STA410 Assignment 3

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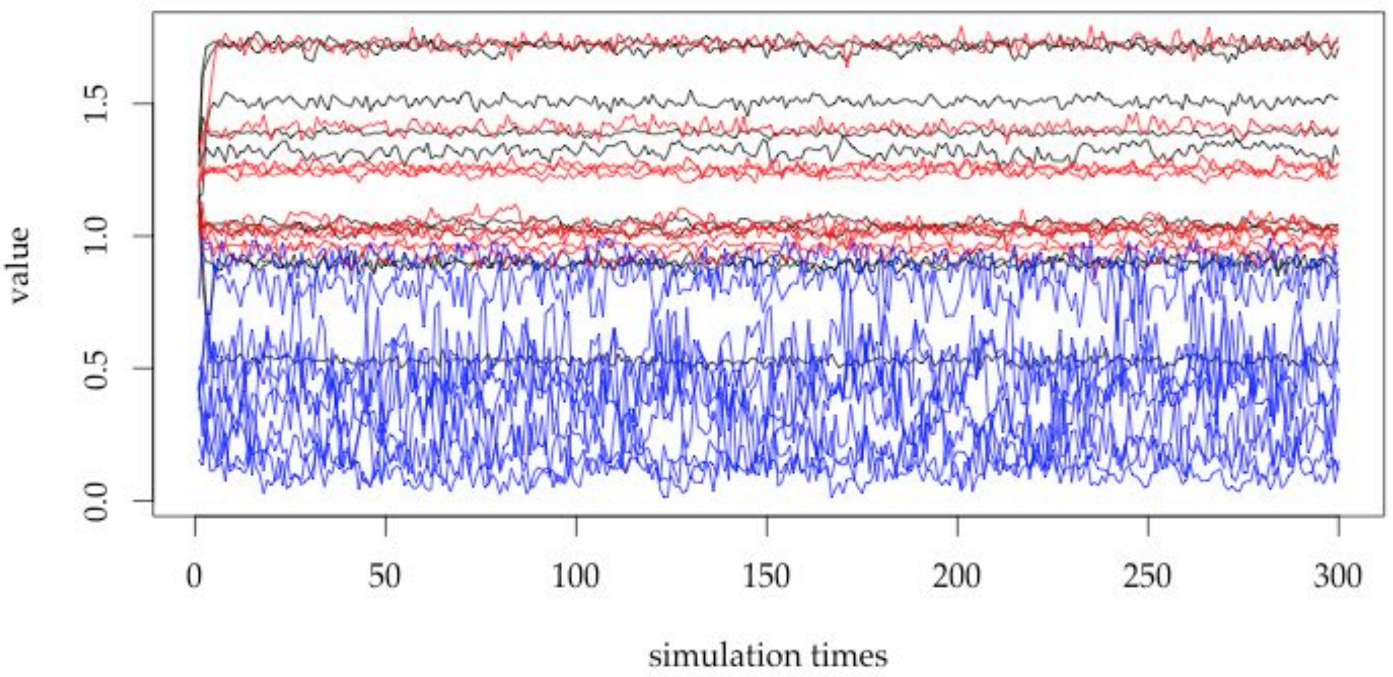
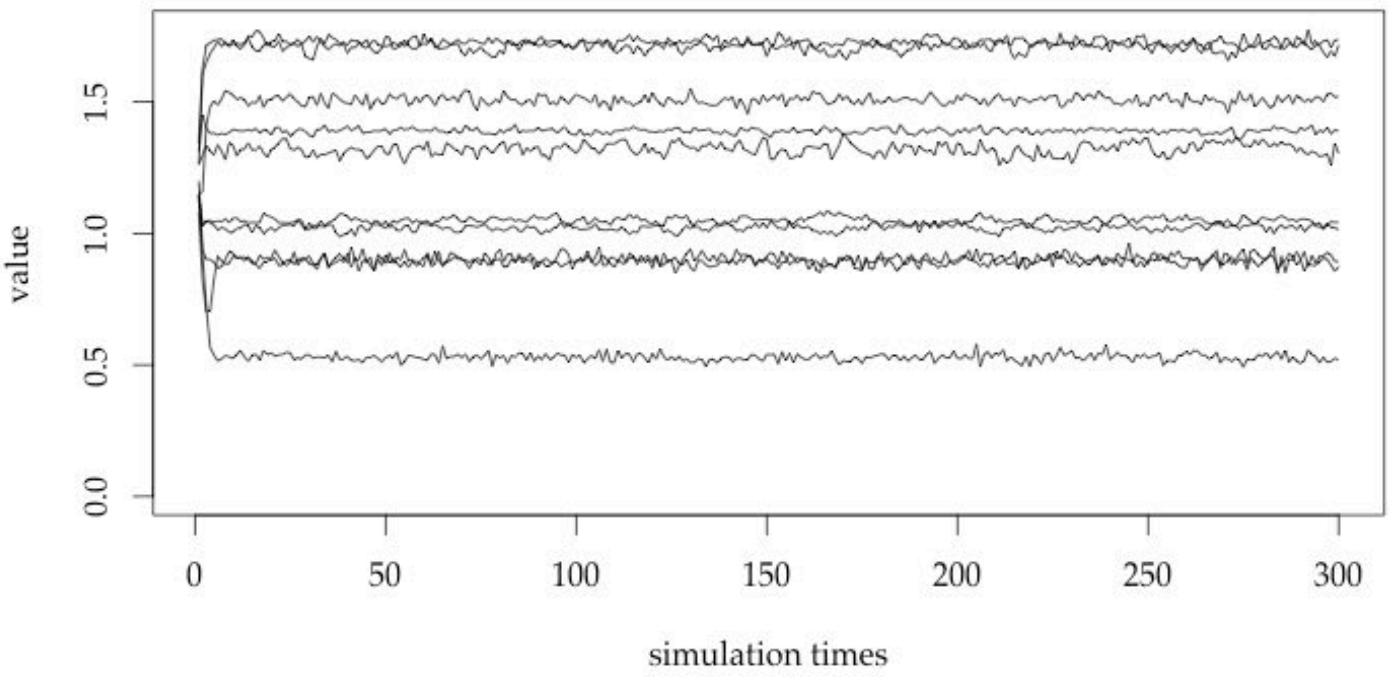
1. Traceplots of parameters



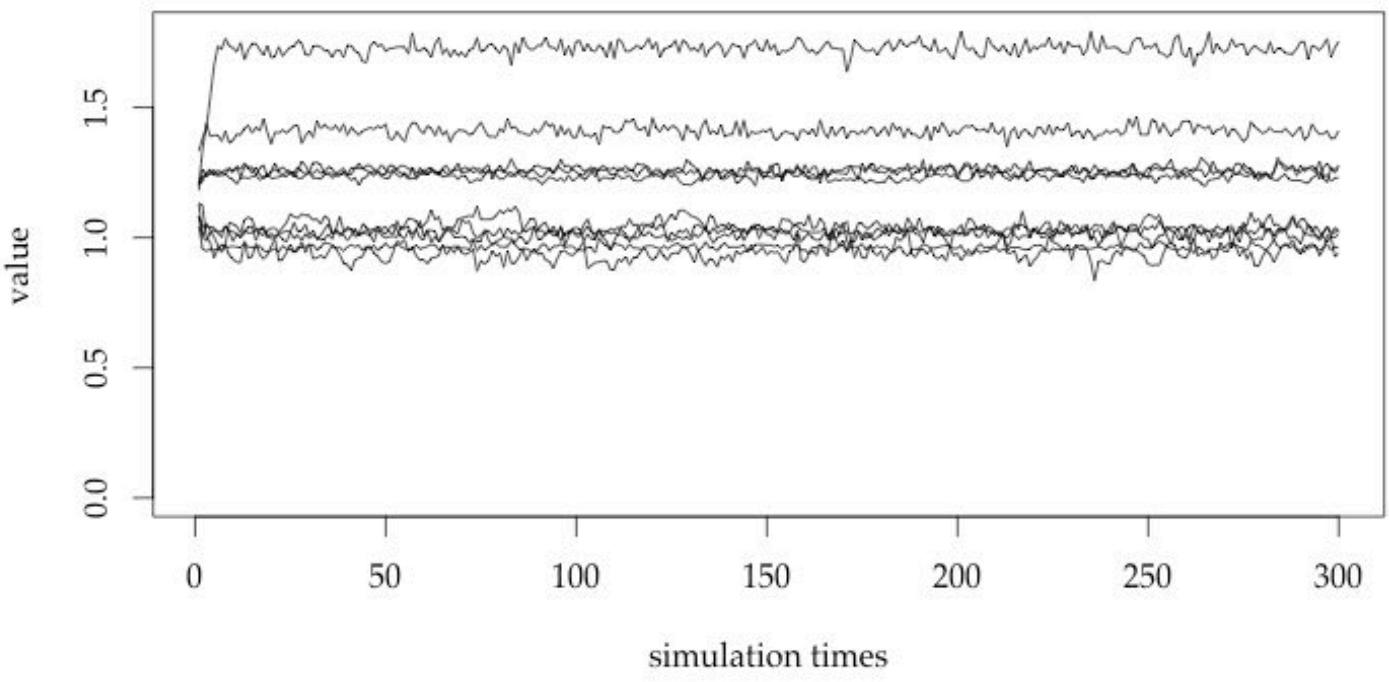
The total traceplot with 3 parameters (black for mu, red for vu, blue for rho).

To clarify, the separate traceplots are listed below:

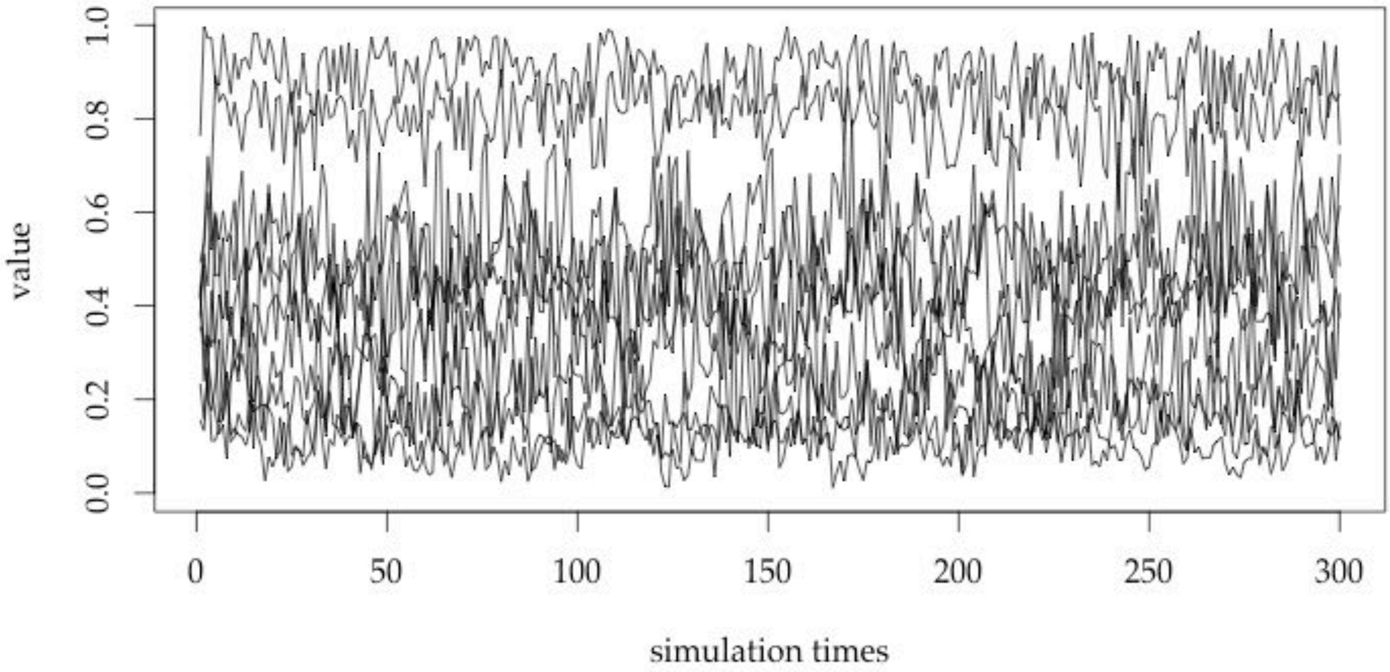
The traceplot of mu.



The traceplot of vu.



The traceplot of rho.



By observation, we are able to make the following statements:

- The value of rho, of any species, is rather chaotic in Gibbs sampling.
- The value of mu and vu have a quite big “jump” at the beginning of Gibbs sampling, so we could consider some “burn-in” iterations.
- The value of mu and vu after some burn-in iterations are somewhat “constant”, although they do have some fluctuations up and down.

2. Estimated posterior mean and standard deviation

If we consider the first 15 iterations are “burn-in” iterations, then we are going to have the following results:

mu:

```
            sp1         sp2        sp3        sp4        sp5        sp6        sp7
mean 0.89217667 1.389672760 1.71534615 0.52909171 1.50745940 1.72127823 1.32025228
sd   0.01528185 0.009622424 0.02339015 0.01483819 0.01647131 0.01248323 0.02279837
            sp8        sp9       sp10
mean 1.04448905 1.02683415 0.90321044
```

```
sd   0.01800056 0.01544346 0.02023304
```

vu:

```
            sp1        sp2        sp3       sp4        sp5        sp6        sp7
mean 1.02552750 0.96268060 1.04027651 1.2599138 1.41086193 1.01502662 0.93990246
sd   0.01919384 0.01036092 0.03199098 0.0163944 0.02054309 0.01718367 0.02953991
            sp8        sp9       sp10
mean 1.25438964 1.23585511 1.72856199
sd   0.01733282 0.01439401 0.02324842
```

rho:

```
            sp1       sp2        sp3        sp4        sp5        sp6       sp7
mean 0.26855897 0.1088104 0.19960786 0.80438839 0.89748316 0.15574658 0.4303648
sd   0.09403528 0.0408743 0.09534101 0.06219955 0.05873907 0.05319458 0.1290998
            sp8        sp9      sp10
mean 0.43081742 0.45978450 0.5301337
sd   0.09564121 0.07666759 0.1195193
```

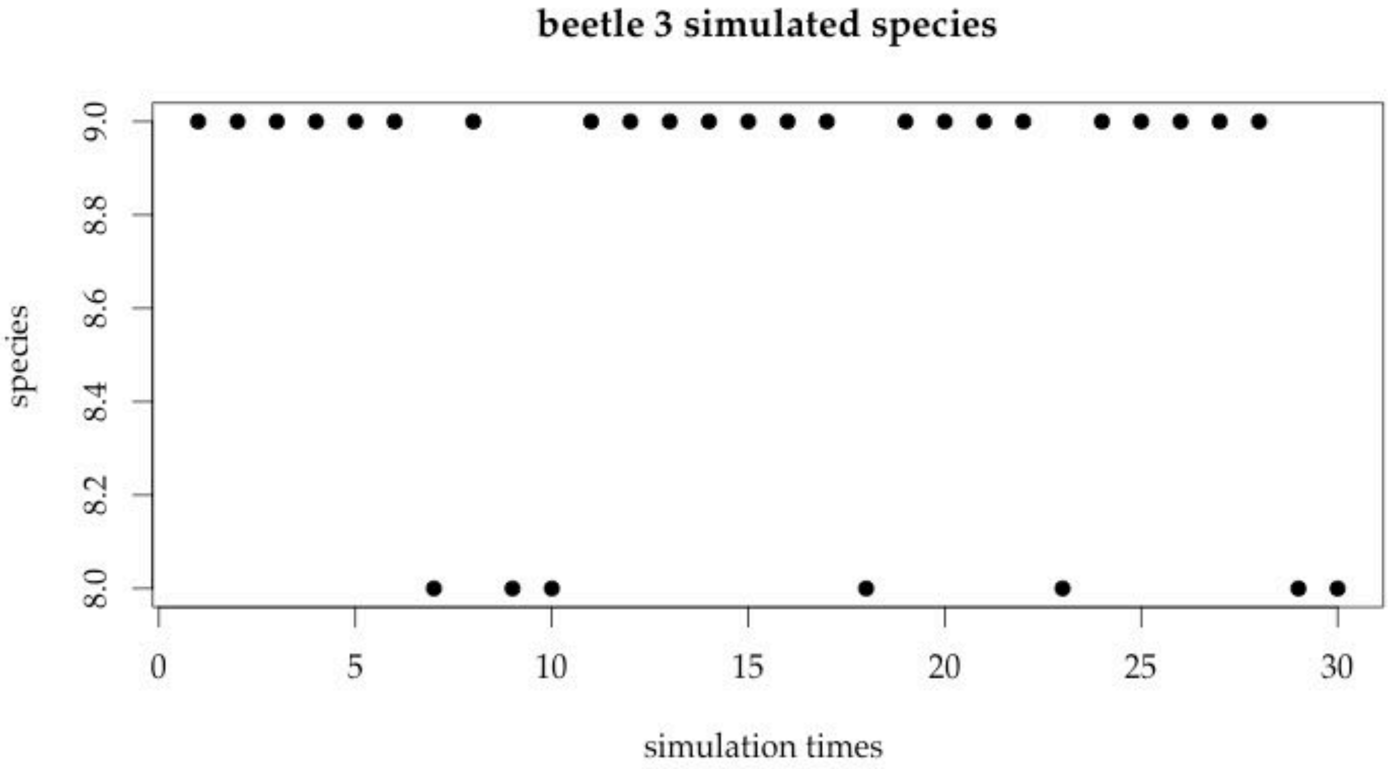
Comparing with the results of EM in Assignment 2, I would consider the results of Gibbs sampling quite satisfying.

```
            mu        vu       rho      alpha
sp1  0.8942923 1.0342643 0.2657339 0.06729892
sp2  1.3899676 0.9623014 0.0993474 0.19440148
sp3  1.7168589 1.0546248 0.1551782 0.07671346
sp4  0.5312401 1.2620517 0.8176918 0.07347779
sp5  1.5094600 1.4086777 0.9183584 0.05511000
sp6  1.7233369 0.9994049 0.1464464 0.10582222
sp7  1.3208239 0.9380040 0.4295160 0.04366880
sp8  1.0519352 1.2553052 0.4406961 0.15757814
sp9  1.0239227 1.2366704 0.4606217 0.19213491
sp10 0.9046637 1.7304230 0.5328304 0.03379428
```

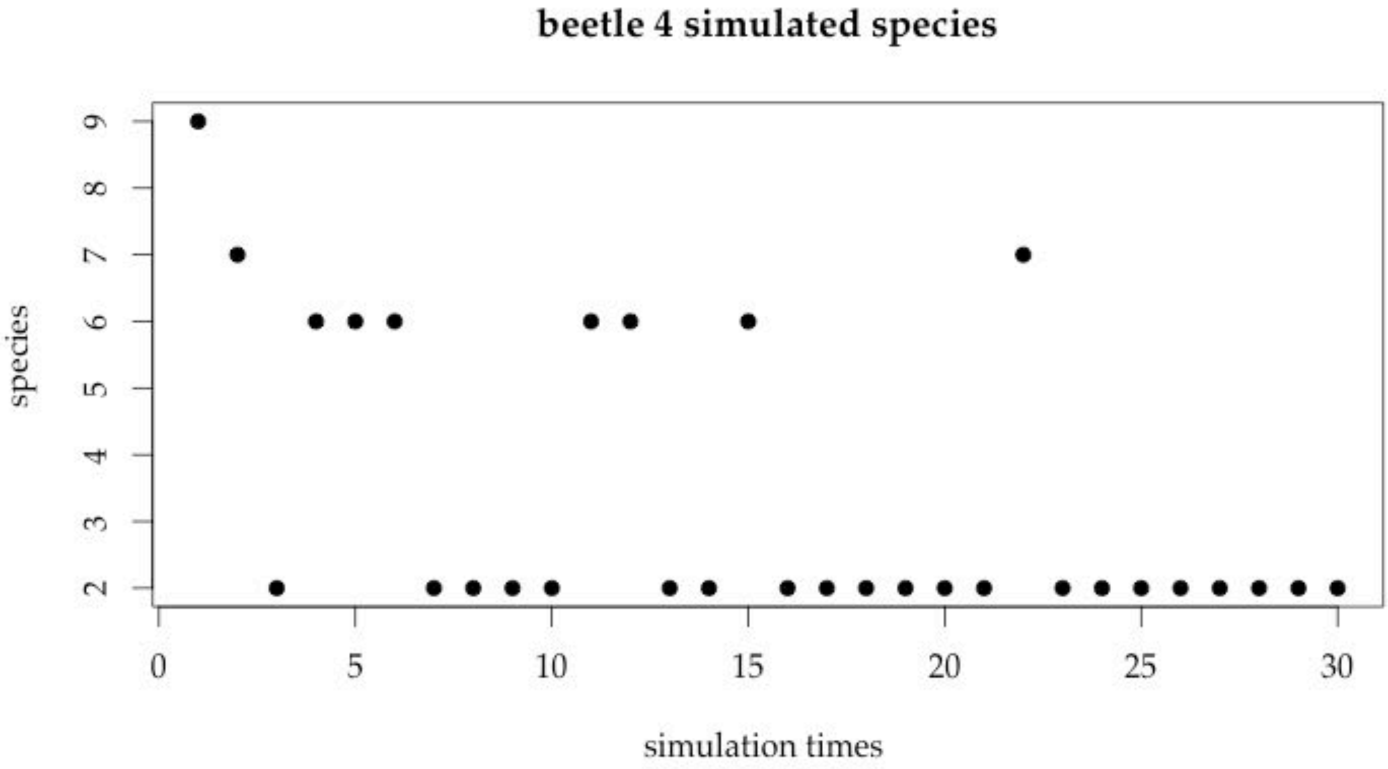
3. Consistency of species sampling

In our Gibbs sampling, we have to put a species for those data without species information in original data, and we want to check whether such “manually-added” speices are consistent.

So we do a test-run with 30 iterations on beetle 3 and beetle 4, and we generate the scatterplots of their speices. (Since we need to update)

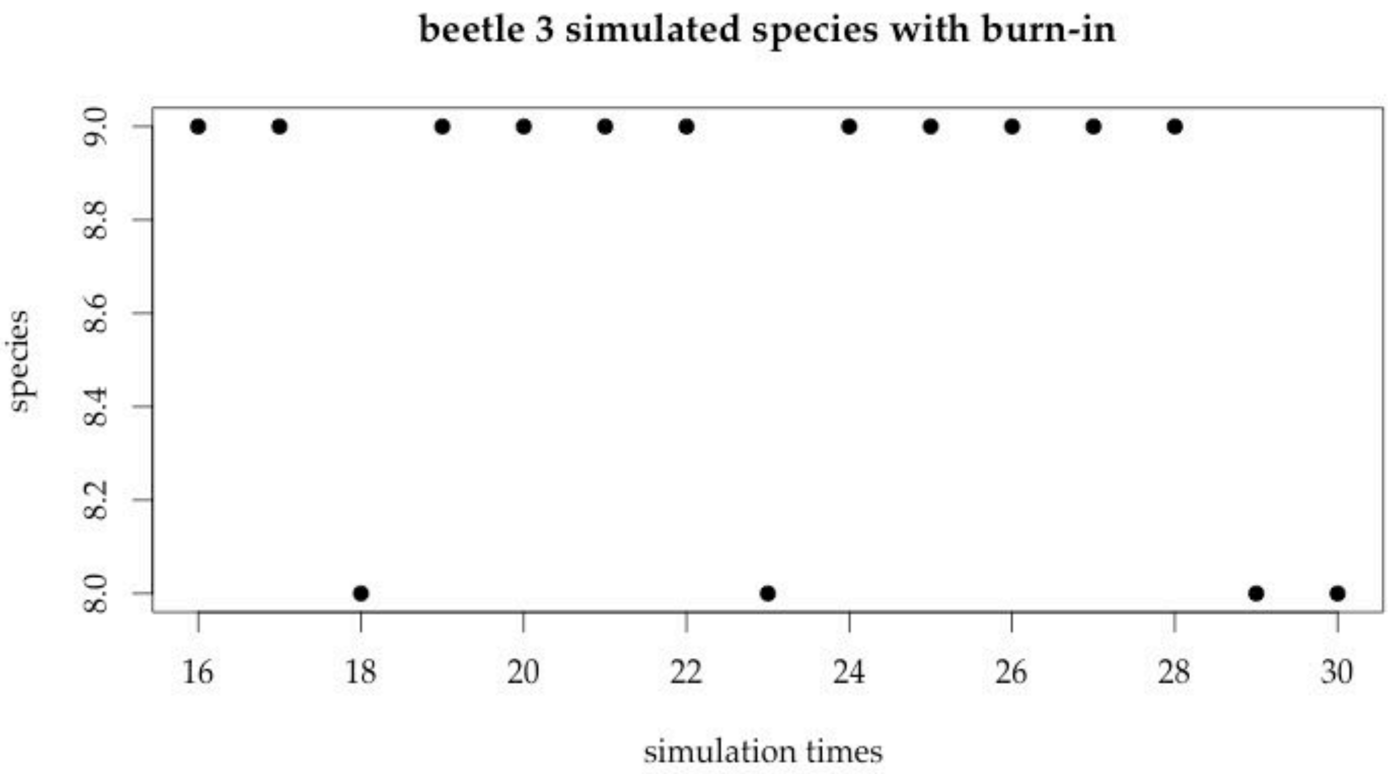


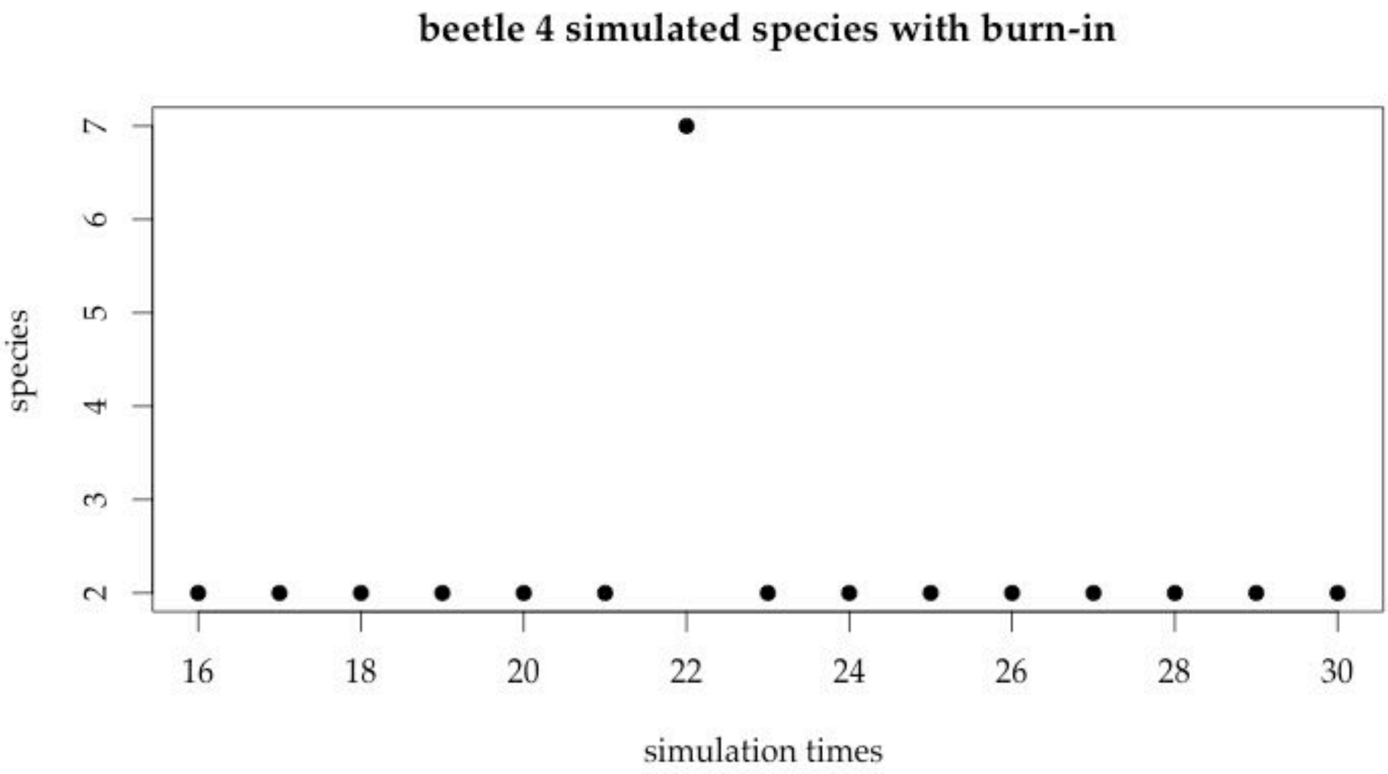
beetle 3 simulated species



beetle 4 simulated species

And consider “burn-in”.


beetle 3 simulated species with burn-in


beetle 4 simulated species with burn-in

4. Summary of Gibbs sampling

- Gibbs sampling converges after about 15 iterations (as “burn-in”), then the value of mu and vu consistently fluctuate near a certain value.
- For mu and vu, the dependencies of previous parameter is rather high; but for rho, the dependency of previous parameter is low.

5. Appendices

Source code.

```
# a function to calculate the probability of each species given a certain k-th beetle
entry
# m := log mass of this beetle
# r := log ratio of this beetle
# sw := swamp condition of this beetle
# para is a 10 by 3 parameter matrix

calcProb <- function(k, data, para, alpha) {

  entry <- data[k,]
  sp <- entry[1, 1]
  g <- entry[1, 2]
  m <- log(entry[1, 3])
  r <- log(entry[1, 4])
  sw <- entry[1, 5]
  up <- rep(0, 10)
  down <- 0

  if (is.na(sp) && is.na(g)) {
    for (i in 1:10) {
      up[i] <- helper(i, para, m, r, sw)
      down <- down+helper(i, para, m, r, sw)
    }
  }

  if (!is.na(g) && is.na(sp)) {
    if (g==1) {
      for (i in 1:3) {
        up[i] <- helper(i, para, m, r, sw)
        down <- down+helper(i, para, m, r, sw)
      }
    }

    if(g==2){
      for(i in 4:5){
        up[i] <- helper(i, para, m, r, sw)
        down <- down+helper(i, para, m, r, sw)
      }
    }

    if(g==3){
      for(i in 6:7){
        up[i] <- helper(i, para, m, r, sw)
        down <- down+helper(i, para, m, r, sw)
      }
    }

    if(g==4){
      for(i in 8:10){
        up[i] <- helper(i, para, m, r, sw)
        down <- down+helper(i, para, m, r, sw)
      }
    }
  }
  up <- up/down
  return(up)
}

helper <- function(i, para, m, r, sw) {
  return(dnorm(m, para[i, 1], 0.08)*dnorm(r, para[i, 2], 0.1)*
    (para[i, 3]^sw)*((1-para[i, 3])^(1-sw))*(alpha[i]))
}

# a function used to generate a species "manually" for those
# beetles that don't have species information at the beginning
dataModify <- function(data,para,alpha) {

  data1 <- data
  for (k in 1:nrow(data1)) {
    if (is.na(data1[k,1])) {
      data1[k,1] <- sample(1:10, 1, prob=calcProb(k, data, para, alpha))
    } else {
      data1[k,1] <- data[k,1]
    }
  }
  return(data1)
}

gibbs <- function(data, initial, iter) {

  results <- list(mu=matrix(nrow=iter, ncol=10), vu=matrix(nrow=iter, ncol=10),
   rho=matrix(nrow=iter, ncol=10))

  para <- initial
  storage <- matrix(0,iter,2)

  for (t in 1:iter) {
    data2 <- dataModify(data,para,alpha)
    # the following if-loop is only used for a test-run
    if (test==1) {
      storage[t, 1] <- data2[3, 1]
      storage[t, 2] <- data2[4, 1]
    }
    for (i in 1:10) {
      n <- sum(data2[, 1]==i)
      rho_temp <- sum(data2[which(data2[, 1]==i), 5])/n
      results$mu[t, i] <- rnorm(1, (0.5+2*sum(log(data2[which(data2[, 1]==i),
3]))/0.08^2)/(2*sqrt(0.25+n/0.08^2)), 1) *
        (1/(sqrt(0.25+n/0.08^2)))
      results$vu[t, i] <- rnorm(1, (0.5+2*sum(log(data2[which(data2[, 1]==i),
4]))/0.1^2)/(2*sqrt(0.25+n/0.1^2)), 1) *
        (1/(sqrt(0.25+n/0.1^2)))
      results$rho[t, i] <- rbeta(1, sum(data2[which(data2[, 1]==i), 5]) + 1, n + 1 -
sum(data2[which(data2[, 1]==i), 5]))
      para[i, 1] <- results$mu[t, i]
      para[i, 2] <- results$vu[t, i]
      para[i, 3] <- results$rho[t, i]
    }
  }
  # also only for a test-run
  if (test==1) {
    return(storage)
  }
  results
}
```

Script.

```
source("a3.r")
data <- read.table("./ass2-data.txt", header=T)
initial <- matrix(0.5, 10, 3)
alpha <- c(0.05, 0.20, 0.05, 0.06, 0.04, 0.15, 0.05, 0.15, 0.20, 0.05)

# To see whether the manually sampled species for "missing-species data" is consistent,
# we want to do this tiny test run. The target beetles are the third and fourth beetles
# in original data which don't have species.

test <- 1

res <- gibbs(data,initial,30)

plot(1:30, res[, 1], main="beetle 3 simulated species",
     xlab="simulation times ", ylab="species", pch=19, family="Palatino")
plot(1:30, res[, 2], main="beetle 4 simulated species",
```

```r
     xlab="simulation times ", ylab="species", pch=19, family="Palatino")

# consider burn-in?
plot(16:30, res[16:30, 1], main="beetle 3 simulated species with burn-in",
     xlab="simulation times ", ylab="species", pch=19, family="Palatino")
plot(16:30, res[16:30, 2], main="beetle 4 simulated species with burn-in",
     xlab="simulation times ", ylab="species", pch=19, family="Palatino")

# Test run swithc off (for better performance)
test <- 0

r <- gibbs(data,initial,300)

plot(NULL, xlim=c(1, 300), ylim=range(c(r$rho, r$mu)), xlab="simulation times",
ylab="value", family="Palatino")
for (i in 1:ncol(r$mu)) lines (r$mu[, i])
for (i in 1:ncol(r$vu)) lines (r$vu[, i], col="red")
for (i in 1:ncol(r$rho)) lines (r$rho[, i], col="blue")

plot(NULL, xlim=c(1, 300), ylim=range(c(0, r$mu)), xlab="simulation times",
ylab="value", family="Palatino")
for (i in 1:ncol(r$mu)) lines (r$mu[, i])

plot(NULL, xlim=c(1, 300), ylim=range(c(0, r$vu)), xlab="simulation times",
ylab="value", family="Palatino")
for (i in 1:ncol(r$vu)) lines (r$vu[, i])

plot(NULL, xlim=c(1,300), ylim=range(c(0, r$rho)), xlab="simulation times",
ylab="value", family="Palatino")
for (i in 1:ncol(r$rho)) lines (r$rho[, i])

# Discard first 15 iterations as burn-in

burn_in <- 15

# print estimated posterior means and standard deviations of each parameters

m1 <- rbind(colMeans(r$mu[(burn_in+1):300, ]),
            apply(r$mu[(burn_in+1):300, ], 2, sd))
colnames(m1) <- c("sp1", "sp2", "sp3", "sp4", "sp5", "sp6", "sp7", "sp8", "sp9", "sp10")
rownames(m1) <- c("mean", "sd")
print(m1)

m2 <- rbind(colMeans(r$vu[(burn_in+1):300, ]),
            apply(r$vu[(burn_in+1):300,], 2, sd))
colnames(m2) <- c("sp1", "sp2", "sp3", "sp4", "sp5", "sp6", "sp7", "sp8", "sp9", "sp10")
rownames(m2) <- c("mean", "sd")
print(m2)

m3 <- rbind(colMeans(r$rho[(burn_in+1):300,] ),
            apply(r$rho[(burn_in+1):300,], 2, sd))
```

```r
colnames(m3) <- c("sp1", "sp2", "sp3", "sp4", "sp5", "sp6", "sp7", "sp8", "sp9", "sp10")
rownames(m3) <- c("mean", "sd")
print(m3)
```

Derivation of 3 posterior distributions :

① Posterior for μ_s for $s=1,\cdots,10$

$$P(\mu_s \mid \log m_i, z_i = s) \propto \prod_{i=1}^{n} P(\log m_i \mid z_i = s, \mu_s) \cdot P(\mu_s \mid z_i = s)$$ species s

Note that n is not 500 or simply the size of data, instead, n is # of beetles of ✓
And z_i is the latent variable which is the species of a certain beetle.

(cont') know $\mu_s \sim N(1, 2^2)$, $\log m_i \sim N(\mu_s, 0.08^2)$

$$① \propto N(1,2^2) \cdot \prod_{i=1}^{n} N(\mu_s, 0.08^2)$$

$$= \frac{1}{2\sqrt{2}} \exp(-\tfrac{1}{2}(\mu_s - 1)^2/4) \prod_{i=1}^{n} \frac{1}{0.08\sqrt{2\pi}} \exp(-\tfrac{1}{2}(\log m_i - \mu_s)^2/0.08^2)$$

$$\propto \exp\left(-\frac{1}{2}\left(\frac{\mu_s^2 - 2\mu_s + 1}{4} + \frac{\sum_{i=1}^{n}\log m_i^2 - 2\mu_s \sum_{i=1}^{n}\log m_i + n\mu_s^2}{0.08^2}\right)\right)$$

$$\propto \exp\left\{-\frac{1}{2}\left(\mu_s^2 \underbrace{\left(\frac{1}{4} + \frac{n}{0.08^2}\right)}_{A} - \mu_s \underbrace{\left(\frac{1}{2} + \frac{2\sum_{i=1}^{n}\log m_i}{0.08^2}\right)}_{B}\right)\right\}$$

$$\propto \exp\left\{-\frac{1}{2}(A\mu_s^2 - \mu_s B)\right\}$$

$$\propto \exp\left\{-\frac{1}{2}\left(\sqrt{A} - \mu_s - \frac{B}{2\sqrt{A}}\right)^2 / 1^2\right\} \cdot \frac{1}{1\sqrt{2\pi}}$$

$$\Rightarrow \sqrt{A}\,\mu_s \sim N\left(\frac{B}{2\sqrt{A}}, 1^2\right)$$

$$\mu_s \sim \frac{1}{\sqrt{A}} N\left(\frac{B}{2\sqrt{A}}, 1^2\right)$$

$$\frac{1}{\sqrt{\frac{1}{4} + \frac{n}{0.08^2}}} N\left(\frac{\frac{1}{2} + 2\sum_{i=1}^{n}\log m_i / 0.08^2}{2\sqrt{\frac{1}{4} + \frac{n}{0.08^2}}}, 1^2\right)$$

Similarily,

② Posterior of $\nu_s \propto \exp\{-\frac{1}{2}(C\nu_s^2 - \nu_s D)\}$ for some C, D
&

$$\nu_s \sim \frac{1}{\sqrt{\frac{1}{4} + \frac{n}{0.1^2}}} N\left(\frac{\frac{1}{2} + 2\sum_{i=1}^{n}\log r_i / 0.1^2}{2\sqrt{\frac{1}{4} + n/0.1^2}}, 1^2\right)$$

③ Posterior of φ_s

$$= P(\varphi_s \mid sw_i, z_i = s)$$

$$\propto P(sw_i \mid z_i = s) \prod_{i=1}^{n} P(\varphi_s \mid z_i = s, sw_i)$$

$$\propto \text{Beta}(1,1) \cdot \text{Beta}(\alpha, \beta)$$

$$\propto \frac{\Gamma(1)^2}{\Gamma(2)} \cdot \varphi_s^{1-1} \cdot (1-\varphi_s)^{1-1} \cdot \varphi_s^{\alpha-1} \cdot (1-\varphi_s)^{\beta-1}$$

where $\alpha = \sum_{i=1}^{n} sw_i + 1$, $\beta = n + 1 - \sum_{i=1}^{n} sw_i$

so $\varphi_s \sim 1 \cdot 1 \cdot 1 \cdot \text{Beta}(\alpha, \beta)$

$$\varphi_s \sim \text{Beta}\left(\sum_{i=1}^{n} sw_i + 1,\ n+1 - \sum_{i=1}^{n} sw_i\right)$$