

SUPPLEMENTAL METHODS

Alpha diversity was calculated using the Shannon index and compared between pre- and post-RT time points using a linear mixed effects model including a fixed effect for time point and a random effect for subject. Beta diversity was calculated using Bray distances between TMM-normalized, log transformed taxon counts. PERMANOVA analyses were conducted using the function `adonis` in the R package `vegan`, version 2.5-7.¹ Analyses were conducted using R version 4.0.1 (2020-06-06).²

References

1. Jari Oksanen, F. Guillaume Blanchet, Michael Friendly, Roeland Kindt, Pierre Legendre, Dan McGlenn, Peter R. Minchin, R. B. O'Hara, Gavin L. Simpson, Peter Solymos, M. Henry H. Stevens, Eduard Szoecs and Helene Wagner. *Package 'Vegan.'*; 2020. <https://CRAN.R-project.org/package=vegan>
2. R Core Team. *R: A Language and Environment for Statistical Computing*. Vienna, Austria; 2020. <https://www.R-project.org/>.