JSS *Journal of Statistical Software*



*MMMMMM YYYY, Volume VV, Issue II.* [*http://www.jstatsoft.org/*](http://www.jstatsoft.org/)

**Selecting priority areas from diversity and individual species abundance** DiversityOccupancy

**Derek Corcoran Elisabeth Webb Dylan Kesler**

University of Missouri University of Missouri, USGS 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 amongsite 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.

# Introduction

## 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, governments, scientists and international organizations such as International Union for Conservation of Nature (IUCN), classify species according to a conservation status, and policies are made to safe-ward the ones that are envisioned as species of conservation concern (Keller and Bollmann 2004; Rodrigues, Pilgrim, Lamoreux, Hoffmann, and Brooks 2006). Single species are easier to manage for, and it is easier to keep track the status of a species than it is to define management for diversity (Simberloff 1998), it is also more complicated to sample and keep track of changes in diversity.

There are several approaches to design management measures based on single species, such as using umbrella species (Crosby, Elmore, Leslie, and Will 2015; Bichet, Dupuch, H´ebert, 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 (Mollmann, Lindegren, Blenckner, Bergstr¨ om, Casini, Diekmann, Flinkman, M¨ uller-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; Plag´anyi, Punt, Hillary, Morello, Th´ebaud, 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, 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 (psi) (MacKenzie 2006). (Burnham and Anderson 2003). We standardized all continuous site covariates t

## 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**

# 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 |

## 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.soilˆ2), 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

## 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.

Time taken for model selection

●

●

●

●

0e+00

1e+07

2e+07

2

4

6

8

10

Processing time [seconds]

Number of Parameters [K]

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.soilˆ2), 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 responseplot.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)*

1

2

3

Abundance

0

0 1 2 3 4

Burn.intensity.soil

## 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.

*glm.Batdiverse <- model.diversity(batmodel.selected, method = "g", delta = 2, squared = TRUE)*

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

\begin{CodeChunk}\begin{CodeInput} class(glm.Batdiverse$Table) \end{CodeInput}

[1] "data.frame"

\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.

*responseplot.diver(glm.Batdiverse, Burn.intensity.soil)*

2.40

2.45

2.50

0

1

2

3

4

Burn.intensity.soil

Diversity

Also since the returned plot is a ggplot type object, it can be easily modified following ggplot2 grammar of graphics. *library(ggplot2) k <- responseplot.diver(glm.Batdiverse, Burn.intensity.soil) k*

2.40

2.45

2.50

0

1

2

3

4

Burn.intensity.soil

Diversity

*k + geom\_line(color = "red")*

2.40

2.45

2.50

0

1

2

3

4

Burn.intensity.soil

Diversity

*k + ylim(c(0,3))*

3

2

Diversity

1

0

0 1 2 3 4

Burn.intensity.soil

## Selecting conservation areas based on alpha diversity and abundanceof species of conservation concern

Of the 17 species modeled, there are at least three of conservation concern, pallid bat (*Antrozous pallidus*), corresponding to species 9th 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.

*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

*data(plumas.stack) plot(plumas.stack)*

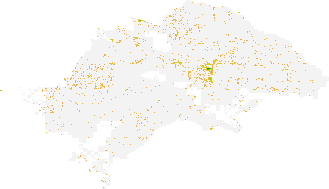
**Distance.to.water Distance.to.road Existing.vegetation**

8000

39.4

39.8

40.2



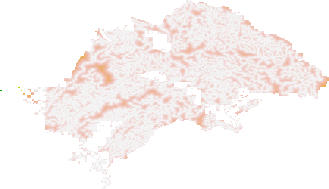
0

200

400

600

800

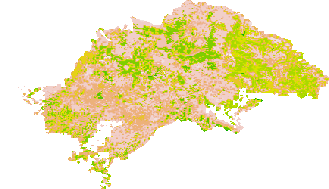


2000

4000

6000

10000



5

10

15

20

25

0

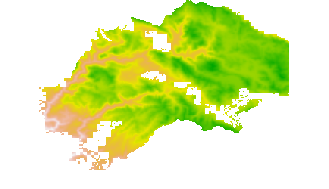
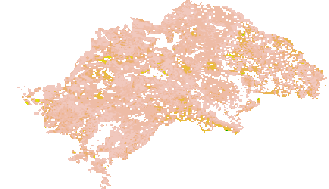
|  |  |  |
| --- | --- | --- |
| **Fire.Interval** | **Altitude** | **Burn.intensity.soil** |

100

39.4

39.8

40.2

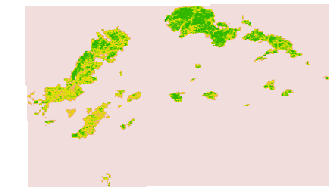


500

1000

1500

2000



0

1

2

3

4

80

60

40

20

|  |  |
| --- | --- |
| **Burn.intensity.Canopy** | **Burn.intensity.basal** |

576

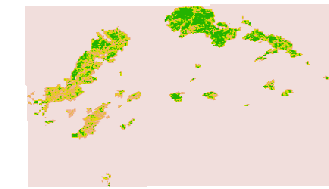
−121.5

−120.5

39.4

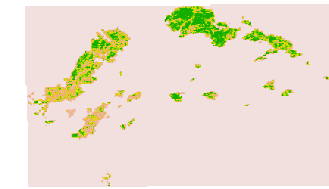
39.8

40.2



−121.5

−120.5



45

34

232

11

00

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).

*Selected.area <- diversity.predict(model = batmodel.selected, diverse = glm.Batdiverse, ne c(F,F,F,F,F,F,F,F,T,F,F,F,F,F,F,F,F))*

−121.5

−121.0

−120.5

−120.0

39.4

39.8

40.2



This function automatically creates a KMZ file that will be stored in the home directory of your session

# 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.

# References

Bichet OM, Dupuch A, H´ebert C, Le Borgne H, Fortin D (2016). “Maintaining animal assemblages through single-species management: the case of threatened caribou in boreal forest.” *Ecological Applications*.

Branton M, Richardson JS (2011). “Assessing the Value of the Umbrella-Species Concept for Conservation Planning with Meta-Analysis.” *Conservation Biology*, **25**(1), 9–20.

Burnham KP, Anderson DR (2003). *Model selection and multimodel inference: a practical information-theoretic approach*. Springer Science & Business Media.

Congress U (1973). “Endangered species act.” *Washington DC*.

Crosby AD, Elmore RD, Leslie DM, Will RE (2015). “Looking beyond rare species as umbrella species: Northern Bobwhites (Colinus virginianus) and conservation of grassland and shrubland birds.” *Biological Conservation*, **186**, 233–240.

Guisan A, Tingley R, Baumgartner JB, Naujokaitis-Lewis I, Sutcliffe PR, Tulloch AI, Regan TJ, Brotons L, McDonald-Madden E, Mantyka-Pringle C, *et al.* (2013). “Predicting species distributions for conservation decisions.” *Ecology letters*, **16**(12), 1424–1435.

Keller V, Bollmann K (2004).“From red lists to species of conservation concern.”*Conservation Biology*, **18**(6), 1636–1644.

MacKenzie DI (2006). *Occupancy estimation and modeling: inferring patterns and dynamics of species occurrence*. Academic Press.

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.](http://www.esajournals.org/doi/abs/10.1890/0012-9658(2002)083%5B2248:ESORWD%5D2.0.CO%3B2)

Mollmann C, Lindegren M, Blenckner T, Bergstr¨ om L, Casini M, Diekmann R, Flinkman J,¨ Muller-Karulis B, Neuenfeldt S, Schmidt JO,¨ *et al.* (2014). “Implementing ecosystem-based fisheries management: from single-species to integrated ecosystem assessment and advice for Baltic Sea fish stocks.” *ICES Journal of Marine Science: Journal du Conseil*, **71**(5), 1187–1197.

Peterson AT (2011). *Ecological niches and geographic distributions (MPB-49)*. 49. Princeton University Press.

Plag´anyi EE, Punt AE, Hillary R, Morello EB, Th´ebaud O, Hutton T, Pillans RD, Thorson´ JT, Fulton EA, Smith AD, *et al.* (2014). “Multispecies fisheries management and conservation: tactical applications using models of intermediate complexity.” *Fish and Fisheries*, **15**(1), 1–22.

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

Reza MIH, Abdullah SA, Nor SBM, Ismail MH (2013). “Integrating GIS and expert judgment in a multi-criteria analysis to map and develop a habitat suitability index: A case study of large mammals on the Malayan Peninsula.” *Ecological indicators*, **34**, 149–158.

ROBERGE JM, Angelstam P (2004). “Usefulness of the umbrella species concept as a conservation tool.” *Conservation Biology*, **18**(1), 76–85.

Rodrigues AS, Pilgrim JD, Lamoreux JF, Hoffmann M, Brooks TM (2006). “The value of the IUCN Red List for conservation.” *Trends in ecology & evolution*, **21**(2), 71–76.

Simberloff D (1998).“Flagships, umbrellas, and keystones: is single-species management pass´e in the landscape era?” *Biological conservation*, **83**(3), 247–257.

Soniat TM, Conzelmann CP, Byrd JD, Roszell DP, Bridevaux JL, Suir KJ, Colley SB (2013).

“Predicting the effects of proposed Mississippi River diversions on oyster habitat quality; application of an oyster habitat suitability index model.” *Journal of Shellfish Research*, **32**(3), 629–638.

Taft OW, Colwell MA, Isola CR, Safran RJ (2002). “Waterbird responses to experimental drawdown: implications for the multispecies management of wetland mosaics.” *Journal of Applied Ecology*, **39**(6), 987–1001.

Tori GM, McLeod S, McKnight K, Moorman T, Reid FA (2002). “Wetland conservation and Ducks Unlimited: Real world approaches to multispecies management.” *Waterbirds*, pp. 115–121.

Waples RS, Nammack M, Cochrane JF, Hutchings JA (2013). “A tale of two acts: endangered species listing practices in Canada and the United States.” *BioScience*, **63**(9), 723–734.

White AM, Zipkin EF, Manley PN, Schlesinger MD (2013). “Conservation of avian diversity in the Sierra Nevada: moving beyond a single-species management focus.” *PloS one*, **8**(5), e63088.

Zohmann M, Pennerstorfer J, Nopp-Mayr U (2013). “Modelling habitat suitability for alpine rock ptarmigan (Lagopus muta helvetica) combining object-based classification of IKONOS imagery and Habitat Suitability Index modelling.” *Ecological modelling*, **254**, 22–32.

**Affiliation:**

Derek Corcoran

University of Missouri

First line Second line

E-mail: corcoranbarriosd@missouri.edu

URL: <http://rstudio.com>

|  |  |
| --- | --- |
| *Journal of Statistical Software* | <http://www.jstatsoft.org/> |
| published by the American Statistical Association | <http://www.amstat.org/> |
| Volume VV, Issue II | *Submitted:* |
| MMMMMM YYYY | *Accepted:* yyyy-mm-dd |