CCOMM

This package expedites the process of analyzing and plotting ecological community data with popular functions from community ecology packages such as 'vegan'. I built this package after spending many hours of frustration attempting to perform the intermediary steps between reading in my community data and getting the pretty plots at the end, and I hope it will help people save themselves similar hours of frustration!

Functions:

givemeDIVERSITY: input is a community matrix (sites by species with abundance data), returns boxplots depicting alpha diversity after rarefaction for each site. Package used for this analysis is ‘BAT’.

givemeNMDS: input is a community matrix (sites by species with abundance or incidence data), returns a stress plot and NMDS plot. Package used for this analysis is ‘vegan’.

givemeTREE: input is a trait matrix (species by traits where values are either 0 (species does NOT have that trait) or 1 (species DOES have that trait)), returns a dendrogram depicting species relationships based on traits.