

SUPPORTING INFORMATION

Mentawai's endemic, relictual fauna: is it evidence for Pleistocene extinctions on Sumatra?

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Appendix S1 Code to simulate species absence on Sumatra, Malaysia, Java and Borneo in R under different scenarios.

```
#####  
### set up data #####  
  
#note that species lost/absent from all four islands are by definition Mentawai endemics and #therefore  
not included in the simulation  
Nvec=c(rep(3,6), rep(2,2), rep(1,11)) #numbers of species lost on 3 (here: 6), 2 (here: 2), 1 (here: 11)  
#islands; example: mammals  
nspec=length(Nvec) # total number of species lost on at least one island  
nsim=10000 #number of simulations  
  
#####  
### 0 model #####  
  
M0 = matrix (nrow=nsim, ncol=4) #matrix to hold simulation results = number of species missing on  
#each of the four islands for each simulation  
for (k in 1:nsim) {  
  llist=vector('list')  
  for (i in 1:nspec) {  
    llist[[i]]<-sample (c(1:4), Nvec[i], replace=FALSE) #randomly select islands species i is missing from  
  }  
  ## 1 = Sumatra  
  ## 2 = Malaysia  
  ## 3 = Java  
  ## 4 = Borneo  
  Ivec=rep(0,4) ### counts how many species were lost on each island  
  for (i in 1: nspec) {
```

```

for(j in 1:4){
if (j %in% Ilist[[i]] == TRUE) Ivec[j]= Ivec[j]+1
}}
M0[k,]<-Ivec
}

```

```

#####
### distance model #####

```

```

pvec=c(0.089,0.281, 0.284, 0.345)
MD = matrix (nrow=nsim, ncol=4)
for (k in 1:nsim) {
IlistD=vector('list')
for (i in 1:nspec) {
IlistD[[i]]<-sample (c(1:4), Nvec[i], prob=pvec, replace=FALSE)
}
IvecD=rep(0,4)
for (i in 1: nspec) {
for(j in 1:4){
if (j %in% IlistD[[i]] == TRUE) IvecD[j]= IvecD[j]+1
}}
MD[k,]<-IvecD
}

```

```

#####
### connectivity model #####

```

```

pvecC=c(0.06,0.301, 0.304, 0.334)
MC = matrix (nrow=nsim, ncol=4)
for (k in 1:nsim) {
IlistC=vector('list')
for (i in 1:nspec) {
IlistC[[i]]<-sample (c(1:4), Nvec[i], prob=pvecC, replace=FALSE)
}
IvecC=rep(0,4)
for (i in 1: nspec) {
for(j in 1:4){
if (j %in% IlistC[[i]] == TRUE) IvecC[j]= IvecC[j]+1
}}

```

```
MC[k,]<-IvecC
}
```

```
#####  
### connectivity + sampling bias model #####
```

```
ICS=c(0.06*2,0.301, 0.304, 0.334)  
pvecCS=ICS/sum(ICS)  
MS3 = matrix (nrow=nsim, ncol=4)  
for (k in 1:nsim) {  
  IlistS3=vector('list')  
  for (i in 1:nspec) {  
    IlistS3[[i]]<-sample (c(1:4), Nvec[i], prob=pvecCS, replace=FALSE)  
  }  
  IvecS3=rep(0,4)  
  for (i in 1: nspec) {  
    for(j in 1:4){  
      if (j %in% IlistS3[[i]] == TRUE) IvecS3[j]= IvecS3[j]+1  
    }  
  }  
  MS3[k,]<-IvecS3  
}
```