

IDM_project

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The following are used for the simulation: We assume $n.genus$ $g = 1, 2, \dots, n.genus$. * For each g genera, we assume $n.species$ in that genus * We assume the data was collected at $n.sites$ * We also assume the total number of visits to each site is $n.visit$. * We also assume that some of the data are collected with species ID * Most of them are collected with genus ID * $shan.index$ is the shannon's index * $p.tag$ is the detection probability for the occurrence model (species data) * $includecov$ (T/F) indicates whether it is a model with a covariate (TRUE) or no covariate (FALSE)

Simulating the data

```
set.seed(2020)
includecov= FALSE
#includecov=TRUE means that there is covariate effect and false otherwise
n.sites=20
n.species = 5
n.visit=3
covte = covariates(n.sites)
data = sim(n.sites, n.species,n.visit,n.sites ,n.sites, cov=covte, includecov) #covte is the covariates
summary(data)
```

```
##           Length Class  Mode
## mat.species 300    -none- numeric
## mat.genus    60     -none- numeric
## covariates   60     -none- numeric
## shan.index   20     -none- numeric
```

Original Parameters

$$\begin{aligned}\sigma_{\alpha}^2 &= 0.4^2 \\ \sigma_{species}^2 &= 2 \\ \sigma_{site}^2 &= 1 \\ p.tag &= 0.7\end{aligned}$$

Running the model

```
mcmc.out <- est(data, code)

## defining model...
## building model...
```

```

## setting data and initial values...
## Warning in model$setData(data): data not used in model: cov
## running calculate on model (any error reports that follow may simply reflect
## missing values in model variables) ...
##
## checking model sizes and dimensions... This model is not fully initialized. This is not an error. To
## model building finished.
## compiling... this may take a minute. Use 'showCompilerOutput = TRUE' to see C++ compilation details.
## compilation finished.
## ===== Monitors =====
## thin = 1: p.tag, shan.index, sigma.alpha, sigma.site, sigma.species
## ===== Samplers =====
## RW sampler (30)
##   - sigma.site
##   - sigma.species
##   - sigma.alpha
##   - p.tag
##   - beta.site[] (20 elements)
##   - beta.species[] (5 elements)
##   - alpha
## binary sampler (100)
##   - z[] (100 elements)
## Monitored nodes are valid for WAIC
## compiling... this may take a minute. Use 'showCompilerOutput = TRUE' to see C++ compilation details.
## compilation finished.
## runMCMC's handling of nburnin changed in nimble version 0.6-11. Previously, nburnin samples were disc
## running chain 1...
## |-----|-----|-----|-----|
## |-----|
## running chain 2...
## |-----|-----|-----|-----|
## |-----|
## WAIC was calculated as NaN. You may need to add monitors to model latent states, in order for a val
#Diagnostics of the model
coda_samples <- mcmc(mcmc.out$mcmc.out$samples)
#mcmcplot(coda_samples)

```

Parameter Estimation

- Mean bias of shannon index
- MSE of shannon index
- Estimate of σ_α , σ_β , σ_γ and $p.tag$

```

true_shan <- data$shan.index #true estimates of shannon index from the simulation
if(includecov==TRUE){
  est_beta <- matrix(mcmc.out$mode.out[1:(n.species*3)],
                    nrow=n.species, ncol=3) #estimates of beta from mcmc

```

```

est_shan = shanest(est_beta,data$covariates, TRUE) #estimation of shannon index
mse_shan = sum(((true_shan-est_shan)^2)/n.sites) #MSE of shannon index
mbias_shan = mean(true_shan-est_shan) #mean bias of shannon index
p_est <- mcmc.out$mode.out[(n.species*3)+1] #detection probability
sig_alpha <- NA
sig_beta <- NA
sig_gamma <- NA
}else{
  est_shan <- mcmc.out$mode.out[2:(n.sites+1)] #estimates of shannon index
  mse_shan = sum(((true_shan-est_shan)^2)/n.sites) #MSE of shannon index
  mbias_shan = mean(true_shan-est_shan)#mean bias of shannon index
p_est <- mcmc.out$mode.out[1] #detection probability
sig_alpha <- tail(mcmc.out$mode.out,3)[1] #variance of intercept
sig_beta <- tail(mcmc.out$mode.out,3)[2] #variance of site effect
sig_gamma <- tail(mcmc.out$mode.out,3)[3] #variance of species effect
}

data = data.frame(p_est, mse_shan, mbias_shan, sig_alpha, sig_beta, sig_gamma)
print(data)

##          p_est    mse_shan  mbias_shan sig_alpha  sig_beta sig_gamma
## p.tag 0.7098417 0.008709304 -0.09332365 0.1455323 0.6132096 0.3414869

```