

# Package ‘wtdr’

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**Type** Package

**Title** Parametric Waiting Time Distribution estimation

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**Author** Sabrina Giometto, Malcolm Gillies, Olga Paoletti, Henrik Støvring

**Maintainer** Henrik Støvring <hersto@rm.dk>

**Description** Estimation of prescription durations and treatment probability based on the parametric Waiting Time Distribution. Pharmacoepidemiologic databases contains information on medication dispensings at pharmacies. Studies using such data typically require some estimate of duration of treatment after a dispensing (known as the prescription duration), which can be estimated using the parametric Waiting Time Distribution.

**License** GPL (>= 3)

**Roxygen** list(markdown = TRUE)

**Imports** bbmle,  
Deriv,  
data.table (>= 1.15.0),  
methods,  
graphics,  
rlang,  
stats

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haven

**Config/testthat/edition** 3

**Encoding** UTF-8

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**Collate** 'wtdr-package.R'  
'dfunctions.R'  
'wtd-class.R'  
'plot.R'  
'pred\_dur\_prob.R'  
'wtdttt.R'  
'ranwtdttt.R'  
'sandwich.R'  
'summary\_wtd-class.R'  
'summaryWtd.R'

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coef,wtd-method	<i>Extract coefficients</i>
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Description

Extract the coefficients from an object of class inheriting from "wtd"

Usage

```
## S4 method for signature 'wtd'  
coef(object)
```

Arguments

object                    a fitted object of class inheriting from "wtd"

Value

A summary of the fitted object

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dexp	<i>The Exponential distribution</i>
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**Description**

The Exponential distribution

**Usage**

```
dexp(x, logitp, lnbeta, delta = 1, log = FALSE)
```

**Arguments**

x	vector of event times (must be between (0; delta))
logitp	log-odds of being a prevalent user
lnbeta	log of beta (scale)
delta	width of interval with positive support (x in (0; delta))
log	logical; if TRUE, probabilities p are given as log(p)

**Value**

Density. The length of the result is the maximum of the lengths of the numerical arguments.

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dlnorm	<i>The Lognormal distribution</i>
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**Description**

The Lognormal distribution

**Usage**

```
dlnorm(x, logitp, mu, lnsigma, delta = 1, log = FALSE)
```

**Arguments**

x	vector of event times (must be between (0; delta))
logitp	log-odds of being a prevalent user
mu	mean on log-scale
lnsigma	log of standard deviation on log-scale
delta	width of interval with positive support (x in (0; delta))
log	logical; if TRUE, density values are returned on log-scale.

**Value**

Density. The length of the result is the maximum of the lengths of the numerical arguments.

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dweib	<i>The Weibull distribution</i>
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### Description

The Weibull distribution

### Usage

```
dweib(x, logitp, lnalpha, lnbeta, delta = 1, log = FALSE)
```

### Arguments

x	vector of event times (must be between (0; delta))
logitp	log-odds of being a prevalent user
lnalpha	log of alpha (shape)
lnbeta	log of beta (scale)
delta	width of interval with positive support (x in (0; delta))
log	logical; if TRUE, probabilities p are given as log(p)

### Value

Density. The length of the result is the maximum of the lengths of the numerical arguments.

---

plot,wtd,ANY-method	<i>Make WTD diagnostic plots</i>
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### Description

Make diagnostic plots showing the fit of an estimated parametric Waiting Time Distribution (WTD) with respect to the observed histogram of prescription redemptions.

### Usage

```
## S4 method for signature 'wtd,ANY'
plot(wtd, x = NULL, y = NULL, ...)
```

### Arguments

wtd	wtd object, typically result of wtdttt
x	ignored
y	ignored
...	other graphical parameters (see par)

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predict,wtd-method	<i>Make WTD predictions</i>
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## Description

Make predictions based on an estimated parametric Waiting Time Distribution (WTD) model, either the probability of a person still being in treatment or the duration of observed prescription redemptions.

## Usage

```
## S4 method for signature 'wtd'
predict(
  object,
  prediction.data = NULL,
  type = "dur",
  iadmean = F,
  distrx = NULL,
  quantile = 0.8,
  se.fit = FALSE,
  na.action = na.pass,
  ...
)
```

## Arguments

object	a fitted object of class inheriting from "wtd"
prediction.data	An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
type	"dur" or "prob". Default "dur".
iadmean	logical; if T, mean duration is predicted.
distrx	For type="prob", a vector of dispensing gaps.
quantile	For type="dur", quantile of distribution. Default 0.8
se.fit	A switch indicating if standard errors are required
na.action	function determining what should be done with missing values in newdata. The default is to predict NA
...	further arguments passed to or from other methods

## Details

#' @section Data format: Covariates in the data provided for wtdttt, used for estimation, must be in the prediction data as well -if used- with identical names The class of the covariate must be the same in the dataset used for estimation and in the one used for prediction - if different - i.e. packsize used as a factor.

## Value

A vector of predictions

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ranwtdttt

*Fit Waiting Time Distribution with random index times*


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## Description

ranwtdttt() estimates maximum likelihood estimates for parametric Waiting Time Distribution (WTD) based on observed prescription redemptions with adjustment for covariates using one or more random index times for each individual. It reports estimates of prevalence fraction and specified percentile of inter-arrival density together with regression coefficients.

## Usage

```
ranwtdttt(
  data,
  form,
  parameters = NULL,
  start = NA,
  end = NA,
  reverse = F,
  id = NA,
  nsamp = 1,
  subset = NULL,
  robust = T,
  na.action = na.omit,
  init = NULL,
  control = NULL,
  ...
)
```

## Arguments

data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which wtdttt is called.
form	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of the model specification are given under 'Details'
parameters	model formulae for distribution parameters
start	start of observation window
end	end of observation window
reverse	logical; Fit the reverse waiting time distribution.
id	the name of the variable that identifies distinct individuals
nsamp	number of samples to take.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
robust	logical; compute a robust estimate of variance.

<code>na.action</code>	a function which indicates what should happen when the data contain NAs. The default is set by the <code>na.action</code> setting of options, and is <code>na.fail</code> if that is unset. The 'factory-fresh' default is <code>na.omit</code> . Another possible value is <code>NULL</code> , no action. Value <code>na.exclude</code> can be useful.
<code>init</code>	starting values for the parameters.
<code>control</code>	a list of parameters for controlling the fitting process.
<code>...</code>	further arguments passed to other methods.

**Value**

`ranwtdttt` returns an object of class "wtd" inheriting from "mle".

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<code>sand_vcov</code>	<i>Calculate a robust variance-covariance matrix using the sandwich estimator</i>
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**Description**

Calculate a robust variance-covariance matrix using the sandwich estimator

**Usage**

```
sand_vcov(fit)
```

**Arguments**

`fit` an object of class "wtd" returned by `ranwtdttt()`

**Value**

`sand_vcov` returns a matrix

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<code>show</code>	<i>Show</i>
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**Description**

Show

**Usage**

```
show(object)
```

**Arguments**

`object` Any R object

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```
show, summary.wtd-method
```

*Formatting of the summary of the model object and the prevalence of drug use*

---

### Description

Formatting of the summary of the model object and the prevalence of drug use

### Usage

```
## S4 method for signature 'summary.wtd'
show(object)
```

### Arguments

object                    a fitted object of class inheriting from "wtd"

### Value

A summary of the fitted object along with the estimated prevalence and its 95% CI

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```
summary, wtd-method      Summarise model object and prevalence of drug use
```

---

### Description

Summarise model object from wtdttt and print the estimated prevalence of drug use along with its 95% confidence interval .

### Usage

```
## S4 method for signature 'wtd'
summary(object)
```

### Arguments

object                    a fitted object of class inheriting from "wtd"

### Value

A summary of the fitted object



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summary.wtd-class	<i>summary.wtd-class - R class definition</i>
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## Description

Register a 'summary.wtd' class, inheriting from 'summary.mle2'

## Slots

call call of the model formula

coef matrix of coefficients estimated through wtdttt function

m2logL log-likelihood

prev\_fin estimate of prevalence of drug use and its 95% confidence interval

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vcov,wtd-method	<i>Extract variance-covariance matrix</i>
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## Description

Extract variance-covariance matrix from an object of class inheriting from "wtd"

## Usage

```
## S4 method for signature 'wtd'
vcov(object)
```

## Arguments

object a fitted object of class inheriting from "wtd"

## Value

A vector of coefficients

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wtd-class	<i>An S4 class representing the result of maximum likelihood estimation for a WTD</i>
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### Description

This class encapsulates results of maximum likelihood estimation for a waiting time distribution.

### Slots

delta value of the delta parameter  
 start window's start  
 end window's end  
 dist name of the WTD distribution family: "lnorm", "weib" or "exp"  
 depvar name of the dependent variable  
 idvar (optional) name of the id variable  
 isreverse logical; indicates whether a forward or backward distribution is used

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wtdttt	<i>Fit Waiting Time Distribution</i>
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### Description

Estimates the maximum likelihood estimate for a parametric Waiting Time Distribution (WTD) based on observed prescription redemptions with adjustment for covariates. Reports estimates of prevalence fraction and specified percentile of inter-arrival density together with regression coefficients.

### Usage

```
wtdttt(
  data,
  form,
  parameters = NULL,
  start = NA,
  end = NA,
  reverse = F,
  id = NA,
  preprocess = T,
  subset = NULL,
  na.action = na.omit,
  init = NULL,
  control = NULL,
  ...
)
```

## Arguments

data	an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>wtdttt</code> is called.
form	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of the model specification are given under 'Details'
parameters	optional model formulae for distribution parameters
start	start of observation window (date or real number)
end	end of observation window (date or real number)
reverse	logical; Fit the reverse waiting time distribution (default F).
id	name of the id variable (optional)
preprocess	logical; Pre-process the data to limit to one observation per id. If id is omitted, defaults to F (default T).
subset	an optional vector specifying a subset of observations to be used in the fitting process. If the variable for which you want to create the subset is a factor, it is necessary to use both double and single quotation marks in the following way: i.e., <code>subset = 'sex=="F"'</code>
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the <code>na.action</code> setting of options, and is <code>na.fail</code> if that is unset. The 'factory-fresh' default is <code>na.omit</code> . Another possible value is <code>NULL</code> , no action. Value <code>na.exclude</code> can be useful.
init	starting values for the parameters.
control	a list of parameters for controlling the fitting process.
...	further arguments passed to other methods.

## Value

`wtdttt` returns an object of class "wtd" inheriting from "mle".

## Model formula

The model formula form follows the pattern `obstime ~ dist(alpha, beta, gamma)` with

- `obstime`: the redemption time variable (date or real number)
- `dist`: the parametric distribution for the forward or backward recurrence density (FRD/BRD), which must be `dexp()`, `dweib()` or `dlnorm()` i.e named after their corresponding interarrival density (IAD).

The model formula parameters follows the pattern `list(alpha ~ "covariate", beta ~ "covariate", gamma ~ 1)` with

- `covariate`: the variable that is informative about the duration to the next prescription redemption and that will affect the estimate of the parameters of the model In the pattern reported above the covariate only affect alpha and beta, but not gamma (since 1 is supplied after ~)

## Data format

The WTD is fit to the first prescription redemption of each individual within an observation window (ordinary WTD), or the last (reverse WTD), respectively.

You may prepare the data to this format, or optionally specify the name of an id variable to select the first or last redemption automatically.

If the redemption time data are of type date, a continuity correction will be applied automatically.

## Examples

```
# Fit the WTD with a lognormal distribution -----

# load data
df <- haven::read_dta(system.file("extdata", "wtddat_dates.dta", package="wtdr"))

# fit the model
fit1 <- wtdttt(data = df,
               form = rx1time ~ dlnorm(logitp, mu, lnsigma),
               id = "pid",
               start = as.Date('2014-01-01'),
               end = as.Date('2014-12-31'))
)
```

```
# Fit a reverse WTD with covariates -----

# load data
df <- haven::read_dta(system.file("extdata", "wtddat_covar.dta", package="wtdr"))

# make packsize a factor
df$packsize <- as.factor(df$packsize)

# fit the model
fit1 <- wtdttt(data = df,
               form = last_rxttime ~ dlnorm(logitp, mu, lnsigma),
               start = 0,
               end = 1,
               reverse = TRUE,
               parameters = list(logitp ~ packsize, mu ~ packsize, lnsigma ~ packsize))
)
```

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