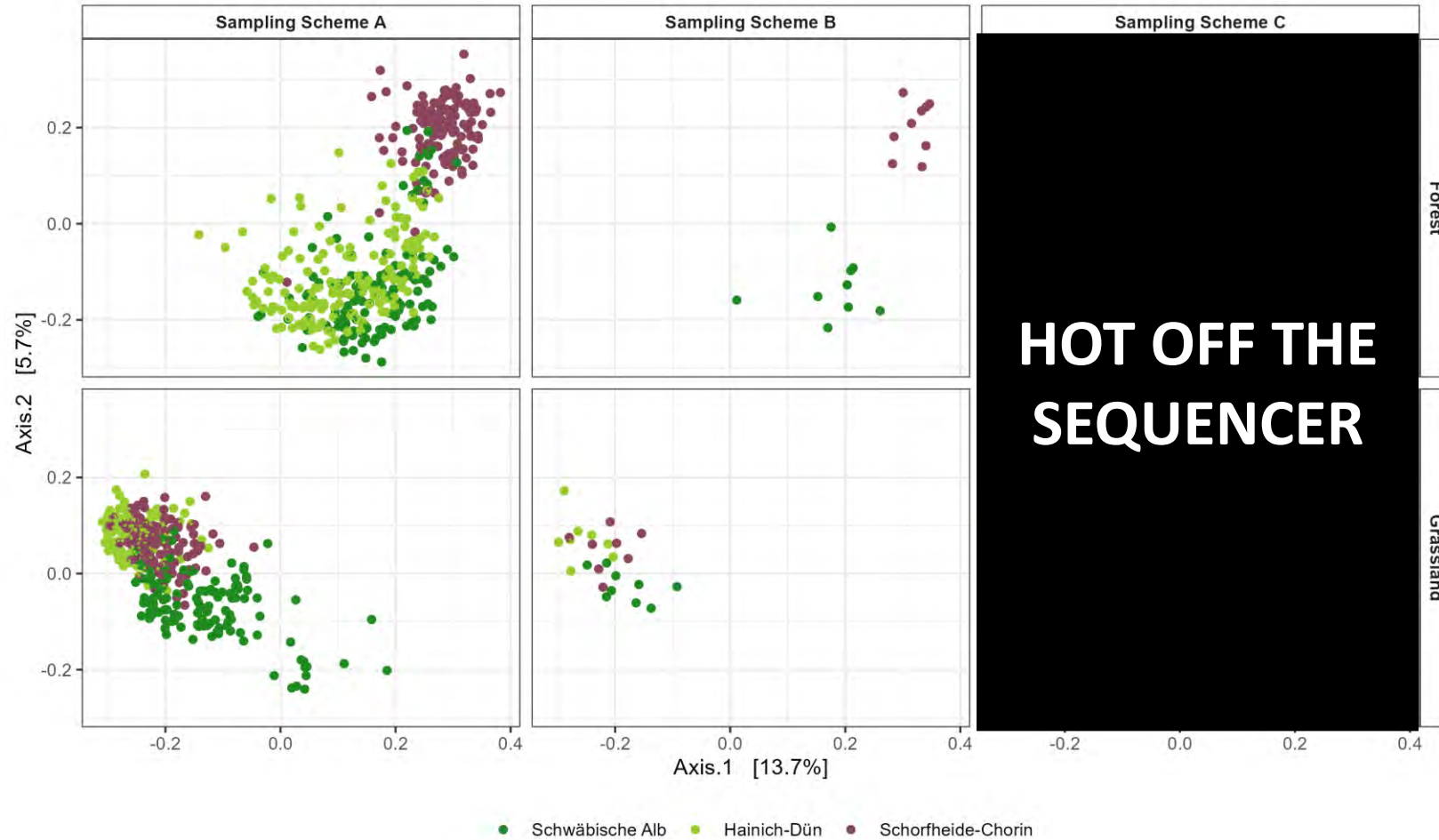- **16S rRNA,** 18S rRNA gene, ITS sequencing

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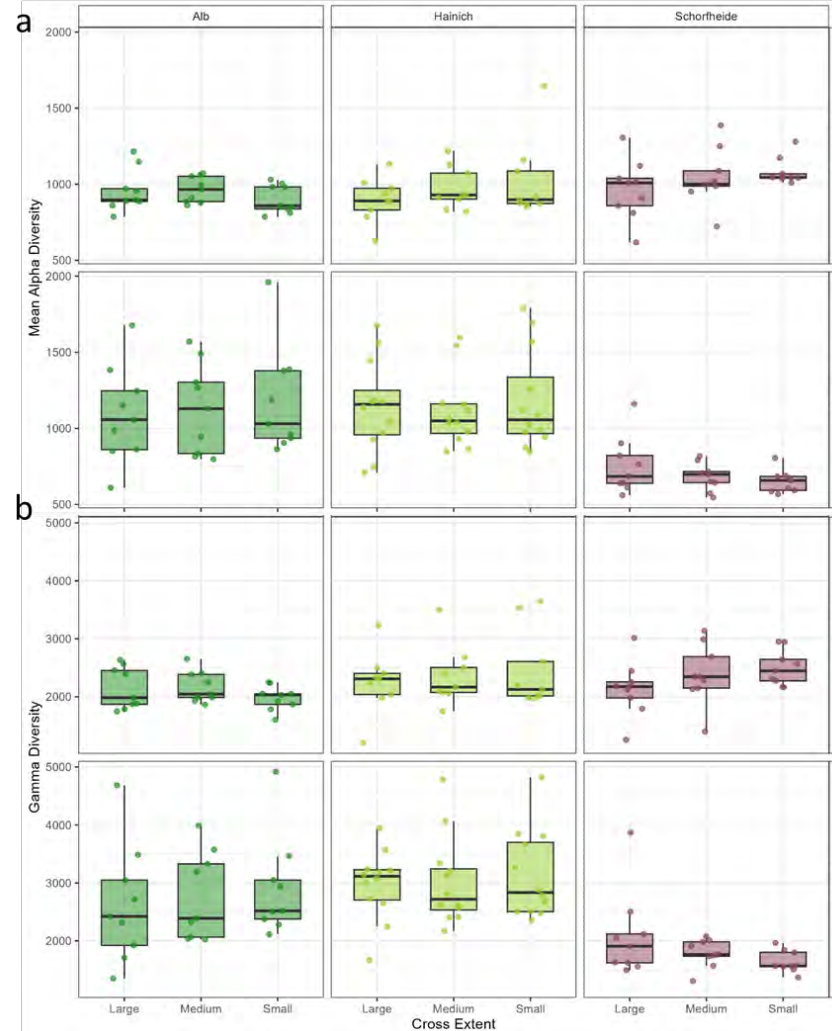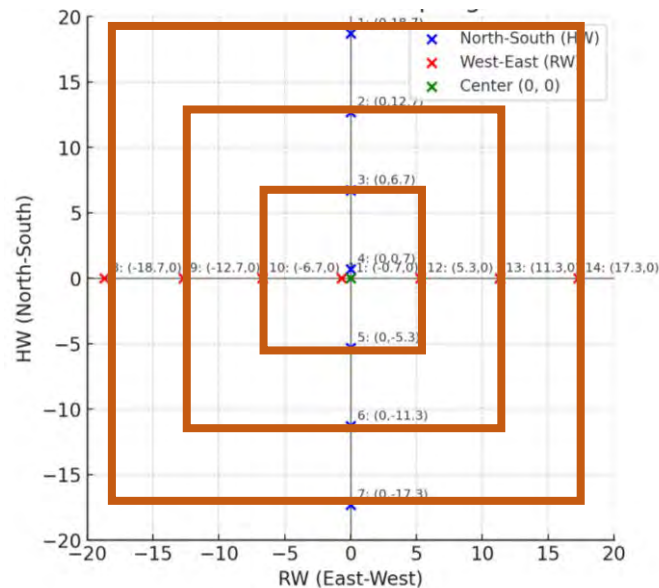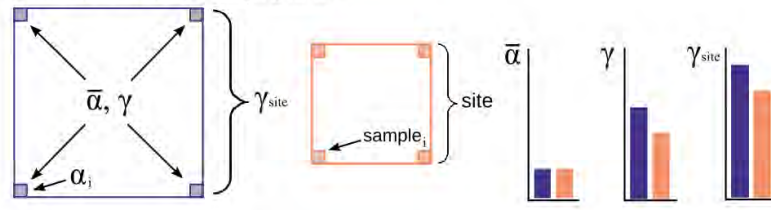

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Jurburg, Keil, Singh, Chase. 2021, Molecular Ecology Resources

Does the diversity captured from different sample extents differ?

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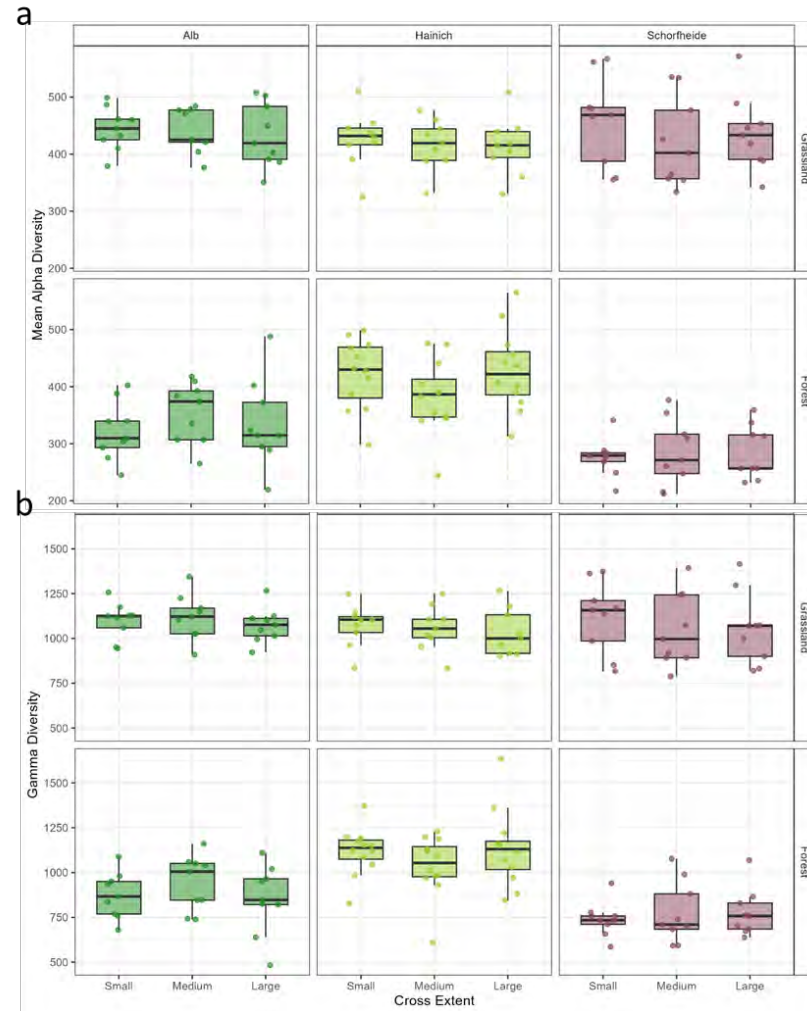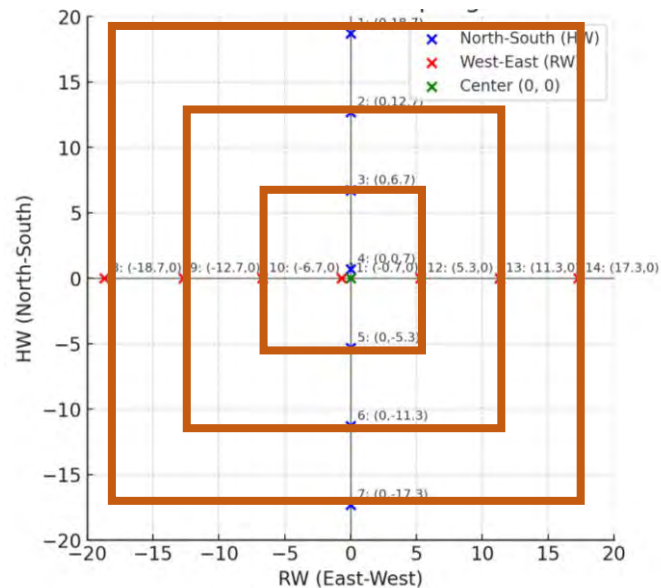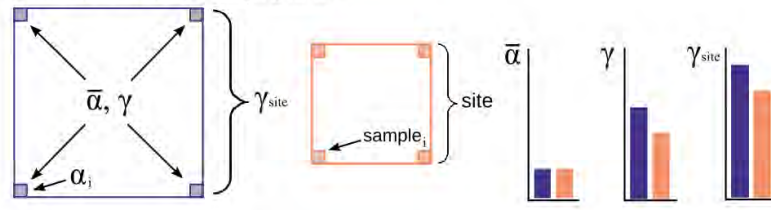
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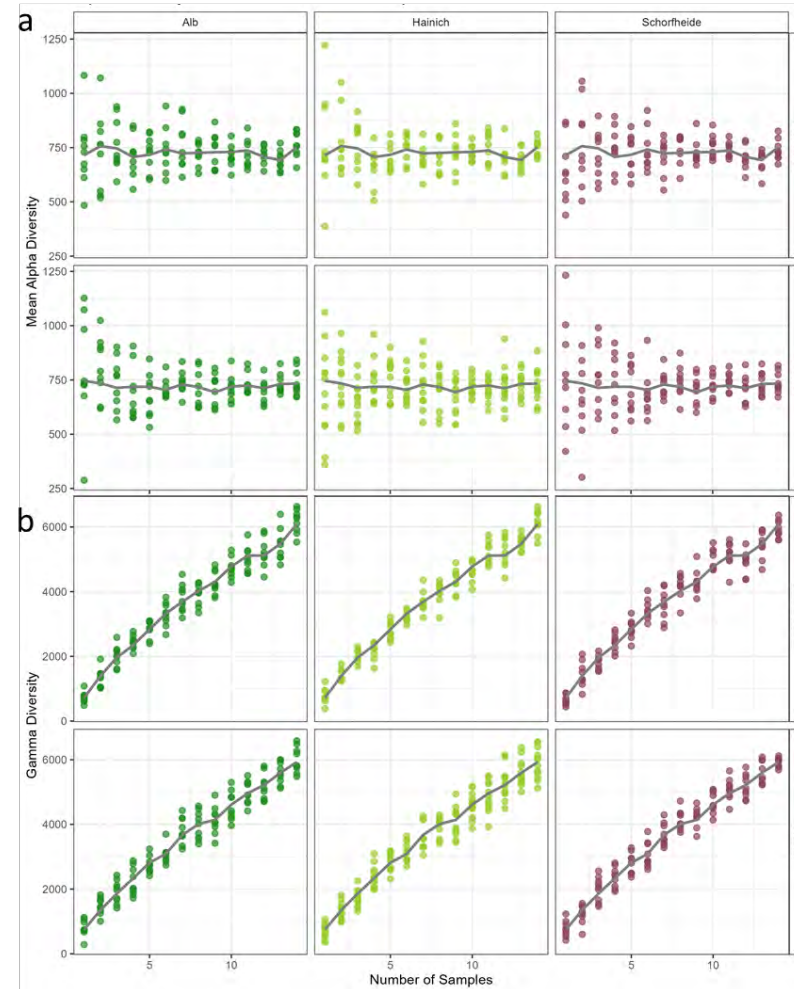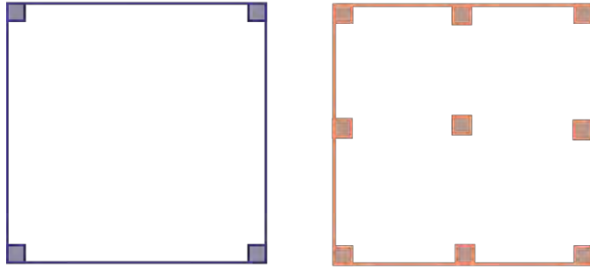

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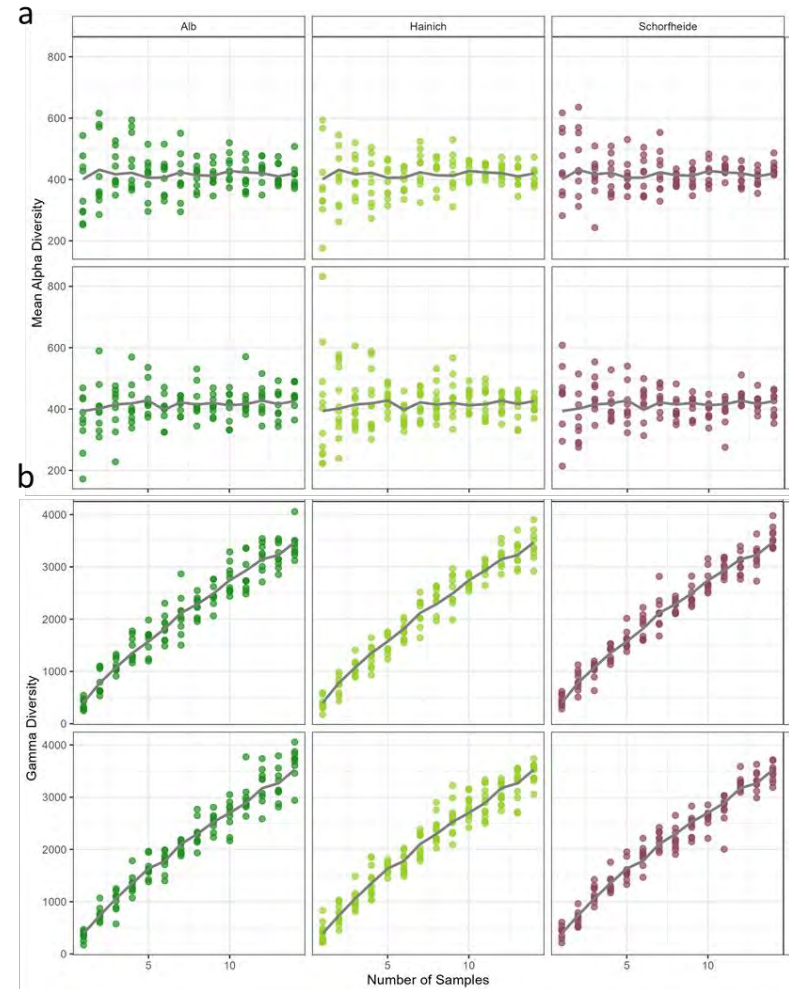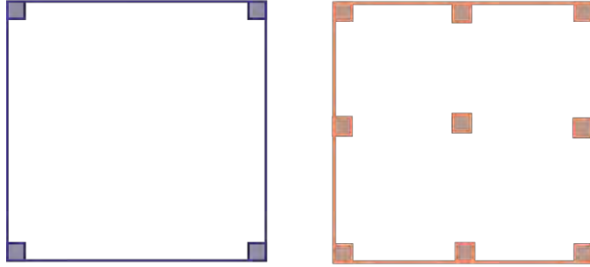
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*Jurburg, Keil, Singh, Chase. 2021, Molecular Ecology Resources*

- Composite samples capture eukaryotic diversity to a greater extent than prokaryotic diversity
- Microbial communities are unaffected by sample extent
- Diversity estimates are *strongly* affected by the number of samples in a composite

Tree-nematode interactions in oak phytometers under changing climate
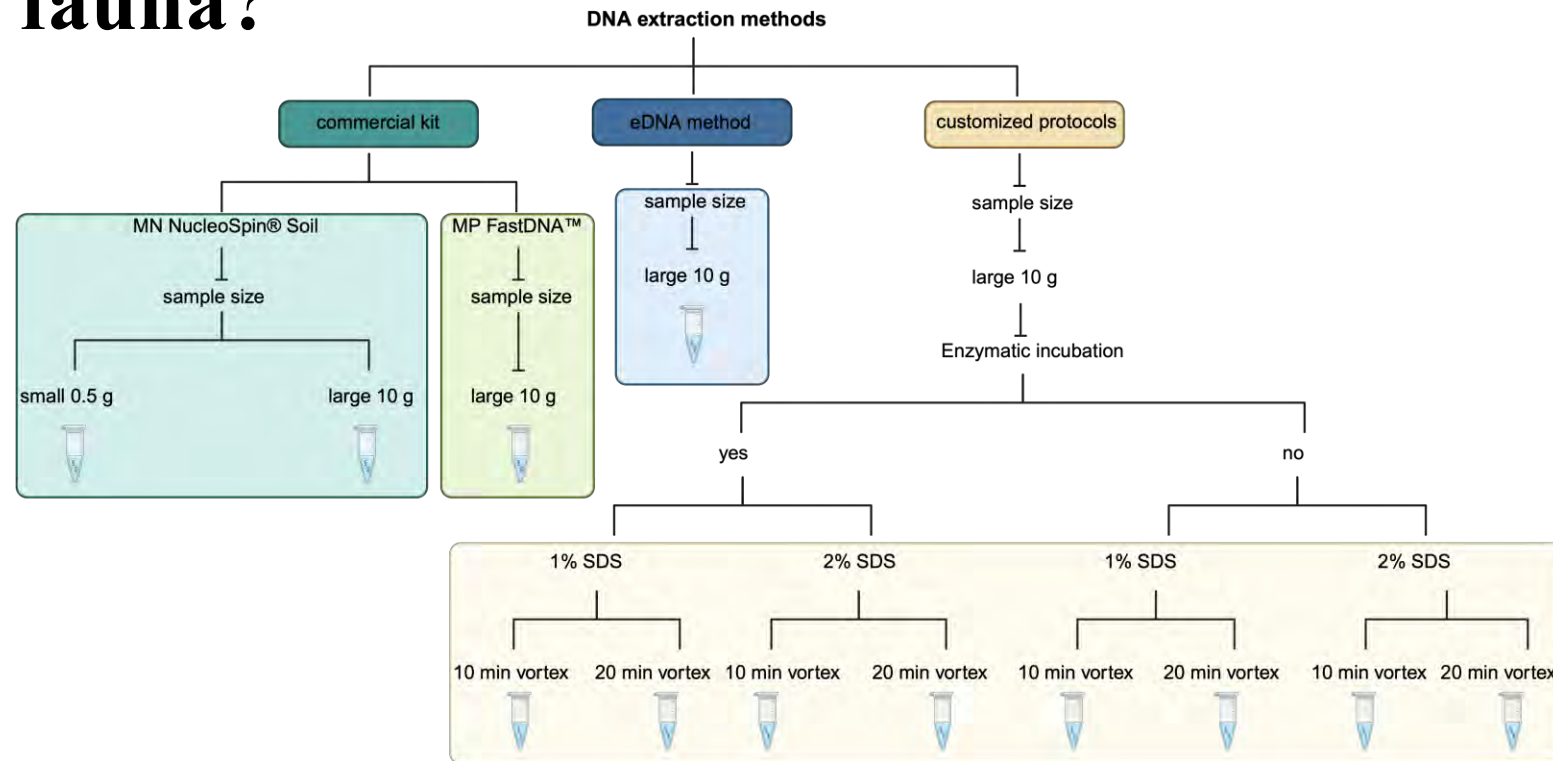
c varying size of samples
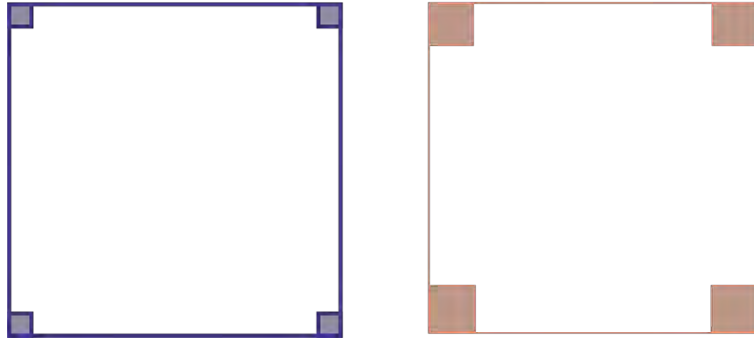
Lu Wang

- Validation and benchmarking of metabarcoding technique for soil nematodes
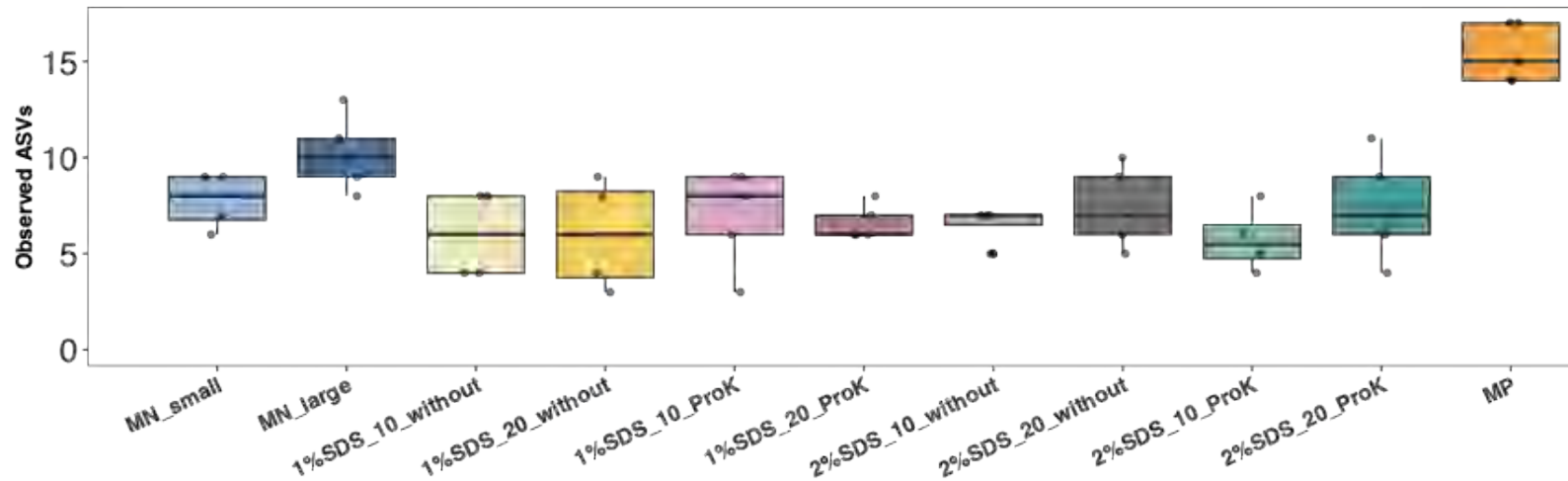
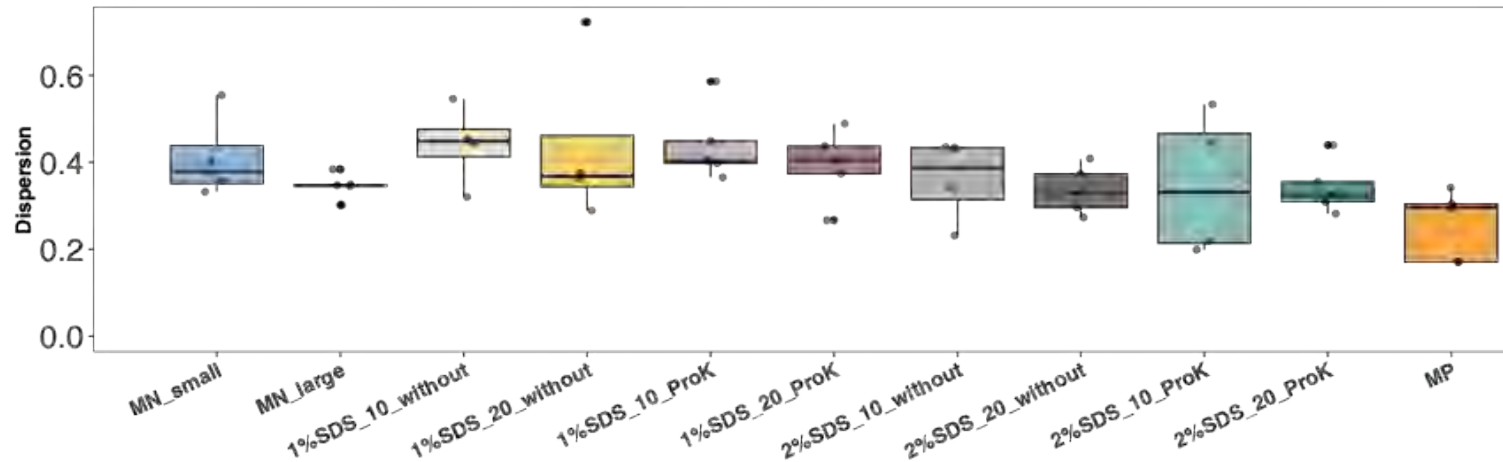# To what extent can we use 'conventional' DNA extraction methods to characterize soil fauna?

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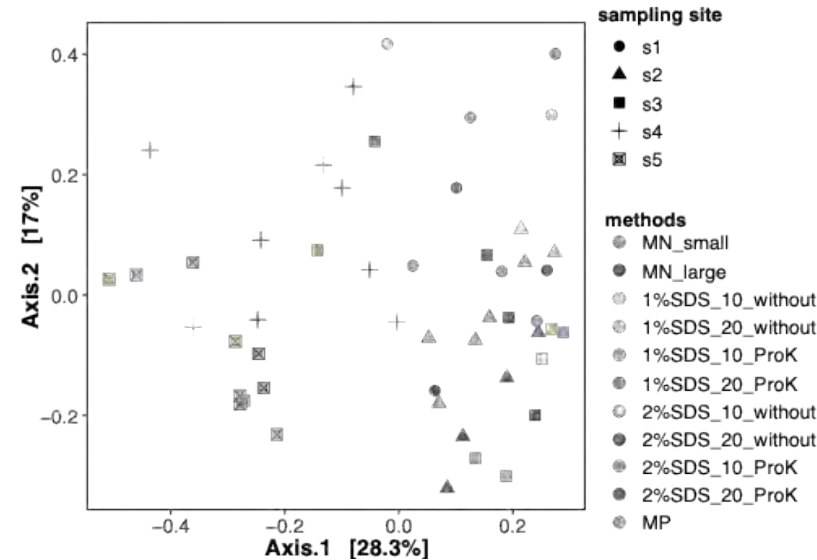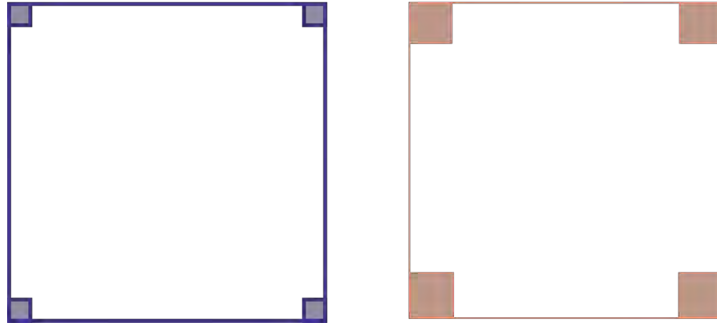
Which DNA extraction method fares best?

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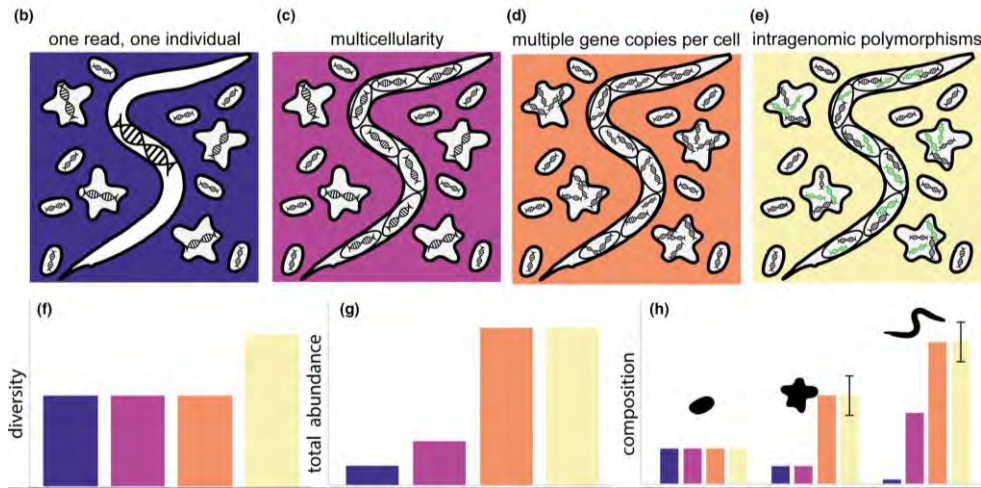
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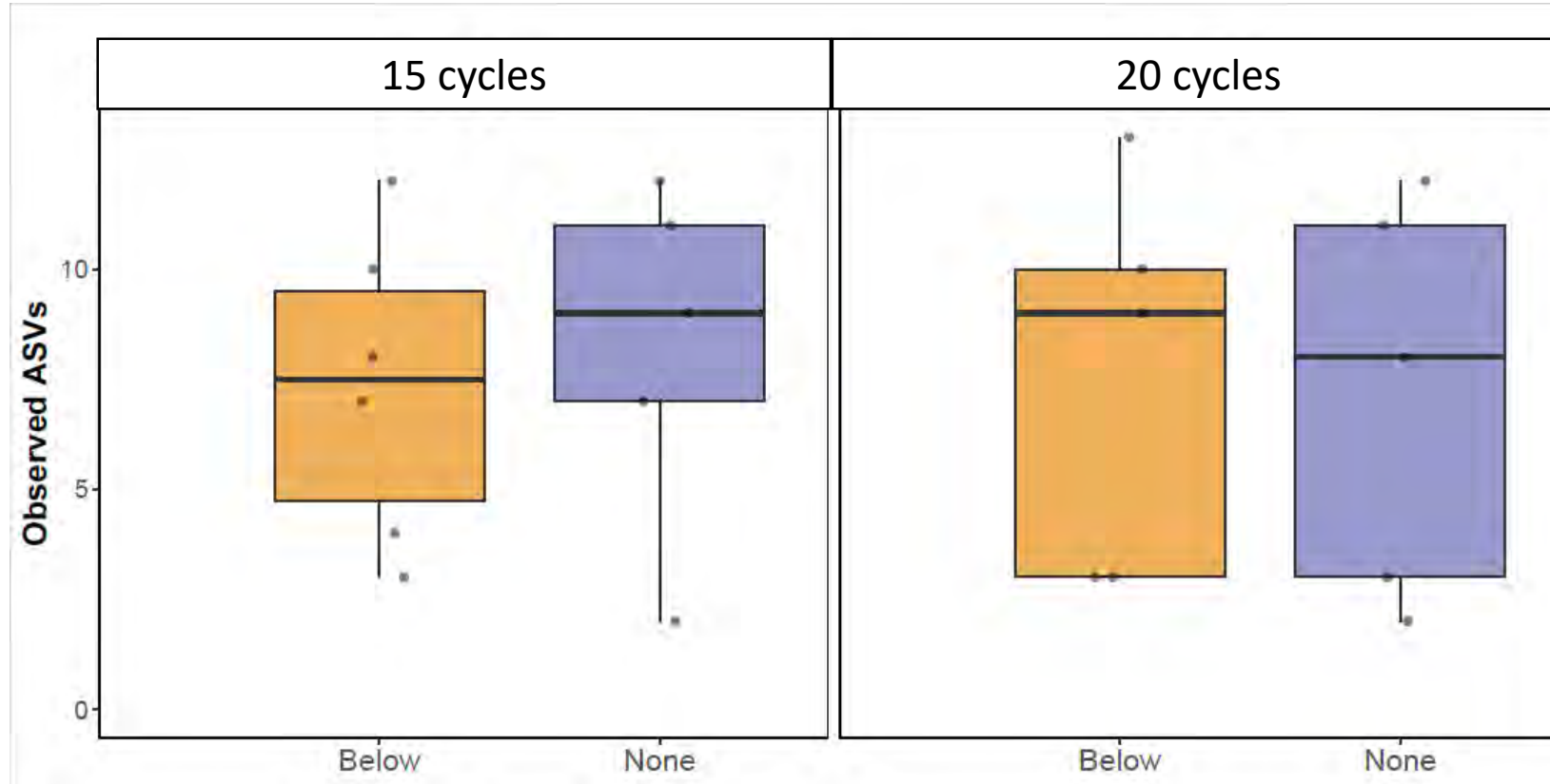# Tree-nematode interactions in oak phytometers under changing climate

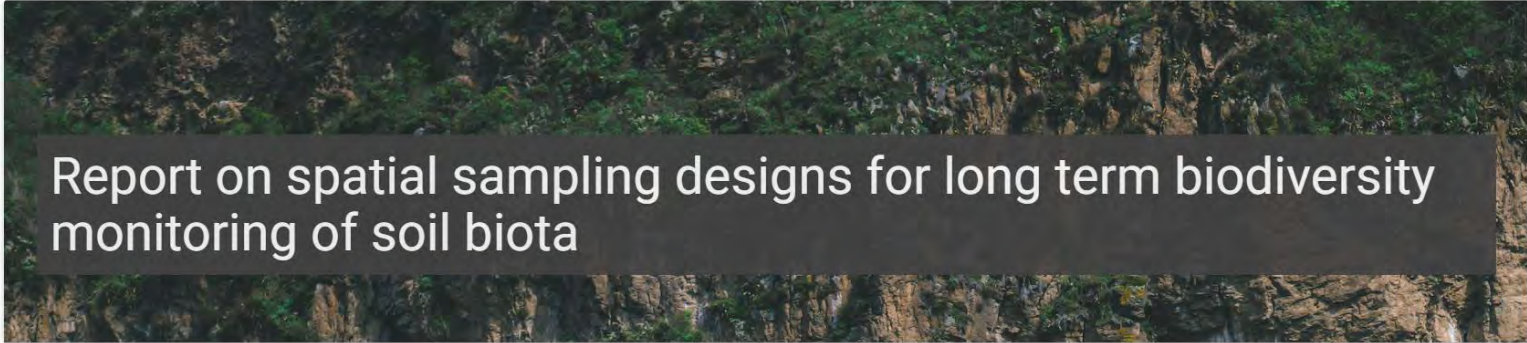- Validation and benchmarking of metabarcoding technique for soil nematodes

- Alpha diversity is affected by DNA extraction protocol and the amount of sample included.
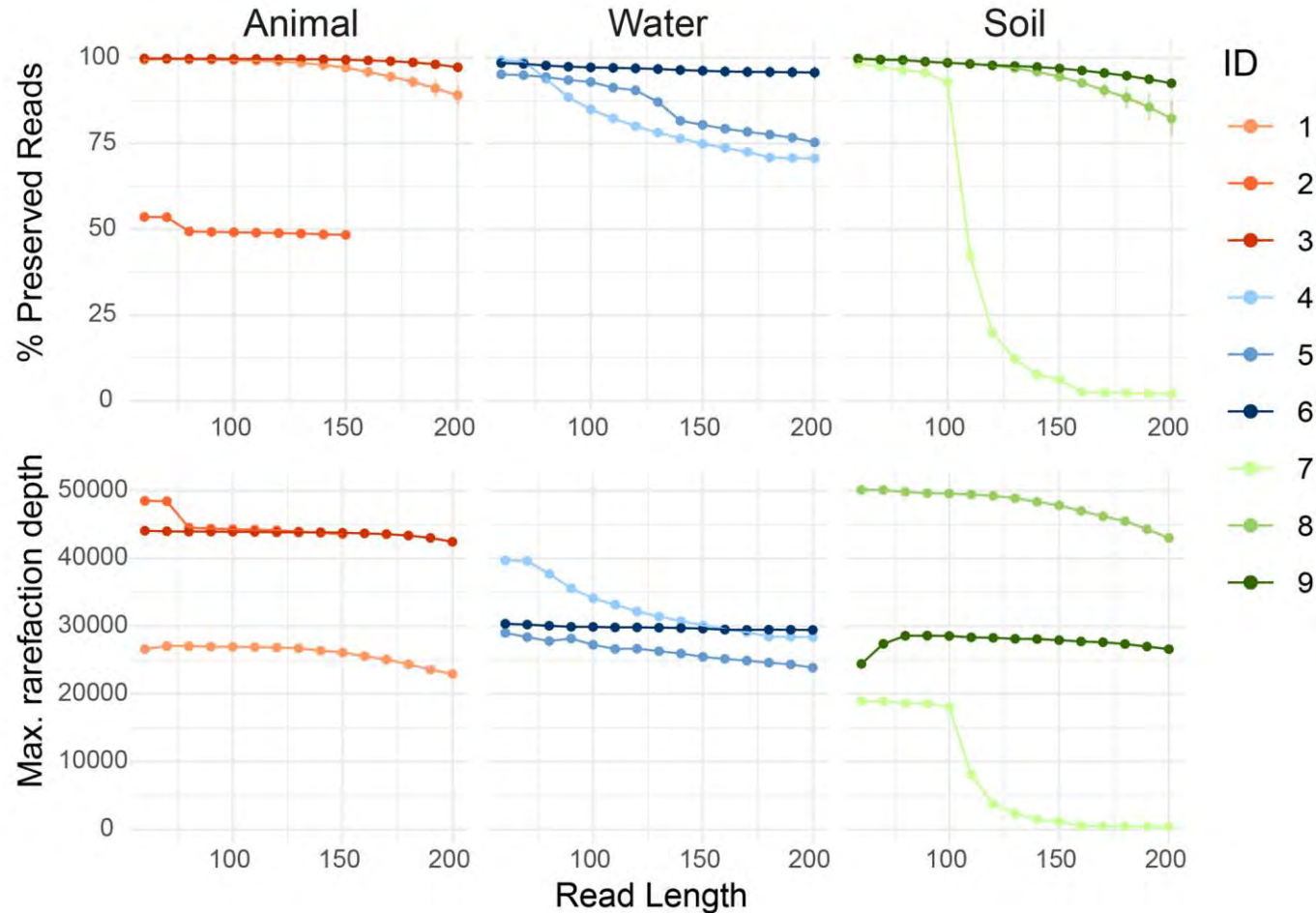- Community variance is consistent across DNA extraction methods

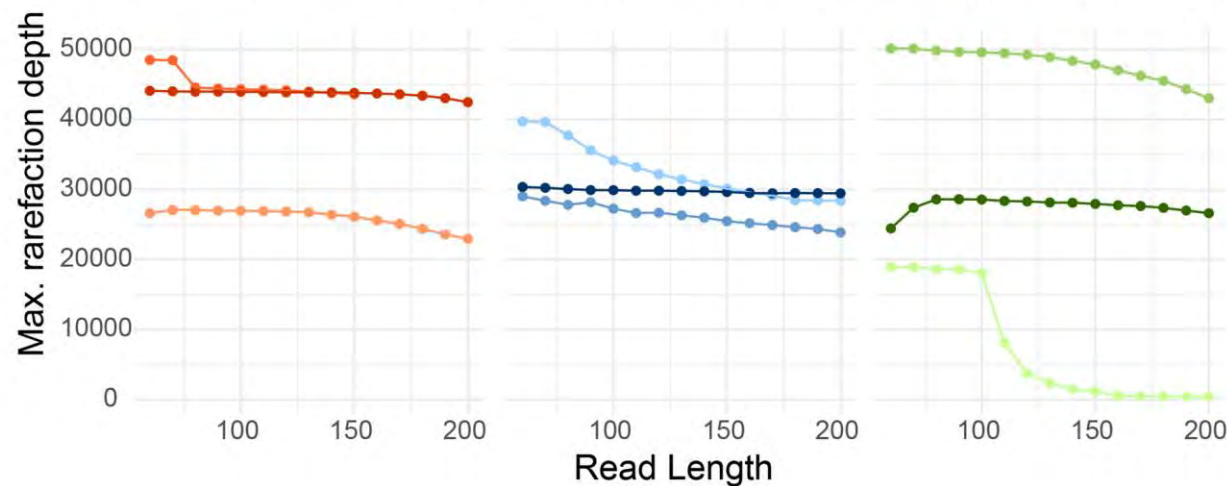Report on spatial sampling designs for long term biodiversity monitoring of soil biota

Empirical tests on the effect of bioinformatics processing on diversity detection

- Reanalysis of 9 16S rRNA gene datasets from aquatic, soil, and animal-associated microbiomes
- Processing at a range of read lengths (50-200 bp)
- Measurement of various diversity parameters

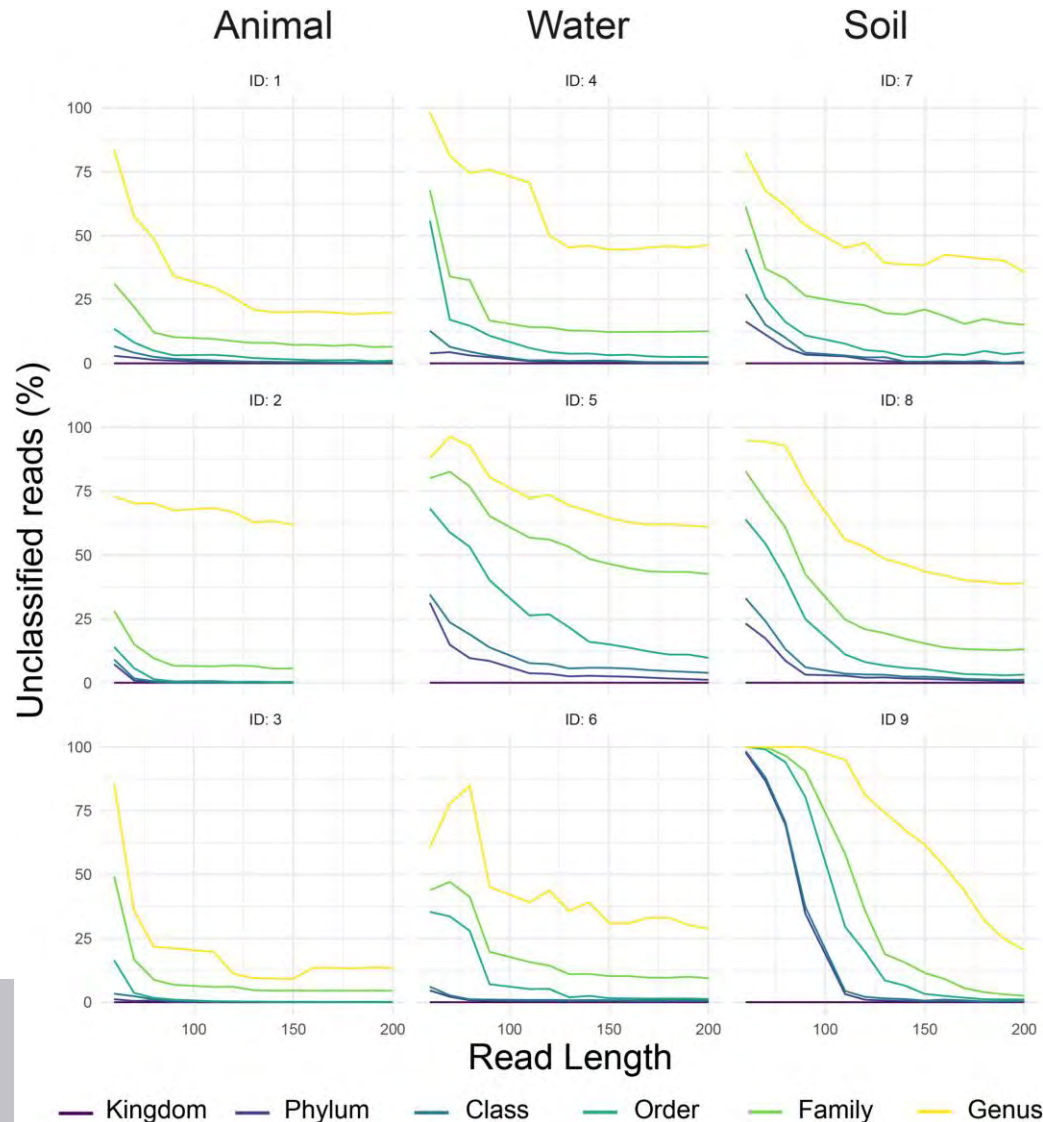# Empirical tests on the effect of bioinformatics processing on diversity detection

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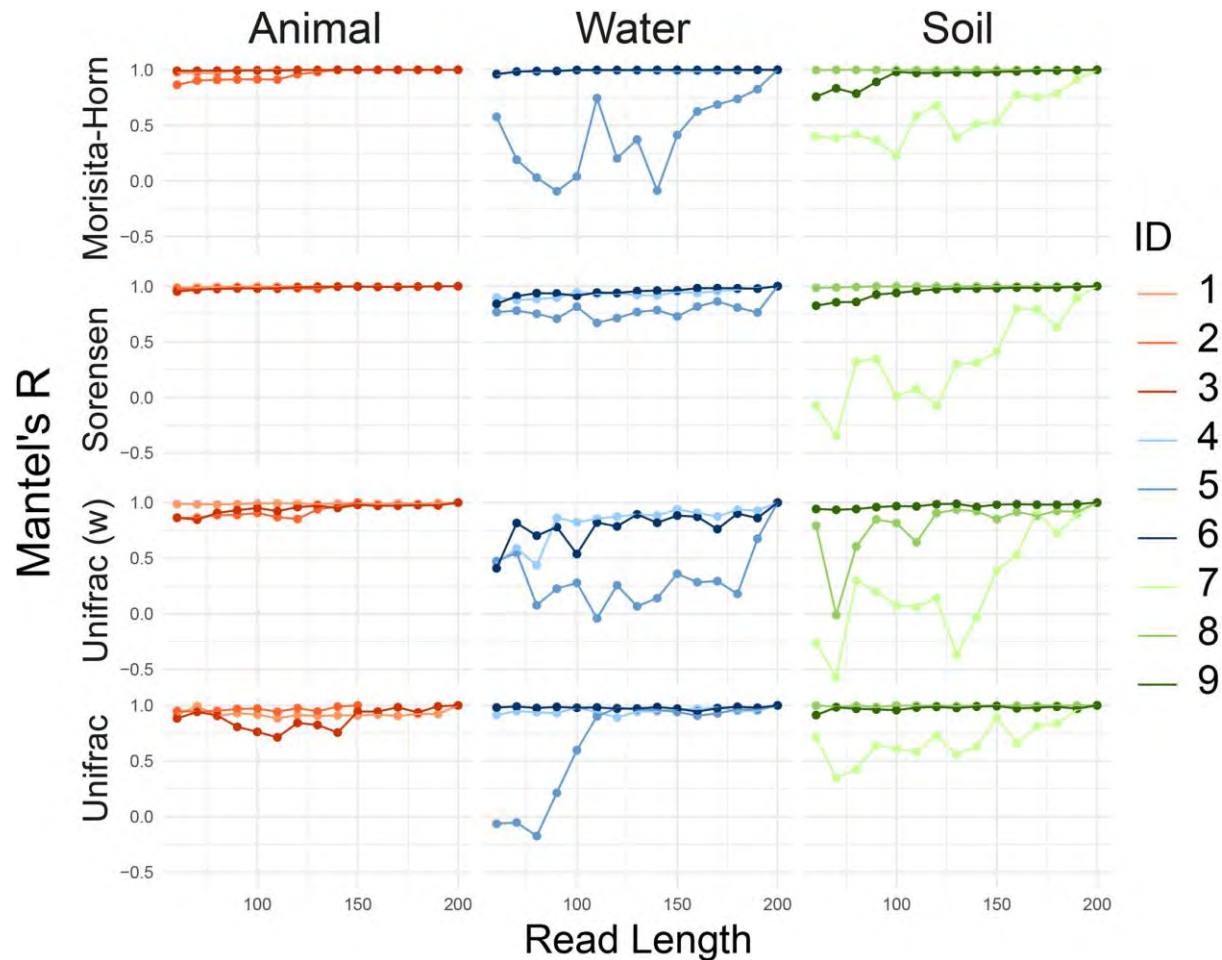- Measurement of various diversity parameters

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- Bioinformatics can improve consensus between sequence datasets when there are differences
- Sequence length matters, but is not limiting

Developing long-term metabarcoding practices requires looking at all steps simultaneously

a. Sample collection

b. Sample preparation

c. Data collection

Nucleotide sequencing, mass spectrometry

d. Data processing

Thank you!

Jurburg and Van Klink, 2020; FAO Children's Book Competition "Protect soil biodiversity"