Package ‘dynamichazard’

October 11, 2021

Type Package

Title Dynamic Hazard Models using State Space Models

Version 1.0.1


License GPL-2

LazyData TRUE

LinkingTo Rcpp, RcppArmadillo

Imports parallel, Rcpp (>= 0.12.6), boot

Depends R (>= 3.5.0), stats, graphics, utils, survival

RoxygenNote 7.1.1

Suggests testthat, knitr, rmarkdown, timereg, captioner, biglm, httr, mgcv, shiny, formatR, R.rsp, speedglm, dichromat, colorspace, plyr, gsl, mvtnorm, nloptr (>= 1.2.0)

VignetteBuilder knitr, R.rsp

BugReports https://github.com/boennecd/dynamichazard/issues

SystemRequirements C++11

URL https://github.com/boennecd/dynamichazard

Encoding UTF-8

NeedsCompilation yes

Author Benjamin Christoffersen [cre, aut]  
<https://orcid.org/0000-0002-7182-1346>,  
Alan Miller [cph],  
Anthony Williams [cph],
Boost developers [cph],
R-core [cph]

Maintainer  Benjamin Christoffersen <boennecd@gmail.com>

Repository  CRAN

Date/Publication  2021-10-11 16:40:02 UTC

R topics documented:

ddFixed ............................................................... 3
ddhazard ............................................................. 4
ddhazard_app ......................................................... 6
ddhazard_boot ......................................................... 7
ddhazard_control ..................................................... 8
get_cloud_means ..................................................... 10
get_cloud_quantiles ............................................... 11
get_Q_0 ............................................................. 12
get_risk_obj ......................................................... 13
get_survival_case_weights_and_data .............................. 14
hatvalues.ddhazard ................................................ 16
hds ................................................................. 17
logLik.ddhazard .................................................... 18
logLik.PF_EM ......................................................... 19
PF_control .......................................................... 20
PF_EM .............................................................. 22
PF_forward_filter .................................................. 28
PF_get_score_n_hess ............................................... 32
plot.ddhazard ....................................................... 35
plot.ddhazard_space_errors ..................................... 36
plot.ddsurvcurve ................................................... 37
plot.PF_clouds ...................................................... 40
plot.PF_EM .......................................................... 41
predict.ddhazard .................................................... 42
print.ddhazard_boot ............................................... 44
print.summary.ddhazard .......................................... 44
residuals.ddhazard ................................................ 45
static_glm ........................................................ 46

Index  49
Auxiliary Functions for Fixed Effects

Description

Functions used in formula of `ddhazard` for time-invariant effects. `ddFixed_intercept` is only used for the intercept.

Usage

```r
ddFixed(object)

ddFixed_intercept(random_intercept = FALSE)
```

Arguments

- **object**: expression that would be used in formula. E.g. `x` or `poly(x, degree = 3)`.
- **random_intercept**: `TRUE` if a zero mean time-varying process should be included as an additional term. Only relevant in stationary models. See the `type` argument in `PF_EM`.

Value

Returns the passed object.

Examples

```r
# we can get a time-invariant effect of `x1` by
set.seed(1)
dat <- data.frame(stop = 1:20, event = rep(c(TRUE, FALSE), 10L), x1 = rnorm(20))

ddhazard(Surv(stop, event) ~ ddFixed(x1), dat,
          Q_0 = diag(1), by = 1, Q = diag(1))

# all of the calls below will yield the same result with a time-invariant # intercept:

# set.seed(1)
dat <- data.frame(stop = 1:20, event = rep(c(TRUE, FALSE), 10L), x1 = rnorm(20))

ddhazard(Surv(stop, event) ~ ddFixed_intercept() + x1, dat,                 
          Q_0 = diag(1), by = 1, Q = diag(1))

ddhazard(Surv(stop, event) ~ -1 + ddFixed_intercept() + x1, dat,          
          Q_0 = diag(1), by = 1, Q = diag(1))
```
ddhazard  

Fitting Dynamic Hazard Models

Description

Function to fit dynamic hazard models using state space models.

Usage

ddhazard(
  formula,  
data, 
  model = "logit", 
  by, 
  max_T, 
  id, 
  a_0, 
  Q_0, 
  Q = Q_0, 
  order = 1, 
  weights, 
  control = ddhazard_control(), 
  verbose = FALSE
)

Arguments

formula  
  coxph like formula with Surv(tstart,tstop,event) on the left hand site of ~.

data  
  data.frame or environment containing the outcome and covariates.

model  
  "logit", "cloglog", or "exponential" for respectively the logistic link function with discrete outcomes, the inverse cloglog link function with discrete outcomes, or for the continuous time model with piecewise constant exponentially distributed arrival times.

by  
  interval length of the bins in which parameters are fixed.

max_T  
  end of the last interval interval.

id  
  vector of ids for each row of the in the design matrix.

a_0  
  vector a_0 for the initial coefficient vector for the first iteration (optional). Default is estimates from static model (see static_glm).

Q_0  
  covariance matrix for the prior distribution.

Q  
  initial covariance matrix for the state equation.

order  
  order of the random walk.

weights  
  weights to use if e.g. a skewed sample is used.

control  
  list of control variables from ddhazard_control.

verbose  
  TRUE if you want status messages during execution.
**Details**

This function can be used to estimate survival models where the regression parameters follows a given order random walk. The order is specified by the `order` argument. 1. and 2. order random walks is implemented. The regression parameters are updated at time by, 2by, ..., max_T. See the vignette("ddhazard","dynamichazard") for details.

All filter methods needs a state covariance matrix $Q_0$ and state vector $a_0$. An estimate from a time-invariant model is used for $a_0$ if it is not supplied (the same model you would get from static_glm). A diagonal matrix with large entries is recommended for $Q_0$. What is large dependents on the data set and model. Further, a covariance matrix for the first iteration $Q$ is needed. The $Q$ and $a_0$ are estimated with an EM-algorithm.

The model is specified through the `model` argument. The discrete outcome models are where outcomes are binned into the intervals. Be aware that there can be "loss" of information due to binning if outcomes are not discrete to start with. It is key for these models that the `id` argument is provided if individuals in the data set have time-varying covariates. The the exponential model use a piecewise constant exponential distribution for the arrival times where there is no "loss" information due to binning. Though, one of the assumptions of the model is not satisfied if outcomes are only observed in discrete time intervals.

It is recommended to see the Shiny app demo for this function by calling `ddhazard_app()`.

**Value**

A list with class ddhazard. The list contains

- `formula` the passed formula.
- `call` the matched call.
- `state_vecs` 2D matrix with the estimated state vectors (regression parameters) in each bin.
- `state_vars` 3D array with smoothed variance estimates for each state vector.
- `lag_one_cov` 3D array with lagged correlation matrix for each for each change in the state vector. Only present when the model is logit and the method is EKF.
- `n_risk` the number of observations in each interval.
- `times` the interval borders.
- `risk_set` the object from `get_risk_obj` if saved.
- `data` the data argument if saved.
- `weights` weights used in estimation if saved.
- `id` ids used to match rows in data to individuals.
- `order` order of the random walk.
- `F_` matrix which map from one state vector to the next.
- `method` method used in the E-step.
- `est_Q_0` TRUE if $Q_0$ was estimated in the EM-algorithm.
- `family` Rcpp Module with C++ functions used for estimation given the `model` argument.
- `discrete_hazard_func` the hazard function corresponding to the `model` argument.
terms

the terms object used.

has_fixed_intercept

TRUE if the model has a time-invariant intercept.

xlev

a record of the levels of the factors used in fitting.

References


See Also

plot, residuals, predict, static_glm, ddhazard_app, ddhazard_boot

Examples

# example with first order model
library(dynamichazard)
fit <- ddhazard(
  Surv(time, status == 2) ~ log(bili), pbc, id = pbc$id, max_T = 3600,
  Q_0 = diag(1, 2), Q = diag(1e-4, 2), by = 50,
  control = ddhazard_control(method = "GMA"))
plot(fit)

# example with second order model
fit <- ddhazard(
  Surv(time, status == 2) ~ log(bili), pbc, id = pbc$id, max_T = 3600,
  Q_0 = diag(1, 4), Q = diag(1e-4, 2), by = 50,
  control = ddhazard_control(method = "GMA"),
  order = 2)
plot(fit)

ddhazard_app  ddhazard Demo

Description

ddhazard_app runs a shiny app with demonstration of models.

Usage

ddhazard_app(quietly = FALSE, ...)
Arguments

- **quietly** TRUE if no messages should be printed when the app is run.
- ... starting values for the shiny app.

Details

Runs a shiny app where you try different model specifications on simulated data.

Value

Returns the object from shiny::shinyApp.

Examples

```r
## Not run:
ddhazard::ddhazard_app()
ddhazard::ddhazard_app(seed = 1, more_options = TRUE)
## End(Not run)
```

```
---

## Bootstrap for ddhazard Object

Description

See the vignette vignette("Bootstrap_illustration", "dynamichazard"). The do_stratify_with_event may be useful when either cases or non-cases are very rare to ensure that the model estimation succeeds.

Usage

```r
ddhazard_boot(
  ddhazard_fit,
  strata,
  unique_id,
  R = 100,
  do_stratify_with_event = FALSE,
  do_sample_weights = FALSE,
  LRs = ddhazard_fit$control$LR * 2^(0:4),
  print_errors = FALSE
)
```
Arguments

- `ddhazard_fit` returned object from a `ddhazard` call.
- `strata` strata to sample within. These need to be on an individual by individual basis and not rows in the design matrix.
- `unique_id` unique ids where entries match entries of `strata`.
- `R` number of bootstrap estimates.
- `do_stratify_with_event` TRUE if sampling should be by strata of whether the individual has an event. An interaction factor will be made if `strata` is provided.
- `do_sample_weights` TRUE if weights should be sampled instead of individuals.
- `LRs` learning rates in decreasing order which will be used to estimate the model.
- `print_errors` TRUE if errors should be printed when estimations fails.

Value

An object like from the `boot` function.

See Also

`ddhazard`, `plot`

Examples

```r
library(dynamichazard)
set.seed(56219373)
fit <- ddhazard(
  Surv(time, status == 2) ~ log(bili), pbc, id = pbc$id, max_T = 3000,
  Q_0 = diag(1, 2), Q = diag(1e-4, 2), by = 100,
  control = ddhazard_control(method = "GMA"))
bt <- ddhazard_boot(fit, R = 999)
plot(fit, ddhazard_boot = bt, level = .9)
```

---

**ddhazard_control  Auxiliary for Controlling Dynamic Hazard Models**

**Description**

Auxiliary for additional settings with `ddhazard`. 
Usage

```
ddhazard_control(
  kappa = NULL,
  alpha = 1,
  beta = 0,
  NR_eps = NULL,
  LR = 1,
  n_max = 10^2,
  eps = 0.001,
  est_Q_0 = FALSE,
  method = "EKF",
  save_risk_set = TRUE,
  save_data = TRUE,
  eps_fixed_parems = 1e-04,
  fixed_parems_start = NULL,
  n_threads = getOption("ddhazard_max_threads"),
  denom_term = 1e-05,
  fixed_terms_method = "E_step",
  Q_0_term_for_fixed_E_step = NULL,
  permu = if (!is.null(method)) method == "SMA" else FALSE,
  posterior_version = "cholesky",
  GMA_max_rep = 25,
  GMA_NR_eps = 1e-04,
  est_a_0 = TRUE,
  ...
)
```

Arguments

- **kappa**: hyper parameter $\kappa$ in the unscented Kalman Filter.
- **alpha**: hyper parameter $\alpha$ in the unscented Kalman Filter.
- **beta**: hyper parameter $\beta$ in the unscented Kalman Filter.
- **NR_eps**: tolerance for the Extended Kalman filter. Default is NULL which means that no extra iteration is made in the correction step.
- **LR**: learning rate.
- **n_max**: maximum number of iteration in the EM-algorithm.
- **eps**: tolerance parameter for the EM-algorithm.
- **est_Q_0**: TRUE if you want the EM-algorithm to estimate $Q_0$. Default is FALSE.
- **method**: set to the method to use in the E-step. Either "EKF" for the Extended Kalman Filter, "UKF" for the Unscented Kalman Filter, "SMA" for the sequential posterior mode approximation method or "GMA" for the global mode approximation method. "EKF" is the default.
- **save_risk_set**: TRUE if you want to save the list from `get_risk_obj` used to estimate the model. It may be needed for later calls to e.g., `residuals`, `plot` and `logLike`.
- **save_data**: TRUE if you want to keep the data argument. It may be needed for later calls to e.g., `residuals`, `plot` and `logLike`. 

get_cloud_means

eps_fixed_parems
tolerance used in the M-step of the Fisher's scoring algorithm for the fixed effects

fixed_parems_start
starting value for fixed terms.

n_threads
maximum number of threads to use.

denom_term
term added to denominators in either the EKF or UKF.

fixed_terms_method
the method used to estimate the fixed effects. Either 'M_step' or 'E_step' for estimation in the M-step or E-step respectively.

Q_0_term_for_fixed_E_step
the diagonal value of the initial covariance matrix, Q_0, for the fixed effects if fixed effects are estimated in the E-step.

permu
TRUE if the risk sets should be permuted before computation. This is TRUE by default for posterior mode approximation method and FALSE for all other methods.

posterior_version
the implementation version of the posterior approximation method. Either "woodbury" or "cholesky".

GMA_max_rep
maximum number of iterations in the correction step if method = 'GMA'.

GMA_NR_eps
tolerance for the convergence criteria for the relative change in the norm of the coefficients in the correction step if method = 'GMA'.

est_a_0
FALSE if the starting value of the state model should be fixed.

...
additional undocumented arguments.

Value
A list with components named as the arguments.

See Also
ddhazard

---

get_cloud_means  Compute Mean Estimates from Particle Cloud

Description
Computes the estimated means from a particle cloud.
### get_cloud_quantiles

**Usage**

```r
get_cloud_quantiles(object, ...)  
## S3 method for class 'PF_EM'
get_cloud_quantiles(object, ...)

## S3 method for class 'PF_clouds'
get_cloud_quantiles(
  object,
  cov_index = NULL,
  qlvls = c(0.05, 0.5, 0.95),
  type = c("smoothed_clouds", "forward_clouds", "backward_clouds"),
  ...
)
```

**Arguments**

- `object`: object with class `PF_EM` or `PF_clouds`.
- `...`: named arguments to pass to the `PF_clouds` method.
- `cov_index`: integer vector with indices of the random effect to include.
- `type`: character with the type of cloud to compute quantiles for.

**Value**

A matrix which rows are time indices and columns are random effect indices.

---

### Description

Computes the estimated quantiles from a particle cloud.

**Usage**

```r
get_cloud_quantiles(object, ...)  
## S3 method for class 'PF_EM'
get_cloud_quantiles(object, ...)

## S3 method for class 'PF_clouds'
get_cloud_quantiles(
  object,
  cov_index = NULL,
  qlvls = c(0.05, 0.5, 0.95),
  type = c("smoothed_clouds", "forward_clouds", "backward_clouds"),
  ...
)
```
get_Q_0

Compute Time-Invariant Covariance Matrix

Description

Computes the invariant covariance matrix for a vector autoregression model.

Usage

get_Q_0(Qmat, Fmat)

Arguments

Qmat                  covariance matrix in transition density.
Fmat                  coefficients in transition density.

Value

The invariant covariance matrix.

Examples

Fmat <- matrix(c(.8, .4, .1, .5), 2, 2)
Qmat <- matrix(c( 1, .5, .5, 2), 2)

x1 <- get_Q_0(Qmat = Qmat, Fmat = Fmat)
x2 <- Qmat
for(i in 1:101)
  x2 <- tcrossprod(Fmat %*% x2, Fmat) + Qmat
stopifnot(isTRUE(all.equal(x1, x2)))
get_risk_obj

Risk Set on an Equidistant Distant Grid

Description

Get the risk set at each bin over an equidistant distant grid.

Usage

get_risk_obj(
  Y,
  by,
  max_T,
  id,
  is_for_discrete_model = TRUE,
  n_threads = 1,
  min_chunk = 5000
)

Arguments

Y vector of outcome variable returned from Surv.
by length of each bin.
max_T last observed time.
id vector with ids where entries match with outcomes Y.

is_for_discrete_model
TRUE if the model outcome is discrete. For example, a logit model is discrete whereas what is is referred to as the exponential model in this package is a dynamic model.

n_threads set to a value greater than one to use mclapply to find the risk object.

min_chunk minimum chunk size of ids to use when parallel version is used.

Value

a list with the following elements

risk_sets list of lists with one for each bin. Each of the sub lists have indices that corresponds to the entries of Y that are at risk in the bin.

min_start start time of the first bin.
I_len length of each bin.

d number of bins.

is_event_in indices for which bin an observation Y is an event. -1 if the individual does not die in any of the bins.

is_for_discrete_model value of is_for_discrete_model argument.
Examples

```r
# small toy example with time-varying covariates
dat <- data.frame(
id = c(1, 1, 2, 2),
tstart = c(0, 4, 0, 2),
tstop = c(4, 6, 2, 4),
event = c(0, 1, 0, 0))

with(dat, get_risk_obj(Surv(tstart, tstop, event), by = 1, max_T = 6, id = id))
```

get_survival_case_weights_and_data

*Get data.frame for Discrete Time Survival Models*

Description

Function used to get `data.frame` with weights for a static fit for survivals.

Usage

```r
get_survival_case_weights_and_data(
  formula,
  data,
  by,
  max_T,
  id,
  init_weights,
  risk_obj,
  use_weights = TRUE,
  is_for_discrete_model = TRUE,
  c_outcome = "y",
  c_weights = "weights",
  c_end_t = "t"
)
```

Arguments

- **formula**: `coxph` like formula with `Surv(tstart,tstop,event)` on the left hand site of `~`.
- **data**: `data.frame` or environment containing the outcome and covariates.
- **by**: interval length of the bins in which parameters are fixed.
- **max_T**: end of the last interval interval.
- **id**: vector of ids for each row of the in the design matrix.
- **init_weights**: weights for the rows in `data`. Useful e.g., with skewed sampling.
get_survival_case_weights_and_data

risk_obj          a pre-computed result from a get_risk_obj. Will be used to skip some computations.
use_weights       TRUE if weights should be used. See details.
is_for_discrete_model
                  TRUE if the model is for a discrete hazard model is used like the logistic model.
c_outcome, c_weights, c_end_t
                  alternative names to use for the added columns described in the return section.
                  Useful if you already have a column named Y, t or weights.

Details

This function is used to get the data.frame for e.g. a glm fit that is comparable to a ddhazard fit in the sense that it is a static version. For example, say that we bin our time periods into (0, 1], (1, 2] and (2, 3]. Next, consider an individual who dies at time 2.5. He should be a control in the first two bins and should be a case in the last bin. Thus the rows in the final data frame for this individual is c(Y = 1, ..., weights = 1) and c(Y = 0, ..., weights = 2) where Y is the outcome, ... is the covariates and weights is the weights for the regression. Consider another individual who does not die and we observe him for all three periods. Thus, he will yield one row with c(Y = 0, ..., weights = 3).

This function use similar logic as the ddhazard for individuals with time varying covariates (see the vignette vignette("ddhazard","dynamichazard") for details).

If use_weights = FALSE then the two previously mentioned individuals will yield three rows each. The first individual will have c(Y = 0, t = 1, ..., weights = 1), c(Y = 0, t = 2, ..., weights = 1), c(Y = 1, t = 3, ..., weights = 1) while the latter will have three rows c(Y = 0, t = 1, ..., weights = 1), c(Y = 0, t = 2, ..., weights = 1), c(Y = 0, t = 3, ..., weights = 1). This kind of data frame is useful if you want to make a fit with e.g. gam function in the mgcv package as described en Tutz et. al (2016).

Value

Returns a data.frame where the following is added (column names will differ if you specified them): column Y for the binary outcome, column weights for weights of each row and additional rows if applicable. A column t is added for the stop time of the bin if use_weights = FALSE. An element Y with the used Surv object is added if is_for_discrete_model = FALSE.

References


See Also

ddhazard, static_glm

Examples

library(dynamichazard)
# small toy example with time-varying covariates
dat <- data.frame(
  id = c( 1, 1, 2, 2),
  tstart = c( 0, 4, 0, 2),
  tstop = c( 4, 6, 2, 6),
  event = c( 0, 1, 0, 0),
  x1 = c(1.09, 1.29, 0, -1.16))

get_survival_case_weights_and_data(
  Surv(tstart, tstop, event) ~ x1, dat, by = 1, id = dat$id)$X
get_survival_case_weights_and_data(
  Surv(tstart, tstop, event) ~ x1, dat, by = 1, id = dat$id, 
  use_weights = FALSE)$X

hatvalues.ddhazard  

---

hatvalues.ddhazard  

**Hat Values for ddhazard Object**

### Description

Computes hat-"like" values from usual L2 penalized binary regression.

### Usage

```r
## S3 method for class 'ddhazard'
hatvalues(model, ...)
```

### Arguments

- `model`  
  a fit from `ddhazard`.

- `...`  
  not used.

### Details

Computes hat-"like" values in each interval for each individual at risk in the interval. See the vignette("ddhazard", "dynamichazard") vignette for details.

### Value

A list of matrices. Each matrix has three columns: the hat values, the row number of the original data point and the id the row belongs to.

### See Also

`ddhazard`
Examples

```r
library(dynamichazard)
fit <- ddhazard(
  Surv(time, status == 2) ~ log(bili), pbc, id = pbc$id, max_T = 3000,
  Q_0 = diag(1, 2), Q = diag(1e-4, 2), by = 100,
  control = ddhazard_control(method = "GMA"))

hvs <- hatvalues(fit)
head(hvs[[1]])
head(hvs[[2]])
```

**hds**

### Hard Drive Failures

**Description**

A data set containing hard drive failures data from Backblaze in the start-stop format used in the survival package.

**Usage**

hds

**Format**

A data.frame with the following columns:

- **serial_number**  Serial number for the hard disk which the row belongs to.
- **model** hard disk model.
- **manufacturer** manufacturer of the hard disk model.
- **tstart,tstop** start and stop times on the SMART 9 attribute scale.
- **fails** 1 if the hard disk fails at tstop.
- **size_tb** hard disk size in terabytes.
- **smart_x** the raw SMART attribute x value. E.g., smart_12 is the power cycle count.
- **smart_x_bin** 1 if the SMART attribute x value is non-zero.
- **..._cumsum** cumulative sum of the prefix . . .
- **n_fails** number of failures in the original data. Hard disk should only fail once but this is not the case in the raw data.
- **n_records** number of records in the original source.
- **min_date,max_date** first and last date in the original source.
- **min_hours,max_hours** smallest and largest value of the SMART 9 attribute in the original source.
Details

Details about the SMART attributes can be found on https://en.wikipedia.org/wiki/S.M.A.R.T. As stated in the original source

"Reported stats for the same SMART stat can vary in meaning based on the drive manufacturer and the drive model. Make sure you are comparing apples-to-apples as drive manufacturers don’t generally disclose what their specific numbers mean."

There are some notes on https://en.wikipedia.org/wiki/S.M.A.R.T. regarding which attributes that have vendor specific raw value. Further,

"The values in the files are the values reported by the drives. Sometimes, those values are out of whack. For example, in a few cases the RAW value of SMART 9 (Drive life in hours) reported a value that would make a drive 10+ years old, which was not possible. In other words, it’s a good idea to have bounds checks when you process the data."

See this github page for the processing steps https://github.com/boennecd/backblaze_survival_analysis_prep.

Source

Raw data from https://www.backblaze.com/b2/hard-drive-test-data.html. Data have been processed to get a start-stop data frame format.

---

**logLik.ddhazard**

*Log Likelihood of Mean Path of ddhazard Object*

Description

Computes the log likelihood of (a potentially new) data set given the estimated:

\[
E_\theta(\alpha_1|y_{1:d}), E_\theta(\alpha_2|y_{1:d}), \ldots, E_\theta(\alpha_d|y_{1:d})
\]

of the ddhazard object. Note that this is not the log likelihood of the observed data given the outcome.

Usage

```r
## S3 method for class 'ddhazard'
logLik(object, data = NULL, id, ...)
```

Arguments

- `object` an object of class ddhazard.
- `data` new data to evaluate the likelihood for.
- `id` the individual identifiers as in ddhazard.
- `...` unused.
Value

Returns an object of class logLik. See logLik.

Examples

```r
library(dynamichazard)
fit <- ddhazard(
  Surv(time, status == 2) ~ log(bili), pbc, id = pbc$id, max_T = 3600,
  Q_0 = diag(1, 2), Q = diag(1e-4, 2), by = 50,
  control = dhdhazard_control(method = "GMA"))
logLik(fit)
```

Description

Computes the approximate log-likelihood using the forward filter clouds. See the vignette("Particle_filtering","dynamichazard") for details.

Usage

```r
## S3 method for class 'PF_EM'
logLik(object, ...)

## S3 method for class 'PF_clouds'
logLik(object, df = NA_real_, nobs = NA_integer_, ...)
```

Arguments

- `object` an object of class PF_clouds or PF_EM.
- `...` unused.
- `df` degrees of freedom used in the model.
- `nobs` integer with number of individuals used to estimate the model.

Value

The approximate log-likelihood value given the observed data and set of parameter used when simulating the clouds. An attribute "P(y_t|y_{1:(t-1)})" has the $P(y_t|y_{1:(t-1)})$ terms.
**PF_control**

**Auxiliary for Controlling Particle Fitting**

**Description**

 Auxiliary for additional settings with **PF_EM**.

**Usage**

```r
PF_control(
    N_fw_n_bw = NULL,
    N_smooth = NULL,
    N_first = NULL,
    eps = 0.01,
    forward_backward_ESS_threshold = NULL,
    method = "AUX_normal_approx_w_cloud_mean",
    n_max = 25,
    n_threads = getOption("ddhazard_max_threads"),
    smoother = "Fearnhead_0_N",
    Q_tilde = NULL,
    est_a_0 = TRUE,
    N_smooth_final = N_smooth,
    nu = 0L,
    covar_fac = -1,
    ftol_rel = 1e-08,
    averaging_start = -1L,
    fix_seed = TRUE
)
```

**Arguments**

- `N_fw_n_bw` number of particles to use in forward and backward filter.
- `N_smooth` number of particles to use in particle smoother.
- `N_first` number of particles to use at time 0 and time $d + 1$.
- `eps` convergence threshold in EM method.
- `forward_backward_ESS_threshold` required effective sample size to not re-sample in the particle filters.
- `method` method for forward, backward and smoothing filter.
- `n_max` maximum number of iterations of the EM algorithm.
- `n_threads` maximum number of threads to use in the computations.
- `smoother` smoother to use.
- `Q_tilde` covariance matrix of additional error term to add to the proposal distributions. NULL implies no additional error term.
est_a_0: FALSE if the starting value of the state model should be fixed. Does not apply for type = "VAR".

N_smooth_final: number of particles to sample with replacement from the smoothed particle cloud with N_smooth particles using the particles' weights. This causes additional sampling error but decreases the computation time in the M-step.

nu: integer with degrees of freedom to use in the (multivariate) t-distribution used as the proposal distribution. A (multivariate) normal distribution is used if it is zero.

covar_fac: factor to scale the covariance matrix with. Ignored if the values is less than or equal to zero.

ftol_rel: relative convergence tolerance of the mode objective in mode approximation.

averaging_start: index to start averaging. Values less then or equal to zero yields no averaging.

fix_seed: TRUE if the same seed should be used. E.g., in PF_EM the same seed will be used in each iteration of the E-step of the MCEM algorithm.

Details

The method argument can take the following values:

- bootstrap_filter for a bootstrap filter.
- PF_normal_approx_w_cloud_mean for a particle filter where a Gaussian approximation is used using a Taylor approximation made at the mean for the current particle given the mean of the parent particles and/or mean of the child particles.
- AUX_normal_approx_w_cloud_mean for an auxiliary particle filter version of PF_normal_approx_w_cloud_mean.
- PF_normal_approx_w_particles for a filter similar to PF_normal_approx_w_cloud_mean and differs by making a Taylor approximation at a mean given each sampled parent and/or child particle.
- AUX_normal_approx_w_particles for an auxiliary particle filter version of PF_normal_approx_w_particles.

The smoother argument can take the following values:

- Fearnhead_O_N for the smoother in Fearnhead, Wyncoll, and Tawn (2010).
- Brier_O_N_square for the smoother in Briers, Doucet, and Maskell (2010).

Value

A list with components named as the arguments.

References


**See Also**

PF_EM

---

**PF_EM**

*EM Estimation with Particle Filters and Smoothers*

**Description**

Method to estimate the hyper parameters with an EM algorithm.

**Usage**

```r
PF_EM(
  formula,
  data,
  model = "logit",
  by,
  max_T,
  id,
  a_0,
  Q_0,
  Q,
  order = 1,
  control = PF_control(...),
  trace = 0,
  seed = NULL,
  type = "RW",
  fixed = NULL,
  random = NULL,
  Fmat,
  fixed_effects,
  G,
  theta,
  J,
  K,
  psi,
  phi,
  ...
)
```
Arguments

- **formula**: coxph like formula with `Surv(tstart,tstop,event)` on the left hand site of `~`.
- **data**: data.frame or environment containing the outcome and covariates.
- **model**: either 'logit' for binary outcomes with the logistic link function, 'cloglog' for binary outcomes with the inverse cloglog link function, or 'exponential' for piecewise constant exponential distributed arrival times.
- **by**: interval length of the bins in which parameters are fixed.
- **max_T**: end of the last interval interval.
- **id**: vector of ids for each row of the in the design matrix.
- **a_0**: vector $a_0$ for the initial coefficient vector for the first iteration (optional). Default is estimates from static model (see `static_glm`).
- **Q_0**: covariance matrix for the prior distribution.
- **Q**: initial covariance matrix for the state equation.
- **order**: order of the random walk.
- **control**: see `PF_control`.
- **trace**: argument to get progress information. Zero will yield no info and larger integer values will yield incrementally more information.
- **seed**: seed to set at the start of every EM iteration. See `set.seed`.
- **type**: type of state model. Either "RW" for a Random Walk or "VAR" for Vector AutoRegression.
- **fixed**: two-sided formula to be used with random instead of formula. It is of the form `Surv(tstart,tstop,event) ~ x` or `Surv(tstart,tstop,event) ~ -1` for no fixed effects.
- **random**: one-sided formula to be used with fixed instead of formula. It is of the form `~ z`.
- **Fmat**: starting value for $F$ when type = "VAR". See 'Details' in `PF_EM`.
- **fixed_effects**: starting values for fixed effects if any. See `ddFixed`.
- **G, theta, J, K, psi, phi**: parameters for a restricted type = "VAR" model. See the vignette mentioned in 'Details' of `PF_EM` and the examples linked to in 'See Also'.
- **...**: optional way to pass arguments to `control`.

Details

Estimates a state model of the form

$$\alpha_t = F \alpha_t + R \epsilon_t, \quad \epsilon_t \sim N(0, Q)$$

where $F \in \mathbb{R}^{p \times p}$ has full rank, $\alpha_t \in \mathbb{R}^p$, $\epsilon_t \in \mathbb{R}^r$, $r \leq p$, and $R = (e_1, e_2, \ldots, e_r)$ where $e_k$ is column from the $p$ dimensional identity matrix and $l_1 < l_2 < \ldots < l_r$. The time zero state is drawn from
\[ \alpha_0 \sim N(a_0, Q_0) \]

with \( Q_0 \in \mathbb{R}^{p \times p} \). The latent states, \( \alpha_t \), are related to the output through the linear predictors

\[ \eta_{it} = X_t (R^+ \alpha_t) + Z_t \beta \]

where \( X_t \in \mathbb{R}^{n_t \times r} \) and \( Z_t \mathbb{R}^{n_t \times c} \) are design matrices and the outcome for an individual \( i \) at time \( t \) is distributed according to an exponential family member given \( \eta_{it} \). \( \beta \) are constant coefficients.

See vignette("Particle_filtering","dynamichazard") for details.

Value

An object of class `PF_EM`.

Warning

The function is still under development so the output and API may change.

See Also

`PF_forward_filter` to get a more precise estimate of the final log-likelihood.

See the examples at https://github.com/boennecd/dynamichazard/tree/master/examples.

Examples

```r
####
# Fit model with lung data set from survival
# Warning: long-ish computation time

library(dynamichazard)
.lung <- lung[!is.na(lung$ph.ecog),]
# standardize
.lung$age <- scale(.lung$age)

# fit
set.seed(43588155)
pf_fit <- PF_EM(
  Surv(time, status == 2) ~ ddFixed(ph.ecog) + age,
  data = .lung, by = 50, id = 1:nrow(.lung),
  Q_0 = diag(1, 2), Q = diag(.5^2, 2),
  max_T = 800,
  control = PF_control(
    # these number should be larger! Small for CRAN checks
    N_fw_n_bw = 100L, N_first = 250L, N_smooth = 100L,
    n_max = 50, eps = .001, Q_tilde = diag(.2^2, 2), est_a_0 = FALSE,
    n_threads = 2))
```
# Plot state vector estimates
plot(pf_fit, cov_index = 1)
plot(pf_fit, cov_index = 2)

# Plot log-likelihood
plot(pf_fit$log_likes)

#######
# example with fixed intercept
# prepare data

temp <- subset(pbc, id <= 312, select=c(id, sex, time, status, edema, age))
pbc2 <- tmerge(temp, temp, id=id, death = event(time, status))
pbc2 <- tmerge(pbc2, pbcseq, id=id, albumin = tdc(day, albumin),
                protime = tdc(day, protime), bili = tdc(day, bili))
pbc2 <- pbc2[, c("id", "tstart", "tstop", "death", "sex", "edema",
                      "age", "albumin", "protime", "bili")]
pbc2 <- within(pbc2, {
    log_albumin <- log(albumin)
    log_protime <- log(protime)
    log_bili <- log(bili)
})

# standardize
for(c. in c("age", "log_albumin", "log_protime", "log_bili"))
    pbc2[[c.]] <- drop(scale(pbc2[[c.]]))

# fit model with extended Kalman filter
ddfit <- ddhazard(
    Surv(tstart, tstop, death == 2) ~ ddFixed_intercept() + ddFixed(age) +
    ddFixed(edema) + ddFixed(log_albumin) + ddFixed(log_protime) + log_bili,
    pbc2, Q_0 = 100, Q = 1e-2, by = 100, id = pbc2$id,
    model = "exponential", max_T = 3600,
    control = ddhazard_control(eps = 1e-5, NR_eps = 1e-4, n_max = 1e4))
summary(ddfit)

# fit model with particle filter
set.seed(88235076)
pf_fit <- PF_EM(
    Surv(tstart, tstop, death == 2) ~ ddFixed_intercept() + ddFixed(age) +
    ddFixed(edema) + ddFixed(log_albumin) + ddFixed(log_protime) + log_bili,
    pbc2, Q_0 = 2^2, Q = ddfit$Q * 100, # use estimate from before
    by = 100, id = pbc2$id,
    model = "exponential", max_T = 3600,
    control = PF_control(
        # these number should be larger! Small for CRAN checks
        N_fw_n_bw = 100, N_smooth = 250, N_first = 100, eps = 1e-3,
        method = "AUX_normal_approx_w_cloud_mean", est_a_0 = FALSE,
        Q_tilde = as.matrix(.1^2),
        n_max = 25, # just take a few iterations as an example
        n_threads = 2))
# compare results
plot(ddfit)
plot(pf_fit)
sqrt(ddfit$Q * 100)
sqrt(pf_fit$Q)
rbind(ddfit$fixed_effects, pf_fit$fixed_effects)

#####
# simulation example with 'random' and 'fixed' argument and a restricted # model

# g groups with k individuals in each
g <- 3L
k <- 400L

# matrices for state equation
p <- g + 1L
G <- matrix(0., p^2, 2L)
for(i in 1:p)
  G[i + (i - 1) * p, 1L + (i == p)] <- 1L

theta <- c(.9, .8)
# coefficients in transition density
(F. <- matrix(as.vector(G %*% theta), 4L, 4L))

J <- matrix(0., ncol = 2L, nrow = p)
J[-p, 1L] <- J[p, 2L] <- 1
psi <- c(log(c(.3, .1)))

K <- matrix(0., p * (p - 1L) / 2L, 2L)
j <- 0L
for(i in (p - 1L):1L){
  j <- j + i
  K[j, 2L] <- 1
}
K[K[, 2L] < 1, 1L] <- 1
phi <- log(-(c(.8, .3) + 1) / (c(.8, .3) - 1))
V <- diag(exp(drop(J %*% psi)))
C <- diag(1, ncol(V))
C[lower.tri(C)] <- 2/(1 + exp(-drop(K %*% phi))) - 1
C[upper.tri(C)] <- t(C)[upper.tri(C)]
(Q <- V %*% C %*% V)  # covariance matrix in transition density
cov2cor(Q)

Q.0 <- get.Q.0(Q, F.)  # time-invariant covariance matrix
beta <- c(rep(-6, g), 0)  # all groups have the same long run mean intercept

# simulate state variables
set.seed(56219373)
n_periods <- 300L
alphas <- matrix(nrow = n_periods + 1L, ncol = p)
alphas[1L, ] <- rnorm(p) %*% chol(Q_0)
for(i in 1:n_periods + 1L)
  alphas[i, ] <- F. %*% alphas[i - 1L, ] + drop(rnorm(p) %*% chol(Q))
alphas <- t(t(alphas) + beta)

# plot state variables
matplot(alphas, type = "l", lty = 1)

# simulate individuals' outcome
n_obs <- g * k
df <- lapply(1:n_obs, function(i){
  # find the group
  grp <- (i - 1L) %/% (n_obs / g) + 1L

  # left-censoring
  tstart <- max(0L, sample.int((n_periods - 1L) * 2L, 1L) - n_periods + 1L)

  # covariates
  x <- c(1, rnorm(1))

  # outcome (stop time and event indicator)
  osa <- NULL
  oso <- NULL
  osx <- NULL
  y <- FALSE
  for(tstop in (tstart + 1L):n_periods){
    sigmoid <- 1 / (1 + exp(- drop(x %*% alphas[tstop + 1L, c(grp, p)])))
    if(sigmoid > runif(1)){
      y <- TRUE
      break
    }
    if(.01 > runif(1L) && tstop < n_periods){
      # sample new covariate
      osa <- c(osa, tstart)
      tstart <- tstop
      oso <- c(oso, tstop)
      osx <- c(osx, x[2])
      x[2] <- rnorm(1)
    }
  }
  cbind(
    tstart = c(osa, tstart), tstop = c(oso, tstop),
    x = c(osx, x[2]), y = c(rep(FALSE, length(osa)), y), grp = grp,
    id = i)
})
df <- data.frame(do.call(rbind, df))
df$grp <- factor(df$grp)

# fit model. Start with "cheap" iterations
fit <- PF_EM(
  fixed = Surv(tstart, tstop, y) ~ x, random = ~ grp + x - 1,
data = df, model = "logit", by = 1L, max_T = max(df$tstop),
Q_0 = diag(1.5^2, p), id = df$id, type = "VAR",
G = G, theta = c(.5, .5), J = J, psi = log(c(.1, .1)),
K = K, phi = log(-(c(.4, 0) + 1) / (c(.4, 0) - 1)),
control = PF_control(
    N_fw_n_bw = 100L, N_smooth = 100L, N_first = 500L,
    method = "AUX_normal_approx_w_cloud_mean",
    nu = 5L, # sample from multivariate t-distribution
    n_max = 60L, averaging_start = 50L,
    smoother = "Fearnhead_0_N", eps = 1e-4, covar_fac = 1.2,
    n_threads = 2L # depends on your cpu(s)
),
trace = 1L)
plot(fit$log_likes) # log-likelihood approximation at each iterations

# you can take more iterations by uncommenting the following
# cl <- fit$call
# ctrl <- cl[["control"]]
# ctrl[c("N_fw_n_bw", "N_smooth", "N_first", "n_max",
#     "averaging_start")] <- list(500L, 2000L, 5000L, 200L, 30L)
# cl[["control"]]] <- ctrl
# cl[c("phi", "psi", "theta")]] <- list(fit$phi, fit$psi, fit$theta)
# fit_extra <- eval(cl)
plot(fit$log_likes) # log-likelihood approximation at each iteration

# check estimates
sqrt(diag(fit$Q))
sqrt(diag(Q))
cov2cor(fit$Q)
cov2cor(Q)
fit$F.

# plot predicted state variables
for(i in 1:p){
    plot(fit, cov_index = i)
    abline(h = 0, lty = 2)
    lines(1:nrow(alphas) - 1, alphas[, i] - beta[i], lty = 3)
}

---

PF_forward_filter

Forward Particle Filter

**Description**

Functions to only use the forward particle filter. Useful for log-likelihood evaluation though there is an $O(d^2)$ variance of the estimate where $d$ is the number of time periods. The number of particles specified in the control argument has no effect.
The function does not alter the `.Random.seed` to make sure the same `rng.kind` is kept after the call. See `PF_EM` for model details.

Usage

```
PF_forward_filter(x, N_fw, N_first, ...)  
## S3 method for class 'PF_EM'
PF_forward_filter(x, N_fw, N_first, seed, ...)
## S3 method for class 'formula'
PF_forward_filter(
  x,  
  N_fw,  
  N_first,  
  data,  
  model = "logit",  
  by,  
  max_T,  
  id,  
  a_0,  
  Q_0,  
  Q,  
  fixed_effects,  
  control = PF_control(...),  
  seed = NULL,  
  trace = 0,  
  G,  
  theta,  
  J,  
  K,  
  psi,  
  phi,  
  type = "RW",  
  Fmat,  
  ...
)
## S3 method for class 'data.frame'
PF_forward_filter(
  x,  
  N_fw,  
  N_first,  
  formula,  
  model = "logit",  
  by,  
  max_T,  
  id,  
  a_0,  
  ...
PF_forward_filter

Q_0,
Q,
fixed_effects,
control = PF_control(...),
seed = NULL,
trace = 0,
fixed = NULL,
random = NULL,
G,
theta,
J,
K,
psi,
phi,
type = "RW",
Fmat,
order = 1,
...

Arguments

x an PF_EM or formula object.
N_fw number of particles.
N_first number of time zero particles to draw.
... optional way to pass arguments to control.
seed .GlobalEnv$.Random.seed to set. Not seed as in set.seed function. Can be used with the .Random.seed returned by PF_EM.
data data.frame or environment containing the outcome and covariates.
model either 'logit' for binary outcomes with the logistic link function, 'cloglog' for binary outcomes with the inverse cloglog link function, or 'exponential' for piecewise constant exponential distributed arrival times.
by interval length of the bins in which parameters are fixed.
max_T end of the last interval interval.
id vector of ids for each row of the in the design matrix.
a_0 vector a_0 for the initial coefficient vector for the first iteration (optional). Default is estimates from static model (see static_glm).
Q_0 covariance matrix for the prior distribution.
Q initial covariance matrix for the state equation.
fixed_effects values for the fixed parameters.
control see PF_control.
trace argument to get progress information. Zero will yield no info and larger integer values will yield incrementally more information.
parameters for a restricted type = "VAR" model. See the vignette mentioned in 'Details' of \texttt{PF_EM} and the examples linked to in 'See Also'.

type \hspace{1cm} \text{type of state model. Either "RW" for a [R]andom [W]alk or "VAR" for [V]ector [A]uto[R]egression.}

Fmat \hspace{1cm} \text{starting value for } F \text{ when type = "VAR". See 'Details' in } \texttt{PF_EM}. 

formula \hspace{1cm} \text{\texttt{coxph} like formula with } \texttt{Surv(tstart,tstop,event)} \text{ on the left hand site of } \sim. 

fixed \hspace{1cm} \text{two-sided formula to be used with random instead of formula. It is of the form } 
\texttt{Surv(tstart,tstop,event)} \sim x \text{ or } \texttt{Surv(tstart,tstop,event)} \sim -1 \text{ for no fixed effects.} 

random \hspace{1cm} \text{one-sided formula to be used with fixed instead of formula. It is of the form } 
\sim z. 

order \hspace{1cm} \text{order of the random walk.} 

\textbf{Value} 

An object of class \texttt{PF_clouds}. 

\textbf{Methods (by class)} 

- \texttt{PF_EM}: Forward particle filter using the estimates of an \texttt{PF_EM} call. 
- \texttt{formula}: Forward particle filter with formula input. 
- \texttt{data.frame}: Forward particle filter with \texttt{data.frame} data input as \texttt{x} instead of \texttt{data}. Can be used with \texttt{fixed} and \texttt{random} argument. 

\textbf{Warning} 

The function is still under development so the output and API may change. 

\textbf{Examples} 

is_censored <- c( 
6, 27, 34, 36, 42, 46, 48:51, 51 + c(15, 30:28, 33, 35:37, 39, 40, 42:45))
head_neck_cancer <- data.frame( 
id = 1:96, 
stop = c( 
1, 2, 2, rep(3, 6), 4, 4, rep(5, 8), 
rep(6, 7), 7, 8, 8, 9, 9, 10, 10, 10, 11, 14, 14, 14, 15, 18, 18, 20, 
20, 37, 37, 38, 41, 45, 47, 47, 
2, 2, 3, rep(4, 4), rep(5, 5), rep(6, 5), 
7, 7, 7, 9, 10, 11, 12, 15, 16, 18, 18, 18, 21, 
21, 24, 25, 27, 36, 41, 44, 52, 54, 59, 59, 63, 67, 71, 76), 
event = !(1:96 %in% is_censored),
group = factor(c(rep(1, 45 + 6), rep(2, 45))))
# fit model
set.seed(61364778)
ctrl <- PF_control(N_fw_n_bw = 500, N_smooth = 2500, N_first = 2000,
n_max = 1, # set to one as an example
n_threads = 2,
eps = .001, Q_tilde = as.matrix(.3^2), est_a_0 = FALSE)
pf_fit <- suppressWarnings(PF_EM(survival::Surv(stop, event) ~ ddFixed(group),
data = head_neck_cancer, by = 1, Q_0 = 1, Q = 0.1^2, control = ctrl,
max_T = 30))

# the log-likelihood in the final iteration
(end_log_like <- logLik(pf_fit))

# gives the same
fw_ps <- PF_forward_filter(survival::Surv(stop, event) ~ ddFixed(group), N_fw = 500, N_first = 2000,
data = head_neck_cancer, by = 1, Q_0 = 1, Q = 0.1^2,
a_0 = pf_fit$a_0, fixed_effects = -0.5370051,
control = ctrl, max_T = 30, seed = pf_fit$seed)
all.equal(c(end_log_like), c(logLik(fw_ps)))

# will differ since we use different number of particles
fw_ps <- PF_forward_filter(survival::Surv(stop, event) ~ ddFixed(group), N_fw = 1000, N_first = 3000,
data = head_neck_cancer, by = 1, Q_0 = 1, Q = 0.1^2,
a_0 = pf_fit$a_0, fixed_effects = -0.5370051,
control = ctrl, max_T = 30, seed = pf_fit$seed)
all.equal(c(end_log_like), c(logLik(fw_ps)))

# will differ since we use the final estimates
fw_ps <- PF_forward_filter(pf_fit, N_fw = 500, N_first = 2000)
all.equal(c(end_log_like), c(logLik(fw_ps)))

---

**PF_get_score_n_hess**  
Approximate Observed Information Matrix and Score Vector

**Description**

Returns a list of functions to approximate the observed information matrix and score vector.

**Usage**

`PF_get_score_n_hess(object, debug = FALSE, use_0_n_sq = FALSE)`
Arguments

object
object of class PF_EM.

debug
TRUE if debug information should be printed to the console.

use_0_n_sq
TRUE if the method from Poyiadjis et al. (2011) should be used.

Details

The score vector and observed information matrix are computed with the (forward) particle filter. This comes at an $O(d^2)$ variance where $d$ is the number of periods. Thus, the approximation may be poor for long series. The score vector can be used to perform stochastic gradient descent.

If use_0_n_sq is TRUE then the method in Poyiadjis et al. (2011) is used. This may only have a variance which is linear in the number of time periods. However, the present implementation is $O(N^2)$ where $N$ is the number of particles. The method uses a particle filter as in Section 3.1 of Lin et al. (2005). There is no need to call run_particle_filter unless one wants a new approximation of the log-likelihood as a separate filter is run with get_get_score_n_hess when use_0_n_sq is TRUE.

Value

A list with the following functions as elements

run_particle_filter
function to run particle filter as with PF_forward_filter.

set_parameters
function to set the parameters in the model. The first argument is a vectorized version of $F$ matrix and $Q$ matrix. The second argument is the fixed effect coefficients.

set_n_particles
sets the number of particles to use in run_particle_filter and get_get_score_n_hess when use_0_n_sq is TRUE.

get_get_score_n_hess
approximate the observed information matrix and score vector. The argument toggles whether or not to approximate the observed information matrix. The last particle cloud from run_particle_filter is used when use_0_n_sq is FALSE.

Warning

The function is still under development so the output and API may change.

References


**See Also**

See the examples at https://github.com/boennecd/dynamichazard/tree/master/examples.

**Examples**

```r
library(dynamichazard)
.lung <- lung[!is.na(lung$ph.ecog), ]
# standardize
.lung$age <- scale(.lung$age)

# fit model
set.seed(43588155)
 pf_fit <- PF_EM(
  fixed = Surv(time, status == 2) ~ ph.ecog + age,
  random = ~ 1, model = "exponential",
  data = .lung, by = 50, id = 1:nrow(.lung),
  Q_0 = as.matrix(1), Q = as.matrix(.5^2), type = "VAR",
  max_T = 800, Fmat = as.matrix(.5),
  control = PF_control(
    N_fw_n_bw = 250, N_first = 2000, N_smooth = 500, covar_fac = 1.1,
    nu = 6, n_max = 1000L, eps = 1e-4, averaging_start = 200L,
    n_threads = 2))

# compute score and observed information matrix
comp_obj <- PF_get_score_n_hess(pf_fit)
comp_obj$set_n_particles(N_fw = 10000L, N_first = 10000L)
comp_obj$run_particle_filter()
(o1 <- comp_obj$get_get_score_n_hess())

# O(N^2) method with lower variance as a function of time
comp_obj <- PF_get_score_n_hess(pf_fit, use_O_n_sq = TRUE)
comp_obj$set_n_particles(N_fw = 2500L, N_first = 2500L)
(o2 <- comp_obj$get_get_score_n_hess())

# approximations may have large variance
o3 <- replicate(10L, {
  runif(1)
  pf_fit$seed <- .Random.seed
  comp_obj <- PF_get_score_n_hess(pf_fit)
  comp_obj$set_n_particles(N_fw = 10000L, N_first = 10000L)
  comp_obj$run_particle_filter()
  comp_obj$get_get_score_n_hess()
}, simplify = FALSE)
sapply(o3, function(x) x$score)
```
sapply(o3, function(x) sqrt(diag(solve(x$obs_info))))

## S3 method for class 'ddhazard'
plot(
  x,
  xlab = "Time",
  ylab = "Hazard",
  type = "cov",
  plot_type = "l",
  cov_index,
  ylim,
  col = "black",
  add = FALSE,
  do_alter_mfcol = TRUE,
  level = 0.95,
  ddhazard_boot,
  ...
)

Arguments

x
result of `ddhazard` call.

xlab, ylab, ylim, col
arguments to override defaults set in the function.

type
type of plot. Currently, only "cov" is available for plot of the state space parameters.

plot_type
the type argument passed to `plot`.

cov_index
the index (indices) of the state space parameter(s) to plot.

add
FALSE if you want to make a new plot.

do_alter_mfcol
TRUE if the function should alter `par(mfcol)` in case that `cov_index` has more than one element.

level
level (fraction) for confidence bounds.

ddhazard_boot
object from a `ddhazard_boot` call which confidence bounds will be based on and where bootstrap samples will be printed with a transparent color.

... arguments passed to `plot.default` or `lines` depending on the value of add.
Details

Creates a plot of state variables or adds state variables to a plot with indices cov_index. Pointwise 1.96 std. confidence intervals are provided with the smoothed co-variance matrices from the fit.

Value

Returns NULL using invisible.

Examples

library(dynamichazard)
fit <- ddhazard(
  Surv(time, status == 2) ~ log(bili), pbc, id = pbc$id, max_T = 3600,
  Q_0 = diag(1, 2), Q = diag(1e-4, 2), by = 50,
  control = ddhazard_control(method = "GMA"))
plot(fit)
plot(fit, cov_index = 2)
### Arguments

- **x**: result of `residuals` with a 'type' argument which yields state space errors.
- **mod**: the `ddhazard` result used in the `residuals` call.
- **cov_index**: the indices of state vector errors to plot. Default is to use all.
- **t_index**: the bin indices to plot. Default is to use all bins.
- **p_cex**: cex argument for the points
- **pch, ylab, xlab**: arguments to override defaults set in the function.
- **x_tick_loc, x_tick_mark**: at and labels arguments passed to `axis`.
- **...**: arguments passed to `plot.default`.

### Value

Returns NULL using `invisible`.

---

**plot.ddsurvcurve**  
*Create and plot survival curves*

### Description

The function creates a predicted survival curve for a new observation using an estimated `ddhazard` model from `ddhazard`. The predicted curve is based on the predicted mean path of the state vector. Thus, the survival curve will not be a "mean" curve due to the non-linear relation between the probability of an event and the state vector.

### Usage

```r
## S3 method for class 'ddsurvcurve'
plot(x, y, xlab = "Time", ylab = "Survival", ylim, xaxs = "i", yaxs = "i", ...)

## S3 method for class 'ddsurvcurve'
lines(x, col = "Black", lty = 1, lwd = par()$lwd, ...)

ddsurvcurve(object, new_data, tstart = "", tstop = "")
```

### Arguments

- **x**: a `ddsurvcurve` object.
- **y**: not used.
- **xlab**: `xlab` passed to `plot`.
- **ylab**: `ylab` passed to `plot`.
- **ylim**: `ylim` passed to `plot`.
- **xaxs**: `xaxs` passed to `plot`.
yaxs  yaxs passed to plot.
... not used.
col  col passed to lines.
lty  lty passed to lines.
lwd  lwd passed to lines.
object  a ddhazard object.
new_data  a data.frame with the new data for the observation who the survival curve should be for. It can have more rows if tstart and tstop is supplied. The rows need to be consecutive and non-overlapping time intervals.
tstart  name of the start time column in new_data. It must be on the same time scale as the tstart used in the Surv(tstart,tstop,event) in the formula passed to ddhazard.
tstop  same as tstart for the stop argument.

Value

ddsurvcurve returns an object of class ddsurvcurve. It elements are the predicted discrete survival curve, time points for the survival curve, point of the first time period, the call, the discrete probabilities of an event in each interval conditional on survival up to that point, and the name of the distribution family. It should be seen as a plug-in estimate.

Methods (by generic)

- plot: method for plotting survival curve.
- lines: Method for adding survival curve to a plot.

plot.ddsurvcurve

Returns the same as lines.ddsurvcurve.

lines.ddsurvcurve

Either returns the objects used in the call to segments for discrete time hazard models, or the time points and survival function used to draw the survival curve.

See Also

ddhazard, and predict.ddhazard.

Examples

```r
###
# example with continuous time model
# setup data set. See `vignette("timedep", "survival")`
library(dynamichazard)
temp <- subset(pbc, id <= 312, select=c(id:sex, stage))
pbc2 <- tmerge(temp, temp, id=id, death = event(time, status))
pbc2 <- tmerge(pbc2, pbcseq, id = id, bili = tdc(day, bili))
```
```r
# fit model
f1 <- ddhazard(
  Surv(tstart, tstop, death == 2) ~ ddFixed(log(bili)), pbc2, id = pbc2$id,
  max_T = 3600, Q_0 = 1, Q = 1e-2, by = 100, model = "exponential",
  control = ddhazard_control(method = "EKF", eps = 1e-4, n_max = 1000,
    fixed_terms_method = "H_step"))

# predict with default which is all covariates set to zero
ddcurve <- ddsurvcurve(f1)
par_old <- par(mar = c(4.5, 4, .5, .5))
plot(ddcurve, col = "DarkBlue", lwd = 2)

# compare with cox model
f2 <- coxph(Surv(tstart, tstop, death == 2) ~ log(bili), data = pbc2)
nw <- data.frame(bili = 1, tstart = 0, tstop = 3000)
lines(survfit(f2, newdata = nw))

# same as above but with bili = 3
nw <- data.frame(bili = 3)
lines(ddsurvcurve(f1, new_data = nw), col = "DarkBlue")
lines(survfit(f2, newdata = nw))

# change to time-varying slope
f3 <- ddhazard(
  Surv(tstart, tstop, death == 2) ~ log(bili), pbc2, id = pbc2$id,
  max_T = 3600, Q_0 = diag(1, 2), Q = diag(1e-2, 2), by = 100, model = "exponential",
  control = ddhazard_control(method = "EKF", eps = 1e-4, n_max = 1000))

# example with time-varying coefficient
nw <- data.frame(
  bili = c(2.1, 1.9, 3.3, 3.9, 3.8, 3.6, 4, 4.9, 4.2, 5.7, 10.2),
  tstart = c(0L, 225L, 407L, 750L, 1122L, 1479L, 1849L, 2193L, 2564L, 2913L, 3284L),
DDcurve <- ddsurvcurve(f3, new_data = nw, tstart = "tstart", tstop = "tstop")
lines(DDcurve, "darkorange", lwd = 2)

# can condition on survival up to some time
DDcurve <- ddsurvcurve(f3, new_data = nw[-(1:5), ], tstart = "tstart",
    tstop = "tstop")
lines(DDcurve, lty = 2, lwd = 2)

#####
# example with discrete time model
is_censored <- c(
  6, 27, 34, 36, 42, 46, 48:51, 51 + c(15, 30:28, 33, 35:37, 39, 40, 42:45))
head_neck_cancer <- data.frame(
  id = 1:96,
  stop = c(
    1, 2, 2, rep(3, 6), 4, 4, rep(5, 8),
```
# fit model
h1 <- ddhazard(
  Surv(stop, event) ~ group, head_neck_cancer, by = 1, max_T = 45,
  Q_0 = diag(2^2, 2), Q = diag(.01^2, 2), control = ddhazard_control(
    method = "GMA", eps = 1e-4, n_max = 200))

# plot predicted survival curve. Notice the steps since the model is discrete
nw <- data.frame(group = factor(1, levels = 1:2), tstart = 0, tstop = 30)
ddcurve <- ddsurvcurve(h1, new_data = nw, tstart = "tstart",
                        tstop = "tstop")
plot(ddcurve, col = "Darkblue")
nw$group <- factor(2, levels = 1:2)
ddcurve <- ddsurvcurve(h1, new_data = nw, tstart = "tstart",
                        tstop = "tstop")
lines(ddcurve, col = "DarkOrange")

# compare with KM
lines(survfit(Surv(stop, event) ~ 1, head_neck_cancer, subset = group == 1),
      col = "DarkBlue")
lines(survfit(Surv(stop, event) ~ 1, head_neck_cancer, subset = group == 2),
      col = "DarkOrange")
par(par_old) # As per CRAN policy, the settings are reset

---

**plot.PF_clouds**  
*Plot of Clouds from a PF_clouds Object*

**Description**  
Plots mean curve along with quantiles through time for the forward, backward or smoothed clouds.

**Usage**  
```r
## S3 method for class 'PF_clouds'
plot(x, y, type = c("smoothed_clouds", "forward_clouds", "backward_clouds"), ylim, add = FALSE, qlvls = c(0.05, 0.5, 0.95),
```
plot.PF_EM

pch = 4,
lty = 1,
col,
..., 
cov_index,
qtype = c("points", "lines")
)

Arguments

x      an object of class PF_clouds.
y      unused.
type    parameter to specify which cloud to plot.
ylim    ylim passed to matplot.
add    TRUE if a new plot should not be made.
qlvls    vector of quantile levels to be plotted.
pch      pch argument for the quantile points.
lty      lty argument for the mean curves.
col      col argument to matplot and matpoints or matlines.
...    unused.
cov_index    indices of the state vector to plot. All are plotted if this argument is omitted.
qtype    character specifying how to show quantiles. Either "points" for crosses or "lines" for dashed lines.

Value

List with quantile levels and mean curve.

plot.PF_EM                  Plot for a PF_EM Object

Description

Short hand to call plot.PF_clouds.

Usage

## S3 method for class 'PF_EM'
plot(x, y, ...)

Arguments

x      an object of class PF_EM.
y      unused.
...    arguments to plot.PF_clouds.
predict.ddhazard

Predict Method for ddhazard Object

Description

Predict method for ddhazard.

Usage

## S3 method for class 'ddhazard'
predict(
  object, 
  new_data,
  type = c("response", "term"),
  tstart = "start",
  tstop = "stop",
  use_parallel,
  sds = FALSE,
  max_threads,
  ...
)

Arguments

object             result of a ddhazard call.
new_data           new data to base predictions on.
type               either "response" for predicted probability of an event or "term" for predicted terms in the linear predictor.
tstart             name of the start time column in new_data. It must be on the same time scale as the tstart used in the Surv(tstart,tstop,event) in the formula passed to ddhazard.
tstop               same as tstart for the stop argument.
use_parallel       not longer supported.
sds                TRUE if point wise standard deviation should be computed. Convenient if you use functions like ns and you only want one term per term in the right hand side of the formula used in ddhazard.
max_threads        not longer supported.
...                 not used.
Details
The function check if there are columns in new_data which names match tstart and tstop. If matched, then the bins are found which the start time to the stop time are in. If tstart and tstop are not matched then all the bins used in the estimation method will be used.

Value
Returns a list with elements as described in the Term and Response sections.

Term
The result with type = "term" is a lists of list each having length equal to nrow(new_data). The lists are
- terms: It’s elements are matrices where the first dimension is time and the second dimension is the terms.
- sds: similar to terms for the point-wise confidence intervals using the smoothed co-variance matrices. Only added if sds = TRUE.
- fixed_terms: contains the fixed (non-time-varying) effect.
- varcov: similar to sds but differs by containing the whole covariance matrix for the terms. It is a 3D array where the third dimension is time. Only added if sds = TRUE.
- start: numeric vector with start time for each time-varying term.
- tstop: numeric vector with stop time for each time-varying term.

Response
The result with type = "response" is a list with the elements below. If tstart and tstop are matched in columns in new_data, then the probability will be for having an event between tstart and tstop conditional on no events before tstart.
- fits: fitted probability of an event.
- istart: numeric vector with start time for each element in fits.
- istop: numeric vector with stop time for each element in fits.

Examples
```r
fit <- ddhazard(
  Surv(time, status == 2) ~ log(bili), pbc, id = pbc$id, max_T = 3600,
  Q_0 = diag(1, 2), Q = diag(1e-4, 2), by = 50,
  control = ddhazard_control(method = "GMA"))
predict(fit, type = "response", new_data =
  data.frame(time = 0, status = 2, bili = 3))
predict(fit, type = "term", new_data =
  data.frame(time = 0, status = 2, bili = 3))
# probability of an event between time 0 and 2000 with bili = 3
predict(fit, type = "response", new_data =
  data.frame(time = 0, status = 2, bili = 3, tstart = 0, tstop = 2000),
  tstart = "tstart", tstop = "tstop")
```
print.ddhazard_boot  Summary Statistics for a ddhazard_boot Object

Description
Arguments have the same effects as for an object from a boot call. See print.

Usage
## S3 method for class 'ddhazard_boot'
print(x, digits = getOption("digits"), index = 1L:ncol(boot.out$t), ...)

Arguments
x returned object from a ddhazard_boot call.
digits the number of digits to be printed in the summary statistics.
index indices indicating for which elements of the bootstrap output summary statistics are required.
... not used.

Value
Returns x using invisible.

See Also
ddhazard_boot

---

print.summary.ddhazard  Summarizing Dynamic Hazard Models Fits

Description
The sd printed for time-varying effects are point-wise standard deviations from the smoothed covariance matrices.

Usage
## S3 method for class 'summary.ddhazard'
print(x, digits = getOption("digits"), ...)

## S3 method for class 'ddhazard'
summary(object, var_indices = 1:ncol(object$state_vecs), max_print = 10, ...)
Arguments

- `x` object returned from `summary.ddhazard`.
- `digits` number of digits to print.
- `...` not used.
- `object` object returned from `ddhazard`.
- `var_indices` variable indices to print for time-varying effects.
- `max_print` maximum number of time points to print coefficients at.

Description

Residuals method for the result of a `ddhazard` call.

Usage

```r
## S3 method for class 'ddhazard'
residuals(
  object,
  type = c("std_space_error", "space_error", "pearson", "raw"),
  data = NULL,
  ...
)
```

Arguments

- `object` result of `ddhazard` call.
- `type` type of residuals. Four possible values: "std_space_error", "space_error", "pearson" and "raw". See the sections below for details.
- `data` data frame with data for the Pearson or raw residuals. This is only needed if the data set is not saved with the object. Must be the same data set used in the initial call to `ddhazard`.
- `...` not used.

Value

Returns a list as described in the Pearson and raw residuals section and in the State space errors section.
Pearson and raw residuals

Is the result of a call with a type argument of either "pearson" or "raw" for Pearson residuals or raw residuals. Returns a list with class "ddhazard_residual" with the following elements.

- residuals: list of residuals for each bin. Each element of the list contains a 2D array where the rows correspond to the passed data and columns are the residuals (residuals), estimated probability of death ($p_{est}$), outcome ($Y$) and row number in the initial data set ($row_{num}$). The data rows will only have a residuals in a given risk list if they are at risk in that risk set.
- type: the type of residual.

State space errors

Is the result of a call with a type argument of either "std_space_error" or "space_error". The former is for standardized residuals while the latter is non-standardized. Returns a list with class "ddhazard_space_errors" with the following elements:

- residuals: 2D array with either standardized or non-standardized state space errors. The row are bins and the columns are the parameters in the regression.
- standardize: TRUE if standardized state space errors.
- Covariances: 3D array with the smoothed co-variance matrix for each set of the state space errors.

Examples

```r
library(dynamichazard)
fit <- ddhazard(
  Surv(time, status == 2) ~ log(bili), pbc, id = pbc$id, max_T = 3600,
  Q_0 = diag(1, 2), Q = diag(1e-4, 2), by = 50,
  control = ddhazard_control(method = "GMA"))
resids <- residuals(fit, type = "pearson")$residuals
head(resids[[1]])
head(resids[[2]])
```

static_glm

Static glm Fit

Description

Method to fit a static model corresponding to a ddhazard fit. The method uses weights to ease the memory requirements. See get_survival_case_weights_and_data for details on weights.

The parallelglm_quick and parallelglm_QR methods are similar to two methods used in bam function in the mgcv package (see the `use.chol` argument or Wood et al. 2015). parallelglm_QR is more stable but slower. See Golub (2013) section 5.3 for a comparison of the Cholesky decomposition method and the QR method.
static_glm

Usage

static_glm(
  formula, data, by, max_T, ...,
  id, family = "logit", model = FALSE,
  weights, risk_obj = NULL,
  speedglm = FALSE, only_coef = FALSE,
  mf, method_use = c("glm", "speedglm", "parallelglm_quick", "parallelglm_QR"),
  n_threads = getOption("ddhazard_max_threads")
)

Arguments

formula  coxph like formula with Surv(tstart,tstop,event) on the left hand site of ~.
data  data.frame or environment containing the outcome and covariates.
by  interval length of the bins in which parameters are fixed.
max_T  end of the last interval interval.
...  arguments passed to glm or speedglm. If only_coef = TRUE then the arguments are passed to glm.control if glm is used.
id  vector of ids for each row of the in the design matrix.
family  "logit", "cloglog", or "exponential" for a static equivalent model of ddhazard.
model  TRUE if you want to save the design matrix used in glm.
weights  weights to use if e.g. a skewed sample is used.
risk_obj  a pre-computed result from a get_risk_obj. Will be used to skip some computations.
speedglm  depreciated.
only_coef  TRUE if only coefficients should be returned. This will only call the speedglm::speedglm.wfit or glm.fit which will be faster.
mf  model matrix for regression. Needed when only_coef = TRUE
method_use  method to use for estimation. glm uses glm.fit, speedglm::speedglm uses speedglm::speedglm.wfit and parallelglm_quick and parallelglm_QR uses a parallel C++ estimation method.
n_threads  number of threads to use when method_use is "parallelglm".
Value

The returned list from the `glm` call or just coefficients depending on the value of `only_coef`.

References


Examples

```r
library(dynamichazard)
fit <- static_glm(
  Surv(time, status == 2) ~ log(bili), pbc, id = pbc$id, max_T = 3600,
  by = 50)
fit$coefficients
```
## Index

### * datasets
- hds, 17
- Random.seed, 29, 30

### boot
- 8, 44

### coxph
- 4, 14, 23, 31, 47

### ddFixed
- 3, 23
- ddFixed_intercept (ddFixed), 3

### ddhazard
- 3, 4, 8, 10, 15, 16, 18, 35–38, 42, 45–47
- ddhazard_app, 5, 6, 6
- ddhazard_boot, 6, 7, 35, 44
- ddhazard_control, 4, 8
- ddsurvcurve (plot.ddsurvcurve), 37

### formula
- 23, 31

### gam
- 15

### get_cloud_means
- 10

### get_cloud_quantiles
- 11

### get_Q_0
- 12

### get_risk_obj
- 5, 9, 13, 15, 47

### get_survival_case_weights_and_data
- 14, 46

### glm
- 47, 48
- glm.control, 47
- glm.fit, 47

### hatvalues.ddhazard
- 16

### hds
- 17

### invisible
- 36, 37, 44

### lines.ddsurvcurve (plot.ddsurvcurve), 37

### logLik
- 19
- logLik.ddhazard, 18
- logLik.PF_clouds (logLik.PF_EM), 19
- logLik.PF_EM, 19

### matlines
- 41

### matplot
- 41

### matpoints
- 41

### mclapply
- 13

### Module
- 5

### ns
- 42

### PF_control
- 20, 23, 30

### PF_EM
- 3, 20–22, 22, 23, 29–31, 33

### PF_forward_filter
- 24, 28, 33

### PF_get_score_n_hess
- 32

### plot
- 6, 8

### plot.ddhazard
- 35

### plot.ddhazard_space_errors
- 36

### plot.ddsurvcurve
- 37

### plot.default
- 35, 37

### plot.PF_clouds
- 40, 41, 42

### plot.PF_EM
- 41

### predict
- 6

### predict.ddhazard
- 38, 42

### print
- 44

### print.ddhazard_boot
- 44

### print.summary.ddhazard
- 44

### residuals
- 6, 37

### residuals.ddhazard
- 45

### segments
- 38

### set.seed
- 23, 30

### speedglm
- 47

### static_glm
- 4–6, 15, 23, 30, 46

### summary.ddhazard
- (print.summary.ddhazard), 44

### Surv
- 4, 13, 14, 23, 31, 38, 42, 47

### terms
- 6

49