Package ‘ungroup’

October 15, 2018

Type Package

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

Version 1.1.1

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>.

License GPL-3

LazyData TRUE

Depends R (>= 3.4.0)

Imports MortalitySmooth (>= 2.3.4), pbapply (>= 1.3), Rcpp (>= 0.12.0), rgl (>= 0.99.0), Rdpack (>= 0.8)

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

VignetteBuilder knitr

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control.pclm  Auxiliary for Controlling pclm Fitting

Description

Auxiliary for Controlling pclm Fitting

Usage

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)
**Arguments**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>lambda</code></td>
<td>Smoothing parameter to be used in pclm estimation. If <code>lambda = NA</code> an algorithm will find the optimal values.</td>
</tr>
<tr>
<td><code>kr</code></td>
<td>Knot ratio. Number of internal intervals used for defining 1 knot in B-spline basis construction. See <code>MortSmooth_bbbase</code>.</td>
</tr>
<tr>
<td><code>deg</code></td>
<td>Degree of the splines needed to create equally-spaced B-splines basis over an abscissa of data.</td>
</tr>
<tr>
<td><code>int.lambda</code></td>
<td>If <code>lambda</code> is optimized an interval to be searched needs to be specified. Format: vector containing the end-points.</td>
</tr>
<tr>
<td><code>diff</code></td>
<td>An integer indicating the order of differences of the components of PCLM coefficients. Default value: 2.</td>
</tr>
<tr>
<td><code>opt.method</code></td>
<td>Selection criterion of the model. Possible values are &quot;AIC&quot; and &quot;BIC&quot;. Default: &quot;BIC&quot;.</td>
</tr>
<tr>
<td><code>max.iter</code></td>
<td>Maximal number of iterations used in fitting procedure.</td>
</tr>
<tr>
<td><code>tol</code></td>
<td>Relative tolerance in PCLM fitting procedure. Default: 0.1% i.e. the estimated aggregate bins should be in the 0.1% error margin.</td>
</tr>
</tbody>
</table>

**Value**

A list with exactly eight control parameters.

**See Also**

`pclm`

**Examples**

```r
control.pclm()
```

---

**control.pclm2D**  
**Auxiliary for Controlling `pclm2D` Fitting**

**Description**

Auxiliary for Controlling `pclm2D` Fitting

**Usage**

```r
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()

pclm  
Univariate Penalized Composite Link Model (PCLM)

Description

Fit univariate penalized composite link model (PCLM) to ungroup binned count data, e.g. age-at-death distributions grouped in age classes.

Usage

pclm(x, y, nlast, offset = NULL, out.step = 1, ci.level = 95, verbose = FALSE, 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**: 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 MortSmooth_base.
  - **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

control.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, 538, 384, 303, 245, 249) * 1000
nlast <- 26 # the size of the last interval

# Example 1 -----------------------------
M1 <- pclm(x, y, nlast)
ls(M1)
summary(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,
Two-Dimensional Penalized Composite Link Model (PCLM-2D)

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. Forthcoming).

Usage

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 pclm2D
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)

plot.pclm

Generic Plot for pclm Class

Description

Generic Plot for pclm Class

Usage

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

plot.pclm
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**: 1-character string giving the type of plot desired. The following values are possible, for details, see `plot`: "p" for points, "1" 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.

Usage

```r
## 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).
- `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

```r
# See complete examples in pclm2D help page
```

Description

Extract PCLM Deviance Residuals

Usage

```r
## 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`. 
Extraction of PCLM-2D Deviance Residuals

**Examples**

```r
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)
```

---

**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.

**Examples**

```r
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)
group <- rep(x, n)
y <- aggregate(Dx, by = list(group), FUN = "sum")[, -1]

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

residuals(P1)
```
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
- Report bugs at https://github.com/mpascariu/ungroup/issues

ungsroup.data Test Dataset in the Package

Description

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

ungsroup.data

Format

An object of class ungroup.data of length 2.

Source

Human Mortality Database

References


See Also

ReadHMD
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