Package ‘pammtools’

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Title Piece-Wise Exponential Additive Mixed Modeling Tools for Survival Analysis

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Description The Piece-wise exponential (Additive Mixed) Model (PAMM; Bender and others (2018) <doi:10.1177/1471082X17748083>) is a powerful model class for the analysis of survival (or time-to-event) data, based on Generalized Additive (Mixed) Models (GA(M)Ms). It offers intuitive specification and robust estimation of complex survival models with stratified baseline hazards, random effects, time-varying effects, time-dependent covariates and cumulative effects (Bender and others (2019)), as well as support for left-truncated, competing risks and recurrent events data.

pammtools provides tidy workflow for survival analysis with PAMMs, including data simulation, transformation and other functions for data preprocessing and model post-processing as well as visualization.

Depends R (>= 3.5.0)

Imports mgcv, survival (>= 2.39-5), checkmate, magrittr, rlang, tidyr (>= 1.0.0), ggplot2 (>= 3.2.2), dplyr (>= 1.0.0), purrr (>= 0.2.3), tibble, lazyeval, Formula, mvtnorm, pec, vctrs (>= 0.3.0)

Suggests testthat

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LazyData true

URL https://adibender.github.io/pammtools/

BugReports https://github.com/adibender/pammtools/issues

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add_cif

Add cumulative incidence function to data

Description

Add cumulative incidence function to data

Usage

add_cif(newdata, object, ...)

## Default S3 method:
add_cif(
  newdata,
  object,
  ci = TRUE,
  overwrite = FALSE,
  alpha = 0.05,
  n_sim = 500L,
  cause_var = "cause",
  time_var = NULL,
  ...
)

Arguments

newdata A data frame or list containing the values of the model covariates at which predictions are required. If this is not provided then predictions corresponding to the original data are returned. If newdata is provided then it should contain all the variables needed for prediction: a warning is generated if not. See details for use with link{linear.functional.terms}.

object a fitted gam object as produced by gam().

... Further arguments passed to predict.gam and get_hazard

Ci logical. Indicates if confidence intervals should be calculated. Defaults to TRUE.

overwrite Should hazard columns be overwritten if already present in the data set? Defaults to FALSE. If TRUE, columns with names c("hazard","se","lower","upper") will be overwritten.

alpha The alpha level for confidence/credible intervals.

n_sim Number of simulations (draws from posterior of estimated coefficients) on which estimation of CIFs and their confidence/credible intervals will be based on.

cause_var Character. Column name of the 'cause' variable.

time_var Name of the variable used for the baseline hazard. If not given, defaults to "tend" for gam fits, else "interval". The latter is assumed to be a factor, the former numeric.
add_hazard

Description

Add (cumulative) hazard based on the provided data set and model. If ci=TRUE confidence intervals (CI) are also added. Their width can be controlled via the se_mult argument. The method by which the CI are calculated can be specified by ci_type. This is a wrapper around predict.gam. When reference is specified, the (log-)hazard ratio is calculated.

Usage

add_hazard(newdata, object, ...)

## Default S3 method:
add_hazard(
  newdata,
  object,
  reference = NULL,
  type = c("response", "link"),
  ci = TRUE,
  se_mult = 2,
  ci_type = c("default", "delta", "sim"),
  overwrite = FALSE,
  time_var = NULL,
  ...
)

add_cumu_hazard(
  newdata,
  object,
  ci = TRUE,
  se_mult = 2,
  overwrite = FALSE,
  time_var = NULL,
  interval_length = "intlen",
  ...
)

Arguments

newdata A data frame or list containing the values of the model covariates at which predictions are required. If this is not provided then predictions corresponding to the original data are returned. If newdata is provided then it should contain all the variables needed for prediction: a warning is generated if not. See details for use with link{linear.functional.terms}.

object a fitted gam object as produced by gam().
add_surv_prob

Further arguments passed to `predict.gam` and `get_hazard`

**reference**
A data frame with number of rows equal to `nrow(newdata)` or one, or a named list with (partial) covariate specifications. See examples.

**type**
Either "response" or "link". The former calculates hazard, the latter the log-hazard.

**ci**
Logical. Indicates if confidence intervals should be calculated. Defaults to TRUE.

**se_mult**
Factor by which standard errors are multiplied for calculating the confidence intervals.

**ci_type**
The method by which standard errors/confidence intervals will be calculated. Default transforms the linear predictor at respective intervals. "delta" calculates CIs based on the standard error calculated by the Delta method. "sim" draws the property of interest from its posterior based on the normal distribution of the estimated coefficients. See here for details and empirical evaluation.

**overwrite**
Should hazard columns be overwritten if already present in the data set? Defaults to FALSE. If TRUE, columns with names c("hazard","se","lower","upper") will be overwritten.

**time_var**
Name of the variable used for the baseline hazard. If not given, defaults to "tend" for `gam` fits, else "interval". The latter is assumed to be a factor, the former numeric.

**interval_length**
The variable in newdata containing the interval lengths. Can be either bare unquoted variable name or character. Defaults to "intlen".

See Also

`predict.gam`, `add_surv_prob`

Examples

```r
ped <- tumor[1:50,] %>% as_ped(Surv(days, status)~ age)
pam <- mgcv::gam(ped_status ~ s(tend)+age, data = ped, family=poisson(), offset=offset)
ped_info(ped) %>% add_hazard(pam, type="link")
ped_info(ped) %>% add_hazard(pam, type = "response")
ped_info(ped) %>% add_cumu_hazard(pam)
```

Description

Given suitable data (i.e. data with all columns used for estimation of the model), this function adds a column `surv_prob` containing survival probabilities for the specified covariate and follow-up information (and CIs `surv_lower`, `surv_upper` if `ci=TRUE`).
add_surv_prob

Usage

add_surv_prob(
    newdata,
    object,
    ci = TRUE,
    se_mult = 2,
    overwrite = FALSE,
    time_var = NULL,
    interval_length = "intlen",
    ...
)

Arguments

newdata A data frame or list containing the values of the model covariates at which predictions are required. If this is not provided then predictions corresponding to the original data are returned. If newdata is provided then it should contain all the variables needed for prediction: a warning is generated if not. See details for use with link\{linear.functional.terms\}.

object a fitted \texttt{gam} object as produced by \texttt{gam()}.

ci logical. Indicates if confidence intervals should be calculated. Defaults to \texttt{TRUE}.

se_mult Factor by which standard errors are multiplied for calculating the confidence intervals.

overwrite Should hazard columns be overwritten if already present in the data set? Defaults to \texttt{FALSE}. If \texttt{TRUE}, columns with names \texttt{c("hazard","se","lower","upper")} will be overwritten.

time_var Name of the variable used for the baseline hazard. If not given, defaults to \texttt{"tend"} for \texttt{gam} fits, else \texttt{"interval"}. The latter is assumed to be a factor, the former numeric.

interval_length The variable in newdata containing the interval lengths. Can be either bare unquoted variable name or character. Defaults to \texttt{"intlen"}.

... Further arguments passed to \texttt{predict.gam} and \texttt{get_hazard}

See Also

\texttt{predict.gam}, \texttt{add_surv_prob}

Examples

ped <- tumor[1:50,] %>% as_ped(Surv(days, status) ~ age)
pam <- mgcv::gam(ped_status ~ s(tend)+age, data=ped, family=poisson(), offset=offset)
ped_info(ped) %>% add_surv_prob(pam, ci=TRUE)
add_tdc

Add time-dependent covariate to a data set

Description
Given a data set in standard format (with one row per subject/observation), this function adds a
column with the specified exposure time points and a column with respective exposures, created
from rng_fun. This function should usually only be used to create data sets passed to sim_pexp.

Usage
add_tdc(data, tz, rng_fun, ...)

Arguments
data A data set with variables specified in formula.
tz A numeric vector of exposure times (relative to the beginning of the follow-up
time t)
rng_fun A random number generating function that creates the time-dependent covari-
ates at time points tz. First argument of the function should be n, the number of
random numbers to generate. Within add_tdc, n will be set to length(tz).
... Currently not used.

add_term
Embeds the data set with the specified (relative) term contribution

Description
Adds the contribution of a specific term to the linear predictor to the data specified by newdata.
Essentially a wrapper to predict.gam, with type="terms". Thus most arguments and their docu-
mentation below is from predict.gam.

Usage
add_term(newdata, object, term, reference = NULL, ci = TRUE, se_mult = 2, ...)

Arguments
newdata A data frame or list containing the values of the model covariates at which pre-
dictions are required. If this is not provided then predictions corresponding to
the original data are returned. If newdata is provided then it should contain all
the variables needed for prediction: a warning is generated if not. See details for
use with link{linear.functional.terms}.
object a fitted gam object as produced by gam().
A character (vector) or regular expression indicating for which term(s) information should be extracted and added to data set.

reference
A data frame with number of rows equal to nrow(newdata) or one, or a named list with (partial) covariate specifications. See examples.

ci
logical. Indicates if confidence intervals should be calculated. Defaults to TRUE.

se_mult
The factor by which standard errors are multiplied to form confidence intervals.

Further arguments passed to `predict.gam`.

### Examples

```r
library(ggplot2)
ped <- as_ped(tumor, Surv(days, status) ~ age, cut = seq(0, 2000, by = 100))
pam <- mgcv::gam(ped_status ~ s(tend) + s(age), family = poisson(),
                offset = offset, data = ped)

# term contribution for sequence of ages
s_age <- ped %>% make_newdata(age = seq_range(age, 50)) %>%
          add_term(pam, term = "age")
ggplot(s_age, aes(x = age, y = fit)) + geom_line() +
      geom_ribbon(aes(ymin = ci_lower, ymax = ci_upper), alpha = .3)

# term contribution relative to mean age
s_age2 <- ped %>% make_newdata(age = seq_range(age, 50)) %>%
          add_term(pam, term = "age", reference = list(age = mean(.$age)))
ggplot(s_age2, aes(x = age, y = fit)) + geom_line() +
      geom_ribbon(aes(ymin = ci_lower, ymax = ci_upper), alpha = .3)
```

### Description

As `data.frame` S3 method for objects of class `crps`.

### Usage

```r
## S3 method for class 'crps'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

### Arguments

- **x**: An object of class `crps`. See `crps`.
- **row.names**: NULL or a character vector giving the row names for the data frame. Missing values are not allowed.
- **optional**: logical. If TRUE, setting row names and converting column names (to syntactic names: see `make.names`) is optional. Note that all of R's `base` package `as.data.frame()` methods use optional only for column names treatment, basically with the meaning of `data.frame(*,check.names = !optional)`. See also the `make.names` argument of the matrix method.
additional arguments to be passed to or from methods.

**Description**

This data set contains the time-dependent covariates (TDCs) for the patient data set. Note that nutrition was protocoted for at most 12 days after ICU admission. The data set includes:

- **CombinedID** Unique patient identifier. Can be used to merge with patient data
- **Study_Day** The calendar (!) day at which calories (or proteins) were administered
- **caloriesPercentage** The percentage of target calories supplied to the patient by the ICU staff
- **proteinGproKG** The amount of protein supplied to the patient by the ICU staff

**Usage**

daily

**Format**

An object of class tbl_df (inherits from tbl, data.frame) with 18797 rows and 4 columns.

**Description**

This is a preprocessed subset of the data discussed in Heyard, et. al 2018 (and provided in a slightly different format as VAP_data in the package TBFmultinomial). In this package, the data is split in two parts, extub_event contains time-to-event data and time-constant covariates and extub_tdc contains the information on the time-dependent covariate SOFA score. The data contains the following variables:

- **ID** Unique patient ID
- **gender** The patients’ gender
- **type** Type of admission, either Medical or Surgical
- **SAPSadmission** SAPS score at admission
- **time** Time (days) until extubation
- **extubation** 0 = no extubation/censoring, 1 = extubation
- **day** Exposure time, i.e., time at which the SOFA score was observed
- **SOFA** The SOFA score at respective days
Usage

text

text

Format

An object of class tbl_df (inherits from tbl, data.frame) with 110 rows and 6 columns.
An object of class tbl_df (inherits from tbl, data.frame) with 1518 rows and 3 columns.

Description

geom_hazard is an extension of the geom_line, and is optimized for (cumulative) hazard plots. Essentially, it adds a (0,0) row to the data, if not already the case. Stolen from the RmcdrPlugin.KMggplot2 (slightly modified).

Usage

geom_hazard(
mapping = NULL,
data = NULL,
stat = "identity",
position = "identity",
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE,
...
)

geom_stephazard(
mapping = NULL,
data = NULL,
stat = "identity",
position = "identity",
direction = "vh",
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE,
...
)

gmod_surv(
mapping = NULL,
...
geom_hazard

data = NULL,
stat = "identity",
position = "identity",
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE,
...
)

Arguments

mapping  Set of aesthetic mappings created by aes() or aes_(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data  The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x,10)).

stat  The statistical transformation to use on the data for this layer, as a string.

position  Position adjustment, either as a string, or the result of a call to a position adjustment function.

na.rm  If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

show.legend  logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes  If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

...  Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

direction  direction of stairs: 'vh' for vertical then horizontal, 'hv' for horizontal then vertical, or 'mid' for step half-way between adjacent x-values.

See Also

geom_line, geom_step.
Examples

```r
library(ggplot2)
library(pammtools)
ped <- tumor[10:50,] %>% as_ped(Surv(days, status)~1)
pam <- mgcv::gam(ped_status ~ s(tend), data=ped, family = poisson(), offset = offset)
ndf <- make_newdata(ped, tend = unique(tend)) %>% add_hazard(pam)
# piece-wise constant hazards
ggplot(ndf, aes(x = tend, y = hazard)) +
gem_vline(xintercept = c(0, ndf$tend[c(1, (nrow(ndf)-2):nrow(ndf))]), lty = 3) +
gem_hline(yintercept = c(ndf$hazard[1:3], ndf$hazard[nrow(ndf)]), lty = 3) +
gem_stephazard() +
gem_step(col=2) +
gem_step(col=2, lty = 2, direction="vh")

# cumulative hazard
ndf <- ndf %>% add_cumu_hazard(pam)
ggplot(ndf, aes(x = tend, y = cumu_hazard)) +
gem_hazard() +
gem_line(col=2) # doesn't start at (0, 0)

# survival probability
ndf <- ndf %>% add_surv_prob(pam)
ggplot(ndf, aes(x = tend, y = surv_prob)) +
gem_surv() +
gem_line(col=2) # doesn't start at c(0,1)
```

**geom_stepribbon**  
Step ribbon plots.

**Description**

`geom_stepribbon` is an extension of the `geom.ribbon`, and is optimized for Kaplan-Meier plots with pointwise confidence intervals or a confidence band.

**Usage**

```r
geom_stepribbon(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...)
```
geom_stepribbon

Arguments

mapping Set of aesthetic mappings created by \texttt{aes()} or \texttt{aes()}(). If specified and \texttt{inherit.aes} = \texttt{TRUE} (the default), it is combined with the default mapping at the top level of the plot. You must supply \texttt{mapping} if there is no plot mapping.

data The data to be displayed in this layer. There are three options:
If \texttt{NULL}, the default, the data is inherited from the plot data as specified in the call to \texttt{ggplot()}.
A \texttt{data.frame}, or other object, will override the plot data. All objects will be fortified to produce a data frame. See \texttt{fortify()} for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a \texttt{data.frame}, and will be used as the layer data. A function can be created from a formula (e.g. \texttt{~ head(x,10)}).

stat The statistical transformation to use on the data for this layer, as a string.

position Position adjustment, either as a string, or the result of a call to a position adjustment function.

na.rm If \texttt{FALSE}, the default, missing values are removed with a warning. If \texttt{TRUE}, missing values are silently removed.

show.legend logical. Should this layer be included in the legends? \texttt{NA}, the default, includes if any aesthetics are mapped. \texttt{FALSE} never includes, and \texttt{TRUE} always includes. It can also be a named logical vector to finely select the aesthetics to display.

\texttt{inherit.aes} If \texttt{FALSE}, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. \texttt{borders()}.

... Other arguments passed on to \texttt{layer()}. These are often aesthetics, used to set an aesthetic to a fixed value, like \texttt{colour = “red”} or \texttt{size = 3}. They may also be parameters to the paired geom/stat.

See Also

\texttt{geom_ribbon} \texttt{geom_stepribbon} inherits from \texttt{geom_ribbon}.

Examples

\begin{verbatim}
library(ggplot2)
huron <- data.frame(year = 1875:1972, level = as.vector(LakeHuron))
h <- ggplot(huron, aes(year))
h + geom_stepribbon(aes(ymin = level - 1, ymax = level + 1), fill = "grey70") +
   geom_step(aes(y = level))
h + geom_ribbon(aes(ymin = level - 1, ymax = level + 1), fill = "grey70") +
   geom_line(aes(y = level))
\end{verbatim}
Description

These functions are designed to extract (or mimic) the cumulative coefficients usually used in additive hazards models (Aalen model) to depict (time-varying) covariate effects. For PAMMs, these are the differences between the cumulative hazard rates where all covariates except one have the identical values. For a numeric covariate of interest, this calculates $\Lambda(t|x + 1) - \Lambda(t|x)$. For non-numeric covariates the cumulative hazard of the reference level is subtracted from the cumulative hazards evaluated at all non reference levels. Standard errors are calculated using the delta method.

Usage

get_cumu_coef(model, data = NULL, terms, ...)

## S3 method for class 'gam'
get_cumu_coef(model, data, terms, ...)

## S3 method for class 'aalen'
get_cumu_coef(model, data = NULL, terms, ci = TRUE, ...)

## S3 method for class 'cox.aalen'
get_cumu_coef(model, data = NULL, terms, ci = TRUE, ...)

Arguments

model Object from which to extract cumulative coefficients.
data Additional data if necessary.
terms A character vector of variables for which the cumulative coefficient should be calculated.
... Further arguments passed to methods.
ci Logical. Indicates if confidence intervals should be returned as well.

get_cumu_eff Calculate (or plot) cumulative effect for all time-points of the follow-up

Description

Calculate (or plot) cumulative effect for all time-points of the follow-up
get_intervals

Usage

get_cumu_eff(data, model, term, z1, z2 = NULL, se_mult = 2)

gg_cumu_eff(data, model, term, z1, z2 = NULL, se_mult = 2, ci = TRUE)

Arguments

data: Data used to fit the model.
model: A suitable model object which will be used to estimate the partial effect of term.
term: A character string indicating the model term for which partial effects should be plotted.
z1: The exposure profile for which to calculate the cumulative effect. Can be either a single number or a vector of same length as unique observation time points.
z2: If provided, calculated cumulative effect is for the difference between the two exposure profiles (g(z1,t)-g(z2,t)).
se_mult: Multiplicative factor used to calculate confidence intervals (e.g., lower = fit - 2*se).
ci: Logical. Indicates if confidence intervals for the term of interest should be calculated/plotted. Defaults to TRUE.

get_intervals

Information on intervals in which times fall

Usage

get_intervals(x, times, ...)

## Default S3 method:
get_intervals(x, times, left.open = TRUE, rightmost.closed = TRUE, ...)

Arguments

x: An object from which interval information can be obtained, see int_info.
times: A vector of times for which corresponding interval information should be returned.
...: Further arguments passed to findInterval.
left.open: logical; if true all the intervals are open at left and closed at right; in the formulas below, <= should be swapped with < (and > with >=), and rightmost.closed means 'leftmost is closed'. This may be useful, e.g., in survival analysis computations.
rightmost.closed: logical; if true, the rightmost interval, vec[N-1] .. vec[N] is treated as closed, see below.
Value

A `data.frame` containing information on intervals in which values of `times` fall.

See Also

`findInterval`, `int_info`

Examples

```r
set.seed(111018)
brks <- c(0, 4.5, 5, 10, 30)
int_info(brks)
x <- runif(3, 0, 30)
x
get_intervals(brks, x)
```

---

**get_laglead**

Construct or extract data that represents a lag-lead window

Description

Constructs lag-lead window data set from raw inputs or from data objects with suitable information stored in attributes, e.g., objects created by `as_ped`.

Usage

```r
get_laglead(x, ...)
```

## Default S3 method:

```r
get_laglead(x, tz, ll_fun, ...)
```

## S3 method for class 'Var'

```r
data.frame
```

Arguments

- `x` Either a numeric vector of follow-up cut points or a suitable object.
- `...` Further arguments passed to methods.
- `tz` A vector of exposure times
- `ll_fun` Function that specifies how the lag-lead matrix should be constructed. First argument is the follow up time second argument is the time of exposure.

Examples

```r
get_laglead(0:10, tz=-5:5, ll_fun=function(t, tz) { t >= tz + 2 & t <= tz + 2 + 3})
gg_laglead(0:10, tz=-5:5, ll_fun=function(t, tz) { t >= tz + 2 & t <= tz + 2 + 3})
```
get_plotinfo

Extract plot information for all special model terms

Description

Given a mgcv gamObject, returns the information used for the default plots produced by plot.gam.

Usage

get_plotinfo(x, ...)

Arguments

x a fitted gam object as produced by gam().
... Further arguments passed to plot.gam

get_terms

Extract the partial effects of non-linear model terms

Description

This function basically creates a new df from data for each term in terms, creating a range from minimum and maximum of the predict(fit,newdata=df,type="terms"). Terms are then stacked to a tidy data frame.

Usage

get_terms(data, fit, terms, ...)

Arguments

data A data frame containing variables used to fit the model. Only first row will be used.
fit A fitted object of class gam.
terms A character vector (can be length one). Specifies the terms for which partial effects will be returned
... Further arguments passed to seq_range.

Value

A tibble with 5 columns.
Examples

```r
library(survival)
fit <- coxph(Surv(time, status) ~ pspline(karno) + pspline(age), data=veteran)
terms_df <- veteran %>% get_terms(fit, terms = c("karno", "age"))
head(terms_df)
tail(terms_df)
```

---

**gg_fixed**

**Forrest plot of fixed coefficients**

Description

Given a model object, returns a data frame with columns `variable`, `coef` (coefficient), `ci_lower` (lower 95\% CI), `ci_upper` (upper 95\% CI).

Usage

```r
gg_fixed(x, intercept = FALSE, ...)
```

Arguments

- `x` A model object.
- `intercept` Logical, indicating whether intercept term should be included. Defaults to `FALSE`.
- `...` Currently not used.

See Also

- `tidy_fixed`

Examples

```r
g <- mgcv::gam(Sepal.Length ~ Sepal.Width + Petal.Length + Petal.Width + Species, data=iris)
gg_fixed(g, intercept=TRUE)
gg_fixed(g)
```
**gg_laglead**

*Plot Lag-Lead windows*

**Description**

Given data defining a Lag-lead window, returns respective plot as a ggplot2 object.

**Usage**

```r
gg_laglead(x, ...)
## Default S3 method:
gg_laglead(x, tz, ll_fun, ...)
## S3 method for class 'LL_df'
gg_laglead(
  x,
  high_col = "grey20",
  low_col = "whitesmoke",
  grid_col = "lightgrey",
  ...)
## S3 method for class 'nested_fdf'
gg_laglead(x, ...)
```

**Arguments**

- **x**
  - Either a numeric vector of follow-up cut points or a suitable object.
- **...**
  - Further arguments passed to methods.
- **tz**
  - A vector of exposure times
- **ll_fun**
  - Function that specifies how the lag-lead matrix should be constructed. First argument is the follow up time second argument is the time of exposure.
- **high_col**
  - Color used to highlight exposure times within the lag-lead window.
- **low_col**
  - Color of exposure times outside the lag-lead window.
- **grid_col**
  - Color of grid lines.

**See Also**

`get_laglead`
Examples

## Example 1: supply t, tz, ll_fun directly

```r
gg_laglead(1:10, tz=-5:5, 
  ll_fun=function(t, tz) { t >= tz + 2 & t <= tz + 2 + 3})
```

## Example 2: extract information on t, tz, ll_from data with respective attributes

```r
data("simdf_elra", package = "pammtools")
gg_laglead(simdf_elra)
```

---

**gg_partial**  
Visualize effect estimates for specific covariate combinations

Description

Depending on the plot function and input, creates either a 1-dimensional slices, bivariate surface or (1D) cumulative effect.

Usage

```r
gg_partial(data, model, term, ..., reference = NULL, ci = TRUE)
```

```r
gg_partial_ll(
  data,
  model,
  term,
  ..., 
  reference = NULL,
  ci = FALSE,
  time_var = "tend"
)
```

```r
get_partial_ll(
  data,
  model,
  term,
  ..., 
  reference = NULL,
  ci = FALSE,
  time_var = "tend"
)
```

Arguments

data: Data used to fit the model.

model: A suitable model object which will be used to estimate the partial effect of term.

term: A character string indicating the model term for which partial effects should be plotted.
Covariate specifications (expressions) that will be evaluated by looking for variables in \( x \). Must be of the form \( z = f(z) \) where \( z \) is a variable in the data set and \( f \) a known function that can be usefully applied to \( z \). Note that this is also necessary for single value specifications (e.g. \( \text{age} = c(50) \)). For data in PED (piece-wise exponential data) format, one can also specify the time argument, but see "Details" an "Examples" below.

**reference**  
If specified, should be a list with covariate value pairs, e.g. \( \text{list}(x1 = 1, x2 = 50) \). The calculated partial effect will be relative to an observation specified in \( \text{reference} \).

**ci**  
Logical. Indicates if confidence intervals for the term of interest should be calculated/plotted. Defaults to \text{TRUE}.

**time_var**  
The name of the variable that was used in \text{model} to represent follow-up time.

---

**gg_re**  
Plot Normal QQ plots for random effects

**Description**  
Plot Normal QQ plots for random effects

**Usage**  
\text{gg_re}(x, \ldots)

**Arguments**  
\text{x}  
a fitted \text{gam} object as produced by \text{gam}().

\ldots  
Further arguments passed to \text{plot.gam}

**See Also**  
\text{tidy_re}

**Examples**  
```r  
library(pammtools)  
data("patient")  
ped <- patient %>%  
dplyr::slice(1:100) %>%  
as_ped(Surv(Survdays, PatientDied) ~ ApacheII Score + CombinedicuID, id="CombinedID")  
pam <- mgcv::gam(ped_status ~ s(tend) + ApacheII Score + s(CombinedicuID, bs="re"),  
data=ped, family=poisson(), offset=offset)  
gg_re(pam)  
plot(pam, select = 2)  
```
**gg_slice**

*Plot 1D (smooth) effects*

**Description**

Flexible, high-level plotting function for (non-linear) effects conditional on further covariate specifications and potentially relative to a comparison specification.

**Usage**

```r
gg_slice(data, model, term, ..., reference = NULL, ci = TRUE)
```

**Arguments**

- **data**: Data used to fit the model.
- **model**: A suitable model object which will be used to estimate the partial effect of `term`.
- **term**: A character string indicating the model term for which partial effects should be plotted.
- **...**: Covariate specifications (expressions) that will be evaluated by looking for variables in `x`. Must be of the form `z = f(z)` where `z` is a variable in the data set and `f` a known function that can be usefully applied to `z`. Note that this is also necessary for single value specifications (e.g. `age = c(50)`). For data in PED (piece-wise exponential data) format, one can also specify the time argument, but see "Details" an "Examples" below.
- **reference**: If specified, should be a list with covariate value pairs, e.g. `list(x1 = 1, x2 = 50)`. The calculated partial effect will be relative to an observation specified in `reference`.
- **ci**: Logical. Indicates if confidence intervals for the term of interest should be calculated/plotted. Defaults to TRUE.

**Examples**

```r
ped <- tumor[1:200, ] %>% as_ped(Surv(days, status) ~ .)
model <- mgcv::gam(ped_status~s(tend) + s(age, by = complications), data=ped, family = poisson(), offset=offset)
make_newdata(ped, age = seq_range(age, 20), complications = levels(complications))

# Plot partial effect of age
gg_slice(ped, model, "age", age=seq_range(age, 20), complications=levels(complications))

# Plot partial effect of age with confidence intervals
gg_slice(ped, model, "age", age=seq_range(age, 20), complications=levels(complications), ci = FALSE)

# Plot partial effect of age relative to age = 50
gg_slice(ped, model, "age", age=seq_range(age, 20), complications=levels(complications), reference=list(age = 50))
```
gg_smooth

Plot smooth 1d terms of gam objects

Description
Given a gam model this convenience function returns a plot of all smooth terms contained in the model. If more than one smooth is present, the different smooth are faceted.

Usage

```r
gg_smooth(x, ...)  
## Default S3 method:  
gg_smooth(x, fit, ...)  
```

Arguments

- `x`: A data frame or object of class `ped`.
- `...`: Further arguments passed to `get_terms`.
- `fit`: A model object.

Value

A `ggplot` object.

See Also

`get_terms`

Examples

```r
g1 <- mgcv::gam(Sepal.Length ~ s(Sepal.Width) + s(Petal.Length), data=iris)  
 gg_smooth(iris, g1, terms=c("Sepal.Width", "Petal.Length"))
```

---

gg_tensor

Plot tensor product effects

Description
Given a gam model this convenience function returns a ggplot2 object depicting 2d smooth terms specified in the model as heat/contour plots. If more than one 2d smooth term is present individual terms are faceted.

Usage

```r
gg_tensor(x, ci = FALSE, ...)
```
Arguments

- **x**
  A fitted gam object as produced by `gam()`.

- **ci**
  A logical value indicating whether confidence intervals should be calculated and returned. Defaults to TRUE.

- **...**
  Further arguments passed to `plot.gam`.

See Also

tidy_smooth2d

Examples

g <- mgcv::gam(Sepal.Length ~ te(Sepal.Width, Petal.Length), data=iris)
gg_tensor(g)
gg_tensor(g, ci=TRUE)
gg_tensor(update(g, .~. + te(Petal.Width, Petal.Length)))

Description

This functions provides a flexible interface to create a data set that can be plugged in as newdata argument to a suitable predict function (or similar). The function is particularly useful in combination with one of the add_* functions, e.g., add_term, add_hazard, etc.

Usage

```r
make_newdata(x, ...)
```

### Default S3 method:
```r
make_newdata(x, ...)
```

### S3 method for class 'ped'
```r
make_newdata(x, ...)
```

### S3 method for class 'fped'
```r
make_newdata(x, ...)
```

Arguments

- **x**
  A data frame (or object that inherits from data.frame).

- **...**
  Covariate specifications (expressions) that will be evaluated by looking for variables in x. Must be of the form $z = f(z)$ where z is a variable in the data set and f a known function that can be usefully applied to z. Note that this is also necessary for single value specifications (e.g. age = c(50)). For data in PED (piece-wise exponential data) format, one can also specify the time argument, but see "Details" an "Examples" below.
Details

Depending on the type of variables in \( x \), mean or modus values will be used for variables not specified in ellipsis (see also \textbf{sample_info}). If \( x \) is an object that inherits from class \textbf{ped}, useful data set completion will be attempted depending on variables specified in ellipsis. This is especially useful, when creating a data set with different time points, e.g. to calculate survival probabilities over time (\textbf{add_surv_prob}) or to calculate a time-varying covariate effects (\textbf{add_term}). To do so, the time variable has to be specified in \ldots\, e.g., \( \text{tend} = \text{seq\_range(tend, 20)} \). The problem with this specification is that not all values produced by \text{seq\_range(tend, 20)} will be actual values of \( \text{tend} \) used at the stage of estimation (and in general, it will often be tedious to specify exact \( \text{tend} \) values). \textbf{make\_newdata} therefore finds the correct interval and sets \( \text{tend} \) to the respective interval endpoint. For example, if the intervals of the PED object are \((0, 1], [1, 2] \) then \( \text{tend} = 1.5 \) will be set to 2 and the remaining time-varying information (e.g. offset) completed accordingly. See examples below.

Examples

# General functionality
tumor %>% make_newdata()
tumor %>% make_newdata(age = c(50))
tumor %>% make_newdata(days = seq_range(days, 3), age = c(50, 55))
tumor %>% make_newdata(days = seq_range(days, 3), status = unique(status), age = c(50, 55))
# mean/modus values of unspecified variables are calculated over whole data
tumor %>% make_newdata(sex = unique(sex))
tumor %>% group_by(sex) %>% make_newdata()
# You can also pass a part of the data sets as data frame to make\_newdata
purrr::cross_df(list(days = c(0, 500, 1000), sex = c("male", "female"))) %>%
  make_newdata(x = tumor)

# Examples for PED data
ped <- tumor %>% slice(1:3) %>% as_ped(Surv(days, status) ~ ., cut = c(0, 500, 1000))
ped %>% make_newdata(age = c(50, 55))

# if time information is specified, other time variables will be specified
# accordingly and offset calculated correctly
ped %>% make_newdata(tend = c(1000), age = c(50, 55))
ped %>% make_newdata(tend = unique(tend))
ped %>% group_by(sex) %>% make_newdata(tend = unique(tend))

# tend is set to the end point of respective interval:
ped <- tumor %>% as_ped(Surv(days, status) ~ .)
seq_range(ped$tend, 3)
make_newdata(ped, tend = seq_range(tend, 3))

\textbf{pammtools:} Piece-wise exponential Additive Mixed Modeling tools.
Description

pammtools provides functions and utilities that facilitate fitting Piece-wise Exponential Additive Mixed Models (PAMMs), including data transformation and other convenience functions for pre- and post-processing as well as plotting.

Details

The best way to get an overview of the functionality provided and how to fit PAMMs is to view the vignettes available at https://adibender.github.io/pammttools/articles/. A summary of the vignettes' content is given below:

- **basics**: Introduction to PAMMs and basic modeling.
- **baseline**: Shows how to estimate and visualize baseline model (without covariates) and comparison to respective Cox-PH model.
- **convenience**: Convenience functions for post-processing and plotting PAMMs.
- **data-transformation**: Transforming data into a format suitable to fit PAMMs.
- **frailty**: Specifying "frailty" terms, i.e., random effects for PAMMs.
- **splines**: Specifying spline smooth terms for PAMMs.
- **strata**: Specifying stratified models in which each level of a grouping variable has a different baseline hazard.
- **tdcovar**: Dealing with time-dependent covariates.
- **tveffects**: Specifying time-varying effects.
- **left-truncation**: Estimation for left-truncated data.
- **competing-risks**: Competing risks analysis.

References


 Survival data of critically ill ICU patients

Description

A data set containing the survival time (or hospital release time) among other covariates. The full data is available here. The following variables are provided:

- **Year** The year of ICU Admission
- **CombinedICU** Intensive Care Unit (ICU) ID
- **CombinedID** Patient identifier
- **Survdays** Survival time of patients. Here it is assumed that patients survive until t=30 if released from hospital.
- **PatientDied** Status indicator; 1=death, 0=censoring
- **surv hosp** Survival time in hospital. Here it is assumed that patients are censored at time of hospital release (potentially informative)
- **Gender** Male or female
- **Age** The patients age at Admission
- **AdmCatID** Admission category: medical, surgical elective or surgical emergency
- **ApacheII Score** The patient’s Apache II Score at Admission
- **BMI** Patient’s Body Mass Index
- **DiagID2** Diagnosis at admission in 9 categories

Usage

patient

Format

An object of class data.frame with 2000 rows and 12 columns.

ped_info

Extract interval information and median/modus values for covariates

Description

Given an object of class ped, returns data frame with one row for each interval containing interval information, mean values for numerical variables and modus for non-numeric variables in the data set.
Usage
ped_info(ped)

## S3 method for class 'ped'
ped_info(ped)

Arguments
ped An object of class ped as returned by as_ped.

Value
A data frame with one row for each unique interval in ped.

See Also
int_info, sample_info

Examples
ped <- tumor[1:4,] %>% as_ped(Surv(days, status) ~ sex + age)
ped_info(ped)

predictSurvProb.pamm  S3 method for pamm objects for compatibility with package pec

Description
S3 method for pamm objects for compatibility with package pec

Usage
## S3 method for class 'pamm'
predictSurvProb(object, newdata, times)

Arguments
object A fitted model from which to extract predicted survival probabilities
newdata A data frame containing predictor variable combinations for which to compute predicted survival probabilities.
times A vector of times in the range of the response variable, e.g. times when the response is a survival object, at which to return the survival probabilities.
seq_range

*Generate a sequence over the range of a vector*

**Description**

Stolen from [here](#).

**Usage**

```r
seq_range(x, n, by, trim = NULL, expand = NULL, pretty = FALSE)
```

**Arguments**

- `x` A numeric vector
- `n, by` Specify the output sequence either by supplying the length of the sequence with `n`, or the spacing between value with `by`. Specifying both is an error. I recommend that you name these arguments in order to make it clear to the reader.
- `trim` Optionally, trim values off the tails. `trim / 2 * length(x)` values are removed from each tail.
- `expand` Optionally, expand the range by `expand * (1 + range(x))` (computed after trimming).
- `pretty` If `TRUE`, will generate a pretty sequence. If `n` is supplied, this will use `pretty()` instead of `seq()`. If `by` is supplied, it will round the first value to a multiple of `by`.

**Examples**

```r
x <- rcauchy(100)
seq_range(x, n = 10)
seq_range(x, n = 10, trim = 0.1)
seq_range(x, by = 1, trim = 0.1)

# Make pretty sequences
y <- runif(100)
seq_range(y, n = 10)
seq_range(y, n = 10, pretty = TRUE)
seq_range(y, n = 10, expand = 0.5, pretty = TRUE)

seq_range(y, by = 0.1)
seq_range(y, by = 0.1, pretty = TRUE)
```
Simulated data with cumulative effects

Description

This is data simulated using the `sim_pexp` function. It contains two time-constant and two time-dependent covariates (observed on different exposure time grids). The code used for simulation is contained in the examples of `?sim_pexp`.

Usage

`simdf_elra`

Format

An object of class `nested_fdf` (inherits from `sim_sdf`, `ped`, `tbl_df`, `tbl`, `data.frame`) with 250 rows and 9 columns.

Simulate survival times from the piece-wise exponential distribution

Description

Simulate survival times from the piece-wise exponential distribution

Usage

`sim_pexp(formula, data, cut)`

Arguments

- `formula`: An extended formula that specifies the linear predictor. If you want to include a smooth baseline or time-varying effects, use `t` within your formula as if it was a covariate in the data, although it is not and should not be included in the data provided to `sim_pexp`. See examples below.
- `data`: A data set with variables specified in `formula`.
- `cut`: A sequence of time-points starting with 0.
Examples

```r
library(survival)
library(dplyr)
library(pammtools)

# set number of observations/subjects
n <- 250
# create data set with variables which will affect the hazard rate.
df <- cbind.data.frame(x1 = runif (n, -3, 3), x2 = runif (n, 0, 6)) %>%
  as_tibble()
# the formula which specifies how covariates affect the hazard rate
f0 <- function(t) {
  dgamma(t, 8, 2) * 6
}
form <- ~ -3.5 + f0(t) - 0.5 * x1 + sqrt(x2)
set.seed(24032018)
sim_df <- sim_pexp(form, df, 1:10)
head(sim_df)
plot(survfit(Surv(time, status) ~ 1, data = sim_df))

# for control, estimate with Cox PH
mod <- coxph(Surv(time, status) ~ x1 + pspline(x2), data = sim_df)
coef(mod)[1]
layout(matrix(1:2, nrow = 1))
termplot(mod, se = TRUE)

# and using PAMs
layout(1)
ped <- sim_df %>% as_ped(Surv(time, status) ~ ., max_time = 10)
library(mgcv)
pam <- gam(ped_status ~ s(tend) + x1 + s(x2), data = ped, family = poisson, offset = offset)
coef(pam)[2]
plot(pam, page = 1)

## Not run:
# Example 2: Functional covariates/cumulative coefficients
# function to generate one exposure profile, tz is a vector of time points
# at which TDC z was observed
rng_z = function(nz) {
  as.numeric(arima.sim(n = nz, list(ar = c(.8, -.6))))
}
# two different exposure times for two different exposures
tz1 <- 1:10
tz2 <- -5:5
# generate exposures and add to data set
df <- df %>%
  add_tdc(tz1, rng_z) %>%
  add_tdc(tz2, rng_z)
df

# define tri-variate function of time, exposure time and exposure z
ft <- function(t, tmax) {
```
\[ -1 \times \cos(t/t_{\max} \pi) \]

```r
fdnorm <- function(x) (dnorm(x,1.5,2)+1.5*dnorm(x,7.5,1))
wdnorm <- function(lag) 15*dnorm(lag,8,10)
wdnorm <- function(lag) 5*(dnorm(lag,4,6)+dnorm(lag,25,4))
f_xyz1 <- function(t, tz, z) {
  ft(t, tmax=10) * 0.8*fdnorm(z)* wpeak2(t - tz)
}
f_xyz2 <- function(t, tz, z) {
  wdnorm(t-tz) * z
}

# define lag-lead window function
ll_fun <- function(t, tz) {t >= tz}
ll_fun2 <- function(t, tz) {t - 2 >= tz}
# simulate data with cumulative effect
sim_df <- sim_pexp(
  formula = ~ -3.5 + f0(t) -0.5*x1 + sqrt(x2) |
        fcumu(t, tz1, z.tz1, f_xyz=f_xyz1, ll_fun=ll_fun) +
        fcumu(t, tz2, z.tz2, f_xyz=f_xyz2, ll_fun=ll_fun2),
  data = df,
  cut = 0:10)
```

## End(Not run)

**staph**

**Time until staphylococcus aureaus infection in children, with possible recurrence**

### Description

This dataset originates from the Drakenstein child health study. The data contains the following variables:

- **id** Randomly generated unique child ID
- **t.start** The time at which the child enters the risk set for the \( k \)-th event
- **t.stop** Time of \( k \)-th infection or censoring.
- **enum** Event number. Maximum of 6.
- **hiv**

### Usage

```
staph
```

### Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 374 rows and 6 columns.
### tidy_re

**Extract random effects in tidy data format.**

**Description**

Extract random effects in tidy data format.

**Usage**

```r
tidy_re(x, keep = c("fit", "main", "xlab", "ylab"), ...)n
```

**Arguments**

- `x`: a fitted `gam` object as produced by `gam()`.
- `keep`: A vector of variables to keep.
- `...`: Further arguments passed to `plot.gam`.

**See Also**

- `qqline`
tidy_smooth2d

Extract 2d smooth objects in tidy format.

Description

Extract 2d smooth objects in tidy format.

Usage

```r
tidy_smooth2d(
  x,
  keep = c("x", "y", "fit", "se", "xlab", "ylab", "main"),
  ci = FALSE,
  ...
)
```

Arguments

- `x`: a fitted `gam` object as produced by `gam()`.
- `keep`: A vector of variables to keep.
- `ci`: A logical value indicating whether confidence intervals should be calculated and returned. Defaults to `TRUE`.
- `...`: Further arguments passed to `plot.gam`

---

tumor

Stomach area tumor data

Description

Information on patients treated for a cancer disease located in the stomach area. The data set includes:

- `days`: Time from operation until death in days.
- `status`: Event indicator (0 = censored, 1 = death).
- `age`: The subject’s age.
- `sex`: The subject’s sex (male/female).
- `charlson_score`: Charlson comorbidity score, 1-6.
- `transfusion`: Has subject received transfusions (no/yes).
- `complications`: Did major complications occur during operation (no/yes).
- `metastases`: Did the tumor develop metastases? (no/yes).
- `resection`: Was the operation accompanied by a major resection (no/yes).
tumor

Usage
tumor

Format
An object of class tbl_df (inherits from tbl, data.frame) with 776 rows and 9 columns.
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