## Working with the *vegan*R package

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## What to show (notes to myself)

```
Matrix transformation
    o use "communities.tsv"
rarefy()
    o use "LMO.16S.dada2.tsv.gz"
specnumber(), diversity(), diversity()/log(specnumber())
vegdist()
    metaMDS() (incl. scores())
```

Microbial model Systems