

# Package ‘dynamichazard’

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**Type** Package

**Title** Dynamic Hazard Models using State Space Models

**Version** 0.6.3

**Description** Contains functions that lets you fit dynamic hazard models using state space models. The first implemented model is described in Fahrmeir (1992) <doi:10.1080/01621459.1992.10475232> and Fahrmeir (1994) <doi:10.1093/biomet/81.2.317>. Extensions hereof are available where the Extended Kalman filter is replaced by an unscented Kalman filter and other options including particle filters. The implemented particle filters support more general state space models.

**License** GPL-2

**LazyData** TRUE

**LinkingTo** Rcpp, RcppArmadillo

**Imports** parallel, Rcpp (>= 0.12.6), boot

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**BugReports** <https://github.com/boennecd/dynamichazard/issues>

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---

ddFixed

*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**

```
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](#).

**Examples**

```
# we can get a time-invariant effect of `x1` by
## Not run:
ddhazard(Surv(stop, event) ~ ddFixed(x1), data)

## End(Not run)

# all of the calls below will yield the same result with a time-invariant
# intercept:
## Not run:
ddhazard(Surv(stop, event) ~ ddFixed_intercept() + x1, data)
ddhazard(Surv(stop, event) ~ -1 + ddFixed_intercept() + x1, data)

## End(Not run)
```

---

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 = F)
```

**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 <a href="#">static_glm</a> ).
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 <a href="#">ddhazard_control</a> .
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 depends 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 <a href="#">get_risk_obj</a> 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 <a href="#">Module</a> with C++ functions used for estimation given the model argument.
discrete_hazard_func	the hazard function corresponding to the model argument.
terms	the <a href="#">terms</a> 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

- Fahrmeir, Ludwig. *Dynamic modelling and penalized likelihood estimation for discrete time survival data*. *Biometrika* 81.2 (1994): 317-330.
- Durbin, James, and Siem Jan Koopman. *Time series analysis by state space methods*. No. 38. Oxford University Press, 2012.

## 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 = F, ...)
```

### 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.

### Examples

```
## Not run:
dynamichazard::ddhazard_app()
dynamichazard::ddhazard_app(seed = 1, more_options = TRUE)

## End(Not run)
```

---

ddhazard\_boot

*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

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

## Arguments

ddhazard_fit	returned object from a <a href="#">ddhazard</a> 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

```
## Not run:
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)

## End(Not run)
```

---

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 = F, method = "EKF",
  save_risk_set = T, save_data = T, 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 F,
  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 <code>get_risk_obj</code> used to estimate the model. It may be needed for later calls to e.g., <code>residuals</code> , <code>plot</code> and <code>logLike</code> .
save_data	TRUE if you want to keep the data argument. It may be needed for later calls to e.g., <code>residuals</code> , <code>plot</code> and <code>logLike</code> .
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	<i>Compute Mean Estimates from Particle Cloud</i>
-----------------	---

---

**Description**

Computes the estimated means from a particle cloud.

**Usage**

```
get_cloud_means(object, ...)

## S3 method for class 'PF_EM'
get_cloud_means(object, ...)

## S3 method for class 'PF_clouds'
get_cloud_means(object, cov_index = NULL,
  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 means for.

**Value**

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

---

get\_cloud\_quantiles     *Compute Quantile Estimates from Particle Cloud*

---

### Description

Computes the estimated quantiles from a particle cloud.

### Usage

```
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.
qlvls	numeric vector with values in [0, 1] with the quantiles to compute.
type	character with the type of cloud to compute quantiles for.

### Value

A 3 dimensional array where the first dimension is the quantiles, the second dimension is the random effect, and the third dimension is the time.

---

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.

---

get_risk_obj	<i>Risk Set on an Equidistant Distant Grid</i>
--------------	--

---

**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 = T,
            n_threads = 1, min_chunk = 5000)
```

**Arguments**

Y	vector of outcome variable returned from <a href="#">Surv</a> .
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 referred to as the exponential model in this package is a dynamic model.
n_threads	set to a value greater than one to use <a href="#">mclapply</a> 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**

```
# 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**

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

**Arguments**

formula	coxph like formula with <code>Surv(tstart, tstop, event)</code> on the left hand site of <code>~</code> .
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.
risk_obj	a pre-computed result from a <code>get_risk_obj</code> . 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 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

Tutz, Gerhard, and Matthias Schmid. *Nonparametric Modeling and Smooth Effects*. Modeling Discrete Time-to-Event Data. Springer International Publishing, 2016. 105-127.

## 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 Hat Values for ddhazard Object
```

---

## Description

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

## Usage

```
## 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

```
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 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](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:

$$E_{\theta}(\alpha_1|y_{1:d}), E_{\theta}(\alpha_2|y_{1:d}), \dots, E_{\theta}(\alpha_d|y_{1:d})$$

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

## Usage

```
## 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 <a href="#">ddhazard</a> .
...	unused.

## 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"))
logLik(fit)
```

---

logLik.PF\_EM

*Approximate Log-Likelihood from a Particle Filter*


---

**Description**

Computes the approximate log-likelihood using the forward filter clouds. See the vignette("Particle\_filtering", "dyn" for details.

**Usage**

```
## 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**

```
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)
```

**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 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.

**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_0_N` for the smoother in Fearnhead, Wyncoll, and Tawn (2010).
- `Brier_0_N_square` for the smoother in Briers, Doucet, and Maskell (2010).

**Value**

A list with components named as the arguments.

## References

- Gordon, N. J., Salmond, D. J., and Smith, A. F. (1993) Novel approach to nonlinear/non-Gaussian Bayesian state estimation. *In IEE Proceedings F (Radar and Signal Processing)*, (Vol. 140, No. 2, pp. 107-113). IET Digital Library.
- Pitt, M. K., and Shephard, N. (1999) Filtering via simulation: Auxiliary particle filters. *Journal of the American statistical association*, **94(446)**, 590-599.
- Fearnhead, P., Wyncoll, D., and Tawn, J. (2010) A sequential smoothing algorithm with linear computational cost. *Biometrika*, **97(2)**, 447-464.
- Briers, M., Doucet, A., and Maskell, S. (2010) Smoothing algorithms for state-space models. *Annals of the Institute of Statistical Mathematics*, **62(1)**, 61.

## 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

```
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	<a href="#">coxph</a> like formula with <a href="#">Surv</a> (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 <a href="#">static_glm</a> ).
Q_0	covariance matrix for the prior distribution.

Q	initial covariance matrix for the state equation.
order	order of the random walk.
control	see <a href="#">PF_control</a> .
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 <a href="#">set.seed</a> .
type	type of state model. Either "RW" for a [R]andom [W]alk or "VAR" for [V]ector [A]uto[R]egression.
fixed	two-sided <a href="#">formula</a> to be used with random instead of formula. It is of the form $\text{Surv}(tstart, tstop, event) \sim x$ or $\text{Surv}(tstart, tstop, event) \sim -1$ for no fixed effects.
random	one-sided <a href="#">formula</a> to be used with fixed instead of formula. It is of the form $\sim z$ .
Fmat	starting value for $F$ when type = "VAR". See 'Details' in <a href="#">PF_EM</a> .
fixed_effects	starting values for fixed effects if any. See <a href="#">ddFixed</a> .
G, theta, J, K, psi, phi	parameters for a restricted type = "VAR" model. See the vignette mentioned in 'Details' of <a href="#">PF_EM</a> 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  $R = (e_{l_1}, e_{l_2}, \dots, e_{l_r})$  where  $e_k$  is column from the  $p$  dimensional identity matrix and  $l_1 < l_2 < \dots < l_r$ . 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  $Z_t \in \mathbb{R}^{n_t \times c}$  are design matrices and the outcome for a 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**

```
## Not run:
#####
# 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(
    N_fw_n_bw = 500, N_first = 2500, N_smooth = 5000,
    n_max = 50, eps = .001, Q_tilde = diag(.2^2, 2), est_a_0 = FALSE,
    n_threads = max(parallel::detectCores(logical = FALSE), 1)))

# Plot state vector estimates
plot(pf_fit, cov_index = 1)
plot(pf_fit, cov_index = 2)

# Plot log-likelihood
plot(pf_fit$log_likes)

## End(Not run)
## Not run:
#####
# 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(
    N_fw_n_bw = 500, N_smooth = 2500, N_first = 1000, 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 = max(parallel::detectCores(logical = FALSE), 1)))

# compare results
plot(ddfit)
plot(pf_fit)
sqrt(ddfit$Q * 100)
sqrt(pf_fit$Q)
rbind(ddfit$fixed_effects, pf_fit$fixed_effects)

## End(Not run)
## Not run:
#####
# 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 - 1L) * 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, 1) - 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 = 50L, # should maybe be larger
    smoother = "Fearnhead_0_N", eps = 1e-4,
    n_threads = 4L # depends on your cpu(s)
  ),
  trace = 1L)
plot(fit$log_likes) # log-likelihood approximation at each iterations

# take more iterations with more particles
cl <- fit$call
ctrl <- cl[["control"]]
ctrl[c("N_fw_n_bw", "N_smooth", "N_smooth_final", "N_first", "n_max")] <- list(

```

```

    500L, 2000L, 500L, 5000L, 30L)
  cl[["control"]] <- ctrl
  cl[c("phi", "psi", "theta")] <- list(fit$phi, fit$psi, fit$theta)
  fit_extra <- eval(cl)

  plot(fit_extra$log_likes) # log-likelihood approximation at each iteration

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

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

  ## End(Not run)

```

---

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, 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 <a href="#">set.seed</a> function. Can be used with the <a href="#">.Random.seed</a> 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 <a href="#">static_glm</a> ).
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 <a href="#">PF_control</a> .
trace	argument to get progress information. Zero will yield no info and larger integer values will yield incrementally more information.
G, theta, J, K, psi, phi	parameters for a restricted type = "VAR" model. See the vignette mentioned in 'Details' of <a href="#">PF_EM</a> and the examples linked to in 'See Also'.
type	type of state model. Either "RW" for a [R]andom [W]alk or "VAR" for [V]ector [A]uto[RE]gression.
Fmat	starting value for $F$ when type = "VAR". See 'Details' in <a href="#">PF_EM</a> .
formula	<a href="#">coxph</a> like formula with <a href="#">Surv</a> (tstart, tstop, event) on the left hand site of ~.
fixed	two-sided <a href="#">formula</a> to be used with random instead of formula. It is of the form <a href="#">Surv</a> (tstart, tstop, event) ~ x or <a href="#">Surv</a> (tstart, tstop, event) ~ - 1 for no fixed effects.
random	one-sided <a href="#">formula</a> to be used with fixed instead of formula. It is of the form ~ z.
order	order of the random walk.

**Value**

An object of class PF\_cclouds.

**Methods (by class)**

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

**Examples**

```
## Not run:
# head-and-neck cancer study data. See Efron, B. (1988) doi:10.2307/2288857
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, 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 = max(parallel::detectCores(logical = FALSE), 1),
  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)))

## End(Not run)

```

---

plot.ddhazard

*Plots for ddhazard Object*


---

## Description

Plot of estimated state space variables from a [ddhazard](#) fit.

## Usage

```

## S3 method for class 'ddhazard'
plot(x, xlab = "Time", ylab = "Hazard",
     type = "cov", plot_type = "l", cov_index, ylim, col = "black",
     add = F, do_alter_mfcol = T, level = 0.95, ddhazard_boot, ...)

```

## Arguments

x	result of <a href="#">ddhazard</a> 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 <code>par(mfcol)</code> in case that <code>cov_index</code> has more than one element.
level	level (fraction) for confidence bounds.
ddhazard_boot	object from a <a href="#">ddhazard_boot</a> call which confidence bounds will be based on and where bootstrap samples will be printed with a transparent color.
...	arguments passed to <a href="#">plot.default</a> or lines depending on the value of <code>add</code> .

**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.

**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)
```

---

```
plot.ddhazard_space_errors
      State Space Error Plot
```

---

**Description**

Plot function for state space errors from [ddhazard](#) fit.

**Usage**

```
## S3 method for class 'ddhazard_space_errors'
plot(x, mod, cov_index = NA,
     t_index = NA, p_cex = par()$cex * 0.2, pch = 16,
     ylab = "Std. state space error", x_tick_loc = NA, x_tick_mark = NA,
     xlab = "Time", ...)
```

**Arguments**

<code>x</code>	result of <a href="#">residuals</a> with a ‘type’ argument which yields state space errors.
<code>mod</code>	the <a href="#">ddhazard</a> result used in the <a href="#">residuals</a> call.
<code>cov_index</code>	the indices of state vector errors to plot. Default is to use all.
<code>t_index</code>	the bin indices to plot. Default is to use all bins.
<code>p_cex</code>	cex argument for the points
<code>pch, ylab, xlab</code>	arguments to override defaults set in the function.
<code>x_tick_loc, x_tick_mark</code>	at and labels arguments passed to axis.
<code>...</code>	arguments passed to <a href="#">plot.default</a> .

---

plot.ddsurve      *Create and plot survival curves*

---

### Description

The function creates a predicted survival curve for a new observation using a 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

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

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

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

### Arguments

x	a ddsurve 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 <a href="#">Surv(tstart, tstop, event)</a> in the formula passed to <a href="#">ddhazard</a> .
tstop	same as tstart for the stop argument.

**Value**

ddsurvcurve returns an object of class ddsurvcurve. Its 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**

```
#####
# 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))

# 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 = "M_step"))

# predict with default which is all covariates set to zero
ddcurve <- ddsurvcurve(f1)
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),
  tstop = c(225L, 407L, 750L, 1122L, 1479L, 1849L, 2193L, 2564L, 2913L,
            3284L, 3600L))
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
# head-and-neck cancer study data. See Efron, B. (1988) doi:10.2307/2288857
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, 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
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")

```

---

plot.PF_clouds	<i>Plot of Clouds from a PF_clouds Object</i>
----------------	---

---

## Description

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

## Usage

```

## 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), 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 <a href="#">matplot</a> .
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 <a href="#">matplot</a> and <a href="#">matpoints</a> or <a href="#">matlines</a> .
...	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	<i>Plot for a PF_EM Object</i>
------------	--------------------------------

---

**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 <a href="#">plot.PF_clouds</a> .

**Value**

See [plot.PF\\_clouds](#)

---

predict.ddhazard	<i>Predict Method for ddhazard Object</i>
------------------	---

---

**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 = F,
  max_threads, ...)
```

**Arguments**

object	result of a <code>ddhazard</code> 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 <code>Surv(tstart, tstop, event)</code> in the formula passed to <code>ddhazard</code> .
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 <code>ns</code> and you only want one term per term in the right hand site of the formula used in <code>ddhazard</code> .
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.

**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**

```
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 <a href="#">ddhazard_boot</a> 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.

**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 <code>summary.ddhazard</code> .
digits	number of digits to print.
...	not used.
object	object returned from <a href="#">ddhazard</a> .
var_indices	variable indices to print for time-varying effects.
max_print	maximum number of time points to print coefficients at.

---

```
residuals.ddhazard
```

*Residuals Method for ddhazard Object*

---

### Description

Residuals method for the result of a [ddhazard](#) call.

### Usage

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

**Arguments**

object	result of <code>ddhazard</code> 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 <code>ddhazard</code> .
...	not used.

**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 corresponds 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**

```
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.

**Usage**

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

**Arguments**

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

**Value**

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

**References**

Wood, S.N., Goude, Y. & Shaw S. (2015) Generalized additive models for large datasets. *Journal of the Royal Statistical Society, Series C* 64(1): 139-155.

Golub, G. H., & Van Loan, C. F. (2013). *Matrix computations* (4th ed.). JHU Press.

**Examples**

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

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