Analysing:

1) Biodiversity of ant communities along an elevational gradient and

2) Taxonomic composition of arthropods along plant diversity gradient in the Jena Experiment

Course: Quantitative Community Ecology in R

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Task 2)

Step by step

1) Does data responds linearly? –> DCA to access gradient length (< 3 = Linear); In any case I personally prefer to use distance-based methods; The most widely used method in ecology is nowadays an NMDS with post-hoc vector analysis; Since we‘re dealing with abundance data I would suggest using the Bray-Curtis Dissimilarity as distance matrix

2) Constrained or unconstrained methods? In our case we do have predictors, but again, I would prefer using an NMDS and post-hoc vector fitting using either the envit() function or the ordisurf() function

… but first lets see how the data looks like etc.