Package ‘ungroup’

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Type Package

Title Penalized Composite Link Model for Efficient Estimation of Smooth Distributions from Coarsely Binned Data

Version 1.1.5

Description Versatile method for ungrouping histograms (binned count data) assuming that counts are Poisson distributed and that the underlying sequence on a fine grid to be estimated is smooth. The method is based on the composite link model and estimation is achieved by maximizing a penalized likelihood. Smooth detailed sequences of counts and rates are so estimated from the binned counts. Ungrouping binned data can be desirable for many reasons: Bins can be too coarse to allow for accurate analysis; comparisons can be hindered when different grouping approaches are used in different histograms; and the last interval is often wide and open-ended and, thus, covers a lot of information in the tail area. Age-at-death distributions grouped in age classes and abridged life tables are examples of binned data. Because of modest assumptions, the approach is suitable for many demographic and epidemiological applications. For a detailed description of the method and applications see Rizzi et al. (2015) <doi:10.1093/aje/kwv020>.

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LinkingTo Rcpp, RcppEigen

Suggests MortalityLaws (>= 1.5.0), knitr (>= 1.20), rmarkdown (>= 1.10), testthat (>= 2.0.0)

RdMacros Rdpack

URL https://github.com/mpascariu/ungroup

BugReports https://github.com/mpascariu/ungroup/issues

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control.pclm

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**control.pclm**  
*Auxiliary for Controlling pclm Fitting*

**Description**

Auxiliary for Controlling pclm Fitting

**Usage**

```r
control.pclm(lambda = NA,
             kr = 2,
             deg = 3,
             int.lambda = c(0.1, 1e+5),
             diff = 2,
             opt.method = c("BIC", "AIC"),
             max.iter = 1e+3,
             tol = 1e-3)
```
control.pclm2D

Arguments

lambda Smoothing parameter to be used in pclm estimation. If lambda = NA an algorithm will find the optimal values.

kr Knot ratio. Number of internal intervals used for defining 1 knot in B-spline basis construction. See MortSmooth_bbase.

deg Degree of the splines needed to create equally-spaced B-splines basis over an abscissa of data.

int.lambda If lambda is optimized an interval to be searched needs to be specified. Format: vector containing the end-points.

diff An integer indicating the order of differences of the components of PCLM coefficients. Default value: 2.

opt.method Selection criterion of the model. Possible values are "AIC" and "BIC". Default: "BIC".

max.iter Maximal number of iterations used in fitting procedure.

tol Relative tolerance in PCLM fitting procedure. Default: 0.1% i.e. the estimated aggregate bins should be in the 0.1% error margin.

Value

A list with exactly eight control parameters.

See Also

pclm

Examples

control.pclm()

countroller.pclm2D

Auxiliary for Controlling pclm2D Fitting

Description

Auxiliary for Controlling pclm2D Fitting

Usage

control.pclm2D(lambda = c(1, 1),
               kr = 7,
               deg = 3,
               int.lambda = c(0.1, 1e+3),
               diff = 2,
               opt.method = c("BIC", "AIC"),
               max.iter = 1e+3,
               tol = 1e-3)
Arguments

lambda

Smoothing parameter to be used in pclm estimation. If lambda = NA an algorithm will find the optimal values.

kr

Knot ratio. Number of internal intervals used for defining 1 knot in B-spline basis construction. See MortSmooth_bbase.

deg

Degree of the splines needed to create equally-spaced B-splines basis over an abscissa of data.

int.lambda

If lambda is optimized an interval to be searched needs to be specified. Format: vector containing the end-points.

diff

An integer indicating the order of differences of the components of PCLM coefficients. Default value: 2.

opt.method

Selection criterion of the model. Possible values are "AIC" and "BIC". Default: "BIC".

max.iter

Maximal number of iterations used in fitting procedure.

tol

Relative tolerance in PCLM fitting procedure. Default: 0.1% i.e. the estimated aggregate bins should be in the 0.1% error margin.

Value

A list with exactly eight control parameters.

See Also

pclm2D

Examples

control.pclm2D()
Arguments

- **x**: Vector containing the starting values of the input intervals/bins. For example: if we have 3 bins \([0,5),[5,10)\) and \([10,15)\), \(x\) will be defined by the vector \(c(0,5,10)\).
- **y**: Vector with counts to be ungrouped. It must have the same dimension as \(x\).
- **nlast**: Length of the last interval. In the example above \(nlast\) would be 5.
- **offset**: Optional offset term to calculate smooth mortality rates. A vector of the same length as \(x\) and \(y\). See Rizzi et al. (2015) for further details.
- **out.step**: Length of estimated intervals in output. Values between 0.1 and 1 are accepted. Default: 1.
- **ci.level**: Level of significance for computing confidence intervals. Default: 95.
- **verbose**: Logical value. Indicates whether a progress bar should be shown or not. Default: FALSE.
- **control**: List with additional parameters:
  - \(\lambda\) – Smoothing parameter to be used in pclm estimation. If \(\lambda = NA\) an algorithm will find the optimal values.
  - \(kr\) – Knot ratio. Number of internal intervals used for defining 1 knot in B-spline basis construction. See \texttt{MortSmooth\_bbase}.
  - \(deg\) – Degree of the splines needed to create equally-spaced B-splines basis over an abscissa of data.
  - \(int.\lambda\) – If \(\lambda\) is optimized an interval to be searched needs to be specified. Format: vector containing the end-points.
  - \(diff\) – An integer indicating the order of differences of the components of PCLM coefficients.
  - \(opt.method\) – Selection criterion of the model. Possible values are "AIC" and "BIC".
  - \(max.iter\) – Maximal number of iterations used in fitting procedure.
  - \(tol\) – Relative tolerance in PCLM fitting procedure.

Details

The PCLM method is based on the composite link model, which extends standard generalized linear models. It implements the idea that the observed counts, interpreted as realizations from Poisson distributions, are indirect observations of a finer (ungrouped) but latent sequence. This latent sequence represents the distribution of expected means on a fine resolution and has to be estimated from the aggregated data. Estimates are obtained by maximizing a penalized likelihood. This maximization is performed efficiently by a version of the iteratively reweighted least-squares algorithm. Optimal values of the smoothing parameter are chosen by minimizing Bayesian or Akaike’s Information Criterion.

Value

The output is a list with the following components:

- **input**: A list with arguments provided in input. Saved for convenience.
fitted

The fitted values of the PCLM model.

ci

Confidence intervals around fitted values.

goodness.of.fit

A list containing goodness of fit measures: standard errors, AIC and BIC.

smoothPar

Estimated smoothing parameters: lambda, kr and deg.

bins.definition

Additional values to identify the bins limits and location in input and output objects.

deep

A list of objects created in the fitting process. Useful in diagnosis of possible issues.

call

An unevaluated function call, that is, an unevaluated expression which consists of the named function applied to the given arguments.

References


See Also

ccontrol.pclm plot.pclm

Examples

# Data
x <- c(0, 1, seq(5, 85, by = 5))
y <- c(294, 66, 32, 44, 170, 284, 287, 293, 361, 600, 998,
      1572, 2529, 4637, 6161, 7369, 10481, 15293, 39016)
offset <- c(114, 440, 509, 492, 628, 618, 576, 580, 634, 657,
          631, 584, 573, 619, 530, 384, 303, 245, 249) * 1000
nlast <- 26 # the size of the last interval

# Example 1 ----------------------
M1 <- pclm(x, y, nlast)
ls(M1)
solitary(M1)
fitted(M1)
plot(M1)

# Example 2 ----------------------
# ungroup even in smaller intervals
M2 <- pclm(x, y, nlast, out.step = 0.5)
head(fitted(M1))
plot(M1, type = "s")
# Note, in example 1 we are estimating intervals of length 1. In example 2 we are estimating intervals of length 0.5 using the same aggregate data.

# Example 3 ----------------------
# Do not optimise smoothing parameters; choose your own. Faster.
M3 <- pclm(x, y, nlast, out.step = 0.5,
control = list(lambda = 100, kr = 10, deg = 10))
plot(M3)

summary(M2)
summary(M3) # not the smallest BIC here, but sometimes is not important.

# Example 4 -----------------------
# Grouped x & grouped offset (estimate death rates)
M4 <- pclm(x, y, nlast, offset)
plot(M4, type = "s")

# Example 5 -----------------------
# Grouped x & ungrouped offset (estimate death rates)
ungrouped_Ex <- pclm(x, y = offset, nlast, offset = NULL)$fitted # ungrouped offset data
M5 <- pclm(x, y, nlast, offset = ungrouped_Ex)

**Description**

Fit two-dimensional penalized composite link model (PCLM-2D), e.g. simultaneous ungrouping of age-at-death distributions grouped in age classes for adjacent years. The PCLM can be extended to a two-dimensional regression problem. This is particularly suitable for mortality analysis when mortality surfaces are to be estimated to capture both age-specific trajectories of coarsely grouped distributions and time trends (Rizzi et al. 2019).

**Usage**

```r
pclm2D(x, y, nlast, offset = NULL, out.step = 1, ci.level = 95, verbose = TRUE, control = list())
```

**Arguments**

- `x` Vector containing the starting values of the input intervals/bins. For example: if we have 3 bins \([0,5),[5,10)\) and \([10,15)\), `x` will be defined by the vector: `c(0,5,10)`.
- `y` data.frame with counts to be ungrouped. The number of rows should be equal with the length of `x`.
- `nlast` Length of the last interval. In the example above `nlast` would be 5.
- `offset` Optional offset term to calculate smooth mortality rates. A vector of the same length as `x` and `y`. See Rizzi et al. (2015) for further details.
- `out.step` Length of estimated intervals in output. Values between 0.1 and 1 are accepted. Default: 1.
- `ci.level` Level of significance for computing confidence intervals. Default: 95.
verbose Logical value. Indicates whether a progress bar should be shown or not. Default: TRUE.

control List with additional parameters:
- lambda – Smoothing parameter to be used in pclm estimation. If lambda = NA an algorithm will find the optimal values.
- kr – Knot ratio. Number of internal intervals used for defining 1 knot in B-spline basis construction. See MortSmooth_bbase.
- deg – Degree of the splines needed to create equally-spaced B-splines basis over an abscissa of data.
- int.lambda – If lambda is optimized an interval to be searched needs to be specified. Format: vector containing the end-points.
- diff – An integer indicating the order of differences of the components of PCLM coefficients.
- opt.method – Selection criterion of the model. Possible values are "AIC" and "BIC".
- max.iter – Maximal number of iterations used in fitting procedure.
- tol – Relative tolerance in PCLM fitting procedure.

Value

The output is a list with the following components:

input A list with arguments provided in input. Saved for convenience.
fitted The fitted values of the PCLM model.
ci Confidence intervals around fitted values.
goodness.of.fit A list containing goodness of fit measures: standard errors, AIC and BIC.
smoothPar Estimated smoothing parameters: lambda, kr and deg.
bins.definition Additional values to identify the bins limits and location in input and output objects.
deep A list of objects created in the fitting process. Useful in diagnosis of possible issues.
call An unevaluated function call, that is, an unevaluated expression which consists of the named function applied to the given arguments.

References


See Also

control.pclm2D plot.pclm2D

Examples

# Input data
Dx <- ungroup.data$Dx
Ex <- ungroup.data$Ex

# Aggregate data to ungroup it in the examples below
x <- c(0, 1, seq(5, 85, by = 5))
nlast <- 26
n <- c(diff(x), nlast)
group <- rep(x, n)
y <- aggregate(Dx, by = list(group), FUN = "sum")[, -1]
offset <- aggregate(Ex, by = list(group), FUN = "sum")[, -1]

# Example 1 ----------------------
# Fit model and ungroup data using PCLM-2D
P1 <- pclm2D(x, y, nlast)
summary(P1)
# plot(P1)

## Not run:
# NOTE: pclm2D does not search for optimal smoothing parameters by default
# (like pclm) because it is more time consuming. If optimization is required
# set lambda = c(NA, NA):

P1 <- pclm2D(x, y, nlast, control = list(lambda = c(NA, NA)))

# Example 2 ----------------------
# Ungroup and build a mortality surface
P2 <- pclm2D(x, y, nlast, offset)
summary(P2)

plot(P2) # plot
library(rgl)
snapshot3d("plotP2.jpeg") # save the plot in jpeg format
aspect3d(x = 1, y = 2, z = 1) # modify the aspect ratio

## End(Not run)
Usage

```r
## S3 method for class 'pclm'
plot(x, xlab, ylab, ylim, type, lwd, col, legend,
    legend.position, ...)
```

Arguments

- `x`: An object of class `pclm`.
- `xlab`: A label for the x axis, defaults to a description of `x`.
- `ylab`: A label for the y axis, defaults to a description of `y`.
- `ylim`: The y limits of the plot.
- `type`: A 1-character string giving the type of plot desired. The following values are possible, for details, see `plot`: "p" for points, "l" for lines, "b" for both points and lines, "c" for empty points joined by lines, "o" for overplotted points and lines, "s" and "S" for stair steps and "h" for histogram-like vertical lines. Finally, "n" does not produce any points or lines.
- `lwd`: Line width, a positive number, defaulting to 2.
- `col`: Three colours to be used in the plot for observed values, fitted values and confidence intervals.
- `legend`: A character or `expression` vector of length ≥ 1 to appear in the legend. Other objects will be coerced by `as.graphicsAnnot`.
- `legend.position`: Legend position, or the x and y co-ordinates to be used to position the legend.
- `...`: Other graphical parameters (see `par` and section ‘Details’ below).

See Also

- `pclm`.

Examples

```r
# See complete examples in pclm help page
```

---

`plot.pclm2D`  
Generic Plot for `pclm2D` Class

Description

The generic plot for a `pclm2D` object is constructed using `rgl` package. And can be modified/improved using the `rgl` tools implemented in the package like: `surface3d`, `axes3d`, `aspect3d`, `title3d` or `snapshot3d`. For a complete guide to 3D visualization using `rgl` see this tutorial.
residuals.pclm

Usage

## S3 method for class 'pclm2D'
plot(x, color = c(1, 2), alpha = c(1, 0.5),
     axes = TRUE, box = TRUE, xlab = "x-axis", ylab = "y-axis",
     zlab = "z-axis", main = "", sub = "", ...)  

Arguments

x    an object of class pclm2D
color vector of R color characters. Represents the diffuse component in case of lighting calculation (lit = TRUE), otherwise it describes the solid color characteristics.
alpha vector of alpha values between 0.0 (fully transparent) .. 1.0 (opaque).
axes add axes to the plot. Logical. Default: TRUE.
box draw a box around the plot. Logical. Default: TRUE.
xlab the axis labels for the plot
ylab the axis labels for the plot
zlab the axis labels for the plot
main the main title for the plot
sub the subtitle for the plot
... Material and texture properties. See rgl.material for details.

See Also

pclm2D surface3d axes3d aspect3d title3d snapshot3d

Examples

# See complete examples in pclm2D help page

residuals.pclm Extract PCLM Deviance Residuals

Description

Extract PCLM Deviance Residuals

Usage

## S3 method for class 'pclm'
residuals(object, ...)
Arguments

object an object for which the extraction of model residuals is meaningful.

... other arguments.

Value

Residuals extracted from the object object.

Examples

```
x <- c(0, 1, seq(5, 85, by = 5))
y <- c(294, 66, 32, 44, 170, 284, 287, 293, 361, 600, 998, 1572, 2529, 4637, 6161, 7369, 10481, 15293, 39016)
M1 <- pclm(x, y, nlast = 26)
residuals(M1)
```

---

residuals.pclm2D Extract PCLM-2D Deviance Residuals

Description

Extract PCLM-2D Deviance Residuals

Usage

```r
## S3 method for class 'pclm2D'
residuals(object, ...)
```

Arguments

object an object for which the extraction of model residuals is meaningful.

... other arguments.

Value

Residuals extracted from the object object.

Examples

```
Dx <- ungroup.data$Dx
Ex <- ungroup.data$Ex

# Aggregate data to ungroup it in the example below
x <- c(0, 1, seq(5, 85, by = 5))
nlast <- 26
n <- c(diff(x), nlast)
```
ungroup <- rep(x, n)
y <- aggregate(Dx, by = list(group), FUN = "sum")[, -1]

# Example
P1 <- pclm2D(x, y, nlast)
residuals(P1)

---

ungroup: Penalized Composite Link Model for Efficient Estimation of Smooth Distributions from Coarsely Binned Data

Description

Versatile method for ungrouping histograms (binned count data) assuming that counts are Poisson distributed and that the underlying sequence on a fine grid to be estimated is smooth. The method is based on the composite link model and estimation is achieved by maximizing a penalized likelihood. Smooth detailed sequences of counts and rates are so estimated from the binned counts. Ungrouping binned data can be desirable for many reasons: Bins can be too coarse to allow for accurate analysis; comparisons can be hindered when different grouping approaches are used in different histograms; and the last interval is often wide and open-ended and, thus, covers a lot of information in the tail area. Age-at-death distributions grouped in age classes and abridged life tables are examples of binned data. Because of modest assumptions, the approach is suitable for many demographic and epidemiological applications. For a detailed description of the method and applications see Rizzi et al. (2015) doi:10.1093/aje/kwv020.

Details

To learn more about the package, start with the vignettes: browseVignettes(package = "ungroup")

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References


### See Also

Useful links:
- [https://github.com/mpascariu/ungroup](https://github.com/mpascariu/ungroup)
- Report bugs at [https://github.com/mpascariu/ungroup/issues](https://github.com/mpascariu/ungroup/issues)

### Description

Test Dataset in the Package

Dataset containing death counts (Dx) and exposures (Ex) by age for a certain population between 1980 and 2014. The data-set is provided for testing purposes only and might be altered and outdated. Download actual demographic data free of charge from Human Mortality Database (2018). Once a username and a password is created on the website the MortalityLaws R package can be used to extract data in R format.

### Usage

`ungroup.data`
Format

An object of class ungroup.data of length 2.

Source

Human Mortality Database

References


See Also

ReadHMD
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