

Package: BivLaplaceRL (via r-universe)

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Type Package

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

Version 1.0.0

Description Implements methods for bivariate and univariate Laplace transforms of residual lives and reversed residual lives, associated stochastic ordering concepts, and entropy measures for reliability analysis. The package covers: (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) ``Bivariate Laplace Transform of Residual Lives and Their Properties" <doi: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); Jayalekshmi, Rajesh, and Nair (2022) ``Bivariate Laplace Transform Order and Ordering of Reversed Residual Lives" <doi:10.1142/S0218539322500061>; (3) Univariate Laplace transform of residual life, hazard rate, mean residual life, and the corresponding stochastic orders (Lt-rl order, hazard rate order, MRL order), together with a nonparametric estimator. Shannon entropy and Golomb's (1966) information generating function are also provided. 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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Contents

BivLaplaceRL-package	3
biv_brlmr_order	4
biv_hazard_gradient	5
biv_mean_residual	6
biv_rhazard_gradient	7
biv_rmrl	8
biv_whr_order	9
biv_wmrl_order	10
biv_wrhr_order	11
biv_wrmrl_order	12
bivpower	13
blt_order_residual	14
blt_order_reversed	15
blt_residual	16
blt_residual_gumbel	17
blt_reversed	18
blt_reversed_fgm	19
blt_reversed_power	20
fgm_biv	21
gumbel_biv	22
hazard_rate	23

hr_order 24
 info_gen_function 25
 lt_residual 26
 lt_rl_order 27
 mean_residual 28
 mrl_order 29
 nbuhr_test 30
 np_blt_residual 31
 np_lt_residual 32
 plot_blt_residual 33
 plot_blt_reversed 34
 schur_biv 35
 shannon_entropy 36
 sim_blt_residual 37

Index **39**

BivLaplaceRL-package *BivLaplaceRL: Bivariate Laplace Transforms, Stochastic Orders, and Entropy Measures in Reliability*

Description

BivLaplaceRL provides a unified framework for reliability analysis covering bivariate and univariate Laplace transforms of residual lives, associated stochastic orders, and entropy measures:

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. Reference: Jayalekshmi, Rajesh, and Nair (2022) [doi:10.1142/S0218539322500061](https://doi.org/10.1142/S0218539322500061).

3. Univariate Residual Life Analysis

Implements the univariate Laplace transform of residual life $L_X(s, t) = E[e^{-sX} | X > t]$, hazard rate, mean residual life, and the corresponding stochastic orders (Lt-rl order, hazard rate order, MRL order), together with a nonparametric estimator.

Parametric families

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

Plotting

[plot_blt_residual](#) and [plot_blt_reversed](#) 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., Nair N.U. (2022). Bivariate Laplace transform order and ordering of reversed residual lives. *International Journal of Reliability, Quality and Safety Engineering*. doi:10.1142/S0218539322500061
- Belzunce F., Ortega E., Ruiz J.M. (1999). The Laplace order and ordering of residual lives. *Statistics & Probability Letters*, 42(2), 145–156. doi:10.1016/S01677152(98)002028
- 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>

biv_brlmr_order

Bivariate Relative Mean Residual Life Order

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_rmr1

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_rmr1(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)
```

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`*Weak Bivariate Reversed Mean Residual Life Order*

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)
```

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))
```

 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 `function(x1, x2)`.

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)
```

hazard_rate

Univariate Hazard Rate Function

Description

Computes the hazard rate (failure rate) of a non-negative continuous random variable:

$$h(t) = \frac{f(t)}{\bar{F}(t)}, \quad t \geq 0.$$

Usage

```
hazard_rate(dens_fn, surv_fn = NULL, t, upper = 100)
```

Arguments

dens_fn	Density function $f(t)$.
surv_fn	Survival function $\bar{F}(t)$; computed by numerical integration if NULL.
t	Scalar or numeric vector of time points.
upper	Upper integration limit (used only when surv_fn = NULL).

Value

Numeric vector of hazard rates at t.

See Also

[mean_residual](#), [hr_order](#)

Examples

```
# Exp(1): constant hazard rate = 1
f <- function(x) dexp(x, 1)
Fb <- function(x) pexp(x, 1, lower.tail = FALSE)
hazard_rate(f, Fb, t = c(0.5, 1, 2))

# Gamma(2,1): increasing hazard rate
fG <- function(x) dgamma(x, shape = 2, rate = 1)
FbG <- function(x) pgamma(x, shape = 2, rate = 1, lower.tail = FALSE)
hazard_rate(fG, FbG, t = c(0.5, 1, 2))
```

hr_order

*Hazard Rate Order***Description**

Checks whether $X \leq_{\text{hr}} Y$ (hazard rate order): the hazard rate of X is pointwise no greater than that of Y :

$$h_X(t) \leq h_Y(t) \quad \forall t \geq 0.$$

Under this order X is stochastically longer-lived than Y . For exponential distributions, $\text{Exp}(\lambda_1) \leq_{\text{hr}} \text{Exp}(\lambda_2)$ iff $\lambda_1 \leq \lambda_2$.

Usage

```
hr_order(
  dens_fn_X,
  surv_fn_X = NULL,
  dens_fn_Y,
  surv_fn_Y = NULL,
  t_grid = seq(0.1, 3, by = 0.5),
  upper = 100
)
```

Arguments

dens_fn_X, dens_fn_Y
Density functions of X and Y .

surv_fn_X, surv_fn_Y
Survival functions; computed if NULL.

t_grid
Grid of time points.

upper
Integration upper bound.

Value

A list with:

order_holds Logical.

max_violation Maximum of $h_X(t) - h_Y(t)$ over the grid.

hazard_X Hazard rate of X at `t_grid`.

hazard_Y Hazard rate of Y at `t_grid`.

See Also

[hazard_rate](#), [mrl_order](#), [lt_rl_order](#)

Examples

```
# Exp(1) <=_hr Exp(2): h_X(t)=1 <= 2=h_Y(t)
fX <- function(x) dexp(x, 1)
FbX <- function(x) pexp(x, 1, lower.tail = FALSE)
fY <- function(x) dexp(x, 2)
FbY <- function(x) pexp(x, 2, lower.tail = FALSE)
hr_order(fX, FbX, fY, FbY, t_grid = c(0.5, 1, 2))$order_holds
```

info_gen_function *Golomb Information Generating Function*

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

[shannon_entropy](#)

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)
```

lt_residual

Univariate Laplace Transform of Residual Life

Description

Computes the Laplace transform of the residual life of a non-negative continuous random variable conditioned on survival past time t :

$$L_X(s, t) = E[e^{-sX} | X > t] = \frac{1}{\bar{F}(t)} \int_t^\infty e^{-sx} f(x) dx, \quad s \geq 0, t \geq 0.$$

At $t = 0$ this reduces to the standard Laplace transform $L_X(s) = E[e^{-sX}]$.

Usage

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

Arguments

dens_fn	Density function $f(x)$.
surv_fn	Survival function $\bar{F}(x)$; computed by numerical integration of dens_fn if NULL.
s	Non-negative Laplace parameter.
t	Truncation time (default 0).
upper	Upper integration limit.

Value

Scalar numeric.

References

Belzunce F., Ortega E., Ruiz J.M. (1999). The Laplace order and ordering of residual lives. **Statistics & Probability Letters**, 42(2), 145–156.

See Also

[hazard_rate](#), [mean_residual](#), [np_lt_residual](#), [lt_rl_order](#), [blt_residual](#)

Examples

```
# Exp(1): L_X(s, 0) = 1/(1+s) = 0.5 at s=1
f <- function(x) dexp(x, 1)
Fb <- function(x) pexp(x, 1, lower.tail = FALSE)
lt_residual(f, Fb, s = 1, t = 0)

# Memoryless property: L_X(s,t) should equal L_X(s,0) for Exp
lt_residual(f, Fb, s = 1, t = 0.5)
```

 lt_rl_order

Univariate Laplace Transform Order of Residual Lives

Description

Checks whether $X \leq_{Lt-rl} Y$: the Laplace transform of the residual life of X is dominated by that of Y pointwise over a grid of (s, t) values:

$$L_X(s, t) \leq L_Y(s, t) \quad \forall s \geq 0, t \geq 0.$$

The order is verified numerically on `s_grid` x `t_grid`.

Usage

```
lt_rl_order(
  dens_fn_X,
  surv_fn_X = NULL,
  dens_fn_Y,
  surv_fn_Y = NULL,
  s_grid = seq(0.5, 3, by = 0.5),
  t_grid = seq(0, 2, by = 0.5),
  upper = 100
)
```

Arguments

dens_fn_X, dens_fn_Y
Density functions of X and Y .

surv_fn_X, surv_fn_Y
Survival functions; computed if NULL.

s_grid
Numeric vector of Laplace parameter values to check.

t_grid
Numeric vector of truncation times to check.

upper
Integration upper bound.

Value

A list with:

order_holds Logical; TRUE if the order holds at all grid points.

max_violation Maximum violation $\max(L_X - L_Y, 0)$.

ratio_matrix Matrix of $L_X(s, t)/L_Y(s, t)$ values (rows = s_grid, columns = t_grid).

See Also

[lt_residual](#), [hr_order](#), [mrl_order](#), [blt_order_residual](#)

Examples

```
# Exp(1) <=_Lt-rl Exp(2): L_{Exp(lambda)}(s,t) = lambda*exp(-s*t)/(s+lambda)
# For s>0: 1/(s+1) < 2/(s+2), so Exp(1) has smaller LT of residual life
fX <- function(x) dexp(x, 1)
FbX <- function(x) pexp(x, 1, lower.tail = FALSE)
fY <- function(x) dexp(x, 2)
FbY <- function(x) pexp(x, 2, lower.tail = FALSE)
lt_rl_order(fX, FbX, fY, FbY,
            s_grid = c(0.5, 1, 2), t_grid = c(0, 0.5, 1))$order_holds
```

mean_residual

Univariate Mean Residual Life

Description

Computes the mean residual life (mean excess function):

$$m(t) = E[X - t \mid X > t] = \frac{1}{F(t)} \int_t^\infty \bar{F}(x) dx, \quad t \geq 0.$$

Usage

```
mean_residual(surv_fn, t = 0, upper = 100)
```

Arguments

surv_fn	Survival function $\bar{F}(x)$.
t	Scalar or numeric vector of time points.
upper	Upper integration limit.

Value

Numeric vector of MRL values at t.

See Also

[hazard_rate](#), [mrl_order](#)

Examples

```
# Exp(1): constant MRL = 1 (memoryless)
Fb <- function(x) pexp(x, 1, lower.tail = FALSE)
mean_residual(Fb, t = c(0, 0.5, 1, 2))

# Gamma(2,1): decreasing MRL
FbG <- function(x) pgamma(x, shape = 2, rate = 1, lower.tail = FALSE)
mean_residual(FbG, t = c(0, 0.5, 1, 2))
```

mrl_order	<i>Mean Residual Life Order</i>
-----------	---------------------------------

Description

Checks whether $X \leq_{\text{mrl}} Y$ (mean residual life order): the MRL of X is pointwise no greater than that of Y :

$$m_X(t) \leq m_Y(t) \quad \forall t \geq 0.$$

Usage

```
mrl_order(surv_fn_X, surv_fn_Y, t_grid = seq(0, 3, by = 0.5), upper = 100)
```

Arguments

surv_fn_X, surv_fn_Y	Survival functions of X and Y .
t_grid	Grid of time points.
upper	Integration upper bound.

Value

A list with:

order_holds Logical.

max_violation Maximum of $m_X(t) - m_Y(t)$ over the grid.

mr1_X MRL of X at `t_grid`.

mr1_Y MRL of Y at `t_grid`.

See Also

[mean_residual](#), [hr_order](#), [lt_rl_order](#)

Examples

```
# Exp(2) <=_mr1 Exp(1): m_X(t)=0.5 <= 1=m_Y(t)
FbX <- function(x) pexp(x, 2, lower.tail = FALSE)
FbY <- function(x) pexp(x, 1, lower.tail = FALSE)
mr1_order(FbX, FbY, t_grid = c(0, 0.5, 1, 2))$order_holds
```

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](https://doi.org/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_lt_residual	<i>Nonparametric Estimator for the Univariate Laplace Transform of Residual Life</i>
----------------	--

Description

Given a sample X_1, \dots, X_n , estimates the Laplace transform of the residual life using the empirical survival function:

$$\hat{L}_X(s, t) = \frac{\sum_{i: X_i > t} e^{-sX_i}}{\#\{i : X_i > t\}}.$$

Usage

```
np_lt_residual(x, s, t = 0)
```

Arguments

x	Numeric vector; observed sample.
s	Non-negative Laplace parameter.
t	Truncation time (default 0).

Value

Scalar numeric estimate of $L_X(s, t)$.

See Also

[lt_residual](#)

Examples

```

set.seed(1)
x <- rexp(300, rate = 1)

# Estimate at s=1, t=0: true value 1/(1+1) = 0.5
np_lt_residual(x, s = 1, t = 0)

# Estimate at s=1, t=0.5: true value still approx 0.5 (memoryless)
np_lt_residual(x, s = 1, t = 0.5)

```

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"))
```

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 lambda.

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.

See Also

[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)
```

Index

biv_brlmr_order, 4
biv_hazard_gradient, 5
biv_mean_residual, 6
biv_rhazard_gradient, 7
biv_rmrl, 8
biv_whr_order, 9, 15
biv_wmrl_order, 10
biv_wrhr_order, 11, 16
biv_wrmrl_order, 12
BivLaplaceRL (BivLaplaceRL-package), 3
BivLaplaceRL-package, 3
bivpower, 13
blt_order_residual, 14, 15, 17, 28
blt_order_reversed, 15, 19
blt_residual, 15, 16, 18, 27
blt_residual_gumbel, 17, 17, 32, 37
blt_reversed, 16, 18
blt_reversed_fgm, 19, 19
blt_reversed_power, 20

dbivpower (bivpower), 13
dfgm_biv (fgm_biv), 21
dgumbel_biv (gumbel_biv), 22

fgm_biv, 21

gumbel_biv, 22

hazard_rate, 23, 25, 27, 29
hr_order, 23, 24, 28, 30

info_gen_function, 25, 36

lt_residual, 26, 28, 32
lt_rl_order, 25, 27, 27, 30

mean_residual, 23, 27, 28, 30
mrl_order, 25, 28, 29, 29

nbuhr_test, 30
np_blt_residual, 17, 31, 37, 38

np_lt_residual, 27, 32

pbivpower (bivpower), 13
pfgm_biv (fgm_biv), 21
pgumbel_biv (gumbel_biv), 22
plot_blt_residual, 4, 33
plot_blt_reversed, 4, 34

rbivpower (bivpower), 13
rfgm_biv (fgm_biv), 21
rgumbel_biv (gumbel_biv), 22
rschur_biv (schur_biv), 35

sbivpower (bivpower), 13
schur_biv, 35
sfgm_biv (fgm_biv), 21
sgumbel_biv (gumbel_biv), 22
shannon_entropy, 26, 36
sim_blt_residual, 32, 37
sschur_biv (schur_biv), 35