

Package: BayesX (via r-universe)

September 15, 2024

Type Package

Title R Utilities Accompanying the Software Package BayesX

Version 0.3-3

Date 2023-10-20

Description Functions for exploring and visualising estimation results obtained with BayesX, a free software for estimating structured additive regression models (<https://www.uni-goettingen.de/de/bayesx/550513.html>). In addition, functions that allow to read, write and manipulate map objects that are required in spatial analyses performed with BayesX.

Depends shapefiles

Imports sp, sf, colorspace, coda, splines, methods, interp

Suggests spdep

LazyLoad yes

License GPL-2 | GPL-3

NeedsCompilation no

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Date/Publication 2023-10-20 07:20:07 UTC

Repository <https://freezenik.r-universe.dev>

RemoteUrl <https://github.com/cran/BayesX>

RemoteRef HEAD

RemoteSha cdf79c8ebeb9d2e6d654b2c71b93ad29e6785a8

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BayesX-package

R Utilities Accompanying the Software Package BayesX

Description

This package provides functionality for exploring and visualising estimation results obtained with the software package **BayesX** for structured additive regression. It also provides functions that allow to read, write and manipulate map objects that are required in spatial analyses performed with **BayesX**.

Author(s)

Nikolaus Umlauf, Thomas Kneib, Nadja Klein, Felix Heinzl, Andreas Brezger, Daniel Sabanes Bove

References

Belitz C, Brezger A, Kneib T, Lang S (2011). **BayesX** - Software for Bayesian Inference in Structured Additive Regression Models. Version 2.0.1. URL <https://www.uni-goettingen.de/de/bayesx/550513.html>.

add.neighbor	<i>Add Neighborhood Relations</i>
--------------	-----------------------------------

Description

Adds a neighborhood relationship between two given regions to a map object in graph format.

Usage

```
add.neighbor(map, region1, region2)
```

Arguments

map	Map object in graph format that should be modified.
region1, region2	Names of the regions that should be connected as neighbors.

Value

Returns an adjacency matrix that represents the neighborhood structure of map plus the new neighborhood relation in graph format.

Author(s)

Felix Heinzl, Thomas Kneib

See Also

[get.neighbor](#), [delete.neighbor](#), [read.gra](#), [write.grabnd2gra](#)

Examples

```
germany <- read.gra(system.file("examples/germany.gra", package="BayesX"))
get.neighbor(germany, c("1001", "7339"))
germany <- add.neighbor(germany, "7339", "1001")
get.neighbor(germany, c("1001", "7339"))
```

`bnd2gra`*Convert Boundary Format to Graph Format*

Description

Converts a map in boundary format to a map in graph format.

Usage

```
bnd2gra(map)
```

Arguments

`map` Map in boundary format that should be converted.

Value

Returns an adjacency matrix that represents the neighborhood structure of the map object in graph format.

Author(s)

Felix Heinzl, Thomas Kneib

References

BayesX Reference Manual. Available from <https://www.uni-goettingen.de/de/bayesx/550513.html>

See Also

[read.bnd](#), [read.gra](#), [write.bnd](#), [write.gra](#)

Examples

```
tanzania.bnd <- read.bnd(system.file("examples/tanzania.bnd", package="BayesX"))
tanzania.gra <- bnd2gra(tanzania.bnd)
```

`createxymap`*Create map objects for some points and a given distance*

Description

Creates a map object from a list of coordinates by treating observations within a certain distance as neighbors. The resulting neighborhood structure is stored in a map object in graph format while a map in boundary format is created to enable visualisation.

Usage

```
createxymap(x, y, districts=NULL, p=2, max.dist)
```

Arguments

<code>x</code>	Vector of x-coordinates of underlying points
<code>y</code>	Vector of y-coordinates of underlying points
<code>districts</code>	Either NULL or a vector of names for labeling points. If <code>districts=NULL</code> , points are labelled by index.
<code>p</code>	Any p-norm with $p \geq 1$ can be chosen as the distance measure with the Euclidian distance ($p=2$) being the default. For $p=Inf$, the maximum of coordinates is used. Except for $p=Inf$, calculations can fail for huge p .
<code>max.dist</code>	Value which determines the neighborhood. Points whose distance is smaller or equal than <code>max.dist</code> are considered as neighbors.

Value

List of two elements: map object in graph format and map object in boundary format.

Author(s)

Felix Heinzl, Thomas Kneib

See Also

[read.gra](#), [read.bnd](#), [drawmap](#)

Examples

```
x <- c(3,3,5,9.5,11,11)
y <- c(2,4,4,6,4.5,5)
xymap <- createxymap(x, y, districts=c("A","B","C","D","E","F"), max.dist=2)
xymap$gra
drawmap(map=xymap$bnd)
```

delete.neighbor	<i>Delete Neighborhood Relations</i>
-----------------	--------------------------------------

Description

Adds the neighborhood relationship between two given regions from a map object in graph format.

Usage

```
delete.neighbor(map, region1, region2)
```

Arguments

map	Map object in graph format that should be modified.
region1, region2	Names of the regions that should no longer be regarded as neighbors.

Value

Returns an adjacency matrix that represents the neighborhood structure of map minus the deleted neighborhood relation in graph format.

Author(s)

Felix Heinzl, Thomas Kneib

See Also

[get.neighbor](#), [add.neighbor](#), [read.gra](#), [write.grabnd2gra](#)

Examples

```
germany <- read.gra(system.file("examples/germany.gra", package="BayesX"))
get.neighbor(germany, c("7339"))
germany <- delete.neighbor(germany, "7339", "7141")
get.neighbor(germany, c("7339"))
```

Description

Visualises variables that are spatially aligned according to a given map object. Each of the regions in a map will be coloured according to the value of the variable.

Usage

```
drawmap(data, map, regionvar=2, plotvar=3, limits, cols="hcl", nrcolors=100,
        swapcolors=FALSE, pcat=FALSE,
        hcl.par=list(h=c(120, 0), c=60, l=c(45,60), power=1.2),
        hsv.par=list(s=1, v=1), legend=TRUE, drawnames=FALSE, cex.names=0.7,
        cex.legend=0.7, mar.min=2, density=15, ...)
```

Arguments

data	Either the name of a file or a data frame containing the variables to be visualised. If missing, the map will be visualised without superposition of any further information
map	Map object containing the required boundary information (as obtained by a call to read.bnd)
regionvar	Defines the variable specifying the geographical regions. Either the name of a variable in data or the index of the corresponding column.
plotvar	Defines the variable that should be visualised. Either the name of a variable in data or the index of the corresponding column.
limits	Restricts (or extends) the coloring scheme to a range of values.
cols	Color scheme to be employed. Could be either a vector of colors or one out of the following pre-defined schemes: hcl, hsv, grey
nrcolors	Number of colors (only meaningful when using one of the pre-defined colour schemes).
swapcolors	Reverse the order of colors (works also with user-specified colours but will be most useful with the pre-defined schemes).
pcat	Option for the visualisation of posterior probabilities. In this case, a three-colour scheme representing significantly positive, insignificant and significantly negative values.
hcl.par	Parameters for the hcl colour scheme (see the documentation of <code>diverge_hcl</code> in package <code>vcd</code> for details).
hsv.par	Parameters for the hsv colour scheme (see the documentation of <code>hsv</code> for details).
legend	Should a legend be added to the figure?
drawnames	Adds the name of each region as a text label to the plot. In most cases the result will be confusing but may be useful when checking the validity of a map.

<code>cex.names</code>	Magnification to be used for the names (if <code>drawnames=TRUE</code>).
<code>cex.legend</code>	Magnification to be used for the legend.
<code>mar.min</code>	Controls the definition of boundaries. Could be either <code>NULL</code> for individual settings of <code>mar</code> or a value which defines <code>mar</code> as follows: The boundaries will be calculated according to the height to width ratio of the map with minimal boundary <code>mar.min</code> .
<code>density</code>	Regions without data will be visualised with diagonal stripes. <code>density</code> defines how dense the stripes should be.
<code>...</code>	Further arguments to be passed to the plot calls that visualise the region boundaries (probably not useful at all).

Author(s)

Felix Heinzl, Thomas Kneib, Andreas Brezger

See Also

[read.bnd](#)

Examples

```

germany <- read.bnd(system.file("examples/germany.bnd", package="BayesX"))
drawmap(map=germany)
drawmap(map=germany, drawnames=TRUE)

res <- read.table(system.file("examples/spatial_f_regions_spatial.res",
                             package="BayesX"), header=TRUE)

drawmap(res, map=germany)
drawmap(res, map=germany, limits=c(-2,4))
drawmap(res, map=germany, regionvar="regions", plotvar="pmed")
drawmap(res, map=germany, legend=FALSE)
drawmap(res, map=germany, legend=FALSE, main="spatial effect")

drawmap(res, map=germany, cols="hsv")
drawmap(res, map=germany, swapcolors=TRUE, cols="hsv")
drawmap(res, map=germany, cols="grey")
drawmap(res, map=germany,
        cols=c('darkgreen', 'green', 'yellow', 'orange', 'red', 'darkred'))

drawmap(res, map=germany, pcat=TRUE, cols="hcl")
drawmap(res, map=germany, pcat=TRUE, cols="hsv")
drawmap(res, map=germany, pcat=TRUE, cols="grey")

drawmap(res, map=germany, nrcolors=10, cols="hcl")
drawmap(res, map=germany, nrcolors=10, cols="hsv")
drawmap(res, map=germany, nrcolors=10, cols="grey")

drawmap(res, map=germany, cols="hcl",
        hcl.par=list(h=c(0,120), c=60, l=c(45,90), power=1.2))

```



```
drawmap(res, map=germany, cols="hcl",
        hcl.par=list(h=c(300,120), c=60, l=c(45,90), power=1.2))
drawmap(res, map=germany, cols="hcl",
        hcl.par=list(h=c(40,260), c=60, l=c(45,90), power=1.2))
drawmap(res, map=germany, cols="hsv", hsv.par=list(s=0.7, v=0.7))
```

extractSamples	<i>Extract MCMC samples from a BayesX results directory</i>
----------------	---

Description

This is a convenience function to extract samples from a BayesX results directory, which processes the log file to e.g. convert the spline coefficients samples to function values samples.

Usage

```
extractSamples(directoryWithBasename,
              logfile = file.path(dirname(directoryWithBasename), "log.txt"))
```

Arguments

directoryWithBasename	The BayesX results directory with basename for the files (e.g. "results/test", if this was specified as outfile in BayesX for the bayesreg object)
logfile	The log file of the MCMC run, defaults to log.txt in the results directory.

Value

Returns a list with the extracted samples of effects and deviances as well as the prediction data.frame:

<function name>	for P-Splines, Random Walks and spatial effects: a list with mcmc objects 'functionSamples' and 'varianceSamples' containing the respective effects/function and variance parameter samples.
FixedEffects	an mcmc object of all fixed simple parametric effects
RandomEffects	if there is at least one random effect in the model, this is a list, with elements in the first hierarchy being the group ID names, and elements in the second hierarchy being the names of the covariates. The leafs are the mcmc objects 'functionSamples' and 'varianceSamples', as for the other non-fixed terms
Deviance	an mcmc object with the (unstandardized and saturated) deviance
means	if the option predictmu was used, this mcmc object contains the mean samples
scale	an mcmc object with the possible scale parameter samples
lassoCoefficients	an mcmc object with the possible lasso regression parameter samples
ridgeCoefficients	an mcmc object with the possible ridge regression parameter samples

PredictMeans data.frame corresponding to the possible predictmean file in the BayesX directory

Additionally, entries for possibly remaining lasso or ridge variance parameters etc. are included in the return list.

Warning

You should be sure that only one MCMC run is saved in the given results directory in order to get sensible results out of this function.

Author(s)

Daniel Sabanes Bove, with contributions by Fabian Scheipl

Examples

```
## get the samples
samples <- extractSamples(file.path(system.file("examples/samples", package="BayesX"),
                                         "res"))

str(samples)

## check deviance convergence
plot(samples$Deviance)

## fixed parametric effects
plot(samples$FixedEffects)

## nonparametric effects:

## handy plot function to get means and pointwise credible intervals
nonpPlot <- function(samplesMatrix,
                      ...)
{
  x <- as.numeric(colnames(samplesMatrix))

  yMeans <- colMeans(samplesMatrix)
  yCredible <- t(apply(samplesMatrix,
                      MARGIN=2,
                      FUN=quantile,
                      prob=c(0.025, 0.975),
                      na.rm=TRUE))

  matplot(x, cbind(yMeans, yCredible),
          type="l",
          lty=c(1, 2, 2),
          lwd=c(2, 1, 1),
          col=c(1, 2, 2),
          ...)
}

nonpPlot(samples$f_x1$functionSamples,
```

```
        xlab=expression(x[1]),
        ylab=expression(hat(f)(x[1])))
nonpPlot(samples$f_x2$functionSamples,
        xlab=expression(x[2]),
        ylab=expression(hat(f)(x[2])))

## spatial effect
tanzania <- read.bnd(file=system.file("examples/tanzania.bnd", package="BayesX"))
drawmap(map=tanzania,
        data=
        with(samples$f_district,
            data.frame(name=colnames(functionSamples),
                estimate=colMeans(functionSamples))),
        regionvar="name",
        plotvar="estimate")
```

fuse

Combine Regions

Description

Combines a list of several regions of a map object in boundary format into a single region.

Usage

```
fuse(map, regions, name)
```

Arguments

map	Map object in boundary format that should be modified.
regions	Vector of regions to be combined
name	Name that should be given to the region arising from fusing the specified regions.

Value

Map object in boundary format with the specified regions combined.

Author(s)

Nadja Klein

See Also

[read.bnd](#), [write.bnd](#)

Examples

```
## Not run: map <- read.bnd(system.file("examples/germany9301.bnd",
  package = "BayesX"))
drawmap(map = map, drawnames = TRUE)

## Vector of regions to be combined.
regions <- c("1056", "1060", "1061")

## New name of combined region.
newname <- "1"
newmap <- fuse(map, regions, newname)
drawmap(map = newmap, drawnames = TRUE)

## Vector of regions to be combined.
germany <- read.bnd(system.file("examples/germany.bnd", package="BayesX"))
drawmap(map = germany, drawnames = TRUE)
regions <- c("9371", "9373", "9374", "9471", "9472", "9474", "9574")

## New name of combined region.
newname <- "1"
newmap <- fuse(germany, regions, newname)
drawmap(map = newmap, drawnames = TRUE)

## End(Not run)
```

get.centroids

Compute Centroids of Polygons

Description

Computes all areas and centroids of the regions of a given map in boundary format.

Usage

```
get.centroids(map)
```

Arguments

map Map object in boundary format.

Value

Matrix of area and centroids.

Author(s)

Felix Heinzl, Thomas Kneib

Examples

```
germany <- read.bnd(system.file("examples/germany.bnd", package="BayesX"))
centroids <- get.centroids(germany)
centroids[1:10,]

plot(c(2100,3700),c(6800,8500),type="n", xlab="", ylab="")
for(i in 1:10){
  polygon(germany[[i]])
  region <- attr(germany,"names")[i]
  text(x=centroids[i,2]+50, y=centroids[i,3]+30, region, cex=0.7)
}
points(centroids[1:10,2:3], col='red', pch=16)
```

`get.neighbor`*Obtain Neighbors of Given Regions*

Description

Extracts the neighbors of a number of regions from a map in graph format.

Usage

```
get.neighbor(map, regions)
```

Arguments

<code>map</code>	Map object in graph format.
<code>regions</code>	Vector of names of regions for which the neighbors should be extracted.

Value

A list of vectors containing the neighbors of the elements in regions.

Author(s)

Felix Heinzl, Thomas Kneib

See Also

[add.neighbor](#), [delete.neighbor](#)

Examples

```
germany <- read.gra(system.file("examples/germany.gra", package="BayesX"))
get.neighbor(germany, "1001")
get.neighbor(germany, c("1001", "7339"))
```

hpd *Computing Highest Posterior Density (HPD) Intervals*

Description

Compute approximate HPD intervals out of MCMC-samples in BayesX

Usage

```
hpd(data, alpha = 0.05, ...)
hpd.coda(data, alpha = 0.05)
```

Arguments

data	Either the name of a file or a data frame containing the sample.
alpha	A numeric scalar in the interval (0,1) such that 1 - alpha is the target probability content of the intervals.. The default is alpha = 0.05.
...	Further parameters to be passed to the internal call of <code>optim</code> and <code>integrate</code> .

Details

`hpd` computes the HPD interval based on a kernel density estimate of the samples. `hpd.coda` computes the HPD interval with the function `HPDinterval` available in package `coda`.

Author(s)

Nadja Klein

Examples

```
res <- read.table(system.file("examples/nonparametric_f_x_p spline_sample.raw",
  package="BayesX"), header = TRUE)
hpd(res)
hpd.coda(res)
```

Interface between nb and gra format
Convert nb and gra format into each other

Description

Convert neighborhood structure objects of class "nb" from R-package `spdep` to graph objects of class "gra" from R-package `BayesX` and vice versa.

Usage

```
nb2gra(nbObject)
gra2nb(graObject)
```

Arguments

```
nbObject      neighborhood structure object of class "nb"
graObject     graph object of class "gra"
```

Value

Equivalent object in the other format.

Author(s)

Daniel Sabanes Bove

See Also

[sp2bnd](#), [bnd2sp](#) for conversion between the geographical information formats and [read.gra](#), [write.gra](#) for the interface to the BayesX files.

Examples

```
## Not run: ## first nb to gra:
if(requireNamespace("sf") &
  requireNamespace("spdep")) {
  library("sf")
  library("spdep")

  columbus <- st_read(system.file("etc/shapes/columbus.shp",
    package = "spdep")[1])
  colNb <- poly2nb(columbus)
  ## ... here manual editing is possible ...
  ## then export to graph format
  colGra <- nb2gra(colNb)

  ## and save in BayesX file
  graFile <- tempfile()
  write.gra(colGra, file=graFile)

  ## now back from gra to nb:
  colGra <- read.gra(graFile)
  newColNb <- gra2nb(colGra)
  newColNb
  ## compare this with the original
  colNb
  ## only the call attribute does not match (which is OK):
  all.equal(newColNb, colNb,
    check.attributes=FALSE)
  attr(newColNb, "call")
}
```

```

    attr(colNb, "call")
  }

  ## End(Not run)

```

Interface between *sp* and *bnd* format

Convert sp and bnd format into each other

Description

Convert geographical information objects of class "SpatialPolygons" (or specializations) from R-package *sp* to objects of class "bnd" from R-package *BayesX* and vice versa.

Usage

```

sp2bnd(spObject, regionNames, height2width, epsilon)
bnd2sp(bndObject)

```

Arguments

<code>spObject</code>	object of class "SpatialPolygons" (or specializations)
<code>regionNames</code>	character vector of region names (parallel to the Polygons list in <code>spObject</code>), defaults to the IDs
<code>height2width</code>	ratio of total height to width, defaults to the bounding box values
<code>epsilon</code>	how much can two polygons differ (in maximum squared Euclidean distance) and still match each other?, defaults to machine precision
<code>bndObject</code>	object of class "bnd"

Value

Equivalent object in the other format.

Author(s)

Daniel Sabanes Bove

See Also

[nb2gra](#), [gra2nb](#) for conversion between the neighborhood structure formats and [read.bnd](#), [write.bnd](#) for the interface to the *BayesX* files.

Examples

```

## Not run: ## bnd to sp:
germany <- read.bnd(system.file("examples/germany2001.bnd", package="BayesX"))
spGermany <- bnd2sp(germany)

## plot the result together with the neighborhood graph
library(sp)
plot(spGermany)
library(spdep)
nbGermany <- poly2nb(spGermany)
plot(nbGermany, coords=coordinates(spGermany), add=TRUE)

## example with one region inside another
spExample <- spGermany[c("7211", "7235"), ]
plot(spExample)
plot(poly2nb(spExample), coords=coordinates(spExample), add=TRUE)

## now back from sp to bnd:
bndGermany <- sp2bnd(spGermany)
drawmap(map=bndGermany)

## compare names and number of polygons
stopifnot(identical(names(bndGermany),
                    names(germany)),
          identical(length(bndGermany),
                    length(germany)))

## compare contains-relations
surrounding <- attr(bndGermany, "surrounding")
whichInner <- which(sapply(surrounding, length) > 0L)
bndContainsData <- data.frame(inner=names(bndGermany)[whichInner],
                              outer=unlist(surrounding))

surrounding <- attr(germany, "surrounding")
whichInner <- which(sapply(surrounding, length) > 0L)
originalContainsData <- data.frame(inner=names(germany)[whichInner],
                                   outer=unlist(surrounding))

stopifnot(all(bndContainsData[order(bndContainsData$inner), ] ==
             originalContainsData[order(originalContainsData$inner), ]))

## End(Not run)

```

Description

Computes and plot autocorrelation functions for samples obtained with MCMC in BayesX

Usage

```
plotautocor(data, ask = TRUE, lag.max=100, ...)
```

Arguments

data	Either the name of a file or a data frame containing the sample.
ask	plotautocor will plot separate autocorrelation functions for each parameter. If ask=TRUE, the user will be prompted before showing the next plot.
lag.max	Maximum number of lags to be considered.
...	Further parameters to be passed to the internal call of plot such as ylim, etc.

Author(s)

Felix Heinzl, Thomas Kneib

Examples

```
res <- read.table(system.file("examples/nonparametric_f_x_p spline_sample.raw",
                             package="BayesX"), header=TRUE)
plotautocor(res)
plotautocor(res, lag.max=50)
```

plotnonp

Plotting Nonparametric Function Estimates

Description

Plots nonparametric function estimates obtained from BayesX

Usage

```
plotnonp(data, x = 2, y = c(3, 4, 5, 7, 8), ylim = NULL,
          lty = c(1, 2, 3, 2, 3), cols = rep(1, length(y)), month, year, step=12,
          xlab, ylab, ...)
```

Arguments

data	Either the name of a file or a data frame containing the estimation results.
x	Defines the x-axis in the plot. Either the name of a variable in data or the index of the corresponding column.
y	Defines the variables to be plotted against x. May be either a vector of names of variables in data or the corresponding indices. The default choice corresponds to the point estimate plus two confidence bands.
ylim	Since plotnonp plots multiple y-variables, it automatically determines the appropriate ylim to make all curves visible. Argument ylim allows to override this default behaviour with fixed values.

lty	Vector of line types used for plotting (must have the same length as y). The default corresponds to solid lines for the point estimate and dashed and dotted lines for the confidence bands.
cols	Vector of colors used for plotting (must have the same length as y). Default are black lines.
month, year, step	Provide specific annotation for plotting estimation results for temporal variables. month and year define the minimum time point whereas step specifies the type of temporal data with step=4, step=2 and step=1 corresponding to quarterly, half yearly and yearly data.
xlab, ylab	plotnonp constructs default labels that can be overwritten by these arguments
...	Further arguments to be passed to the interval call of plot such as type, etc.

Author(s)

Felix Heinzl, Andreas Brezger and Thomas Kneib

See Also

[drawmap](#), [plotautocor](#), [plotsample](#), [plotsurf](#)

Examples

```
res <- read.table(system.file("examples/nonparametric_f_x_pspline.res",
                             package="BayesX"), header=TRUE)

plotnonp(res)
plotnonp(res, x="x")
plotnonp(res, x="x", y="pmean")
plotnonp(res, x="x", y="pmed")
plotnonp(res, x="x", y="pmed", ylim=c(-2,2))
plotnonp(res, x="x", y=c("pmean", "pqu10", "pqu90"), lty=c(1,1,1),
          col=c("red", "blue", "blue"))
plotnonp(res, xlab="some variable", ylab="f(some variable)",
          main="Nonlinear effect of some variable", sub="penalised spline")

res <- read.table(system.file("examples/nonparametric2_f_time_pspline.res",
                             package="BayesX"), header=TRUE)

plotnonp(res)
plotnonp(res, month=1, year=1980, step=12)

res <- res[1:18,]
plotnonp(res, month=1, year=1980, step=12)
```

`plotsample`*Plotting Sampling Paths*

Description

Plots sampling paths obtained with MCMC-sampling in BayesX

Usage

```
plotsample(data, ask = TRUE, ...)  
plotsample.coda(data, ask = TRUE, ...)
```

Arguments

<code>data</code>	Either the name of a file or a data frame containing the sample.
<code>ask</code>	<code>plotsample</code> will plot separate sampling paths for each parameter. If <code>ask=TRUE</code> , the user will be prompted before showing the next plot.
<code>...</code>	Further parameters to be passed to the internal call of <code>plot</code> such as <code>ylim</code> , etc.

Details

`plotsample` simply plots sampling paths while `plotsampe.coda` makes use of the plotting facilities available in package `coda`.

Author(s)

Felix Heinzl, Andreas Brezger, Thomas Kneib

See Also

[drawmap](#), [plotautocor](#), [plotnonp](#), [plotsurf](#),

Examples

```
res <- read.table(system.file("examples/nonparametric_f_x_pspline_sample.raw",  
                             package="BayesX"), header=TRUE)  
plotsample(res)
```

plotsurf *Visualise Surface Estimates*

Description

Visualises surface estimates obtained with BayesX.

Usage

```
plotsurf(data, x=2, y=3, z=4, mode=1, ticktype="detailed",
         expand=0.75, d=100, theta=-30, phi=25, ...)
```

Arguments

data	Either the name of a file or a data frame containing the estimation results.
x	Defines the x-axis in the plot. Either the name of a variable in data or the index of the corresponding column.
y	Defines the y-axis in the plot. Either the name of a variable in data or the index of the corresponding column.
z	Defines the z-axis in the plot. Either the name of a variable in data or the index of the corresponding column.
mode	plotsurf is mostly a convenient interface to the functions persp (mode=1), image (mode=2) and contour (mode=3).
ticktype, expand, d, theta, phi	Overwrite the default behaviour of persp
...	Further parameteres that are parsed to the internal call to persp, image or contour

Author(s)

Felix Heinzl, Thomas Kneib

See Also

[drawmap](#), [plotautocor](#), [plotsample](#), [plotnonp](#)

Examples

```
res <- read.table(system.file("examples/surface_f_x1_x2_pspline.res",
                             package="BayesX"), header=TRUE)

plotsurf(res)
plotsurf(res, mode=2)
plotsurf(res, mode=3)

plotsurf(res, x="x1", y="x2", z="pmed")

plotsurf(res, ticktype="simple")
```

```
plotsurf(res, main="3D-Plot", xlab="myx", ylab="myy", zlab="f(myx,myy)")
```

read.bnd

Read Geographical Information in Boundary Format

Description

Reads the geographical information provided in a file in boundary format (see Ch. 5 of the BayesX Reference Manual) and stores it in a map object.

Usage

```
read.bnd(file, sorted=FALSE)
```

Arguments

file	Name of the boundary file to be read.
sorted	Should the regions be ordered by the numbers specifying the region names (sorted=TRUE)?

Value

Returns a list of polygons that form the map. Additional attributes are

surrounding	Parallel list where for each polygon, the name of a possible surrounding region is saved.
height2width	Ratio between height and width of the map. Allows customised drawing and storage in files by specifying the appropriate height and width.
class	Indicates whether the map is stored in boundary format (bnd) or graph format (gra). Maps returned by read.bnd are of class bnd

Author(s)

Daniel Sabanes Bove, Felix Heinzl, Thomas Kneib, Andreas Brezger

References

BayesX Reference Manual. Available from <https://www.uni-goettingen.de/de/bayesx/550513.html>

See Also

[write.bnd](#), [drawmap](#), [read.gra](#), [write.gra](#)

Examples

```

germany <- read.bnd(system.file("examples/germany.bnd", package="BayesX"))
drawmap(map=germany)
attributes(germany)

germany <- read.bnd(system.file("examples/germany2001.bnd", package="BayesX"))
drawmap(map=germany)
attributes(germany)

```

read.gra

Read Geographical Information in Graph Format

Description

Reads the geographical information provided in a file in graph format (see Ch. 5 of the BayesX Reference Manual) and stores it in a map object.

Usage

```
read.gra(file, sorted=FALSE)
```

Arguments

<code>file</code>	Name of the graph file to be read.
<code>sorted</code>	Should the regions be ordered by the numbers specifying the region names (<code>sorted=TRUE</code>)?

Value

Returns an adjacency matrix that represents the neighborhood structure defined in the graph file. Additional attributes are

<code>dim</code>	Dimension of the (square) adjacency matrix.
<code>dimnames</code>	List of region names corresponding to rows and columns of the adjacency matrix.
<code>class</code>	Indicates whether the map is stored in boundary format (<code>bnd</code>) or graph format (<code>gra</code>). Maps returned by <code>read.gra</code> are of class <code>gra</code>

Author(s)

Thomas Kneib, Felix Heinzl

References

BayesX Reference Manual. Available from <https://www.uni-goettingen.de/de/bayesx/550513.html>

See Also

[write.gra](#),[read.bnd](#),[write.bnd](#),[get.neighbor](#),[add.neighbor](#),[delete.neighbor](#)

Examples

```
germany <- read.gra(system.file("examples/germany.gra", package="BayesX"))
attributes(germany)
```

shp2bnd

convert a shape-file into a boundary object

Description

Converts the geographical information provided in a shape-file into a boundary object (see Ch. 5 of the Reference Manual)

Usage

```
shp2bnd(shpname, regionnames, check.is.in = TRUE)
```

Arguments

shpname	Base filename of the shape-file (including path)
regionnames	Either a vector of region names or the name of the variable in the dbf-file representing these names
check.is.in	Test whether some regions are surrounded by other regions (FALSE speeds up the execution time but may result in a corrupted bnd-file)

Value

Returns a boundary object, i.e. a list of polygons that form the map. See [read.bnd](#) for more information on the format.

Author(s)

Felix Heinzl, Daniel Sabanes Bove, Thomas Kneib with contributions by Michael Hoehle and Frank Sagerer

References

BayesX Reference Manual. Available from <https://www.uni-goettingen.de/de/bayesx/550513.html>

See Also

[write.bnd](#),[drawmap](#),[read.bnd](#)

Examples

```
## read shapefile into bnd object
shpName <- sub(pattern="(.*)\.dbf", replacement="\1",
              x=system.file("examples/northamerica_adm0.dbf",
                           package="BayesX"))
north <- shp2bnd(shpname=shpName, regionnames="COUNTRY")

## draw the map
drawmap(map=north)

## compare with shipped bnd file
shippedBnd <- read.bnd(system.file("examples/northamerica.bnd", package="BayesX"))
stopifnot(all.equal(north, shippedBnd))
```

smooth.bnd

Round Boundary Information

Description

Rounds the boundary information in a map object in boundary format to a specified precision.

Usage

```
smooth.bnd(map, digits = 2, scale = 1)
```

Arguments

map	Map object in boundary format that should be modified.
digits	Number of digits to round to.
scale	Scaling factor that should be applied for rounding. For example, with scale=0.1 all polygons are divided by 10 before rounding.

Value

Map object in boundary format rounded to the specified precision.

Author(s)

Felix Heinzl, Thomas Kneib

See Also

[read.bnd](#), [write.bnd](#)

write.bnd *Saving Maps in Boundary Format*

Description

Writes the information of a map object to a file (in boundary format)

Usage

```
write.bnd(map, file, replace = FALSE)
```

Arguments

map	Map object ot be saved (should be in boundary format).
file	Name of the file to write to
replace	Should an existing file be overwritten with the new version?

Author(s)

Thomas Kneib, Felix Heinzl

References

BayesX Reference Manual. Available from <https://www.uni-goettingen.de/de/bayesx/550513.html>

See Also

[write.gra](#), [read.gra](#), [read.bnd](#)

write.gra *Saving Maps in Graph Format*

Description

Writes the information of a map object to a file (in graph format)

Usage

```
write.gra(map, file, replace = FALSE)
```

Arguments

map	Map object ot be saved (should be in graph format, see bnd2gra for the conversion of boundary format to graph format).
file	Name of the file to write to
replace	Should an existing file be overwritten with the new version?

Author(s)

Thomas Kneib, Felix Heinzl

References

BayesX Reference Manual. Available from <https://www.uni-goettingen.de/de/bayesx/550513.html>

See Also

[write.bnd](#),[read.gra](#),[read.bnd](#)

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