

# Package: PWEXP (via r-universe)

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**Type** Package

**Title** Piecewise Exponential Distribution Prediction Model

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**Depends** survival, fastmatch

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**Description** Build piecewise exponential survival model for study design (planning) and event/timeline prediction.

**URL** <https://github.com/zjph602xtc/PWEXP>

**BugReports** <https://github.com/zjph602xtc/PWEXP/issues>

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boot.pwexp.fit	<i>Bootstrap a Piecewise Exponential Model</i>
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## Description

Bootstrap a existing piecewise exponential model or build a piecewise exponential model with bootstrapping.

## Usage

```
## Default S3 method:
boot.pwexp.fit(time, event, nsim=100, breakpoint=NULL, nbreak=0,
               exclude_int=NULL, min_pt_tail=5, max_set=1000, seed=1818,
               optimizer='mle', tol=1e-4, parallel=FALSE, mc.core=4, ...)
## S3 method for class 'pwexp.fit'
boot.pwexp.fit(time, nsim=100, max_set=1000, seed=1818,
               optimizer='mle', tol=1e-4, parallel=FALSE, mc.core=4, ...)
```

## Arguments

time	observed time from randomization or a <a href="#">pwexp.fit</a> object.
event	the status indicator. See <a href="#">pwexp.fit</a> .
nsim	the number of repeated bootstrapping.
breakpoint	pre-specified breakpoints. See <a href="#">pwexp.fit</a> .
nbreak	total number of breakpoints. See <a href="#">pwexp.fit</a> .
exclude_int	an interval that excludes any estimated breakpoints. See <a href="#">pwexp.fit</a> .
min_pt_tail	the minimum number of events used for estimating the tail (the hazard rate of the last piece). See <a href="#">pwexp.fit</a> .
max_set	maximum estimated combination of breakpoints. See <a href="#">pwexp.fit</a> .
seed	a random seed.
optimizer	one of the optimizers: mle, ols, or hybrid. See <a href="#">pwexp.fit</a> .
tol	the minimum allowed gap between two breakpoints. The gap is calculated as $(\max(\text{time}) - \min(\text{time})) * \text{tol}$ . Keep it as default in most cases.
parallel	logical. If TRUE, use <b>doSNOW</b> package to run in parallel.
mc.core	number of processes allowed to be run in parallel.
...	internal function reserved.

**Details**

Use bootstrap to repeatedly call `pwexp.fit` to estimate the uncertainty of parameters.

**Value**

A data frame (`res`) containing these columns:

<code>brk1, ..., brkx</code>	estimated breakpoints. The <code>attr(res, 'brk')</code> can extract the result of breakpoint from each bootstrap sample ( <code>res</code> is the returned model from <code>boot.pwexp.fit</code> ).
<code>lam1, ..., lamx</code>	estimated piecewise hazard rates. The <code>attr(res, 'lam')</code> can extract the result of hazard rates from bootstrap sample ( <code>res</code> is the returned model from <code>boot.pwexp.fit</code> ).
<code>likelihood</code>	the log-likelihood of the model.
<code>AIC</code>	the Akaike information criterion of the model.
<code>BIC</code>	the Bayesian information criterion of the model.

**Author(s)**

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**See Also**

[pwexp.fit](#)

**Examples**

```
event_dist <- function(n)rpwexp(n, rate = c(0.1, 0.01, 0.2), breakpoint = c(5,14))
dat <- simdata(rand_rate = 20, drop_rate = 0.03, total_sample = 1000,
              advanced_dist = list(event_dist=event_dist),
              add_column = c('censor_reason', 'event', 'followT', 'followT_abs'))

fit_res3 <- pwexp.fit(dat$followT, dat$event, nbreak = 2)
fit_res_boot <- boot.pwexp.fit(fit_res3, nsim = 10) # here nsim=10 is for demo purpose,
                                                # pls increase it in practice

plot_survival(dat$followT, dat$event, xlim=c(0,40))
plot_survival(fit_res_boot, col='red', CI_par = list(col='red'))
brk_ci <- apply(attr(fit_res_boot, 'brk'), 2, function(x)quantile(x,c(0.025,0.975)))
abline(v=brk_ci, col='grey', lwd=2)
```

---

conditional piecewise exponential

*The Conditional Piecewise Exponential Distribution*

---

**Description**

Distribution function, quantile function and random generation for the piecewise exponential distribution  $t$  with piecewise rate `rate` given  $t > qT$ .

**Usage**

```
ppwexp_conditional(q, qT, rate=1, breakpoint=NULL, lower.tail=TRUE,
                  log.p=FALSE, one_piece, safety_check=TRUE)
qpwexp_conditional(p, qT, rate=1, breakpoint=NULL, lower.tail=TRUE,
                  log.p=FALSE, one_piece, safety_check=TRUE)
rpwexp_conditional(n, qT, rate, breakpoint=NULL)
```

**Arguments**

q	vector of quantiles.
p	vector of probabilities.
qT	the distribution is conditional on $t > qT$ . qT can be a scalar or a vector with the same length of q or p.
n	number of observations. Must be a positive integer with length 1.
rate	a vector of rates in each piece.
breakpoint	a vector of breakpoints. The length is $\text{length}(\text{rate})-1$ . Can be NULL if rate is a single value.
log, log.p	logical; if TRUE, probabilities p are given as $\log(p)$ .
lower.tail	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .
one_piece	(only required when <code>safety_check=FALSE</code> ) whether the distribution only has one piece (i.e., rate is a single value and <code>breakpoint=NULL</code> ).
safety_check	logical; whether check the input arguments; if FALSE, function has better computing performance by skipping all safety checks.

**Details**

See webpage <https://zjph602xtc.github.io/PWEXP/> for more details for its survival function, cumulative density function, quantile function.

**Value**

ppwexp\_conditional gives the conditional distribution function, qpwexp\_conditional gives the conditional quantile function, and rpwexp\_conditional generates conditional random variables.

The length of the result is determined by q, p or n for ppwexp\_conditional, qpwexp\_conditional or rpwexp\_conditional. You can only specify a single piecewise exponential distribution every time you call these functions. This is different from the exponential distribution functions in package **stats**.

When the length of qT is 1, then all results are conditional on the same  $t > qT$ . In rpwexp\_conditional, qT must be a scalar. When the length of qT equals to the length of q or p, then each value in the result is conditional on  $t > qT$  for each value in qT.

Arguments rate and breakpoint must match. The length of rate is the length of breakpoint + 1.

**Author(s)**

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**See Also**

[dpwexp](#), [ppwexp](#), [qpwexp](#), [rpwexp](#)

**Examples**

```
# CDF and quantile function of conditional piecewise exp with rate 2, 1, 3 given t > 0.1
t <- seq(0.1, 1.2, 0.01)
F2_con <- ppwexp_conditional(t, qT=0.1, rate=c(2, 1, 3), breakpoint=c(0.3, 0.8))
plot(t, F2_con, type='l', col='red', lwd=2, main="CDF and Quantile Function of
  Conditional \nPiecewise Exp Dist", xlim=c(0, 1.2), ylim=c(0, 1.2))
lines(F2_con, qpwexp_conditional(F2_con, qT=0.1, rate=c(2, 1, 3),
  breakpoint=c(0.3,0.8)), lty=2, lwd=2, col='red')

# compare with CDF and quantile function of unconditional piecewise exp with rate 2, 1, 3
t <- seq(0, 1.2, 0.01)
F2 <- rpwexp(t, rate=c(2, 1, 3), breakpoint=c(0.3,0.8))
lines(t, F2, lwd=2)
lines(F2, qpwexp(F2, rate=c(2, 1, 3), breakpoint=c(0.3,0.8)), lty=2, lwd=2)
abline(v=0.1, col='grey')
abline(h=0.1, col='grey')
legend('topleft', c('CDF of piecewise exp dist given t > 0.1', 'quantile
  function of piecewise exp dist given t > 0.1', 'CDF of piecewise exp dist',
  'quantile function of piecewise exp dist'), col=c('red', 'red', 'black', 'black'),
  lty=c(1, 2, 1, 2), lwd=2)

# use rpwexp_conditional function to generate piecewise exp samples with rate 2, 1, 3 given t > 0.1
r_sample_con <- rpwexp_conditional(3000, qT=0.1, rate=c(2, 1, 3), breakpoint=c(0.3,0.8))
plot(ecdf(r_sample_con), col='red', lwd=2, main="Empirical CDF of Conditional
  Piecewise Exp Dist", xlim=c(0, 1.2), ylim=c(0, 1))

# compare with its CDF
lines(seq(0.1, 1.2, 0.01), F2_con, lwd=2)
legend('topleft', c('empirical CDF of piecewise exp dist given t > 0.1',
  'true CDF of piecewise exp dist given t > 0.1'), col=c('red', 'black'), lty=c(1,2), lwd=2)
```

---

cut\_dat

*Cut Data before a Specified Time*

---

**Description**

Take a subset of a dataset by constraining the randomization time  $\leq$  cut time. Additionally, it updates the follow-up time, censor/event indicator, censor reason, accordingly.

**Usage**

```
cut_dat(cut, data, var_randT=NULL, var_followT=NULL, var_followT_abs=NULL,
  var_censor=NULL, var_event=NULL, var_censor_reason='status_at_end')
```

**Arguments**

cut	cut time (from the beginning of the trial); only rows with randomization time $\leq$ cut will be kept.
data	a data frame.
var_randT	character; the variable name of randomization time. If missing, then the randomization time will be treated as 0 and NO subjects will be filtered by cut time.
var_followT	character; the variable name of follow-up time (from randomization)
var_followT_abs	character; the variable name of follow-up time (from the beginning of the trial)
var_censor	character; the variable name of censoring (drop-out or death) indicator (1=censor, 0=event)
var_event	character; the variable name of event indicator (1=event, 0=censor)
var_censor_reason	character; the variable name of censoring reason (character variable). This variable will be created, if data does not contain it.

**Details**

We first filter rows that randomization time is equal to or less than cut time. Then we modify these columns (if provided):

- var\_followT: change values to (cut - randomization time) if (follow-up time + randomization time) > cut
- var\_followT\_abs: change values to cut if (follow-up time from beginning) > cut
- var\_censor: change values to 1 if (follow-up time from beginning) > cut
- var\_event: change values to 0 if (follow-up time from beginning) > cut
- var\_censor\_reason: change values to 'cut' if (follow-up time from beginning) > cut

**Value**

A subset data frame with the same columns as data.

var\_censor\_reason is the only variable that is allowed to be absent in data. The function will create this variable in the returned data frame and set values 'cut' to the subjects whose (follow-up time from beginning) > cut.

**Note**

The original dataset data will NOT be modified.

**Author(s)**

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**Examples**

```

event_dist <- function(n)rpwexp(n, rate = c(0.1, 0.01, 0.2), breakpoint = c(5,14))
dat <- simdata(rand_rate = 20, total_sample = 1000, drop_rate = 0.03,
              advanced_dist = list(event_dist=event_dist),
              add_column = c('censor_reason','event','followT','followT_abs'))
cut <- quantile(dat$randT, 0.8)
train <- cut_dat(var_randT = 'randT', cut = cut, data = dat,
                var_followT = 'followT', var_followT_abs = 'followT_abs',
                var_event = 'event', var_censor_reason = 'censor_reason')

```

cv.pwexp.fit

*Cross Validate a Piecewise Exponential Model***Description**

Cross Validate a existing piecewise exponential model.

**Usage**

```

## Default S3 method:
cv.pwexp.fit(time, event, nfold=5, nsim=100, breakpoint=NULL,
             nbreak=0, exclude_int=NULL, min_pt_tail=5, max_set=1000, seed=1818,
             optimizer='mle', tol=1e-4, parallel=FALSE, mc.core=4, ...)
## S3 method for class 'pwexp.fit'
cv.pwexp.fit(time, nfold=5, nsim=100, max_set=1000, seed=1818,
             optimizer='mle', tol=1e-4, parallel=FALSE, mc.core=4, ...)

```

**Arguments**

time	observed time from randomization or a <a href="#">pwexp.fit</a> object.
event	the status indicator. See <a href="#">pwexp.fit</a> .
nfold	the number of folds used in CV.
nsim	the number of simulations.
breakpoint	pre-specified breakpoints. See <a href="#">pwexp.fit</a> .
nbreak	total number of breakpoints. See <a href="#">pwexp.fit</a> .
exclude_int	an interval that excludes any estimated breakpoints. See <a href="#">pwexp.fit</a> .
min_pt_tail	the minimum number of events used for estimating the tail (the hazard rate of the last piece). See <a href="#">pwexp.fit</a> .
max_set	maximum estimated combination of breakpoints. See <a href="#">pwexp.fit</a> .
seed	a random seed.
optimizer	one of the optimizers: mle, ols, or hybrid. See <a href="#">pwexp.fit</a> .
tol	the minimum allowed gap between two breakpoints. The gap is calculated as $(\max(\text{time}) - \min(\text{time})) * \text{tol}$ . Keep it as default in most cases.
parallel	logical. If TRUE, use <b>doSNOW</b> package to run in parallel.
mc.core	number of processes allowed to be run in parallel.
...	internal function reserved.

**Details**

Use cross validation obtain the prediction log likelihood.

**Value**

A vector of length nsim containing the CV log likelihood in each round of simulation.

**Author(s)**

Tianchen Xu <zjph602xutianchen@gmail.com>

**See Also**

[pwexp.fit](#)

**Examples**

```
event_dist <- function(n)rpwexp(n, rate = c(0.1, 0.01, 0.2), breakpoint = c(5,14))
dat <- simdata(rand_rate = 20, drop_rate = 0.03, total_sample = 1000,
              advanced_dist = list(event_dist=event_dist),
              add_column = c('censor_reason','event','followT','followT_abs'))

# here nsim=10 is for demo purpose, pls increase it in practice!!

cv0 <- cv.pwexp.fit(dat$followT, dat$event, nsim = 10, nbreak = 0)
cv1 <- cv.pwexp.fit(dat$followT, dat$event, nsim = 10, nbreak = 1)
cv2 <- cv.pwexp.fit(dat$followT, dat$event, nsim = 10, nbreak = 2)
sapply(list(cv0,cv1,cv2), median)
```

---

piecewise exponential *The Piecewise Exponential Distribution*

---

**Description**

Density, distribution function, quantile function and random generation for the piecewise exponential distribution with piecewise rate rate.

**Usage**

```
dpwexp(x, rate = 1, breakpoint = NULL, log = FALSE, one_piece, safety_check = TRUE)
ppwexp(q, rate = 1, breakpoint = NULL, lower.tail = TRUE, log.p = FALSE,
       one_piece, safety_check = TRUE)
qpwexp(p, rate = 1, breakpoint = NULL, lower.tail = TRUE, log.p = FALSE,
       one_piece, safety_check = TRUE)
rpwexp(n, rate = 1, breakpoint = NULL)
```



**Arguments**

x, q	vector of quantiles.
p	vector of probabilities.
n	number of observations. Must be a positive integer with length 1.
rate	a vector of rates in each piece.
breakpoint	a vector of breakpoints. The length is $\text{length}(\text{rate})-1$ . Can be NULL if rate is a single value.
log, log.p	logical; if TRUE, probabilities p are given as $\log(p)$ .
lower.tail	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .
one_piece	(only required when <code>safety_check=FALSE</code> ) whether the distribution only has one piece (i.e., rate is a single value and <code>breakpoint=NULL</code> ).
safety_check	logical; whether check the input arguments; if FALSE, function has better computing performance by skipping all safety checks.

**Details**

The piecewise distribution function with piecewise rate  $\lambda_1, \dots, \lambda_r$  is

$$f(t) = \lambda_{r+1} \exp\left[\sum_{i=1}^r (\lambda_{i+1} - \lambda_i) d_i - \lambda_{r+1} t\right]$$

for  $d_r \leq t < d_{r+1}$ .

See webpage <https://zjph602xtc.github.io/PWEXP/> for more details for its hazard function, cumulative hazard function, survival function, cumulative density function, quantile function.

**Value**

dpwexp gives the density, ppwexp gives the distribution function, qpwexp gives the quantile function, and rpwexp generates random deviates.

The length of the result is determined by x, q, p or n for dpwexp, ppwexp, qpwexp or rpwexp. You can only specify a single piecewise exponential distribution every time you call these functions. This is different from the exponential distribution functions in package **stats**.

Arguments `rate` and `breakpoint` must match. The length of `rate` is the length of `breakpoint` + 1.

**Note**

When `breakpoint=NULL`, the function calls exponential function in **stats**.

**Author(s)**

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**See Also**

[ppwexp\\_conditional](#), [qpwexp\\_conditional](#), [rpwexp\\_conditional](#)

**Examples**

```

# use rpwexp function to generate piecewise exp samples with rate 2, 1, 3
r_sample <- rpwexp(50000, rate=c(2, 1, 3), breakpoint=c(0.3, 0.8))
hist(r_sample, freq=FALSE, breaks=200, main="Density of Piecewise Exp Dist",
     xlab='t', xlim=c(0, 1.2))

# piecewise exp density with rate 2, 1, 3
t <- seq(0, 1.5, 0.01)
f2 <- dpwexp(t, rate=c(2, 1, 3), breakpoint=c(0.3, 0.8))
points(t, f2, col='red', pch=16)

# exp distribution can be a special case of piecewise exp distribution
f1 <- dpwexp(t, rate=2)
lines(t, f1, lwd=2)
legend('topright', c('exp dist with rate 2', 'piecewise exp dist with rate 2, 1,
3', 'histogram of piecewise exp dist with rate 2, 1, 3'),
     col=c('black', 'red'), fill=c(NA, NA, 'grey'), border=c('white', 'white',
'black'), lty=c(1, NA, NA), pch=c(NA, 16, NA), lwd=2)

# CDF of piecewise exp with rate 2, 1, 3
F2 <- ppwexp(t, rate=c(2, 1, 3), breakpoint=c(0.3, 0.8), lower.tail=TRUE)
plot(t, F2, type='l', col='red', lwd=2, main="CDF and Quantile Function of
Piecewise Exp Dist", xlim=c(0, 1.5), ylim=c(0, 1.5))

# CDF of exp dist is compatible with our package
F1 <- ppwexp(t, rate=2, lower.tail=TRUE)
lines(t, F1, lwd=2)

# plot quantile functions of both distributions
lines(F1, qpwexp(F1, rate=2, lower.tail=TRUE), lty=2, lwd=2)
lines(F2, qpwexp(F2, rate=c(2, 1, 3), breakpoint=c(0.3,0.8), lower.tail=TRUE),
     col='red', lty=2, lwd=2)

abline(0, 1, col='grey')
legend('topleft', c('CDF of piecewise exp with rate 2, 1, 3', 'quantile
function of piecewise exp with rate 2, 1, 3', 'CDF of exp with rate 2',
'quantile function of exp with rate 2'), col=c('red', 'red', 'black',
'black'), lty=c(1, 2, 1, 2), lwd=2)

```

---

plot\_event

*Plot Cumulative Event Curve*


---

**Description**

Plot cumulative event curve with right censoring data.

**Usage**

```

## Default S3 method:
plot_event(time, event, abs_time=TRUE, additional_event=0,

```

```

        add=FALSE, plot=TRUE, xyswitch=FALSE, ...)
## S3 method for class 'predict.pwexp.fit'
plot_event(time, abs_time=TRUE, add=TRUE, plot=TRUE,
           xyswitch=FALSE, eval_at=NULL, ...)
## S3 method for class 'predict.boot.pwexp.fit'
plot_event(time, abs_time=TRUE, alpha=0.1, type='confidence',
           add=TRUE, plot=TRUE, xyswitch=FALSE, eval_at=NULL,
           show_CI=TRUE, CI_par=NULL, ...)

```

## Arguments

time	observed/follow-up time from individual randomization time ( <code>abs_time=FALSE</code> ) or from the first subject randomization time ( <code>abs_time=TRUE</code> ); or a predicted object from <a href="#">predict.pwexp.fit</a> , or a predicted object with bootstrapping from <a href="#">predict.boot.pwexp.fit</a> .
abs_time	logical; if <code>TRUE</code> , time is the time from first randomization of the trial. if <code>FALSE</code> , time is the time from the randomization of each subject.
event	the status indicator, 0=censor, 1=event. Other choices are <code>TRUE/FALSE</code> ( <code>TRUE = event</code> ).
additional_event	adding the cumulative number of events by a constant number from the beginning.
add	logical; if <code>TRUE</code> add lines to current plot.
plot	logical; if <code>FALSE</code> , do not plot any lines, but return the line data
xyswitch	logical; if <code>TRUE</code> , x-axis will be cumulative number of events and y will be the time.
eval_at	a vector of the time (when <code>xyswitch=FALSE</code> ) or the number of events (when <code>xyswitch=TRUE</code> ) that you want to make prediction on.
alpha	the significance level of the confidence interval.
type	the type of prediction required. The default <code>confidence</code> returns the confidence interval without random error; the alternative <code>predictive</code> returns the predictive interval.
show_CI	logical; if <code>TRUE</code> add confidence interval of the estimated event curve.
CI_par	a list of parameters to control the appearance of lines of confidence intervals. The values pass to <a href="#">lines</a> .
...	other arguments (e.g., <code>lwd</code> , etc.) are passed over to <a href="#">plot</a> .

## Details

A convenient function to calculate and plot the cumulative number of events.

Parameters in ... are passed to [plot](#) function to control the appearance of the event curve; parameters in `CI_par` are passed to [lines](#) function to control the appearance of confidence intervals. See examples for usage.

By default, `plot_event` plots a data frame in a new figure; and plots a predicted model in existing figure.

**Value**

A data frame containing these columns:

time	sorted time
n_event	cumulative number of events

**Author(s)**

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**See Also**

[plot\\_survival](#)

**Examples**

```
set.seed(1818)
event_dist <- function(n)rpwexp(n, rate = c(0.1, 0.01, 0.2), breakpoint = c(5,14))
dat <- simdata(rand_rate = 20, drop_rate = 0.03, total_sample = 1000,
              advanced_dist = list(event_dist=event_dist),
              add_column = c('censor_reason','event','followT','followT_abs'))
cut <- quantile(dat$randT, 0.8)
train <- cut_dat(var_randT = 'randT', cut = cut, data = dat,
                var_followT = 'followT', var_followT_abs = 'followT_abs',
                var_event = 'event', var_censor_reason = 'censor_reason')

fit_res3 <- pwexp.fit(train$followT, train$event, nbreak = 2)
fit_res_boot <- boot.pwexp.fit(fit_res3, nsim = 8) # here nsim=8 is for demo purpose,
                                                # pls increase it in practice

drop_indicator <- ifelse(train$censor_reason=='drop_out' & !is.na(train$censor_reason),1,0)
fit_res_censor <- pwexp.fit(train$followT, drop_indicator, nbreak = 0)
fit_res_censor_boot <- boot.pwexp.fit(fit_res_censor, nsim = 8)

cut_indicator <- train$censor_reason=='cut'
cut_indicator[is.na(cut_indicator)] <- 0

predicted_boot <- predict(fit_res_boot, cut_indicator = cut_indicator,
                        analysis_time = cut, censor_model_boot=fit_res_censor_boot,
                        future_rand=list(rand_rate=20, total_sample=NROW(dat)-NROW(train)))

plot_event(dat$followT_abs, abs_time = TRUE, event=dat$event, ylim=c(0,800))
plot_event(predicted_boot, eval_at = seq(40,90,5), CI_par = list(lty=3, lwd=2))

plot_event(dat$followT_abs, xlim=c(0,800), event=dat$event, xyswitch = TRUE)
plot_event(predicted_boot, xyswitch = TRUE, eval_at = seq(600,900,50))
```

---

plot_survival	<i>Plot Survival Curve</i>
---------------	----------------------------

---

### Description

Plot KM curve with right censoring data or the survival curve of a fitted piecewise exponential model.

### Usage

```
## Default S3 method:
plot_survival(time, event, add=FALSE, conf.int=FALSE, mark.time=TRUE,
              lwd=2, xlab='Follow-up time', ylab='Survival function', ...)
## S3 method for class 'pweexp.fit'
plot_survival(time, add=TRUE, show_breakpoint=TRUE,
              breakpoint_par=NULL, ...)
## S3 method for class 'boot.pweexp.fit'
plot_survival(time, add=TRUE, alpha=0.1, show_breakpoint=TRUE,
              breakpoint_par=NULL, show_CI=TRUE, CI_par=NULL, ...)
```

### Arguments

time	observed time from randomization or a <a href="#">pweexp.fit</a> / <a href="#">boot.pweexp.fit</a> object.
event	the status indicator, normally 0=censor, 1=event. Other choices are TRUE/FALSE (TRUE = event).
add	logical; if TRUE add lines to current plot.
show_breakpoint	logical; if TRUE add vertical dashed lines to indicate breakpoints.
breakpoint_par	a list of parameters to control the appearance of vertical lines of breakpoints. The values pass to <a href="#">abline</a> .
alpha	the significance level of the confidence interval.
show_CI	logical; if TRUE add confidence interval of the estimated curve. For KM estimator, use <code>conf.int=TRUE</code> to show CI band.
CI_par	a list of parameters to control the appearance of lines of confidence intervals. The values pass to <a href="#">lines</a> .
conf.int	determines whether pointwise confidence intervals will be plotted. Passed over to <a href="#">plot.survfit</a> .
mark.time	controls the labeling of the curves. Passed over to <a href="#">plot.survfit</a> .
lwd	line width of the KM curve.
xlab	x label.
ylab	y label.
...	other arguments are passed over to <a href="#">plot.survfit</a> (default method) or <a href="#">plot</a> (for class <code>pweexp.fit</code> ).

**Details**

For the default method, this a wrapper of `plot.survfit` function to plot right censoring data.

For class `pwexp.fit`, parameters in `...` are passed to `plot` function to control the appearance of the survival curve; parameters in `breakpoint_par` are passed to `abline` function to control the appearance of vertical lines of breakpoints. See examples for usage.

For class `boot.pwexp.fit`, parameters in `...` are passed to `plot` function to control the appearance of the survival curve; parameters in `breakpoint_par` are passed to `abline` function to control the appearance of vertical lines of breakpoints; parameters in `CI_par` are passed to `lines` function to control the appearance of confidence intervals. See examples for usage.

**Value**

No return value.

**Author(s)**

Tianchen Xu <zjph602xutianchen@gmail.com>

**See Also**

[plot\\_event](#)

**Examples**

```
event_dist <- function(n)rpwexp(n, rate = c(0.1, 0.01, 0.2), breakpoint = c(5,14))
dat <- simdata(rand_rate = 20, drop_rate = 0.03, total_sample = 1000,
              advanced_dist = list(event_dist=event_dist),
              add_column = c('censor_reason','event','followT','followT_abs'))

plot_survival(dat$followT, dat$event, xlim=c(0,40))

fit_res <- pwexp.fit(dat$followT, dat$event, nbreak = 2)
plot_survival(fit_res, col='red', lwd=3, breakpoint_par = list(col='grey', lwd=2.5))
```

---

predict

*Predict Events for Piecewise Exponential Model*

---

**Description**

Obtains event prediction and (optionally) confidence interval from a piecewise exponential model.

**Usage**

```
## S3 method for class 'pwexp.fit'
predict(object, cut_indicator=NULL, analysis_time, censor_model=NULL,
        n_each=100, future_rand=NULL, seed=1818, ...)
## S3 method for class 'boot.pwexp.fit'
predict(object, cut_indicator=NULL, analysis_time,
        censor_model_boot=NULL, n_each=10, future_rand=NULL,
        seed=1818, ...)
```

**Arguments**

object	a <code>pwexp.fit</code> or <code>boot.pwexp.fit</code> object. It is the event model for the primary endpoint.
cut_indicator	(optional) A vector indicates which subject is censored due to the end of the trial. The length of the vector is the number of rows of the data used in <code>event_model/event_model_boot</code> . Value 0 means the subject had event or drop-out or death before the end of the trial; 1 means the subject didn't have any of these. See details.
analysis_time	the analysis time. This is the time length from the start of the trial to the time collecting data for the model.
censor_model	an object of class <code>pwexp.fit</code> returned by the <code>pwexp.fit</code> function. It is the censoring model for drop-out and death.
censor_model_boot	an object of class <code>boot.pwexp.fit</code> returned by the <code>boot.pwexp.fit</code> function. It is the censoring model with bootstrapping for drop-out and death.
n_each	the number of iterations for each bootstrapping sample to obtain predictive CI. Typically, a value of 10 to 100 should be enough.
future_rand	the randomization curve in the following times. Can be NULL if all subjects have been randomized. You can specify <b>future</b> rand rate and <b>future</b> total number of samples to be randomized by <code>list(rand_rate= , total_sample= )</code> or specify the <b>future</b> number of randomization each month by <code>list(n_rand= )</code> . See details.
seed	a random seed.
...	internal function reserved.

**Details**

The prediction will have a confidence interval only if the event model and censor model are bootstrap models.

`cut_indicator` indicates the status of each subject in the `event_model/event_model_boot` model at the end of the trial. Value 1 means the subject didn't have events, drop-out or death at the end of the trial (or say, the subject was censored due to the end of the trial). When `cut_indicator` is NOT provided, we assign value 1 to the subject who didn't have event (or drop-out, or death) in both `event_model/event_model_boot` and `censor_model/censor_model_boot` models.

`future_rand` is a list determining the parameter of randomization curve in the following times. For example, you specify randomization rate=10pt/month and total sample size=1000 by `list(rand_rate=10 , total_sample=1000)` or specify the number of randomization each month (e.g., 10,15,30,30 in four months) by `list(n_rand=c(10, 15, 30, 30))`.

**Value**

A list containing:

- event\_fun number of events vs. time curve function in each bootstrap.
- time\_fun time vs. number of events curve function in each bootstrap.

This returned list should be used in [plot\\_event](#) function for summarizing its result.

**Author(s)**

Tianchen Xu <zjph602xutianchen@gmail.com>

**See Also**

[plot\\_event](#)

**Examples**

```
set.seed(1818)
event_dist <- function(n)rpwexp(n, rate = c(0.1, 0.2), breakpoint = 14)
dat <- simdata(rand_rate = 20, drop_rate = 0.03, total_sample = 500,
              advanced_dist = list(event_dist=event_dist),
              add_column = c('censor_reason','event','followT','followT_abs'))
cut <- quantile(dat$randT, 0.8)
train <- cut_dat(var_randT = 'randT', cut = cut, data = dat,
               var_followT = 'followT', var_followT_abs = 'followT_abs',
               var_event = 'event', var_censor_reason = 'censor_reason')

fit_res3 <- pwerp.fit(train$followT, train$event, nbreak = 1)
fit_res_boot <- boot.pwerp.fit(fit_res3, nsim = 8) # here nsim=8 is for demo purpose,
                                                # pls increase it in practice

drop_indicator <- ifelse(train$censor_reason=='drop_out' & !is.na(train$censor_reason),1,0)
fit_res_censor <- pwerp.fit(train$followT, drop_indicator, nbreak = 0)
fit_res_censor_boot <- boot.pwerp.fit(fit_res_censor, nsim = 8)

cut_indicator <- train$censor_reason=='cut'
cut_indicator[is.na(cut_indicator)] <- 0

predicted_boot <- predict(fit_res_boot, cut_indicator = cut_indicator,
                        analysis_time = cut, censor_model_boot=fit_res_censor_boot,
                        future_rand=list(rand_rate=20, total_sample=NROW(dat)-NROW(train)))
plot_event(train$followT_abs, train$event, xlim=c(0,69), ylim=c(0,800))
plot_event(predicted_boot, eval_at = 40:90)
plot_event(train$followT_abs, train$event, xyswitch = TRUE, ylim=c(0,69), xlim=c(0,800))
plot_event(predicted_boot, xyswitch = TRUE, eval_at = 600:900)
```



pwexp.fit

*Fit the Piecewise Exponential Distribution***Description**

Fit the piecewise exponential distribution with right censoring data. User can specify all breakpoints, some of the breakpoints or let the function estimate the breakpoints.

**Usage**

```
pwexp.fit(time, event, breakpoint=NULL, nbreak=0, exclude_int=NULL, min_pt_tail=5,
          max_set=10000, seed=1818, trace=FALSE, optimizer='mle', tol=1e-4)
```

**Arguments**

time	observed time from randomization. For right censored data, this is the follow-up time.
event	the status indicator, normally 0=censor, 1=event. Other choices are TRUE/FALSE (TRUE = event).
breakpoint	fixed breakpoints. Pre-specify some breakpoints. The maximum value must be earlier than the last event time.
nbreak	total number of breakpoints in the model. This number includes the points specified in breakpoint. If nbreak=NULL, then nbreak=ceiling(8*(# unique events)^0.2).
exclude_int	an interval that excludes any estimated breakpoints (e.g., exclude_int=c(10, Inf) will exclude any estimated breakpoints after t=10). See details.
min_pt_tail	the minimum number of events used for estimating the tail (the hazard rate of the last piece). See details.
max_set	maximum estimated combination of breakpoints.
seed	a random seed.
trace	(internal use) logical; if TRUE, the returned data frame contains the log-likelihood of all possible breakpoints instead of the one with maximum likelihood.
optimizer	one of the optimizers: mle, ols, or hybrid.
tol	the minimum allowed gap between two breakpoints. The gap is calculated as (max(time)-min(time))*tol. Keep it as default in most cases.

**Details**

See webpage <https://zjph602xtc.github.io/PWEXP/> for a detailed description of the model and optimizers.

If user specifies breakpoint, we will check the values to make the model identifiable. Any breakpoints after the last event time will be removed; Any breakpoints before the first event time will be removed; a mid-point will be used if there are NO events between any two consecutive breakpoints. A warning will be given.

If user sets `nbreak=NULL`, then the function will automatically apply `nbreak=ceiling(8*(# unique events)^0.2)`. This empirical number of breakpoints is for the reference below, and it may be too large in many cases.

Argument `exclude_int` is a vector of two values such as `exclude_int=c(a, b)` (`b` can be `Inf`). It defines an interval that excludes any estimated breakpoints. It is helpful when excluding breakpoints that are too close to the tail.

In order to obtain a more robust hazard rate estimation of the tail, user can set `min_pt_tail` to the minimum number of events for estimating the tail (last piece of the piecewise exponential). It only works for `optimizer='mle'`.

### Value

A data frame (`res`) containing these columns:

<code>brk1, ..., brkx</code>	estimated breakpoints. The <code>attr(res, 'brk')</code> can extract the vector of breakpoint from the model ( <code>res</code> is the returned model from <code>pwexp.fit</code> ).
<code>lam1, ..., lamx</code>	estimated piecewise hazard rates. The <code>attr(res, 'lam')</code> can extract the vector of hazard rates from the model ( <code>res</code> is the returned model from <code>pwexp.fit</code> ).
<code>likelihood</code>	the log-likelihood of the model.
<code>AIC</code>	the Akaike information criterion of the model.
<code>BIC</code>	the Bayesian information criterion of the model.

### Author(s)

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### References

Muller, H. G., & Wang, J. L. (1994). Hazard rate estimation under random censoring with varying kernels and bandwidths. *Biometrics*, 61-76.

### See Also

[boot.pwexp.fit](#), [cv.pwexp.fit](#)

### Examples

```
event_dist <- function(n)rpwexp(n, rate=c(0.1, 0.01, 0.2), breakpoint=c(5,14))
dat <- simdata(rand_rate = 20, total_sample = 1000, drop_rate = 0.03,
              advanced_dist = list(event_dist=event_dist),
              add_column = c('censor_reason', 'event', 'followT', 'followT_abs'))
cut <- quantile(dat$randT, 0.8)
train <- cut_dat(var_randT = 'randT', cut = cut, data = dat,
               var_followT = 'followT', var_followT_abs = 'followT_abs',
               var_event = 'event', var_censor_reason = 'censor_reason')

fit_a0 <- pwexp.fit(train$followT, train$event, breakpoint = c(5,14))
fit_a1 <- pwexp.fit(train$followT, train$event, nbreak = 2, breakpoint = c(14))
fit_b0 <- pwexp.fit(train$followT, train$event, nbreak = 0)
```

```
fit_b1 <- pwexp.fit(train$followT, train$event, nbreak = 1)
fit_b2 <- pwexp.fit(train$followT, train$event, nbreak = 2)
```

---

simdata *Simulate Survival Data*

---

## Description

simdata is used to simulate a clinical trial data with time-to-event endpoints.

## Usage

```
simdata(group="Group 1", strata="Strata 1", allocation=1,
        event_lambda=NA, drop_rate=NA, death_lambda=NA, n_rand=NULL,
        rand_rate=NULL, total_sample=NULL, add_column=c('followT'),
        simplify=TRUE, advanced_dist=NULL)
```

## Arguments

group	a character vector of the names of each group (e.g., c('treatment', 'control')).
strata	a character vector of the names of strata in groups (e.g., c('young', 'old')).
allocation	the relative ratio of sample size in each subgroup (group*strata). See details. The value will be recycled if the length is less than needed.
event_lambda	the hazard rate of the primary endpoint (event). See details. The value will be recycled if the length is less than needed.
drop_rate	(optional) the drop-out rate (patients/month). Not hazard rate. See details. The value will be recycled if the length is less than needed.
death_lambda	(optional) the hazard rate of death. The value will be recycled if the length is less than needed.
n_rand	(required when rand_rate=NULL) a vector of the number of randomization each month; can be non-integers.
rand_rate	(required when n_rand=NULL) the randomization rate (patients/month; can be non-integer).
total_sample	(required when n_rand=NULL) total scheduled sample size.
add_column	request additional columns of the returned data frame. Valid options are: <ul style="list-style-type: none"> <li>• 'eventT_abs': absolute event time from the beginning of the trial (=eventT+randT)</li> <li>• 'dropT_abs': absolute drop-out time from the beginning of the trial (=dropT+randT)</li> <li>• 'deathT_abs': absolute death time from the beginning of the trial (=deathT+randT)</li> <li>• 'censor': censoring (drop-out or death) indicator</li> <li>• 'event': event indicator</li> <li>• 'censor_reason': censoring reason ('drop_out', 'death', 'never_event'(eventT=inf))</li> <li>• 'followT': follow-up time (true observed time) from randT</li> </ul>

	<ul style="list-style-type: none"> <li>'followT_abs': absolute follow-up time from the beginning of the trial (=followT+randT)</li> </ul>
simplify	whether drop unused columns (e.g., the group variable when there is only one group). See details.
advanced_dist	use user-specified distributions for event, drop-out and death. A list containing random generation functions. See details and examples.

## Details

See webpage <https://zjph602xtc.github.io/PWEXP/> for a diagram illustration of the relationship between returned variables.

The total number of subgroups will be '# treatment groups' \* '# strata'. The strata variable will be distributed into each treatment group. For example, if `group = c('trt', 'placebo')`, `strata = c('A', 'B', 'C')`, then there will be 6 subgroups: `trt+A`, `trt+B`, `trt+C`, `placebo+A`, `placebo+B`, `placebo+C`. The lengths of `allocation`, `event_lambda`, `drop_rate`, `death_lambda` should be 6 as well. Note that the values will be recycled for these variables. For example, if `allocation = c(1, 2, 3)`, then the proportion of 6 subgroups is actually 1:2:3:1:2:3, which means 1:1 ratio for groups, 1:2:3 ratio in each stratum.

The `event_lambda` ( $\lambda$ ) is the hazard rate of the interested events. The density function of events is  $f(t) = \lambda e^{-\lambda * t}$ . Similarly, the `death_lambda` is the hazard rate of death.

The `drop_rate` is the probability of drop-out at  $t = 1$ , which means the hazard rate of drop-out is  $-\log(1 - \text{drop\_rate})$  (or say,  $\text{drop\_rate} = 1 - e^{-\text{hazardrate}}$ ).

When `simplify=TRUE`, these columns will NOT be included:

- `group` when only one group is specified
- `strata` when only one stratum is specified
- `eventT` when `event_lambda=NA`
- `dropT` when `drop_rate=NA`
- `deathT` when `death_lambda=NA`

`advanced_dist` is used to define non-exponential distributions for event, drop-out or death. It is a list containing at least one of the elements: `event_dist`, `drop_dist`, `death_dist`. Each element has random generation functions for each subgroups. For example, `advanced_dist = list(event_dist = c(function1, function2), drop_dist = c(function3, function4))`. Here `function1`, `function3` are the event, drop-out generation function for the first subgroup; `function2`, `function4` for the second. If there is a third subgroup, `function1`, `function3` will be reused. Each data generation function (`functionX`) is a function with only one input argument `n` (sample size). If any of the `event_dist`, `drop_dist`, `death_dist` is missing, then we search for `event_lambda`, `drop_rate`, `death_lambda` to generate a exp distribution; if they are also missing, then corresponding variable will not be generated.

## Value

A data frame containing the some of these columns:

ID	subject ID
group	group indicator

strata	stratum indicator
randT	randomization time (from the beginning of the trial)
eventT	event time (from randT)
eventT_abs	event time (from the beginning of the trial)
dropT	drop-out time (from randT)
dropT_abs	drop-out time (from the beginning of the trial)
deathT	death time (from randT)
deathT_abs	death time (from the beginning of the trial)
censor	censoring (drop-out or death) indicator
censor_reason	censoring reason ('drop_out','death','never_event'(followT=inf))
event	event indicator
followT	follow-up time / observed time (from randT)
followT_abs	follow-up time / observed time (from the beginning of the trial)

**Note**

event\_lambda, drop\_rate, death\_lambda can be 0, which means the corresponding subgroup will have an Inf value for each variable.

**Author(s)**

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**See Also**

[rpwexp](#), [rpwexp\\_conditional](#)

**Examples**

```
# Two groups with two strata. In the treatment group, there is a treatment
# sensitive stratum and a non-sensitive stratum. In the placebo group, all
# subjects are the same. Treatment:place=1:2. Drop rate=1% only in treatment group.
dat <- simdata(group=c('trt', 'place'), strata = c('sensitive','non-sensitive'),
              allocation = c(1,1,2,2), rand_rate = 20, total_sample = 1000,
              event_lambda = c(0.1, 0.2, 0.01, 0.01),
              drop_rate = c(0.01, 0.01, 0, 0))

# randomized subjects
table(dat$group,dat$strata)
# randomization curve
plot(sort(dat$randT), 1:1000, xlab='time', ylab='randomized subjects')
# event time in treatment group
plot(ecdf(dat$eventT[dat$group=='trt' & dat$strata=='sensitive']))
lines(ecdf(dat$eventT[dat$group=='trt' & dat$strata=='non-sensitive']), col='red')

# One group. Event follows a piecewise exponential distribution; drop-out follows
# a Weibull; death follows a exponential.
```

```

dist_trt <- function(n)rpwexp(n, rate=c(0.01, 0.05, 0.01), breakpoint = c(30,60))
dist_placebo <- function(n)rpwexp(n, rate=c(0.01, 0.005), breakpoint = c(50))
dat <- simdata(group = c('trt','placebo'), n_rand = c(rep(10,50),rep(20,10)),
              death_lambda = 0.01,
              advanced_dist = list(event_dist=c(dist_trt, dist_placebo),
                                   drop_dist=function(n)rweibull(n,3,40))

# randomized subjects
table(dat$group)
# randomization curve
plot(sort(dat$randT), 1:700, xlab='time', ylab='randomized subjects')
# event time in both groups
plot(ecdf(dat$eventT[dat$group=='trt']), xlim=c(0,100))
lines(ecdf(dat$eventT[dat$group=='placebo']), col='red')
# drop-out time
plot(ecdf(dat$dropT), xlim=c(0,100))

# mixture cure distribution, 20% of the subject are cured and will not have events
dat <- simdata(strata=c('cure','non-cure'), allocation=c(20,80),
              event_lambda=c(0, 0.38), n_rand = rep(20,30),
              add_column = c('eventT_abs', 'censor', 'event',
                             'censor_reason', 'followT', 'followT_abs'))

```

---

sim\_followup

*Estimate follow up time and number of events by simulation*


---

## Description

sim\_followup is used to estimate follow-up time and number of events (given calander time, or number of randomized samples, or number of events).

## Usage

```

sim_followup(at, type = 'calander', group="Group 1", strata='Strata 1',
             allocation=1, event_lambda=NA, drop_rate=NA, death_lambda=NA,
             n_rand=NULL, rand_rate=NULL, total_sample=NULL, extra_follow=0,
             by_group=FALSE, by_strata=FALSE, advanced_dist=NULL,
             stat=c(mean, median, sum), follow_up_endpoint=c('death', 'drop_out',
             'cut'), count_in_extra_follow=FALSE, count_insufficient_event=FALSE,
             start_date=NULL, rep=300, seed=1818)

```

## Arguments

at	specify a vector of occasions. When type='calander', at is the time from first randomization; when type='event', at is the number of accumulated events; when type='sample', at is the number of randomized samples.
type	specify the type of at. Must be 'calander', event or sample.
group	a character vector of the names of each group (e.g., c('treatment', 'control')). See <a href="#">simdata</a> .

strata	a character vector of the names of strata in groups (e.g., c('young', 'old')). See <a href="#">simdata</a> .
allocation	the relative ratio of sample size in each subgroup (group*strata). The value will be recycled if the length is less than needed. See <a href="#">simdata</a> .
event_lambda	the hazard rate of the primary endpoint (event). The value will be recycled if the length is less than needed. See <a href="#">simdata</a> .
drop_rate	(optional) the drop-out rate (patients/month). Not hazard rate. The value will be recycled if the length is less than needed. See <a href="#">simdata</a> .
death_lambda	(optional) the hazard rate of death. The value will be recycled if the length is less than needed. See <a href="#">simdata</a> .
n_rand	(required when rand_rate=NULL) a vector of the number of randomization each month; can be non-integers. See <a href="#">simdata</a> .
rand_rate	(required when n_rand=NULL) the randomization rate (patients/month; can be non-integer). See <a href="#">simdata</a> .
total_sample	(required when n_rand=NULL) total scheduled sample size. See <a href="#">simdata</a> .
extra_follow	delay the analysis time by extra time (extra_follow) after the time specified by at. See details.
by_group	logical; if TRUE, also return results by each group.
by_strata	logical; if TRUE, also return results by each stratum.
advanced_dist	use user-specified distributions for event, drop-out and death. A list containing random generation functions. See details and examples in <a href="#">simdata</a> .
stat	a vector of functions to summarize the follow-up time. See example.
follow_up_endpoint	Which endpoints can be regarded as the end of follow-up. Choose from 'death', 'drop_out', 'cut' (censored at the end of the trial) or 'event'.
count_in_extra_follow	logical; whether to count subjects who are randomized after the time specified by at but before the time specified by at + extra_follow.
count_insufficient_event	logical; only affects the result when type='event'. If TRUE, for samples that cannot achieve required number of events, the last follow-up time is the analysis time. If FALSE, these samples will be dropped.
start_date	the start date of the first randomization; in the format: "2000-01-30"
rep	number simulated iterations.
seed	a random seed.

## Details

See the help document of [simdata](#) for most arguments details.

When type='calander', the function estimates the follow-up time and number of events at time at plus extra\_follow; when type='event', the function estimates these at the time when total number of events is at plus time extra\_follow; when type='sample', the function estimates these at the time when total number of randomized subjects is at plus time extra\_follow.

The stat specifies a vector of user defined functions. Each of them must take a vector of individual follow-up time as input and return a single summary value. See example.

**Value**

A data frame containing the some of these columns:

ID	subject ID
group	group indicator
strata	stratum indicator
randT	randomization time (from the beginning of the trial)
eventT	event time (from randT)
eventT_abs	event time (from the beginning of the trial)
dropT	drop-out time (from randT)
dropT_abs	drop-out time (from the beginning of the trial)
deathT	death time (from randT)
deathT_abs	death time (from the beginning of the trial)
censor	censoring (drop-out or death) indicator
censor_reason	censoring reason ('drop_out','death','never_event'(followT=inf))
event	event indicator
followT	follow-up time / observed time (from randT)
followT_abs	follow-up time / observed time (from the beginning of the trial)

**Note**

event\_lambda, drop\_rate, death\_lambda can be 0, which means the corresponding subgroup will have an Inf value for each variable.

**Author(s)**

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**See Also**

[simdata](#)

**Examples**

```
# Two groups. Treatment:place=1:2. Drop rate=3%/month. Hazard ratio=0.7.

# define the piecewise exponential event generation function
myevent_dist_trt <- function(n)rpwexp(n, rate=c(0.1, 0.01, 0.2)*0.7, breakpoint=c(5,14))
myevent_dist_con <- function(n)rpwexp(n, rate=c(0.1, 0.01, 0.2), breakpoint=c(5,14))

# user defined summary function, the proportion of subjects that follow more than 12 month
prop_12 <- function(x)mean(x >= 12)

# estimate the event curve or timeline:
# (here rep=60 is for demo purpose only, please increase this value in practice!)
event_curve <- sim_followup(at=seq(20,90,10), type = 'calendar', group = c('trt','con'),
```



```
rand_rate = 20, total_sample = 1000, drop_rate = 0.03, allocation = 1:2,
advanced_dist = list(event_dist=c(myevent_dist_trt, myevent_dist_con)),
by_group = TRUE, stat = c(median, mean, prop_12), start_date = "2020-01-01",
rep=60)
time_curve <- sim_followup(at=seq(200,600,100), type = 'event', group = c('trt','con'),
rand_rate = 20, total_sample = 1000, drop_rate = 0.03, allocation = 1:2,
advanced_dist = list(event_dist=c(myevent_dist_trt, myevent_dist_con)),
stat = c(median, mean, prop_12), start_date = "2020-01-01", rep=60)
# plot event curve or timeline
plot(event_curve$T_all$analysis_time_c, event_curve$T_all$event, xlab='Time',
ylab='Number of events', type='b')
plot(time_curve$T_all$event, time_curve$T_all$analysis_time_c, xlab='Number of
events', ylab='Time', type='b')
```

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