Processing and Analysis of Biological Data

Joint Species Distribution Modelling

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Introduction

In community ecology, chemical ecology and many other sub-fields, data are often multivariate in comprising e.g. many species or many chemical compounds. Traditionally, these data have normally been analysed by ordination methods such as principal component analysis, (detrended) correspondence analysis, redundancy analysis, non-metric multidimensional scaling (NMDS) etc. Recently however, there has been an explosive development of model-based approaches falling into the category of "joint models". In this chapter we will consider such joint models applied to multivariate data on species communities, thus fitting *joint species distribution models*.

The HMSC framework

Hierarchical Modelling of Species Communities (Hmsc) is a conceptual framework for analysis of community-ecological data, currently implemented in the Bayesian framework in the `R` package `Hmsc`. For a complete introduction to the framework, have a look at the paper

Ovaskainen, O., G. Tikhonov, A. Norberg, F. G. Blanchet, L. Duan, D. Dunson, T. Roslin, and N. Abrego. 2017. How to make more out of community data? A conceptual framework and its implementation as models and software. Ecol Lett 20:561-576.

In the following sections, we will go through the basics of model fitting and interpretation of an `Hmsc` model. As an example, we will analyse a dataset on Euglossine bee communities from the Brazilian atlantic forest.

Model fitting

When fitting models with Bayesian inference, the model fitting can take a long time and is always performed separately from subsequent postprocessing. First, we read in and format a set of datafiles that we will use in the analysis.

```
Y = read.csv(file="datasets/euglossini/Y.csv")
XData = read.csv(file="datasets/euglossini/XData.csv")
XData$method = as.factor(XData$method)

TrData = read.csv(file="datasets/euglossini/TrData.csv")
TrData = as.data.frame(TrData)
rownames(TrData) = colnames(Y)
names(TrData) = "genus"

dfPi = read.csv(file="datasets/euglossini/dfPi.csv")
```

```
dfPi$SA = as.factor(dfPi$SA)
dfPi$SU = as.factor(dfPi$SU)
```

After reading the data, it is good to check that all the data components have the same number of samples and species. For example, the predictor variables (`XData`) should have as many rows as the response variables (`Y`).

```
dim(Y)
```

```
## [1] 178  61
```

```
dim(XData)
```

```
## [1] 178   9
```

Similarly, the trait data (`TrData`) should have as many species as the response data (`Y`).

```
dim(Y)
```

```
## [1] 178  61
```

```
dim(TrData)
```

```
## [1] 61  1
```

Next, we proceed to set up our model. In the current model we will fit two hierarchical random factors, study area (SA) and sampling unit (SU). The sampling units correspond to the rows in the dataset. While in a univariate model we would usually not include a random effect with no replication within each level, in a joint model this makes sense because we have several (many) species sampled in the same sampling units, and we want to model the non-independence of these.

```
library(Hmsc)
rL1 = HmscRandomLevel(units = unique(dfPi$SA))
rL2 = HmscRandomLevel(units = unique(dfPi$SU))
rL1
```

```
## Hmsc random level object with 72 units. Spatial dimensionality is 0 and number of covariates is 0.
```

```
rL2
```

```
## Hmsc random level object with 178 units. Spatial dimensionality is 0 and number of covariates is 0.
```

Next, we set the formulae for the predictors. We also include a "trait" genus, which tells us which genus the species belong to. This will act as a very simple phylogenetic structure in the model. (`Hmsc` also allows using an actual phylogeny, but we skip that here for simplicity).

```
XFormula = ~ method + effort + altitude + MAT + MAP + Tseason + Pseason +
              forest. + lu_het

TrFormula= ~genus
```

Now, we are ready to set up the model. We will fit a presence-absence model, which means that we only ask whether a species is present (1) or absent (0) in each sample. We therefore choose a binomial model with a *probit* link function (recall that the probit link is very similar to the logit link, but works better in the context of Bayesian model fitting).

```
m1 = Hmsc(Y = as.matrix((Y>0)*1),
          XData = XData,  XFormula = XFormula,
          TrData = TrData, TrFormula = TrFormula,
          distr = "probit",
          studyDesign = dfPi,
          ranLevels = list(SA=rL1, SU=rL2))
```

The next step is to set the sampling parameters and run the MCMC sampling. The chain below will run for a total of 15000 iterations, with the first 5000 discarded as a transient, and one sample taken every 10th iteration after this initial "burn-in period". Because the sampling takes a long time, we save the model object once the sampling is done.

```
thin = 10
samples = 10
adaptNf = ceiling(0.4*samples*thin)
transient = ceiling(0.5*samples*thin)
nChains = 2

a=Sys.time()
m1 = sampleMcmc(m1, samples = samples, thin = thin,
                adaptNf = rep(adaptNf, 2),
                transient = transient,
                nChains = nChains, nParallel = 2, updater=list(GammaEta=FALSE))
Sys.time()-a

filename = paste0("model_thin_", thin, ".RData")
save(m1, file=filename)
```

Postprocessing

We are now ready to start exploring the fitted model. First, we read the model object and explore convergence by computing effective sample sizes and potential scale reduction factors.

```
load("model_thin_10.RData")

mpost = convertToCodaObject(m1)

esBeta = effectiveSize(mpost$Beta)
summary(esBeta)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   82.44  395.47  552.11  607.09  761.05 1726.59
```

```
psrf = gelman.diag(mpost$Beta, multivariate=FALSE)$psrf
summary(psrf)
```

```
##    Point est.       Upper C.I.
##  Min.   :0.9993   Min.   :0.9993
##  1st Qu.:1.0007   1st Qu.:1.0025
##  Median :1.0027   Median :1.0096
##  Mean   :1.0060   Mean   :1.0228
##  3rd Qu.:1.0067   3rd Qu.:1.0269
##  Max.   :1.0931   Max.   :1.3326
```

Next, we assess the explanatory (discriminatory) power of the model, as quantified by the coefficient of discrimination (`TjurR2`) and the area under curve (`AUC`) statistic (a common measure of model performance in presence-absence model, for which 0.5 means the model is just as good as expected by chance, and 1 means the model is very good).

```
predY = computePredictedValues(m1, expected=T)
MF = evaluateModelFit(hM=m1, predY = predY)

mean(MF$TjurR2, na.rm=T)
```

```
## [1] 0.4753148
```

```
mean(MF$AUC, na.rm=T)
```

```
## [1] 0.9656342
```

```
range(MF$TjurR2)
```

```
## [1] 0.08660067 0.86351826
```

```
range(MF$AUC)
```

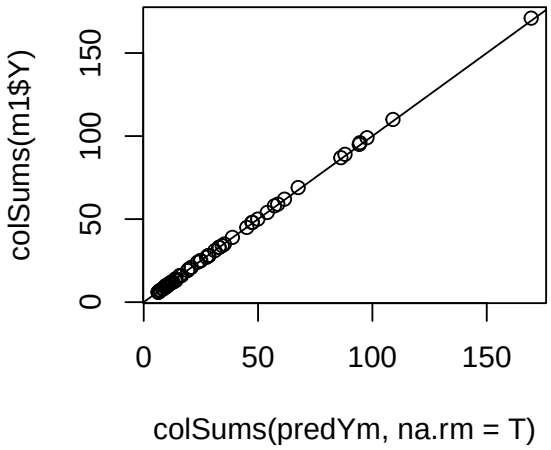
```
## [1] 0.860048 1.000000
```

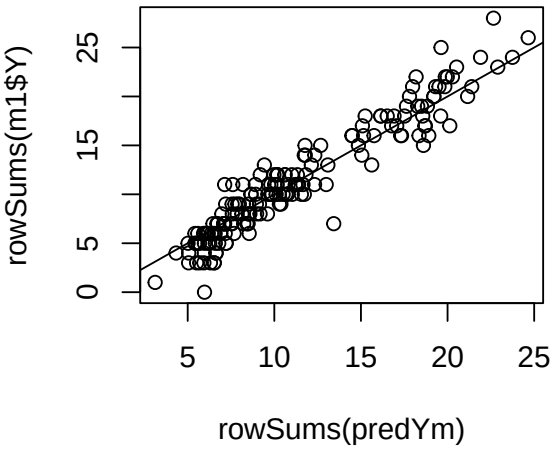
We can also check if the model predicts well the number of species per site (species richness), and the number of occurrences per species. These are given by the row and column sums of the matrix `Y`.

```
predYm = apply(predY, 1:2, mean)

par(mfrow=c(1,2))
plot(colSums(predYm,na.rm=T), colSums(m1$Y))
lines(-1000:1000, -1000:1000)
#cor(colSums(predYm), colSums(m1$Y))^2

plot(rowSums(predYm), rowSums(m1$Y))
lines(-1000:1000, -1000:1000)
```






```
#cor(rowSums(predYm), rowSums(m1$Y))^2
```

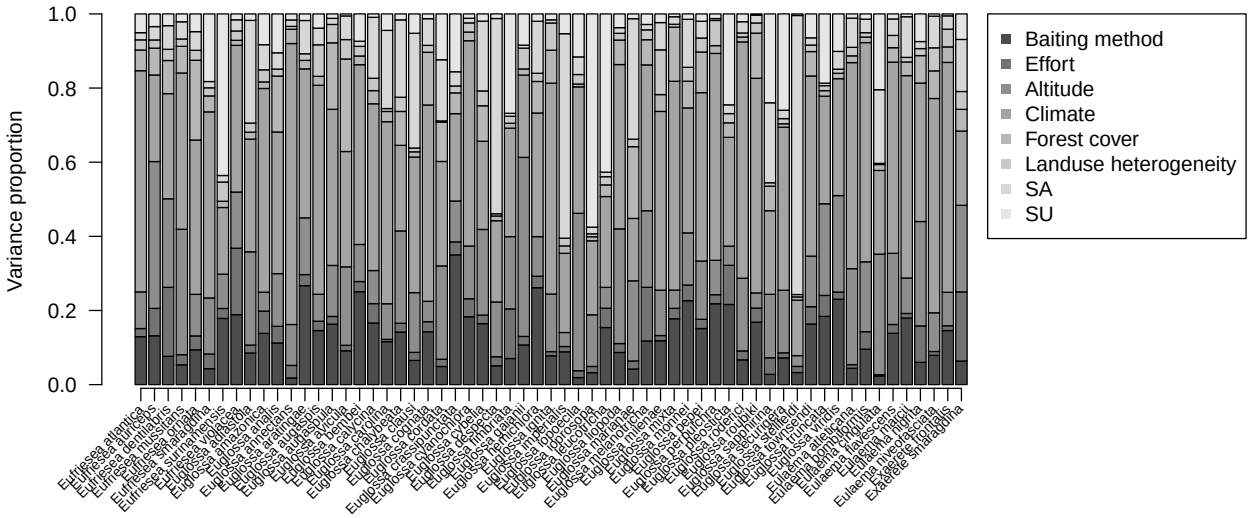
The `Hmsc` package has a build-in function for performing variance partitioning for the fixed and random parts of the model.

```
group = c(rep(1,3), 2, rep(3,1) ,rep(4,4), rep(5,1), rep(6,1))
cbind(m1$covNames, group)
```

```
##                         group
##  [1,] "(Intercept)"     "1"
##  [2,] "methodNetTraps"  "1"
##  [3,] "methodTraps"     "1"
##  [4,] "effort"          "2"
##  [5,] "altitude"        "3"
##  [6,] "MAT"             "4"
##  [7,] "MAP"             "4"
##  [8,] "Tseason"         "4"
##  [9,] "Pseason"         "4"
## [10,] "forest."         "5"
## [11,] "lu_het"          "6"
```

```
groupnames = c("Baiting method", "Effort", "Altitude", "Climate", "Forest cover", "Landuse heterogeneit
VP = computeVariancePartitioning(hM = m1, group = group, groupnames = groupnames)
#VP$vals = VP$vals[,rev(order(colSums(VP$vals[1:6,])))]
```

```
leg = c(VP$groupnames, m1$rLNames)
par(mar=c(8,4,2,10), xpd=T)
bp = barplot(VP$vals, xlab = "", ylab = "Variance proportion",
        las = 1, col=grey.colors(8), xaxt="n")
axis(1, at=bp, labels=F)
legend(75, 1, leg, pch=15, col=grey.colors(8))
text(bp, -0.06, srt = 45, adj = 1,cex=.7,
     labels = gsub("_", " ", m1$spNames), xpd = TRUE)
```

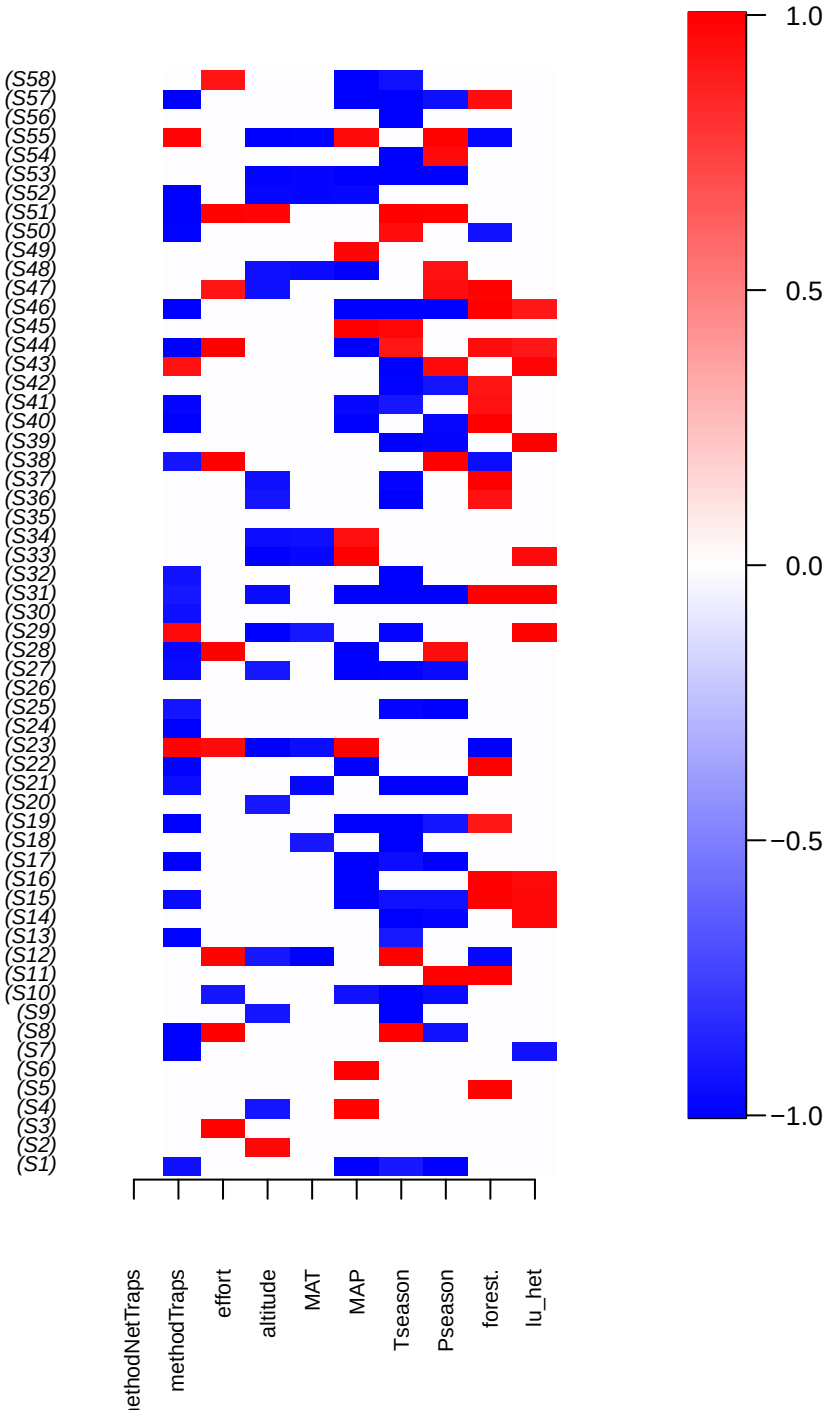


Extracting parameter estimates

The HMSC model includes a lot of parameters, and it rarely makes sense to report all of them in a table (at least not in the main text). One option is to plot the matrix of parameter estimates (or their support, as in the example below).

```
pbeta = getPostEstimate(m1, "Beta")

plotBeta(m1, post=pbeta, param = "Support", covOrder="Vector", covVector=c(2:11),
         supportLevel = .95, SpeciesOrder = "Vector", SpVector = 1:58,
         spNamesNumbers=c(F,T), covNamesNumbers = c(T,F))
```



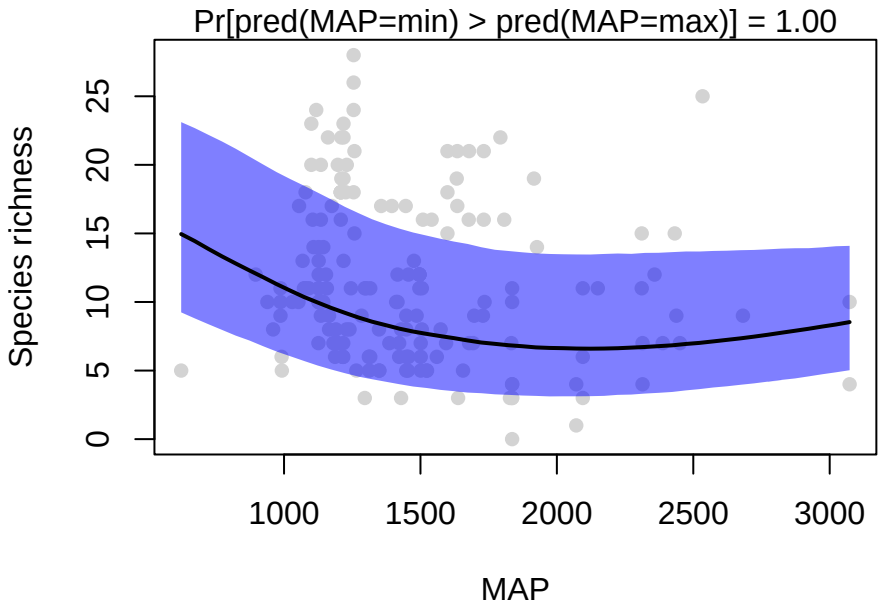
Because there are so many parameters, it can also be useful to summarize the results across species by plotting e.g. a covariate against the predicted species richness.

```
x=2
Gradient=constructGradient(m1, focalVariable = "MAP", ngrid=50,
```

```
                              non.focalVariables = list(
                                method = list(1),
                                effort = list(1),
                                altitude = list(x),
                                MAT = list(x),
                                Tseason = list(x),
                                Pseason = list(x),
                                forest = list(x),
                                lu_het = list(x)))

predY = predict(m1, Gradient=Gradient, expected=TRUE, predictEtaMean=FALSE)

plotGradient(m1, Gradient, predY, measure="S", showData = T)
```




```
## [1] 0.0035
```