Parameter Estimated from JAGS Model

Once obtaining the true abundance results, we aim to perform another simulation modeling to estimate the parameter base on the true abundance results. We can verify the accuracy of the true abundance model by processing the parameter estimated model and result from the new model. The result of true abundance is coming from four freely set parameters whatand an independent variable that cannot randomly changed. Therefore, alpha, theta, sigma, and rho are four parameters should be estimated in our JAGS simulation model.

Alpha parameter is used to control the probability of biological zero ~~present~~. As the alpha is greater and greater, the taxon is going to be the structural zero. The alpha values are in range from negative infinity to positive infinity. Huokai specifies that delta can only output one or zero, with delta following a Bernoulli distribution controlled by alpha at randomly determined probability. The variance component sigma parameter may simulate the uncertainty microbial structure. Larger value of sigma indicates the taxon more variability. Rho represent the evolutionary rate in between two taxon and value of rho closer zero means slower evolution, so rho should choose from zero to positive infinity value. The variance-covariate matrix computed by parameters sigma and evolutionary rate, rho. Theta parameter is proportion to discovery sampling zero in existing taxa. Smaller theta value has larger probability to obtaining sampling zero.

We consider building new simulation models to estimate parameters by use the rjags or runjags package in RStudio. We are certain that non-zero values in true abundance occur when delta equal zero and calculated through the multivariate normal distribution with theta representing the mean parameters and variance-covariate matrix as variance. Initially, we construct the JAGS simulation model to sample from the prior distribution of parameters’ values given true abundance and compile the simulation model, specifying the data, initial values, and the number of chains. Based on the initial values and chains and Bayesian inference, we can obtain the posterior distribution, which represent likelihood rather than exact values. Next, we will sample the JAGS model to estimate the likelihood value.

In the JAGS model, we should estimate the theta values first. Then, based on theta value to estimate the var-covariate matrix. From the var-covariate matrix, we attempt to estimate the sigma and rho. I believe estimating alpha should be done separately with rho, sigma, and theta, because the respond variable is filtered once delta is zero, and zero value of delta is computed from Bernoulli probability of alpha controlled.