Package: sharx (via r-universe)

October 8, 2026

Type Package

Title Models and Data Sets for the Study of Species-Area Relationships

Version 1.0-7

Date 2025-07-12

Maintainer Peter Solymos <psolymos@gmail.com>

Description Hierarchical models for the analysis of species-area relationships (SARs) by combining several data sets and covariates; with a global data set combining individual SAR studies; as described in Solymos and Lele (2012) <doi:10.1111/j.1466-8238.2011.00655.x>.

Depends methods, stats4, Formula, dcmle, dclone

SystemRequirements jags (>= 1.0.3)

URL https://github.com/psolymos/sharx

BugReports https://github.com/psolymos/sharx/issues

License GPL-2

LazyLoad yes

LazyData true

NeedsCompilation no

Author Peter Solymos [aut, cre] (ORCID: <https://orcid.org/0000-0001-7337-1740>)

Config/pak/sysreqs jags

Repository https://cran.r-universe.dev

Date/Publication 2025-07-13 22:40:02 UTC

RemoteUrl https://github.com/cran/sharx

RemoteRef HEAD

RemoteSha 302d029837195c90b77dc6fd106e8a4b62d37569

Contents

sharx-package 2
hsarx 2
sardata 4
sie 5

Index **7**

`sharx-package` *Models and Data Sets for the Study of the Species-Area Relationships*

Description

Data sets and SAR, SARX, HSAR and HSARX models as described in Solymos and Lele (2012).

Details

See `sardata` and `hsarx`

Author(s)

Peter Solymos

Maintainer: Peter Solymos <solymos@ualberta.ca>

References

Solymos, P. and Lele, S. R., 2012. Global pattern and local variation in species-area relationships. *Global Ecology and Biogeography* 21, 109–120.

`hsarx` *Fit SAR, SARX, HSAR and HSARX models to data*

Description

Fit SAR, SARX, HSAR and HSARX models to data as described in Solymos and Lele (2012).

Usage

```
hsarx(formula, data, n.clones, cl = NULL, ...)
```

Arguments

`formula`	Formula.
`data`	Data.
`n.clones`	Number of clones to be used.
`cl`	Cluster object for parallel computations.
`...`	Other arguments for MCMC.

Details

Fit SAR, SARX, HSAR and HSARX models to data as described in Solymos and Lele (2012).

Value

An S4 object object of class 'hsarx'. It inherits from 'dcMle', and has additional slots for storing the data.

Author(s)

Peter Solymos

References

Solymos, P. and Lele, S. R., 2012. Global pattern and local variation in species-area relationships. *Global Ecology and Biogeography* 21, 109–120.

See Also

sardata for data sets.

Examples

```
## Not run:
## to reproduce results from Solymos and Lele (Table 1)
data(sardata)
DAT <- data.frame(sardata$islands,
    sardata$studies[match(sardata$islands$study,
    rownames(sardata$studies)),])
x <- hsarx(log(S+0.5) ~ log(A) | (taxon.group + island.type +
    abs(latitude) + I(log(extent)))^2 | study, DAT,
    n.clones=5, n.adapt=2000, n.update=3000, n.iter=1000)

## SAR
DATS <- DAT[1:191,]
(x1 <- hsarx(log(S+0.5) ~ log(A),
    DATS[DATS$study=="abbott1978bird",], n.clones=2))

## SARX
DATS$rnd <- rnorm(nrow(DATS), log(DATS$extent))
(x2 <- hsarx(log(S+0.5) ~ log(A) * rnd,
    DATS[DATS$study=="abbott1978bird",], n.clones=2))

## HSAR
(x3 <- hsarx(log(S+0.5) ~ log(A) | 1 | study,
    DATS, n.clones=2, n.iter=1000))

## HSARX
(x4 <- hsarx(log(S+0.5) ~ log(A) | abs(latitude) | study,
    DATS, n.clones=2, n.iter=1000))

## End(Not run)
```

sardata *Data Sets for the Study of the Species-Area Relationship*

Description

Data sets for the study of the species-area relationship

Usage

```
data(sardata)
```

Format

A list of two data frames, see Details.

Details

The element `sardata$islands` is a data frame with variables:

`study` Factor, levels are the study identifiers.

`id` Numeric, island identifiers according to the original references.

`S` Numeric, number of species according to the original references.

`A` Numeric, area of the island in square kilometres, according to the original references.

The element `sardata$studies` is a data frame with variables:

`study` Factor, levels are the study identifiers.

`taxon.group` Factor, taxonomic group.

`island.type` Factor, island type.

`latitude` Numeric, middle band of latitude for the study calculated as (min + max) / 2, where min is the latitude close to the Equator, max is the latitude close to the poles.

`extent` Numeric, latitudinal extent of the study.

`location` Character, location of the study.

References

References are in the files `sardata.txt` and `sardata.bib` in the `sharx` library of `R`, labelled by study identifiers. See examples on how to recall the files from the console.

Examples

```
## data structure
data(sardata)
str(sardata$islands)
str(sardata$studies)
## references
file.show(system.file(package = "sharx", "sardata.txt"))
file.show(system.file(package = "sharx", "sardata.bib"))
```

`sie` *Small Island Effect (SIE) via Breakpoint Regression*

Description

Fit a breakpoint regression model to data to find threshold for the small island effect (SIE) as described in Lomolino...

Usage

```
sie(S, A, method = "Nelder-Mead", ...)
sieplot(x, add = FALSE, ...)
```

Arguments

`S`	untransformed species richness, vector.
`A`	untransformed area, vector.
`x`	a fitted model object of class 'sie'.
`method`	optimization method.
`add`	logical, if lines should be added to existing plot (`TRUE`), or a new plot is to be drawn (`FALSE`, default).
`...`	graphical arguments passed to `plot`.

Details

`sie` fits the breakpoint regression to the data, richness is `log(S+0.5)` transformed, area is `log(A)` transformed before analysis. There is a `coef`, `summary`, `print` method for fitted objects.

`sieplot` plots the observed (transformed) data and the fitted line.

Value

An S4 object of class 'sie' inheriting from class 'mle'.

Author(s)

Peter Solymos

References

Lomolino, M. V., and M. D. Weiser. 2001. Towards a more general species-area relationship: diversity on all islands, great and small. *Journal of Biogeography*, 28, 431–445.

Examples

```
data(sardata)
DAT <- sardata$islands[sardata$islands$study=="abbott1978plant",]
(x <- sie(DAT$S, DAT$A))
coef(x)
summary(x)
sieplot(x)
```

Index

∗ **datasets**
    sardata, 4
∗ **htest**
    hsarx, 2
    sie, 5
∗ **models**
    hsarx, 2
∗ **package**
    sharx-package, 2

hsarx, 2, *2*
hsarx-class *(*hsarx*)*, 2

plot, *5*

sardata, *2, 3*, 4
sharx *(*sharx-package*)*, 2
sharx-package, 2
show,hsarx-method *(*hsarx*)*, 2
show,sie-method *(*sie*)*, 5
sie, 5
sie-class *(*sie*)*, 5
sieplot *(*sie*)*, 5