

# Package ‘sharx’

January 15, 2016

**Type** Package

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

**Version** 1.0-5

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**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, *Global Ecology and Biogeography* 21, 109-120).

**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

**Repository** CRAN

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 sharx-package

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


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### 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.

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 hsarx

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


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### 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)
```

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sardata

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

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### 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  $(\text{min} + \text{max}) / 2$ , 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"))
```

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

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### 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

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

### 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)
```

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