

Package ‘BGPhazard’

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Title Markov Beta and Gamma Processes for Modeling Hazard Rates

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Description Computes the hazard rate estimate as described by Nieto-Barajas & Walker (2002), Nieto-Barajas (2003), Nieto-Barajas & Walker (2007) and Nieto-Barajas & Yin (2008).

License GPL (>= 2)

URL <https://github.com/EAMI91/BGPhazard>

BugReports <https://github.com/EAMI91/BGPhazard/issues>

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BeMRes

Markov Beta Model

Description

Posterior inference for the Bayesian non-parametric Markov beta model for discrete survival times.

Usage

```
BeMRes(
  times,
  delta = rep(1, length(times)),
  alpha = rep(1e-04, K),
  beta = rep(1e-04, K),
  c.r = rep(0, K - 1),
  a.eps = 0.1,
  b.eps = 0.1,
  type.c = 4,
  epsilon = 1,
  iterations = 2000,
```

```

    burn.in = floor(iterations * 0.2),
    thinning = 5,
    printtime = TRUE
  )

```

Arguments

times	Numeric positive vector. Failure times.
delta	Logical vector. Status indicator. TRUE (1) indicates exact lifetime is known, FALSE (0) indicates that the corresponding failure time is right censored.
alpha	Nonnegative vector. Small entries are recommended in order to specify a non-informative prior distribution.
beta	Nonnegative vector. Small entries are recommended in order to specify a non-informative prior distribution.
c.r	Nonnegative vector. The higher the entries, the higher the correlation of two consecutive failure times.
a.eps	Numeric. Shape parameter for the prior gamma distribution of epsilon when type.c = 4.
b.eps	Numeric. Scale parameter for the prior gamma distribution of epsilon when type.c = 4.
type.c	Integer. 1=defines c.r as a zero-entry vector; 2=lets the user define c.r freely; 3=assigns c.r an exponential prior distribution with mean epsilon; 4=assigns c.r an exponential hierarchical distribution with mean epsilon which in turn has a Ga(a.eps, b.eps) distribution.
epsilon	Double. Mean of the exponential distribution assigned to c.r
iterations	Integer. Number of iterations including the burn.in and thinning to be computed for the Markov chain.
burn.in	Integer. Length of the burn-in period for the Markov chain.
thinning	Integer. Factor by which the chain will be thinned. Thinning the Markov chain is to reduce autocorrelation.
printtime	Logical. If TRUE, prints out the execution time.

Details

Computes the Gibbs sampler given by the full conditional distributions of u and Π (Nieto-Barajas & Walker, 2002) and arranges the resulting Markov chain into a tibble which can be used to obtain posterior summaries.

Note

It is recommended to verify chain's stationarity. This can be done by checking each partition element individually. See [BePlotDiag](#).

References

- Nieto-Barajas, L. E. & Walker, S. G. (2002). Markov beta and gamma processes for modelling hazard rates. *Scandinavian Journal of Statistics* **29**: 413-424.

See Also

[BePlotDiag](#), [BePloth](#)

Examples

```
## Simulations may be time intensive. Be patient.

## Example 1
# data(psych)
# timesP <- psych$time
# deltaP <- psych$death
# BEX1 <- BeMRes(timesP, deltaP, iterations = 3000, burn.in = 300, thinning = 1)

## Example 2
# data(gehan)
# timesG <- gehan$time[gehan$treat == "control"]
# deltaG <- gehan$cens[gehan$treat == "control"]
# BEX2 <- BeMRes(timesG, deltaG, type.c = 2, c.r = rep(50, 22))
```

BePlotDiag

Diagnosis plots for PI, U, C and Epsilon

Description

Diagnostic plots for hazard rate (PI), latent variable (U), dependence parameter (C) and parameter of the hierarchical model (Epsilon).

Usage

```
BePlotDiag(M, variable = "PI", pos = 1)
```

Arguments

M	Tibble. Contains the output by BeMRes
variable	Either "PI", "U", "C" or "Epsilon". Variable for which diagnostic plot will be shown.
pos	Positive integer. Position of the selected variable to be plotted.

Details

This function returns a diagnostics plot for the chain of the selected variable. The diagnostics includes trace, ergodic mean, autocorrelation function and histogram.

References

- Nieto-Barajas, L. E. & Walker, S. G. (2002). Markov beta and gamma processes for modelling hazard rates. *Scandinavian Journal of Statistics* **29**: 413-424.

See Also

[BeMRes](#)

Examples

```
## Simulations may be time intensive. Be patient.

## Example 1
# data(psych)
# timesP <- psych$time
# deltaP <- psych$death
# BEX1 <- BeMRes(timesP, deltaP, iterations = 3000, burn.in = 300, thinning = 1)
# BePlotDiag(BEX1, variable = "PI", pos = 2)
# BePlotDiag(BEX1, variable = "U", pos = 3)

## Example 2
# data(gehan)
# timesG <- gehan$time[gehan$treat == "control"]
# deltaG <- gehan$cens[gehan$treat == "control"]
# BEX2 <- BeMRes(timesG, deltaG, type.c = 2, c.r = rep(50, 22))
# BePlotDiag(BEX2, variable = "PI", pos = 5)
# BePlotDiag(BEX2, variable = "U", pos = 4)
```

BePloth

Plots for the discrete Hazard and Survival Function Estimates

Description

Plots the resulting hazard function along with the survival function estimates defined by the Markov beta process (Nieto-Barajas and Walker, 2002).

Usage

```
BePloth(  
  M,  
  type.h = "dot",  
  add.survival = T,  
  intervals = T,  
  confidence = 0.95,
```

```
summary = FALSE
)
```

Arguments

M	tibble. Contains the output generated by BeMRres.
type.h	character, "line" = plots the hazard rate of each interval joined by a line, "dot" = plots the hazard rate of each interval with a dot.
add.survival	logical, If TRUE, plots the Nelson-Aalen based estimate in the same graphic of the hazard rate and the Kaplan-Meier estimates of the survival function.
intervals	logical. If TRUE, plots confidence bands for the selected functions including Nelson-Aalen and/or Kaplan-Meier estimate.
confidence	Numeric. Confidence band width.
summary	Logical. If TRUE, a summary for hazard and survival functions is returned as a tibble.

Details

This function returns estimators plots for the hazard rate as computed by [BeMRes](#) together with the Nelson-Aalen estimate along with their confidence intervals for the data set given. Additionally, it plots the survival function and the Kaplan-Meier estimate with their corresponding credible intervals.

Value

SUM.h	Numeric tibble. Summary for the mean, median, and a $\text{confint} / 100$ confidence interval for each failure time of the hazard function.
SUM.S	Numeric tibble. Summary for the mean, median, and a $\text{confint} / 100$ confidence interval for each failure time of the survival function.

References

- Nieto-Barajas, L. E. & Walker, S. G. (2002). Markov beta and gamma processes for modelling hazard rates. *Scandinavian Journal of Statistics* **29**: 413-424.

See Also

[BeMRes](#), [BePlotDiag](#)

Examples

```
## Simulations may be time intensive. Be patient.

## Example 1
# data(psych)
# timesP <- psych$time
# deltaP <- psych$death
```

```
# BEX1 <- BeMRes(timesP, deltaP, iterations = 3000, burn.in = 300, thinning = 1)
# BePloth(BEX1)
# sum <- BePloth(BEX1, type.h = "line", summary = T)

## Example 2
# data(gehan)
# timesG <- gehan$time[gehan$treat == "control"]
# deltaG <- gehan$cens[gehan$treat == "control"]
# BEX2 <- BeMRes(timesG, deltaG, type.c = 2, c.r = rep(50, 22))
# BePloth(BEX2)
```

BGP Hazard

BGP Hazard: A package bayesian nonparametric inference in survival analysis.

Description

The BGP Hazard package provides three categories of important functions: simulating, diagnostic and result.

Simulating functions

The simulating functions are used to make posterior inference for the bayesian survival semiparametric models as described by Nieto-Barajas and Walker (2002), Nieto-Barajas (2003) and Nieto-Barajas, L. E., & Yin, G. (2008)

Diagnostic functions

The diagnostic functions are used to make convergence diagnostics plots about the simulations of the parameters/variables.

Result functions

The result functions are used to produce estimators plots of the hazard function along with the survival function defined by the model.

BMTKleinbook	<i>Times to death or relapse (in days) for patients with bone marrow transplants for Hodgkin and non-Hodgkin lymphoma</i>
--------------	---

Description

Was collected on 43 bone marrow transplant patients at The Ohio State University Bone Marrow Transplant Unit. Details of this study can be found in Avalos et al. (1993).

Usage

```
data(BMTKleinbook)
```

Format

A data frame with 43 observations containing:

times time to death or relapse in days

delta Status indicator: 1 = death or relapse; 0 = otherwise

tTransplant Allogeneic transplant from an HLA match sibling donor (1) or an autogeneic transplant (0)

hodgkin Hodgkin disease (1), or non-Hodgkin lymphoma (0)

karnofsky The pretransplant Karnofsky score

waiting Waiting time to transplant

Source

Klein, J. P., and Moeschberger, M. L. (2003). Survival analysis: techniques for censored and truncated data. Springer Science & Business Media.

References

Copelan, E. A., Biggs, J. C., Thompson, J. M., Crilley, P., Szer, J., Klein, J. P., Kapoor, N., Avalos, B. R., Cunningham, I., Atkinson, K., Downs, K., Harmon, G. S., Daly, M. B., Brodsky, I., Bulova, S. I., and Tutschka, P. J. Treatment for Acute Myelocytic Leukemia with Allogeneic Bone Marrow Transplantation Following Preparation with Bu/Cy. Blood 78 (1991): 838-843.

Examples

```
## Cox Cure Gama Process Example 1
# data(BMTKleinbook)
# res <- CCuMRes(BMTKleinbook, covs.x = c("tTransplant", "hodgkin", "karnofsky", "waiting"),
#               covs.y = c("tTransplant", "hodgkin", "karnofsky", "waiting"),
#               type.t = 2, K = 72, length = 30,
#               alpha = rep(2,72), beta = rep(2,72), c.r = rep(50, 71), type.c = 2,
#               var.delta.str = .1, var.theta.str = 1,
#               var.delta.ini = 100, var.theta.ini = 100,
#               iterations = 100, burn.in = 10, thinning = 1)
```

BSBHaz *BSBHaz posterior samples using Gibbs Sampler*

Description

BSBHaz samples posterior observations from the bivariate survival model (BSBHaz model) proposed by Nieto-Barajas & Walker (2007).

Usage

```
BSBHaz(
  bsb_init,
  iter,
  burn_in = 0,
  omega_d = NULL,
  gamma_d = NULL,
  theta_d = NULL,
  seed = 42
)
```

Arguments

<code>bsb_init</code>	An object of class 'BSBinit' created by BSBInit .
<code>iter</code>	A positive integer. Number of samples generated by the Gibbs Sampler.
<code>burn_in</code>	A positive integer. Number of iterations that should be discarded as burn in period.
<code>omega_d</code>	A positive double. This parameter defines the interval used in the Metropolis-Hastings algorithm to sample proposals for omega. See details.
<code>gamma_d</code>	A positive double. This parameter defines the interval used in the Metropolis-Hastings algorithm to sample proposals for gamma. See details.
<code>theta_d</code>	A positive double. This parameter defines the interval used in the Metropolis-Hastings algorithm to sample proposals for theta. See details.
<code>seed</code>	Random seed used in sampling.

Details

BSBHaz (Nieto-Barajas & Walker, 2007) is a bayesian semiparametric model for bivariate survival data. The marginal densities are nonparametric survival models and the joint density is constructed via a mixture. Dependence between failure times is modeled using two frailties, and the dependence between these frailties is modeled with a copula.

This command obtains posterior samples from model parameters. The samples from omega, gamma, and theta are obtained using the Metropolis-Hastings algorithm. The proposal distributions are uniform for the three parameters. The parameters `omega_d`, `gamma_d` and `theta_d` modify the intervals from which the uniform proposals are sampled. If these parameters are too large, the acceptance rates will decrease and the chains will get stuck. On the other hand, if these parameters are small, the acceptance rates will be too high and the chains will not explore the posterior support effectively.

Value

An object of class 'BSBHaz' containing the samples from the variables of interest.

Examples

```
t1 <- survival::Surv(c(1, 2, 3))
t2 <- survival::Surv(c(1, 2, 3))

init <- BSBInit(t1 = t1, t2 = t2, seed = 0)
samples <- BSBHaz(init, iter = 10, omega_d = 2,
  gamma_d = 10, seed = 10)
```

 BSBInit

Initial setup for BSBHaz model

Description

BSBInit creates the necessary data structure for use in [BSBHaz](#).

Usage

```
BSBInit(
  df = NULL,
  t1 = NULL,
  t2 = NULL,
  alpha = 0.001,
  beta = 0.001,
  c = 1000,
  part_len = 1,
  seed = 42
)
```

Arguments

df	A data frame with columns 't1', 't2', 'delta1', 'delta2'. Any other columns not named 'id' are taken to be predictors. These predictors must be numeric, i.e., categorical predictors must be one-hot encoded .
t1, t2	Objects of class 'Surv' as created by Surv .
alpha, beta, c	Doubles. Parameters for Markov gamma hazard priors.
part_len	A double that gives the length of time partition intervals.
seed	Random seed for variable initialization.

Details

This function reads and formats censored bivariate survival data in the following way. If `df` is provided, failure times and censoring indicators are assumed to be columns named 't1', 't2', 'delta1', and 'delta2'. Other columns not named 'id' (ignoring case) are taken to be predictors. If `df` has no columns 'delta1' or 'delta2', observations are taken as exact.

If `df` is not provided, then `t1` and `t2` are expected to be objects of class 'Surv' created by [Surv](#) and the model does not use predictors. Only right-censored observations are supported. Only `df` or `t1` and `t2` must be supplied. `df` argument comes first for use in pipes.

Value

An object of class 'BSBinit'

Examples

```
t1 <- survival::Surv(c(1, 2, 3))
t2 <- survival::Surv(c(1, 2, 3))

init <- BSBInit(t1 = t1, t2 = t2, seed = 0)
```

 BSBPlotDiag

Plot diagnostics for BSBHaz model

Description

Plot diagnostics for BSBHaz model

Usage

```
BSBPlotDiag(
  bsbhaz,
  variable = c("omega1", "omega2", "lambda1", "lambda2", "gamma", "theta"),
  type = c("traceplot", "ergodic_means")
)
```

Arguments

`bsbhaz` An object of class 'BSBHaz' created by [BSBHaz](#).

`variable` A character indicating which variable to get the plot from.

`type` A character indicating if the plot should be a traceplot or plot the ergodic means.

Examples

```
t1 <- survival::Surv(c(1, 2, 3))
t2 <- survival::Surv(c(1, 2, 3))

init <- BSBInit(t1 = t1, t2 = t2, seed = 0)
samples <- BSBHaz(init, iter = 10, omega_d = 2,
  gamma_d = 10, seed = 10)

BSBPlotDiag(samples, variable = "omega1", type = "traceplot")
```

BSBPlotSumm

Plot summaries for BSBHaz model

Description

Plot summaries for BSBHaz model

Usage

```
BSBPlotSumm(bsbhaz, variable = c("lambda1", "lambda2", "s1", "s2"))
```

Arguments

`bsbhaz` An object of class 'BSBHaz' created by [BSBHaz](#).

`variable` A character indicating the variable to plot.

Examples

```
t1 <- survival::Surv(c(1, 2, 3))
t2 <- survival::Surv(c(1, 2, 3))

init <- BSBInit(t1 = t1, t2 = t2, seed = 0)
samples <- BSBHaz(init, iter = 10, omega_d = 2,
  gamma_d = 10, seed = 10)

BSBPlotSumm(samples, "s1")
```

BSBSumm

*Get posterior summaries for BSBHaz model***Description**

Get posterior summaries for BSBHaz model

Usage

```
BSBSumm(
  bsbhaz,
  variable = c("omega1", "omega2", "lambda1", "lambda2", "gamma", "theta", "s1", "s2")
)
```

Arguments

`bsbhaz` An object of class 'BSBHaz' created by [BSBHaz](#).
`variable` A character indicating which variable to get summaries from.

Value

A data frame with posterior sample means and a 95 % probability interval. For `omega1`, `omega2`, `gamma`, and `theta` also includes a column with the acceptance rates for the Metropolis-Hastings algorithm.

Examples

```
t1 <- survival::Surv(c(1, 2, 3))
t2 <- survival::Surv(c(1, 2, 3))

init <- BSBIInit(t1 = t1, t2 = t2, seed = 0)
samples <- BSBHaz(init, iter = 10, omega_d = 2,
  gamma_d = 10, seed = 10)

BSBSumm(samples, variable = "gamma")
BSBSumm(samples, variable = "omega1")
BSBSumm(samples, variable = "lambda1")
```

CCuMRes

*Bayesian Semiparametric Cure Rate Model with an Unknown Threshold and Covariate Information***Description**

Posterior inference for the bayesian semiparmetric cure rate model with covariates in survival analysis.

Usage

```

CCuMRes(
  data,
  covs.x = names(data)[seq.int(3, ncol(data))],
  covs.y = names(data)[seq.int(3, ncol(data))],
  type.t = 3,
  K = 50,
  utao = NULL,
  alpha = rep(0.01, K),
  beta = rep(0.01, K),
  c.r = rep(0, K - 1),
  c.nu = 1,
  var.theta.str = 25,
  var.delta.str = 25,
  var.theta.ini = 100,
  var.delta.ini = 100,
  type.c = 4,
  a.eps = 0.1,
  b.eps = 0.1,
  epsilon = 1,
  iterations = 5000,
  burn.in = floor(iterations * 0.2),
  thinning = 3,
  printtime = TRUE
)

```

Arguments

<code>data</code>	Double tibble. Contains failure times in the first column, status indicator in the second, and, from the third to the last column, the covariate(s).
<code>covs.x</code>	Character. Names of covariables to be part of the multiplicative part of the hazard
<code>covs.y</code>	Character. Names of covariables to determine the cure threshold por each patient.
<code>type.t</code>	Integer. 1=computes uniformly-dense intervals; 2= partition arbitrarily defined by the user with parameter <code>utao</code> and 3=same length intervals.
<code>K</code>	Integer. Partition length for the hazard function.
<code>utao</code>	vector. Partition specified by the user when <code>type.t = 2</code> . The first value of the vector has to be 0 and the last one the maximum observed time, either censored or uncensored.
<code>alpha</code>	Nonnegative entry vector. Small entries are recommended in order to specify a non-informative prior distribution.
<code>beta</code>	Nonnegative entry vector. Small entries are recommended in order to specify a non-informative prior distribution.
<code>c.r</code>	Nonnegative vector. The higher the entries, the higher the correlation of two consecutive intervals.

<code>c.nu</code>	Tuning parameter for the proposal distribution for <code>c</code> . Only when <code>type.c</code> is 3 or 4.
<code>var.theta.str</code>	Double. Variance of the proposal normal distribution for <code>theta</code> in the Metropolis-Hastings step.
<code>var.delta.str</code>	Double. Variance of the proposal normal distribution for <code>delta</code> in the Metropolis-Hastings step.
<code>var.theta.ini</code>	Double. Variance of the prior normal distribution for <code>theta</code> .
<code>var.delta.ini</code>	Double. Variance of the prior normal distribution for <code>delta</code> . from the acceptance ratio in the Metropolis-Hastings algorithm for <code>delta</code> *.
<code>type.c</code>	1=defines <code>c.r</code> as a zero-entry vector; 2=lets the user define <code>c.r</code> freely; 3=assigns <code>c.r</code> an exponential prior distribution with mean 1; 4=assigns <code>c.r</code> an exponential hierarchical distribution with mean <code>epsilon</code> which in turn has a $Ga(a.eps, b.eps)$ distribution.
<code>a.eps</code>	Double. Shape parameter for the prior gamma distribution of <code>epsilon</code> when <code>type.c</code> = 4.
<code>b.eps</code>	Double. Scale parameter for the prior gamma distribution of <code>epsilon</code> when <code>type.c</code> = 4.
<code>epsilon</code>	Double. Mean of the exponential distribution assigned to <code>c.r</code> when <code>type.c</code> = 3.
<code>iterations</code>	Integer. Number of iterations including the <code>burn.in</code> to be computed for the Markov chain.
<code>burn.in</code>	Integer. Length of the burn-in period for the Markov chain.
<code>thinning</code>	Integer. Factor by which the chain will be thinned. Thinning the Markov chain reduces autocorrelation.
<code>printtime</code>	Logical. If TRUE, prints out the execution time.

Details

Computes the Gibbs sampler with the full conditional distributions of all model parameters (Nieto-Barajas & Yin, 2008) and arranges the resulting Markov chain into a tibble which can be used to obtain posterior summaries. Prior distributions for the regression coefficients `Theta` and `Delta` are assumed independent normals with zero mean and variance `var.theta.ini`, `var.delta.ini`, respectively.

Note

It is recommended to verify chain's stationarity. This can be done by checking each element individually. See [CCuPlotDiag](#).

References

- Nieto-Barajas, L. E., & Yin, G. (2008). Bayesian semiparametric cure rate model with an unknown threshold. *Scandinavian Journal of Statistics*, 35(3), 540-556. <https://doi.org/10.1111/j.1467-9469.2007.00589.x>
- Nieto-barajas, L. E. (2002). Discrete time Markov gamma processes and time dependent covariates in survival analysis. *Statistics*, 2-5.

See Also

[CCuPlotDiag](#), [CCuPlot](#)

Examples

```
# data(BMTKleinbook)
# res <- CCuMRes(BMTKleinbook, covs.x = c("tTransplant", "hodgkin", "karnofsky", "waiting"),
#             covs.y = c("tTransplant", "hodgkin", "karnofsky", "waiting"),
#             type.t = 2, K = 72, length = 30,
#             alpha = rep(2,72), beta = rep(2,72), c.r = rep(50, 71), type.c = 2,
#             var.delta.str = .1, var.theta.str = 1,
#             var.delta.ini = 100, var.theta.ini = 100,
#             iterations = 100, burn.in = 10, thinning = 1)
```

CCuPlotDiag

*Diagnostics plots for Lambda, Theta, Delta, U, C, Pi, Z and Epsilon.
Hazard function, cure proportion and cure time for the median obser-
vation.*

Description

Diagnostic plots for hazard rate (Lambda), regression parameters for the hazard (Theta), regression parameters for the cure rate (Delta), latent variable (U), dependence parameter (C), mean of cure threshold (Mu), cure proportion (Pi), cure threshold (Z) and the parameter of the hierarchical prior (Epsilon).

Usage

```
CCuPlotDiag(M, variable = "Lambda", pos = 1)
```

Arguments

M	tibble. Contains the output by CCuMRes.
variable	Either "Lambda", "U", "C", "Mu", "Pi", "Z" or "Epsilon". Variable for which diagnostic plot will be shown.
pos	Positive integer. Position of the selected variable to be plotted.

Details

This function returns a diagnostics plot for which the chain for the selected variable can be monitored. Diagnostics includes trace, ergodic mean, autocorrelation function and histogram.

References

Nieto-Barajas, L. E., & Yin, G. (2008). Bayesian semiparametric cure rate model with an unknown threshold. *Scandinavian Journal of Statistics*, **35**(3), 540-556. <https://doi.org/10.1111/j.1467-9469.2007.00589.x>

See Also

[CCuMRes](#)

Examples

```
## Simulations may be time intensive. Be patient.

## Example 1
# data(BMTKleinbook)
# res <- CCuMRes(BMTKleinbook, covs.x = c("tTransplant", "hodgkin", "karnofsky", "waiting"),
#               covs.y = c("tTransplant", "hodgkin", "karnofsky", "waiting"),
#               type.t = 2, K = 72, length = 30,
#               alpha = rep(2,72), beta = rep(2,72), c.r = rep(50, 71), type.c = 2,
#               var.delta.str = .1, var.theta.str = 1,
#               var.delta.ini = 100, var.theta.ini = 100,
#               iterations = 100, burn.in = 10, thinning = 1)
# CCuPlotDiag(M = res, variable = "Z")
# CCuPlotDiag(M = res, variable = "Pi.m")
# CCuPlotDiag(M = res, variable = "Lambda", pos = 2)
# CCuPlotDiag(M = res, variable = "U", pos = 4)
```

CCuPloth

Plots for the Hazard and Survival Function Estimates

Description

Plots the resulting hazard function and the survival function estimates defined by the bayesian semi-parametric cure rate model with an unknown threshold (Nieto-Barajas & Yin, 2008).

Usage

```
CCuPloth(
  M,
  new_obs = NULL,
  type.h = "segment",
  qn = 0.5,
  intervals = T,
  confidence = 0.95,
```

```
summary = FALSE
)
```

Arguments

M	tibble. Contains the output generated by CuMRres.
new_obs	tibble. Contains the covariate information for new observations.
type.h	character. "segment"= use segments to plot hazard rates, "line" = link hazard rates by a line
qn	Numeric. Quantile for Tao (cure time) that should be visualized on the plot.
intervals	logical. If TRUE, plots credible intervals.
confidence	Numeric. Confidence level.
summary	Logical. If TRUE, a summary for the hazard and survival functions is returned as a tibble.

Details

This function returns estimators plots for the hazard rate as it is computed by [CCuMRes](#) and the cure time (quantile of Tao specified by the user) together with credible intervals. Additionally, it plots the survival function and the cure proportion estimates with their corresponding credible intervals.

Value

SUM.h	Numeric tibble. Summary for the mean, median, and a $confint / 100$ confidence interval for each segment of the hazard function. If <code>summary = TRUE</code>
SUM.S	Numeric tibble. Summary for the mean, median, and a $confint / 100$ confidence interval for each segment of the survival function. If <code>summary = TRUE</code>

References

- Nieto-Barajas, L. E. (2003). Discrete time Markov gamma processes and time dependent covariates in survival analysis. *Bulletin of the International Statistical Institute 54th Session*. Berlin. (CD-ROM).
- Nieto-Barajas, L. E., & Yin, G. (2008). Bayesian semiparametric cure rate model with an unknown threshold. *Scandinavian Journal of Statistics*, **35(3)**, 540-556. <https://doi.org/10.1111/j.1467-9469.2007.00589.x>

See Also

[CCuMRes](#),

Examples

```
## Simulations may be time intensive. Be patient.

## Example 1
# data(BMTKleinbook)
```

```

# res <- CCuMRes(BMTKleinbook, covs.x = c("tTransplant","hodgkin","karnofsky","waiting"),
#             covs.y = c("tTransplant","hodgkin","karnofsky","waiting"),
#             type.t = 2, K = 72, length = 30,
#             alpha = rep(2,72), beta = rep(2,72), c.r = rep(50, 71), type.c = 2,
#             var.delta.str = .1, var.theta.str = 1,
#             var.delta.ini = 100, var.theta.ini = 100,
#             iterations = 100, burn.in = 10, thinning = 1)
#
# CCuPloth(res, type.h = "segment",qn=.5, summary = T)
#
# new_obs <- tibble(tTransplant=c(0,0,0,0),
#                 hodgkin=c(0,1,0,1),
#                 karnofsky=c(90,90,60,60),
#                 waiting=c(36,36,36,36)
# )
#
# ind <- CCuPloth(res, new_obs, qn = .5)
# ind

```

CGaMRes

Markov Gamma Model with Covariates

Description

Posterior inference for the Bayesian non-parametric Markov gamma model with covariates in survival analysis.

Usage

```

CGaMRes(
  data,
  type.t = 2,
  length = 1,
  K = 5,
  alpha = rep(0.01, K),
  beta = rep(0.01, K),
  c.r = rep(1, K - 1),
  c.nu = 1,
  var.theta.str = 25,
  var.theta.ini = 100,
  a.eps = 0.1,
  b.eps = 0.1,
  type.c = 4,
  epsilon = 1,
  iterations = 1000,
  burn.in = floor(iterations * 0.2),

```

```

    thinning = 3,
    printtime = TRUE
  )

```

Arguments

<code>data</code>	Double tibble. Contains failure times in the first column, status indicator in the second, and, from the third to the last column, the covariate(s).
<code>type.t</code>	Integer. 1=computes uniformly-dense intervals; 2=length intervals defined by user and 3=same length intervals.
<code>length</code>	Integer. Interval length of the partition.
<code>K</code>	Integer. Partition length for the hazard function.
<code>alpha</code>	Nonnegative entry vector. Small entries are recommended in order to specify a non-informative prior distribution.
<code>beta</code>	Nonnegative entry vector. Small entries are recommended in order to specify a non-informative prior distribution.
<code>c.r</code>	Nonnegative vector. The higher the entries, the higher the correlation of two consecutive intervals.
<code>c.nu</code>	Tuning parameter for the proposal distribution for <code>c</code> .
<code>var.theta.str</code>	Double. Variance of the proposal normal distribution for <code>theta</code> in the Metropolis-Hastings step.
<code>var.theta.ini</code>	Double. Variance of the prior normal distribution for <code>theta</code> .
<code>a.eps</code>	Double. Shape parameter for the prior gamma distribution of <code>epsilon</code> when <code>type.c = 4</code> .
<code>b.eps</code>	Double. Scale parameter for the prior gamma distribution of <code>epsilon</code> when <code>type.c = 4</code> .
<code>type.c</code>	1=defines <code>c.r</code> as a zero-entry vector; 2=lets the user define <code>c.r</code> freely; 3=assigns <code>c.r</code> by computing an exponential prior distribution with mean 1; 4=assigns <code>c.r</code> an exponential hierarchical distribution with mean <code>epsilon</code> which in turn has a <code>Ga(a.eps, b.eps)</code> distribution.
<code>epsilon</code>	Double. Mean of the exponential distribution assigned to <code>c.r</code> when <code>type.c = 3</code> .
<code>iterations</code>	Integer. Number of iterations including the <code>burn.in</code> to be computed for the Markov chain.
<code>burn.in</code>	Integer. Length of the burn-in period for the Markov chain.
<code>thinning</code>	Integer. Factor by which the chain will be thinned. Thinning the Markov chain reduces autocorrelation.
<code>printtime</code>	Logical. If TRUE, prints out the execution time.

Details

Computes the Gibbs sampler with the full conditional distributions of `Lambda` and `Theta` (Nieto-Barajas, 2003) and arranges the resulting Markov chain into a matrix which can be used to obtain posterior summaries. Prior distributions for the regression coefficients (`Theta`) are assumed independent normals with zero mean and variance `var.theta.ini`.

Note

It is recommended to verify chain's stationarity. This can be done by checking each element individually. See [CGaPlotDiag](#) To obtain posterior summaries of the coefficients use function [CGaPloth](#).

References

- Nieto-Barajas, L. E. (2003). Discrete time Markov gamma processes and time dependent co-variates in survival analysis. *Bulletin of the International Statistical Institute 54th Session*. Berlin. (CD-ROM).
- Nieto-Barajas, L. E. & Walker, S. G. (2002). Markov beta and gamma processes for modelling hazard rates. *Scandinavian Journal of Statistics* **29**: 413-424.

See Also

[CGaPlotDiag](#), [CGaPloth](#)

Examples

```
## Simulations may be time intensive. Be patient.

## Example 1
# data(leukemiaFZ)
# leukemia1 <- leukemiaFZ
# leukemia1$wbc <- log(leukemiaFZ$wbc)
# CGEX1 <- CGaMRes(data = leukemia1, K = 10, iterations = 100, thinning = 1)

## Example 2. Refer to "Cox-gamma model example" section in package vignette for details.
# SampWeibull <- function(n, a = 10, b = 1, beta = c(1, 1)) {
#   M <- tibble(i = seq(n), x_i1 = runif(n), x_i2 = runif(n),
#             t_i = rweibull(n, shape = b,
#                           scale = 1 / (a * exp(x_i1*beta[1] + x_i2*beta[2]))),
#             c_i = rexp(n), delta = t_i > c_i,
#             `min{c_i, d_i}` = min(t_i, c_i))
#   return(M)
# }
# dat <- SampWeibull(100, 0.1, 1, c(1, 1))
# dat <- dat %>% select(4,6,2,3)
# CG <- CGaMRes(data = leukemia1, K = 10, iterations = 100, thinning = 1)
# CGaPloth(CG)
```

CGaPlotDiag

*Diagnostics plots for lambda, U, C, Epsilon and Theta***Description**

Diagnostics plots for hazard rate (Lambda), latent variable (U), dependence variable (C), parameter of the hierarchical model (Epsilon) and regression coefficients (Theta).

Usage

```
CGaPlotDiag(M, variable = "Lambda", pos = 1)
```

Arguments

M	Tibble. Contains the output by CGaMRes
variable	Either "Lambda", "U", "C", "Epsilon" or "Theta". Variable for which diagnostics plot will be shown.
pos	Positive integer. Position of the selected variable to be plotted.

Details

This function returns a diagnostics plot for the chain of the selected variable. The diagnostics includes trace, ergodic mean, autocorrelation function and histogram.

References

- Nieto-Barajas, L. E. (2003). Discrete time Markov gamma processes and time dependent covariates in survival analysis. *Bulletin of the International Statistical Institute 54th Session*. Berlin. (CD-ROM).
- Nieto-Barajas, L. E. & Walker, S. G. (2002). Markov beta and gamma processes for modelling hazard rates. *Scandinavian Journal of Statistics* **29**: 413-424.

See Also

[CGaMRes](#)

Examples

```
## Simulations may be time intensive. Be patient.

## Example 1
# data(leukemiaFZ)
# leukemia1 <- leukemiaFZ
# leukemia1$wbc <- log(leukemiaFZ$wbc)
# CGEX1 <- CGaMRes(data = leukemia1, K = 10, iterations = 1000, thinning = 1)
# CGaPlotDiag(CGEX1,variable="Theta",pos=1)
```

CGaPloth	<i>Plots for the Hazard and Survival Function Estimates for the Bayesian non-parametric Markov gamma model with covariates in survival analysis.</i>
----------	--

Description

Plots the resulting hazard function along with the survival function estimate defined by the Markov gamma process with covariates (Nieto-Barajas, 2003).

Usage

```
CGaPloth(
  M,
  new_obs = NULL,
  type.h = "segment",
  coxSurv = T,
  intervals = T,
  confidence = 0.95,
  summary = FALSE
)
```

Arguments

M	tibble. Contains the output generated by CuMRres.
new_obs	tibble. The function calculates the hazard rates and survival function estimates for specific individuals expressed in a tibble, the names of the columns have to be the same as the data input.
type.h	character. "segment"= use segments to plot hazard rates, "line" = link hazard rates by a line
coxSurv	logical. Add estimated Survival function with the Cox-Model
intervals	logical. If TRUE, plots confidence bands for the selected functions including Cox-Model.
confidence	Numeric. Confidence level.
summary	logical. If TRUE, a summary for hazard and survival functions is returned as a tibble.

Details

This function return plots for the resulting hazard rate as it is computed by [CGaMRes](#) and the quantile of Tao specified by the user aswell as an annotation. In the same plot the credible intervals for both variables are plotted; The mean of Pi is also annotated. Additionally, it plots the survival function with their corresponding credible intervals.

Value

SUM.h	Numeric tibble. Summary for the mean, median, and a $\text{confint} / 100$ confidence interval for each segment of the hazard function. If <code>summary = TRUE</code>
SUM.S	Numeric tibble. Summary for the mean, median, and a $\text{confint} / 100$ confidence interval for each segment of the survival function. If <code>summary = TRUE</code>

References

- Nieto-Barajas, L. E. (2003). Discrete time Markov gamma processes and time dependent covariates in survival analysis. *Bulletin of the International Statistical Institute 54th Session*. Berlin. (CD-ROM).
- Nieto-Barajas, L. E. & Walker, S. G. (2002). Markov beta and gamma processes for modelling hazard rates. *Scandinavian Journal of Statistics* **29**: 413-424.

See Also

[CGaMRes](#),

Examples

```
## Simulations may be time intensive. Be patient.

# ## Example 1
# data(leukemiaFZ)
# leukemia1 <- leukemiaFZ
# leukemia1$wbc <- log(leukemiaFZ$wbc)
# CGEX1 <- CGaMRes(data = leukemia1, K = 10, iterations = 100, thinning = 1)
# CGaPloth(CGEX1)
```

cpo

Conditional Predictive Ordinate (CPO) Statistic

Description

Makes the CPO Plot and calculates the logarithm of the Pseudomarginal likelihood (LPML).

Usage

```
cpo(res)
```

Arguments

`res` tibble. The output from the `*Res` functions, where `*` could either be `BeM`, `GaM`, `CGaM`, `CuM`, `CCuM`

Details

Computes de CPO as a goodness of fit measure

Value

LPML	The value of the logarithm of the Pseudomarginal likelihood
plot	CPO Plot

References

See Geisser (1993); Gelfand, Dey, and Chang (1992); Dey, Chen, and Chang (1997); and Sinha and Dey (1997)

Examples

```
## Example 1
# data(gehan)
# timesG <- gehan$time[gehan$treat == "6-MP"]
# deltaG <- gehan$cens[gehan$treat == "6-MP"]
# GEX1 <- GaMRes(timesG, deltaG, K = 8, iterations = 3000)
# cpo(GEX1)
```

crm3	<i>Simulated data from the proportional hazards cure rate model of Yakolev & Tsodikov (1996) by taking a baseline density with a bounded support.</i>
------	---

Description

Triangular distribution $\text{Tri}(a, c, b)$ as the baseline density, which puts a probability of one to the interval $[a, b]$ and the mode at c .

Usage

```
data("crm3")
```

Format

A data frame with 100 observations with the following 2 variables.

times Simulated time

delta Simulated censoring

Details

In particular we took, $a = 0$, $c = 1$ and $b = 4$. The censoring time was independently generated from a uniform distribution to yield a 30% censoring rate. Sample size $n = 100$ and the cure proportion $\exp\{-\theta\} = 0.2$.

Source

Nieto-Barajas, L. E., & Yin, G. (2008)

Examples

```
## Cure Gama model Example 1
# data(crm3)
# times<-crm3$times
# delta<-crm3$delta
# res <- CuMRes(times, delta, type.t = 2,
#               K = 100, length = .1, alpha = rep(1, 100 ),
#               beta = rep(1, 100),c.r = rep(50, 99),
#               iterations = 100, burn.in = 10, thinning = 1, type.c = 2)
```

CuMRes

Bayesian Semiparametric Cure Rate Model with an Unknown Threshold

Description

Posterior inference for the bayesian semiparametric cure rate model in survival analysis.

Usage

```
CuMRes(
  times,
  delta = rep(1, length(times)),
  type.t = 3,
  K = 5,
  utao = NULL,
  alpha = rep(0.01, K),
  beta = rep(0.01, K),
  c.r = rep(1, (K - 1)),
  type.c = 4,
  epsilon = 1,
  c.nu = 1,
  a.eps = 0.1,
  b.eps = 0.1,
  a.mu = 0.01,
  b.mu = 0.01,
  iterations = 1000,
  burn.in = floor(iterations * 0.2),
```

```

    thinning = 5,
    printtime = TRUE
)

```

Arguments

<code>times</code>	Numeric positive vector. Failure times.
<code>delta</code>	Logical vector. Status indicator. TRUE (1) indicates exact lifetime is known, FALSE (0) indicates that the corresponding failure time is right censored.
<code>type.t</code>	Integer. 1=computes uniformly-dense intervals; 2= partition arbitrarily defined by the user with parameter <code>utao</code> and 3=same length intervals.
<code>K</code>	Integer. Partition length for the hazard function if <code>type.t=1</code> or <code>type.t=3</code> .
<code>utao</code>	vector. Partition specified by the user when <code>type.t = 2</code> . The first value of the vector has to be 0 and the last one the maximum observed time, either censored or uncensored.
<code>alpha</code>	Nonnegative entry vector. Small entries are recommended in order to specify a non-informative prior distribution.
<code>beta</code>	Nonnegative entry vector. Small entries are recommended in order to specify a non-informative prior distribution.
<code>c.r</code>	Nonnegative vector. The higher the entries, the higher the correlation of two consecutive intervals.
<code>type.c</code>	1=defines <code>c.r</code> as a zero-entry vector; 2=lets the user define <code>c.r</code> freely; 3=assigns <code>c.r</code> by computing an exponential prior distribution with mean <code>epsilon</code> ; 4=assigns <code>c.r</code> by computing an exponential hierarchical distribution with mean <code>epsilon</code> which in turn has a $Ga(a.eps, b.eps)$ distribution.
<code>epsilon</code>	Double. Mean of the exponential distribution assigned to <code>c.r</code> when <code>type.c = 3</code> . When <code>type.c = 4</code> , <code>epsilon</code> is assigned a $Ga(a.eps, b.eps)$ distribution.
<code>c.nu</code>	Tuning parameter for the proposal distribution for <code>c</code> .
<code>a.eps</code>	Numeric. Shape parameter for the prior gamma distribution of <code>epsilon</code> when <code>type.c = 4</code> .
<code>b.eps</code>	Numeric. Scale parameter for the prior gamma distribution of <code>epsilon</code> when <code>type.c = 4</code> .
<code>a.mu</code>	Numeric. Shape parameter for the prior gamma distribution of <code>mu</code>
<code>b.mu</code>	Numeric. Scale parameter for the prior gamma distribution of <code>mu</code>
<code>iterations</code>	Integer. Number of iterations including the <code>burn.in</code> to be computed for the Markov Chain.
<code>burn.in</code>	Integer. Length of the burn-in period for the Markov chain.
<code>thinning</code>	Integer. Factor by which the chain will be thinned. Thinning the Markov chain is to reduces autocorrelation.
<code>printtime</code>	Logical. If TRUE, prints out the execution time.

Details

Computes the Gibbs sampler with the full conditional distributions of all model parameters (Nieto-Barajas & Yin 2008) and arranges the resulting Markov chain into a tibble which can be used to obtain posterior summaries.

Note

It is recommended to verify chain's stationarity. This can be done by checking each element individually. See [CuPlotDiag](#).

Examples

```
## Simulations may be time intensive. Be patient.
## Example 1
# data(crm3)
# times<-crm3$times
# delta<-crm3$delta
# res <- CuMRes(times, delta, type.t = 2,
#               K = 100, length = .1, alpha = rep(1, 100 ),
#               beta = rep(1, 100),c.r = rep(50, 99),
#               iterations = 100, burn.in = 10, thinning = 1, type.c = 2)
```

CuPlotDiag

Diagnosis plots for Lambda, U, C, Mu, Pi, Z and Epsilon

Description

Diagnostics plots for hazard rate (Lambda), latent variable (U), dependence variable (C), mean of cure threshold (Mu), cure proportion (Pi), cure threshold (Z) and the parameter of the hierarchical prior (Epsilon).

Usage

```
CuPlotDiag(M, variable = "Lambda", pos = 1)
```

Arguments

M	List. Contains the output by CuMRes.
variable	Either "Lambda", "U", "C", "Mu", "Pi", "Z" or "Epsilon". Variable for which diagnostic plot will be shown.
pos	Positive integer. Position of the selected variable to be plotted.

Details

This function returns a diagnostics plot for which the chain for the selected variable can be monitored. Diagnostics includes trace, ergodic mean, autocorrelation function and histogram.

References

Nieto-Barajas, L. E., & Yin, G. (2008). Bayesian semiparametric cure rate model with an unknown threshold. *Scandinavian Journal of Statistics*, **35**(3), 540-556. <https://doi.org/10.1111/j.1467-9469.2007.00589.x>

See Also

[CuMRes](#)

Examples

```
## Simulations may be time intensive. Be patient.

## Example 1
# data(crm3)
# times<-crm3$times
# delta<-crm3$delta
# res <- CuMRes(times, delta, type.t = 2,
#               K = 100, length = .1, alpha = rep(1, 100 ),
#               beta = rep(1, 100),c.r = rep(50, 99),
#               iterations = 100, burn.in = 10, thinning = 1, type.c = 2)
# CuPlotDiag(M = res, variable = "Mu")
# CuPlotDiag(M = res, variable = "Z")
# CuPlotDiag(M = res, variable = "Pi")
# CuPlotDiag(M = res, variable = "Lambda", pos = 2)
# CuPlotDiag(M = res, variable = "U", pos = 4)
# CuPlotDiag(M = res, variable = "C", pos = 3)
```

CuPloth

Plots for the Hazard and Survival Function Estimates

Description

Plots the hazard function and the survival function estimates defined by the bayesian semiparametric cure rate model with an unknown threshold (Nieto-Barajas & Yin, 2008).

Usage

```
CuPloth(
  M,
  type.h = "segment",
  intervals = T,
  confidence = 0.95,
  qn = 0.5,
  summary = FALSE,
```

```
    position_label = "right"
  )
```

Arguments

M	tibble. Contains the output generated by CuMRes.
type.h	character. "segment"= use segments to plot hazard rates, "line" = link hazard rates by a line
intervals	logical. If TRUE, plots credible intervals.
confidence	Numeric. Confidence level.
qn	Numeric. Quantile for Tao that should be visualized on the plot.
summary	Logical. If TRUE, a summary for hazard and survival functions is returned as a tibble.
position_label	character. Labels on the right or left side of the plot.

Details

This function return estimators plots for the resulting hazard rate as it is computed by [CuMRes](#) and the cure time (quantile of Tao specified by the user), together with credible intervals. Additionally, it plots the survival function and the cure proportion estimates with their corresponding credible intervals.

Value

SUM.h	Numeric tibble. Summary for the mean, median, and a confint / 100 confidence interval for each segment of the hazard function. If summary = TRUE
SUM.S	Numeric tibble. Summary for the mean, median, and a confint / 100 confidence interval for a grid of the survival function. If summary = TRUE

References

- Nieto-Barajas, L. E. (2003). Discrete time Markov gamma processes and time dependent co-variates in survival analysis. *Bulletin of the International Statistical Institute 54th Session*. Berlin. (CD-ROM).
- Nieto-Barajas, L. E., & Yin, G. (2008). Bayesian semiparametric cure rate model with an unknown threshold. *Scandinavian Journal of Statistics*, **35(3)**, 540-556. <https://doi.org/10.1111/j.1467-9469.2007.00589.x>

See Also

[CuMRes](#),

Examples

```
## Simulations may be time intensive. Be patient.

## Example 1
```

```

# data(crm3)
# times<-crm3$times
# delta<-crm3$delta
# res <- CuMRes(times, delta, type.t = 2, length = .1,
#               K = 100, alpha = rep(1, 100 ),
#               beta = rep(1, 100),c.r = rep(50, 99),
#               iterations = 100, burn.in = 10, thinning = 1, type.c = 2)
# CuPloth(res, type.h = "segment",qn=.5, summary = T)
# CuPloth(res, type.h = "line",qn=.5)

```

GaMRes

Markov Gamma Model

Description

Computes the Gibbs sampler given by the full conditional distributions of U, Lambda, C and Epsilon (Nieto-Barajas & Walker, 2002) and arranges the resulting Markov chain into a tibble which can be used to obtain posterior summaries.

Usage

```

GaMRes(
  times,
  delta = rep(1, length(times)),
  type.t = 3,
  K = 5,
  utao = NULL,
  alpha = rep(0.01, K),
  beta = rep(0.01, K),
  c.r = rep(1, (K - 1)),
  c.nu = 1,
  a.eps = 0.1,
  b.eps = 0.1,
  type.c = 4,
  epsilon = 1,
  iterations = 1000,
  burn.in = floor(iterations * 0.2),
  thinning = 5,
  printtime = TRUE
)

```

Arguments

`times` Numeric positive vector. Failure times.

delta	Logical vector. Status indicator. TRUE (1) indicates exact lifetime is known, FALSE (0) indicates that the corresponding failure time is right censored.
type.t	Integer. 1=computes uniformly-dense intervals; 2= partition arbitrarily defined by the user with parameter utao and 3=same length intervals.
K	Integer. Partition length for the hazard function if type.t=1 or type.t=3.
utao	vector. Partition specified by the user when type.t = 2. The first value of the vector has to be 0 and the last one the maximum observed time, either censored or uncensored.
alpha	Nonnegative entry vector. Small entries are recommended in order to specify a non-informative prior distribution.
beta	Nonnegative entry vector. Small entries are recommended in order to specify a non-informative prior distribution.
c.r	Nonnegative vector. The higher the entries, the higher the correlation of two consecutive intervals.
c.nu	Tuning parameter for the proposal distribution for c.
a.eps	Numeric. Shape parameter for the prior gamma distribution of epsilon when type.c = 4.
b.eps	Numeric. Scale parameter for the prior gamma distribution of epsilon when type.c = 4.
type.c	1=assigns c.r a zero-entry vector; 2=lets the user define c.r freely; 3=assigns c.r an exponential prior distribution with mean 1; 4=assigns c.r an exponential hierarchical distribution with mean epsilon which in turn has a Ga(a.eps, b.eps) distribution.
epsilon	Double. Mean of the exponential distribution assigned to c.r when type.c = 3
iterations	Integer. Number of iterations including the burn.in to be computed for the Markov chain.
burn.in	Integer. Length of the burn-in period for the Markov chain.
thinning	Integer. Factor by which the chain will be thinned. Thinning the Markov chain is to reduce autocorrelation.
printtime	Logical. If TRUE, prints out the execution time.

Details

Posterior inference for the Bayesian non-parametric Markov gamma model in survival analysis.

Examples

```
## Simulations may be time intensive. Be patient.

## Example 1
data(gehan)
timesG <- gehan$time[gehan$treat == "6-MP"]
deltaG <- gehan$cens[gehan$treat == "6-MP"]
GEX1 <- GaMRes(timesG, deltaG, K = 8, iterations = 3000)
```

```
## Example 2
data(leukemiaFZ)
timesFZ <- leukemiaFZ$time
deltaFZ <- leukemiaFZ$delta
GEX2 <- GaMRes(timesFZ, deltaFZ, type.c = 4)
```

GaPlotDiag

Diagnosis plots for Lambda, U, C and Epsilon

Description

Diagnostics plots for hazard rate (Lambda), latent variable (U), dependence parameter (C) and the parameter of the hierarchical prior (Epsilon).

Usage

```
GaPlotDiag(M, variable = "Lambda", pos = 1)
```

Arguments

M	List. Contains the output by GaMRes.
variable	Either "Lambda", "U", "C" or "Epsilon". Variable for which informative plot will be shown.
pos	Positive integer. Position of the selected variable to be plotted.

Details

This function returns a diagnostics plot for which the chain of the selected variable can be monitored. Diagnostics includes trace, ergodic mean, autocorrelation function and histogram.

References

- Nieto-Barajas, L. E. & Walker, S. G. (2002). Markov beta and gamma processes for modelling hazard rates. *Scandinavian Journal of Statistics* **29**: 413-424.

See Also

[GaMRes](#)

Examples

```
## Simulations may be time intensive. Be patient.

## Example 1
# data(gehan)
# timesG <- gehan$time[gehan$treat == "6-MP"]
# deltaG <- gehan$cens[gehan$treat == "6-MP"]
# GEX1 <- GaMRes(timesG, deltaG, K = 8, iterations = 3000)
# GaPlotDiag(GEX1, variable = "Lambda", pos = 2)
# GaPlotDiag(GEX1, variable = "U", pos = 5)

## Example 2
# data(leukemiaFZ)
# timesFZ <- leukemiaFZ$time
# deltaFZ <- leukemiaFZ$delta
# GEX2 <- GaMRes(timesFZ, deltaFZ, type.c = 4)
# GaPlotDiag(GEX2, variable = "Lambda", pos = 2)
# GaPlotDiag(GEX2, variable = "U", pos = 3)
```

GaPloth

Plots for the Hazard and Survival Function Estimates

Description

Plots the hazard function and with the survival function estimates defined by the Markov gamma process with and without covariates (Nieto-Barajas & Walker, 2002).

Usage

```
GaPloth(
  M,
  type.h = "segment",
  addSurvival = T,
  intervals = T,
  confidence = 0.95,
  summary = FALSE
)
```

Arguments

M	tibble. Contains the output by CGaMRres and GaMRes.
type.h	character. "segment"= use segments to plot hazard rates, "line" = link hazard rates by a line

addSurvival	Logical. If TRUE, Nelson-Aalen estimate is plotted over the hazard function and Kaplan-Meier estimate is plotted over the survival function.
intervals	logical. If TRUE, plots confidence bands for the selected functions including Nelson-Aalen and/or Kaplan-Meier estimate.
confidence	Numeric. Confidence level.
summary	Logical. If TRUE, a summary for hazard and survival functions is returned as a tibble.

Details

This function returns estimators plots for the resulting hazard rate as it is computed by [GaMRes](#) and [CGaMRes](#) and the Nelson-Aalen estimate along with their confidence intervals for the data set given. Additionally, it plots the survival function and the Kaplan-Meier estimate with their corresponding credible/confidence intervals.

Value

SUM.h	Numeric tibble. Summary for the mean, median, and a confint / 100 confidence interval for each segment of the hazard function. If summary = TRUE
SUM.S	Numeric tibble. Summary for the mean, median, and a confint / 100 confidence interval for a grid of the survival function. If summary = TRUE

References

- Nieto-Barajas, L. E. (2003). Discrete time Markov gamma processes and time dependent covariates in survival analysis. *Bulletin of the International Statistical Institute 54th Session*. Berlin. (CD-ROM).
- Nieto-Barajas, L. E. & Walker, S. G. (2002). Markov beta and gamma processes for modelling hazard rates. *Scandinavian Journal of Statistics* **29**: 413-424.

See Also

[GaMRes](#), [CGaMRes](#), [CGaPlotDiag](#), [GaPlotDiag](#)

Examples

```
## Simulations may be time intensive. Be patient.

## Example 1
# data(gehan)
# timesG <- gehan$time[gehan$treat == "6-MP"]
# deltaG <- gehan$cens[gehan$treat == "6-MP"]
# GEX1 <- GaMRes(timesG, deltaG, K = 8, iterations = 3000)
# GaPloth(GEX1)

## Example 2
```

```
# data(leukemiaFZ)
# timesFZ <- leukemiaFZ$time
# deltaFZ <- leukemiaFZ$delta
# GEX2 <- GaMRes(timesFZ, deltaFZ, type.c = 4)
# GaPloth(GEX2)
```

gehan

Times of Remission of Leukemia Patients (Gehan)

Description

Freireich et al. (1963) report the results of a clinical trial of a drug 6-mercaptopurine (6-MP) versus a placebo (control) in 42 children with acute leukemia. The trial was conducted at 11 American hospitals. The trial was conducted by matching pairs of patients at a given hospital by remission status (complete or partial) and randomizing within the pair to either a 6-MP or placebo maintenance therapy. Patients were followed until their leukemia returned (relapse) or until the end of the study (in weeks). The data was taken from Klein & Moeschberger (2003) and is contained in the MASS package.

Usage

```
data(gehan)
```

Format

A data frame with 42 observations containing:

`pair` Pair index.

`time` Remission time (weeks).

`cens` Status: 0=censored.

`treat` Treatment: control or 6-MP.

Source

Klein, J. P., & Moeschberger, M. L. (2003). *Survival analysis: techniques for censored and truncated data*. Springer Science & Business Media.

References

Freireich, E. J., et al. (1963). The effect of 6-mercaptopurine on the duration of steroid-induced remissions in acute leukemia: A model for evaluation of other potentially useful therapy. *Blood*, **21**(6), 699-716.

Examples

```
## Gamma Process Example 1
# data(gehan)
# timesG <- gehan$time[gehan$treat == "6-MP"]
# deltaG <- gehan$cens[gehan$treat == "6-MP"]
# GEX1 <- GaMRes(timesG, deltaG, K = 8, iterations = 3000)
# GaPloth(GEX1)
```

KIDNEY

Recurrent infection of kidney catheters

Description

Data on the recurrent times to infection, at the point of insertion of the catheter, for kidney patients using portable dialysis equipment. Catheters may be removed for reasons other than infection, in which case the observation is censored. Each patient has exactly 2 observations. Only sex was kept as an explanatory variable.

Usage

KIDNEY

Format

A data frame with 38 rows and 6 variables:

id patient ID

t1,t2 times to infection

delta1,delta2 censorship indicators (1 = exact, 0 = right-censored)

sex 0 = female, 1 = male

Source

<https://www.mayo.edu/research/documents/kidneyhtml/doc-10027569>

`leukemiaFZ`*Survival Times of Patients with Leukemia (Feigl and Zelen)*

Description

Survival times of 33 patients with leukemia (Feigl and Zeelen, 1965). Times are measured in weeks from diagnosis. Reported covariates are white blood cell counts (WBC) and a binary variable AG that indicates a positive or negative test related to the white blood cell characteristics. Three of the observations were censored. The data was taken from Lawless (2003).

Usage

```
data(leukemiaFZ)
```

Format

A data frame with 33 observations on the following 4 variables.

`time` Weeks from diagnosis.

`delta` Status indicator: 0=censored.

`AG` Indicates a positive or negative test related to the white blood cell characteristics. (1=AG-positive, 2=AG-negative).

`wbc` White blood cell counts in thousands (reported covariates).

Source

Lawless, J.F. (2003). *Statistical Models and Methods for Lifetime Data*. Wiley: New Jersey.

References

Feigl, P. and Zelen, M. (1965). Estimation of Exponential Survival Probabilities with Concomitant Information. *Biometrics* **21**, 826-838.

Examples

```
## Cox-Gamma Process Example 1
# data(leukemiaFZ)
# leukemia1 <- leukemiaFZ
# leukemia1$wbc <- log(leukemiaFZ$wbc)
# CGEX1 <- CGaMRes(data = leukemia1, K = 10, iterations = 100, thinning = 1)
```

psych

Death Times of Psychiatric Patients (Woolson)

Description

Woolson (1981) has reported survival data on 26 psychiatric inpatients admitted to the University of Iowa hospitals during the years 1935-1948. This sample is part of a larger study of psychiatric inpatients discussed by Tsuang and Woolson (1977) and it is contained in the KMsurv package.

Usage

```
data(psych)
```

Format

A data frame with 26 observations containing:

sex Patient sex: 1=male, 2=female.

age Age at first admission to the hospital.

time Number of years of follow-up.

death Patient status at the follow-up time: 0=alive, 1=dead.

Source

Klein, J. P., and Moeschberger, M. L. (2003). *Survival analysis: techniques for censored and truncated data*. Springer Science & Business Media.

References

Tsuang, M. T. and Woolson, R. F. (1977). Mortality in Patients with Schizophrenia, Mania and Depression. *British Journal of Psychiatry*, **130**: 162-166.

Woolson, R. F. (1981). Rank Tests and a One-Sample Log Rank Test for Comparing Observed Survival Data to a Standard Population. *Biometrics* **37**: 687-696.

Examples

```
## Beta Process Example 1
## Example 1
# data(psych)
# timesP <- psych$time
# deltaP <- psych$death
# BEX1 <- BeMRes(timesP, deltaP, iterations = 3000, burn.in = 300, thinning = 1)
```

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