Journal of Statistical Software

MMMMMM YYYY, Volume VV, Issue II. http://www.jstatsoft.org/

Selecting priority areas from diversity and individual species abundance DiversityOccupancy

Derek Corcoran
University of Missouri

Elisabeth Webb
University of Missouri, USGS

Dylan Kesler
Institute Of Bird Population

Abstract

Lately occupancy modeling has been vastly used as a tool for ecological research and management planing. However mostly it is used by interpreting single species models. We present the **DiversityOccupancy** in the R environment. The objective of this package is to simultaneously model factors associated with occupancy and abundance of individual species using a detection history file, and to use predicted abundances to calculate species diversity for each sampling site. The package then models factor(s) associated with among-site species diversity, which can then be combined with spatial data to identify areas that contain both high abundance of species of conservation concern and high species diversity.

Keywords: **DiversityOccupancy**, Occupancy Modeling, R.

1. Introduction

1.1. Single-species or multiple-species management

The ecological and management literature has usually valued the idea of managing for diversity. This, however clashes with the classic way in which conservation takes place. conservation agencies, goverments and scientists usually classify species according to a conservation status, and policies are made to safeward the ones that are envisioned as species of conservation concerned. Single species are easier to manage for, and it is easier to keep track the status of a specie than it is to define management for diversity, it is also more complicated to sample to keep track of changes in diversity.

One of the problems of managing simple species, is that is usually very difficult to predict what will happend to other species and because of that it is hard to predict what will happend to diversity (Pulliam 2000)

In this paper we present package **DiversityOccupancy**, used in the R environment, The objective of this package is to simultaneously model factors associated with occupancy and abundance of individual species using a detection history file, and to use predicted abundances to calculate species diversity for each sampling site. The package then models factor(s) associated with among-site species diversity, which can then be combined with spatial data to identify areas that contain both high abundance of species of conservation concern and high species diversity.

Single species conservation methods vs multiple species method, possibility of using both for taking decisions

In the last decade, Occupancy modeling has been used more and more as a method to account for how species respond to environmental or anthropogenic factors. It has also been shown to be useful as a species distribution modeling tool when species have imperfect detection. Anthore use for what it has been used is for managers to change the environment of managed areas in order to improve the status of species of conservation concern. Unfortunantely this decision usually comes without taking into account the effect of such management action on species diversity. There has been several authors championing for the use of species specific or diversity related approaches to plan conservation issues, (Hill 1982; MacKenzie, Nichols, Lachman, Droege, Andrew Royle, and Langtimm 2002) but as far as we know this is the first method that takes into account both species diversity and individual species abundance in order to select conservation areas (MacKenzie *et al.* 2002).

1.2. Installing DiversityOccupancy

Requirements

To use this package you need R version 3.2.2 or newer (use the function `sessionInfo()` in your R session to check your current version).

Installing the package

Install from cran repository

```
install.packages("DiversityOccupancy")
```

1.3. Objectives of the Package

2. Use of the package

In order to calculate abundance and alpha diversity we need at least three files:

Detection history of multiple species A data frame consisting on the detection history of at least two species. As an example **DiversityOccupancy** has the data-set BatOccu which contains detection histories of 17 species of bats in the Plumas National Forest for 3 consecutive days (Columns) in 49 different sites (Rows). The data set includes a 1 for each time a species was detected, and a 0 for each time it was not detected.

A detection for the first three species is presented below:

```
library(DiversityOccupancy)
data("BatOccu")
head(BatOccu[1:9])
```

```
  Myyu1 Myyu2 Myyu3 Myca1 Myca2 Myca3 Myci1 Myci2 Myci3
1     0     0     0     0     0     0     0     0     0
2     1     0     0     1     0     0     0     0     0
3     0     0     0     0     1     0     0     0     0
4     0     0     0     0     0     0     0     0     0
5     0     0     0     1     1     1     0     0     0
6     1     0     0     1     1     1     0     0     0
```

Site covariates Site covariates are presented in a data frame consisting of measurements taken at each site. The covariates are used singly and in combination to model occupancy or abundance, and they should be variables that are stable within the scope of the length of the study. In **DiversityOccupancy** there is an example concordant with the BatOccu data set called sampling.cov:

```
data("sampling.cov")
head(sampling.cov)
```

```
  Distance.to.water Distance.to.road Existing.vegetation Fire.Interval Altitude
1                 0         325.2647            3.000000      14.79164 1859.337
2                 0           0.0000           15.294588      11.00000 1839.813
3                 0           0.0000            4.769200      16.00000 1890.586
4                 0           0.0000            4.705464      18.27010 1927.237
5                 0           0.0000           14.224747      14.97247 1682.559
6                 0        2308.6010           15.727460      15.81841 1515.009
  Burn.intensity.soil Burn.intensity.Canopy Burn.intensity.basal
1          0.00000000            0.00000000           0.00000000
2          0.24802029            0.12812701           0.12812701
3          0.00000000            0.00000000           0.00000000
4          0.00000000            0.00000000           0.00000000
5          3.42075635            3.84151252           5.30799686
6          0.01135227            0.01135223           0.01135223
```

Detection covariates A list of data frames, in which each data frame includes a daily measurement of variables with the potential to affect detection probabilities. It is important that each element (data frame) of the list has a name, so that it can be called to fit the occupancy model. These variables are used to model the probability of detection.

DiversityOccupancy has a data set called *Dailycov* which illustrates how the Daily covariates have to be structured:

```
#All the items of the ist must have names
names(Dailycov)
```

```
[1] "Julian"   "Maxhum"   "Maxtemp"  "Meanhum"  "Meantemp" "Minhum"   "Mintemp"
[8] "sdhum"    "sdtemp"
```

```
#here we see the first dataframe of the Dailycov dataset
head(Dailycov[[1]])
```

```
  Julian.Julian1 Julian.Julian2 Julian.Julian3
1      -1.683391      -1.683391      -1.683019
2      -1.620723      -1.620723      -1.620362
3      -1.684443      -1.684443      -1.684071
4      -1.557310      -1.557310      -1.556958
5      -1.429475      -1.429475      -1.434405
6      -1.241253      -1.241253      -1.240951
```

2.1. Fiting models for abundance and predicting alpha diversity

In this example we will fit and model the abundance for 17 bat species and calculate alpha diversity from those results.

\begin{CodeChunk} \begin{CodeInput} BatDiversity <-diversityoccu(pres = BatOccu, sitecov = sampling.cov, obscov = Dailycov,spp = 17, form = ~ Julian + Meanhum ~ Burn.intensity.soil + I(Burn.intensity.soil^2), dredge = FALSE) \end{CodeInput} \end{CodeChunk}

The resulting object of class diversityoccupancy has the following elements

```
names(BatDiversity)
```

```
[1] "Covs"      "models"    "Diversity" "species"
```

If you need to see the parameters of the model of one of the species, you call the species number with the element$models. For example extract the model for the second species:

```
BatDiversity$models[[2]]
```

```
Call:
occuRN(formula = form, data = models[[i]])

Abundance:
                          Estimate     SE      z P(>|z|)
(Intercept)               0.000567 0.2829  0.002   0.998
Burn.intensity.soil       0.543374 0.3826  1.420   0.156
I(Burn.intensity.soil^2) -0.092936 0.0996 -0.933   0.351

Detection:
            Estimate    SE      z P(>|z|)
(Intercept)    0.113 0.357  0.317  0.7512
```

```
Julian        -0.097 0.267 -0.364  0.7159
Meanhum       -0.548 0.246 -2.228  0.0259

AIC: 180.113
```

The species parameter for a diversityoccupancy object shows us a table with the abundance and alpha diversity calculated for each sampled point:

summary(BatDiversity$species)

```
       h             species.1          species.2          species.3           species.4
 Min.   :2.115   Min.   :0.3528   Min.   :1.001   Min.   :0.1156   Min.   :0.4802
 1st Qu.:2.115   1st Qu.:0.3528   1st Qu.:1.001   1st Qu.:0.1156   1st Qu.:0.5504
 Median :2.277   Median :0.5153   Median :1.300   Median :0.1883   Median :0.5863
 Mean   :2.291   Mean   :0.7520   Mean   :1.523   Mean   :0.3401   Mean   :0.6125
 3rd Qu.:2.488   3rd Qu.:1.2428   3rd Qu.:2.045   3rd Qu.:0.6356   3rd Qu.:0.5870
 Max.   :2.553   Max.   :1.3027   Max.   :2.214   Max.   :0.6695   Max.   :0.8884
   species.5          species.6            species.7          species.8        species.9
 Min.   :0.3020   Min.   :0.0000223   Min.   : 2.776   Min.   :1.716   Min.   :0.1006
 1st Qu.:0.3020   1st Qu.:0.0000223   1st Qu.: 4.261   1st Qu.:1.716   1st Qu.:0.2089
 Median :0.5035   Median :0.0004349   Median : 6.424   Median :2.035   Median :0.3037
 Mean   :0.6907   Mean   :0.0983938   Mean   : 6.267   Mean   :2.603   Mean   :0.4328
 3rd Qu.:1.1210   3rd Qu.:0.1874298   3rd Qu.: 6.424   3rd Qu.:3.584   3rd Qu.:0.3037
 Max.   :1.2776   Max.   :0.3654810   Max.   :12.836   Max.   :4.150   Max.   :1.6148
   species.10         species.11         species.12         species.13       species.14
 Min.   :0.3994   Min.   :0.5758   Min.   :0.3391   Min.   :1.638   Min.   :1.016
 1st Qu.:0.5334   1st Qu.:0.5770   1st Qu.:0.3391   1st Qu.:1.638   1st Qu.:1.239
 Median :0.5334   Median :0.5816   Median :0.5080   Median :1.750   Median :1.360
 Mean   :1.5900   Mean   :0.8988   Mean   :0.5584   Mean   :2.746   Mean   :1.472
 3rd Qu.:1.3059   3rd Qu.:1.0866   3rd Qu.:0.7826   3rd Qu.:3.533   3rd Qu.:1.369
 Max.   :7.1212   Max.   :1.9802   Max.   :0.9358   Max.   :6.038   Max.   :2.525
   species.15         species.16          species.17
 Min.   :0.1267   Min.   : 0.7016   Min.   :0.06252
 1st Qu.:0.1267   1st Qu.: 0.7016   1st Qu.:0.06252
 Median :0.2016   Median : 0.7636   Median :0.12145
 Mean   :0.2653   Mean   : 2.9118   Mean   :0.36548
 3rd Qu.:0.4187   3rd Qu.: 3.3637   3rd Qu.:0.74717
 Max.   :0.4708   Max.   :11.9074   Max.   :0.90081
```

2.2. Automatic model selection for abundance models

If the option of dredge is set to "TRUE", then diversityoccu attempts to fit all first order models, and it selects the one with the lowest AICc value, for each species. Be aware that processing times rapidly increases with added numbers of parameters, and that processing can require many hours or days for complex data sets. The following graph and table shows the processing time for the BatOccu data set.

From now on we will work with automatically selected models for bat abundance and diversity using an information theoretic approach (AICc).

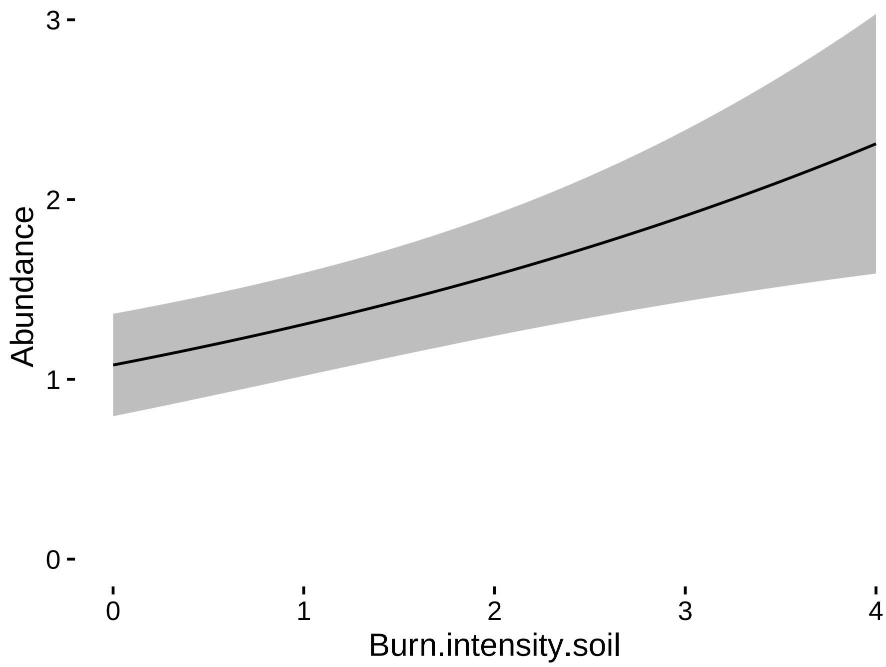
\begin{CodeChunk} \begin{CodeInput} batmodel.selected <- diversityoccu(pres = BatOccu, sitecov = sampling.cov, obscov = Dailycov,spp = 17, form = ~ Julian + Meanhum ~ Burn.intensity.soil + I(Burn.intensity.soil^2), dredge = TRUE) \end{CodeInput} \end{CodeChunk}

Below we present an example of an analysis with the full model (includes all variables) and subsequently results from a model selection analysis, both of them only for the second species:

```
BatDiversity$models[[2]]



Call:
occuRN(formula = form, data = models[[i]])

Abundance:
                          Estimate     SE      z P(>|z|)
(Intercept)               0.000567 0.2829  0.002   0.998
Burn.intensity.soil       0.543374 0.3826  1.420   0.156
I(Burn.intensity.soil^2) -0.092936 0.0996 -0.933   0.351

Detection:
            Estimate    SE      z P(>|z|)
(Intercept)    0.113 0.357  0.317  0.7512
Julian        -0.097 0.267 -0.364  0.7159
Meanhum       -0.548 0.246 -2.228  0.0259

AIC: 180.113

batmodel.selected$models[[2]]



Call:
occuRN(formula = ~Meanhum + 1 ~ Burn.intensity.soil + 1, data = data2)

Abundance:
                    Estimate     SE     z P(>|z|)
(Intercept)           0.0767 0.2637 0.291  0.7712
Burn.intensity.soil   0.1901 0.0973 1.953  0.0508

Detection:
            Estimate    SE      z P(>|z|)
(Intercept)    0.143 0.351  0.407  0.6840
Meanhum       -0.530 0.242 -2.190  0.0285

AIC: 177.0765
```

The responses of individual species to specific variables can be shown using the function respnseplot.abund, bellow we show the response of abundance in species 2 to the Burn intensity soil. Note that this function automatically bounds the limits of the variable to the maximum and minimum observable values in the field.

```
responseplot.abund(batmodel.selected, spp = 2, variable = Burn.intensity.soil)
```



2.3. Model selection for alpha diversity modeling

3. Discussion

The **DiversityOccupancy** package lets scientists and managers take dessitions based on species information, diversity information or both. In some countries, laws require that the decision is taken based on endangered species information, the possibility on selecting an area, or manage environments based on both diversity and species specific information, gives a possibility to managers or decision makers wanting to use diversity with laws requiring them to take species into account.

References

Hill EP (1982). "Beaver (Castor canadensis)." In JA Chapman, GA Feldhamer (eds.), *Wild mammals of North America: biology, management, and economics*, first edition, pp. 256–281. John Hopkins University Press, Michigan.

MacKenzie DI, Nichols JD, Lachman GB, Droege S, Andrew Royle J, Langtimm CA (2002). "Estimating site occupancy rates when detection probabilities are less than one." *Ecology*, **83**(8), 2248–2255. URL http://www.esajournals.org/doi/abs/10.1890/0012-9658(2002)083%5B2248:ESORWD%5D2.0.CO%3B2.

Pulliam HR (2000). "On the relationship between niche and distribution." *Ecology letters*, **3**(4), 349–361.

Affiliation:

Derek Corcoran
University of Missouri
First line Second line
E-mail: corcoranbarriosd@missouri.edu
URL: http://rstudio.com