

We use R function phylocurve.R to rarefy phylogenetic diversity (PD) as a function of OTU number. We construct a rooted Maximum Likelihood tree for each MID and graph in Excel.

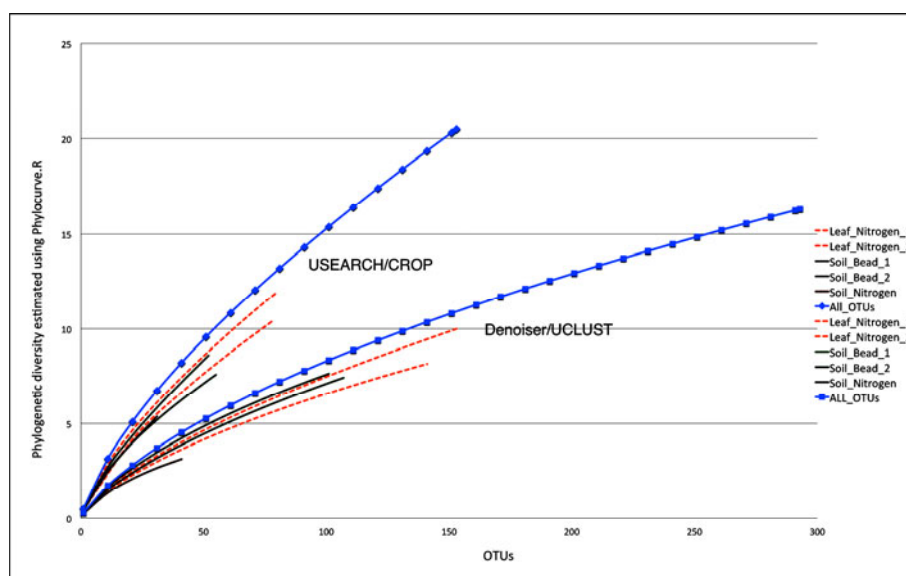


Figure S1 compares alpha PD from the USEACRCH/CROP and Denoiser/UCLUST pipelines. Red dotted lines, leaf litter using liquid nitrogen; green lines, soil, using bead-beating; brown line, soil, using liquid nitrogen; blue line, all MIDs together.

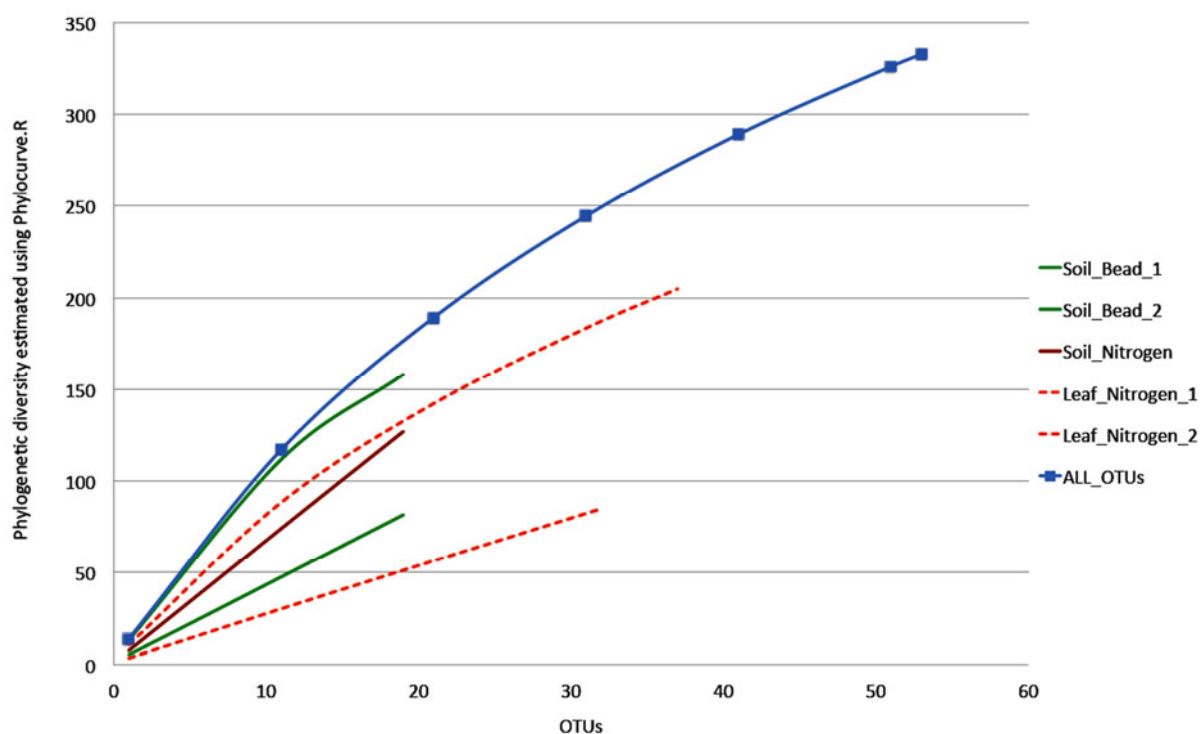


Figure S2 plots by the OCTUPUS MIDs. Note that the MID-specific lines differ in total OTU numbers by more than a factor of 3, but PD is more similar amongst the MIDs, suggesting that total OTU number is perhaps a reliable index of alpha diversity.