



DiversityOccupancy: A package to model occupancy, abundance, diversity and selection of priority areas based on repeated presence-absence sampling

Derek Corcoran
University of Missouri

Elisabeth Webb
University of Missouri, USGS Institute for Bird Populations

Dylan Kesler

Abstract

Occupancy modeling has been widely used as a tool for ecological research and management planning in the context of single species models. We present the package **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 to model occupancy and/or abundance. This new package also uses predicted abundances to calculate species diversity for each sampling site. **DiversityOccupancy** models factor(s) associated with among-site species diversity, which can 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, alpha diversity, Protected areas.

1. Introduction

1.1. Imperfect detection in wildlife surveys

One of the main objectives of ecology is to study the abundance and distribution of species and populations. The problem is that estimation of population is time consuming, hard to replicate and almost impossible in rare species due to the fact that they are hard to detect, which leads to false absences that might cause underestimation of abundances and distribution. Despite this, most sampling and analysis techniques don't take into account the inherent imperfect detection found in natural populations. One of the tools used to overcome this limitation is occupancy modeling.

1.2. Occupancy models, taking into account detection probability

In the last decade, Occupancy modeling has been increasingly used 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. Another 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 (MacKenzie, Nichols, Lachman, Droege, Andrew Royle, and Langtimm 2002; MacKenzie 2006) 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. Occupancy models use detection-nondetection data from repeat surveys to simultaneously estimate probabilities of detection (p) and occupancy ψ (Kellner and Swihart 2014, MacKenzie 2006). Occupancy is defined as the proportion of habitat occupied by a species (MacKenzie et al. 2002)

1.3. Occupancy modeling y formulacion matematica

1.4. Single-species or multiple-species management

The ecological and management literature has historically valued the idea of managing for diversity. This, however, clashes with the classic way in which conservation takes place. Conservation agencies, governments, scientists and international organizations such as International Union for Conservation of Nature (IUCN), classify species according to a conservation status, and policies are enacted to safeguard the ones that species of conservation concern (Keller and Bollmann 2004; Rodrigues, Pilgrim, Lamoreux, Hoffmann, and Brooks 2006). Managing for single species is often less complicated than simultaneously addressing suites of species, and it is may be simpler to track the status of a species than it is to define management for diversity (Simberloff 1998). Further, tracking the conservation status of a single species is often more straightforward than tracking multiple species or diversity.

There are several approaches to designing management measures based on single species, such as using umbrella species (Crosby, Elmore, Leslie, and Will 2015; Bichet, Dupuch, Hébert, Le Borgne, and Fortin 2016), Habitat Suitability Indices (HSI) (Reza, Abdullah, Nor, and Ismail 2013; Soniat, Conzelmann, Byrd, Roszell, Bridevaux, Suir, and Colley 2013; Zohmann, Pennerstorfer, and Nopp-Mayr 2013) and Species distribution modeling (SDM) (Peterson 2011; Guisan, Tingley, Baumgartner, Naujokaitis-Lewis, Sutcliffe, Tulloch, Regan, Brotons, McDonald-Madden, Mantyka-Pringle *et al.* 2013) among others. Even when the literature mostly criticizes the use of such approaches due to the ineffectiveness in preventing loss of biodiversity (ROBERGE and Angelstam 2004; Branton and Richardson 2011).

One of the problems of managing simple species, is that is usually very difficult to predict what will happen to other species and because of that it is hard to predict what will happen to diversity (Pulliam 2000), with some examples showing that even management measurements that use some species as umbrella species for conservation of ecosystems leading to undesired community effects (White, Zipkin, Manley, and Schlesinger 2013).

Managing for multiple-species, although desirable, it has shown to be difficult to implement (Möllmann, Lindegren, Blenckner, Bergström, Casini, Diekmann, Flinkman, Müller-Karulis, Neuenfeldt, Schmidt *et al.* 2014; ?), most multimodel species only take into account only the number of species in an area, not accounting for how rare or common some species are, or

they do not take into account the presence of some endangered species, since they are only trying to account for higher number of species, and not their identity (Taft, Colwell, Isola, and Safran 2002; Tori, McLeod, McKnight, Moorman, and Reid 2002; Plagányi, Punt, Hillary, Morello, Thébaud, Hutton, Pillans, Thorson, Fulton, Smith *et al.* 2014)

There are scenarios where a manager could want to manage for biodiversity, but in many countries, laws such as the Endangered Species Act in the United States or Canada's Species at Risk Act (Congress 1973; Waples, Nammack, Cochrane, and Hutchings 2013), will require the manager or scientist to focus at the species level. The package presented in this article pretends to be a tool to change this either/or scenario and take information of both diversity and individual species models.

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.

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. Another 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 (MacKenzie *et al.* 2002; MacKenzie 2006) 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.

Occupancy models use detection-nondetection data from repeat surveys to simultaneously estimate probabilities of detection (p) and occupancy (ψ) (MacKenzie 2006). (Burnham and Anderson 2003). We standardized all continuous site covariates t

1.5. Occupancy modeling

Imperfect detection and the need for occupancy modeling

One of the main objectives of ecology is to study the abundance and distribution of species and populations. The problem is that estimation of population is time consuming, hard to replicate and almost impossible in rare species due to the fact that they are really hard to detect, which leads to false absences that might bias estimates. Despite this most sampling and analysis techniques don't deal with imperfect detection. Occupancy models use detection-nondetection data from repeat surveys to simultaneously estimate probabilities of detection and occupancy (Kellner and Swihart 2014). Occupancy is defined as the proportion of habitat occupied by a species (MacKenzie *et al.* 2002)

History of occupancy modeling

Occupancy modeling was first proposed in 2002 (MacKenzie *et al.* 2002)

Math of Occupancy modeling

Lets suppose we are trying to determine the probability of a species presence in a site (ψ), given the probability of detection (p). There are t Trials in the field to detect the species in a site, and the detections (1) and non-detections (0) are tallied as a detection history. Then after the estimation of p , we can say that the cumulative probability of detection is:

$$p^* = 1 - (1 - p)^t$$

If S sites are sampled and the species was detected Sd times, our estimation of ψ is:

$$\psi = \frac{Sd}{S \times p^*}$$

Furthermore, both the probability of detection (p) and occupancy (ψ) may be a function of covariates. We can extent the model to include covaiates using the following formula.

$$\psi = \frac{\exp(Cov \times \beta)}{1 + \exp(Cov \times \beta)}$$

History of occupancy modeling software's and it's limitation (the need for DiversityOccupancy)

Comparison of DiversityOccupancy and other occupancy softwares (TABLE)

- camptrapR (R)
- downscale (R)
- hillmakerR (R)
- pom (R)
- Presence
- stocc (R)
- Unmarked (R)

% latex table generated in R 3.2.4 by xtable 1.8-2 package % Mon Feb 20 15:34:32 2017

| | | Diversityoccupancy | Unmarked | stocc | Presence | Pom | camptrapR |
|---|--|--------------------|----------|-------|----------|-----|-----------|
| 1 | Single Species Single Season occupancy | x | x | x | x | x | x |
| 2 | Multiple Species Single Season occupancy | x | | | | | |
| 3 | Single Species Abundance | x | x | | x | | |
| 4 | Multiple Species Abundance | x | | | | | |
| 5 | Alpha diversity models | x | | | | | |
| 6 | Single Species Dynamic occupancy | | x | | x | | |
| 7 | Priority area selection | x | | | | | |
| 8 | Build in model selection | x | | | | | |
| 9 | Built in response plot | x | | | | | |

1.6. 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

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

Objectives of the Package

Multiple species occupancy modeling

Abundance from multiple species occupancy modeling

Diversity from abundance

Spacially explicit predictions

Selection of priority areas

Graphical advantages from the package

Example dataset

As an example we provide part of the dataset collected in Pohnpei Island ([Oleiro 2014](#)), containing the detection history of five species in four consecutive days in 120 different locations of the Island.

1.7. Pohnpei in the federal states of micronesia

The Island of Pohnpei is a 334 squared kilometer island, in Oceania. it is the largest and most populated Island in the Federal States of Micronesia. Like every oceanic Island it has high endemism. It has a rich mosaic of ecosystems composed by manglars, palm forest, dwarf forests among others ([Raynor 1994](#); [Buden 2000](#); [Merlin and Raynor 2005](#)).

1.8. Bird Species

$$\begin{aligned}\dot{x} &= \sigma(y - x) \\ \dot{y} &= \rho x - y - xz\end{aligned}$$

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 *Islandbirds* which contains detections history of 5 species in the Pohnpei Island for 4 consecutive days (Columns) in 120 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 two species is presented below:

```
R> library(DiversityOccupancy)
```

```
Warning: package 'lattice' was built under R version 3.2.5
```

```
Warning: package 'Rcpp' was built under R version 3.2.5
```

```
R> data("IslandBirds")
```

```
R> head(IslandBirds[1:8], 10)
```

| | CICA.1 | CICA.2 | CICA.3 | CICA.4 | CIRW.1 | CIRW.2 | CIRW.3 | CIRW.4 |
|----|--------|--------|--------|--------|--------|--------|--------|--------|
| 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 6 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| 7 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 8 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 10 | 0 | 0 | 0 | 0 | 0 | 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 *IslandBirds* data set called *siteCov*:

```
R> data("siteCov")
```

```
R> head(siteCov, 10)
```

| | Elev | AgroFo | SecVec | Wetland | Upland |
|---|-------|------------|-------------|---------|-----------|
| 1 | 214.6 | 0.04536772 | 0.309614772 | 0 | 0.6450175 |
| 2 | 254.7 | 0.00000000 | 0.013053168 | 0 | 0.9869468 |
| 3 | 321.5 | 0.00000000 | 0.009073543 | 0 | 0.9909265 |
| 4 | 68.2 | 0.00000000 | 0.000000000 | 0 | 1.0000000 |
| 5 | 346.5 | 0.00000000 | 0.106972302 | 0 | 0.8930277 |
| 6 | 74.5 | 0.00000000 | 0.000000000 | 0 | 1.0000000 |

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 *Daily_Cov* which illustrates how the Daily covariates have to be structured:

```
R> #All the items of the list must have names
R> names(Daily_Cov)

[1] "Day"      "Wind"     "Obs"      "Time"     "Rain"     "Noise"    "Clouds"

R> #here we see the first dataframe of the Daily_Cov dataset
R> head(Daily_Cov[[1]])

      Day1 Day2 Day3 Day4
3       25  27  33  42
5       25  27  33  42
7       25  27  33  41
11      19  22  25  51
13      19  22  25  51
16      19  22  25  51
```

2.1. Fiting models for occupancy

As an example of batch fitting occupancy models, we will use the *IslandBirds* dataset, at first we will do a simple occupancy model without automatic model selection:

```
R> BirdOccupancy <- batchoccu(pres = IslandBirds, sitecov = siteCov, obscov = Daily_Cov, spp =
R+ Elev + AgroFo + SecVec + Wetland)

[1] "Species 1 ready!"
[1] "Species 2 ready!"
[1] "Species 3 ready!"
[1] "Species 4 ready!"
[1] "Species 5 ready!"
```

In this case *pres* expects the detection history file explained above, *sitecov*, expects a dataframe with the covariates used to estimate occupancy, *obscov* is a list of dataframes with the variables expected to affect the probability of detection, *spp* is the number of species in the *pres* file, and *form* is the formula used to fit the model

This creates an object of the class *batchoccupancy* We can check the fitted model accesing the *models* element

```
\begin{CodeChunk}
\begin{CodeInput} R> BirdOccupancy$models \end{CodeInput}
\end{CodeChunk}
```

[[1]]

Call:

occu(formula = form, data = data2)

Occupancy:

| | Estimate | SE | z | P(> z) |
|-------------|----------|--------|--------|---------|
| (Intercept) | -10.012 | 20.73 | -0.483 | 0.629 |
| Elev | 0.508 | 0.77 | 0.659 | 0.510 |
| AgroFo | -100.296 | 138.41 | -0.725 | 0.469 |
| SecVec | -408.270 | NaN | NaN | NaN |
| Wetland | 13.093 | 20.65 | 0.634 | 0.526 |

Detection:

| | Estimate | SE | z | P(> z) |
|-------------|----------|--------|--------|---------|
| (Intercept) | -3.34368 | 0.9853 | -3.393 | 0.00069 |
| Day | 0.03082 | 0.0224 | 1.375 | 0.16898 |
| Wind | -0.41709 | 0.2346 | -1.778 | 0.07543 |
| Rain | -0.42307 | 0.7931 | -0.533 | 0.59373 |
| Noise | -0.06591 | 0.1909 | -0.345 | 0.72985 |
| Clouds | 0.00131 | 0.0085 | 0.154 | 0.87797 |

AIC: 144.0011

[[2]]

Call:

occu(formula = form, data = data2)

Occupancy:

| | Estimate | SE | z | P(> z) |
|-------------|-----------|----------|--------|---------|
| (Intercept) | 5.32e-01 | 7.78e-01 | 0.685 | 0.4936 |
| Elev | -4.96e-03 | 2.29e-03 | -2.168 | 0.0301 |
| AgroFo | 6.28e-01 | 1.45e+00 | 0.433 | 0.6653 |
| SecVec | 1.21e+00 | 1.74e+00 | 0.694 | 0.4874 |
| Wetland | -1.55e+02 | 4.44e+02 | -0.350 | 0.7266 |

Detection:

| | Estimate | SE | z | P(> z) |
|-------------|----------|---------|---------|---------|
| (Intercept) | -2.42376 | 0.78176 | -3.1004 | 0.00193 |
| Day | 0.03711 | 0.02031 | 1.8267 | 0.06775 |
| Wind | 0.01807 | 0.20904 | 0.0865 | 0.93111 |
| Rain | -0.55340 | 0.90311 | -0.6128 | 0.54003 |
| Noise | -0.41490 | 0.19083 | -2.1743 | 0.02969 |
| Clouds | 0.00802 | 0.00853 | 0.9398 | 0.34734 |

AIC: 206.9414

[[3]]

Call:

occu(formula = form, data = data2)

Occupancy:

| | Estimate | SE | z | P(> z) |
|-------------|----------|--------|-------|---------|
| (Intercept) | -3.4645 | 1.9877 | -1.74 | 0.0813 |
| Elev | 0.0473 | 0.0246 | 1.92 | 0.0546 |
| AgroFo | -5.5331 | 3.2742 | -1.69 | 0.0910 |
| SecVec | 12.3461 | 9.7284 | 1.27 | 0.2044 |
| Wetland | 3.4146 | 2.2217 | 1.54 | 0.1243 |

Detection:

| | Estimate | SE | z | P(> z) |
|-------------|----------|---------|---------|---------|
| (Intercept) | -1.46061 | 0.61125 | -2.3896 | 0.0169 |
| Day | 0.00864 | 0.01551 | 0.5573 | 0.5773 |
| Wind | 0.01269 | 0.15015 | 0.0845 | 0.9326 |
| Rain | -0.53391 | 0.57192 | -0.9335 | 0.3505 |
| Noise | -0.27912 | 0.12870 | -2.1687 | 0.0301 |
| Clouds | -0.00144 | 0.00539 | -0.2672 | 0.7893 |

AIC: 316.6923

[[4]]

Call:

occu(formula = form, data = data2)

Occupancy:

| | Estimate | SE | z | P(> z) |
|-------------|----------|---------|--------|---------|
| (Intercept) | -0.3594 | 0.96212 | -0.374 | 0.7087 |
| Elev | 0.0101 | 0.00662 | 1.518 | 0.1289 |
| AgroFo | -1.9886 | 1.10864 | -1.794 | 0.0729 |
| SecVec | -0.3248 | 1.48768 | -0.218 | 0.8272 |
| Wetland | -2.5379 | 1.47523 | -1.720 | 0.0854 |

Detection:

| | Estimate | SE | z | P(> z) |
|-------------|----------|---------|--------|---------|
| (Intercept) | 0.37017 | 0.53559 | 0.691 | 0.4895 |
| Day | -0.01375 | 0.01310 | -1.049 | 0.2940 |
| Wind | 0.16717 | 0.12158 | 1.375 | 0.1692 |
| Rain | 0.06358 | 0.31754 | 0.200 | 0.8413 |
| Noise | -0.17355 | 0.08924 | -1.945 | 0.0518 |
| Clouds | -0.00423 | 0.00441 | -0.959 | 0.3377 |

AIC: 469.6008

[[5]]

Call:

```
occu(formula = form, data = data2)
```

Occupancy:

| | Estimate | SE | z | P(> z) |
|-------------|----------|---------|--------|---------|
| (Intercept) | -1.25268 | 0.53130 | -2.358 | 0.0184 |
| Elev | 0.00424 | 0.00199 | 2.133 | 0.0329 |
| AgroFo | -3.21615 | 1.49323 | -2.154 | 0.0313 |
| SecVec | -0.85353 | 1.54730 | -0.552 | 0.5812 |
| Wetland | 1.31017 | 0.75086 | 1.745 | 0.0810 |

Detection:

| | Estimate | SE | z | P(> z) |
|-------------|-----------|---------|---------|---------|
| (Intercept) | 0.891117 | 0.73667 | 1.2097 | 0.226 |
| Day | -0.020304 | 0.01586 | -1.2802 | 0.200 |
| Wind | -0.158150 | 0.15018 | -1.0531 | 0.292 |
| Rain | -0.294663 | 0.41554 | -0.7091 | 0.478 |
| Noise | 0.015623 | 0.10563 | 0.1479 | 0.882 |
| Clouds | -0.000341 | 0.00526 | -0.0648 | 0.948 |

AIC: 374.6705

\end{CodeChunk}

In order to do automatic model selection for the occupancy models, you have to change the option of dredge to TRUE:

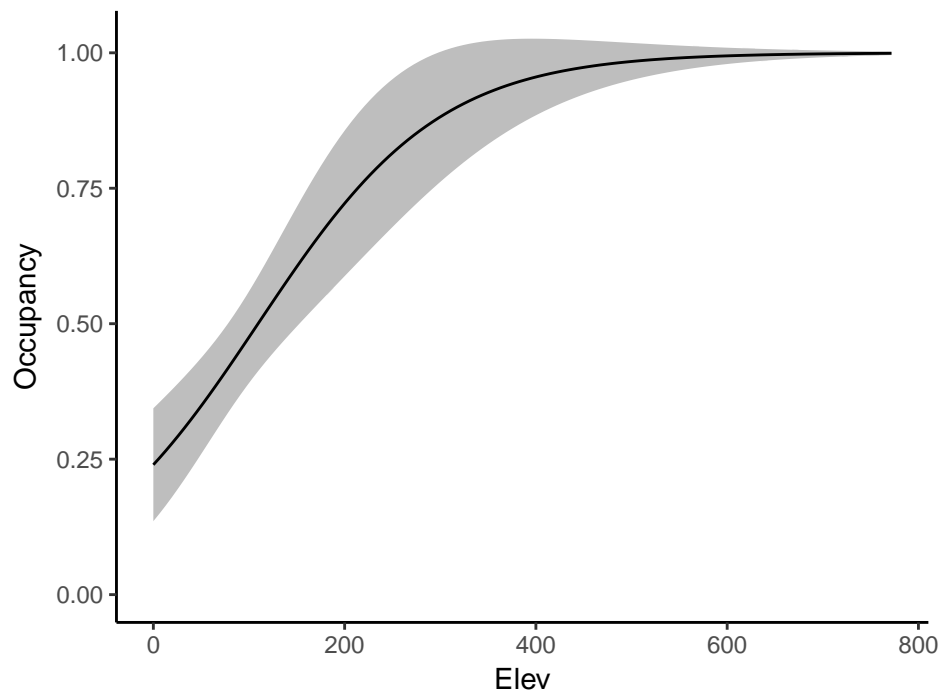
```
R> BirdOccupancy <- batchoccu(pres = IslandBirds, sitecov = siteCov, obscov = Daily_Cov, sp
R+ Elev + AgroFo + SecVec + Wetland, dredge = TRUE)
```

```
[1] "Species 1 ready!"
[1] "Species 2 ready!"
[1] "Species 3 ready!"
[1] "Species 4 ready!"
[1] "Species 5 ready!"
```

Plotting the response of occupancy for each species and each variable

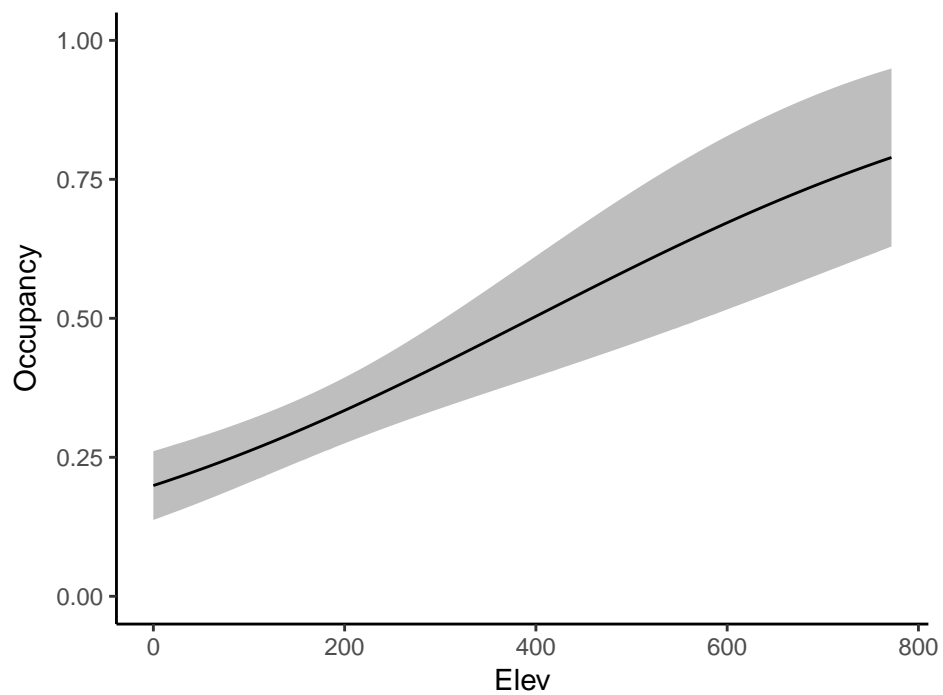
DiversityOccupancy, has a build in function *responseplot.occu* that will automatically plot the occupancy response to the variation of any of the covariates from the *sitecov* file. To use this function you need a *batchoccupancy* model to feed the batch parameter, and then you have to select which species and variable to plot. In the next graph, we are plotting the response of the fourth species (*Rukia longirostra*), for elevation. This function automatically limits the variable of interest between the minimum and maximum value found in the field.

```
R> responseplot.occu(batch = BirdOccupancy, spp = 4, variable = Elev)
```



This next plot shows again, the response to elevation, but in this case for species 5 (*Ducula oceanica*).

```
R> responseplot.occu(batch = BirdOccupancy, spp = 5, variable = Elev)
```



2.2. Fiting models for abundance and predicting alpha diversity

In this example we will fit and model the abundance for 5 bird species and calculate alpha diversity from those results.

```
R> birdDiversity <-diversityoccu(pres = IslandBirds, sitecov = siteCov,
R+ obscov = Daily_Cov,spp = 5, form = ~ Day + Wind + Time ~ Elev + Wetland + Upland, dred

[1] "Species 1 ready!"
[1] "Species 2 ready!"
[1] "Species 3 ready!"
[1] "Species 4 ready!"
[1] "Species 5 ready!"
```

The resulting object of class diversityoccupancy has the following elements

```
R> names(birdDiversity)

[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:

```
R> birdDiversity$models[[2]]
```

Call:

```
occuRN(formula = form, data = data2)
```

Abundance:

| | Estimate | SE | z | P(> z) |
|-------------|-----------|----------|--------|---------|
| (Intercept) | 0.66046 | 7.41e-01 | 0.891 | 0.3731 |
| Elev | -0.00398 | 1.73e-03 | -2.305 | 0.0212 |
| Wetland | -47.31278 | 1.72e+02 | -0.276 | 0.7828 |
| Upland | -0.42087 | 5.56e-01 | -0.756 | 0.4494 |

Detection:

| | Estimate | SE | z | P(> z) |
|-------------|----------|---------|--------|---------|
| (Intercept) | -2.36626 | 1.80923 | -1.308 | 0.1909 |
| Day | 0.03480 | 0.01801 | 1.932 | 0.0534 |
| Wind | -0.10959 | 0.19166 | -0.572 | 0.5675 |
| Time | -0.00114 | 0.00375 | -0.305 | 0.7605 |

AIC: 208.1134

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

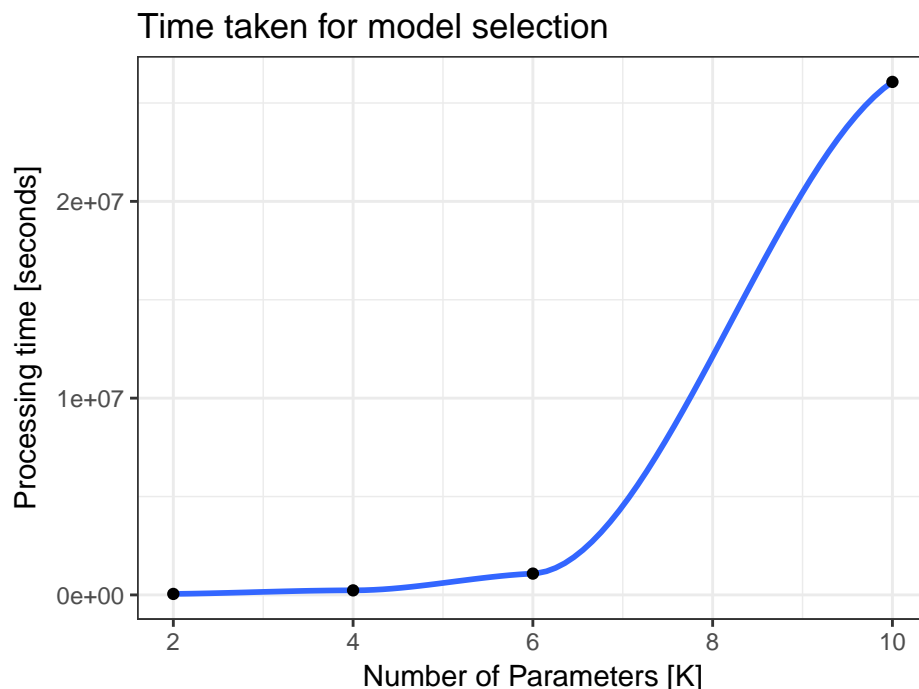
```
R> summary(birdDiversity$species)
```

| h | species.1 | species.2 | species.3 | species.4 |
|----------------|----------------|----------------|---------------|----------------|
| Min. :0.9332 | Min. :0.1863 | Min. :0.0000 | Min. :1.636 | Min. :0.1107 |
| 1st Qu.:1.2299 | 1st Qu.:0.4451 | 1st Qu.:0.1188 | 1st Qu.:2.128 | 1st Qu.:0.7577 |
| Median :1.2952 | Median :0.6292 | Median :0.5799 | Median :3.051 | Median :2.4028 |
| Mean :1.2679 | Mean :0.6486 | Mean :0.5679 | Mean :2.740 | Mean :1.9794 |
| 3rd Qu.:1.3262 | 3rd Qu.:0.7794 | 3rd Qu.:0.8910 | 3rd Qu.:3.275 | 3rd Qu.:3.0071 |
| Max. :1.3616 | Max. :1.2106 | Max. :1.8616 | Max. :3.553 | Max. :3.7061 |

| species.5 |
|-----------------|
| Min. :0.04913 |
| 1st Qu.:0.29879 |
| Median :0.56381 |
| Mean :0.60893 |
| 3rd Qu.:0.74995 |
| Max. :2.01430 |

2.3. 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 `IslandBirds` data set.



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

```
R> birdmodel.selected <- diversityoccu(pres = IslandBirds, sitecov = siteCov,
R+ obscov = Daily_Cov, spp = 5, form = ~ Day + Wind + Time ~ Elev + Wetland + Upland, dred

[1] "Species 1 ready!"
[1] "Species 2 ready!"
[1] "Species 3 ready!"
[1] "Species 4 ready!"
[1] "Species 5 ready!"
```

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:

```
R> birdDiversity$models[[2]]
```

Call:

```
occuRN(formula = form, data = data2)
```

Abundance:

| | Estimate | SE | z | P(> z) |
|-------------|-----------|----------|--------|---------|
| (Intercept) | 0.66046 | 7.41e-01 | 0.891 | 0.3731 |
| Elev | -0.00398 | 1.73e-03 | -2.305 | 0.0212 |
| Wetland | -47.31278 | 1.72e+02 | -0.276 | 0.7828 |
| Upland | -0.42087 | 5.56e-01 | -0.756 | 0.4494 |

Detection:

| | Estimate | SE | z | P(> z) |
|-------------|----------|---------|--------|---------|
| (Intercept) | -2.36626 | 1.80923 | -1.308 | 0.1909 |
| Day | 0.03480 | 0.01801 | 1.932 | 0.0534 |
| Wind | -0.10959 | 0.19166 | -0.572 | 0.5675 |
| Time | -0.00114 | 0.00375 | -0.305 | 0.7605 |

AIC: 208.1134

```
R> birdmodel.selected$models[[2]]
```

Call:

```
occuRN(formula = ~Day + 1 ~ Elev + Wetland + 1, data = data2)
```

Abundance:

| | Estimate | SE | z | P(> z) |
|-------------|----------|---------|--------|---------|
| (Intercept) | 0.50953 | 0.66082 | 0.771 | 0.44067 |
| Elev | -0.00446 | 0.00164 | -2.725 | 0.00643 |
| Wetland | -5.05318 | 2.71875 | -1.859 | 0.06308 |

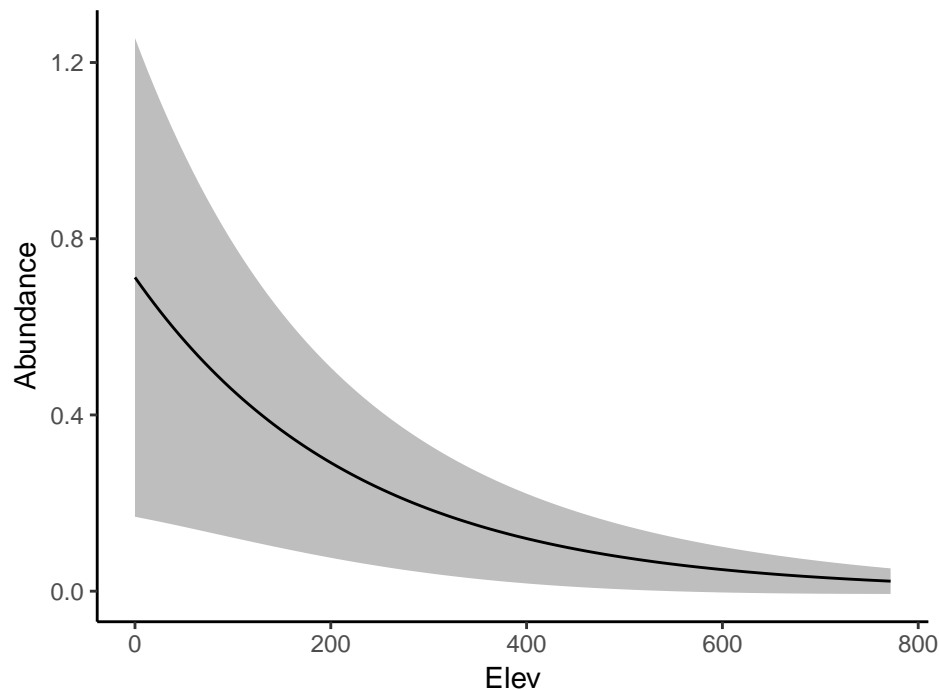
Detection:

| | Estimate | SE | z | P(> z) |
|-------------|----------|--------|-------|----------|
| (Intercept) | -3.1681 | 0.8008 | -3.96 | 7.62e-05 |
| Day | 0.0324 | 0.0174 | 1.86 | 6.29e-02 |

AIC: 204.0382

The responses of individual species to specific variables can be shown using the function `responseplot.abund.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.

```
R> responseplot.abund(birdmodel.selected, spp = 2, variable = Elev)
```



2.4. Model selection for alpha diversity modeling

The next step is to select the best model for predicting alpha diversity using the `model.diversity` function. The function takes a `diversityoccupancy` object, and fits all possible glm models and ranks them by AICc. Other than the `diversityoccupancy` object, there are three other parameters to select: 1) `Method`, which can be either “h” which fits every possible model, or “g”, which uses genetic algorithms to select models (recommended for large candidate sets); 2) `Delta`, which allows the user to identify an AICc delta threshold, which returns all models with AICc values below the threshold; 3) `Squared`, which includes only linear combinations when set to FALSE (Default), and both linear and quadratic (second order) if set to TRUE.

```
R> glm.BirdDiverse <- model.diversity(birdmodel.selected, method = "g", delta = 2,
R+ squared = TRUE)
```

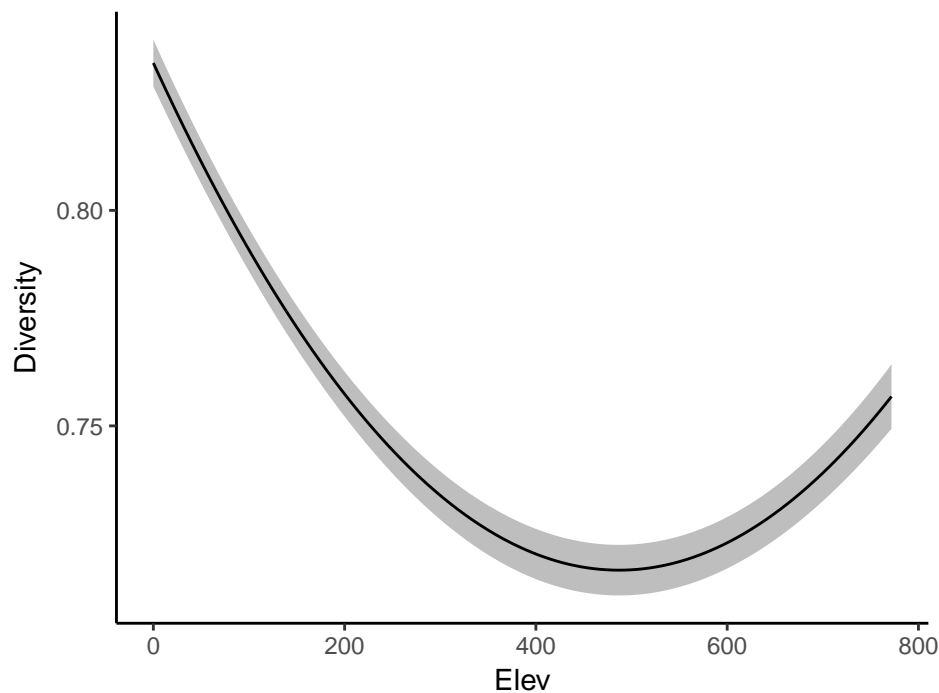
To see the top models extract the Table element of the modelselection object

```
\begin{CodeChunk}
```

```
\begin{CodeOutput} model 1 Diversity ~ 1 + Elev + AgroFo + Wetland + I(Elev^2) +
I(AgroFo^2) + I(SecVec^2) + I(Wetland^2) + I(Upland^2) 2 Diversity ~ 1 + Elev + AgroFo +
Wetland + I(Elev^2) + I(AgroFo^2) + I(Wetland^2) + I(Upland^2) 3 Diversity ~ 1 + Elev +
AgroFo + Wetland + Upland + I(Elev^2) + I(AgroFo^2) + I(Wetland^2) + I(Upland^2) 4 Di-
versity ~ 1 + Elev + SecVec + Wetland + Upland + I(Elev^2) + I(AgroFo^2) + I(Wetland^2)
+ I(Upland^2) 5 Diversity ~ 1 + Elev + AgroFo + SecVec + Wetland + I(Elev^2) +
I(AgroFo^2) + I(Wetland^2) + I(Upland^2) aicc weights Delta.AICc 1 -681.3992 0.2610582
0.0000000 2 -681.1351 0.2287691 0.2640605 3 -680.7723 0.1908161 0.6268668 4 -680.4609
0.1632999 0.9383094 5 -680.3701 0.1560568 1.0290469 \end{CodeOutput} \end{CodeChunk}
```

The `responseplot.diver` function takes a `modeldiversity` object and one of the variables used to predict the alpha diversity index, and makes a plot showing the response of the diversity index against the selected variable. This function automatically limits the values of that variable to the maximum and minimum values of the dataset. It also shows the standard deviation of the estimation.

```
R> responseplot.diver(glm.BirdDiverse, Elev)
```

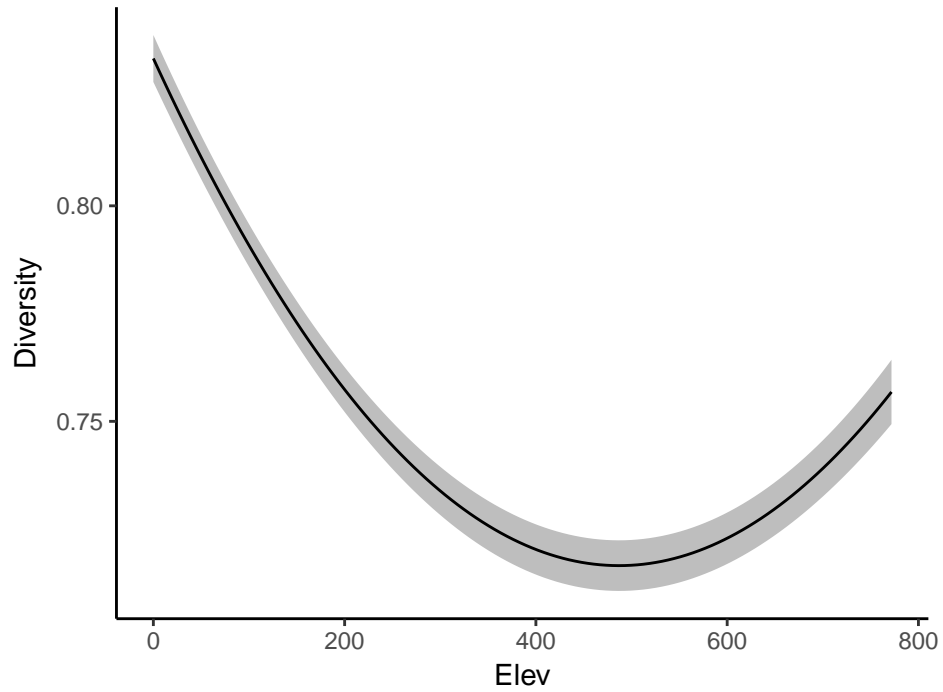


Also since the returned plot is a ggplot type object, it can be easily modified following ggplot2 grammar of graphics.

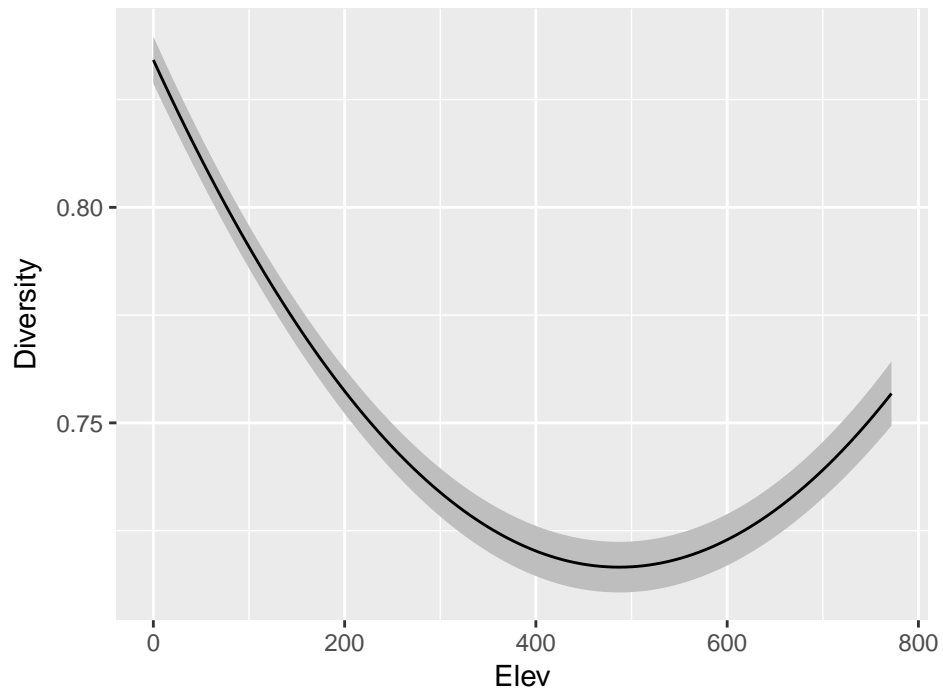
```
R> library(ggplot2)
```

Warning: package 'ggplot2' was built under R version 3.2.5

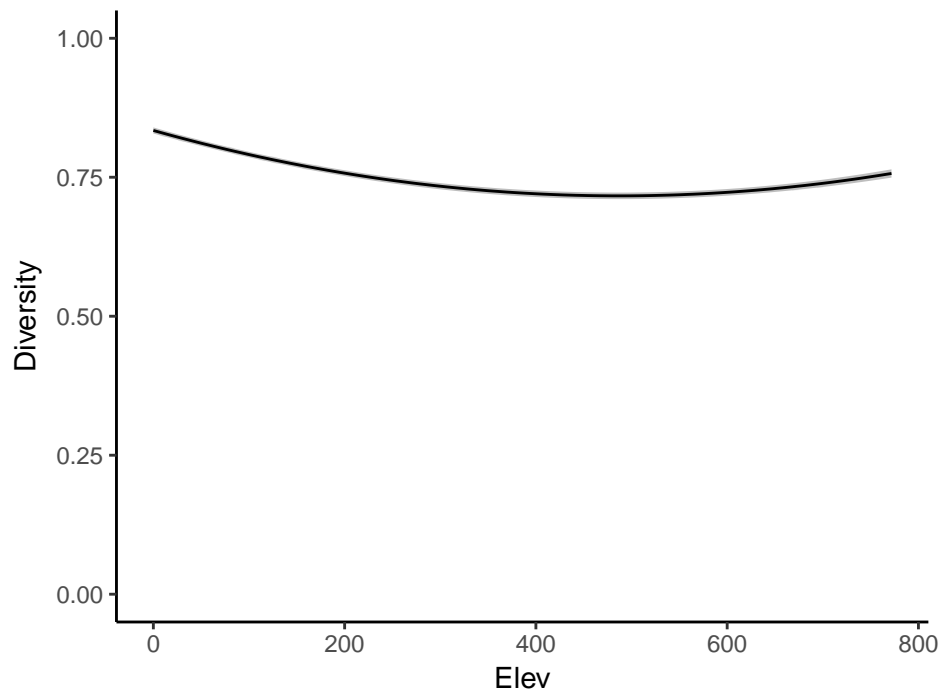

```
R> k <- responseplot.diver(glm.BirdDiverse, Elev)
R> k
```



```
R> k + theme_gray()
```



```
R> k + ylim(c(0,1))
```



2.5. Selecting conservation areas based on alpha diversity and abundance of species of conservation concern

Of the 5 species modeled, let's say that there are at least two of conservation concern, the second and thirds of our list. Since we already have models relating site characteristics to species abundance and a model relating site characteristics to alpha diversity, with the use of a spatial raster layers (rasterstack) with the modeled variables we can choose an area with high species diversity and/or abundance. In order for this function to work properly the stack has to be in lon lat projection, and Birdstack is in UTM, so we reproject the data.

```
R> library(raster)
```

```
Loading required package: sp
```

```
Attaching package: 'sp'
```

```
The following object is masked from 'package:unmarked':
```

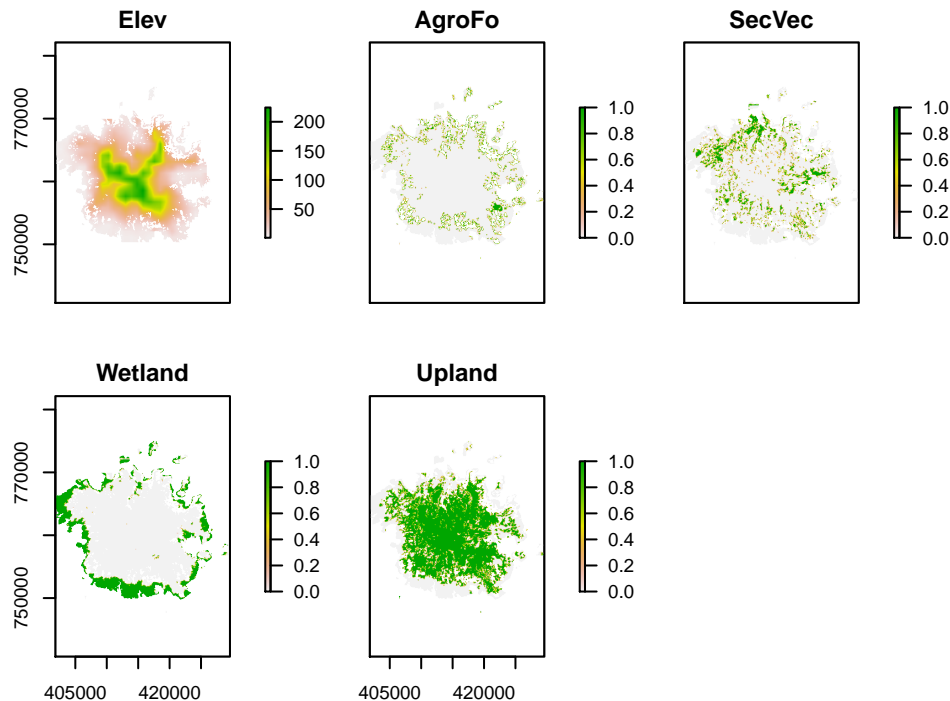
```
coordinates
```

```
Attaching package: 'raster'
```

```
The following objects are masked from 'package:unmarked':
```

```
getData, projection
```

```
R> data(Birdstack)
R> plot(Birdstack)
```



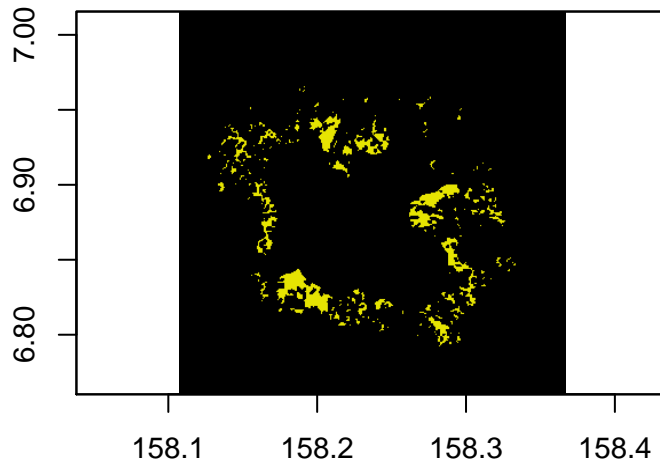
```
R> newproj <- '+proj=longlat +datum=WGS84 +ellps=WGS84 +towgs84=0,0,0'
R> library(rgdal)
```

```
rgdal: version: 1.1-10, (SVN revision 622)
Geospatial Data Abstraction Library extensions to R successfully loaded
Loaded GDAL runtime: GDAL 2.0.1, released 2015/09/15
Path to GDAL shared files: C:/Users/corcoranbarriosd/Documents/R/win-library/3.2/rgdal/gdal
GDAL does not use iconv for recoding strings.
Loaded PROJ.4 runtime: Rel. 4.9.1, 04 March 2015, [PJ_VERSION: 491]
Path to PROJ.4 shared files: C:/Users/corcoranbarriosd/Documents/R/win-library/3.2/rgdal/proj
Linking to sp version: 1.2-3
```

```
R> Birdstack <- stack(projectRaster(Birdstack, crs=newproj))
```

In order to find areas of high conservation value, we use the `predict.diversity` function. We need both a `diversityoccupancy` and a `modeldiversity` class object, used in the model, and diverse parameters respectfully, a spatial representation of site covariates as raster files (`rasterstack`), with the variables in the `new.data` parameter, a boolean vector in the `species` parameter indicating which species shall be considered (T or F), and the `quantile.nth` parameter, which indicates a quantile threshold that is used for abundance and/or richness to indicate conservation value (areas above the threshold will be returned).

```
R> Selected.area <- diversity.predict(model = birdmodel.selected, diverse = glm.BirdDivers
R+ c(F,T,T,F,F))
```



From the object `Selected.area` we can extract and plot not only the area that was selected with the attributes, but also the layers that show the predicted diversity for the island and also the predicted abundance for each of the species that were used for the analysis.

3. Discussion

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Affiliation:

Derek Corcoran

University of Missouri

First line Second line

E-mail: corcoranbarriosd@missouri.eduURL: <http://rstudio.com>

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