

Package ‘JointSurvey’

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Type Package

Title Joint Survey Analysis for Seabird Populations

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Description

Pooling multiple survey data for marine populations requires us to take into account the biases of each survey methodology and the spatial/temporal extent of each survey. This package provides functions for the Bayesian hierarchical modelling of multiple survey data sets. Some more description here.

Depends R (>= 3.5.0), RColorBrewer, runjags, coda

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.0.2

Suggests knitr, rmarkdown

NeedsCompilation no

R topics documented:

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| | |
|----------|--|
| colambda | <i>colambda: Spatial intensity for collection of colonies and covariates</i> |
|----------|--|

Description

Generates aggregate layer of expected usage from multiple colonies and covariates

Usage

```
colambda(cols, acoef, ccoef, Xpred, Dist, mask)
```

Arguments

| | |
|--------|--|
| cols | A data frame with the coordinates and sizes of colonies |
| acoef | The habitat variable coefficients |
| ccoeff | The density dependence coefficients |
| Xpred | A dataframe with covariate data in the columns |
| Dist | A dataframe with distance data in the columns |
| mask | A matrix the size of the map which has zero for land and 1 for sea |

Details

The ‘Dist’ dataframe has points in space as its rows and different colonies as its columns.

Value

A map with the same dimensions as ‘mask’ representing intensity for all accessible points in space.

Author(s)

Jason Matthiopoulos

| | |
|----------|-----------------|
| Colonies | <i>Colonies</i> |
|----------|-----------------|

Description

Colonies

Usage

```
Colonies
```

Format

Rdata

Details

An example data-frame of the locations and sizes of three colonies on the TestlandscapeDat map.

| | |
|------------|--|
| colonyDist | <i>colonyDist:Distance from colony map</i> |
|------------|--|

Description

A distance-from-colony based on Euclidean distances. An optional mask layer may be provided to exclude land. In future versions, the mask layer will be used to generate at-sea distances, instead of Euclidean.

Usage

```
colonyDist(xo, yo, map, masked = NULL)
```

Arguments

| | |
|--------|--|
| xo, yo | Scalars or vectors. The x and y locations of the colony. |
| map | The map on which distances are required. To be used as a mask, it must have values 0 on land and 1 at sea. |
| masked | An optional argument that declares whether the map matrix should be used to exclude land. If so, then the map matrix needs to have entries 1 for sea and 0 for land. If masked, the distances on land are set to the masked value. |

Details

The coordinate system used must be distance-preserving because Euclidean distances are employed for spacing the transects. The centred argument is useful for constructing distances in colonies that are variably "shaded" by land. It allows several different colonies to have the same mean for the frequency distribution of distances.

Value

A matrix of distances. If xo and yo are vectors, then an array is returned with layers of distances.

Author(s)

Jason Matthiopoulos

| | |
|--------|--|
| counts | <i>counts: Sampling of species distribution along given transects.</i> |
|--------|--|

Description

Produces simulated counts of individuals along a set of sampling locations, based on the underlying (but unknown distribution of the species)

Usage

```
counts(tr, u, w, l, p)
```

Arguments

| | |
|----|---|
| tr | A nx2 matrix with coordinates of sampling points along the transects |
| u | The underlying distribution to be surveyed |
| w | The effective detection distance from the transect |
| l | The spacing between successive survey points (This is related to speed along transect) |
| p | The detection probability of each bird within the effective detection area of the survey point. |

Details

The algorithm assumes that the cell of the map has a unitary area (area=1). The detection probability 'p' captures availability bias.

Value

A vector of length n

Author(s)

Jason Matthiopoulos

jointHSF

jointHSF: Bayesian inference on pooled survey data.

Description

MCMC and JAGS modelling of joint survey data. Several different models are possible.

Usage

```
jointHSF(
  count,
  X,
  dist,
  surv,
  ll,
  w,
  p0,
  N,
  model = "IPP",
  disp = NULL,
  ABS = c(1000, 1000, 1000)
)
```

Arguments

| | |
|-------|---|
| count | The number of individuals counted at each step of the transect |
| X | A matrix of covariate data. Rows represent survey point, columns represent covariates |
| dist | A matrix of distances from each colony. Rows represent survey point, columns represent colonies |
| surv | A vector of index values pointing to the survey serial number from which the count arose |
| ll | Distance between successive transect points. |
| w | Width of strip transect. |
| p0 | Probability of detection of each individual at distance zero. |
| N | A vector of colony sizes. |
| disp | Distance between every pair of points in the dataset. A square matrix only used for spatial models. |

Details

The coordinate system used must be distance-preserving because Euclidean distances are employed for spacing the transects.

Value

A JAGS object of results from the model run.

Author(s)

Jason Matthiopoulos

Examples

```
pts<-survey(c(0,150),c(0,150),1,10,10)
plot(pts)
```

jointHSF.predict

jointHSF.predict: Bayesian prediction from pooled survey data.

Description

MCMC and JAGS modelling of joint survey data. Several different models are possible.

Usage

```
jointHSF.predict(results, aLocs, cLocs, Xpred, Dist, mask, Colonies)
```

Arguments

| | |
|----------|---|
| results | The output object of the jointHSF command |
| alocs | A vector of integers declaring the positions, in the 'results', of the environmental covariate parameters |
| clocs | A vector of integers declaring the positions, in the 'results', of the colony ranging parameters |
| Xpred | A matrix with covariate data in the columns |
| Dist | A dataframe with distance data in the columns |
| mask | A matrix the size of the map which has zero for land and 1 for sea |
| Colonies | A matrix with the locations and sizes of the colonies modelled (xloc in col 1, yloc in col 2 and size in col 3) |

Details

This function redeploys the 'colambda' function repeatedly, using different parameterisations from the sample of the joint posterior distribution

Value

A list with two maps, one for the expected usage and one for the associated standard deviation

Author(s)

Jason Matthiopoulos

JointSurvey

JointSurvey: Integrated Bayesian analysis of transect surveys.

Description

This package provides functions for the integrated Bayesian analysis of transect survey data that have originated from surveys of differing design. The applications are motivated from a Marine Scotland grant enquiring about the inferential feasibility of joint analyses of current and historic seabird surveys.

JointSurvey functions

[survey](#), [synthDistr](#), [colonyDist](#), [counts](#), [jointHSF](#), [jointHSF.predict](#)

JointSurvey data-sets

[TestlandscapeDat](#)

Author(s)

Jason Matthiopoulos

References

References for this implementation:

Matthiopoulos et al. (2011) Generalized functional responses for species distributions. *Ecology* 92 (3), 583-589

Matthiopoulos et al. (2015) Establishing the link between habitat selection and animal population dynamics. *Ecological Monographs* 85 (3), 413-436

Background references:

Morales et al. (2010) Building the bridge between animal movement and population dynamics *Phil. Trans. R. Soc. B* 2010 365 2289-2301; DOI: 10.1098/rstb.2010.0082.

Examples

```
# FITTING A GENERALISED FUNCTIONAL RESPONSE MODEL (see Matthiopoulos et al. 2011)
```

| | |
|--------|--|
| survey | <i>survey: Transect generation for rectangular region.</i> |
|--------|--|

Description

Generates regular transects with a particular design profile, within a rectangular region of predefined boundaries.

Usage

```
survey(xlim, ylim, le, disp, df = 0, mask = NULL)
```

Arguments

| | |
|------------|---|
| xlim, ylim | Two-element vectors containing the limits of the rectangular region (in arbitrary coordinates) |
| le | The spacing between successive sampling points on the transect (in units of length) |
| disp | The perpendicular distance between transects (in units of length) |
| df | The orientation of the transects with reference to the rectangular boundaries. It is an angle measured in rad anti-clockwise from the horizontal. |
| mask | An optional matrix that can be used to mask out survey points. |

Details

The coordinate system used must be distance-preserving because Euclidean distances are employed for spacing the transects.

Value

A nx2 matrix of sampling coordinates (where n is the number of points that were required to survey the rectangular study region)

Author(s)

Jason Matthiopoulos

Examples

```
pts<-survey(c(0,150),c(0,150),1,10,10)
plot(pts)
```

| | |
|------------|--|
| synthDistr | <i>synthDistr: Point generation given underlying intensity map for IPP</i> |
|------------|--|

Description

Allows the generation of occurrences from the map of an intensity function lambda, provided as a matrix, allowing for overdispersion.

Usage

```
synthDistr(lambda, q = 1)
```

Arguments

| | |
|--------|---|
| lambda | A matrix of non-negative values (intensities) |
| q | The overdispersion parameter. |

Details

The value q cannot be <1. Set to 1 for a Poisson and >1 for overdispersed values from a negative binomial. When q>1, no zero values are allowed in lambda.

Value

A matrix with the same dimensions as lambda containing integer counts

Author(s)

Jason Matthiopoulos

| | |
|------------------|-------------------------|
| TestlandscapeDat | <i>TestlandscapeDat</i> |
|------------------|-------------------------|

Description

TestlandscapeDat

Usage

```
TestlandscapeDat
```

Format

Rdata

Details

Contains three covariate layers (stored as matrices). The first 'u1' corresponds to bathymetry an the second 'u2' refers to an aspect of sediment. The third, 'land' has the indicator values of 1 for sea and 0 for land. # @examples image(u1)

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