Package 'DiversityOccupancy'

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Type Package

Title Building Diversity Models from Multiple Species Occupancy Models

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Description
Predictions of alpha diversity are fitted from presence data, first abundance is modeled from occupancy models and then, several diversity indices are calculated and finally GLM models are used to predict diversity in different environments and select priority areas.

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Imports dplyr, ggplot2, glmulti, qpcR, raster, vegan

Suggests knitr, rgdal, rmarkdown,

License GPL-3

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VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

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batchoccu   *Fits occupancy models for multiple species detection history*

Description

This function takes a data.frame with multiple detection history from various species in different
sites, covariates of each site to calculate occupancy, variables specific to sampling days to calculate
probability of detection. It features an automatic model selection when dredge = TRUE.

Usage

```
batchoccu(pres, sitecov, obscov, spp, form, dredge = FALSE)
```

Arguments

pres	a data.frame where rows are the sites and columns are a series of presence-absence observation from multiple species, every species needs to have the same number of observations.
sitecov	a data.frame where every row is a site, and every column is a measurement of that site, such as elevation or slope, this covariates are usually more constant.
obscov	a list where every element is a data frame with the daily covariates for each site, that is a measurement for each day, such as average temperature of a day, this covariates are usually very .
spp	the number of species in the pres data.frame
form	a formula in the format ~ obscov ~ sitcov, the first arguments will be used to calculate probability of detection and the second part the occupancy.
dredge	default = FALSE, if TRUE, for each species, the best occupancy model will be determined by fitting all possible models and ranking by AICc.

Details

This function fits the single season occupancy model of MacKenzie et al (2002), for multiple species
and it can automatically select the best model for each specie based on AICc.

Value

A list with the fitted models for each species and the calculated Alpha diversity for each site.

Author(s)

Derek Corcoran <derek.corcoran.barrios@gmail.com>

See Also

diversityoccu

Examples

```
## Not run:
data("IslandBirds")
data("Daily_Cov")
data("siteCov")
BirdOccupancy <-batchoccu(pres = IslandBirds, sitecov = siteCov, obscov =
Daily_Cov, spp =  5, form = ~ Day + Wind + Rain + Noise + Clouds ~
Elev + AgroFo + SecVec + Wetland)
#plot the response of occupancy to individual variables for species 4 and  5

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

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

## End(Not run)
#Dredge for all species
BirdOccupancy2 <- batchoccu(pres = IslandBirds, sitecov = siteCov, obscov =
Daily_Cov, spp = 5, form = ~ 1 ~
Elev + AgroFo, dredge = TRUE)
```

---

batchoccuavg	*Fits occupancy models for multiple species detection history and calculated model average*

Description

This function takes a data.frame with multiple detection history from various species in different sites, covariates of each site to calculate occupancy, variables specific to sampling days to calculate probability of detection. It features an automatic model selection when dredge = TRUE.

Usage

```
batchoccuavg(pres, sitecov, obscov, spp, form, dredge = FALSE, delta = 2)
```

Arguments

pres	a data.frame where rows are the sites and columns are a series of presence-absence observation from multiple species, every species needs to have the same number of observations.
sitecov	a data.frame where every row is a site, and every column is a measurement of that site, such as elevation or slope, this covariates are usually more constant.
obscov	a list where every element is a data frame with the daily covariates for each site, that is a measurement for each day, such as average temperature of a day, this covariates are usually very .
spp	the number of species in the pres data.frame
form	a formula in the format ~ obscov ~ sitcov, the first arguments will be used to calculate probability of detection and the second part the occupancy.
dredge	default = FALSE, if TRUE, for each species, the best occupancy model will be determined by fitting all possible models and ranking by AICc.
delta	default = 2, AICc difference used for model averaging

Details

This function fits the single season occupancy model of MacKenzie et al (2002), for multiple species and it can automatically select the best model for each specie based on AICc, ther result of this function is the model average.

Value

A list with the average models for each species.

Author(s)

Derek Corcoran <derek.corcoran.barrios@gmail.com>

See Also

diversityoccu

Examples

```
## Not run:
data("IslandBirds")
data("Daily_Cov")
data("siteCov")
BirdOccupancy <-batchoccuavg(pres = IslandBirds, sitecov = siteCov, obscov =
Daily_Cov, spp =  5, form = ~ Day + Wind + Rain + Noise + Clouds ~
Elev + AgroFo + SecVec + Wetland)
#Summary of averaged model for species 2
summary(BirdOccupancy$models[[2]])

## End(Not run)
#Dredge for all species
```

Birdstack	*Raster Stack with five variables measured in Pohnpei Island in Micronesia*

Description

A Raster Stack containing five rasters from in the Pohnpei Island in Micronesia where the detection histories of the IslandBirds where taken.

Elev Metres above sea level of the sampled point

AgroFo Proportion of a station (from 0 to 1) corresponding to agricultural forest incudes areas withsubsistence or commercial staple crops mixed with undisturbed forest

SecVec Proportion of a station (from 0 to 1) corresponding to secondary vegetation which represents anthropogenic habitats (e.g., savannah) and early colonizers and invasive species (e.g. *Hibiscus spp.* and *Merremia peltata)*

Wetland Proportion of a station (from 0 to 1) corresponding to areas classified as mangroves, marshes, swamp forest and fresh water bodies

Upland Proportion of a station (from 0 to 1) corresponding to upland and undisturbed forest habitats

Usage

    Birdstack

Format

A raster stack with 5 layers:

See Also

IslandBirds

Daily_Cov

siteCov

Daily_Cov	*Seven covariables measured at 120 survey stations in an island in micronesia*

Description

A list containing the measurements of seven variables correspondant to 120 different survey stations (Rows) in Pohnpei Island where the detection histories of the IslandBirds where taken.

Usage

```
Daily_Cov
```

Format

A list with 6 elements, each of them with a data frame

Details

Day Ordinal day

Wind Wind intensity using a modified Beafourt scale

Obs First initial of the observer

Time Survey time (minutes after sunrise)

Rain Categorical variable where 0 = no rain, 1 = light rain and 2 = heavy rain

Noise Ambient noise (1-10 being 10 the loudest)

Clouds Cloud cover in percentage

References

Oleiro P. 2014. Avian population responses to anthropogenic landscape changes in Pohnpei, Federated Stats of Micronesia. Masters Thesis University of Missouri.

See Also

IslandBirds

siteCov

---

diversity.predict	*Makes a spacially explicit prediction of the occupancy of multiple species and alpha diversity, and select the area where*

Description

This function takes an deiversityoccu object and predicts occupancy for all species in new data, either a data.frame or a rasterstack. It can also return a subset of the total area of a rasterstack, where diversity and occupancy/abundance are higher than the nth quantile.

Usage

```
diversity.predict(model, diverse, new.data, quantile.nth = 0.8, species,
  kml = TRUE, name = "Priority_Area.kml")
```

Arguments

`model`	A result from diversityoccu
`diverse`	A result from the model.diversity function.
`new.data`	a rasterstack, or a dataframe containing the same variables as the siteCovs variable in diversityoccu or batchoccu
`quantile.nth`	the nth quantile, over which is a goal to keep both diversity and selected species. default = NULL
`species`	a boolean vector of the species to take into acount
`kml`	if TRUE builds a kml file of the selected area and saves it in your working directry
`name`	the name of the kml file if kml is TRUE

Value

a data frame with predicted values, or a raster stack with predictions for each species, a raster for diversity and a raster with the area meeting the quantile criteria.

Author(s)

Derek Corcoran <derek.corcoran.barrios@gmail.com>

See Also

diversityoccu

batchoccu

model.diversity

Examples

```
## Not run:
#Load the data
data("IslandBirds")
data("Daily_Cov")
data("siteCov")
data("Birdstack")

#Model the abundance for  5 bat species and calculate alpha diversity from that

#Model the abundance for  5 bat species and calculate alpha diversity from that

BirdDiversity <-diversityoccu(pres = IslandBirds, sitecov = siteCov,
obscov = Daily_Cov,spp =  5, form = ~ Day + Wind + Time ~ Elev + Wetland + Upland)

#Select the best model that explains diversity using genetic algorithms
set.seed(123)
glm.Birdiversity <- model.diversity(BirdDiversity, method = "g")

# get the area where the first two bird species are most abundant
```

```
# and the diversity is high

library(rgdal)
Selected.area <- diversity.predict(model = BirdDiversity, diverse = glm.Birdiversity,
new.data = Birdstack, quantile.nth = 0.65, species =
c(TRUE, TRUE, FALSE, FALSE, FALSE))

Selected.area

## End(Not run)
```

---

diversityoccu   *Calculates alpha diversity from multiple species occupancy data*

Description

This function takes a data.frame with multiple presence absence-data from various species in different sites, covariates of each site to calculate occupancy, variables specific to sampling days to calculate probability of detection, and it calculates the alpha diversity for each site.

Usage

```
diversityoccu(pres, sitecov, obscov, spp, form, index = "shannon",
  dredge = FALSE)
```

Arguments

pres	a data.frame where rows are the sites and columns are a series of presence-absence observation from multiple species, every species needs to have the same number of observations.
sitecov	a data.frame where every row is a site, and every column is a measurement of that site, such as elevation or slope, this covariates are usually more constant.
obscov	a list where every element is a data frame with the daily covariates for each site, that is a measurement for each day, such as average temperature of a day, this covariates are usually very .
spp	the number of species in the pres data.frame
form	a formula in the format ~ obscov ~ sitcov, the first arguments will be used to calculate probability of detection and the second part the occupancy.
index	Diversity index, one of "shannon", "simpson" or "invsimpson".
dredge	default = FALSE, if TRUE, for each species, the best occupancy model will be determined by fitting all possible models and ranking by AICc.

Details

This function fits the latent abundance mixture model described in Royle and Nichols (2003), to calculate the abundance of every species in each site, the using that abundance it calculates the alpha diversity index for each site based on that abundance.

Value

A list with the fitted models for each species, the calculated Alpha diversity for each site, and a dataframe with the abundance of each species and diversity.

Author(s)

Derek Corcoran <derek.corcoran.barrios@gmail.com>

Nicole L. Michel

Mike Meredith

See Also

[diversity](#)

[model.diversity](#)

Examples

```
## Not run:
#Load the data
data("IslandBirds")
data("Daily_Cov")
data("siteCov")

#Model the abundance for  5 bird species and calculate alpha diversity from that

BirdDiversity <-diversityoccu(pres = IslandBirds, sitecov = siteCov,
obscov = Daily_Cov,spp =  5, form = ~ Day + Wind + Time + Rain +
Noise ~ Elev + AgroFo + SecVec + Wetland + Upland)

#To see the estimates and p values for each model:

BirdDiversity$models

## End(Not run)
```

IslandBirds   *Occupancy data of 5 bird species in Micronesia.*

Description

A dataset containing the detections history of 5 species in the Pohnpei Island for 4 consecutive days (Columns) in 120 different sites (Rows).

CICA.1 Detection history of *Coracina tenurostris*: on day 1

CICA.2 Detection history of *Coracina tenurostris*: on day 2

CICA.3 Detection history of *Coracina tenurostris*: on day 3

CICA.4 Detection history of *Coracina tenurostris*: on day 4

CIRW.1 Detection history of *Acrocephalus syrinx*: on day 1

CIRW.2 Detection history of *Acrocephalus syrinx*: on day 2

CIRW.3 Detection history of *Acrocephalus syrinx*: on day 3

CIRW.4 Detection history of *Acrocephalus syrinx*: on day 4

CIWE.1 Detection history of *Zosterops semperi*: on day 1

CIWE.2 Detection history of *Zosterops semperi*: on day 2

CIWE.3 Detection history of *Zosterops semperi*: on day 3

CIWE.4 Detection history of *Zosterops semperi*: on day 4

LBWE.1 Detection history of *Rukia longirostra*: on day 1

LBWE.2 Detection history of *Rukia longirostra*: on day 2

LBWE.3 Detection history of *Rukia longirostra*: on day 3

LBWE.4 Detection history of *Rukia longirostra*: on day 4

MIPI.1 Detection history of *Ducula oceanica*: on day 1

MIPI.2 Detection history of *Ducula oceanica*: on day 2

MIPI.3 Detection history of *Ducula oceanica*: on day 3

MIPI.4 Detection history of *Ducula oceanica*: on day 4

Usage

```
IslandBirds
```

Format

A data frame with 120 rows and 20 variables

References

Oleiro P. 2014. Avian population responses to anthropogenic landscape changes in Pohnpei, Federated Stats of Micronesia. Masters Thesis University of Missouri.

See Also

Daily_Cov

siteCov

---

model.diversity   *Find the best GLM model explaining the alpha divesity of the species*

Description

This function takes a diversityoccu object and heuristically searches for the glm that best explains the alpha diversity of the modelled species.

Usage

```
model.diversity(DivOcc, method = "h", delta = 2, squared = FALSE)
```

Arguments

DivOcc   is an object returned by the divesityoccu function of this package

method   The method to be used to explore the candidate set of models. If "h" an exhaustive screening is undertaken. If "g" the genetic algorithm is employed (recommended for large candidate sets). If "l", a very fast exhaustive branch-and-bound algorithm is used. Package leaps must then be loaded, and this can only be applied to linear models with covariates and no interactions.

delta   The number of models that will be returned will be the ones that have a maximum AICc difference with the top model equal to delta.

squared,   if FALSE (Default), only GLMs with linear components will be evaluated; If TRUE, GLMs with both linear and quadratic components will be evaluated. WARNING if squared is TRUE, the number of parameters duplicates and the models grow exponentially, this may result in to many variables for a CPU to compute.

Details

This function fits every first order glm possible and ranks them by AICc.

Value

An object with the best fitted model, the coefficients of that model, a table with the top 5 fitted models ranked by AICc and the data used for the model

Author(s)

Derek Corcoran <derek.corcoran.barrios@gmail.com>

See Also

diversityoccu

Examples

```
## Not run:
#Load the data
data("IslandBirds")
data("Daily_Cov")
data("siteCov")

#Model the abundance for  5 bat species and calculate alpha diversity from that

BirdDiversity <-diversityoccu(pres = IslandBirds, sitecov = siteCov,
obscov = Daily_Cov,spp =  5, form = ~ Day + Wind + Time + Rain +
Noise ~ Elev + AgroFo + SecVec + Wetland + Upland)

#Select the best model that explains diversity using genetic algorithms
set.seed(123)
glm.Birdiversity <- model.diversity(BirdDiversity, method = "g")

#see the best models

glm.Birdiversity$Best.model

#plot the response of diversity to individual variables

plot(glm.Birdiversity, elev)

#To add the quadratic components of models

glm.birdiversity <- model.diversity(BirdDiversity , method = "g", squared = TRUE)

responseplot.diver(glm.birdiversity, Elev)

## End(Not run)
```

---

occupancy.predict   *Predicts occupancy for all the species in a batchoccupancy class object*

Description

This function takes an batchoccupancy object and predicts occupancy for all species in new data, either a data.frame or a rasterstack.

Usage

```
occupancy.predict(batch, new.data)
```

Arguments

batch   A result from the batchoccu

new.data   a rasterstack, or a dataframe containing the same variables as the siteCovs vari-
                   able in batchoccu

Value

a raster stack with predictions for each species.

Author(s)

Derek Corcoran <derek.corcoran.barrios@gmail.com>

See Also

batchoccu

Examples

```
## Not run:
#Load the data
data("IslandBirds")
data("Daily_Cov")
data("siteCov")
data("Birdstack")
BirdOccupancy <-batchoccu(pres = IslandBirds, sitecov = siteCov, obscov =
Daily_Cov, spp =  5, form = ~ Day + Wind + Rime + Noise + Clouds ~
Elev + AgroFo + SecVec + Wetland)

Occupancy.stack <- occupancy.predict(batch = BirdOccupancy, new.data =
Birdstack)

## End(Not run)
```

---

responseplot.abund	*plot the response of an abundance model to the change of aparticular variable*

Description

This function takes a diversityoccupancy object and one of the variables used to predict abundance, and makes a plot showing the response of occupancyt against the selected variable. This function automatically limits the values of that variable to the maximum and minimum values of the dataset.

Usage

```
responseplot.abund(batch, spp, variable)
```

Arguments

batch	A result from the diversityoccu function.
spp	The species number of which response is going to be ploted.
variable	The variable of which the response is to be ploted.

Value

a ggplot object plotting the alpha diversity response to the selected variable.

Author(s)

Derek Corcoran <derek.corcoran.barrios@gmail.com>

See Also

batchoccu

Examples

```
## Not run:
data("IslandBirds")
data("Daily_Cov")
data("siteCov")

#Model the abundance for 5 bird species and calculate alpha diversity from that

BirdDiversity <-diversityoccu(pres = IslandBirds, sitecov = siteCov,
obscov = Daily_Cov,spp = 5, form = ~ Day + Wind + Time + Rain +
Noise ~ Elev + AgroFo + SecVec + Wetland + Upland)

#plot the response of abundance to individual variables for species 4, 11

responseplot.abund(batch = BirdDiversity, spp = 4, variable = Elev)

responseplot.abund(batch = BirdDiversity, spp = 11, variable = Elev)

## End(Not run)
```

---

responseplot.diver	*plot the response of the calculated alpha diversity to the change of a particular variable*

Description

This 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.

Usage

```
responseplot.diver(model, variable)
```

Arguments

model   A result from the model.diversity function.

variable   The variable of which the response is to be ploted.

Value

a ggplot object plotting the alpha diversity response to the selected variable.

Author(s)

Derek Corcoran <derek.corcoran.barrios@gmail.com>

See Also

diversityoccu

model.diversity

Examples

```
## Not run:
#Load the data
data("IslandBirds")
data("Daily_Cov")
data("siteCov")

#Model the abundance for 5 bird species and calculate alpha diversity from that

BirdDiversity <-diversityoccu(pres = IslandBirds, sitecov = siteCov,
obscov = Daily_Cov,spp = 5, form = ~ Day + Wind + Time + Rain +
Noise ~ Elev + AgroFo + SecVec + Wetland + Upland)

#Select the best model that explains diversity using genetic algorithms
set.seed(123)
glm.Birdiversity <- model.diversity(BirdDiversity, method = "g")

#see the best models

glm.Birdiversity$Best.model

#plot the response of diversity to individual variables

plot(glm.Birdiversity, elev)

## End(Not run)
```

---

responseplot.occu   *plot the response of an occupancy model to the change of aparticular*
                           variable

Description

This function takes a batchoccupancy object and one of the variables used to predict occupacy,
and makes a plot showing the response of occupancyt against the selected variable. This function
automatically limits the values of that variable to the maximum and minimum values of the dataset.

Usage

```
responseplot.occu(batch, spp, variable)
```

Arguments

batch   A result from the batchoccu function.

spp   The species number of which response is going to be ploted.

variable   The variable of which the response is to be ploted.

Value

a ggplot object plotting the alpha diversity response to the selected variable.

Author(s)

Derek Corcoran <derek.corcoran.barrios@gmail.com>

See Also

batchoccu

Examples

```
## Not run:
data("IslandBirds")
data("Daily_Cov")
data("siteCov")
BirdOccupancy <-batchoccu(pres = IslandBirds, sitecov = siteCov, obscov =
Daily_Cov, spp = 5, form = ~ Day + Wind + Rime + Noise + Clouds ~
Elev + AgroFo + SecVec + Wetland)
#plot the response of occupancy to individual variables for species 4 and 5

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


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

## End(Not run)
```

---

siteCov	*Nine covariables measured at 120 survey stations in an island in micronesia*

Description

A dataframe containing the measurements of 5 variables (columns) correspondant to 120 different survey stations (Rows) in Pohnpei Island where the detection histories of the IslandBirds where taken.

Elev Metres above sea level of the sampled point

AgroFo Proportion of a station (from 0 to 1) corresponding to agricultural forest incudes areas withsubsistence or commercial staple crops mixed with undisturbed forest

SecVec Proportion of a station (from 0 to 1) corresponding to secondary vegetation which represents anthropogenic habitats (e.g., savannah) and early colonizers and invasive species (e.g. *Hibiscus spp.* and *Merremia peltata)*

Wetland Proportion of a station (from 0 to 1) corresponding to areas classified as mangroves, marshes, swamp forest and fresh water bodies

Upland Proportion of a station (from 0 to 1) corresponding to upland and undisturbed forest habitats

Usage

    siteCov

Format

A data frame with 120 rows and 52 variables:

References

Oleiro P. 2014. Avian population responses to anthropogenic landscape changes in Pohnpei, Federated Stats of Micronesia. Masters Thesis University of Missouri.

See Also

Daily_Cov

IslandBirds

Index