

# Phylogenetic Diversity - Communities

*Z620: Quantitative Biodiversity, Indiana University*

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**Pruning trees to only include species from phylogeny (phy) that are present in the community (comm)**

```
# # Prune a phylogenetic tree to include only species present
# # It's not clear that we will need the `prune.sample` function
# # Need to make sure OTU names in comm match names in phy
# prunedphy <- prune.sample(comm, phy)
#
# par(mfrow = c(2, 3)) # figure with 2 rows and 3 columns
#
# for (i in row.names(comm)) {
#   plot(prunedphy, show.tip.label = FALSE, main = i)
#   tiplabels(tip = which(prunedphy$tip.label %in% names(which(comm[i, ] > 0))), pch = 19, cex = 2)
# }
```

One common way to test for phylogenetic clustering and overdispersion is to use the Net Relatedness Index (NRI). NRI is calculated with the following equation:  $-\frac{MPD_{obs} - \overline{MPD}_{null}}{\sigma(MPD_{null})}$  where  $MPD_{obs}$  is the mean phylogenetic distance calculated from pairwise branch lengths in a sample,  $\overline{MPD}_{null}$  is the mean of the MPD values generated via randomization, and  $\sigma MPD_{null}$  is the standard deviation of the MPD values generated via randomization. Negative NRI values indicate that a sample is phylogenetically overdispersed; that is, taxa are less related to one another than expected. Positive NRI values indicate that a sample is phylogenetically underdispersed, or clustered, such that taxa are more closely related to one another than expected. Let's use `picante` to calculate NRI: