Package 'simIC'

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Title Simulate and Analyze Interval- and Mixed-Censored Survival Data

Version 0.1.0

Description Provides tools to simulate and analyze survival data with interval-, left-, right-, and uncensored observations under common parametric distributions, including ``Weibull'', ``Exponential'', ``Log-Normal'', ``Log-Logistic'', ``Gamma'', ``Gompertz'', ``Normal'', ``Logistic'', and ``EMV''. The package supports both direct maximum likelihood estimation and imputation-based methods, making it suitable for methodological research, simulation benchmarking, and teaching. A web-based companion app is also available for demonstration purposes.

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Encoding UTF-8

RoxygenNote 7.3.2

URL https://github.com/jayarasan/simIC

BugReports https://github.com/jayarasan/simIC/issues

NeedsCompilation no

Author Jayanthi Arasan [aut, cre]

Maintainer Jayanthi Arasan <jayanthi@upm.edu.my>

Repository CRAN

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mle_imp *Imputation-Based MLE for Censored Data*

Description

Estimates distribution parameters using imputed event times.

Usage

```
mle_imp(
  left,
  right,
  dist = "weibull",
 impute = c("midpoint", "random", "median", "harmonic_median", "geometric_median",
    "random_survival")
)
```

Arguments

left	Left bounds of censoring intervals
right	Right bounds of censoring intervals
dist	Distribution name (e.g. "weibull", "loglogistic", "EMV")
impute	Imputation method: "midpoint", "random", "median", "harmonic_median", "geometric_median", "random_survival"

Value

A list containing estimates, standard errors, and log-likelihood

Examples

```
# Simulate interval-censored data from a Weibull distribution
set.seed(123)
dat <- simIC(n = 100, dist = "weibull", shape = 1.5, scale = 5, width = 2,
             study_start = 1, study_end = 8, uncensored_tol = 0.1)

# Fit model using harmonic median imputation
fit <- mle_imp(left = dat$left, right = dat$right, dist = "weibull", impute = "harmonic_median")

# Inspect results
print(fit$estimates)
print(fit$logLik)
print(fit$converged)
```

mle_int *Interval-Censored Maximum Likelihood Estimation*

Description

Estimates distribution parameters by maximizing the interval-censored likelihood.

Usage

```
mle_int(left, right, dist)
```

Arguments

left	Left bounds of censoring intervals
right	Right bounds of censoring intervals
dist	Distribution name (e.g. "weibull", "loglogistic", "EMV")

Value

A list containing estimates, standard errors, log-likelihood, and convergence status

Examples

```
# Simulate data from a log-logistic distribution
set.seed(123)
data <- simIC(n = 100, dist = "loglogistic", shape = 1.5, scale = 5, width = 2,
              study_start = 1, study_end = 8, uncensored_tol = 0.1)
# Fit the model
fit <- mle_int(left = data$left, right = data$right, dist = "loglogistic")
print(fit$estimates)
print(fit$logLik)
print(fit$converged)
```

simIC *Simulate Interval-, Left-, Right-, and Uncensored Survival Data*

Description

Simulates survival data with optional left-censoring, right-censoring, and uncensoring thresholds.

Usage

```
simIC(
  n = 100,
  dist = "weibull",
  shape = 2,
  scale = 1,
  meanlog = 0,
  sdlog = 1,
  location = 0,
  width = 1,
  visit_start = 0,
  study_start = NULL,
  study_end = NULL,
  uncensored_tol = 0.1
)
```

Arguments

n	Number of samples.
dist	Distribution name ("weibull", "exp", "lognormal", "loglogistic", "normal", "logistic", "EMV", "gamma", "gompertz").
shape, scale	Distribution parameters for applicable distributions.
meanlog, sdlog	For lognormal.
location	For normal, logistic, and EMV.
width	Visit interval width.
visit_start	First visit time.
study_start	Optional: left-censoring cutoff.
study_end	Optional: right-censoring cutoff.
uncensored_tol	Tolerance to treat (left, right) as exact event.

Value

A data frame with columns: id, left, right, true_time, censoring

Examples

```
# Simulate 100 survival times from a log-normal distribution
set.seed(123)
data <- simIC(n = 100, dist = "lognormal", meanlog = 1.5, sdlog = 0.5, width = 2,
              study_start = 1, study_end = 8, uncensored_tol = 0.1)
head(data)
```

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