

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 and Walker (2002) and Nieto-Barajas (2003).

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BGPhazard-package

Markov Beta and Gamma Processes for Modeling Hazard Rates

Description

Computes the hazard rate estimate as described by Nieto-Barajas and Walker (2002) and Nieto-Barajas (2003).

Details

Package: BGPhazard
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Author(s)

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References

- Feigl, P. and Zelen, M. (1965). Estimation of Exponential Survival Probabilities with Concomitant Information. *Biometrics* **21**: 826-838.
- 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.
- Klein, J. P., & Moeschberger, M. L. (2003). Survival analysis: techniques for censored and truncated data. Springer Science & Business Media.
- Lawless, J.F. (2003). Statistical Models and Methods for Lifetime Data. Wiley: New Jersey.
- Nieto-Barajas, L. E. (2003). Discrete time Markov gamma processes and time dependent co-variables 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.
- 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

```
## The list of active function is {BeMRes, BePlotDiag, BePloth, GaMRes, GaPlotDiag,
## GaPloth, CGaMRes, CGaPlotDiag, CGaPloth, CGaPred, PlotTheta}. The list of data sets
## is {gehan, psych and leukemiaFZ}.

## Simulations may be time intensive. Be patient.

## Example 1
# data(leukemiaFZ)
# timesFZ <- leukemiaFZ$time
# deltaFZ <- leukemiaFZ$delta
# GEX2 <- GaMRes(timesFZ, deltaFZ, type.c = 4)
# GaPloth(GEX2, fun = "both", confint = TRUE)

## 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, confint = TRUE, confidence = 0.95)

## Example 3
# data(leukemiaFZ)
# leukemia1 <- leukemiaFZ
# leukemia1$wbc <- log(leukemiaFZ$wbc)
# CGEX1 <- CGaMRes(data = leukemia1, K = 10, iterations = 10000, thpar = 10)
# CGaPloth(CGEX1, fun = "both", confint = TRUE)
# PlotTheta(CGEX1)

## Example 4. Refer to "Cox-gamma model example" section in package vignette for details.
# SampWeibull <- function(n, a = 10, b = 1, beta = c(1, 1)) {
#   M <- matrix(0, ncol = 7, nrow = n)
#   for(i in 1:n){
#     M[i, 1] <- i
#     M[i, 2] <- x1 <- runif(1)
#     M[i, 3] <- x2 <- runif(1)
#     M[i, 4] <- rweibull(1, shape = b,
#                       scale = 1 / (a * exp(cbind(x1, x2) %*% beta)))
#     M[i, 5] <- rexp(1)
#     M[i, 6] <- M[i, 4] > M[i, 5]
#     M[i, 7] <- min(M[i, 4], M[i, 5])
#   }
#   colnames(M) <- c("i", "x_i1", "x_i2", "t_i", "c_i", "delta", "min{c_i, d_i}")
#   return(M)
# }
# dat <- SampWeibull(100, 0.1, 1, c(1, 1))
# dat <- cbind(dat[, c(4, 6)], dat[, c(2, 3)])
# CG <- CGaMRes(dat, K = 10, iterations = 3000, thpar = 10)
# CGaPloth(CG)
# PlotTheta(CG)
# CGaPred(CG)
```

BeMRes

*Markov Beta Model***Description**

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

Usage

```
BeMRes(times, delta = rep(1, length(times)), alpha = rep(1e-04, K),
beta = rep(1e-04, K), c.r = rep(0, K), type.c = 4, epsilon = 1,
iterations = 1000, burn.in = floor(iterations * 0.2), thinning = TRUE,
thpar = 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 intervals.
type.c	Integer. 1=defines c.r as a zero-entry vector; 2=lets the user define c.r feely; 3=defines c.r by computing an exponential distribution with mean 1; 4=defines c.r by computing an exponential distribution with mean epsilon which has assigned a Ga(0.01, 0.01) distribution.
epsilon	Double. Mean of the exponential distribution assigned to c.r when type.c = 3. When type.c = 4, epsilon is assigned a Ga(0.01,0.01) distribution.
iterations	Integer. Number of iterations including the burn.in to be computed by the model.
burn.in	Integer. Length of the burn-in period for the Markov chain.
thinning	Logical. TRUE thins the Markov chain to reduce autocorrelation.
thpar	Integer. Factor by which the chain will be thinned if thinning=TRUE.
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 matrix which can be used to obtain posterior summaries.

Value

times	Numeric vector. Failure times.
delta	Numeric vector. Status indicator.
tao	Numeric vector. Partition for hazard function's support.
K	Integer. Partition length.
t.unc	Numeric vector. Uncensored failure times sorted ascendingly.
iterations	Integer.
summary	Numeric matrix. Contains the resulting Markov chain for Pi, u, c.r and epsilon (if applicable).
S	Numeric matrix. Survival estimates for each state of the chain.

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)

## 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

Informative plots for hazard rate (Pi), latent variable (u), dependence variable (c) and parameter of the hierarchical model (epsilon).

Usage

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

Arguments

M	List. Contains the information given for Pi and u by BeMRes
variable	Either "Pi", "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 diagnosis plot for the chain of the selected variable. The diagnosis 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)
# 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)
```

Description

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

Usage

```
BePloth(M, fun = "both", confint = TRUE, h.NA = TRUE, KM = TRUE,
confidence = 0.95, summary = FALSE, legend = TRUE)
```

Arguments

M	List. Contains the information given for Pi and u (generated by BeMRes).
fun	"h"=plots hazard function, "S"= plots survival function and "both"=plots both the hazard and survival functions.
confint	Logical. If TRUE, plots confidence bands for the selected functions including Nelson-Aalen and/or Kaplan-Meier estimate.
h.NA	Logical. If TRUE, Nelson-Aalen estimate is plotted over the hazard function.
KM	Logical. If TRUE, Kaplan-Meier estimate is plotted over the survival function.
confidence	Numeric. Confidence band width.
summary	Logical. If TRUE, a summary for hazard and survival functions is returned as a list.
legend	Logical. If FALSE, legend is not shown.

Details

This function returns plots for the resulting hazard rate as it is computed by [BeMRes](#) 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 confidence intervals.

Value

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

Warning

The argument `fun` is case-sensitive and requires quotations as its class is character.

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)
# BePloth(BEX1, confint = FALSE)
# BePloth(BEX1, fun = "both", confint = TRUE)

## Example 2
# data(gehan)
# timesG <- gehan$time[gehan$treat == "control"]
# deltaG <- gehan$scens[gehan$treat == "control"]
# BEX2 <- BeMRes(timesG, deltaG, type.c = 2, c.r = rep(50, 22))
# BePloth(BEX2, confint = TRUE, confidence = 0.95)
```

 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 = 1, K = 5, alpha = rep(0.001, K.aux),
beta = rep(1e-04, K.aux), c.r = rep(0, K.aux - 1), type.c = 4,
epsilon = 1, iterations = 1000, burn.in = floor(iterations * 0.2),
thinning = TRUE, thpar = 3, printtime = TRUE)
```


Arguments

data	Numeric matrix. Contains failure times in the first column, status indicator in the second, and, from the third to the last column, the varying covariate(s).
type.t	Integer. 1=computes uniformly-dense intervals; 2=unitary length intervals and 3=same length intervals.
K	Integer. Partition length for the hazard function if type.t=1 or type.t=3.
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	Correlation vector. Its entries must be nonnegative integers.
type.c	1=defines c.r as a zero-entry vector; 2=lets the user define c.r freely; 3=defines c.r by computing an exponential distribution with mean 1; 4=defines c.r by computing an exponential distribution with mean epsilon which has assigned a Ga(0.01, 0.01) distribution.
epsilon	Double. Mean of the exponential distribution assigned to c.r when type.c = 3. When type.c = 4, epsilon is assigned a Ga(0.01,0.01) distribution.
iterations	Integer. Number of iterations including the burn.in to be computed by the model.
burn.in	Integer. Length of the burn-in period for the Markov chain.
thinning	Logical. TRUE thins the Markov chain to reduce autocorrelation.
thpar	Integer. Factor by which the chain will be thinned if thinning=TRUE.
printtime	Logical. If TRUE, prints out the execution time.

Details

Computes the Gibbs sampler given by the full conditional distributions of h , λ and θ (Nieto-Barajas, 2003) and arranges the resulting Markov chain into a matrix which can be used to obtain posterior summaries. Prior distributions for the coefficients (θ) are assumed independent normals with zero mean and standard deviation 10.

Value

times	Numeric vector. Failure times.
delta	Numeric vector. Status indicator.
covar	Numeric matrix. Matrix of covariates.
type.t	Integer.
tao	Numeric vector. Partition for hazard function's support.
K	Integer. Partition length.
t.unc	Numeric vector. Uncensored failure times sorted ascendingly.
iterations	Integer.
summary	Numeric matrix. Contains the resulting Markov chain for λ , u , $c.r$, ϵ (if applicable) and the coefficients.

S	Numeric matrix. Survival estimates for each state of the chain.
H	Numeric matrix. Cumulative hazard rate estimates for each state of the chain.
p	Integer. Number of covariates for the data set given.

Note

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

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

[PlotTheta](#), [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 = 10000, thpar = 10)

## 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 <- matrix(0, ncol = 7, nrow = n)
#   for(i in 1:n){
#     M[i, 1] <- i
#     M[i, 2] <- x1 <- runif(1)
#     M[i, 3] <- x2 <- runif(1)
#     M[i, 4] <- rweibull(1, shape = b,
#                       scale = 1 / (a * exp(cbind(x1, x2) %*% beta)))
#     M[i, 5] <- rexp(1)
#     M[i, 6] <- M[i, 4] > M[i, 5]
#     M[i, 7] <- min(M[i, 4], M[i, 5])
#   }
#   colnames(M) <- c("i", "x_i1", "x_i2", "t_i", "c_i", "delta", "min{c_i, d_i}")
#   return(M)
# }
# dat <- SampWeibull(100, 0.1, 1, c(1, 1))
# dat <- cbind(dat[, c(4, 6)], dat[, c(2, 3)])
# CG <- CGaMRes(dat, K = 10, iterations = 3000, thpar = 10)
```

CGaPlotDiag

*Diagnosis plots for lambda, u, c, epsilon and theta***Description**

Informative plots for hazard rate (π), latent variable (u), dependence variable (c), parameter of the hierarchical model (ϵ) and regression coefficients (θ).

Usage

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

Arguments

M	List. Contains the information given for lambda and u by CGaMRes
variable	Either "lambda", "u", "c", "epsilon" or "theta". Variable for which informative plot will be shown.
pos	Positive integer. Position of the selected variable to be plotted.

Details

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

References

- Nieto-Barajas, L. E. (2003). Discrete time Markov gamma processes and time dependent co-variables 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 = 10000, thpar = 10)
# CGaPlotDiag(CGEX1, variable = "lambda", pos = 2)
# CGaPlotDiag(CGEX1, variable = "u", pos = 3)
```

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, fun = "both", confint = TRUE, h.NA = FALSE, KM = FALSE,
confidence = 0.95, summary = FALSE, legend = TRUE)
```

Arguments

M	List. Contains the information given for lambda and u (generated by CGaMRes).
fun	"h"=plots hazard function; "S"= plots survival function and "both"=plots both the hazard and survival functions.
confint	Logical. If TRUE, plots confidence bands for the selected functions including Nelson-Aalen and/or Kaplan-Meier estimate.
h.NA	Logical. If TRUE, Nelson-Aalen estimate is plotted over the hazard function.
KM	Logical. If TRUE, Kaplan-Meier estimate is plotted over the survival function.
confidence	Numeric. Confidence band width.
summary	Logical. If TRUE, a summary for hazard and survival functions is returned as a list.
legend	Logical. If FALSE, legend is not shown.

Details

This function return plots for the resulting hazard rate as it is computed by [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 confidence intervals.

Value

SUM.h	Numeric matrix. Summary for the mean, median, and a <code>confint / 100</code> confidence interval for each segment of the hazard function.
SUM.S	Numeric matrix. Summary for the mean, median, and a <code>confint / 100</code> confidence interval for each segment of the survival function.

Warning

The argument `fun` is case-sensitive and requires quotations as its class is character.

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

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

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 = 10000, thpar = 10)
# CGaPloth(CGEX1, fun = "both", confint = TRUE)

## 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 <- matrix(0, ncol = 7, nrow = n)
#   for(i in 1:n){
#     M[i, 1] <- i
#     M[i, 2] <- x1 <- runif(1)
#     M[i, 3] <- x2 <- runif(1)
#     M[i, 4] <- rweibull(1, shape = b,
#                       scale = 1 / (a * exp(cbind(x1, x2) %*% beta)))
#     M[i, 5] <- rexp(1)
#     M[i, 6] <- M[i, 4] > M[i, 5]
#     M[i, 7] <- min(M[i, 4], M[i, 5])
#   }
#   colnames(M) <- c("i", "x_i1", "x_i2", "t_i", "c_i", "delta", "min{c_i, d_i}")
#   return(M)
# }
# dat <- SampWeibull(100, 0.1, 1, c(1, 1))
# dat <- cbind(dat[, c(4, 6)], dat[, c(2, 3)])
# CG <- CGaMRes(dat, K = 10, iterations = 3000, thpar = 10)
# CGaPloth(CG)
```

CGaPred

Predictive hazard function

Description

Estimates the hazard function for a given vector of covariates.

Usage

```
CGaPred(M, xf = "median", confidence = 0.95)
```

Arguments

M	List. Contains the information given for lambda and u by CGaMRes.
xf	Vector. Varying covariates that are used to generate the predictive hazard function estimate.
confidence	Numeric. Confidence band width.

Details

If no vector of varying covariates is specified, a vector of medians of each covariate will be taken.

Value

theta.summary	Numeric matrix. Summary for the regression coefficients.
h.xf	Numeric vector. Estimate for the hazard function given covariates vector xf.
S.xf	Numeric vector. Estimate for the survival function given covariates vector xf.

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](#), [CLambdaSumm](#)

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 = 10000, thpar = 10)
# CGaPred(CGEX1)
```

Description

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

Usage

```
GaMRes(times, delta = rep(1, length(times)), type.t = 1, K = 5,
alpha = rep(0.0001, K.aux), beta = rep(1e-04, K.aux),
c.r = rep(0, (K.aux - 1)), type.c = 4, epsilon = 1, iterations = 1000,
burn.in = floor(iterations * 0.2), thinning = TRUE, thpar = 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=uniformly-dense intervals; 2=unitary length intervals and 3=computes same length intervals.
K	Integer. Partition length for the hazard function if type.t=1 or type.t=3.
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	Correlation vector. Its entries must be nonnegative integers.
type.c	1=defines c.r as a zero-entry vector; 2=lets the user define c.r feely; 3=defines c.r by computing an exponential distribution with mean 1; 4=defines c.r by computing an exponential distribution with mean epsilon which has assigned a Ga(0.01, 0.01) distribution.
epsilon	Double. Mean of the exponential distribution assigned to c.r when type.c = 3. When type.c = 4, epsilon is assigned a Ga(0.01,0.01) distribution.
iterations	Integer. Number of iterations including the burn.in to be computed by the model.
burn.in	Integer. Length of the burn-in period for the Markov chain.
thinning	Logical. TRUE thins the Markov chain to reduce autocorrelation.
thpar	Integer. Factor by which the chain will be thinned if thinning=TRUE.
printtime	Logical. If TRUE, prints out the execution time.

Details

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

Value

times	Numeric vector. Failure times.
delta	Numeric vector. Status indicator.
type.t	Integer.
tao	Numeric vector. Partition for hazard function's support.
K	Integer. Partition length.
t.unc	Numeric vector. Uncensored failure times sorted ascendingly.
iterations	Integer.
summary	Numeric matrix. Contains the resulting Markov chain for lambda, u, c.r and epsilon (if applicable).
S	Numeric matrix. Survival estimates for each state of the chain.

Note

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

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

[GaPlotDiag](#), [GaPloth](#)

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)
```


Description

Informative plots for hazard rate (λ), latent variable (u), dependence variable (c) and the parameter of the hierarchical model ϵ .

Usage

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

Arguments

M	List. Contains the information given for λ and u 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 diagnosis plot for which the chain for the selected variable can be monitored. Diagnosis 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 resulting hazard function along with the survival function estimate defined by the Markov gamma process (Nieto-Barajas and Walker, 2002).

Usage

```
GaPloth(M, fun = "both", confint = TRUE, h.NA = TRUE, KM = TRUE,
confidence = 0.95, summary = FALSE, legend = TRUE)
```

Arguments

M	List. Contains the information given for lambda and u (generated by GaMRes).
fun	"h"=plots hazard function; "S"= plots survival function and "both"=plots both the hazard and survival functions.
confint	Logical. If TRUE, plots confidence bands for the selected functions including Nelson-Aalen and/or Kaplan-Meier estimate.
h.NA	Logical. If TRUE, Nelson-Aalen estimate is plotted over the hazard function.
KM	Logical. If TRUE, Kaplan-Meier estimate is plotted over the survival function.
confidence	Numeric. Confidence band width.
summary	Logical. If TRUE, a summary for hazard and survival functions is returned as a list.
legend	Logical. If FALSE, legend is not shown.

Details

This function return plots for the resulting hazard rate as it is computed by [GaMRes](#) 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 confidence intervals.

Value

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

Warning

The argument `fun` is case-sensitive and requires quotations as its class is character.

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](#), [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, confint = FALSE)
# GaPloth(GEX1, fun = "both", confint = TRUE)

## Example 2
# data(leukemiaFZ)
# timesFZ <- leukemiaFZ$time
# deltaFZ <- leukemiaFZ$delta
# GEX2 <- GaMRes(timesFZ, deltaFZ, type.c = 4)
# GaPloth(GEX2, fun = "both", confint = TRUE)
```

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, confint = FALSE)
# GaPloth(GEX1, fun = "both", confint = TRUE)
```

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 = 10000, thpar = 10)
# CGaPloth(CGEX1, fun = "both", confint = TRUE)
```

PlotTheta

Plots and summarises the covariate coefficients

Description

Plots density and histogram for one or all covariate coefficients and computes summaries.

Usage

```
PlotTheta(M, i = 1, plot.all = TRUE, quantiles = TRUE)
```

Arguments

M	List. Output object generated by command CGaMRes.
i	Integer. If plot.all == FALSE, only the <i>ith</i> position is plot.
plot.all	Logical. If TRUE plots all p covariate coefficients.
quantiles	Logical. If TRUE returns a matrix containing mean, standar deviation and quantiles for theta.

Value

quant Data frame. Mean, standard deviation, 0.025, 0.05, 0.5, 0.95 and 0.975 quantiles for theta.

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

[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 = 10000, thpar = 10)
# PlotTheta(CGEX1)
```

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
# data(psych)
# timesP <- psych$time
# deltaP <- psych$death
# BEX1 <- BeMRes(timesP, deltaP, iterations = 3000)
# BePloth(BEX1, confint = FALSE)
# BePloth(BEX1, fun = "both", confint = TRUE)
```

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