

# Package ‘reslife’

May 9, 2026

**Type** Package

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

**Version** 0.2.1

**Date** 2023-10-26

**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

**NeedsCompilation** no

**Author** Andrew Crawford [cre, aut],  
Zekai Wang [aut],  
Ka Lok Lee [aut]

**Maintainer** Andrew Crawford <[atcrawford18@gmail.com](mailto:atcrawford18@gmail.com)>

**Repository** CRAN

**Date/Publication** 2023-10-26 19:50:02 UTC

## Contents

residlife	2
reslifefsr	3

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**

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

# Index

residlife, 2  
reslifefsr, 3