



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

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, 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.(?).

1.1. 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")
```

1.2. Objectives of the Package

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.

1.3. 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
1	0	325.2647	3.000000	14.79164
2	0	0.0000	15.294588	11.00000
3	0	0.0000	4.769200	16.00000
4	0	0.0000	4.705464	18.27010
5	0	0.0000	14.224747	14.97247
6	0	2308.6010	15.727460	15.81841

	Altitude	Burn.intensity.soil	Burn.intensity.Canopy	Burn.intensity.basal
1	1859.337	0.00000000	0.00000000	0.00000000
2	1839.813	0.24802029	0.12812701	0.12812701
3	1890.586	0.00000000	0.00000000	0.00000000
4	1927.237	0.00000000	0.00000000	0.00000000
5	1682.559	3.42075635	3.84151252	5.30799686
6	1515.009	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 list must have names
names(Dailycov)

[1] "Julian"    "Maxhum"    "Maxtemp"   "Meanhum"   "Meantemp"  "Minhum"
[7] "Mintemp"   "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

1.4. 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.

```
BatDiversity <-diversityoccu(pres = BatOccu, sitecov = sampling.cov, obscov =
Dailycov,spp = 17, form = ~ Julian + Meanhum ~ Burn.intensity.soil +
I(Burn.intensity.soil^2), dredge = FALSE)
```

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:

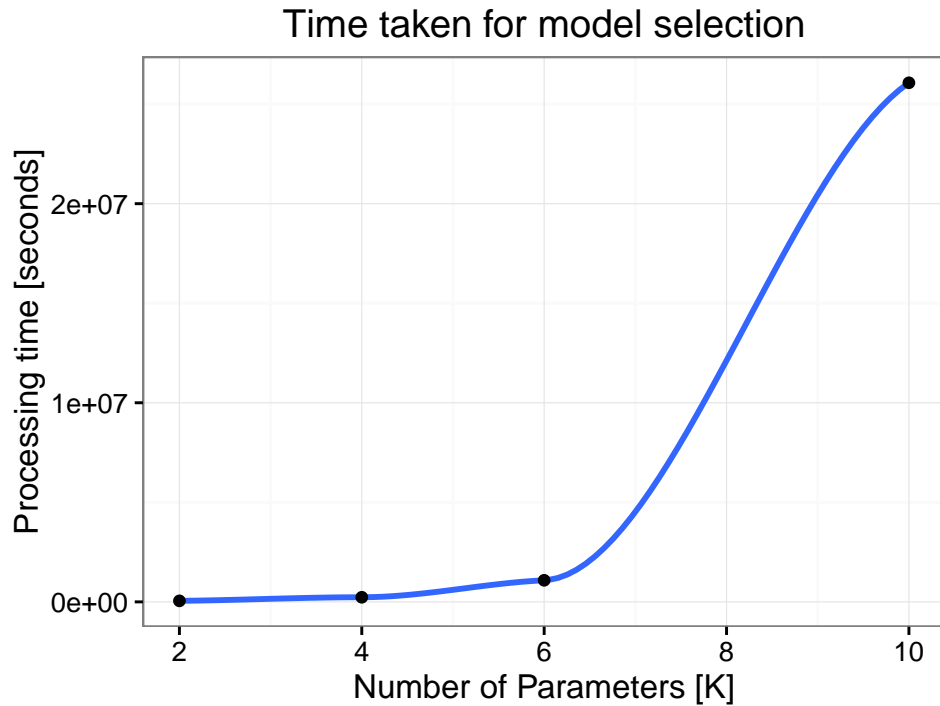
```
summary(BatDiversity$species)
```

h	species.1	species.2	species.3
Min. :2.115	Min. :0.3528	Min. :1.001	Min. :0.1156
1st Qu.:2.115	1st Qu.:0.3528	1st Qu.:1.001	1st Qu.:0.1156
Median :2.277	Median :0.5153	Median :1.300	Median :0.1883
Mean :2.291	Mean :0.7520	Mean :1.523	Mean :0.3401
3rd Qu.:2.488	3rd Qu.:1.2428	3rd Qu.:2.045	3rd Qu.:0.6356
Max. :2.553	Max. :1.3027	Max. :2.214	Max. :0.6695
species.4	species.5	species.6	species.7

Min. :0.4802	Min. :0.3020	Min. :0.0000223	Min. : 2.776
1st Qu.:0.5504	1st Qu.:0.3020	1st Qu.:0.0000223	1st Qu.: 4.261
Median :0.5863	Median :0.5035	Median :0.0004349	Median : 6.424
Mean :0.6125	Mean :0.6907	Mean :0.0983938	Mean : 6.267
3rd Qu.:0.5870	3rd Qu.:1.1210	3rd Qu.:0.1874298	3rd Qu.: 6.424
Max. :0.8884	Max. :1.2776	Max. :0.3654810	Max. :12.836
species.8	species.9	species.10	species.11
Min. :1.716	Min. :0.1006	Min. :0.3994	Min. :0.5758
1st Qu.:1.716	1st Qu.:0.2089	1st Qu.:0.5334	1st Qu.:0.5770
Median :2.035	Median :0.3037	Median :0.5334	Median :0.5816
Mean :2.603	Mean :0.4328	Mean :1.5900	Mean :0.8988
3rd Qu.:3.584	3rd Qu.:0.3037	3rd Qu.:1.3059	3rd Qu.:1.0866
Max. :4.150	Max. :1.6148	Max. :7.1212	Max. :1.9802
species.12	species.13	species.14	species.15
Min. :0.3391	Min. :1.638	Min. :1.016	Min. :0.1267
1st Qu.:0.3391	1st Qu.:1.638	1st Qu.:1.239	1st Qu.:0.1267
Median :0.5080	Median :1.750	Median :1.360	Median :0.2016
Mean :0.5584	Mean :2.746	Mean :1.472	Mean :0.2653
3rd Qu.:0.7826	3rd Qu.:3.533	3rd Qu.:1.369	3rd Qu.:0.4187
Max. :0.9358	Max. :6.038	Max. :2.525	Max. :0.4708
species.16	species.17		
Min. : 0.7016	Min. :0.06252		
1st Qu.: 0.7016	1st Qu.:0.06252		
Median : 0.7636	Median :0.12145		
Mean : 2.9118	Mean :0.36548		
3rd Qu.: 3.3637	3rd Qu.:0.74717		
Max. :11.9074	Max. :0.90081		

1.5. 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).

```
batmodel.selected <- diversityoccu(pres = BatOccu, sitecov = sampling.cov, obscov = Dailycov)
```

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

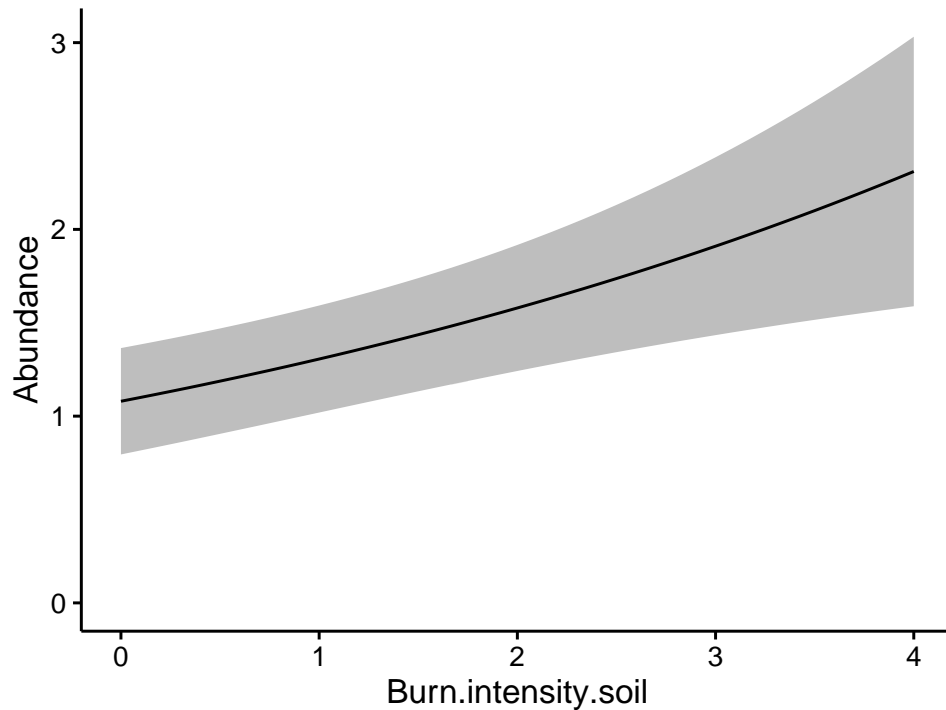
Detection:

	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 `responseplot.abund`, below 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)
```



1.6. Model selection for alpha diversity modeling

2. Discussion

The **DiversityOccupancy** package lets scientists and managers take decisions 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.

Affiliation:

Derek Corcoran

University of Missouri

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E-mail: corcoranbarriosd@missouri.edu

URL: <http://rstudio.com>