In this folder you'll find code for the R package DTMbvs for the manuscript:

“*DTMbvs: Dirichlet-Tree Multinomial Regression Models with Bayesian Variable Selection for Microbiome Data – an R Package*” by MD Koslovsky and M Vannucci

The main functions operate in C++ via the R package Rcpp. These functions can be sourced by a set of wrapper functions that enable easy implementation of the code in the R environment. Various functions are available that produce, summarize, and plot the results for inference.

This package relies on various R packages that need to be installed in the R environment before running. To install, use the install.packages(‘’) command for the following packages:

Rcpp

RcppArmadillo

MCMCpack

mvtnorm

ggplot2

ape

GGMselect

To install the ‘DTMbvs’ package, run

install.packages(‘devtools’)

library( devtools )

Download the ‘DTMbvs’ folder from [https://github.com/mkoslovsky/DTMbvs](https://github.com/mkoslovsky/bvsDMLM). Unzip the file, and then in RStudio, navigate to the File dropdown and select ‘Open Project…’ Then select the DTMbvs folder.

In the Rstudio command line, run

devtools::build()

and

devtools::install()

In its current state, simulated data will automatically be produced and modeled if all arguments are left blank in the main wrapper function DTMbvs\_R(). Adjusting the arguments in this command can generate various simulation scenarios. A worked example and technical details are provided in the vignette.

The output produced includes the MCMC samples for alpha, zeta, phi, Omega, and G.