

Package: reslife (via r-universe)

September 3, 2024

Type Package

Title Calculate Mean Residual Life (MRL) and Related Values for Different Distributions

Version 0.2.1

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Description A pair of functions for calculating mean residual life (MRL), median residual life, and percentile residual life using the outputs of either the 'flexsurv' package or parameters provided by the user. Input information about the distribution, the given 'life' value, the percentile, and the type of residual life, and the function will return your desired values. For the 'flexsurv' option, the function allows the user to input their own data for making predictions. This function is based on Jackson (2016) [<doi:10.18637/jss.v070.i08>](https://doi.org/10.18637/jss.v070.i08).

License GPL (>= 3)

Encoding UTF-8

RoxygenNote 7.2.3

Depends pracma, flexsurv, gsl

URL <https://github.com/an-crawford/reslife>

Suggests knitr, rmarkdown

VignetteBuilder knitr

Repository <https://an-crawford.r-universe.dev>

RemoteUrl <https://github.com/an-crawford/reslife>

RemoteRef HEAD

RemoteSha 350310d614df0dce94db35bcdf384c18a34c62bc

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residlife

*Calculating Residual Life Values***Description**

Calculates residual life values over a range of values. Allows the user to specify the distribution and the parameters.

Usage

```
residlife(values, distribution, parameters, p = 0.5, type = "mean")
```

Arguments

values	Range of values over which residual life is calculated. Usually given as a vector.
distribution	Name of the distribution. Needs to be one of 'weibull', 'gompertz', 'gamma', 'gengamma.orig', 'exponential', 'lnorm', or 'llogis', 'genf', or 'genf.orig'.
parameters	Parameters of the survival function. Needs to be inputted in order as a vector, with the name of the parameter included.
p	Percentile at which to calculate residual life. Default is .5.
type	Type of residual life outputted. Must be "mean", "median", "percentile", or "all". Default is "mean".

Value

The residual life for a specified sequence of values.

References

Jackson CH (2016). "flexsurv: a platform for parametric survival modeling in R." *Journal of statistical software*, 70.

Poynor V (2010). "Bayesian inference for mean residual life functions in survival analysis." Masters diss., University of California, Santa Cruz.

Prentice RL (1975). "Discrimination among some parametric models." *Biometrika*, 62(3), 607–614.

Stacy EW (1962). "A generalization of the gamma distribution." *The Annals of mathematical statistics*, pp. 1187–1192

Examples

```
residlife(values = 0:60, distribution= 'weibull', parameters = c(shape = 1.2, scale = 3))
residlife(values = 15:35, distribution= 'gamma', parameters = c(shape = 1.2, rate = 1.7),
p = .25, type = 'all')
```

`reslifefsr`*Calculate Residual Life Values Using a flexsurvreg() Object*

Description

Calculate residual life values using a `flexsurvreg()` object. Contains an option to supply new data and returns the output as a vector.

Usage

```
reslifefsr(obj, life, p = 0.5, type = "mean", newdata = data.frame())
```

Arguments

<code>obj</code>	Name of a <code>flexsurvreg()</code> object from which data is extracted.
<code>life</code>	Value at which the user wants to calculate residual life. Must be a scalar.
<code>p</code>	percentile for percentile residual life, default is .5
<code>type</code>	can be 'mean', 'median', 'percentile', or 'all'. Default is 'mean'.
<code>newdata</code>	a data frame containing new data values to calculate residual life for. Default is a blank data frame.

Value

A vector of residual life values

References

Jackson CH (2016). "flexsurv: a platform for parametric survival modeling in R." *Journal of statistical software*, 70.

Poynor V (2010). "Bayesian inference for mean residual life functions in survival analysis." Masters diss., University of California, Santa Cruz.

Prentice RL (1975). "Discrimination among some parametric models." *Biometrika*, 62(3), 607–614.

Stacy EW (1962). "A generalization of the gamma distribution." *The Annals of mathematical statistics*, pp. 1187–1192

Examples

```
library(flexsurv)
fitg <- flexsurv::flexsurvreg(formula = Surv(futime, fustat) ~ 1,
  data = ovarian, dist="gengamma")
reslifefsr(obj = fitg, life = 6, p= .75, type= 'all')

fitg2 <- flexsurv::flexsurvreg(formula = Surv(futime, fustat) ~ age,
  data = ovarian, dist="gengamma")
df_new = data.frame(age = 12)
reslifefsr(obj = fitg2, life = 3, type = 'median', newdata = df_new)
```

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