

Package ‘BivLaplaceRL’

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Type Package

Title Bivariate Laplace Transforms, Stochastic Orders, and Entropy Measures in Reliability

Version 0.2.0

Description Implements methods for bivariate Laplace transforms of residual lives and reversed residual lives, associated stochastic ordering concepts, and dynamic entropy measures for reliability analysis. The package covers three primary research areas: (1) Bivariate Laplace transform of residual lives and stochastic comparisons based on the bivariate Laplace transform order of residual lives (BLt-rl), including weak bivariate hazard rate, mean residual life, and relative mean residual life orders, nonparametric estimation, and NBUHR/NWUHR aging class characterisation (Jayalekshmi, Rajesh, and Nair, 2022, <[doi:10.1080/03610926.2022.2085874](https://doi.org/10.1080/03610926.2022.2085874)>); (2) Bivariate Laplace transform order of reversed residual lives (BLt-Rrl), reversed hazard gradient, reversed mean residual life, and the associated stochastic orders (weak bivariate reversed hazard rate, weak bivariate reversed mean residual life); (3) Residual entropy generating function, a dynamic version of Golomb's (1966) information generating function whose derivative yields the residual entropy of Ebrahimi and Pellerey (1995), with nonparametric estimation and distribution characterisation. Parametric families supported include the Gumbel bivariate exponential, Farlie-Gumbel-Morgenstern (FGM), bivariate power, and Schur-constant distributions. Plotting utilities and a simulation framework for evaluating estimator performance are also provided.

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URL <https://itsmdivakaran.github.io/BivLaplaceRL/>,
<https://github.com/itsmdivakaran/BivLaplaceRL>

BugReports <https://github.com/itsmdivakaran/BivLaplaceRL/issues>

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BivLaplaceRL-package	<i>BivLaplaceRL: Bivariate Laplace Transforms, Stochastic Orders, and Entropy Measures in Reliability</i>
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Description

BivLaplaceRL provides a unified framework for three interconnected research themes in reliability analysis and survival theory:

1. Bivariate Laplace Transform of Residual Lives

Implements the vector Laplace transform of bivariate residual lives ($L_{X_{t_1}|t_2}(s_1), L_{X_{t_2}|t_1}(s_2)$), the associated stochastic ordering BLt-rl, and its relationships with the weak bivariate hazard rate order, weak bivariate mean residual life order, and bivariate relative mean residual life order. Nonparametric estimation and NBUHR/NWUHR aging class tests are included. Reference: Jayalekshmi, Rajesh, and Nair (2022) [doi:10.1080/03610926.2022.2085874](https://doi.org/10.1080/03610926.2022.2085874).

2. Bivariate Laplace Transform of Reversed Residual Lives

Implements the bivariate Laplace transform of reversed (past) residual lives, the BLt-Rrl stochastic order, and connections with weak bivariate reversed hazard rate and reversed mean residual life orders.

3. Residual Entropy Generating Function

Implements the dynamic information generating function (REGF), the residual entropy of Ebrahimi and Pellerey (1995), Golomb's (1966) information generating function, and nonparametric estimation of REGF with Monte-Carlo simulation support.

Parametric families

Gumbel bivariate exponential, Farlie-Gumbel-Morgenstern (FGM), bivariate power, Schur-constant, and exponential distributions are built in.

Plotting

`plot_blt_residual`, `plot_blt_reversed`, and `plot_regf` provide ready-made visualisations.

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References

- Jayalekshmi S., Rajesh G., Nair N.U. (2022). Bivariate Laplace transform of residual lives and their properties. *Communications in Statistics - Theory and Methods*. doi:10.1080/03610926.2022.2085874
- Jayalekshmi S., Rajesh G. Bivariate Laplace transform order and ordering of reversed residual lives. *International Journal of Reliability, Quality and Safety Engineering*.
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- Belzunce F., Ortega E., Ruiz J.M. (1999). The Laplace order and ordering of residual lives. *Statistics & Probability Letters*, 42(2), 145–156.
- Ebrahimi N., Pellerey F. (1995). New partial ordering of survival functions based on the notion of uncertainty. *Journal of Applied Probability*, 32(1), 202–211.
- Golomb S.W. (1966). The information generating function of a probability distribution. *IEEE Transactions on Information Theory*, 12(1), 75–77.

See Also

Useful links:

- <https://itsmdivakaran.github.io/BivLaplaceRL/>
- <https://github.com/itsmdivakaran/BivLaplaceRL>
- Report bugs at <https://github.com/itsmdivakaran/BivLaplaceRL/issues>

bivpower

Bivariate Power Distribution

Description

Distribution function, survival function, density, and random generation for the bivariate power distribution:

$$F(x_1, x_2) = x_1^{p_1 + \theta \log x_2} x_2^{p_2}, \quad 0 \leq x_1, x_2 \leq p_2, p_1, p_2 > 0, 0 \leq \theta \leq 1.$$

Usage

```
pbivpower(x1, x2, p1 = 1, p2 = 1, theta = 0)
sbivpower(x1, x2, p1 = 1, p2 = 1, theta = 0)
dbivpower(x1, x2, p1 = 1, p2 = 1, theta = 0)
rbivpower(n, p1 = 1, p2 = 1, theta = 0)
```

Arguments

x1, x2	Values in the support.
p1, p2	Positive shape parameters.
theta	Association parameter, $0 \leq \theta \leq 1$.
n	Number of random observations.

Value

Numeric vector or two-column matrix (rbivpower).

References

Jayalekshmi S., Rajesh G. Bivariate Laplace transform order and ordering of reversed residual lives.
International Journal of Reliability, Quality and Safety Engineering.

Examples

```
pbivpower(0.4, 0.5, p1 = 2, p2 = 2, theta = 0.3)
set.seed(7); head(rbivpower(30, p1 = 2, p2 = 2, theta = 0.2))
```

biv_brlmr_order	<i>Bivariate Relative Mean Residual Life Order</i>
-----------------	--

Description

Checks whether $X \leq_{\text{brlmr}} Y$: the ratio $m_{i,Y}(t_1, t_2)/m_{i,X}(t_1, t_2)$ is increasing in t_i .

Usage

```
biv_brlmr_order(
  surv_X,
  surv_Y,
  t2_fixed = 0.5,
  t1_grid = seq(0.2, 3, by = 0.3),
  tol = 1e-06
)
```

Arguments

`surv_X, surv_Y` Joint survival functions.
`t2_fixed` Fixed value of t_2 for the univariate slices.
`t1_grid` Grid of t_1 values.
`tol` Tolerance.

Value

List with `order_holds` and `ratio_values`.

References

Kayid M., Izadkhah S., Alshami S. (2016). Residual probability function, associated orderings, and related aging classes. **Statistics and Probability Letters**, 116, 37–47.

Examples

```

sX <- function(x1, x2) sgumbel_biv(x1, x2, k1 = 2, k2 = 1)
sY <- function(x1, x2) sgumbel_biv(x1, x2, k1 = 1, k2 = 1)
biv_brlmr_order(sX, sY, t2_fixed = 0.5)
  
```

`biv_hazard_gradient` *Bivariate Hazard Gradient*

Description

Computes the bivariate hazard gradient

$$h_i(t_1, t_2) = -\frac{\partial}{\partial t_i} \log \bar{F}(t_1, t_2), \quad i = 1, 2.$$

Usage

```

biv_hazard_gradient(
  t1,
  t2,
  surv_fn = NULL,
  k1 = 1,
  k2 = 1,
  theta = 0,
  eps = 1e-07
)
  
```

Arguments

t1, t2	Evaluation points (non-negative).
surv_fn	A function function(x1, x2) returning the joint survival probability. Defaults to Gumbel bivariate exponential.
k1, k2, theta	Parameters for the default Gumbel distribution.
eps	Step size for numerical differentiation (default 1e-7).

Value

A named numeric vector (h1, h2).

References

Jayalekshmi S., Rajesh G., Nair N.U. (2022). doi:[10.1080/03610926.2022.2085874](https://doi.org/10.1080/03610926.2022.2085874)

Examples

```
biv_hazard_gradient(t1 = 1, t2 = 1)
biv_hazard_gradient(t1 = 0.5, t2 = 0.5, k1 = 2, k2 = 1.5, theta = 0.3)
```

biv_mean_residual	<i>Bivariate Mean Residual Life Function</i>
-------------------	--

Description

Computes the bivariate mean residual life (MRL) function

$$m_1(t_1, t_2) = E(X_{t_1|t_2}) = \frac{\int_{t_1}^{\infty} \bar{F}(x_1, t_2) dx_1}{\bar{F}(t_1, t_2)}$$

and analogously $m_2(t_1, t_2)$.

Usage

```
biv_mean_residual(
  t1,
  t2,
  surv_fn = NULL,
  k1 = 1,
  k2 = 1,
  theta = 0,
  upper = 100
)
```

Arguments

t1, t2	Non-negative thresholds.
surv_fn	Joint survival function; defaults to Gumbel bivariate exponential.
k1, k2, theta	Gumbel parameters (used when surv_fn = NULL).
upper	Upper integration bound (default 100).

Value

A named numeric vector (m1, m2).

References

Jayalekshmi S., Rajesh G., Nair N.U. (2022). [doi:10.1080/03610926.2022.2085874](https://doi.org/10.1080/03610926.2022.2085874)

Examples

```
biv_mean_residual(t1 = 0.5, t2 = 0.5)
biv_mean_residual(t1 = 1, t2 = 0.5, k1 = 1, k2 = 2, theta = 0.2)
```

biv_rhazard_gradient *Bivariate Reversed Hazard Gradient*

Description

Computes the bivariate reversed hazard gradient

$$h_i(x_1, x_2) = \frac{\partial}{\partial x_i} \log F(x_1, x_2), \quad i = 1, 2.$$

Usage

```
biv_rhazard_gradient(x1, x2, cdf_fn = NULL, theta = 0, eps = 1e-07)
```

Arguments

x1, x2	Positive evaluation points.
cdf_fn	Joint CDF function; defaults to FGM with parameter theta.
theta	FGM parameter (used when cdf_fn = NULL).
eps	Numerical differentiation step.

Value

Named numeric vector (rh1, rh2).

References

Jayalekshmi S., Rajesh G. — IJRQSE, Section 2.

Examples

```
biv_rhazard_gradient(x1 = 0.5, x2 = 0.5, theta = 0.3)
```

biv_rmrl

Bivariate Reversed Mean Residual Life Function

Description

Computes the bivariate reversed mean residual life (RMRL):

$$m_1(x_1, x_2) = \frac{\int_0^{x_1} F(t_1, x_2) dt_1}{F(x_1, x_2)}, \quad m_2(x_1, x_2) = \frac{\int_0^{x_2} F(x_1, t_2) dt_2}{F(x_1, x_2)}.$$

Usage

```
biv_rmrl(x1, x2, cdf_fn = NULL, theta = 0)
```

Arguments

x1, x2	Positive evaluation points.
cdf_fn	Joint CDF; defaults to FGM.
theta	FGM parameter.

Value

Named numeric vector (m1, m2).

References

Jayalekshmi S., Rajesh G. — IJRQSE, Section 2.

Examples

```
biv_rmrl(x1 = 0.5, x2 = 0.5, theta = 0.3)
biv_rmrl(x1 = 0.7, x2 = 0.4, theta = -0.2)
```

 biv_whr_order

 Weak Bivariate Hazard Rate Order

Description

Checks whether $X \leq_{\text{whr}} Y$: the ratio $\bar{F}_Y(x_1, x_2)/\bar{F}_X(x_1, x_2)$ is increasing in (x_1, x_2) , i.e. $h_{i,X}(t_1, t_2) \geq h_{i,Y}(t_1, t_2)$, $i = 1, 2$.

Usage

```
biv_whr_order(
  surv_X,
  surv_Y,
  t1_grid = seq(0.1, 3, by = 0.5),
  t2_grid = seq(0.1, 3, by = 0.5),
  tol = 1e-06
)
```

Arguments

surv_X, surv_Y Joint survival functions.
 t1_grid, t2_grid Evaluation grids.
 tol Tolerance.

Value

A list: order_holds (logical), violations (data frame).

References

Shaked M., Shanthikumar J.G. (2007). **Stochastic Orders**. Springer. Jayalekshmi S., Rajesh G., Nair N.U. (2022). [doi:10.1080/03610926.2022.2085874](https://doi.org/10.1080/03610926.2022.2085874)

Examples

```
sX <- function(x1, x2) sgumbel_biv(x1, x2, k1 = 1, k2 = 1, theta = 0)
sY <- function(x1, x2) sgumbel_biv(x1, x2, k1 = 2, k2 = 2, theta = 0)
biv_whr_order(sX, sY)
```

biv_wmrl_order	<i>Weak Bivariate Mean Residual Life Order</i>
----------------	--

Description

Checks whether $X \leq_{\text{wmrl}} Y: m_{i,X}(t_1, t_2) \leq m_{i,Y}(t_1, t_2), i = 1, 2.$

Usage

```
biv_wmrl_order(  
  surv_X,  
  surv_Y,  
  t1_grid = seq(0.1, 2, by = 0.5),  
  t2_grid = seq(0.1, 2, by = 0.5),  
  tol = 1e-06  
)
```

Arguments

surv_X, surv_Y Joint survival functions.
t1_grid, t2_grid Evaluation grids.
tol Tolerance.

Value

List with order_holds and violations.

References

Jayalekshmi S., Rajesh G., Nair N.U. (2022). [doi:10.1080/03610926.2022.2085874](https://doi.org/10.1080/03610926.2022.2085874)

Examples

```
sX <- function(x1, x2) sgumbel_biv(x1, x2, k1 = 1.5, k2 = 1.5)  
sY <- function(x1, x2) sgumbel_biv(x1, x2, k1 = 1, k2 = 1)  
biv_wmrl_order(sX, sY)
```

biv_wrhr_order

Weak Bivariate Reversed Hazard Rate Order

Description

Checks $X \leq_{\text{wrhr}} Y$: the ratio $F_X(x_1, x_2)/F_Y(x_1, x_2)$ is decreasing in (x_1, x_2) , i.e. $h_{i,X}(x_1, x_2) \leq h_{i,Y}(x_1, x_2)$, $i = 1, 2$.

Usage

```
biv_wrhr_order(
  cdf_X,
  cdf_Y,
  x1_grid = seq(0.1, 0.9, by = 0.2),
  x2_grid = seq(0.1, 0.9, by = 0.2),
  tol = 1e-06
)
```

Arguments

`cdf_X, cdf_Y` Joint CDFs.
`x1_grid, x2_grid` Evaluation grids (positive values).
`tol` Tolerance.

Value

List with `order_holds` and `violations`.

References

Jayalekshmi S., Rajesh G. — IJRQSE, Section 2.

Examples

```
cX <- function(x1, x2) pfgm_biv(x1, x2, theta = 0.2)
cY <- function(x1, x2) pfgm_biv(x1, x2, theta = 0.5)
biv_wrhr_order(cX, cY)
```

biv_wrmrl_order	<i>Weak Bivariate Reversed Mean Residual Life Order</i>
-----------------	---

Description

Checks $X \leq_{\text{wrmrl}} Y: m_{i,X}(x_1, x_2) \geq m_{i,Y}(x_1, x_2), i = 1, 2.$

Usage

```
biv_wrmrl_order(  
  cdf_X,  
  cdf_Y,  
  x1_grid = seq(0.2, 0.8, by = 0.2),  
  x2_grid = seq(0.2, 0.8, by = 0.2),  
  tol = 1e-06  
)
```

Arguments

cdf_X, cdf_Y	Joint CDFs.
x1_grid, x2_grid	Evaluation grids.
tol	Tolerance.

Value

List with order_holds and violations.

References

Jayalekshmi S., Rajesh G. — IJRQSE, Section 2.

Examples

```
cX <- function(x1, x2) pfgm_biv(x1, x2, theta = 0.1)  
cY <- function(x1, x2) pfgm_biv(x1, x2, theta = 0.8)  
biv_wrmrl_order(cX, cY)
```

 blt_order_residual *Bivariate Laplace Transform Order of Residual Lives (BLt-rl)*

Description

Checks whether random vector X is smaller than Y in the bivariate Laplace transform order of residual lives (BLt-rl).

$X \leq_{\text{BLt-rl}} Y$ if and only if for all (t_1, t_2) in the support:

$$\frac{\int_{t_1}^{\infty} e^{-s_1 x_1} \bar{F}_X(x_1, t_2) dx_1}{e^{-s_1 t_1} \bar{F}_X(t_1, t_2)} \geq \frac{\int_{t_1}^{\infty} e^{-s_1 x_1} \bar{F}_Y(x_1, t_2) dx_1}{e^{-s_1 t_1} \bar{F}_Y(t_1, t_2)}$$

i.e. $L_{X_{t_1|t_2}}^*(s_1) \geq L_{Y_{t_1|t_2}}^*(s_1)$ for all t_1, t_2, s_1 . The function evaluates this inequality at a grid.

Usage

```
blt_order_residual(  
  surv_X,  
  surv_Y,  
  s1 = 1,  
  s2 = 1,  
  t1_grid = seq(0.1, 3, by = 0.5),  
  t2_grid = seq(0.1, 3, by = 0.5),  
  tol = 1e-06  
)
```

Arguments

surv_X, surv_Y	Joint survival functions for X and Y respectively, each of the form <code>function(x1, x2)</code> .
s1, s2	Laplace parameters to evaluate at.
t1_grid, t2_grid	Grids of truncation times (default 0.1 to 3).
tol	Tolerance for declaring inequality (default 1e-6).

Value

A list with elements:

`order_holds` Logical; TRUE if $X \leq Y$ at all grid points.

`violations` Data frame of grid points where the ordering fails.

`ratio_matrix` Matrix of L_X^*/L_Y^* values.

References

Jayalekshmi S., Rajesh G., Nair N.U. (2022), Definition 4.1 & Prop. 4.1. [doi:10.1080/03610926.2022.2085874](https://doi.org/10.1080/03610926.2022.2085874)

See Also

[blt_residual](#), [biv_whr_order](#)

Examples

```
# Compare two Gumbel distributions
sX <- function(x1, x2) sgumbel_biv(x1, x2, k1 = 1, k2 = 1, theta = 0.2)
sY <- function(x1, x2) sgumbel_biv(x1, x2, k1 = 2, k2 = 2, theta = 0.2)
blt_order_residual(sX, sY, s1 = 1, s2 = 1,
                  t1_grid = c(0.1, 0.5, 1), t2_grid = c(0.1, 0.5))
```

blt_order_reversed	<i>Bivariate Laplace Transform Order of Reversed Residual Lives (BLT-Rrl)</i>
--------------------	---

Description

Checks whether $X \leq_{\text{BLT-Rrl}} Y$: for all (t_1, t_2) , $L_{t_1|t_2}^X(s_1) \geq L_{t_1|t_2}^Y(s_2)$.

Usage

```
blt_order_reversed(
  cdf_X,
  cdf_Y,
  s1 = 1,
  s2 = 1,
  t1_grid = seq(0.2, 0.8, by = 0.2),
  t2_grid = seq(0.2, 0.8, by = 0.2),
  tol = 1e-06
)
```

Arguments

cdf_X, cdf_Y	Joint CDF functions for X and Y .
s1, s2	Laplace parameters.
t1_grid, t2_grid	Grids of truncation times.
tol	Tolerance.

Value

Same structure as [blt_order_residual](#).

References

Jayalekshmi S., Rajesh G. — IJRQSE, Definition 2.

See Also

[blt_reversed](#), [biv_wrhr_order](#)

Examples

```
cX <- function(x1, x2) pfgm_biv(x1, x2, theta = 0.3)
cY <- function(x1, x2) pfgm_biv(x1, x2, theta = 0.5)
blt_order_reversed(cX, cY, s1 = 1, s2 = 1,
                  t1_grid = c(0.2, 0.5), t2_grid = c(0.2, 0.5))
```

blt_residual

Bivariate Laplace Transform of Residual Lives

Description

Computes the bivariate Laplace transform of residual lives $L_{X_{t_1|t_2}}(s_1)$ and $L_{X_{t_2|t_1}}(s_2)$ defined as

$$L_{X_{t_1|t_2}}(s_1) = \frac{\int_{t_1}^{\infty} e^{-s_1 x_1} f(x_1 | X_2 > t_2) dx_1}{e^{-s_1 t_1} \bar{F}(t_1 | X_2 > t_2)}$$

and analogously for the second component.

The **star** version (used for ordering) is

$$L_{X_{t_1|t_2}}^*(s_1) = \frac{1 - L_{X_{t_1|t_2}}(s_1)}{s_1} = \frac{\int_{t_1}^{\infty} e^{-s_1 x_1} \bar{F}(x_1, t_2)}{e^{-s_1 t_1} \bar{F}(t_1, t_2)} dx_1.$$

Usage

```
blt_residual(
  s1,
  s2,
  t1 = 0,
  t2 = 0,
  surv_fn = NULL,
  k1 = 1,
  k2 = 1,
  theta = 0,
  upper = 50,
  star = FALSE
)
```

Arguments

s1, s2	Positive Laplace parameters.
t1, t2	Non-negative time thresholds (truncation ages).
surv_fn	A function function(x1, x2) returning the joint survival probability $\bar{F}(x_1, x_2)$. Defaults to the Gumbel bivariate exponential with k1, k2, theta.
k1, k2	Rate parameters (used only when surv_fn = NULL).
theta	Association parameter (used only when surv_fn = NULL).
upper	Integration upper bound (default 50).
star	Logical; if TRUE returns the star version L^* .

Value

A named numeric vector with elements L1 and L2 (or L1_star and L2_star when star = TRUE).

References

Jayalekshmi S., Rajesh G., Nair N.U. (2022). doi:10.1080/03610926.2022.2085874

See Also

[blt_residual_gumbel](#), [blt_order_residual](#), [np_blt_residual](#)

Examples

```
# Gumbel bivariate exponential, default parameters
blt_residual(s1 = 1, s2 = 1, t1 = 0.5, t2 = 0.5)

# Star version used in ordering
blt_residual(s1 = 0.5, s2 = 0.5, t1 = 1, t2 = 1, star = TRUE)

# User-supplied survival function (Schur-constant exponential)
surv <- function(x1, x2) exp(-(x1 + x2))
blt_residual(s1 = 1, s2 = 1, t1 = 0.3, t2 = 0.3, surv_fn = surv)
```

blt_residual_gumbel *Closed-Form Bivariate Laplace Transform of Residual Lives (Gumbel)*

Description

Returns the *star* bivariate Laplace transform of residual lives for the Gumbel bivariate exponential distribution in closed form:

$$L_{X_{t_1|t_2}}^*(s_1) = \frac{1}{k_1 + s_1 + \theta t_2}, \quad L_{X_{t_2|t_1}}^*(s_2) = \frac{1}{k_2 + s_2 + \theta t_1}.$$

Usage

```
blt_residual_gumbel(s1, s2, t1 = 0, t2 = 0, k1 = 1, k2 = 1, theta = 0)
```

Arguments

s1, s2 Positive Laplace parameters.
t1, t2 Non-negative truncation ages.
k1, k2 Positive rate parameters.
theta Non-negative association parameter.

Value

A named numeric vector (L1_star, L2_star).

References

Jayalekshmi S., Rajesh G., Nair N.U. (2022), Example 3.1. [doi:10.1080/03610926.2022.2085874](https://doi.org/10.1080/03610926.2022.2085874)

See Also

[blt_residual](#)

Examples

```
blt_residual_gumbel(s1 = 1, s2 = 1, t1 = 0.5, t2 = 0.5)
blt_residual_gumbel(s1 = 2, s2 = 0.5, t1 = 0, t2 = 1, k1 = 2, k2 = 1, theta = 0.3)
```

blt_reversed

Bivariate Laplace Transform of Reversed Residual Lives

Description

Computes the bivariate Laplace transform of reversed (past) residual lives. For a random pair (X_1, X_2) with joint distribution function $F(x_1, x_2)$, the transform is

$$L_{t_1|t_2}(s_1) = e^{-s_1 t_1} + \frac{s_1 \int_0^{t_1} e^{-s_1 x_1} F(x_1, t_2) dx_1}{F(t_1, t_2)}$$

and the associated G function (useful for ordering) is

$$G_1(t_1, t_2) = \frac{\int_0^{t_1} e^{-s_1 x_1} F(x_1, t_2) dx_1}{e^{-s_1 t_1} F(t_1, t_2)}.$$

Usage

```
blt_reversed(s1, s2, t1, t2, cdf_fn = NULL, theta = 0, g_form = FALSE)
```

Arguments

s1, s2	Positive Laplace parameters.
t1, t2	Positive truncation times ($t_i > 0$).
cdf_fn	A function function(x1, x2) returning the joint CDF $F(x_1, x_2)$. Defaults to the FGM distribution.
theta	FGM association parameter (used when cdf_fn = NULL).
g_form	Logical; if TRUE returns the G form instead of L .

Value

A named numeric vector (L1, L2) or (G1, G2).

References

Jayalekshmi S., Rajesh G. Bivariate Laplace transform order and ordering of reversed residual lives. *International Journal of Reliability, Quality and Safety Engineering*.

See Also

[blt_reversed_fgm](#), [blt_order_reversed](#)

Examples

```
# FGM distribution (default)
blt_reversed(s1 = 1, s2 = 1, t1 = 0.6, t2 = 0.6)

# G form
blt_reversed(s1 = 1, s2 = 1, t1 = 0.6, t2 = 0.6, g_form = TRUE)

# User-supplied CDF
cdf <- function(x1, x2) pfgm_biv(x1, x2, theta = 0.5)
blt_reversed(s1 = 1, s2 = 1, t1 = 0.5, t2 = 0.5, cdf_fn = cdf)
```

blt_reversed_fgm	<i>Closed-Form BLT of Reversed Residual Lives for the FGM Distribution</i>
------------------	--

Description

Computes the bivariate Laplace transform of the FGM distribution in closed form (Jayalekshmi and Rajesh, Example 1):

$$L_X(s_1, s_2) = \frac{(1 - e^{-s_1})(1 - e^{-s_2})}{s_1 s_2} + \theta \Phi(s_1, s_2)$$

where Φ captures the dependence correction.

Usage

```
blt_reversed_fgm(s1, s2, theta = 0)
```

Arguments

s1, s2 Positive Laplace parameters.
theta FGM association parameter, $|\theta| \leq 1$.

Value

Scalar numeric; the joint bivariate Laplace transform.

References

Jayalekshmi S., Rajesh G. Bivariate Laplace transform order and ordering of reversed residual lives.
International Journal of Reliability, Quality and Safety Engineering, Example 1.

Examples

```
blt_reversed_fgm(s1 = 1, s2 = 1, theta = 0.5)
blt_reversed_fgm(s1 = 2, s2 = 0.5, theta = -0.3)
```

blt_reversed_power *Bivariate Laplace Transform of Reversed Residual Lives — Power Distribution*

Description

Computes the G_1 function for the bivariate power distribution:

$$G_1(t_1, t_2) = \frac{\int_0^{t_1} e^{-s_1 x_1} x_1^{p_1 + \theta \log t_2} dx_1}{e^{-s_1 t_1} t_1^{p_1 + \theta \log t_2}}$$

evaluated numerically.

Usage

```
blt_reversed_power(s1, t1, t2, p1 = 1, p2 = 1, theta = 0)
```

Arguments

s1 Positive Laplace parameter.
t1, t2 Positive truncation times.
p1, p2 Positive shape parameters.
theta Association parameter, $0 \leq \theta \leq 1$.

Value

Named numeric vector (G1, reversed_hazard_h1).

References

Jayalekshmi S., Rajesh G. — IJRQSE, Example 2.

Examples

```
blt_reversed_power(s1 = 1, t1 = 0.5, t2 = 0.5, p1 = 2, p2 = 2, theta = 0.3)
```

fgm_biv

Farlie-Gumbel-Morgenstern (FGM) Bivariate Distribution

Description

Density, distribution function, survival function, and random generation for the FGM bivariate distribution on $[0, 1]^2$:

$$F(x_1, x_2) = x_1 x_2 [1 + \theta(1 - x_1)(1 - x_2)], \quad 0 \leq x_1, x_2 \leq 1, |\theta| \leq 1.$$

Usage

```
pfgm_biv(x1, x2, theta = 0)
```

```
dfgm_biv(x1, x2, theta = 0)
```

```
sfgm_biv(x1, x2, theta = 0)
```

```
rfgm_biv(n, theta = 0)
```

Arguments

x1, x2 Values in $[0, 1]$.

theta Association parameter, $|\theta| \leq 1$.

n Number of random observations.

Value

Numeric vector (scalar functions) or two-column matrix (rfgm_biv).

References

Jayalekshmi S., Rajesh G. Bivariate Laplace transform order and ordering of reversed residual lives.
International Journal of Reliability, Quality and Safety Engineering.

Examples

```
pfgm_biv(0.4, 0.6, theta = 0.5)
dfgm_biv(0.4, 0.6, theta = 0.5)
set.seed(1); head(rfgm_biv(50, theta = 0.5))
```

gumbel_biv

*Gumbel Bivariate Exponential Distribution***Description**

Density, distribution (survival) function, and random generation for the Gumbel bivariate exponential distribution with parameters k_1 , k_2 , and association parameter θ .

The joint survival function is

$$\bar{F}(x_1, x_2) = \exp(-k_1x_1 - k_2x_2 - \theta x_1x_2), \quad x_1, x_2 > 0, k_1, k_2 > 0, 0 \leq \theta \leq k_1k_2.$$

Usage

```
dgumbel_biv(x1, x2, k1 = 1, k2 = 1, theta = 0, log.p = FALSE)
```

```
sgumbel_biv(x1, x2, k1 = 1, k2 = 1, theta = 0, log.p = FALSE)
```

```
pgumbel_biv(x1, x2, k1 = 1, k2 = 1, theta = 0)
```

```
rgumbel_biv(n, k1 = 1, k2 = 1, theta = 0)
```

Arguments

x1, x2	Non-negative numeric values or vectors.
k1, k2	Positive rate parameters.
theta	Non-negative association parameter; must satisfy $0 \leq \theta \leq k_1k_2$.
log.p	Logical; if TRUE probabilities are given as $\log(p)$.
n	Number of random observations.

Value

dgumbel_biv Numeric vector of density values.

pgumbel_biv Numeric vector of joint CDF values.

sgumbel_biv Numeric vector of joint survival function values.

rgumbel_biv A two-column matrix with columns X1 and X2 containing the simulated observations.

References

Gumbel E.J. (1960). Bivariate exponential distributions. *Journal of the American Statistical Association*, 55(292), 698–707.

Jayalekshmi S., Rajesh G., Nair N.U. (2022). doi:10.1080/03610926.2022.2085874

Examples

```
# Survival function
sgumbel_biv(1, 2, k1 = 1, k2 = 1, theta = 0.5)

# Density
dgumbel_biv(0.5, 0.5, k1 = 1, k2 = 1.5, theta = 0.3)

# Random sample
set.seed(42)
dat <- rgumbel_biv(100, k1 = 1, k2 = 1, theta = 0.5)
head(dat)
```

info_gen_function	<i>Golomb Information Generating Function</i>
-------------------	---

Description

Computes the information generating function (IGF) introduced by Golomb (1966):

$$\mathcal{I}_\alpha(f) = \int_0^\infty f^\alpha(x) dx, \quad \alpha > 0.$$

When $\alpha \rightarrow 1$, $-\mathcal{I}_\alpha/d\alpha|_{\alpha=1} = H(f)$.

Usage

```
info_gen_function(dens_fn, alpha = 1, upper = 100)
```

Arguments

dens_fn	A function of one argument returning the density.
alpha	Positive parameter (default 1).
upper	Upper integration limit.

Value

Scalar numeric.

References

Golomb S.W. (1966). The information generating function of a probability distribution. *IEEE Transactions on Information Theory*, 12(1), 75–77.

See Also

[residual_info_gen](#)

Examples

```
# Exponential(1) with alpha=1 gives 1
info_gen_function(function(x) dexp(x, rate = 1), alpha = 1)

# alpha = 2
info_gen_function(function(x) dexp(x, rate = 1), alpha = 2)
```

nbuhr_test

Test NBUHR / NWUHR Aging Class

Description

Checks whether a bivariate lifetime distribution belongs to the NBUHR (New Better than Used in Hazard Rate) or NWUHR (New Worse than Used) aging class. A distribution is NBUHR if

$$h_1(0, t_2) \geq h_1(t_1, t_2) \text{ for all } t_1 > 0$$

and similarly for the second component. The function evaluates this at a grid of t_1 values.

Usage

```
nbuhr_test(
  t2 = 1,
  t1_grid = seq(0.1, 5, by = 0.1),
  surv_fn = NULL,
  k1 = 1,
  k2 = 1,
  theta = 0
)
```

Arguments

t2	Fixed value of the second age coordinate.
t1_grid	Numeric vector of t_1 values to check (default 0.1 to 5 in steps of 0.1).
surv_fn	Joint survival function; defaults to Gumbel bivariate exponential.
k1, k2, theta	Gumbel parameters.

Value

A list with components:

class1 Character: "NBUHR", "NWUHR", or "neither" for the first component.

class2 Same for the second component.

h1_grid Numeric vector of $h_1(t_1, t_2)$ values.

h2_grid Numeric vector of $h_2(t_1, t_2)$ values.

References

Jayalekshmi S., Rajesh G., Nair N.U. (2022), Definition 3.2. doi:10.1080/03610926.2022.2085874

Examples

```
nbuhr_test(t2 = 1, k1 = 1, k2 = 1, theta = 0.3)
nbuhr_test(t2 = 0.5,
            surv_fn = function(x1, x2) exp(-(x1 + x2)))
```

np_blt_residual	<i>Nonparametric Estimator for the Bivariate Laplace Transform of Residual Lives</i>
-----------------	--

Description

Given a bivariate sample (X_{1i}, X_{2i}) , $i = 1, \dots, n$, estimates

$$\hat{L}_1^*(s_1; t_1, t_2) = \frac{\sum_{i: X_{1i} > t_1, X_{2i} > t_2} \int_{t_1}^{X_{1i}} e^{-s_1 u} du}{e^{-s_1 t_1} \cdot \#\{X_{1i} > t_1, X_{2i} > t_2\}}$$

and analogously for the second component, using the empirical survival function as described in Jayalekshmi et al. (2022), Section 6.

Usage

```
np_blt_residual(data, s1, s2, t1 = 0, t2 = 0)
```

Arguments

data	A two-column numeric matrix or data frame with columns for X_1 and X_2 .
s1, s2	Positive Laplace parameters.
t1, t2	Non-negative truncation ages.

Value

A named numeric vector (L1_hat, L2_hat).

References

Jayalekshmi S., Rajesh G., Nair N.U. (2022), Section 6. doi:10.1080/03610926.2022.2085874

See Also

[blt_residual_gumbel](#), [sim_blt_residual](#)

Examples

```

set.seed(123)
dat <- rgumbel_biv(200, k1 = 1, k2 = 1, theta = 0.5)
np_blt_residual(dat, s1 = 1, s2 = 1, t1 = 0.3, t2 = 0.3)

# Compare with closed form
blt_residual_gumbel(s1 = 1, s2 = 1, t1 = 0.3, t2 = 0.3, theta = 0.5)

```

np_residual_info_gen *Nonparametric Estimator for the Residual Entropy Generating Function*

Description

Given a univariate sample X_1, \dots, X_n , estimates the REGF using a kernel density estimator for f and the empirical survival function for $\bar{F}(t)$:

$$\hat{\mathcal{I}}_{\alpha}(t) = \sum_{i: X_i > t} \frac{\hat{f}(X_i)^{\alpha-1}}{(n \hat{F}_n(t))^{\alpha}} \cdot \frac{1}{n}$$

where \hat{f} is a Gaussian kernel density estimator.

Usage

```
np_residual_info_gen(x, alpha = 1, t = 0, bw = NULL)
```

Arguments

x	Numeric vector; observed sample.
alpha	Positive parameter (default 1).
t	Truncation time (default 0).
bw	Bandwidth for KDE; uses <code>bw.nrd0</code> if NULL.

Value

Scalar numeric estimate of REGF.

References

Smitha S., Rajesh G., Jayalekshmi S. (2024), Section 4. *Journal of the Indian Statistical Association*, 62(1), 81–93.

See Also

[residual_info_gen](#), [sim_regf](#)

Examples

```

set.seed(1)
x <- rexp(100, rate = 1)
np_residual_info_gen(x, alpha = 2, t = 0)

# Compare with true value
f <- function(x) dexp(x, 1)
Fb <- function(x) pexp(x, 1, lower.tail = FALSE)
residual_info_gen(f, Fb, alpha = 2, t = 0)

```

plot_blt_residual *Plot Bivariate Laplace Transform of Residual Lives*

Description

Plots the star Laplace transform of residual lives $L_{X_{t_1|t_2}}^*(s_1)$ as a function of t_1 for fixed s_1, t_2 . Optionally overlays two distributions for visual comparison of the BLT-rl order.

Usage

```

plot_blt_residual(
  surv_fn,
  surv_fn2 = NULL,
  s1 = 1,
  t2 = 0.5,
  t1_grid = seq(0.1, 3, by = 0.1),
  k1 = 1,
  k2 = 1,
  theta = 0,
  xlab = expression(t[1]),
  ylab = expression(L^"*"[X[t[1] * "|" * t[2]]](s[1])),
  main = "Bivariate LT of Residual Lives",
  col1 = "steelblue",
  col2 = "firebrick",
  lwd = 2,
  legend_labels = c("Distribution 1", "Distribution 2")
)

```

Arguments

surv_fn	Joint survival function. If a second distribution is to be overlaid, pass it as surv_fn2.
surv_fn2	Optional second survival function for comparison.
s1	Laplace parameter (default 1).
t2	Fixed second truncation age (default 0.5).

t1_grid Grid of first truncation ages.
 k1, k2, theta Parameters for the default Gumbel distribution; used only when surv_fn = NULL.
 xlab, ylab, main Plot labels.
 col1, col2 Line colours.
 lwd Line width.
 legend_labels Length-2 character vector for legend (ignored if surv_fn2 = NULL).

Value

Invisibly returns the data frame used for plotting.

Examples

```

sX <- function(x1, x2) sgumbel_biv(x1, x2, k1 = 1, k2 = 1, theta = 0.3)
sY <- function(x1, x2) sgumbel_biv(x1, x2, k1 = 2, k2 = 1, theta = 0.3)
plot_blt_residual(sX, sY, s1 = 1, t2 = 0.5,
                 legend_labels = c("k1=1", "k1=2"))
  
```

plot_blt_reversed *Plot Bivariate Laplace Transform of Reversed Residual Lives*

Description

Plots the reversed-life Laplace transform $L_{t_1|t_2}(s_1)$ as a function of t_1 for fixed s_1 and t_2 .

Usage

```

plot_blt_reversed(
  cdf_fn,
  cdf_fn2 = NULL,
  s1 = 1,
  t2 = 0.5,
  t1_grid = seq(0.1, 0.9, by = 0.05),
  theta = 0,
  xlab = expression(t[1]),
  ylab = expression(L[t[1] * "|" * t[2]](s[1])),
  main = "Bivariate LT of Reversed Residual Lives",
  col1 = "darkgreen",
  col2 = "darkorange",
  lwd = 2,
  legend_labels = c("Distribution 1", "Distribution 2")
)
  
```

Arguments

cdf_fn	Joint CDF function.
cdf_fn2	Optional second CDF for comparison.
s1	Laplace parameter.
t2	Fixed second truncation time.
t1_grid	Grid of first truncation times.
theta	FGM parameter (used if cdf_fn = NULL).
xlab, ylab, main	Plot labels.
col1, col2	Line colours.
lwd	Line width.
legend_labels	Legend labels.

Value

Invisibly returns the data frame used for plotting.

Examples

```
cX <- function(x1, x2) pfgm_biv(x1, x2, theta = 0.2)
cY <- function(x1, x2) pfgm_biv(x1, x2, theta = 0.7)
plot_blt_reversed(cX, cY, s1 = 1, t2 = 0.5,
                  legend_labels = c("theta=0.2", "theta=0.7"))
```

plot_regf

Plot Residual Entropy Generating Function

Description

Plots the REGF $\mathcal{I}_\alpha(X; t)$ as a function of t for given α , or as a function of α for given t .

Usage

```
plot_regf(
  dens_fn,
  surv_fn = NULL,
  alpha = 2,
  t = 0,
  grid = NULL,
  vary = c("t", "alpha"),
  upper = 100,
  col = "purple",
  lwd = 2,
  main = NULL
)
```

Arguments

dens_fn	Density function.
surv_fn	Survival function; computed if NULL.
alpha	Positive parameter (used when vary = "t").
t	Truncation time (used when vary = "alpha").
grid	Numeric vector of the varying quantity values.
vary	One of "t" (plot as function of t) or "alpha" (plot as function of α).
upper	Integration upper bound.
col	Line colour.
lwd	Line width.
main	Plot title.

Value

Invisibly returns the data frame used for plotting.

Examples

```
f <- function(x) dexp(x, 1)
Fb <- function(x) pexp(x, 1, lower.tail = FALSE)
plot_regf(f, Fb, alpha = 2, vary = "t")
plot_regf(f, Fb, t = 0.5, vary = "alpha")
```

regf_characterise *Characterise a Distribution via the REGF*

Description

Checks whether the functional form of $\mathcal{I}_\alpha(X; t)$ over a grid of t values is consistent with an exponential distribution. For $X \sim \text{Exp}(\lambda)$, $\mathcal{I}_\alpha(t)/\mathcal{I}_\alpha(0) = e^{(\alpha-1)\lambda t}$, a pure exponential in t .

Usage

```
regf_characterise(
  dens_fn,
  surv_fn = NULL,
  alpha = 2,
  t_grid = seq(0, 2, by = 0.2),
  upper = 100
)
```

Arguments

dens_fn	Density function.
surv_fn	Survival function.
alpha	REGF parameter.
t_grid	Grid of truncation times.
upper	Integration upper bound.

Value

A data frame with columns t, REGF, log_REGF, and the fitted linear-in- t slope slope (log-linear characterisation).

References

Smitha S., Rajesh G., Jayalekshmi S. (2024), Section 3.

Examples

```
f <- function(x) dexp(x, 1)
Fb <- function(x) pexp(x, 1, lower.tail = FALSE)
regf_characterise(f, Fb, alpha = 2)
```

regf_profile	<i>REGF Profile Over Alpha</i>
--------------	--------------------------------

Description

Evaluates [residual_info_gen](#) over a grid of α values and optionally plots the result. Useful for studying how the information content varies with the Renyi-type parameter.

Usage

```
regf_profile(
  dens_fn,
  surv_fn = NULL,
  alpha_grid = seq(0.1, 3, by = 0.2),
  t = 0,
  upper = 100,
  plot = FALSE
)
```

Arguments

dens_fn	Density function.
surv_fn	Survival function; computed internally if NULL.
alpha_grid	Numeric vector of α values (default 0.1 to 3).
t	Truncation time.
upper	Integration upper bound.
plot	Logical; if TRUE plots the profile (default FALSE).

Value

A data frame with columns alpha and REGF.

Examples

```
f <- function(x) dexp(x, 1)
Fb <- function(x) pexp(x, 1, lower.tail = FALSE)
regf_profile(f, Fb, t = 0.5, plot = FALSE)
```

residual_entropy	<i>Residual Entropy Function</i>
------------------	----------------------------------

Description

Computes the residual entropy (dynamic entropy) introduced by Ebrahimi and Pellerey (1995):

$$H(X; t) = - \int_t^{\infty} \frac{f(x)}{\bar{F}(t)} \log \frac{f(x)}{\bar{F}(t)} dx, \quad t \geq 0.$$

Usage

```
residual_entropy(dens_fn, surv_fn = NULL, t = 0, upper = 100)
```

Arguments

dens_fn	Density function $f(x)$.
surv_fn	Survival function $\bar{F}(x)$; if NULL it is computed from dens_fn by integration.
t	Truncation time (default 0, which returns Shannon entropy).
upper	Upper integration limit.

Value

Scalar numeric.

References

Ebrahimi N., Pellerey F. (1995). New partial ordering of survival functions based on the notion of uncertainty. *Journal of Applied Probability*, 32(1), 202–211.

See Also

[residual_info_gen](#), [shannon_entropy](#)

Examples

```
# Exponential(1)
f <- function(x) dexp(x, 1)
Fb <- function(x) pexp(x, 1, lower.tail = FALSE)
residual_entropy(f, Fb, t = 0) # = 1
residual_entropy(f, Fb, t = 1) # = 1 + exp(-1) * log(exp(1)-1) or similar
```

residual_info_gen *Residual Entropy Generating Function (REGF)*

Description

Computes the residual entropy generating function proposed by Smitha, Rajesh, and Jayalekshmi (2024):

$$\mathcal{I}_\alpha(X; t) = \int_t^\infty \left(\frac{f(x)}{\bar{F}(t)} \right)^\alpha dx, \quad \alpha > 0, t \geq 0.$$

Note that:

- At $t = 0$, $\mathcal{I}_\alpha(X; 0) = \mathcal{I}_\alpha(f)$, Golomb's IGF.
- $-\partial \mathcal{I}_\alpha / \partial \alpha |_{\alpha=1} = H(X; t)$, the residual entropy.

Usage

```
residual_info_gen(dens_fn, surv_fn = NULL, alpha = 1, t = 0, upper = 100)
```

Arguments

dens_fn	Density function $f(x)$.
surv_fn	Survival function $\bar{F}(x)$; computed by integration if NULL.
alpha	Positive parameter (default 1).
t	Truncation time (default 0).
upper	Upper integration limit.

Value

Scalar numeric.

References

Smitha S., Rajesh G., Jayalekshmi S. (2024). On residual entropy generating function. *Journal of the Indian Statistical Association*, 62(1), 81–93.

See Also

[info_gen_function](#), [residual_entropy](#), [np_residual_info_gen](#)

Examples

```
f <- function(x) dexp(x, 1)
Fb <- function(x) pexp(x, 1, lower.tail = FALSE)

# At t=0, alpha=1: should equal 1
residual_info_gen(f, Fb, alpha = 1, t = 0)

# Dynamic version at t = 0.5
residual_info_gen(f, Fb, alpha = 2, t = 0.5)

# Derivative recovers residual entropy
(residual_info_gen(f, Fb, alpha = 1 + 1e-5, t = 0) -
 residual_info_gen(f, Fb, alpha = 1, t = 0)) / 1e-5 # approx -H(f)
```

schur_biv

Schur-Constant Bivariate Distribution

Description

Random generation and survival function for a Schur-constant bivariate distribution with survival function

$$\bar{F}(x_1, x_2) = S(x_1 + x_2), \quad x_1, x_2 > 0,$$

where S is a given univariate survival function. The default marginal is exponential with rate λ .

Usage

```
sschur_biv(x1, x2, lambda = 1)
```

```
rschur_biv(n, lambda = 1)
```

Arguments

x1, x2	Non-negative values.
lambda	Exponential rate parameter for the generating survival function.
n	Number of random observations.

Value

Numeric vector (sschur_biv) or two-column matrix (rschur_biv).

References

Barlow R.E., Mendel M.B. (1992). De Finetti-type representations for life distributions. **Journal of the American Statistical Association**, 87(420), 1116–1122.

Examples

```
sschur_biv(0.5, 1, lambda = 1)
set.seed(2); head(rschur_biv(40, lambda = 1))
```

shannon_entropy	<i>Shannon Differential Entropy</i>
-----------------	-------------------------------------

Description

Computes the Shannon differential entropy

$$H(f) = - \int_0^{\infty} f(x) \log f(x) dx$$

for a non-negative continuous random variable with density dens_fn.

Usage

```
shannon_entropy(dens_fn, upper = 100)
```

Arguments

dens_fn	A function of one argument returning the density $f(x)$.
upper	Upper integration limit (default 100).

Value

Scalar numeric.

References

Shannon C.E. (1948). A mathematical theory of communication. **Bell System Technical Journal**, 27(3), 379–423.

Smitha S., Rajesh G., Jayalekshmi S. (2024). **Journal of the Indian Statistical Association**, 62(1), 81–93.

See Also

[residual_entropy](#), [info_gen_function](#)

Examples

```
# Exponential(1): H = 1
shannon_entropy(function(x) dexp(x, rate = 1))

# Exponential(2): H = 1 - log(2)
shannon_entropy(function(x) dexp(x, rate = 2))
```

 sim_blt_residual

Monte-Carlo Simulation Study for the BLT Residual Estimator

Description

Evaluates the performance of `np_blt_residual` via repeated simulation from the Gumbel bivariate exponential distribution and compares estimates to the closed-form `blt_residual_gumbel` values. Returns bias, variance, and mean squared error (MSE).

Usage

```
sim_blt_residual(
  n_obs = 200,
  n_sim = 100,
  s1 = 1,
  s2 = 1,
  t1 = 0.3,
  t2 = 0.3,
  k1 = 1,
  k2 = 1,
  theta = 0.5,
  seed = 42L
)
```

Arguments

<code>n_obs</code>	Sample size per replicate.
<code>n_sim</code>	Number of simulation replicates.
<code>s1, s2</code>	Laplace parameters.
<code>t1, t2</code>	Truncation ages.
<code>k1, k2, theta</code>	Gumbel parameters.
<code>seed</code>	Random seed for reproducibility.

Value

A data frame with columns `component`, `true_value`, `mean_est`, `bias`, `variance`, `mse`.

References

Jayalekshmi S., Rajesh G., Nair N.U. (2022), Section 6. [doi:10.1080/03610926.2022.2085874](https://doi.org/10.1080/03610926.2022.2085874)

See Also

[np_blt_residual](#)

Examples

```
sim_blt_residual(n_obs = 100, n_sim = 50, s1 = 1, s2 = 1,
                t1 = 0.3, t2 = 0.3, k1 = 1, k2 = 1, theta = 0.5)
```

 sim_regf

Monte-Carlo Simulation for the REGF Nonparametric Estimator

Description

Evaluates the performance of [np_residual_info_gen](#) via repeated simulation from the exponential distribution and compares to the true REGF $\mathcal{I}_\alpha(\text{Exp}(\lambda); t) = \lambda^{\alpha-1} e^{(\alpha-1)\lambda t} / (\alpha - 1)$.

Usage

```
sim_regf(lambda = 1, alpha = 2, t = 0, n_obs = 200, n_sim = 100, seed = 42L)
```

Arguments

lambda	Exponential rate.
alpha	REGF parameter.
t	Truncation time.
n_obs	Sample size per replicate.
n_sim	Number of replicates.
seed	Random seed.

Value

A data frame with true_value, mean_est, bias, variance, mse.

References

Smitha S., Rajesh G., Jayalekshmi S. (2024), Section 4.

See Also

[np_residual_info_gen](#)

Examples

```
sim_regf(lambda = 1, alpha = 2, t = 0, n_obs = 100, n_sim = 30)
```

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