

Solution:

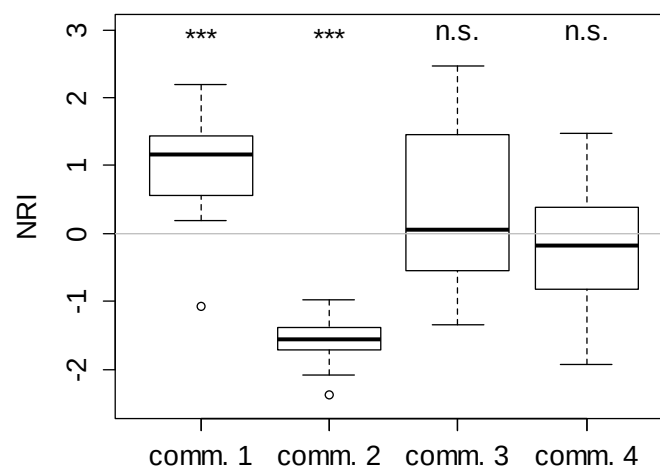
TASK 1:

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((gen1_sp9:24.05, ((gen1_sp8:14.15, gen1_sp7:14.15):4.93, (gen1_sp6:17.29, ((gen1_sp5:9.09, gen1_sp4:9.09):3.85, ((gen1_sp3:9.02, gen1_sp2:9.02):0.71, gen1_sp1:9.73):3.2):4.36):1.78):4.97):14.4, ((gen8_sp17:12.41, gen8_sp16:12.41):7.15, (((gen8_sp15:8.82, gen8_sp14:8.82):6.57, gen8_sp13:15.39):1.68, gen8_sp12:17.07):2.1, (gen8_sp11:18.2, (((gen8_sp10:8.13, gen8_sp9:8.13):7.86, gen8_sp8:15.99):1.63, (((((gen8_sp7:4.43, gen8_sp6:4.43):1.33, gen8_sp5:5.76):1.05, gen8_sp4:6.81):3.03, gen8_sp3:9.84):3.51, gen8_sp2:13.35):0.98, gen8_sp1:14.33):3.3):0.57):0.96):0.39):6.47, ((gen7_sp2:20.68, gen7_sp1:20.68):5.07, ((gen6_sp13:23.27, (((gen6_sp12:8.49, gen6_sp11:8.49):6.41, ((gen6_sp10:9.56, gen6_sp9:9.56):3.85, gen6_sp8:13.41):1.48):7.07, (gen6_sp7:19.98, (((gen6_sp6:2.75, gen6_sp5:2.75):1.5, gen6_sp4:4.25):3.63, gen6_sp3:7.88):8.19, (gen6_sp2:7.88, gen6_sp1:7.88):8.19):3.91):1.99):1.3):1.93, (((gen5_sp17:13.78, gen5_sp16:13.78):7.44, (((gen5_sp15:8.05, (gen5_sp13:6.97, gen5_sp14:6.97):1.08):3.08, gen5_sp12:11.13):5.98, (gen5_sp11:11.38, gen5_sp10:11.38):5.73):2.37, ((gen5_sp9:10.14, (gen5_sp8:4.08, gen5_sp7:4.08):6.06):1.95, gen5_sp6:12.08):4.19, ((gen5_sp5:12.12, gen5_sp4:12.12):1.07, gen5_sp3:13.18):2.39, gen5_sp2:15.57):0.7):3.22):1.74):1.18, gen5_sp1:22.4):2.6, ((gen4_sp6:15.57, (gen4_sp5:12.32, gen4_sp4:12.32):3.25):4.43, (gen4_sp3:13.34, (gen4_sp2:9.98, gen4_sp1:9.98):3.35):6.66):5):0.21):0.55):0.27):2.35, gen3_sp1:28.38):2.56, gen2_sp1:30.94):7.5);
```

TASK 2:

See the attached R-script: Tutorial_WE.R

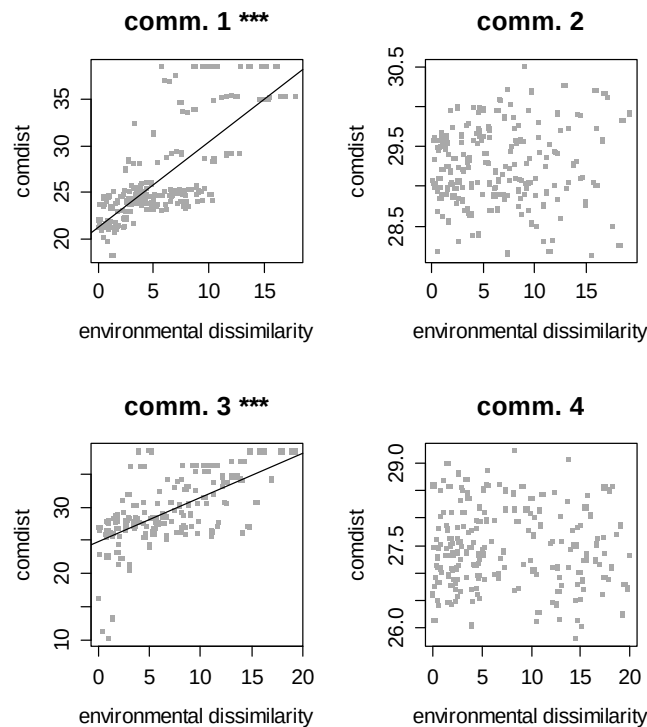
The Net Relatedness Index = $-1 \times \text{SES}(\text{MPD})$ shows that local assemblages in community 1 are overall phylogenetically clustered ($\text{NRI} > 0$), in community 2 they are phylogenetically overdispersed ($\text{NRI} < 0$), and in communities 3 and 4 there is random phylogenetic structure.



Phylogenetic signal analysis using Blomberg's K indicates that characters 1–3 are related to phylogeny (variance of Phylogenetically Independent Contrasts significantly smaller than random), with character 1 showing almost perfect phylogenetic signal ($K \approx 1$) and C3 and C4 showing a tendency towards phylogenetic niche conservatism ($K > 1$).

Character	Class	K	PIC.variance.P
C1	Environmental tolerance	1.02	0
C2	Environmental tolerance	1.31	0
C3	Ressource use	2.83	0
C4	Ressource use	0.41	0.71

Phylogenetic “beta diversity” analysis with the comdist measure of Webb *et al.* (2008) shows that assemblages in similar environments are phylogenetically closer related than assemblages in different environments in communities 1 and 3. A phylogenetic randomization test using reshuffling of taxa shows that this pattern is highly significant ($P < 0.001$ in both communities).



Conclusions:

Community 1: Clustered phylogenetic structure ($NRI > 0$) and a positive relationship between comdist and environmental dissimilarity suggest that different clades occupy different environments, and the community is assembled by environmental filtering. This is supported by the strong phylogenetic signal in the environmental tolerances (C1, C2).

Indeed, community 1 was simulated using environmental filtering based on C1.

Community 2: Overdispersed phylogenetic structure ($NRI < 0$), phylogenetic signal in the resource use traits C3, and no relationship between comdist and environmental dissimilarity suggests that this community is structured by resource competition among close relatives with similar resource needs.

Indeed, community 2 was simulated with a competition model based on C3.

Community 3: Random phylogenetic structure suggests superficially that this community is neutrally assembled, but the relationship between comdist and environmental dissimilarity suggests that there is environmental filtering (just like in community 1). The random phylogenetic structure could thus arise from the opposing forces of environmental filtering and a phylogenetically repulsive process like competition.

Indeed, community 3 was simulated with a two-step model: environmental filtering based on C2 followed by competition based on C3.

Community 4: Random phylogenetic structure and the lack of a relationship between comdist and environmental dissimilarity suggest neutral assembly. However, there might be other processes related to unmeasured traits or environmental variation that cancel out like in community 3 – absence of phylogenetic structure is no strong evidence for neutrality.

In fact, this community was simulated at random.

NB: In natural systems, where numerous processes can occur – not just environmental filtering, competition and stochasticity, like in this simplistic example – it is often impossible to derive unambiguous predictions of phylogenetic structure for certain hypotheses of community assembly. Nevertheless, tests like this can be very useful for generating hypotheses that can be tested further using other methods (e.g. trait-based approaches) that allow more specific predictions.