Package 'reslife'

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Type Package

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

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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>.

License GPL (>= 3)

Encoding UTF-8

Depends pracma, flexsurv, gsl

URL https://github.com/an-crawford/reslife, https://kaloklee.github.io/reslife/

Suggests knitr, rmarkdown, survival, testthat (>= 3.0.0)

VignetteBuilder knitr

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NeedsCompilation no

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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 fitted `flexsurvreg` object. Allows specifying covariate profiles via `newdata`.

Usage

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

Arguments

`obj`	A fitted `flexsurvreg` object from package **flexsurv**.
`life`	Scalar numeric value of elapsed time at which to calculate residual life.
`p`	Percentile for quantile residual life. Default is 0.5.
`type`	Type of residual life to return: `"mean"`, `"median"`, `"quantile"`, `"percentile"`, or `"all"`. Default is `"mean"`.
`newdata`	A data frame containing covariate values to evaluate. Default is empty (evaluates baseline).

Value

A numeric vector (if `type` is `"mean"`, `"median"`, or `"quantile"`) or a data frame (if `type == "all"`), with one row per covariate profile in `newdata`.

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 <- flexsurvreg(Surv(futime, fustat) ~ 1, data = ovarian, dist = "gengamma")
reslifefsr(obj = fitg, life = 6, p = 0.75, type = "all")

fitg2 <- flexsurvreg(Surv(futime, fustat) ~ age, data = ovarian, dist = "gengamma")
df_new <- data.frame(age = c(50, 65))
reslifefsr(obj = fitg2, life = 3, type = "median", newdata = df_new)
```

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