

Package ‘MultiFrailty’

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Title Shared Frailty Regression Models with Inverse Gaussian,
Generalized Lindley, and Gamma Frailty Distributions

Version 0.1.0

Description Implements shared frailty regression models for survival data under eight censoring mechanisms: exact, right censoring (Kalbfleisch and Prentice, 2002), left censoring, interval censoring (Sun, 2006), progressive Type I censoring, and progressive Type II censoring (Balakrishnan and Aggarwala, 2000 <[doi:10.1007/978-1-4612-1334-5](https://doi.org/10.1007/978-1-4612-1334-5)>). Combines four frailty distributions -- Gamma (Clayton, 1978), Inverse Gaussian (Hougaard, 1984), and two variants of the Generalized Lindley (GL) distribution: GL Type 1, a two-component gamma mixture with distribution-specific scale/shape linkage (Pandey, Hanagal, and Tyagi, 2022), and GL Type 2, a two-component gamma mixture with a common rate parameter (Pandey and Tyagi, 2021 <[doi:10.1134/S1995080222010140](https://doi.org/10.1134/S1995080222010140)>) -- with two baseline hazard distributions: the two-parameter Weibull distribution (Weibull, 1951) and the three-parameter Generalized (Exponentiated) Weibull distribution (Mudholkar and Srivastava, 1993 <[doi:10.1109/24.229504](https://doi.org/10.1109/24.229504)>). A no-frailty baseline-only model is also supported for nested model comparison. Maximum likelihood estimation is conducted using Newton-Raphson and Broyden-Fletcher-Goldfarb-Shanno (BFGS) algorithms via the 'maxLik' package (Henningsen and Toomet, 2011 <[doi:10.1007/s00180-010-0217-1](https://doi.org/10.1007/s00180-010-0217-1)>). Provides standard errors, confidence intervals, hypothesis tests, Akaike Information Criterion (AIC, Akaike, 1974 <[doi:10.1109/TAC.1974.1100705](https://doi.org/10.1109/TAC.1974.1100705)>), Bayesian Information Criterion (BIC, Schwarz, 1978 <[doi:10.1214/aos/1176344136](https://doi.org/10.1214/aos/1176344136)>), corrected Akaike Information Criterion (AICc, Hurvich and Tsai, 1989), Hannan-Quinn Information Criterion (HQIC, Hannan and Quinn, 1979), a bootstrap approximation of the Widely Applicable Information Criterion (WAIC, Watanabe, 2010), k-fold cross-validation, frailty variance estimation, survival, hazard, median, risk, and marginal predictions, Cox-Snell (Cox and Snell, 1968), martingale (Barlow and Prentice, 1988), and deviance residuals with a Kolmogorov-Smirnov goodness-of-fit test, influence diagnostics (leverage, Cook's distance, difference in fits (DFFITS), difference in betas (DFBETAS); Belsley, Kuh, and Welsch, 1980), random data generation under all eight censoring mechanisms, a Monte Carlo simulation-study function, and a diagnostic and survival plotting suite.

License GPL-3

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Contents

baseline_hazard	3
bootstrap_waic	4
compare_models	4
cv_frailty	5
diagnostics_table	6
fit_frailty	6
forecast_frailty	8
frailty_functions	8
frailty_laplace	9
influence_frailty	10
loglik_frailty	11
multifrailty	12
plot_all	13
plot_baseline	14
plot_coef_forest	14
plot_dfbetas	15
plot_frailty_density	15
plot_leverage	16
plot_qq_residuals	16
plot_residuals_fitted	17
plot_residuals_leverage	17
plot_scale_location	18
plot_survival_km	18

predict_frailty	19
print.multifrailty_fit	20
residuals_frailty	21
risk_predict	22
r_frailty	23
r_gl1	24
r_gl2	25
r_gw	26
r_ig	26
simulate_mle_performance	27
simulation_study	28
survival_at	29
Index	30

baseline_hazard	<i>Baseline Hazard and Cumulative Hazard Evaluation</i>
-----------------	---

Description

Computes baseline hazard $\phi(t)$ and cumulative baseline hazard $\Phi(t)$ for Weibull and Generalized Weibull (GW) distributions.

Usage

```
baseline_hazard(t, baseline = c("weibull", "gw"), par)
```

Arguments

t	Positive numeric vector of time points.
baseline	Character string specifying baseline distribution: "weibull" or "gw".
par	Numeric vector of parameters: c(lambda, gamma) for Weibull, or c(delta, zeta, xi) for GW.

Value

A named list with components:

H0	Cumulative baseline hazard $\Phi(t)$.
h0	Baseline hazard $\phi(t)$.

References

Mudholkar, G. S., & Srivastava, D. K. (1993). Exponentiated Weibull family for analyzing bathtub failure-rate data. IEEE Transactions on Reliability, 42(2), 299-302.

Examples

```
bh_weib <- baseline_hazard(1:5, baseline = "weibull", par = c(2, 1.5))
bh_gw <- baseline_hazard(1:5, baseline = "gw", par = c(0.5, 1.2, 1.1))
```

bootstrap_waic	<i>Bootstrapped WAIC Computation</i>
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Description

Bootstrapped WAIC Computation

Usage

```
bootstrap_waic(fit, B = 200)
```

Arguments

fit	Fitted multifrailty_fit object.
B	Number of bootstrap replications. Default is 200.

Value

Numeric value of bootstrapped WAIC.

compare_models	<i>Model Comparison, Bootstrapped WAIC, and Cross-Validation for MultiFrailty Models</i>
----------------	--

Description

Compares multiple fitted shared frailty models using AIC, BIC, AICc, HQIC, optional bootstrapped WAIC, and k-fold cross-validation.

Usage

```
compare_models(
  ...,
  criteria = c("AIC", "BIC", "AICc", "HQIC"),
  compute_waic = FALSE,
  waic_B = 100L
)
```

Arguments

...	Fitted "multifrailty_fit" objects passed individually or as a list.
criteria	Character vector of selection criteria to include.
compute_waic	Logical; if TRUE computes bootstrapped WAIC. Default is FALSE.
waic_B	Number of bootstrap samples for WAIC. Default is 100.

Value

A data frame summarizing model comparisons ranked by AIC.

References

Pandey, A., Hanagal, D. D., & Tyagi, S. (2022). Shared Frailty Models Based on Cancer Data. *International Journal of Statistics and Reliability Engineering*, 9(3), 461-474.

Pandey, A., & Tyagi, S. (2021). Comparison of Multiplicative Frailty Models Under Weibull Base-line Distribution. *Lobachevskii Journal of Mathematics*, 42(13), 3184-3195.

Examples

```
set.seed(123)
dat <- r_frailty(n = 60, baseline = "weibull", bpar = c(2, 1.5), frailty = "gamma", fpar = c(0.8))
fit1 <- fit_frailty(time = dat$time, status = dat$status, baseline = "weibull", frailty = "none")
fit2 <- fit_frailty(time = dat$time, status = dat$status, baseline = "weibull", frailty = "gamma")
cmp <- compare_models(fit1, fit2)
print(cmp)
```

cv_frailty

K-Fold Cross Validation for MultiFrailty Models

Description

K-Fold Cross Validation for MultiFrailty Models

Usage

```
cv_frailty(
  time,
  status,
  x = matrix(nrow = length(time), ncol = 0),
  baseline = "weibull",
  frailty = "gamma",
  k = 5L,
  time2 = NULL
)
```

Arguments

time	Time vector.
status	Status vector.
x	Covariate matrix.
baseline	Baseline distribution.
frailty	Frailty distribution.
k	Number of folds. Default is 5L.
time2	Optional upper interval bound vector.

Value

Out-of-sample total log-likelihood score.

diagnostics_table	<i>Diagnostic Summary Table</i>
-------------------	---------------------------------

Description

Diagnostic Summary Table

Usage

```
diagnostics_table(fit)
```

Arguments

fit Fitted multifrailty_fit object.

Value

Data frame of influence diagnostics.

fit_frailty	<i>Low-Level Maximum Likelihood Estimator for MultiFrailty Models</i>
-------------	---

Description

Fits shared frailty regression models using Maximum Likelihood Estimation (MLE) across all 10 baseline-frailty combinations with robust optimizer fallbacks.

Usage

```
fit_frailty(  
  time,  
  status,  
  x = matrix(nrow = length(time), ncol = 0),  
  baseline = c("weibull", "gw"),  
  frailty = c("none", "gamma", "ig", "gl1", "gl2"),  
  time2 = NULL,  
  prog_cen = NULL,  
  init = NULL,  
  method = "NR",  
  ...  
)
```

Arguments

time	Primary survival/censoring time vector.
status	Event indicator vector (0 = right-censored, 1 = event, 2 = left-censored, 3 = interval-censored).
x	Design matrix of covariates (n x p). Default is a 0-column matrix.
baseline	Character string for baseline hazard: "weibull" or "gw".
frailty	Character string for frailty family: "none", "gamma", "ig", "gl1", or "gl2".
time2	Vector of upper interval bounds when status == 3. Default is NULL.
prog_cen	Vector of progressive censoring counts. Default is NULL.
init	Vector of initial values on the estimation scale. Default is NULL (automatic).
method	Optimization method passed to maxLik: "NR" (Newton-Raphson) or "BFGS".
...	Additional arguments passed to optimization algorithms.

Value

An object of class "multifrailty_fit" containing parameter estimates, standard errors, information criteria, variance-covariance matrix, and diagnostic statistics.

References

- Hougaard, P. (1984). Life table methods for heterogeneous populations: distributions of frailties. *Biometrika*, 71(1), 75-83.
- Pandey, A., Hanagal, D. D., & Tyagi, S. (2022). Shared Frailty Models Based on Cancer Data. *International Journal of Statistics and Reliability Engineering*, 9(3), 461-474.
- Pandey, A., & Tyagi, S. (2021). Comparison of Multiplicative Frailty Models Under Weibull Baseline Distribution. *Lobachevskii Journal of Mathematics*, 42(13), 3184-3195.

Examples

```
set.seed(123)
dat <- r_frailty(n = 100, baseline = "weibull", bpar = c(2, 1.5),
               frailty = "gamma", fpar = c(0.8),
               x = matrix(rnorm(100), ncol = 1), beta = 0.5)
fit <- fit_frailty(time = dat$time, status = dat$status, x = as.matrix(dat[, "X1", drop=FALSE]),
                  baseline = "weibull", frailty = "gamma")
print(fit)
```

forecast_frailty	<i>Future Survival Forecast</i>
------------------	---------------------------------

Description

Future Survival Forecast

Usage

```
forecast_frailty(fit, horizon, n_grid = 200, newdata = NULL)
```

Arguments

fit	Fitted multifrailty_fit object.
horizon	Forecast horizon time.
n_grid	Number of evaluation points. Default 200.
newdata	Optional new data frame.

Value

Matrix of forecasted survival probabilities.

frailty_functions	<i>Unified Survival, Density, Hazard, and Cumulative Hazard Combiner</i>
-------------------	--

Description

Evaluates unconditional survival function $S(t)$, probability density function $f(t)$, hazard function $h(t)$, and cumulative hazard function $H(t)$ for any specified combination of frailty distribution and baseline hazard.

Usage

```
frailty_functions(
  t,
  eta = 1,
  frailty = c("none", "gamma", "ig", "gl1", "gl2"),
  fpar = numeric(0),
  baseline = c("weibull", "gw"),
  bpar
)
```


Arguments

t	Positive numeric vector of time points.
eta	Linear predictor risk scores $\rho = \exp(X \% \% \beta)$ (numeric vector of same length as t or scalar).
frailty	Character string specifying frailty family: "none", "gamma", "ig", "gl1", or "gl2".
fpar	Numeric vector of parameters for frailty distribution.
baseline	Character string specifying baseline hazard: "weibull" or "gw".
bpar	Numeric vector of parameters for baseline hazard.

Value

A named list containing:

S	Unconditional survival probabilities $S(t)$.
f	Unconditional density values $f(t)$.
h	Unconditional hazard values $h(t)$.
H	Unconditional cumulative hazard values $H(t)$.

References

- Pandey, A., Hanagal, D. D., & Tyagi, S. (2022). Shared Frailty Models Based on Cancer Data. *International Journal of Statistics and Reliability Engineering*, 9(3), 461-474.
- Pandey, A., & Tyagi, S. (2021). Comparison of Multiplicative Frailty Models Under Weibull Baseline Distribution. *Lobachevskii Journal of Mathematics*, 42(13), 3184-3195.

Examples

```
gf <- frailty_functions(1:5, eta = 1, frailty = "gl1", fpar = c(2.13, 1.53),
  baseline = "gw", bpar = c(0.71, 2.13, 1.54))
```

frailty_laplace

Laplace Transform and Derivatives for Frailty Distributions

Description

Computes Laplace transform $L(s)$, first derivative $L'(s)$, and frailty variance $\text{Var}(W)$ for five frailty families: "none", "gamma", "ig", "gl1", and "gl2".

Usage

```
frailty_laplace(
  s,
  frailty = c("none", "gamma", "ig", "gl1", "gl2"),
  par = numeric(0)
)
```

Arguments

s	Non-negative numeric vector.
frailty	Character string specifying frailty family: "none", "gamma", "ig", "gl1", or "gl2".
par	Numeric vector of parameters per family: numeric(0) for "none", c(theta) for "gamma", c(eta) for "ig", c(eta, epsilon) for "gl1", or c(theta, mu) for "gl2".

Value

A named list with components:

L	Laplace transform $L(s)$.
L1	First derivative $L'(s)$.
Var	Variance of frailty distribution $\text{Var}(W)$, evaluated as $L''(0) - 1$.

References

- Hougaard, P. (1984). Life table methods for heterogeneous populations: distributions of frailties. *Biometrika*, 71(1), 75-83.
- Pandey, A., Hanagal, D. D., & Tyagi, S. (2022). Shared Frailty Models Based on Cancer Data. *International Journal of Statistics and Reliability Engineering*, 9(3), 461-474.
- Pandey, A., & Tyagi, S. (2021). Comparison of Multiplicative Frailty Models Under Weibull Base-line Distribution. *Lobachevskii Journal of Mathematics*, 42(13), 3184-3195.

Examples

```
fl_gamma <- frailty_laplace(s = 0.5, frailty = "gamma", par = c(0.8))
fl_gl1  <- frailty_laplace(s = 0.5, frailty = "gl1", par = c(1.2, 0.5))
fl_gl2  <- frailty_laplace(s = 0.5, frailty = "gl2", par = c(1.5, 0.8))
```

influence_frailty *Influence Diagnostics for MultiFrailty Models*

Description

Computes leverage (hat values), Cook's distance, DFBETAS, and DFFITS for regression parameters.

Usage

```
influence_frailty(fit)
```

Arguments

fit A fitted object of class "multifrailty_fit".

Value

A list containing leverage, Cook's distance, DFBETAS matrix, DFFITS vector, and a summary diagnostic table.

References

Belsley, D. A., Kuh, E., & Welsch, R. E. (1980). Regression diagnostics: Identifying influential data and sources of collinearity. John Wiley & Sons.

Examples

```
set.seed(123)
dat <- r_frailty(n = 50, baseline = "weibull", bpar = c(2, 1.5), frailty = "gamma", fpar = c(0.8))
fit <- fit_frailty(time = dat$time, status = dat$status, baseline = "weibull", frailty = "gamma")
inf <- influence_frailty(fit)
head(inf$diagnostics_table)
```

loglik_frailty

*Log-Likelihood Function for MultiFrailty Models***Description**

Computes the log-likelihood for shared frailty models across all 10 baseline-frailty combinations with support for right, exact, left, and interval censoring, plus optional progressive censoring.

Usage

```
loglik_frailty(
  par_all,
  time,
  status,
  x = matrix(nrow = length(time), ncol = 0),
  baseline = c("weibull", "gw"),
  frailty = c("none", "gamma", "ig", "gl1", "gl2"),
  time2 = NULL,
  prog_cen = NULL
)
```

Arguments

par_all	Vector of all model parameters on estimation scale (log/logit transformed).
time	Primary event/censoring time vector.
status	Event status vector (0 = right-censored, 1 = exact event, 2 = left-censored, 3 = interval-censored).
x	Matrix of covariates (n x p). Default is 0-column matrix.
baseline	Baseline hazard distribution ("weibull" or "gw").

frailty	Frailty distribution ("none", "gamma", "ig", "gl1", or "gl2").
time2	Vector of upper interval bounds when status == 3. Default is NULL.
prog_cen	Vector of progressive censoring counts R_i per observation. Default is NULL.

Value

Scalar log-likelihood value. Returns $-1e12$ sentinel on numerical invalidity.

Examples

```
par_all <- c(log(2), log(1.5), log(0.8), 0.1) # Weibull + Gamma + 1 beta
time <- c(1, 2, 3, 4)
status <- c(1, 0, 1, 0)
x <- matrix(c(0.5, -0.2, 0.1, 0.8), ncol = 1)
ll <- loglik_frailty(par_all, time, status, x, baseline = "weibull", frailty = "gamma")
```

multifrailty

*Formula Interface for Shared Frailty Regression Models***Description**

Fits shared frailty regression models using a formula specifying survival response (e.g., `survival::Surv(time, status) ~ x1 + x2`) and data frame.

Usage

```
multifrailty(
  formula,
  data,
  baseline = c("weibull", "gw"),
  frailty = c("none", "gamma", "ig", "gl1", "gl2"),
  method = "NR",
  ...
)
```

Arguments

formula	Model formula of the form <code>survival::Surv(time, status) ~ x1 + x2</code> .
data	Data frame containing variables in formula.
baseline	Character string specifying baseline hazard: "weibull" or "gw".
frailty	Character string specifying frailty family: "none", "gamma", "ig", "gl1", or "gl2".
method	Optimization method for <code>maxLik</code> : "NR" (Newton-Raphson) or "BFGS".
...	Additional arguments passed to fit_frailty .

Value

Object of class `c("multifrailty", "multifrailty_fit")`.

References

Pandey, A., Hanagal, D. D., & Tyagi, S. (2022). Shared Frailty Models Based on Cancer Data. *International Journal of Statistics and Reliability Engineering*, 9(3), 461-474.

Pandey, A., & Tyagi, S. (2021). Comparison of Multiplicative Frailty Models Under Weibull Baseline Distribution. *Lobachevskii Journal of Mathematics*, 42(13), 3184-3195.

Examples

```
set.seed(123)
df <- data.frame(
  time = stats::rexp(50, rate = 0.1),
  status = sample(c(0, 1), 50, replace = TRUE),
  age = stats::rnorm(50, mean = 50, sd = 10),
  sex = sample(c(0, 1), 50, replace = TRUE)
)
fit <- multifrailty(survival::Surv(time, status) ~ age + sex, data = df,
  baseline = "weibull", frailty = "gamma")
print(fit)
```

plot_all

Full Diagnostic Plot Suite

Description

Displays comprehensive multi-panel diagnostic plot suite.

Usage

```
plot_all(fit, ask = grDevices::dev.interactive(), save_to_file = NULL)
```

Arguments

<code>fit</code>	Fitted model.
<code>ask</code>	Logical; if TRUE prompts user.
<code>save_to_file</code>	Optional file path to save plot grid.

Value

No return value, called for side effects (displays a 2x3 grid of diagnostic plots or saves them to a file).

plot_baseline	<i>Baseline Hazard Plot</i>
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Description

Baseline Hazard Plot

Usage

```
plot_baseline(  
  baseline = c("weibull", "gw"),  
  par,  
  t_range = c(0.01, 3),  
  n_grid = 300  
)
```

Arguments

baseline	Baseline distribution.
par	Baseline parameters.
t_range	Time range vector.
n_grid	Grid resolution.

Value

No return value, called for side effects (displays baseline hazard and cumulative baseline hazard plots).

plot_coef_forest	<i>Coefficient Forest Plot</i>
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Description

Coefficient Forest Plot

Usage

```
plot_coef_forest(fit)
```

Arguments

fit	Fitted model.
-----	---------------

Value

No return value, called for side effects (displays a forest plot of parameter estimates with 95% confidence intervals).

plot_dfbetas	<i>DFBETAS Plot</i>
--------------	---------------------

Description

DFBETAS Plot

Usage

```
plot_dfbetas(fit)
```

Arguments

fit	Fitted model.
-----	---------------

Value

No return value, called for side effects (displays boxplots of DFBETAS values across parameters).

plot_frailty_density	<i>Frailty Density Overlay Plot across Families</i>
----------------------	---

Description

Frailty Density Overlay Plot across Families

Usage

```
plot_frailty_density(t_max = 3)
```

Arguments

t_max	Maximum grid value.
-------	---------------------

Value

No return value, called for side effects (displays frailty density overlay curves across distributions).

plot_leverage	<i>Leverage Index Plot</i>
---------------	----------------------------

Description

Leverage Index Plot

Usage

plot_leverage(fit)

Arguments

fit Fitted model.

Value

No return value, called for side effects (displays an index plot of observation leverage values).

plot_qq_residuals	<i>Q-Q Plot of Cox-Snell Residuals vs Exp(1)</i>
-------------------	--

Description

Q-Q Plot of Cox-Snell Residuals vs Exp(1)

Usage

plot_qq_residuals(fit)

Arguments

fit Fitted model.

Value

No return value, called for side effects (displays a Q-Q plot of Cox-Snell residuals versus standard exponential distribution).

`plot_residuals_fitted` *Residuals vs Fitted Plot*

Description

Residuals vs Fitted Plot

Usage

```
plot_residuals_fitted(fit)
```

Arguments

`fit` Fitted model.

Value

No return value, called for side effects (displays a plot of martingale residuals against fitted survival probabilities).

`plot_residuals_leverage`
Residuals vs Leverage Plot

Description

Residuals vs Leverage Plot

Usage

```
plot_residuals_leverage(fit)
```

Arguments

`fit` Fitted model.

Value

No return value, called for side effects (displays a plot of standardized residuals against leverage values).

plot_scale_location	<i>Scale-Location Plot</i>
---------------------	----------------------------

Description

Scale-Location Plot

Usage

```
plot_scale_location(fit)
```

Arguments

fit	Fitted model.
-----	---------------

Value

No return value, called for side effects (displays a scale-location plot of square-root absolute standardized residuals against fitted survival probabilities).

plot_survival_km	<i>Diagnostic and Visualization Suite for MultiFrailty Models</i>
------------------	---

Description

Provides specialized plotting capabilities for fitted shared frailty models, including frailty density overlays across all five families, baseline hazard curves, Kaplan-Meier survival curves, residual diagnostic plots, coefficient forest plots, and influence diagnostic plots.

Usage

```
plot_survival_km(fit)
```

Arguments

fit	A fitted object of class "multifrailty_fit".
-----	--

Value

No return value, called for side effects (displays a Kaplan-Meier survival curve with fitted Multi-Frailty model overlay).

References

- Pandey, A., Hanagal, D. D., & Tyagi, S. (2022). Shared Frailty Models Based on Cancer Data. *International Journal of Statistics and Reliability Engineering*, 9(3), 461-474.
- Pandey, A., & Tyagi, S. (2021). Comparison of Multiplicative Frailty Models Under Weibull Base-line Distribution. *Lobachevskii Journal of Mathematics*, 42(13), 3184-3195.

Examples

```
set.seed(123)
dat <- r_frailty(n = 60, baseline = "weibull", bpar = c(2, 1.5), frailty = "gamma", fpar = c(0.8))
fit <- fit_frailty(time = dat$time, status = dat$status, baseline = "weibull", frailty = "gamma")
plot_survival_km(fit)
```

predict_frailty	<i>Predictions for MultiFrailty Regression Models</i>
-----------------	---

Description

Computes survival probabilities, hazard rates, median survival times, expected survival times, risk scores, marginal survival curves, or future survival forecasts for a fitted multifrailty model.

Usage

```
predict_frailty(
  fit,
  newdata = NULL,
  newtime = NULL,
  type = c("survival", "hazard", "median", "expected", "risk", "marginal", "forecast"),
  window = NULL
)
```

Arguments

fit	A fitted object of class "multifrailty_fit".
newdata	Optional data frame of new covariate values. If NULL, uses training data.
newtime	Optional vector of evaluation time points. If NULL, uses default grid.
type	Type of prediction: "survival", "hazard", "median", "expected", "risk", "marginal", or "forecast".
window	Optional forecast window or horizon parameter.

Value

Vector or matrix of predictions depending on type.

References

Pandey, A., Hanagal, D. D., & Tyagi, S. (2022). Shared Frailty Models Based on Cancer Data. *International Journal of Statistics and Reliability Engineering*, 9(3), 461-474.

Pandey, A., & Tyagi, S. (2021). Comparison of Multiplicative Frailty Models Under Weibull Baseline Distribution. *Lobachevskii Journal of Mathematics*, 42(13), 3184-3195.

Examples

```
set.seed(123)
dat <- r_frailty(n = 60, baseline = "weibull", bpar = c(2, 1.5), frailty = "gamma", fpar = c(0.8))
fit <- fit_frailty(time = dat$time, status = dat$status, baseline = "weibull", frailty = "gamma")
pred_surv <- predict_frailty(fit, type = "survival", newtime = c(1, 2, 3))
```

```
print.multifrailty_fit
```

S3 Methods for MultiFrailty Fit Objects

Description

Provides standard print, summary, coef, vcov, logLik, AIC, BIC, and confint S3 methods for objects of class "multifrailty_fit".

Usage

```
## S3 method for class 'multifrailty_fit'
print(x, ...)

## S3 method for class 'multifrailty_fit'
summary(object, ...)

## S3 method for class 'summary.multifrailty_fit'
print(x, ...)

## S3 method for class 'multifrailty_fit'
coef(object, ...)

## S3 method for class 'multifrailty_fit'
vcov(object, ...)

## S3 method for class 'multifrailty_fit'
logLik(object, ...)

## S3 method for class 'multifrailty_fit'
AIC(object, ...)

## S3 method for class 'multifrailty_fit'
```

```
BIC(object, ...)

## S3 method for class 'multifrailty_fit'
confint(object, parm, level = 0.95, ...)
```

Arguments

x	An object of class "multifrailty_fit".
...	Additional arguments.
object	An object of class "multifrailty_fit".
parm	Optional parameter vector or names.
level	Confidence level for interval. Default 0.95.

Value

Formatted console output or numeric objects depending on method.

References

Pandey, A., Hanagal, D. D., & Tyagi, S. (2022). Shared Frailty Models Based on Cancer Data. *International Journal of Statistics and Reliability Engineering*, 9(3), 461-474.

Pandey, A., & Tyagi, S. (2021). Comparison of Multiplicative Frailty Models Under Weibull Base-line Distribution. *Lobachevskii Journal of Mathematics*, 42(13), 3184-3195.

residuals_frailty	<i>Residual Diagnostics and Goodness-of-Fit Tests for MultiFrailty Models</i>
-------------------	---

Description

Computes Cox-Snell, Martingale, Deviance, raw, standardized, and studentized residuals along with Kolmogorov-Smirnov (K-S) goodness-of-fit statistics against standard Exponential(1).

Usage

```
residuals_frailty(fit)
```

Arguments

fit	A fitted object of class "multifrailty_fit".
-----	--

Value

A list containing residual vectors, summary accuracy metrics (MSE, RMSE, MAE, R_square, Adj_R_square), and K-S test results (KS_stat, KS_pvalue).

References

- Cox, D. R., & Snell, E. J. (1968). A general definition of residuals. *Journal of the Royal Statistical Society: Series B (Methodological)*, 30(2), 248-265.
- Pandey, A., Hanagal, D. D., & Tyagi, S. (2022). Shared Frailty Models Based on Cancer Data. *International Journal of Statistics and Reliability Engineering*, 9(3), 461-474.
- Pandey, A., & Tyagi, S. (2021). Comparison of Multiplicative Frailty Models Under Weibull Baseline Distribution. *Lobachevskii Journal of Mathematics*, 42(13), 3184-3195.

Examples

```
set.seed(123)
dat <- r_frailty(n = 60, baseline = "weibull", bpar = c(2, 1.5), frailty = "gamma", fpar = c(0.8))
fit <- fit_frailty(time = dat$time, status = dat$status, baseline = "weibull", frailty = "gamma")
res <- residuals_frailty(fit)
print(res$KS_pvalue)
```

risk_predict

Risk Score Predictions

Description

Risk Score Predictions

Usage

```
risk_predict(fit, newdata, times = NULL)
```

Arguments

fit	Fitted multifrailty_fit object.
newdata	Data frame of new observations.
times	Optional time grid.

Value

Numeric vector of risk scores $\exp(X \%*\% \beta)$.

r_frailty

*Random Data Generation under Eight Censoring Schemes***Description**

Generates survival times and censoring indicators for shared frailty regression models across all 10 baseline-frailty combinations under eight distinct censoring mechanisms.

Usage

```
r_frailty(
  n,
  baseline = c("weibull", "gw"),
  bpar,
  frailty = c("none", "gamma", "ig", "gl1", "gl2"),
  fpar = numeric(0),
  x = matrix(nrow = n, ncol = 0),
  beta = numeric(0),
  cen_type = c("none", "right", "left", "interval", "type1", "type2", "progressive",
    "progressive_type1"),
  cen_rate = 0.2,
  left_threshold = NULL,
  int_width = NULL,
  cen_time = NULL,
  r_failures = NULL,
  prog_scheme = NULL,
  prog_times = NULL
)
```

Arguments

n	Number of observations to generate.
baseline	Baseline hazard distribution ("weibull" or "gw").
bpar	Baseline parameter vector.
frailty	Frailty distribution ("none", "gamma", "ig", "gl1", or "gl2").
fpar	Frailty parameter vector.
x	Matrix of covariates (n x p). Default is 0-column matrix.
beta	Regression coefficient vector matching columns of x.
cen_type	Censoring mechanism: "none", "right", "left", "interval", "type1", "type2", "progressive", or "progressive_type1".
cen_rate	Exponential rate for right-censoring time generation. Default is 0.2.
left_threshold	Threshold for left censoring. Default is 20th percentile.
int_width	Width of censoring window for interval censoring. Default is 20% of mean time.
cen_time	Fixed cutoff time for Type-I censoring. Default is 70th percentile.

r_failures	Target number of failures for Type-II censoring. Default is $\text{floor}(0.7 * n)$.
prog_scheme	Vector of progressive removal counts for progressive censoring.
prog_times	Inspection time points for progressive Type-I censoring.

Value

A data frame containing generated time, time2 (for interval), status, and covariates.

References

Hougaard, P. (1984). Life table methods for heterogeneous populations: distributions of frailties. *Biometrika*, 71(1), 75-83.

Pandey, A., Hanagal, D. D., & Tyagi, S. (2022). Shared Frailty Models Based on Cancer Data. *International Journal of Statistics and Reliability Engineering*, 9(3), 461-474.

Pandey, A., & Tyagi, S. (2021). Comparison of Multiplicative Frailty Models Under Weibull Base-line Distribution. *Lobachevskii Journal of Mathematics*, 42(13), 3184-3195.

Examples

```
set.seed(123)
dat <- r_frailty(n = 100, baseline = "weibull", bpar = c(2, 1.5),
               frailty = "gll", fpar = c(1.2, 0.5),
               cen_type = "right", cen_rate = 0.1)
head(dat)
```

r_gll	<i>Random Generation for Generalized Lindley Type 1 (GL1) Frailty Distribution</i>
-------	--

Description

Generates random variates from GL Type 1 frailty distribution (two-component Gamma mixture).

Usage

```
r_gll(n, eta, epsilon)
```

Arguments

n	Number of observations to generate.
eta	Parameter $\eta > 0$.
epsilon	Parameter $\epsilon > 0$.

Value

Numeric vector of length n.

References

Pandey, A., Hanagal, D. D., & Tyagi, S. (2022). Shared Frailty Models Based on Cancer Data. *International Journal of Statistics and Reliability Engineering*, 9(3), 461-474.

Examples

```
set.seed(123)
w_gl1 <- r_gl1(100, eta = 1.2, epsilon = 0.5)
```

r_gl2	<i>Random Generation for Generalized Lindley Type 2 (GL2) Frailty Distribution</i>
-------	--

Description

Generates random variates from GL Type 2 frailty distribution (two-component Gamma mixture with common rate).

Usage

```
r_gl2(n, theta, mu)
```

Arguments

n	Number of observations to generate.
theta	Parameter $\theta > 0$.
mu	Parameter μ in $(0, 1 + \theta)$.

Value

Numeric vector of length n.

References

Pandey, A., & Tyagi, S. (2021). Comparison of Multiplicative Frailty Models Under Weibull Baseline Distribution. *Lobachevskii Journal of Mathematics*, 42(13), 3184-3195.

Examples

```
set.seed(123)
w_gl2 <- r_gl2(100, theta = 1.5, mu = 0.8)
```

r_gw	<i>Random Generation for Generalized Weibull (GW) Baseline Distribution</i>
------	---

Description

Generates random variates from the 3-parameter Generalized Weibull baseline distribution.

Usage

```
r_gw(n, delta, zeta, xi)
```

Arguments

n	Number of observations to generate.
delta	Scale parameter ($\delta > 0$).
zeta	Shape parameter ($\zeta > 0$).
xi	Shape parameter ($\xi > 0$).

Value

Numeric vector of length n containing random samples.

References

Mudholkar, G. S., & Srivastava, D. K. (1993). Exponentiated Weibull family for analyzing bathtub failure-rate data. *IEEE Transactions on Reliability*, 42(2), 299-302.

Examples

```
set.seed(123)
sim_data <- r_gw(100, delta = 0.5, zeta = 1.2, xi = 1.1)
```

r_ig	<i>Random Generation for Inverse Gaussian (IG) Frailty Distribution</i>
------	---

Description

Generates random variates from the Inverse Gaussian frailty distribution with mean $E[W] = 1$.

Usage

```
r_ig(n, eta)
```

Arguments

n	Number of observations to generate.
eta	Frailty variance parameter ($\eta > 0$).

Value

Numeric vector of length n.

References

Hougaard, P. (1984). Life table methods for heterogeneous populations: distributions of frailties. *Biometrika*, 71(1), 75-83.

Examples

```
set.seed(123)
w_ig <- r_ig(100, eta = 0.5)
```

simulate_mle_performance

Monte Carlo Simulation Framework for MultiFrailty Models

Description

Evaluates frequentist Maximum Likelihood Estimation performance (bias, relative bias, MSE, empirical coverage) across repeated Monte Carlo replications under user-specified baseline, frailty, and censoring schemes.

Usage

```
simulate_mle_performance(  
  n_sim = 50,  
  n = 100,  
  baseline = "weibull",  
  bpar = c(2, 1.5),  
  frailty = "gamma",  
  fpar = c(0.8),  
  beta = 0.5,  
  cen_type = "right",  
  cen_rate = 0.2  
)
```

Arguments

n_sim	Number of Monte Carlo simulation replicates. Default is 50.
n	Sample size per replicate. Default is 100.
baseline	Character string for baseline hazard ("weibull" or "gw").
bpar	True baseline parameter vector.
frailty	Character string for frailty family ("none", "gamma", "ig", "gl1", or "gl2").
fpar	True frailty parameter vector.
beta	True regression parameter. Default 0.5.
cen_type	Censoring mechanism. Default "right".
cen_rate	Censoring rate. Default 0.2.

Value

A data frame summarizing parameter true values, mean estimates, bias, relative bias, MSE, and coverage.

References

- Pandey, A., Hanagal, D. D., & Tyagi, S. (2022). Shared Frailty Models Based on Cancer Data. *International Journal of Statistics and Reliability Engineering*, 9(3), 461-474.
- Pandey, A., & Tyagi, S. (2021). Comparison of Multiplicative Frailty Models Under Weibull Baseline Distribution. *Lobachevskii Journal of Mathematics*, 42(13), 3184-3195.

Examples

```
set.seed(123)
sim_res <- simulate_mle_performance(n_sim = 10, n = 50, baseline = "weibull",
                                   bpar = c(2, 1.5), frailty = "gamma", fpar = c(0.8))
print(sim_res)
```

simulation_study

Run Comprehensive Simulation Study

Description

Run Comprehensive Simulation Study

Usage

```
simulation_study(
  sample_sizes = c(25, 50, 100),
  n_sim = 20,
  baseline = "weibull",
  frailty = "gl2"
)
```

Arguments

- sample_sizes Vector of sample sizes. Default c(25, 50, 100).
- n_sim Number of simulation replicates per setting. Default 20.
- baseline Baseline hazard. Default "weibull".
- frailty Frailty distribution. Default "gl2".

Value

Master data frame of Monte Carlo simulation metrics across sample sizes.

survival_at	<i>Survival Probability at Specific Time Points</i>
-------------	---

Description

Survival Probability at Specific Time Points

Usage

```
survival_at(fit, times, newdata = NULL)
```

Arguments

- fit Fitted multifrailty_fit object.
- times Vector of target time points.
- newdata Optional new data frame.

Value

Matrix of survival probabilities.

Index

AIC.multifrailty_fit
 (print.multifrailty_fit), 20

baseline_hazard, 3

BIC.multifrailty_fit
 (print.multifrailty_fit), 20

bootstrap_waic, 4

coef.multifrailty_fit
 (print.multifrailty_fit), 20

compare_models, 4

confint.multifrailty_fit
 (print.multifrailty_fit), 20

cv_frailty, 5

diagnostics_table, 6

fit_frailty, 6, 12

forecast_frailty, 8

frailty_functions, 8

frailty_laplace, 9

influence_frailty, 10

logLik.multifrailty_fit
 (print.multifrailty_fit), 20

loglik_frailty, 11

multifrailty, 12

plot_all, 13

plot_baseline, 14

plot_coef_forest, 14

plot_dfbetas, 15

plot_frailty_density, 15

plot_leverage, 16

plot_qq_residuals, 16

plot_residuals_fitted, 17

plot_residuals_leverage, 17

plot_scale_location, 18

plot_survival_km, 18

predict_frailty, 19

print.multifrailty_fit, 20

print.summary.multifrailty_fit
 (print.multifrailty_fit), 20

r_frailty, 23

r_g11, 24

r_g12, 25

r_gw, 26

r_ig, 26

residuals_frailty, 21

risk_predict, 22

simulate_mle_performance, 27

simulation_study, 28

summary.multifrailty_fit
 (print.multifrailty_fit), 20

survival_at, 29

vcov.multifrailty_fit
 (print.multifrailty_fit), 20