

Package ‘gofmalm’

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Type Package

Title Goodness-of-Fit Tests for Type-II Censored Samples via the Malmquist Transformation

Version 0.1.0

Description Goodness-of-fit tests for an arbitrary user-specified continuous distribution under Type-II right- or left-censoring. Implements the transformation-based method of Lin, Huang and Balakrishnan (2008) [<doi:10.1109/TR.2008.2005860>](https://doi.org/10.1109/TR.2008.2005860), which uses a property of order statistics due to Malmquist (1950) to convert an r-out-of-n Type-II censored uniform sample into a complete sample of size r, alongside the earlier transformation of Michael and Schucany (1979) [<doi:10.1080/00401706.1979.10489813>](https://doi.org/10.1080/00401706.1979.10489813). Also implements the direct (untransformed) censored-sample statistics of Barr and Davidson (1973) [<doi:10.1080/00401706.1973.10489108>](https://doi.org/10.1080/00401706.1973.10489108) and Pettitt and Stephens (1976) [<doi:10.1093/biomet/63.2.291>](https://doi.org/10.1093/biomet/63.2.291), and the modified-statistic maximum-likelihood procedure of Chen and Balakrishnan (1995) for testing composite hypotheses. General background on empirical-distribution-function goodness-of-fit methods follows D'Agostino and Stephens (1986, ISBN:982-0-8247-7487-5).

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fit_mle	<i>Maximum Likelihood Estimation for Type-II Censored Samples</i>
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Description

Estimates distribution parameters under Type-II right- or left-censoring.

Usage

```
fit_mle(  
  data,  
  n,  
  pdf,  
  cdf,  
  sf = NULL,  
  params,  
  censoring = c("right", "left"),  
  optim_control = list()  
)
```

Arguments

- data Numeric vector of length r, sorted ascending.
- n Total sample size (n >= r).
- pdf Probability density function.
- cdf Cumulative distribution function.
- sf Survival function. If NULL, computed as 1 - cdf(x, params).

params Named list or vector of starting parameter values.
 censoring Type of censoring: "right" or "left".
 optim_control Optional control list passed to `optim`.

Value

A list containing `par` (estimated parameters), `value` (negative log-likelihood), convergence status code, and message.

Examples

```

data_exp <- c(0.1, 0.2, 0.3, 0.4, 0.7, 1.0, 1.4)
fit <- fit_mle(
  data = data_exp, n = 20,
  pdf = function(x, p) dexp(x, rate = p$rate),
  cdf = function(x, p) pexp(x, rate = p$rate),
  params = list(rate = 0.1),
  censoring = "right"
)
fit$par

```

gof_censored

Goodness-of-Fit Testing for Type-II Censored Samples

Description

Performs goodness-of-fit tests for arbitrary user-specified continuous parametric distributions under Type-II right- or left-censoring using the Malmquist and Michael-Schucany transformations.

Usage

```

gof_censored(
  data,
  n,
  pdf,
  cdf,
  sf = NULL,
  params = NULL,
  estimate = TRUE,
  censoring = c("right", "left"),
  transform = c("both", "malmquist", "ms"),
  statistics = c("all", "direct7", "complete_ad", "composite_mle", "direct_censored"),
  pvalue_method = c("auto", "distribution_free", "parametric_bootstrap"),
  nsim = 2000,
  seed = NULL,
  optim_control = list()
)

```

Arguments

data	Numeric vector of observed order statistics, length r .
n	Total sample size ($n \geq \text{length}(\text{data})$).
pdf	Probability density function $f(x, \text{params})$.
cdf	Cumulative distribution function $F(x, \text{params})$.
sf	Survival function $S(x, \text{params})$. If NULL, computed as $1 - \text{cdf}(x, \text{params})$.
params	Named list/vector of fixed parameter values (if <code>estimate = FALSE</code>) or starting values for MLE (if <code>estimate = TRUE</code>).
estimate	Logical; TRUE for composite hypothesis (unknown parameters estimated via MLE), FALSE for simple hypothesis.
censoring	Type of censoring: "right" or "left".
transform	Transformations to compute: "both", "malmquist", or "ms".
statistics	Subset of statistics to compute: "all", "direct7", "complete_ad", "composite_mle", or "direct_censored".
pvalue_method	Method for p-values: "auto", "distribution_free", or "parametric_bootstrap".
nsim	Number of Monte Carlo or bootstrap simulation replicates.
seed	Optional random seed.
optim_control	Optional control list passed to <code>optim</code> .

Value

An S3 object of class "gofmalm".

Examples

```
# Simple hypothesis test on Uniform(0,1) with r=5, n=10
data_unif <- c(0.03, 0.06, 0.10, 0.11, 0.13)
res <- gof_censored(
  data = data_unif, n = 10,
  pdf = dunif, cdf = punif,
  estimate = FALSE, pvalue_method = "distribution_free",
  nsim = 500, seed = 123
)
print(res)
```

pvalue_distribution_free

Compute Distribution-Free p-values for Simple Hypotheses

Description

Obtains p-values for EDF goodness-of-fit statistics via Monte Carlo simulation from Uniform(0,1) order statistics.

Usage

```
pvalue_distribution_free(
  u_obs,
  n,
  r,
  censoring = c("right", "left"),
  nsim = 2000,
  seed = NULL
)
```

Arguments

u_obs	Observed order statistics $u_{1:n} < \dots < u_{r:n}$.
n	Total sample size.
r	Number of observed failures.
censoring	Type of censoring: "right" or "left".
nsim	Number of Monte Carlo simulation replicates (default 2000).
seed	Optional random seed.

Value

Named numeric vector of empirical p-values for each statistic.

pvalue_parametric_bootstrap

Compute Parametric Bootstrap p-values for Composite Hypotheses

Description

Obtains p-values for composite hypothesis tests where parameters are estimated from data.

Usage

```
pvalue_parametric_bootstrap(
  data,
  n,
  pdf,
  cdf,
  sf = NULL,
  params_hat,
  censoring = c("right", "left"),
  transform = c("both", "malmquist", "ms"),
  nsim = 2000,
  seed = NULL,
  optim_control = list()
)
```

Arguments

data	Observed data vector of length r .
n	Total sample size.
pdf	Density function.
cdf	Distribution function.
sf	Survival function.
params_hat	Estimated parameter list from observed data.
censoring	Type of censoring.
transform	Transformation method ("ms", "malmquist", or "both").
nsim	Number of bootstrap replicates (default 2000).
seed	Optional random seed.
optim_control	Optional control list passed to optim.

Value

A list containing empirical p-values and number of valid replicates.

stat_composite_mle	<i>Composite Hypothesis Procedure for Type-II Censored Samples</i>
--------------------	--

Description

Evaluates goodness-of-fit under unknown parameters using MLE estimation, transformation to complete sample, normal residual standardization, and modified CvM/AD statistics.

Usage

```
stat_composite_mle(
  data,
  n,
  pdf,
  cdf,
  sf = NULL,
  params,
  censoring = c("right", "left"),
  transform = c("malmquist", "ms"),
  optim_control = list()
)
```

Arguments

data	Numeric vector of observed order statistics.
n	Total sample size ($n \geq \text{length}(\text{data})$).
pdf	Probability density function taking (x, params).
cdf	Cumulative distribution function taking (x, params).
sf	Survival function taking (x, params). If NULL, computed as $1 - \text{cdf}(x, \text{params})$.
params	Named list/vector of starting parameter values for MLE.
censoring	Type of censoring: "right" or "left".
transform	Transformation method: "ms" (Michael-Schucany) or "malmquist".
optim_control	Optional control list passed to optim .

Value

A list containing:

stat_W2	Modified Cramér-von Mises statistic ($_{mW2}$ or $_{lW2}$).
stat_A2	Modified Anderson-Darling statistic ($_{mA2}$ or $_{lA2}$).
W2	Raw Cramér-von Mises statistic on standardized residuals.
A2	Raw Anderson-Darling statistic on standardized residuals.
theta_hat	Estimated parameter values.
convergence	Optimization convergence code.

Examples

```
data_exp <- c(0.1, 0.2, 0.3, 0.4, 0.7, 1.0, 1.4)
stat_composite_mle(
  data = data_exp, n = 20,
  pdf = function(x, p) dexp(x, rate = p$rate),
  cdf = function(x, p) pexp(x, rate = p$rate),
  params = list(rate = 0.1),
  censoring = "right",
  transform = "malmquist"
)
```

stat_direct_censored *Compute Direct Censored EDF Statistics (Pettitt & Stephens, 1976)*

Description

Computes the untransformed direct censored Cramér-von Mises and Anderson-Darling statistics.

Usage

```
stat_direct_censored(u_cens, n)
```

Arguments

`u_cens` Numeric vector of order statistics $u_{1:n} < \dots < u_{r:n}$ in $(0, 1)$.
`n` Total sample size ($n \geq \text{length}(u_cens)$).

Value

Named numeric vector containing `W2_2_rn` and `A2_2_rn`.

Examples

```
u <- c(0.03, 0.06, 0.10, 0.11, 0.13)
stat_direct_censored(u, n = 10)
```

<code>stat_edf_censored</code>	<i>Compute EDF Statistics for Type-II Censored Samples</i>
--------------------------------	--

Description

Computes the nine EDF test statistics described in Lin, Huang & Balakrishnan (2008).

Usage

```
stat_edf_censored(u_cens, n, u_ms = NULL, u_malmquist = NULL)
```

Arguments

`u_cens` Numeric vector of order statistics $u_{1:n} < \dots < u_{r:n}$ in $(0, 1)$.
`n` Total sample size ($n \geq \text{length}(u_cens)$).
`u_ms` Optional pre-computed Michael & Schucany transformed sample.
`u_malmquist` Optional pre-computed Malmquist transformed sample.

Value

A named numeric vector of 9 statistics: `D_rn`, `G_rn`, `T_rn`, `W2_star_rn`, `W2_rn`, `A2_rn`, `U2_rn`, `TA2_r`, and `star_TA2_r`.

Examples

```
u <- c(0.03, 0.06, 0.10, 0.11, 0.13)
stat_edf_censored(u, n = 10)
```

transform_malmquist	<i>Malmquist (1950) Transformation for Type-II Censored Samples</i>
---------------------	---

Description

Converts an r-out-of-n Type-II right- or left-censored uniform sample into an independent complete Uniform(0,1) sample of size r (Lin, Huang & Balakrishnan, 2008).

Usage

```
transform_malmquist(u_cens, n, censoring = c("right", "left"))
```

Arguments

u_cens	Numeric vector of length r containing PIT-transformed order statistics.
n	Total sample size ($n \geq \text{length}(u_cens)$).
censoring	Type of censoring: "right" or "left".

Value

A list containing:

W	Sorted complete sample $W_{1:r} < \dots < W_{r:r}$ of size r.
V	Vector of intermediate Beta-distributed random variables $V_n, \dots, V_{\{n-r+1\}}$.

Examples

```
u <- c(0.03, 0.06, 0.10, 0.11, 0.13)
transform_malmquist(u, n = 10, censoring = "right")
```

transform_ms	<i>Michael & Schucany (1979) Transformation</i>
--------------	---

Description

Transforms an r-out-of-n Type-II right-censored uniform sample into a complete sample of size r.

Usage

```
transform_ms(u_cens, n)
```

Arguments

u_cens	Numeric vector of order statistics $u_{1:n} < \dots < u_{r:n}$ in (0, 1).
n	Total sample size ($n \geq \text{length}(u_cens)$).

Value

Numeric vector of length r representing the transformed complete sample $Z_{1:r} < \dots < Z_{r:r}$.

Examples

```
u <- c(0.03, 0.06, 0.10, 0.11, 0.13)
transform_ms(u, n = 10)
```

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