Package 'dMrs'

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Type Package

Title Competing Risk in Dependent Net Survival Analysis

Version 1.0.0

Date 2025-01-09

Description Provides statistical tools for
analyzing net and relative survival, with a key feature
of relaxing the assumption of independent censoring and
incorporating the effect of dependent competing risks.
It employs a copula-based methodology, specifically the
Archimedean copula, to simulate data, conduct survival
analysis, and offer comparisons with other methods.
This approach is detailed in the work of
Adatorwovor et al. (2022) <doi:10.1515/ijb-2021-0016>.

Encoding UTF-8

Imports methods, Rcpp, Rmpfr, copula, gplots, ggplot2, viridis, sqldf,
data.table, relsurv

LinkingTo Rcpp, RcppArmadillo

Suggests knitr, rmarkdown, markdown

VignetteBuilder knitr

License GPL (>= 3)

RoxygenNote 7.2.3

NeedsCompilation yes

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Repository CRAN

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Contents

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opt_sum	*opt_sum*

Description

Summarizes the solutions post-optimization

Usage

```
opt_sum(OPT)
```

Arguments

OPT   Output list from run_analyses()

Value

A dataframe containing a summary of each successfully optimized configuration of copula and density with corresponding constrained maximum likelihood estimates, and Bayesian Information Criteria.

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plot_SURVs	*plot_SURVs*

Description

Plot net survival probabilities per model

Usage

```
plot_SURVs(run_ANA, MULTIPLE, ncol = 1, ALPHA = 0.5)
```

Arguments

run_ANA   The object outputted from run_analyses function.

MULTIPLE   A boolean set to TRUE to display a survival plot per theta with accompanying maximum log likelihood. Otherwise, the survival plots will be overlayed with a legend.

ncol   Integer number of columns of plots to display

ALPHA   A numeric value between 0 and 1 to control the confidence band transparency.

Value

Returns a ggplot object of survival predictions and corresponding confidence intervals, Bayesian Information Criteria, maximum likelihood estimates. The user may apply their own customized graphic edits prior to visualizing the final graphic with the `print()` function.

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refData_match   *refData_match*

Description

This function takes as input a working dataset of interest and a reference dataset.

Usage

```
refData_match(wDAT, rDAT, ncores = 1)
```

Arguments

wDAT	A working dataset data.frame containing required columns `age`, `time`, `datediag_yr`, and `sex` corresponding to age, observed time (in years), diagnosis year, and sex (coded 'female'/'male'), respectively.
rDAT	A reference dataset data.frame containing required columns `year`, `age`, `qx`, and `sex` corresponding to reference year, reference age, event's interval hazard, and sex, respectively.
ncores	Integer number of parallel threads to decrease matching runtime.

Value

A dataframe containing calculated log-transformed density and log-transformed cumulative distribution

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run_analyses   *run_analyses*

Description

This function performs a full analysis of an inputted dataframe. The user may specify one of two copulas, a `theta` value, a parametric grid to search over, and a vector of times for predicting survival.

Usage

```
run_analyses(
  DATA,
  THETAs = NULL,
  upKAPPA,
  gTHRES = 0.1,
  COPULAS,
  param_grid,
  vec_time,
  ncores = 1,
  max_iter = 200,
  verb,
  PLOT
)
```

Arguments

DATA	A data.frame containing column names `time` (in years), `delta` (event indicator), `log_dens_t2` (log-transformed population-based density), and `log_cdf_t2` (log-transformed population-based cumulative density).
THETAs	A vector of theta values to explore and optimize over.
upKAPPA	An integer value taking values 0 or 1. If set to 1, the exponentiated Weibull distribution is assumed. Otherwise, the Weibull distribution is assumed and optimized over. If undefined, the optimization will search over both distributions.
gTHRES	A numeric threshold on the L2 norm of the gradient evaluated at the MLE.
COPULAS	If undefined, will optimize over all copulas. Otherwise set to 'Independent', 'Clayton' or 'Gumbel'
param_grid	Vector of values spanning possible log(alpha1), log(lambda1), log(kappa1), unconstrained theta parameters
vec_time	Vector of times in years to calculate predicted survival.
ncores	A positive integer for the number of threads to evaluate log-likelihoods across the parameter grid.
max_iter	Maximum Newton Raphson and Gradient Descent iterations to set.
verb	Boolean value to display verbose information or not
PLOT	A logical variable, set to `TRUE` by default to show the two-dimensional heatmap of the profile likelihood if `verb = TRUE`.

Value

Returns a parsable list of results per successfully optimized configuration of copula and density with accompanying net survival predictions, survival confidence intervals, maximum likelihood estimates, MLE confidence intervals (constrained and unconstrained), Bayesian Information Criteria for model selection, and extra statistical metrics to confirm convergence.

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