Figure captions

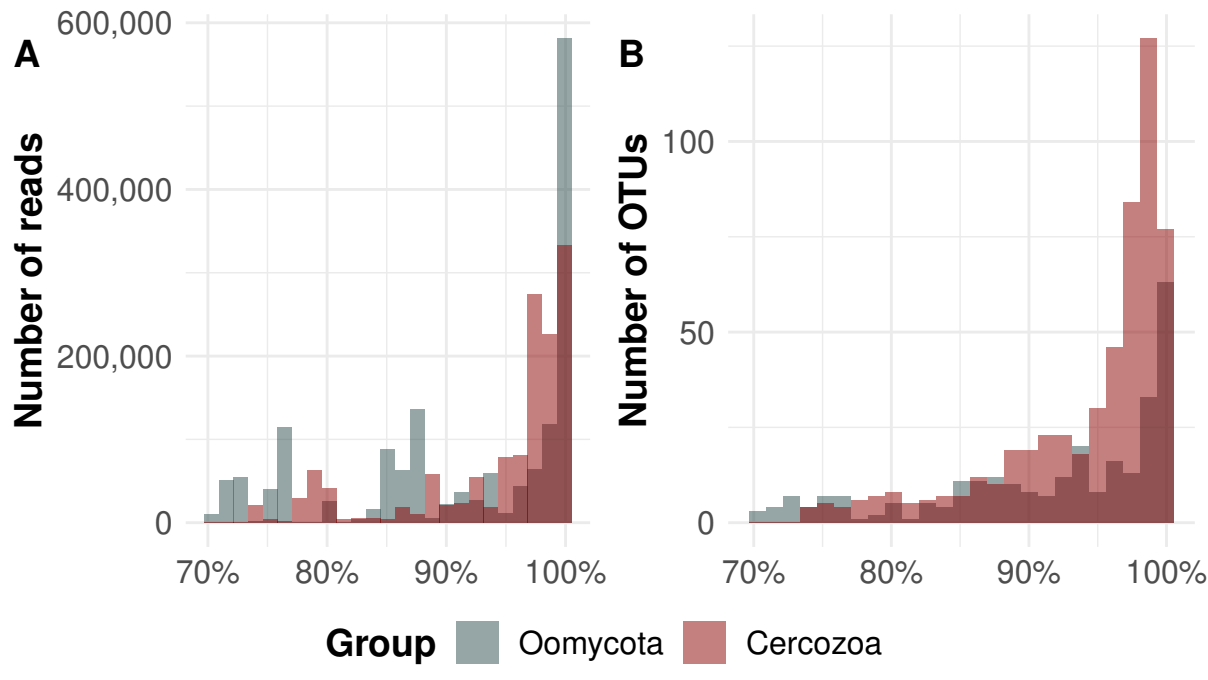
Figure 1: Similarity of protistan sequences to the taxonomic reference database. Oomycete sequences and OTUs are given in grey bars, cercozoan in red. Dark colour represents the overlap between the bars. The majority of all reads (A) and OTUs (B) were ≥ 97% similar to the respective database. 17.2% of all oomycete OTUs had <70% similarity to known reference sequences, whereas only 0.5% of the cercozoan reads had a similarity of <70% (not shown).

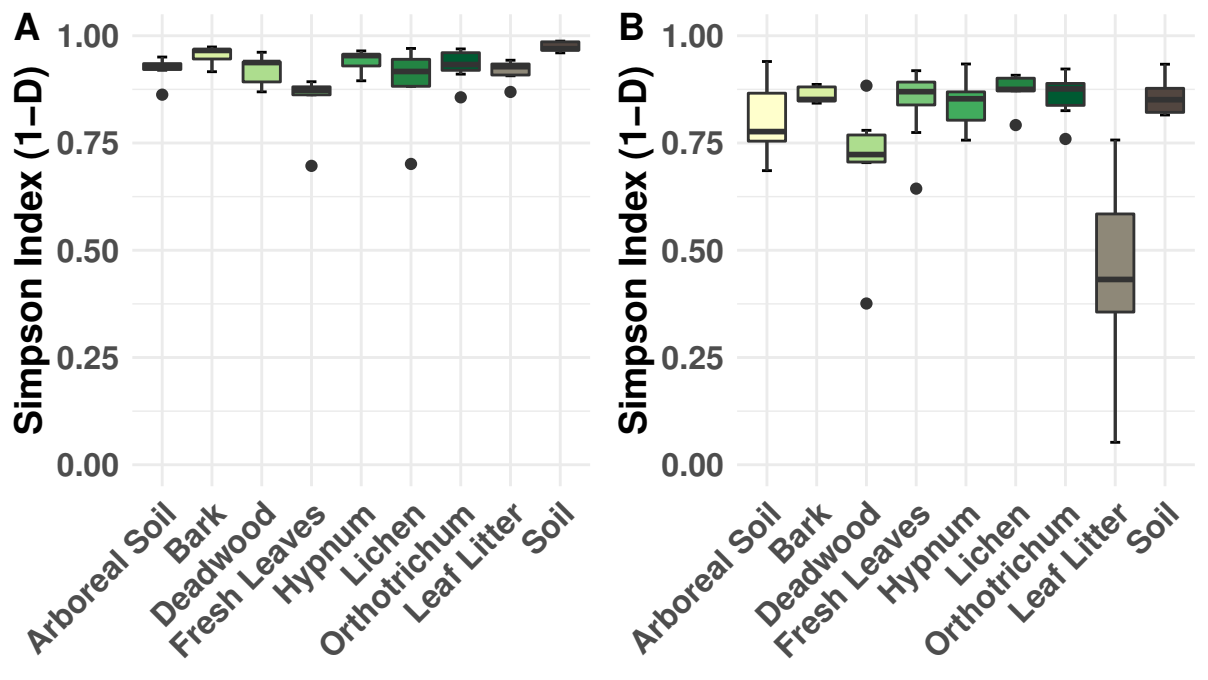
Figure 2: Alpha diversity of microhabitats for cercozoan (A) and oomycete (B) communities. Boxplots describe the Simpson Index of the samples grouped by microhabitat, outliers are given by dots. Simpson Index revealed high alpha diversity irrespective of the investigated protistan group, with the exception of lower alpha diversity of the leaf litter samples within the Oomycota.

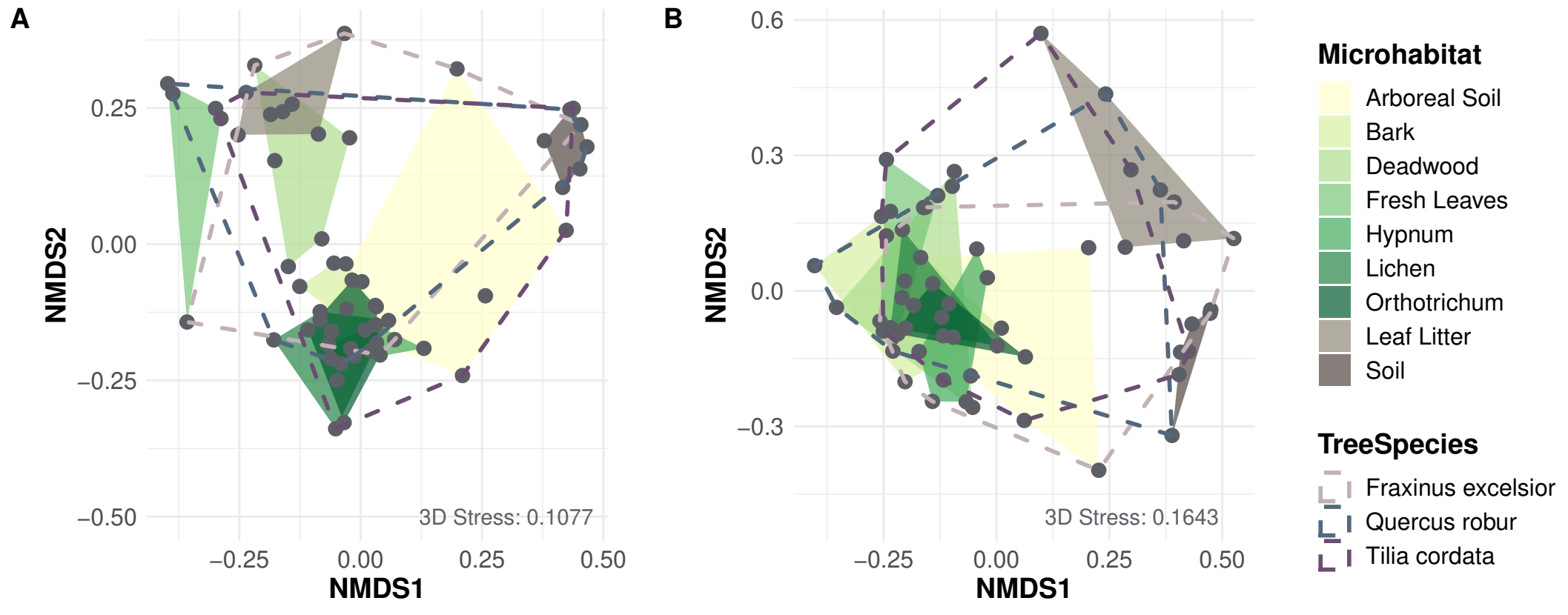
Figure 3: Non-metric multidimensional scaling (NMDS) of Bray-Curtis dissimilarities of cercozoan (A) and oomycete (B) communities among microhabitats. Cercozoan communities showed a finer separation between canopy microhabitats compared to oomycetes, while the latter showed a clearer separation of communities between canopy (green and yellow) and ground (brown). Stress values of NMDS are shown in the lower right of each graph. Microhabitats were more influential for protistan community composition than tree species (Supplementary Table 7).

Figure 4: Redundancy analysis (db-RDA) of cercozoan (A) and oomycete (B) OTUs, microhabitats and tree species. Environmental factors of microhabitat identity and tree species were included in the analysis. Dots represent OTUs. The percentages of variability explained by each axis (RDA1 and RDA2) are given in the labels. RDA ordination resulted in three clusters explaining a comparable amount of variance respectively.

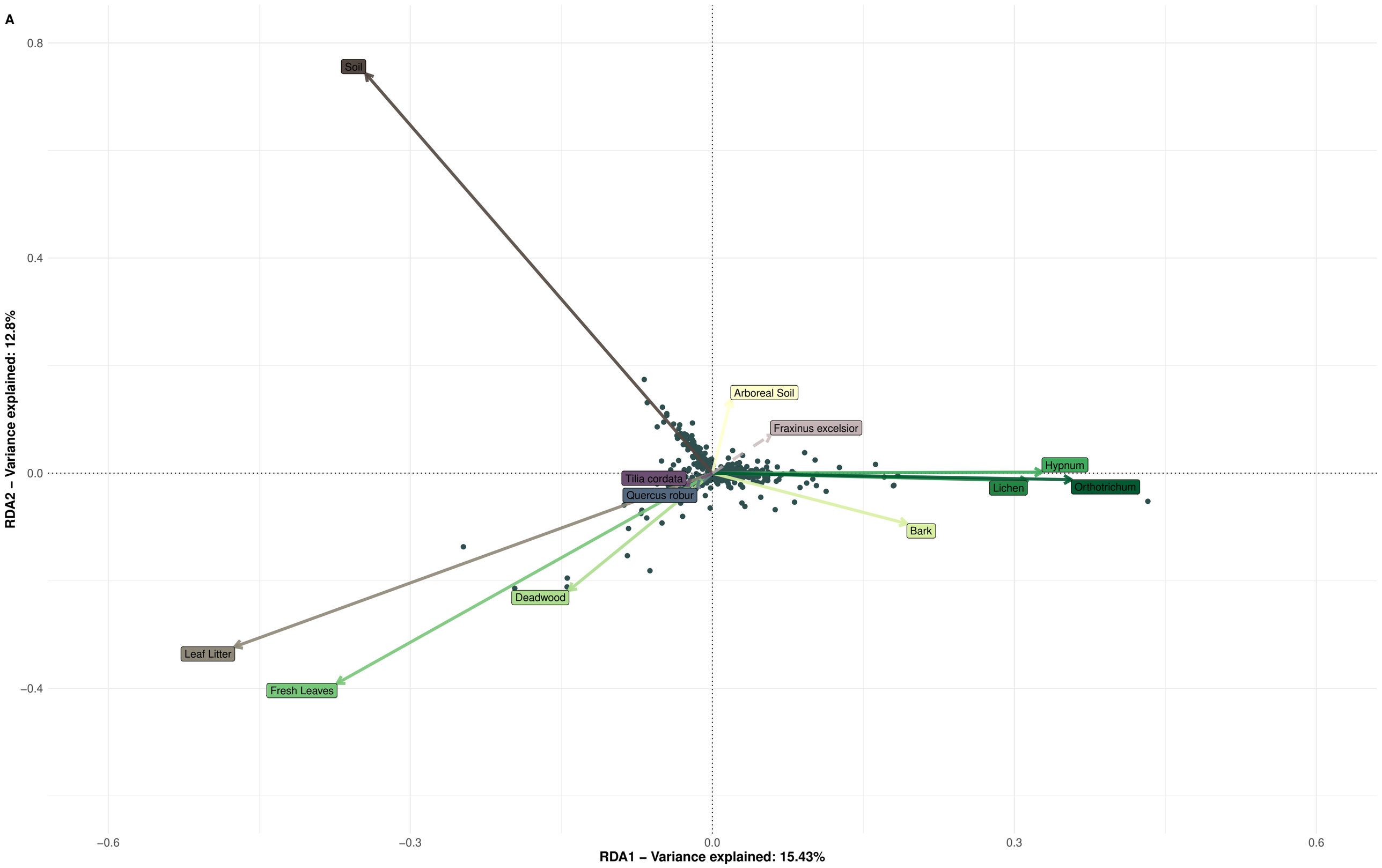
Figure 5: Shared OTUs of cercozoans (A) and oomycetes (B) between microhabitats. Top bar chart represents the sum of the number of shared OTUs resulting from the combination of microhabitats in the matrix below. Only the 15 combinations with the highest numbers of shared OTUs are shown. The majority of OTUs were shared between all microhabitats, irrespective of the investigated protistan phylum.


A
Number of reads
600,000
400,000
200,000
0
70%
80%
90%
100%
B
Number of OTUs
100
50
0
70%
80%
90%
100%
Group
Oomycota
Cercozoa

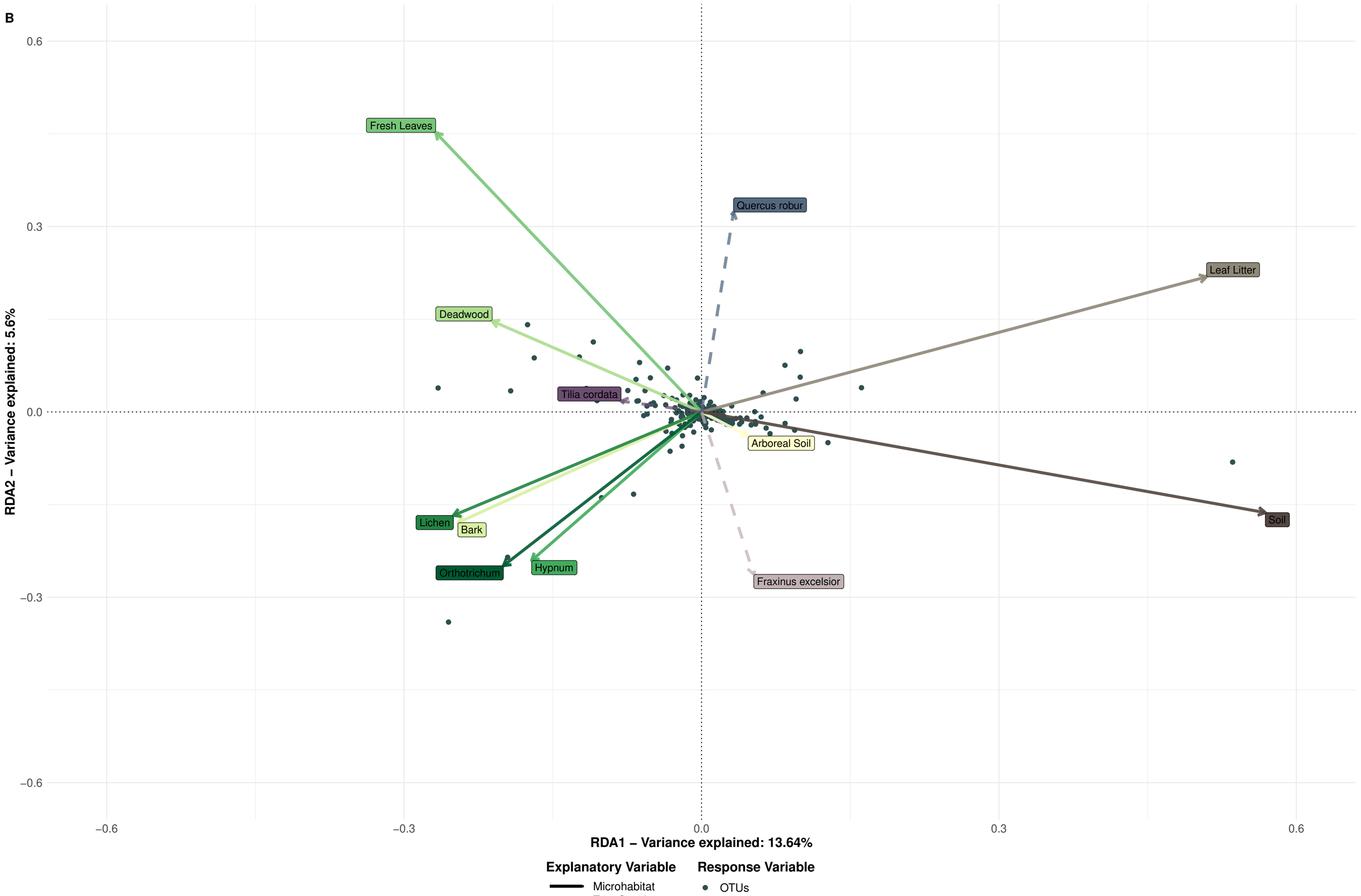

A
B
Simpson Index (1–D)
1.00
0.75
0.50
0.25
0.00
Arboreal Soil
Bark
Deadwood
Fresh Leaves
Hypnum
Lichen
Orthotrichum
Leaf Litter
Soil

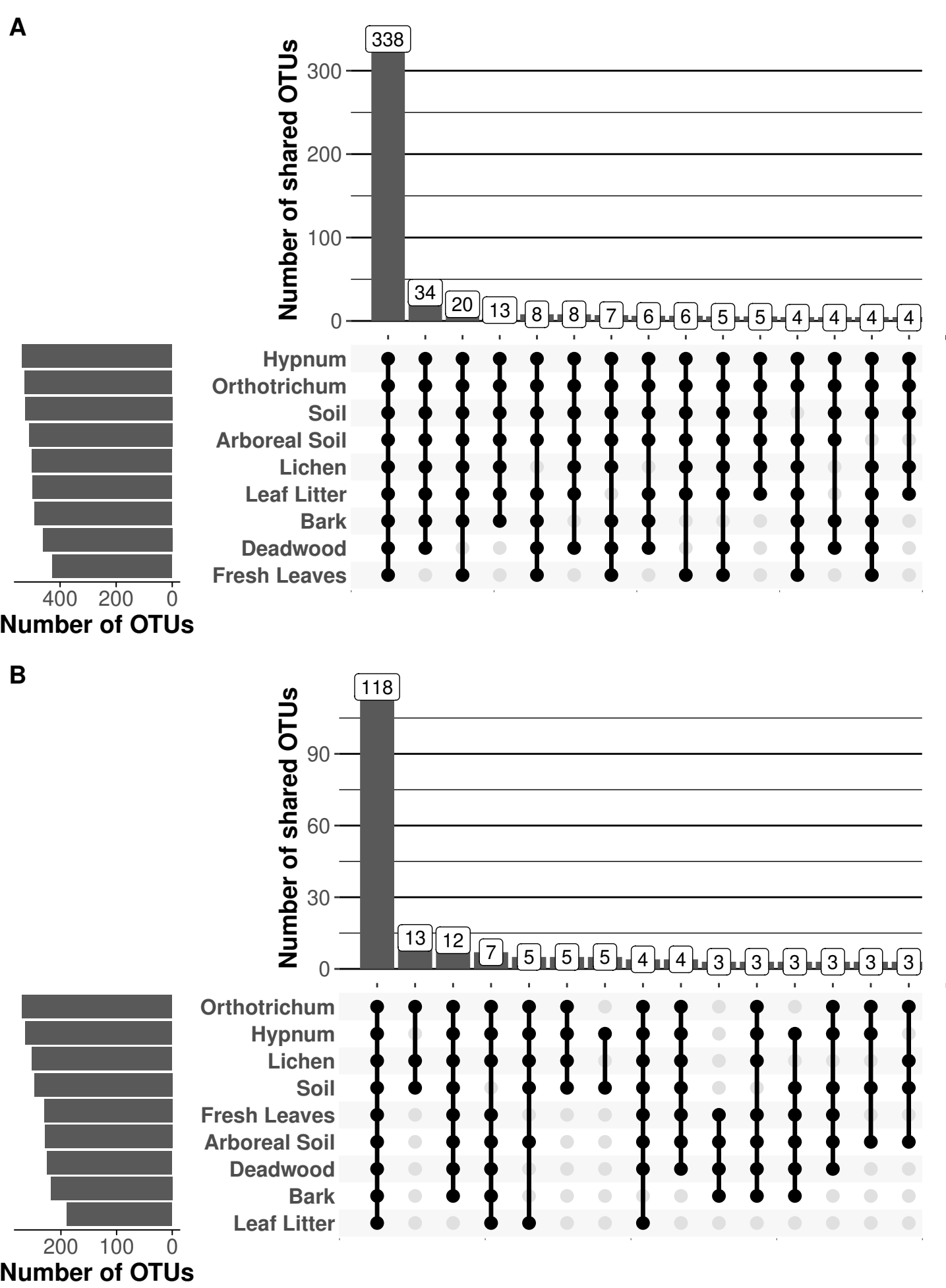

A
B
NMDS1
NMDS2
3D Stress: 0.1077
3D Stress: 0.1643
Microhabitat
Arboreal Soil
Bark
Deadwood
Fresh Leaves
Hypnum
Lichen
Orthotrichum
Leaf Litter
Soil
TreeSpecies
Fraxinus excelsior
Quercus robur
Tilia cordata

A


Soil
Arboreal Soil
Fraxinus excelsior
Hypnum
Lichen
Orthotrichum
Tilia cordata
Quercus robur
Bark
Deadwood
Leaf Litter
Fresh Leaves
0.8
0.4
0.0
−0.4
−0.6
−0.3
0.0
0.3
0.6
RDA2 – Variance explained: 12.8%
RDA1 – Variance explained: 15.43%

B


Fresh Leaves
Quercus robur
Leaf Litter
Deadwood
Tilia cordata
Arboreal Soil
Soil
Lichen
Bark
Hypnum
Orthotrichum
Fraxinus excelsior
0.6
0.3
0.0
−0.3
−0.6
−0.6
−0.3
0.0
0.3
0.6
RDA2 – Variance explained: 5.6%
RDA1 – Variance explained: 13.64%
Explanatory Variable
Microhabitat
Tree Species
Response Variable
OTUs


A
Number of shared OTUs
300
200
100
0
338
34
20
13
8
8
7
6
6
5
5
4
4
4
4
Hypnum
Orthotrichum
Soil
Arboreal Soil
Lichen
Leaf Litter
Bark
Deadwood
Fresh Leaves
400
200
0
Number of OTUs
B
Number of shared OTUs
90
60
30
0
118
13
12
7
5
5
5
4
4
3
3
3
3
3
3
Orthotrichum
Hypnum
Lichen
Soil
Fresh Leaves
Arboreal Soil
Deadwood
Bark
Leaf Litter
200
100
0
Number of OTUs