

Package ‘sharx’

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Type Package

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

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

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 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 (in press).

Details

See [sardata](#) and [hsarx](#)

Author(s)

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References

Solymos, P. and Lele, S. R. (in press), Global pattern and local variation in species-area relationships. *Global Ecology and Biogeography*, xx: xx-xx.

 hsarx

Fit SAR, SARX, HSAR and HSARX models to data

Description

Fit SAR, SARX, HSAR and HSARX models to data

Usage

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

Arguments

formula	Formula.
data	Data.
n.clones	Number of clones to be used.
cl	Cluster object for parallel computations.
subset	Subset to data argument.
na.action	Handling of NA values.
...	Other arguments for MCMC.

Details

Fit SAR, SARX, HSAR and HSARX models to data as described in Solymos and Lele

Value

An mcmc.list object.

Author(s)

Peter Solymos

References

Solymos, P. and Lele, S. R. (in press), Global pattern and local variation in species-area relationships. *Global Ecology and Biogeography*, xx: xx–xx.

See Also

jags.fit, etc.

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-srea 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 kilometers, 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"))
```

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