
[FULL] Primer 6 And Permanova User Manual Fix



the data were analyzed using the qiime (caporaso et al. 2010) software to generate rarefied otu tables and produce alpha and beta diversity measures. singleton otus were removed and the rarefaction depth was set at 2,500 sequences per sample (2,500 sequences were rarefied per sample). diversity and richness estimates for each sample were obtained by calculating the ace and chao1 indices. the shannon and simpson diversity indices were calculated for each sample. calculation of the beta diversity was based on the bray-curtis dissimilarity metric, and a pcoa plot was generated using primer 6 & permanova+(clarke and gorley, 2006) to visualize and compare the overall clustering of samples and taxa. a permanova was performed on the bray-curtis dissimilarity matrix with the qiime (caporaso et al. 2010) software. to examine variation within the data the permdisp was also used in qiime. p-values were obtained by comparing the observed and expected values using 9999 random permutations. the observed values were compared against the expected values of the observed median square distance from the centroid of the group. groups were compared using a 9999 monte carlo permutation test. the p-value was then adjusted for multiple comparisons using the benjamini-hochberg false discovery rate (fdr) correction (benjamini and hochberg 1995). a euclidean distance was calculated in qiime (caporaso et al. 2010) and a pcoa plot was generated using primer 6 software (clarke and gorley, 2006). the pcoa plot was based on the weighted unifrac metric of the input data (lozupone et al. 2007). to determine the significance of differences in community composition between habitats or restoration treatments, the permanova test was performed on the weighted unifrac distance matrix using 9999 permutations. if the p-value was significant at the 0.05 level, pairwise comparisons were performed using a multiple comparison test. for pairwise comparisons of habitat means, a permutation-based, nonparametric t-test (significance level, alpha=0.05) was used. for pairwise comparisons of treatment means, a permutation-based, nonparametric t-test was used (significance level, alpha=0.05).

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