

Package ‘MapGAM’

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Type Package

Title Mapping Smoothed Effect Estimates from Individual-Level Data

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Description Contains functions for mapping odds ratios, hazard ratios, or other effect estimates using individual-level data such as case-control study data, using generalized additive models (GAMs) or Cox models for smoothing with a two-dimensional predictor (e.g., geolocation or exposure to chemical mixtures) while adjusting linearly for confounding variables, using methods described by Kelsall and Diggle (1998), Webster et al. (2006), and Bai et al. (2020). Includes convenient functions for mapping point estimates and confidence intervals, efficient control sampling, and permutation tests for the null hypothesis that the two-dimensional predictor is not associated with the outcome variable (adjusting for confounders).

License GPL-3

Depends R (>= 2.10.0), sp, gam, survival

Imports maptools, colorspace

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MapGAM-package	<i>Mapping Smoothed Effect Estimates from Individual-Level Spatial Data</i>
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Description

Contains functions for estimating and mapping hazard ratios, odds ratios, rate ratios, and continuous outcomes from individual-level data such as case-control study data, using generalized additive models (GAMs) or extended Cox models. This allows for smoothing with a two-dimensional predictor such as geolocation or exposure to chemical mixtures, while adjusting for confounding variables using methods described by Kelsall and Diggle (1998), Webster et al. (2006), and Bai et al. (2020). Includes convenient functions for mapping, efficient control sampling, confidence intervals, and permutation tests for the null hypothesis that the two-dimensional predictor is not associated with the outcome variable, adjusting for confounders.

Details

Package: MapGAM
Type: Package
Version: 1.2-6
Date: 2022-05-25
License: GPL-3

Typical spatial applications will start with the `predgrid` function to create a regular grid of points within the study area, with optional map boundaries (e.g., a country, state, or regional map). Crude or adjusted odds ratios, hazard ratios, or continuous outcomes are then estimated at each grid point using the `modgam` function to smooth by geolocation. Finally, the predicted values (and optionally, "clusters"—areas of significantly increased or decreased values determined via permutation tests or confidence intervals) are plotted using the `plot` or `colormap` functions. Most users will use the `plot` function to create maps from `modgam` objects, but `colormap` is provided for backwards compatibility as well as for creating maps from models fit using functions other than `modgam`. The `trimdata` and `sampcont` functions can be used to restrict data to those within map boundaries and to conduct simple or spatiotemporal stratified sampling from eligible controls. The `optspan` function can be used to find an optimal span size for the LOESS smoother used by the `modgam` function; it is automatically used within the `modgam` function when the span size is not provided by the user. These functions can also be applied to non-spatial data when two-dimensional smoothing is of interest, such as investigation of the effects of a mixture of two chemicals.

Author(s)

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Send bug reports to <sbartell@uci.edu>.

References

- Bai L, Gillen DL, Bartell SM, Vieira VM. [Mapping smoothed spatial effect estimates from individual-level data: MapGAM](#). *The R Journal* 2020, 12:32-48.
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- Young RL, Weinberg J, Vieira V, Ozonoff A, Webster TF. [A power comparison of generalized additive models and the spatial scan statistic in a case-control setting](#). *International Journal of Health Geographics* 2010, 9:37.

See Also

[trimdata](#), [sampcont](#), [predgrid](#), [optspan](#), [modgam](#), [colormap](#), [plot.modgam](#).

Examples

```
# Load synthetic data and a preformatted base map
data(MAmap)
data(MAdata)

# Create a grid on the base map (PBSmapping package recommended)
if(require(PBSmapping)) gamgrid <- predgrid(MAdata, map=MAmap) else
  gamgrid <- predgrid(MAdata)
# Fit a GAM with a smooth term for spatial location
fit1 <- modgam(data=MAdata, rgrid=gamgrid, m="crude", sp=0.5)
# Display odds ratio estimates on the base map
plot(fit1, MAmap, exp=TRUE)

#### See colormap and modgam help files for more examples
```

AIC.modgam

AIC of the [modgam](#) Object

Description

This function summarizes the AIC of a modgam object produced by [modgam](#).

Usage

```
## S3 method for class 'modgam'
AIC(object, ...)
```

Arguments

`object` a modgam object.
`...` extra arguments for S3 generic, ignored by `AIC.modgam`.

Author(s)

Lu Bai
 Send bug reports to <sbartell@uci.edu>.

See Also

[modgam](#) [gamcox](#), [predict.gamcox](#).

beertweets

Geocoded Tweets with Beer Indicator

Description

Geocoded tweets from Twitter, with an indicator variable for any mention of beer, time stamp, and state of origin.

Usage

```
data(MAmap)
```

Format

A data frame with 10000 observations on 5 variables:

`beer` 1 for tweets about beer, 0 for other tweets.

`longitude` geocoded longitude.

`latitude` geocoded latitude.

`state` a factor with the name of the state.

`time` a list of POSIXlt format dates and times for the tweets.

Details

A sample of geocoded tweets from within in the contiguous US, from June to October of 2012. Tweets mentioning beer (cases) are oversampled by a factor of 100. Geocoding is typically at the level of city or town; tweets that could not be geocoded were excluded from this data set.

Source

Dr. Matthew Zook, University of Kentucky

<http://www.floatingsheep.org/2012/07/church-or-beer-americans-on-twitter.html>

Examples

```
data(beertweets)
attach(beertweets)
plot(longitude,latitude,col=beer+1) # beer in red, non-beer in black
```

CAdata

Deidentified Survival Data for California

Description

Survival time, censoring status, and geolocations (jittered to preserve anonymity) for 5000 ovarian cancer patients in California, using a Lambert projection (in meters). [CAmap](#) is a map of California using the same projection.

Usage

```
data(CAdata)
```

Format

A data frame with 5000 observations on the following 6 variables.

time survival time.

event censoring status.

X projected X coordinate.

Y projected Y coordinate.

AGE patient age.

INS insurance type: Mng (Managed Care: managed care, HMO, PPO and other private insurance), Mcr (Medicare), Mcd (Medicaid), Oth: (Other Insurance: military, county-funded), Uni (Not Insured, self-pay) and Unk (Unknown).

Examples

```
data(CAdata)
summary(CAdata)
plot(CAdata$X, CAdata$Y)
```

CAgrid

A Grid on State of California

Description

An evenly-spaced grid of prediction points approximately 5km apart that extended across the latitude and longitude coordinates of participants' locations throughout California with over 7,500 points. Areas with sparse population data are clipped.

Usage

```
data(CAgrid)
```

Format

A data frame with 7579 geolocations.

X projected X coordinate.

Y projected Y coordinate.

Source

Dr. Veronica Vieira, University of California, Irvine

Examples

```
data(CAgrid)
data(CAmap)
plot(CAmap)
points(CAgrid)
```

CAmap

Map of California

Description

A map of the outline of CA in SpatialPolygonsDataFrame format, converted from an ESRI shapefile using the readShapePoly function in the **maptools** package.

Usage

```
data(CAmap)
```

Format

The format is class SpatialPolygonsDataFrame (package "sp").

Details

State Plane Projected coordinate system, North America Datum 1983 (NAD_1983_StatePlane_California_I_FIPS_0401) for California, using standard parallels 40.00000000 and 41.66666667. The latitude of origin is 39.3, the central meridian is -122.0 and the projection units are meters (False Easting: 200000 m; False Northing: 500000 m).

Source

Dr. Veronica Vieira, University of California, Irvine

Examples

```
data(CAmap)
plot(CAmap)
```

`coef.gamcox`*Coefficients of the `gamcox` Object*

Description

This function provides coefficients of a `gamcox` object produced by `gamcox`.

Usage

```
## S3 method for class 'gamcox'  
coef(object, ...)
```

Arguments

```
object      a gamcox object.  
...         .
```

Author(s)

Lu Bai
Send bug reports to <sbartell@uci.edu>.

See Also

`modgam.gamcox`, `predict.gamcox`.

Examples

```
data(CAdata)  
fit <- gamcox(Surv(time,event)~lo(X,Y)+AGE+INS,data=CAdata, span = 0.2)  
coef(fit)
```

`coef.modgam`*Coefficients of the `modgam` Object*

Description

This function provides coefficients of a `modgam` object produced by `modgam`.

Usage

```
## S3 method for class 'modgam'  
coef(object, ...)
```


Arguments

object a modgam object.
 ... extra arguments for S3 generic, ignored by `coef.modgam`.

Author(s)

Lu Bai
 Send bug reports to <sbartell@uci.edu>.

See Also

[modgam](#) [gamcox](#), [predict.gamcox](#).

 colormap

Maps Predicted Values and Clusters on a Two-Dimensional Map

Description

Displays a color image map, including a legend, scale bar, and optional North arrow, showing values for a grid of points. Irregular grids are allowed. Also draws contour lines for regions of significantly increased or decreased predicted values ("clusters").

Usage

```
colormap(obj, map=NULL, exp=FALSE, add=FALSE, mapmin=NULL, mapmax=NULL,
  col.seq=rev(rainbow(201,start=0,end=0.66)), anchor=FALSE,
  border.gray = 0.3, contours="none",
  contours.drawlabels=FALSE, contours.lty=1,
  contours.lwd=1, contours.levels, contours.labcex=0.7,
  interval.exclude=0, arrow=TRUE, axes=FALSE, ptsize=0.9, mai,
  legend.name = "predicted values", legend.cex=1,
  legend.add.line,alpha,...)
```

Arguments

obj (Required) A list containing at least these two elements: "grid" (a 2 column data frame with X and Y coordinates) and "fit" (the value to displayed on the map).

map Can be used to map `fit` on a base map from the `map` function in the **maps** package, or on a base map produced by the `readOGR` function in the **rgdal** package. `readOGR` reads maps from external files in the ESRI shapefile format. `map=NULL` produces a color image without any base map.

exp If `exp=T`, `fit` will be displayed in exponential scale.

add Use `add=T` to add the color map to an existing plot. This will often result in loss of the legend and scale, which are added outside of the normal map boundaries. `add` is ignored when a map is provided using the `map` argument.

mapmin	The minimum value for the color scale legend. When not specified, it will be set to the minimum predicted value.
mapmax	The maximum value for the color scale legend. When not specified, it will be set to the maximum predicted value.
col.seq	The color sequence (palette) used to display the predicted values on the map. The default is a rainbow palette, but divergent or sequential palettes may be better for some applications. See the <code>colspace</code> library and the example below for other options.
anchor	Use <code>anchor=TRUE</code> to center the color palette on <code>legend.add.line</code> . When <code>anchor=FALSE</code> (the default) or when <code>legend.add.line</code> is not specified, the color palette will be centered halfway between <code>mapmin</code> and <code>mapmax</code> . <code>anchor=TRUE</code> is recommended when using a divergent palette.
border.gray	Gray scale for the border of map, ranges from 0 to 1. It is white with <code>border.gray=1</code> , and black with <code>border.gray=0</code> . The default scale is 0.9.
contours	When <code>contours="interval"</code> , two other elements <code>conf.low</code> and <code>conf.high</code> must be included in <code>obj</code> , and regions excluding a user-specified <code>interval.exclude</code> will be circled on the map. By specifying an element name in <code>obj</code> for contours, contour lines for the specified element will be added on the map, e.g. <code>contours="fit"</code> or <code>contours="exp.fit"</code> for a <code>modgam</code> object. The default is "none" which produces no contour lines.
contours.drawlabels	Use <code>contours.drawlabels = TRUE</code> add labels on contour lines.
contours.lty	The line type for contour lines
contours.lwd	The width for contour lines.
contours.levels	The levels for contour lines. When <code>exp=T</code> , the levels will also be used in an exponential scale.
contours.labcex	cex for contour labelling. This is an absolute size, not a multiple of <code>par("cex")</code>
interval.exclude	If <code>contours="interval"</code> , regions with confidence intervals excluding <code>interval.exclude</code> will be circled
arrow	Use <code>arrow=T</code> to add a North arrow to the map.
axes	Use <code>axes=T</code> to add axes to the map (useful for chemical mixture isoboles).
ptsize	The size of the points used to fill in colors on the map. Increase to remove white space inside the map or decrease to remove color outside the map boundaries. NOTE: white space can also be eliminated by increasing the grid size in <code>predgrid</code> , which is often preferable as it results in a higher resolution map.
mai	The margins of the plot. Details see par ,
legend.name	The name of displayed for the legend bar.
legend.cex	A numerical value giving the amount by which legend text should be magnified relative to the default.
legend.add.line	A numerical value at which a line will be added on the legend bar to indicate the color for the value.

Arguments

Y	a list including two elements: time for survival times and event for censoring status.
X	a data frame containing the variables in the model. The data must be structured so that the X and Y coordinates for two-dimensional predictor (e.g., geolocation) are in the 1st and 2nd columns, respectively.
which	matrix index for smooth term.
eta	current estimated subject log hazard ratio compared to the baseline.
span	smoothing parameter that been used to smoothing the second derivative of the log partial likelihood.
adjust	adjust=TRUE means there are confounders included in the model.

Details

For data that having tied failure times, Efron's approximation method is used to calculate the log partial likelihood and corresponding derivatives. Let η denote the log hazard ratio, and l denote the partial likelihood. When fitting a Cox proportional hazard additive model, η is updated by

$$\eta^{new} = \eta^{old} - \frac{dl/d\eta}{smooth(d^2l/d\eta^2)}$$

Value

deltaeta	difference between the input eta and the new updated eta.
w	inverse of smoothed second derivatives.
l	partial likelihood based on input eta.

Author(s)

Lu Bai and Scott Bartell

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References

Hastie TJ, Tibshirani RJ. Generalized Additive Models. (Chapman & Hall/CRC Monographs on Statistics & Applied Probability, Boca Raton, Florida, 1990).

Bristow RE, Chang J, Ziogas A, Gillen DL, Bai L, Vieira VM. Spatial Analysis of Advanced-stage Ovarian Cancer Mortality in California. American Journal of Obstetrics and Gynecology 2015, 213(1), e1-43).

See Also

[gamcox](#), [predict.gamcox](#).

Examples

```
data(CAdata)
Y = CAdata[,c("time", "event")]
X = CAdata[,c(3:5)]
eta = coxph(Surv(time, event)~AGE, data=CAdata)$linear.predictors
result = dls(Y, X, 1:2, eta, span=0.2)
plot(eta, result$deltaeta)
```

formula.gamcox

Formula of the [gamcox](#) Object

Description

This function provides the formula of a gamcox object produced by [gamcox](#).

Usage

```
## S3 method for class 'gamcox'
formula(x, ...)
```

Arguments

x a gamcox object.
... .

Author(s)

Lu Bai
Send bug reports to <sbartell@uci.edu>.

See Also

[modgam](#) [gamcox](#), [predict.gamcox](#).

Examples

```
data(CAdata)
fit <- gamcox(Surv(time, event)~lo(X, Y)+AGE+INS, data=CAdata, span = 0.2)
formula(fit)
```

formula.modgam	<i>Formula of the <code>modgam</code> Object</i>
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Description

This function provide the formula of a modgam object produced by `modgam`.

Usage

```
## S3 method for class 'modgam'
formula(x, ...)
```

Arguments

x	a modgam object.
...	extra arguments for S3 generic, ignored by <code>formula.modgam</code> .

Author(s)

Lu Bai
Send bug reports to <sbartell@uci.edu>.

See Also

[modgam](#) [gamcox](#), [predict.gamcox](#).

gamcox	<i>Fit a Cox Additive Model with a Two-Dimensional Smooth</i>
--------	---

Description

Fits a Cox proportional hazard additive model with a two-dimensional LOESS smooth for geolocation (or any other two-dimensional predictor). `gamcox` uses the backfitting algorithm to combine the smoothing and fitting methods. The smoothing method currently supported is local regression (LOESS).

Usage

```
gamcox(formula, data, subset, weights, span=0.5, I.span=0.2, degree = 1,
        loess.trace = "exact", Maxiter = 40, tol = 1e-07)

gamcox.fit(Y, X, smooth.frame, weights, span=0.5, I.span=0.2, degree = 1,
           loess.trace = "exact", Maxiter = 40, tol = 1e-07)
```

Arguments

formula	a formula expression (required), with the response on the left of a ~ operator, and the predictors on the right. The response must be a survival object as returned by the Surv function. A built-in nonparametric smoothing term is indicated by lo for loess smooth terms. The two-dimensional predictor (e.g., geolocation) should be specified as arguments in lo().
data	a data frame containing the variables in the model. If not found in data, the variables are taken from environment(formula).
Y, X	for gamcox.fit: Y is a list including two elements: time for survival times and event for censoring status. X is a data frame containing the variables in the model. The data must be structured so that the X and Y coordinates for two-dimensional predictor (e.g., geolocation) are in the 1st and 2nd columns, respectively.
smooth.frame	the model matrix for the smooth term.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of weights to be used in the fitting process.
span	the span size for the LOESS smooth of the two-dimensional predictor, which controls the degree of smoothing.
I.span	the span size for the LOESS smooth of the Fisher information.
degree	the degree of the polynomials to be used for LOESS smooth, normally 1 or 2.
loess.trace	whether the trace of the smoother matrix be computed exactly ("exact") or approximately ("approximate"). It is recommended to use "approximate" for more than about 1000 data points.
Maxiter	the maximum number of iterations in backfitting algorithm.
tol	the tolerance threshold for convergence.

Details

The model used to fit the data is a Cox proportional hazard additive model with a LOESS smooth for a two-dimensional predictor such as geolocation (Hastie and Tibshirani, 1990):

$$\lambda(t) = \lambda_0(t) \exp \{S(x_i, y_i) + \mathbf{Z}_i \boldsymbol{\beta}\}$$

where $\lambda(t)$ is the hazard at time t for participant i , x_i and y_i are predictor coordinates for participant i (i.e., projected distance east and north, respectively, from an arbitrarily defined origin location), $S(.,.)$ is a 2-dimensional smoothing function (currently LOESS), \mathbf{Z}_i is a row vector of covariate values for participant i , and $\boldsymbol{\beta}$ is a vector of unknown regression parameters. See the references for more details.

Value

gamcox returns an object of class gamcox. It can be examined by print and predict.

coefficients	a named vector of coefficients for the parametric part of the additive predictors, which multiply the columns of the model matrix. The names of the coefficients are the names of the single-degree-of-freedom effects (the columns of the model matrix). If the model is overdetermined there will be missing values in the coefficients corresponding to inestimable coefficients.
additive.predictors	the additive fit, given by the product of the model matrix and the coefficients, plus the columns of the \$smooth component.
smooth	estimated smoothing term. Nonlinear part of the spatial effect on survival rates.
var	the approximate pointwise variances for the columns of smooth.
residuals	the residuals from the final weighted additive fit; also known as residuals, these are typically not interpretable without rescaling by the weights.
deviance	up to a constant, minus twice the maximized log-likelihood. Similar to the residual sum of squares. Where sensible, the constant is chosen so that a saturated model has deviance zero.
df.residual	the residual degrees of freedom.
aic	AIC of the fitted model.

Author(s)

Lu Bai

Send bug reports to <sbartell@uci.edu>.

References

Hastie TJ, Tibshirani RJ. Generalized Additive Models. (Chapman & Hall/CRC Monographs on Statistics & Applied Probability, Boca Raton, Florida, 1990).

Bristow RE, Chang J, Ziogas A, Gillen DL, Bai L, Vieira VM. Spatial Analysis of Advanced-stage Ovarian Cancer Mortality in California. American Journal of Obstetrics and Gynecology 2015, 213(1), e1-43)

See Also

[modgam](#), [predict.gamcox](#).

Examples

```
data(CAdata)
data(CAmap)

fit <- gamcox(Surv(time,event)~AGE + factor(INS) + lo(X,Y),data=CAdata,
span=0.2,loess.trace="approximate")
fit
pred = predict(fit)
colormap(list(fit=pred$pred,grid=data.frame(X=CAdata$X,Y=CAdata$Y)),map=CAmap,
border.gray=0.5)
```


Description

90 cases and 910 controls with random smoking covariate values and random geolocations within Massachusetts, geocoded on a Lambert projection (in meters). [MMap](#) is a map of Massachusetts using the same projection.

Usage

```
data(MAdata)
```

Format

A data frame with 1000 observations on the following 6 variables.

Case 0 for controls, 1 for cases.

Xcoord projected X coordinate.

Ycoord projected Y coordinate.

Smoking 0 for nonsmokers, 1 for smokers.

Mercury continuous variable for mercury exposure.

Selenium continuous variable for selenium exposure.

Details

Lambert conformal conic projection for the State of Massachusetts, using standard parallels 41.7166667 and 42.68333333. The latitude of origin is 41.0, the central meridian is -71.5, and the projection units are meters (False Easting: 200000 m; False Northing: 750000 m).

Source

Simulated data provided by package authors

Examples

```
data(MAdata)
summary(MAdata)
attach(MAdata)
# map participants, cases in red and controls in black
plot(Xcoord,Ycoord,col=Case+1)
```

MMap

Map of Massachusetts

Description

A map of the outline of MA in SpatialPolygonsDataFrame format, converted from an ESRI shapefile using the readShapePoly function in the **maptools** package.

Usage

```
data(MMap)
```

Format

The format is class SpatialPolygonsDataFrame (package "sp").

Details

Lambert conformal conic projection for the State of Massachusetts, using standard parallels 41.71666667 and 42.68333333. The latitude of origin is 41.0, the central meridian is -71.5, and the projection units are meters (False Easting: 200000 m; False Northing: 750000 m).

Source

Dr. Veronica Vieira, University of California, Irvine

Examples

```
data(MMap)
plot(MMap)
```

MapGAM.version*Revision Dates for MapGAM Functions*

Description

Print version and dates for MapGAM package and functions.

Usage

```
MapGAM.version()
```

Author(s)

Scott Bartell Send bug reports to <sbartell@uci.edu>.

See Also

[MapGAM-package](#),

modgam	<i>Fit a Generalized Additive Model (GAM) with a Two-Dimensional Smooth and Make Predictions</i>
--------	--

Description

Fits a crude or adjusted regression on a user-supplied grid for spatial analysis using a generalized additive model with a two-dimensional LOESS smooth for geolocation (or any other two-dimensional predictor). Includes optional pointwise confidence intervals and permutation tests for global and local tests of the null hypothesis that the two-dimensional predictor (e.g., geolocation) is not associated with the outcome. Most applications will pass the output of this function to `plot.modgam` to map the resulting odds ratios or other effect estimates.

Usage

```
modgam(formula, rgrid, data, subset, offset, family = binomial(), permute = 0,
        conditional = TRUE, pointwise = FALSE, m = "adjusted", sp = seq(0.05, 0.95, 0.05),
        degree=1, keep=FALSE, type=c("spatial", "all"), reference = "median",
        se.fit = FALSE, alpha = 0.05, verbose = TRUE, ...)
```

Arguments

formula	a formula expression, with the response on the left of a <code>~</code> operator, and the predictors on the right. If fitting a Cox additive model, the response must be a survival object as returned by the <code>Surv</code> function. A built-in nonparametric smoothing term is indicated by <code>lo</code> for loess smooth terms. The two-dimensional predictor (e.g., geolocation) should be specified as arguments in <code>lo()</code> . <code>formula</code> can be missing if <code>data</code> and <code>family</code> are specified.
rgrid	a data frame containing the values of X and Y coordinates at which to generate predictions. If missing, the predictions will be generated for the two-dimensional predictor in <code>data</code> . The <code>predgrid</code> function can be used to supply an appropriate <code>rgrid</code> for <code>rdata</code> , with the grid clipped according to any specified base map (see examples below).
data	a data frame containing the variables in the model. If <code>formula</code> is specified, <code>data</code> is optional. In this way, if not found in <code>data</code> , the variables are taken from <code>environment(formula)</code> . If <code>formula</code> is missing, the data must be structured so that the outcome is in the 1st column (1st and 2nd columns for survival data) and the X and Y coordinates for two-dimensional predictor (e.g., geolocation) are in the 2nd and 3rd columns (3rd and 4th columns for survival data), respectively. If more than 3 (4 for survival data) columns are provided and <code>m = "adjusted"</code> , the additional columns will be entered as linear predictors in the GAM model.

family	a description of the error distribution and link function to be used in the model. This can be a character string naming a family function, a family function or the result of a call to a family function. (See family for details of family functions. Note that unlike other packages, MapGAM defaults to the binomial family and logit link, i.e., a logistic model.). If formula is missing, family = "survival" must be specified to fit a Cox proportional hazard additive model.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
offset	name in data and rgrid that will be used as offset in the model. It will be ignored if offset is specified in formula. offset will be ignored if family="survival"
permute	the number of permutations of the data set for testing the significance of the two-dimensional predictor. permute = 0 (default) produces no permutation tests. If permute > 0, the paired coordinates for the two-dimensional predictor are randomly permuted in order to simulate the distribution of results under the null hypothesis that location is not associated with the outcome. 1000 permutations are recommended for reasonable accuracy of p-values. WARNING: Because each permutation requires refitting the GAM, permutation tests can be quite slow.
conditional	a logical value indicating whether to run a conditional or unconditional permutation test; this argument is used only when permute > 0. The default is a conditional permutation test: the span size is held fixed throughout all permutations even if sp = NULL to optimize the span size for the original data (see Young et al., 2012). The unconditional permutation test repeats the span size optimization for each permutation, which is more conservative but takes about 20 times longer to compute. If conditional = FALSE the sp argument is ignored when fitting both the original and permuted data sets.
pointwise	a logical value indicated whether to include pointwise permutation tests for every grid point. This argument is only used when permute > 0. Using se.fit = TRUE to determine grid points with significantly different outcomes is usually preferable to using pointwise permutation tests.
m	model type for the GAM. Options are "crude" or "adjusted" (default). If "crude", only the smooth for the two-dimensional predictor is included in the model (i.e., "crude" is a synonym for "unadjusted"). If "adjusted", all covariates in the data set (columns >= 4) are included in the model.
sp	the span size for the LOESS smooth of the two-dimensional predictor. If sp is a vector an optimal span size will be determined using the optspan function, using the vector as candidate values. By default the optimal span is chosen from among a sequence of values ranging from 0.05 to 0.95, in increments of 0.05. See the help file for optspan for more details. It will be ignored if span is indicated in formula.
degree	the degree of the polynomials to be used for LOESS smooth, normally 1 or 2. It will be ignored if the degree is indicated in formula.
keep	a logical value indicating whether to store and return the pointwise odds ratios, and if conditional = FALSE the span size, for every permuted data set. These values aren't necessary for mapping or cluster identification, and storing them slows the permutation tests, so the default is keep = FALSE.

type	use type="spatial"(default for censored survival data) to estimate the spatial effect, or type="all"(default for univariate outcome) to estimate the effect of all covariates included in the model.
reference	referent for the predicted values or effects. If reference="none", the output will be predicted values at each grid point for either the spatial effect (type="spatial") or the linear predictor including all covariates (type="all"). If reference = "median", the output will be the difference between the estimated effect/predictor at each grid point and the median effect/predictor (e.g., the log odds ratio for a binomial model with logit link). If reference = "mean", the output will be the difference between the estimated effect/predictor at each grid point and the mean effect/predictor. If reference is a data frame indicating a specific geolocation, the output will be the difference between the estimated effect/predictor at each grid point and the effect/predictor at the geolocation specified by reference.
se.fit	if TRUE, pointwise standard errors and confidence intervals are computed along with the predictions. Results can be passed to plot.modgam with contours = "interval" to identify clusters of the outcome (e.g., spatial regions with statistically significant outcomes—e.g., unusually high or low risks).
alpha	the significance level used for confidence intervals when se.fit = TRUE
verbose	a logical value indicating whether to print the GAM model statement, the percentile rank for the global deviance statistic in the permutation test, and the progress of the permutation test (report completion of every 10 permutations). The default is verbose = TRUE.
...	further arguments to be passed to the gam or gamcox function (e.g., weights).

Details

The model used to fit the data is a generalized additive model with a LOESS smooth for a two-dimensional predictor such as geolocation (Hastie and Tibshirani, 1990; Kelsall and Diggle, 1998; Webster et al., 2006). Although any family and link function supported by the gam function is supported, the default binomial family with logit link yields the following model:

$$\ln\left(\frac{\pi_i}{1 - \pi_i}\right) = S(x_i, y_i) + \mathbf{Z}_i\boldsymbol{\beta}$$

where π_i is the probability that the outcome is 1 for participant i , x_i and y_i are predictor coordinates for participant i (i.e., projected distance east and north, respectively, from an arbitrarily defined origin location), $S(\cdot, \cdot)$ is a 2-dimensional smoothing function (currently LOESS), \mathbf{Z}_i is a row vector of covariate values for participant i , and $\boldsymbol{\beta}$ is a vector of unknown regression parameters (including an intercept). When a permutation test is requested, for each permutation the paired X and Y coordinates in the data set are randomly reassigned to participants, consistent with the null hypothesis that the geolocation (or another two-dimensional predictor entered in place of X and Y) is not associated with the outcome. Note that this procedure intentionally preserves associations between other covariates and the outcome variable so the permutation test reflects the significance of geolocation. See the references for more details.

Value

modgam returns an object of class modgam. It can be examined by print and plot.

<code>grid</code>	a data frame with X and Y coordinates from <code>rgrid</code> .
<code>span</code>	the span size used for the LOESS smooth. If <code>keep = TRUE</code> and <code>conditional = FALSE</code> , a vector with optimized span sizes for the original data set and each of the permuted data sets.
<code>gamobj</code>	the <code>gam</code> or <code>gamcox</code> model object from the fit to the data.
<code>predobj</code>	the <code>mypredict.gam</code> or <code>predict.gamcox</code> model object from the fit to the data.
<code>family</code>	the family and link function used for the model.
<code>fit</code>	the predicted values for each point on the grid. For Gaussian family models, predicted values are for the outcome variable at each grid point. For non-Gaussian families, predicted values are for the spatial effect alone on the scale of the linear predictor, compared to a referent specified through <code>augument reference</code> (e.g., for a binomial family logit link model with <code>reference = "median"</code> , the fit values are the difference in log odds of the outcome between the grid point and the median log odds, holding other predictors constant). If predicted responses are desired for non-Gaussian families, they can be obtained from the fit values by setting <code>reference="none"</code> and applying the inverse link function.
<code>exp.fit</code>	the exponential of <code>fit</code> . Primarily useful for logit or log link functions (e.g., this provides odds ratios for a binomial family with logit link function.)
<code>global.pvalue</code>	the p-value based on the likelihood ratio test comparing models with and without geolocation (or other two-dimensional predictor).

If `se.fit = TRUE` then the following values are provided:

<code>se</code>	an estimated standard error for each predicted value.
<code>conf.low</code>	the lower bounds for pointwise (1-alpha) confidence intervals.
<code>conf.high</code>	the higher bounds for pointwise (1-alpha) confidence intervals.

If `permute > 0` then the following values are also provided:

<code>global.permt</code>	the p-value based on the deviance statistic comparing models with and without geolocation (or other two-dimensional predictor), using the distribution of deviance statistics from the permuted data sets to represent the null distribution. For a test of H_0 : geolocation is unassociated with the outcome variable (adjusting for any covariates if <code>m = "adjusted"</code>), reject H_0 if the percentile rank is below alpha. WARNING: by default <code>modgam</code> uses a conditional permutation test which produces inflated type I error rates; Young et al. (2012) recommend using <code>alpha=0.025</code> to limit the type I error rate to approximately 5%.
<code>pointwise.permt</code>	Only provided when <code>pointwise = TRUE</code> . For each point on the grid, the percentile rank of the local linear predictor for the model compared to the local linear predictor distribution from the permuted data sets. This result can be used to define clusters of the outcome (e.g., spatial regions with statistically significant outcomes—e.g., unusually high or low risks), as in <code>plot.modgam</code> with <code>contours="permrank"</code> .

If `permute > 0` and `keep = T` then the following values are also provided:

permutations a matrix containing null permuted values for each point on the grid, with the results for each permutation in a separate column. For the binomial family and logit link these are provided as odds ratios, otherwise they are reported as linear predictors.

deviances.permt a vector containing deviances for each permutation.

Warning

Permutation tests are computationally intensive, often requiring several hours or more.

Author(s)

Lu Bai, Scott Bartell, Robin Bliss, and Veronica Vieira

Send bug reports to <sbartell@uci.edu>.

References

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Hastie TJ, Tibshirani RJ. *Generalized Additive Models*. (Chapman & Hall/CRC Monographs on Statistics & Applied Probability, Boca Raton, Florida, 1990).

Kelsall J, Diggle P. Spatial variation in risk of disease: a nonparametric binary regression approach. *J Roy Stat Soc C-App* 1998, 47:559-573.

Vieira V, Webster T, Weinberg J, Aschengrau A, Ozonoff D. [Spatial analysis of lung, colorectal, and breast cancer on Cape Cod: An application of generalized additive models to case-control data](#). *Environmental Health* 2005, 4:11.

Webster T, Vieira V, Weinberg J, Aschengrau A. [Method for mapping population-based case-control studies using Generalized Additive Models](#). *International Journal of Health Geographics* 2006, 5:26.

Young RL, Weinberg J, Vieira V, Ozonoff A, Webster TF. [A power comparison of generalized additive models and the spatial scan statistic in a case-control setting](#). *International Journal of Health Geographics* 2010, 9:37.

See Also

[predgrid](#), [optspan](#), [plot.modgam.colormap](#), [readShapePoly](#).

Examples

```
# Load base map in SpatialPolygonsDataFrame format
# This map was read from ESRI shapefiles using the readShapePoly function
data(MAmap)
# Load data and create grid on base map
data(MAdata)
gamgrid <- predgrid(MAdata, map=MAmap) # requires PBSmapping package
# Fit crude logistic GAM to the MA data using span size of 50%
```

```

# and predict odds ratios for every point on gamgrid
fit1 <- modgam(data=MAdata, rgrid=gamgrid, m="crude", sp=0.5)
# Summary statistics for pointwise crude odds ratios
summary(fit1$exp.fit)
# Summary stats for pointwise crude log odds (linear predictor)
summary(fit1$fit)

# fit adjusted GAM using span size of 50%,
# including a (too small) conditional permutation test
fit2 <- modgam(data=MAdata, rgrid=gamgrid, permute=25, m="adjusted", sp=0.5)
fit2

# fit adjusted GAM by specifying formula
fit2.f <- modgam(Case~lo(Xcoord,Ycoord)+Smoking + Mercury + Selenium,data=MAdata,
                rgrid=gamgrid, sp=0.5)
fit2.f

# Detailed example with a continuous outcome variable, map projections,
# and data trimming: investigating tweet times by geolocation
# NOTE: this example requires the maps, mapproj, and PBSmapping packages
# Convert base map and beer tweet data locations to US Albers projection
# for better distance estimates than using (lat,long) as (X,Y) coords
if(require(maps) & require(mapproj) & require(PBSmapping)) {
  USmap <- map("state",projection="albers",parameters=c(29.5,45.5),
              plot=FALSE,fill=TRUE,col="transparent")
  data(beertweets)
  # Reuse last map projection to convert data coordinates
  XY <- mapproject(beertweets$longitude,beertweets$latitude)[1:2]
  jtime <- julian(beertweets$time)
  # Convert tweet dates and times to time of day (24-hour)
  tweettime <- as.numeric(jtime-trunc(jtime))*24
  beerproj <- data.frame(tweettime, XY[1], XY[2], beertweets$beer)
  # Generate grid on the US map, trimmed to range of beer data
  USgrid <- predgrid(beerproj, map=USmap)
  # Fit adjusted model--adjusting for beer indicator variable
  fit3 <- modgam(data=beerproj, rgrid=USgrid, family=gaussian,
                reference="none", m="adjusted", sp=0.05)
  # Get summary statistics for predicted tweet times across grid points
  summary(fit3$fit)
}

# Smoothing survival rates over geolocations with adjustment of Age and Insurance
# Including generating pointwise standard errors and confidence intervals
data(CAdata)
data(CAgrid)
data = CAdata[1:1000,] # use a subset of the California data
# manually set the categorical variables as factors
data$INS = factor(data$INS)
# no formula needed if data are arranged in a specific order (see \code{data} argument)
fit4 <- modgam(data=data, rgrid=CAgrid, family="survival", sp=0.2)
fit4
# fit the same model using the formula argument, with data columns in any order
fit4.f <- modgam(Surv(time,event)~AGE+factor(INS)+lo(X,Y), data=data,

```



```

rgrid = CAGrid, family="survival", sp=0.2)

# Smoothing for two-dimensional chemical exposure instead of geolocation
# case status in 1st column, mercury and selenium in 2nd and 3rd columns
ma2 <- MAdata[,c(1,5:6)]
expgrid <- predgrid(ma2)
fit5 <- modgam(data=ma2,rgrid=expgrid,sp=.5,m="crude")
summary(fit5$exp.fit)
# plot the results, with mercury on the X axis and selenium on the Y axis
plot(fit5, contours="response", arrow=FALSE, axes=TRUE)

```

mypredict.gam

Prediction for GAM Fits

Description

Obtains spatial effects predictions and optionally estimates standard errors and confidence intervals of those predictions from a fitted generalized additive model object.

Usage

```

mypredict.gam(object, newdata, se.fit = FALSE, type=c("all","spatial"),
reference = "median", level = 0.05,verbose=FALSE)

```

Arguments

object	a fitted gam object.
newdata	a data frame containing the values at which predictions are required. This argument can be missing, in which case predictions are made at the same values used to compute the object. Only two-dimensional predictor need be present by name in newdata.
se.fit	if TRUE, pointwise standard errors and confidence intervals are computed along with the predictions.
type	use type="spatial" to estimate spatial effect, and use type="all"(default) to estimate the effect of all covariates included in the model.
reference	the type of reference for the estimated effect. If reference = "median", the output will be the estimated effect difference (or log ratio) compared to the median effect. If reference = "mean",the output will be the estimated effect difference (or log-ratio) compared to the mean effect.If reference is a data frame indicating a specific geolocation, the output will be the estimated effect difference (or log-ratio) compared to the effect of the geolocation specified by reference.
level	the significance level used when se.fit=TRUE.
verbose	a logical value indicating whether to print filling values for newdata. The default is verbose = FALSE.

Value

pred	the estimated effect difference or (log ratio) compare to the effect specified by reference.
se	the standard errors along with the predictions.
conf.low	the lower bounds for pointwise (1-level) confidence intervals.
conf.high	the higher bounds for pointwise (1-level) confidence intervals.

Author(s)

Lu Bai

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References

Hastie TJ, Tibshirani RJ. Generalized Additive Models. (Chapman & Hall/CRC Monographs on Statistics & Applied Probability, Boca Raton, Florida, 1990).

See Also

[modgam](#), [predict.gamcox](#).

Examples

```
data(MAdata)
data(MAmap)
gamgrid <- predgrid(MAdata, map=MAmap)

fit <- gam(Case~lo(Xcoord,Ycoord,span=0.2)+Smoking,data=MAdata,family=binomial())
pred1 = mypredict.gam(fit)
colormap(list(fit=pred1$pred,grid=data.frame(X=MAdata$X,Y=MAdata$Y)),map=MAmap)

pred2 = mypredict.gam(fit,gamgrid)
colormap(list(fit=pred2$pred,grid=data.frame(X=gamgrid$X,Y=gamgrid$Y)),map=MAmap)

pred3 = mypredict.gam(fit,gamgrid,se.fit=TRUE)
colormap(list(fit=pred3$pred,conf.low = pred3$conf.low, conf.high = pred3$conf.high,
             grid=data.frame(X=gamgrid$X,Y=gamgrid$Y)),map=MAmap,contours = "interval")
```

 optspan

Determine the Optimal Span Size for [modgam](#)

Description

Determines the optimal span size for `modgam`, a spatial generalized additive model (GAM) with a two-dimensional LOESS smooth for location, by minimizing the AIC.

Usage

```
optspan(formula, data, offset, spans = seq(0.05, 0.95, by = 0.05), m = "adjusted",
        family = binomial(), verbose = TRUE, degree = 1, ...)
```

Arguments

formula	a formula expression for the model, with the response on the left of a <code>~</code> operator, and the predictors on the right. If fitting a Cox additive model, the response must be a survival object as returned by the <code>Surv</code> function. A built-in nonparametric smoothing term is indicated by <code>lo</code> for loess smooth terms. The two-dimensional predictor (e.g., <code>geolocation</code>) should be specified as arguments in <code>lo()</code> . <code>formula</code> can be missing if data is well structured and <code>family</code> is specified.
data	a data frame containing the variables in the model. <code>data</code> can be missing if <code>formula</code> is specified. If <code>formula</code> is missing, the data must be structured so that the outcome variable is in the 1st (1st and 2nd for survival data) column and X and Y location values are in the 2nd and 3rd (3rd and 4th for survival data) columns. Any additional columns will be entered as covariates with linear effects in the model.
offset	the name in <code>data</code> that will be used as offset in the model. It will be ignored if offset is specified in <code>formula</code> .
spans	a vector of candidate span sizes that the optimal span is chosen from.
m	the model type. Options are "crude" or "adjusted" (default). If "crude", only the spatial smooth term for location is included in the model. If "adjusted", all covariates in the data set (columns ≥ 4) are included in the model.
family	a family function or the result of a call to a family function. (See family for details of family functions. <code>family = "survival"</code> for survival data.
verbose	a logical argument; if TRUE shows the AIC for each candidate span size.
degree	a smoothing parameter used in modgam .
...	any additional arguments to pass to the <code>gam</code> function.

Value

The optimal span size, determined by minimizing the AIC

Note

This function does not return model predictions—only the optimal span size. To obtain model predictions use the `modgam` function.

Author(s)

Lu Bai, Scott Bartell, Robin Bliss, and Veronica Vieira

Send bug reports to <sbartell@uci.edu>.

See Also

[predgrid](#), [modgam](#), [colormap](#).

Examples

```
data(MAdata)
optspan(data=MAdata, m="crude")

data(CAdata)
optspan(Surv(time,event)~AGE+factor(INS)+lo(X,Y), data=CAdata,
        spans=c(0.1,0.2,0.3),family="survival")
```

plot.modgam

Maps Predicted Values and Clusters for `modgam` Objects

Description

Displays a color image map, including a legend, scale bar, and optional North arrow, showing crude or adjusted odds ratios (or linear predictors) for a grid of points. Irregular grids are allowed. Also draws contour lines for regions of significantly increased or decreased values of the outcome variable ("clusters"), if permutation ranks are provided. Designed to display `modgam` objects but can be used with other model results if the `modgamobj` list contains the correct elements.

Usage

```
## S3 method for class 'modgam'
plot(x, map = NULL, exp = FALSE, add = FALSE, intervals=TRUE,
     mapmin = NULL, mapmax = NULL, col.seq = diverge_hsv(201), anchor=FALSE,
     border.gray = 0.3, contours=c("none","response","permrnk","interval"),
     contours.drawlabels=FALSE, contours.lty=1, contours.lwd=1,
     contours.levels, contours.labcex=0.7, arrow=TRUE, axes=FALSE, ptsize=0.9,
     alpha=0.05, mai, legend.name = "predicted values", legend.cex=1, ...)
```

Arguments

x	(required) an object of class modgam, usually returned by the modgam function.
map	can be used to map predicted values on a base map from the map function in the maps package, or on a base map produced by the readShapePoly function in mapttools package. ReadShapePoly reads maps from external files in the ESRI shapefile format. map=NULL produces a color image without any base map.
exp	if exp=T, fit will be displayed in exponential scale.
add	use add=T to add the color map to an existing plot. This will often result in loss of the legend and scale, which are added outside of the normal map boundaries. add is ignored when a map is provided using the map argument.
intervals	if the modgam object contains confidence intervals, the lower and higher intervals will be plotted if intervals=T.
mapmin	the minimum value for the color scale legend.
mapmax	the maximum value for the color scale legend.
col.seq	The color sequence (palette) used to display the predicted values on the map.
anchor	Use anchor=TRUE to center the color palette on legend.add.line. When anchor=FALSE or when legend.add.line is not specified, the color palette will be centered halfway between mapmin and mapmax. anchor=TRUE is recommended when using a divergent palette.
border.gray	gray scale for the border of map, ranges from 0 to 1. It is white with border.gray=1, and black with border.gray=0. The default scale is 0.3.
contours	use contours="response" to add contour lines for the predicted response, for example to draw isoboles for mixtures of exposures. Use contours="permrank" to add contour lines for pointwise p-values computed from the permutation ranks, at alpha/2 and (1-alpha)/2. use contours = "intervals" to add contour lines for areas where the confidence intervals do not include 0. The default is "none" which produces no contour lines.
contours.drawlabels	use contours.drawlabels = TRUE add labels on contour lines.
contours.lty	the line type for contour lines.
contours.lwd	the width for contour lines.
contours.levels	the levels for contour lines. When exp=T, the levels will also be used in an exponential scale.
contours.labcex	cex for contour labelling. This is an absolute size, not a multiple of par("cex")
arrow	use arrow=T to add a North arrow to the map.
axes	use axes=T to add axes to the map (useful for chemical mixture isoboles).
ptsize	the size of the points used to fill in colors on the map. Increase to remove white space inside the map or decrease to remove color outside the map boundaries. NOTE: white space can also be eliminated by increasing the grid size in predgrid, which is often preferable as it results in a higher resolution map.
alpha	the nominal pointwise type I error rate; only used when contours="permrank".

mai	the margins of the plot. Details see par .
legend.name	the name of displayed for the legend bar.
legend.cex	a numerical value giving the amount by which legend text should be magnified relative to the default.
...	other arguments to be passed to colormap function.

Value

Produces an image map showing crude or adjusted linear predictors (or odds ratios). If the base map is in readShapePoly format a scale bar is included. The scale bar assumes that the X and Y coordinates are provided in meters.

Warning

Note that the contour lines use a pointwise nominal type I error rate of alpha; the chance of a type I error occurring for **at least** one point on the map is much higher, typically approaching 100% at alpha=0.05, because a spatial prediction grid generally contains many points.

Author(s)

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See Also

[trimdata](#), [predgrid](#), [optspan](#), [modgam](#), [colormap](#).

Examples

```
data(MAmap)
data(MAdata)
# Create a grid on the base map (PBSmapping package recommended)
if(require(PBSmapping)) MAgrid <- predgrid(MAdata, map=MAmap) else
MAgrid <- predgrid(MAdata)
# fit crude GAM model to the MA data using span size of 50%
fit1 <- modgam(data=MAdata, rgrid=MAgrid, m="crude", sp=0.5)
# Plot a map showing crude odds ratios
plot(fit1, MAmap)

#### A detailed example including map projections and data trimming
# NOTE: this example requires the maps, mapproj, and PBSmapping packages
# Convert base map and beer tweet data locations to US Albers projection
# projected coords yield better distance estimates than (lat,long)
if(require(maps) & require(mapproj) & require(PBSmapping)) {
  USmap <- map("state", projection="albers", parameters=c(29.5,45.5),
    plot=FALSE, fill=TRUE, col="transparent")
  data(beertweets)
  case <- beertweets$beer
  # Reuse last map projection to convert data coordinates
```

```

XY <- mapproject(beertweets$longitude,beertweets$latitude)[1:2]
beerproj <- data.frame(case, XY[1], XY[2])
# Generate grid on the US map, trimmed to range of beer data
USgrid <- predgrid(beerproj, map=USmap)
# Fit unadjusted model--geolocation only
fit2 <- modgam(data=beerproj, rgrid=USgrid, m="unadjusted", sp=0.05)
dev.new(width=7,height=5)
plot(fit2, USmap)
title(main="Beer Tweet Odds Ratios")
}

```

predgrid

Create a Grid and Clip It to a Map and Data Bounds

Description

Creates a data frame containing a rectangular grid of points to cover the range of X and Y coordinates provided in a data set, and trims the grid so that the points do not extend beyond the boundaries shown on a map. Users can omit a data set to create a grid covering the whole map, or omit a map to create a grid covering the whole data set. This function requires PBSmapping package.

Usage

```
predgrid(dataXY = NULL, map = NULL, nrow = 100, ncol = 100, X = NULL, Y = NULL)
```

Arguments

dataXY	A data frame with X and Y coordinates. If the data frame has more than 2 columns, the X and Y coordinates must be in the 2nd and 3rd columns, respectively (the format for the data argument in the modgam function). If the data frame has only 2 columns, the X coordinates must be in the 1st column and Y coordinates in the 2nd column. If no data are provided for this argument or for the X and Y arguments, the grid will cover the entire map.
map	a map for clipping the grid, provided in a recognized format. Supported classes include "map", the format produced by the maps package, and "SpatialPolygonsDataFrame", which can be produced from an ESRI shapefile using the readShapePoly function in the maptools package. If map = NULL (default), a rectangular grid is produced covering the range of geolocations within dataXY. If no map is provided the grid will cover the whole data set.
nrow	the number of rows in the grid (default=100).
ncol	the number of columns in the grid (default=100).
X	a vector of X coordinates, supplied instead of (or in addition to) dataXY. If both X and dataXY are provided, X will be used instead of the corresponding column of dataXY.
Y	a vector of Y coordinates, supplied instead of (or in addition to) dataXY. If both Y and dataXY are provided, Y will be used instead of the corresponding column of dataXY.

Details

predgrid creates a grid of dimensions nrow*ncol using the range of X and Y coordinates (e.g., longitude and latitude) in the data frame supplied as dataXY. If the map argument is used, the function trimdata is used to clip the grid. Users should be sure to use the same projection for the map and the data; putting both on the same plot can help reveal differing projections. If the map centroid is not in the range of the data a warning message is printed; this might indicate differing projections but can occur naturally when the data were not sampled from the entire extent of the map or when map boundaries are concave.

Value

A data frame with X and Y coordinates in the first two columns. The column names from dataXY are used for the output. If the columns of dataXY are unnamed then the names "X" and "Y" are assigned to the data frame.

Author(s)

Veronica Vieira, Scott Bartell, and Robin Bliss

Send bug reports to <sbartell@uci.edu>.

See Also

[trimdata](#), [optspan](#), [modgam](#), [colormap](#).

Examples

```
# define a rectangular 100x100 grid covering the MA data
data(MAdata)
gamgrid <- predgrid(MAdata)
# plot the grid points
plot(gamgrid$Xcoord, gamgrid$Ycoord, cex=0.1, col="red")
# and the data locations
points(MAdata$Xcoord, MAdata$Ycoord)

# But that grid extends beyond the state boundaries and into the ocean!
# Better to also clip the grid to a map of MA using the following code
# which requires the PBSmapping package:

if (require(PBSmapping)) {
  # Clip a 50x50 grid covering the MA data to a map of MA
  data(MAmap)
  gamgrid2 <- predgrid(MAdata, map=MAmap, nrow=50, ncol=50)
  # plot the MA map and grid points
  plot(MAmap)
  points(gamgrid2, cex=0.1, col="red")
}
```

predict.gamcox	<i>Prediction Method for gamcox Fits</i>
----------------	--

Description

Obtains spatial effects predictions and optionally estimates standard errors and confidence intervals of those predictions from a fitted Cox proportional hazard additive model object.

Usage

```
## S3 method for class "gamcox"
## S3 method for class 'gamcox'
predict(object, newdata = object$data, se.fit = FALSE, type=c("spatial", "all"),
        reference = "median", level = 0.05, verbose=FALSE,...)
```

Arguments

object	a fitted gamcox object.
newdata	a data frame containing the values at which predictions are required. This argument can be missing, in which case predictions are made at the same values used to compute the object. A comprehensive effect (hazard ratio) of the covariates included in newdata will be predicted.
se.fit	if TRUE, pointwise standard errors and confidence intervals are computed along with the predictions.
type	use type="spatial"(default) to estimate spatial effect, and use type="all" to estimate the effect of all covariates included in the model.
reference	the type of reference for the estimated effect. If reference = "median", the output will be the estimated hazard ratio (or log-ratio) compared to the median effect. If reference = "mean", the output will be the estimated hazard ratio (or log-ratio) compared to the mean effect. If reference is a data frame indicating a specific geolocation, the output will be the estimated hazard ratio (or log ratio) compared to the hazard of the geolocation specified by reference.
level	the confidence level for confidence bands.
verbose	a logical value indicating whether to print filling values for newdata. The default is verbose = FALSE.
...	extra arguments for S3 generic, ignored by predict.gamcox.

Value

pred	the estimated log hazards ratio compared to the effect specified by reference.
se	the standard errors along with the predictions.
conf.low	the lower bounds for pointwise (1-level) confidence intervals.
conf.high	the higher bounds for pointwise (1-level) confidence intervals.

Author(s)

Lu Bai

Send bug reports to <sbartell@uci.edu>.

References

Hastie TJ, Tibshirani RJ. Generalized Additive Models. (Chapman & Hall/CRC Monographs on Statistics & Applied Probability, Boca Raton, Florida, 1990).

See Also

[modgam](#), [predict.gamcox](#).

Examples

```
data(CAdata)
data(CAmap)
fit <- gamcox(Surv(time,event)~AGE + factor(INS) + lo(X,Y),data=CAdata,
             span=0.2,loess.trace="approximate")
fit
pred1 = predict(fit)
colormap(list(fit=pred1$pred,grid=data.frame(X=CAdata$X,Y=CAdata$Y)),map=CAmap,
         border.gray=0.5)

data(CAgrid)
pred2 = predict(fit,CAgrid[,c("X","Y")])
colormap(list(fit=pred2$pred,grid=data.frame(X=CAgrid$X,Y=CAgrid$Y)),map=CAmap,
         border.gray=0.5, legend.name="log hazard ratio")

## Circle significant areas based on the confidence intervals specified by conf.low and conf.high
pred3 = predict(fit,CAgrid[,c("X","Y")],se.fit=TRUE)
colormap(list(fit=pred3$pred,conf.low = pred3$conf.low, conf.high = pred3$conf.high,
             grid=data.frame(X=CAgrid$X,Y=CAgrid$Y)),map=CAmap,border.gray = 0.7,
         contours = "interval",legend.name="log hazard ratio")
```

print.gamcox

Print the [gamcox](#) Object

Description

This function displays information about a gamcox object produced by [gamcox](#).

Usage

```
## S3 method for class 'gamcox'
print(x,...)
```

Arguments

x a gamcox object.
... .

Author(s)

Lu Bai
Send bug reports to <sbartell@uci.edu>.

See Also

[modgam gamcox](#), [predict.gamcox](#).

Examples

```
data(CAdata)
fit <- gamcox(Surv(time,event)~lo(X,Y)+AGE+INS,data=CAdata, span = 0.2)
print(fit)
```

`print.modgam` *Print the [modgam](#) Object*

Description

This function displays information about a `modgam` object produced by [modgam](#).

Usage

```
## S3 method for class 'modgam'
print(x, ...)
```

Arguments

x a `modgam` object.
... extra arguments for S3 generic, ignored by `print.modgam`.

Author(s)

Lu Bai
Send bug reports to <sbartell@uci.edu>.

See Also

[modgam gamcox](#), [predict.gamcox](#).

residuals.gamcox *Residuals of the [gamcox](#) Object*

Description

This function provides residuals of a gamcox object produced by [gamcox](#).

Usage

```
## S3 method for class 'gamcox'  
residuals(object,...)
```

Arguments

object a gamcox object.
... .

Author(s)

Lu Bai
Send bug reports to <sbartell@uci.edu>.

See Also

[modgam gamcox](#), [predict.gamcox](#).

Examples

```
data(CAdata)  
fit <- gamcox(Surv(time,event)~lo(X,Y)+AGE+INS,data=CAdata, span = 0.2)  
residuals(fit)
```

residuals.modgam *Residuals of the [modgam](#) Object*

Description

This function provides residuals of a modgam object produced by [modgam](#).

Usage

```
## S3 method for class 'modgam'  
residuals(object, ...)
```

Arguments

object a modgam object.
 ... extra arguments for S3 generic, ignored by residuals.modgam.

Author(s)

Lu Bai
 Send bug reports to <sbartell@uci.edu>.

See Also

[modgam](#), [gamcox](#), [predict.gamcox](#).

 smpcont

Unmatched Control Sampling

Description

Take all cases and a random sample of controls from a data frame. Simple random sampling and stratified random sampling are available. For stratified random sampling, strata can be defined by region, or by region and time. If no specific regions are specified then the function will create a regular grid for sampling.

Usage

```
smpcont(rdata, type = "stratified", casecol=1, Xcol=2, Ycol=3, regions = NULL,
addstrat = NULL, times = NULL, n = 1, nrow = 100, ncol = 100)
```

Arguments

rdata a data frame with case status in the casecol column (by default, the 1st column), and the geocoordinates (e.g., X and Y) in the Xcol and Ycol columns (by default, the 2nd and 3rd columns). Additional columns are not used in the sampling scheme but are retained in the sampled data frame.

casecol the column number in rdata for the case status (coded with 0 for controls, 1 for cases).

Xcol the column number in rdata for the X geocoordinate.

Ycol the column number in rdata for the Y geocoordinate.

type "stratified" (default) or "simple". If "simple" then a simple random sample of n controls (rows of rdata with outcome=0) is obtained. If "stratified" then a stratified random sample of controls is obtained, with up to n controls per stratum. Sampling strata are defined by the regions and times arguments. All cases (rows with outcome=1) are taken for the sample regardless of the value supplied for type.

regions	a vector of length equal to the number of rows in <code>rdata</code> , used to construct sampling strata. Only used if <code>type = "stratified"</code> . If <code>regions = NULL</code> and the <code>PBSmapping</code> package is available then the function will define <code>regions</code> as a vector of specific grid cells on a regular grid with <code>nrow</code> rows and <code>ncol</code> columns. If <code>times = NULL</code> then the nonempty regions are used as the sampling strata. If <code>times</code> is a vector, then the sampling strata are all nonempty combinations of <code>regions</code> and <code>times</code> .
addstrat	a vector of length equal to the number of rows in <code>rdata</code> , used along with <code>regions</code> to construct sampling strata. If <code>addstrat = NULL</code> then the sampling strata are defined only by the <code>regions</code> argument. If <code>addstrat</code> is a vector, then the sampling strata are all nonempty combinations of <code>regions</code> and <code>addstrat</code> . Continuous variables should generally be binned before being passed through this argument, as there are no efficiency gains if each value in <code>addstrat</code> is unique.
times	included for backward compatibility; now replaced by the <code>addstrat</code> argument which serves the same purpose.
n	the number of controls to sample from the eligible controls in each stratum. All available controls will be taken for strata with fewer than <code>n</code> eligible controls.
nrow	the number of rows used to create a regular grid for sampling regions. Only used when <code>regions = NULL</code> .
ncol	the number of columns used to create a regular grid for sampling regions. Only used when <code>regions = NULL</code> .

Value

<code>rdata</code>	a data frame with all cases and a random sample of controls.
<code>w</code>	the inverse probability weights for the rows in <code>rdata</code> . Important to include as weights in subsequent analyses.
<code>ncont</code>	the total number of controls in the sample.
<code>type</code>	stratified or simple sampling, as specified by the same argument described above.
<code>gridsize</code>	a vector with the numbers of rows and columns for the stratified sampling grid.
<code>grid</code>	the stratified sampling grid in PolySet format.

Author(s)

Scott M. Bartell and Ian W. Tang <sbartell@uci.edu>.

See Also

[modgam](#)

Examples

```
#### load beertweets data, which has 719 cases and 9281 controls
data(beertweets)
# take a simple random sample of 1000 controls
samp1 <- smpcont(beertweets, type="simple", n=1000)
```

```

# take a stratified random sample of controls on a 80x50 grid
# requires PBSmapping package
samp2 <- NULL

if(require(PBSmapping)) samp2 <- sampcont(beertweets, nrow=80, ncol=50)

# Compare locations for the two sampling designs (cases in red)
par(mfrow=c(2,1), mar=c(0,3,4,3))
plot(samp1$rdata$longitude, samp1$rdata$latitude, col=3-samp1$rdata$beer,
cex=0.5, type="p", axes=FALSE, ann=FALSE)
# Show US base map if maps package is available
mapUS <- require(maps)
if (mapUS) map("state", add=TRUE)
title("Simple Random Sample, 1000 Controls")

if (!is.null(samp2)) {
plot(samp2$rdata$longitude, samp2$rdata$latitude,
col=3-samp2$rdata$beer, cex=0.5, type="p", axes=FALSE,
ann=FALSE)
if (mapUS) map("state", add=TRUE)
title(paste("Spatially Stratified Sample,", samp2$ncont, "Controls"))
}

par(mfrow=c(1,1))

## Note that weights are needed in statistical analyses
# Prevalence of cases in sample--not in source data
mean(samp1$rdata$beer)
# Estimated prevalence of cases in source data
weighted.mean(samp1$rdata$beer, w=samp1$w)
## Do beer tweet odds differ below the 36.5 degree parallel?
# Using full data
glm(beer~I(latitude<36.5), family=binomial, data=beertweets)
# Stratified sample requires sampling weights
if (!is.null(samp2)) glm(beer~I(latitude<36.5), family=binomial,
data=samp2$rdata, weights=samp2$w)

```

summary.gamcox

Summarize the gamcox Object

Description

This function summarizes information about a gamcox object produced by [gamcox](#).

Usage

```

## S3 method for class 'gamcox'
summary(object,...)

```

Arguments

object a gamcox object.
... .

Author(s)

Lu Bai
Send bug reports to <sbartell@uci.edu>.

See Also

[modgam gamcox](#), [predict.gamcox](#).

Examples

```
data(CAdata)
fit <- gamcox(Surv(time,event)~lo(X,Y)+AGE+INS,data=CAdata, span = 0.2)
summary(fit)
```

summary.modgam

Summarize the [modgam](#) Object

Description

This function summarizes information about a modgam object produced by [modgam](#).

Usage

```
## S3 method for class 'modgam'
summary(object, ...)
```

Arguments

object a modgam object.
... extra arguments for S3 generic, ignored by summary.modgam.

Author(s)

Lu Bai
Send bug reports to <sbartell@uci.edu>.

See Also

[modgam gamcox](#), [predict.gamcox](#).

`toformula`*Build a Formula Based on Data for `modgam` Function*

Description

Based on the arguments in `modgam`, build a formula used for model fitting.

Usage

```
toformula(formula, data,m="adjusted",surv = FALSE, span=0.5,degree=2,  
          smooth = TRUE,offset='')
```

Arguments

<code>formula</code>	a user specified formula expression (for <code>modgam</code>).
<code>data</code>	a well structured data frame with the two geolocation parameters in the first and second columns. <code>data</code> is ignored if <code>formula</code> is specified.
<code>m</code>	use <code>m="adjusted"</code> to specify a model including adjusted confounders. Use <code>m="unadjusted"</code> to specify a unadjusted model.
<code>surv</code>	<code>surv=TRUE</code> specifies a model for censored survival dataset.
<code>span, degree</code>	smoothing parameters used for smoothing functions (see details in <code>modgam</code>) if <code>smooth=TRUE</code> .
<code>smooth</code>	<code>smooth=TRUE</code> specifies a smooth term in the model.
<code>offset</code>	the name for offset.

Value

The function returns the formula for the model.

Author(s)

Lu Bai

Send bug reports to <sbartell@uci.edu>.

See Also

[modgam](#), .

Examples

```
data(CAdata)  
toformula(data=CAdata, surv=TRUE)
```

trimdata	<i>Trim a Data Set To Map Boundaries</i>
----------	--

Description

Takes a subset of a data frame: returns rows with geolocations inside the boundaries determined by a map. If `rectangle=FALSE`, strict map boundaries are used. If `rectangle=TRUE`, a rectangular boundary is determined based on the range of X and Y coordinates for the map, along with an optional buffer.

Usage

```
trimdata(rdata, map, Xcol=2, Ycol=3, rectangle=F, buffer=0.05)
```

Arguments

<code>rdata</code>	the data set (required). If <code>rdata</code> has only 2 columns then they are assumed to be the X and Y coordinates, in that order. If <code>rdata</code> has more than 2 columns then identify the positions of the X and Y coordinates with <code>Xcol</code> and <code>Ycol</code> , respectively.
<code>map</code>	a map for clipping the grid, provided in a recognized format. Supported classes include "map", the format produced by the <code>maps</code> package, and "SpatialPolygonsDataFrame", which can be produced from an ESRI shapefile using the <code>readOGR</code> function in the <code>rgdal</code> package.
<code>Xcol</code>	the column number of <code>rdata</code> for the X coordinates of geolocation. Only used if <code>rdata</code> has >2 columns.
<code>Ycol</code>	the column number of <code>rdata</code> for the Y coordinates of geolocation. Only used if <code>rdata</code> has >2 columns.
<code>rectangle</code>	if <code>rectangle=FALSE</code> (default), only data with geolocations strictly within the map boundaries are retained. If <code>rectangle=TRUE</code> , only data with geolocations within a rectangular boundary are retained. The rectangular boundary coordinates are determined using the ranges of X and Y coordinates for the map, along with an optional buffer.
<code>buffer</code>	a fraction of the map range to add to either side of the rectangular boundary before trimming the data (default 5%). The buffer argument is ignored if <code>rectangle=FALSE</code> . If a vector of length 2 is supplied, the first value is used as the buffer fraction for the X coordinate range and the second value is used as the buffer fraction for the Y coordinate range.

Details

Various functions from the `PBSmapping` package and `maptools` package are used to convert map formats, check whether the map and data are aligned, and clip the grid. Without the `PBSmapping` package only `rectangle=TRUE` will work. Be sure to use `fill=T` when using the `map` function to produce maps for `trimdata`: maps produced using the default `fill=F` argument do not work properly with this function. If the map centroid is not in the range of the data and the `PBSmapping`

package is available a warning message is printed; this might indicate differing projections but can occur naturally when the data were not sampled from the entire extent of the map or when map boundaries are concave.

Value

A subset of the rdata data frame containing only those rows with geolocations within the specified boundaries.

Author(s)

Veronica Vieira, Scott Bartell, and Robin Bliss

Send bug reports to <sbartell@uci.edu>.

See Also

[predgrid](#), [optspan](#), [modgam](#), [colormap](#).

Examples

```
# These examples require the "PBSmapping" and "maps" packages
if (require(maps) & require(PBSmapping)) {
  data(beertweets)
  dim(beertweets)

  ### Trim data to US base map, and plot them
  basemap1 <- map("usa", fill=TRUE, col="transparent")
  dUS <- trimdata(beertweets, basemap1)
  # Plot tweet locations (beer tweets in red)
  points(dUS$longitude, dUS$latitude, col=dUS$beer+1, cex=0.5)

  ### Trim data to Texas base map, and plot them
  basemap2 <- map("state", regions="texas", fill=TRUE, col="transparent")
  dTX <- trimdata(beertweets, basemap2)
  # Plot tweet locations (beer tweets in red)
  points(dTX$longitude, dTX$latitude, col=dTX$beer+1, cex=0.5)
}
```

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