

# Package ‘Rwtdttt’

April 29, 2024

**Type** Package

**Title** Parametric Waiting Time Distribution estimation

**Version** 0.1.0

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**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,  
class,  
data.table,  
dplyr,  
haven,  
methods,  
graphics,  
stats,  
numDeriv

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.3

**Collate** 'Rwtdttt-package.R'  
'dfunctions.R'  
'wtd-class.R'  
'plot.R'  
'pred\_dur\_prob.R'  
'wtdttt.R'  
'ranwtdttt.R'  
'sandwich.R'

R topics documented:

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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 prescription redemption times               |
| logitp | log-odds of being a prevalent user                    |
| lnbeta | log of beta (scale)                                   |
| delta  | XXXX  |
| log    | logical; if TRUE, probabilities p are given as log(p) |

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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 prescription redemption times                |
| logitp  | log-odds of being a prevalent user                     |
| mu      | mean on log-scale                                      |
| lnsigma | log of standard deviation on log-scale                 |
| delta   | XXXX   |
| log     | logical; if TRUE, probabilities p are given as log(p). |

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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 prescription redemption times
logitp	log-odds of being a prevalent user
lnalpha	log of alpha (shape)
lnbeta	log of beta (scale)
delta	XXXX
log	logical; if TRUE, probabilities p are given as log(p)

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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. HS 240108: I think this needs to incorporate information on time period of observations (start and end specified in call to wtdttt)

### Usage

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

### Arguments

wtd	wtd object, typically result of wtdttt
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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,
  newdata = NULL,
  type = "dur",
  distrx = NULL,
  quantile = 0.8,
  se.fit = FALSE,
  na.action = na.pass,
  ...
)
```

### Arguments

wtd                      a fitted object of class inheriting from "wtd"

### Value

A vector of predictions

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ranwtdttt	<i>Fit Waiting Time Distribution with random index times</i>
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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. Reports estimates of prevalence fraction and specified percentile of inter-arrival density together with regression coefficients.

### Usage

```
ranwtdttt(
  form,
  parameters = NULL,
  data,
  id,
  start,
  end,
```

```

    reverse = F,
    nsamp = 4,
    subset,
    na.action = na.pass,
    init,
    control = NULL,
    ...
  )

```

### Arguments

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
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.
id	the name of the variable that identifies distinct individuals
start	start of observation window
end	end of observation window
reverse	logical; Fit the reverse waiting time distribution.
nsamp	number of samples to take.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options, and is na.fail if that is unset. The 'factory-fresh' default is na.omit. Another possible value is NULL, no action. Value na.exclude 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".

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sand_vcov	<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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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,
  subset = NA,
  na.action = na.pass,
  init = NULL,
  control = NULL,
  ...
)
```

**Arguments**

<code>data</code>	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.
<code>form</code>	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'
<code>parameters</code>	optional model formulae for distribution parameters
<code>start</code>	start of observation window (date or real number)
<code>end</code>	end of observation window (date or real number)
<code>reverse</code>	logical; Fit the reverse waiting time distribution (default F).
<code>id</code>	name of the id variable (optional)

subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options, and is na.fail if that is unset. The 'factory-fresh' default is na.omit. Another possible value is NULL, no action. Value na.exclude 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).

**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.

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