Package: BASSLINE (via r-universe)

November 12, 2024

Type Package

Title Bayesian Survival Analysis Using Shape Mixtures of Log-Normal Distributions

Version 0.0.0.9010

Description Mixtures of life distributions provide a convenient framework for survival analysis: particularly when standard models such as the Weibull are unable to capture some features from the data. These mixtures can also account for unobserved heterogeneity or outlying observations. BASSLINE uses shape mixtures of log-normal distributions and has particular applicability to data with fat tails.

License GPL-3

Depends R (>= 3.5.0)

Imports MASS, truncnorm, VGAM, MCMCpack, mvtnorm, Rcpp, ggplot2

Suggests testthat, knitr, msm, rmarkdown, coda, spelling

LazyData true

URL https://www.constantine-cooke.com/BASSLINE/
https://github.com/nathansam/BASSLINE

BugReports https://github.com/nathansam/BASSLINE/issues

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

Encoding UTF-8

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NeedsCompilation yes

Language en-US

Repository https://nathansam.r-universe.dev

RemoteUrl https://github.com/nathansam/BASSLINE

RemoteRef HEAD

RemoteSha d0cc4e82cc4cd04a049efc3eaf03d9820bf95962

Contents

`BASSLINE_convert` *Convert dataframe with mixed variables to a numeric matrix*

Description

BASSLINE's functions require a numeric matrix be provided. This function converts a dataframe of mixed variable types (numeric and factors) to a matrix. A factor with m levels is converted to m columns with binary values used to denote which level the observation belongs to.

Usage

```
BASSLINE_convert(df)
```

Arguments

df	A dataframe intended for conversion

Value

A numeric matrix suitable for BASSLINE functions

Examples

```
library(BASSLINE)
Time <- c(5,15,15)
Cens <- c(1,0,1)
experiment <- as.factor(c("chem1", "chem2", "chem3"))
age <- c(15,35,20)
df <- data.frame(Time, Cens, experiment, age)
converted <- BASSLINE_convert(df)
```

BF_lambda_obs_LLAP *Outlier detection for observation for the log-Laplace model*

Description

This returns a unique number corresponding to the Bayes Factor associated to the test $M_0 : \Lambda_{obs} = \lambda_{ref}$ versus $M_1 : \Lambda_{obs} \neq \lambda_{ref}$ (with all other $\Lambda_j, \neq obs$ free). The value of λ_{ref} is required as input. The user should expect long running times for the log-Student's t model, in which case a reduced chain given $\Lambda_{obs} = \lambda_{ref}$ needs to be generated

Usage

```
BF_lambda_obs_LLAP(obs, ref, X, chain)
```

Arguments

obs	Indicates the number of the observation under analysis
ref	Reference value λ_{ref} or u_{ref}
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function updates

Examples

```
#' library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.
```

```
LLAP <- MCMC_LLAP(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                  Cens = cancer[, 2], X = cancer[, 3:11])
LLAP.outlier <- BF_lambda_obs_LLAP(1,1, X = cancer[, 3:11], chain = LLAP)
```

`BF_lambda_obs_LLOG` *Outlier detection for observation for the log-logistic model*

Description

This returns a unique number corresponding to the Bayes Factor associated to the test $M_0 : \Lambda_{obs} = \lambda_{ref}$ versus $M_1 : \Lambda_{obs} \neq \lambda_{ref}$ (with all other $\Lambda_j, \neq obs$ free). The value of λ_{ref} is required as input. The user should expect long running times for the log-Student's t model, in which case a reduced chain given $\Lambda_{obs} = \lambda_{ref}$ needs to be generated

Usage

```
BF_lambda_obs_LLOG(ref, obs, X, chain)
```

Arguments

`ref`	Reference value λ_{ref} or u_{ref}
`obs`	Indicates the number of the observation under analysis
`X`	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
`chain`	MCMC chains generated by a BASSLINE MCMC function

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LLOG <- MCMC_LLOG(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                  Cens = cancer[, 2], X = cancer[, 3:11])
LLOG.Outlier <- BF_lambda_obs_LLOG(1,1, X = cancer[, 3:11], chain = LLOG)
```

BF_lambda_obs_LST *Outlier detection for observation for the log-student's t model*

Description

This returns a unique number corresponding to the Bayes Factor associated to the test $M_0 : \Lambda_{obs} = \lambda_{ref}$ versus $M_1 : \Lambda_{obs} \neq \lambda_{ref}$ (with all other $\Lambda_j, \neq obs$ free). The value of λ_{ref} is required as input. The user should expect long running times for the log-Student's t model, in which case a reduced chain given $\Lambda_{obs} = \lambda_{ref}$ needs to be generated

Usage

```
BF_lambda_obs_LST(
  N,
  thin,
  burn,
  ref,
  obs,
  Time,
  Cens,
  X,
  chain,
  Q = 1,
  prior = 2,
  set = TRUE,
  eps_l = 0.5,
  eps_r = 0.5,
  ar = 0.44
)
```

Arguments

N	Total number of iterations. Must be a multiple of thin.
thin	Thinning period.
burn	Burn-in period
ref	Reference value λ_{ref} or u_{ref}
obs	Indicates the number of the observation under analysis
Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
Q	Update period for the λ_i's
prior	Indicator of prior (1: Jeffreys, 2: Type I Ind. Jeffreys, 3: Ind. Jeffreys).

set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)
ar	Optimal acceptance rate for the adaptive Metropolis-Hastings updates

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LST <- MCMC_LST(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                Cens = cancer[, 2], X = cancer[, 3:11])

LST.Outlier <- BF_lambda_obs_LST(N = 100, thin = 20 , burn = 1, ref = 1,
                                 obs = 1, Time = cancer[, 1],
                                 Cens = cancer[, 2], X = cancer[, 3:11],
                                 chain = LST)
```

BF_u_obs_LEP *Outlier detection for observation for the log-exponential power model*

Description

This returns a unique number corresponding to the Bayes Factor associated to the test $M_0 : \Lambda_{obs} = \lambda_{ref}$ versus $M_1 : \Lambda_{obs} \neq \lambda_{ref}$ (with all other $\Lambda_j, \neq obs$ free). The value of λ_{ref} is required as input. The user should expect long running times for the log-Student's t model, in which case a reduced chain given $\Lambda_{obs} = \lambda_{ref}$ needs to be generated

Usage

```
BF_u_obs_LEP(
  N,
  thin,
  burn,
  ref,
  obs,
  Time,
  Cens,
  X,
  chain,
```

```
  prior = 2,
  set = TRUE,
  eps_l = 0.5,
  eps_r = 0.5,
  ar = 0.44
)
```

Arguments

N	Total number of iterations. Must be a multiple of thin.
thin	Thinning period.
burn	Burn-in period
ref	Reference value u_{ref}. Vallejos & Steel recommends this value be set to $1.6+1_{\alpha}$ for the LEP model.
obs	Indicates the number of the observation under analysis
Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
prior	Indicator of prior (1: Jeffreys, 2: Type I Ind. Jeffreys, 3: Ind. Jeffreys).
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)
ar	Optimal acceptance rate for the adaptive Metropolis-Hastings updates

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations (especially for the log-exponential power model).

LEP <- MCMC_LEP(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                Cens = cancer[, 2], X = cancer[, 3:11])
alpha <- mean(LEP[, 11])
uref <- 1.6 + 1 / alpha
LEP.Outlier <- BF_u_obs_LEP(N = 100, thin = 20, burn =1 , ref = uref,
                            obs = 1, Time = cancer[, 1], Cens = cancer[, 2],
                            cancer[, 3:11], chain = LEP)
```

cancer *VA Lung Cancer Trial Dataset*

Description

Data from a trial in which a therapy (standard or test chemotherapy) was randomly applied to 137 patients who were diagnosed with inoperable lung cancer. The survival times of the patients were measured in days since treatment.

Usage

```
cancer
```

Format

A matrix with 137 rows and 8 variables:

Time Survival time (in days)

Cens 0 or 1. If 0 the observation is right censored

Intercept The intercept

Treat The treatment applied to the patient (0: standard, 1: test)

Type.1 The histological type of the tumor (1: type 1, 0: otherwise)

Type.2 The histological type of the tumor (1: type 2, 0: otherwise)

Type.3 The histological type of the tumor (1: type 3, 0: otherwise)

Status A continuous index representing the status of the patient: 10—30 completely hospitalized, 40—60 partial confinement, 70—90 able to care for self.

MFD The time between the diagnosis and the treatment (in months)

Age Age (in years)

Prior Prior therapy, 0 or 10

Source

Appendix I of Kalbfleisch and Prentice (1980).

`CaseDeletion_LEP` *Case deletion analysis for the log-exponential power model*

Description

Leave-one-out cross validation analysis. The function returns a matrix with n rows. The first column contains the logarithm of the CPO (Geisser and Eddy, 1979). Larger values of the CPO indicate better predictive accuracy of the model. The second and third columns contain the KL divergence between $\pi(\beta, \sigma^2, \theta|t_{-i})$ and $\pi(\beta, \sigma^2, \theta|t)$ and its calibration index p_i, respectively.

Usage

```
CaseDeletion_LEP(Time, Cens, X, chain, set = TRUE, eps_l = 0.5, eps_r = 0.5)
```

Arguments

`Time`	Vector containing the survival times.
`Cens`	Censoring indication (1: observed, 0: right-censored).
`X`	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
`chain`	MCMC chains generated by a BASSLINE MCMC function
`set`	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
`eps_l`	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
`eps_r`	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations (especially for the log-exponential power model).

LEP <- MCMC_LEP(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                Cens = cancer[, 2], X = cancer[, 3:11])
LEP.CD <- CaseDeletion_LEP(Time = cancer[, 1], Cens = cancer[, 2],
                           X = cancer[, 3:11], chain = LEP)
```

`CaseDeletion_LLAP` *Case deletion analysis for the log-Laplace model*

Description

Leave-one-out cross validation analysis. The function returns a matrix with n rows. The first column contains the logarithm of the CPO (Geisser and Eddy, 1979). Larger values of the CPO indicate better predictive accuracy of the model. The second and third columns contain the KL divergence between $\pi(\beta, \sigma^2, \theta|t_{-i})$ and $\pi(\beta, \sigma^2, \theta|t)$ and its calibration index p_i, respectively.

Usage

```
CaseDeletion_LLAP(Time, Cens, X, chain, set = TRUE, eps_l = 0.5, eps_r = 0.5)
```

Arguments

`Time`	Vector containing the survival times.
`Cens`	Censoring indication (1: observed, 0: right-censored).
`X`	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
`chain`	MCMC chains generated by a BASSLINE MCMC function
`set`	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
`eps_l`	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
`eps_r`	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LLAP <- MCMC_LLAP(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                  Cens = cancer[, 2], X = cancer[, 3:11])
LLAP.CD <- CaseDeletion_LLAP(Time = cancer[, 1], Cens = cancer[, 2],
                             X = cancer[, 3:11], chain = LLAP)
```

CaseDeletion_LLOG *Case deletion analysis for the log-logistic model*

Description

Leave-one-out cross validation analysis. The function returns a matrix with n rows. The first column contains the logarithm of the CPO (Geisser and Eddy, 1979). Larger values of the CPO indicate better predictive accuracy of the model. The second and third columns contain the KL divergence between $\pi(\beta, \sigma^2, \theta|t_{-i})$ and $\pi(\beta, \sigma^2, \theta|t)$ and its calibration index p_i, respectively.

Usage

```
CaseDeletion_LLOG(Time, Cens, X, chain, set = TRUE, eps_l = 0.5, eps_r = 0.5)
```

Arguments

Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LLOG <- MCMC_LLOG(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                  Cens = cancer[, 2], X = cancer[, 3:11])
LLOG.CD <- CaseDeletion_LLOG(Time = cancer[, 1], Cens = cancer[, 2],
                             X = cancer[, 3:11], chain = LLOG)
```

CaseDeletion_LN *Case deletion analysis for the log-normal model*

Description

Leave-one-out cross validation analysis. The function returns a matrix with n rows. The first column contains the logarithm of the CPO (Geisser and Eddy, 1979). Larger values of the CPO indicate better predictive accuracy of the model. The second and third columns contain the KL divergence between $\pi(\beta, \sigma^2, \theta|t_{-i})$ and $\pi(\beta, \sigma^2, \theta|t)$ and its calibration index p_i, respectively.

Usage

```
CaseDeletion_LN(Time, Cens, X, chain, set = TRUE, eps_l = 0.5, eps_r = 0.5)
```

Arguments

Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.LM

LN <- MCMC_LN(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
              Cens = cancer[, 2], X = cancer[, 3:11])
LN.CD <- CaseDeletion_LN(Time = cancer[, 1], Cens = cancer[, 2],
                         X = cancer[, 3:11], chain = LN)
```

CaseDeletion_LST *Case deletion analysis for the log-student's t model*

Description

Leave-one-out cross validation analysis. The function returns a matrix with n rows. The first column contains the logarithm of the CPO (Geisser and Eddy, 1979). Larger values of the CPO indicate better predictive accuracy of the model. The second and third columns contain the KL divergence between $\pi(\beta, \sigma^2, \theta|t_{-i})$ and $\pi(\beta, \sigma^2, \theta|t)$ and its calibration index p_i, respectively.

Usage

```
CaseDeletion_LST(Time, Cens, X, chain, set = TRUE, eps_l = 0.5, eps_r = 0.5)
```

Arguments

Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LST <- MCMC_LST(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                Cens = cancer[, 2], X = cancer[, 3:11])
LST.CD <- CaseDeletion_LST(Time = cancer[, 1], Cens = cancer[, 2],
                           cancer[, 3:11], chain = LST)
```

DIC_LEP *Deviance information criterion for the log-exponential power model*

Description

Deviance information criterion is based on the deviance function $D(\theta, y) = -2log(f(y|\theta))$ but also incorporates a penalization factor of the complexity of the model

Usage

```
DIC_LEP(Time, Cens, X, chain, set = TRUE, eps_l = 0.5, eps_r = 0.5)
```

Arguments

Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations (especially for the log-exponential power model).

LEP <- MCMC_LEP(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                Cens = cancer[, 2], X = cancer[, 3:11])
LEP.DIC <- DIC_LEP(Time = cancer[, 1], Cens = cancer[, 2],
                   X = cancer[, 3:11], chain = LEP)
```

DIC_LLAP *Deviance information criterion for the log-Laplace model*

Description

Deviance information criterion is based on the deviance function $D(\theta, y) = -2log(f(y|\theta))$ but also incorporates a penalization factor of the complexity of the model

Usage

```
DIC_LLAP(Time, Cens, X, chain, set = TRUE, eps_l = 0.5, eps_r = 0.5)
```

Arguments

Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LLAP <- MCMC_LLAP(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                  Cens = cancer[, 2], X = cancer[, 3:11])
LLAP.DIC <- DIC_LLAP(Time = cancer[, 1], Cens = cancer[, 2],
                     X = cancer[, 3:11], chain = LLAP)
```

DIC_LLOG *Deviance information criterion for the log-logistic model*

Description

Deviance information criterion is based on the deviance function $D(\theta, y) = -2log(f(y|\theta))$ but also incorporates a penalization factor of the complexity of the model

Usage

```
DIC_LLOG(Time, Cens, X, chain, set = TRUE, eps_l = 0.5, eps_r = 0.5)
```

Arguments

Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LLOG <- MCMC_LLOG(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                  Cens = cancer[, 2], X = cancer[, 3:11])
LLOG.DIC <- DIC_LLOG(Time = cancer[, 1], Cens = cancer[, 2],
                     X = cancer[, 3:11], chain = LLOG)
```

DIC_LN *Deviance information criterion for the log-normal model*

Description

Deviance information criterion is based on the deviance function $D(\theta, y) = -2log(f(y|\theta))$ but also incorporates a penalization factor of the complexity of the model

Usage

```
DIC_LN(Time, Cens, X, chain, set = TRUE, eps_l = 0.5, eps_r = 0.5)
```

Arguments

Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.LM

LN <- MCMC_LN(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
              Cens = cancer[, 2], X = cancer[, 3:11])
LN.DIC <- DIC_LN(Time = cancer[, 1], Cens = cancer[, 2], X = cancer[, 3:11],
                 chain = LN)
```

DIC_LST *Deviance information criterion for the log-student's t model*

Description

Deviance information criterion is based on the deviance function $D(\theta, y) = -2log(f(y|\theta))$ but also incorporates a penalization factor of the complexity of the model

Usage

```
DIC_LST(Time, Cens, X, chain, set = TRUE, eps_l = 0.5, eps_r = 0.5)
```

Arguments

Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LST <- MCMC_LST(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                Cens = cancer[, 2], X = cancer[, 3:11])
LST.DIC <- DIC_LST(Time = cancer[, 1], Cens = cancer[, 2],
                   X = cancer[, 3:11], chain = LST)
```

LML_LEP *Log-marginal likelihood estimator for the log-exponential power model*

Description

Log-marginal likelihood estimator for the log-exponential power model

Usage

```
LML_LEP(
  thin,
  Time,
  Cens,
  X,
  chain,
  prior = 2,
  set = TRUE,
  eps_l = 0.5,
  eps_r = 0.5
)
```

Arguments

thin	Thinning period.
Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
prior	Indicator of prior (1: Jeffreys, 2: Type I Ind. Jeffreys, 3: Ind. Jeffreys).
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=100 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations (especially for the log-exponential power model).
```

```
LEP <- MCMC_LEP(N = 100, thin = 2, burn = 20, Time = cancer[, 1],
                Cens = cancer[, 2], X = cancer[, 3:11])
LEP.LML <- LML_LEP(thin = 2, Time = cancer[, 1], Cens = cancer[, 2],
                   X = cancer[, 3:11], chain = LEP)
```

LML_LLAP *Log-marginal likelihood estimator for the log-Laplace model*

Description

Log-marginal likelihood estimator for the log-Laplace model

Usage

```
LML_LLAP(
  thin,
  Time,
  Cens,
  X,
  chain,
  Q = 1,
  prior = 2,
  set = TRUE,
  eps_l = 0.5,
  eps_r = 0.5
)
```

Arguments

thin	Thinning period.
Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
Q	Update period for the λ_i's
prior	Indicator of prior (1: Jeffreys, 2: Type I Ind. Jeffreys, 3: Ind. Jeffreys).
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LLAP <- MCMC_LLAP(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                  Cens = cancer[, 2], X = cancer[, 3:11])
```

LML_LLOG *Log-marginal likelihood estimator for the log-logistic model*

Description

Log-marginal likelihood estimator for the log-logistic model

Usage

```
LML_LLOG(
  thin,
  Time,
  Cens,
  X,
  chain,
  Q = 10,
  prior = 2,
  set = TRUE,
  eps_l = 0.5,
  eps_r = 0.5,
  N.AKS = 3
)
```

Arguments

thin	Thinning period.
Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
Q	Update period for the λ_i's
prior	Indicator of prior (1: Jeffreys, 2: Type I Ind. Jeffreys, 3: Ind. Jeffreys).

set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)
N.AKS	Maximum number of terms of the Kolmogorov-Smirnov density used for the rejection sampling when updating mixing parameters (default value: 3)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LLOG <- MCMC_LLOG(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                  Cens = cancer[, 2], X = cancer[, 3:11])
LLOG.LML <- LML_LLOG(thin = 20, Time = cancer[, 1], Cens = cancer[, 2],
                     X = cancer[, 3:11], chain = LLOG)
```

LML_LN *Log-marginal Likelihood estimator for the log-normal model*

Description

Log-marginal Likelihood estimator for the log-normal model

Usage

```
LML_LN(
  thin,
  Time,
  Cens,
  X,
  chain,
  prior = 2,
  set = TRUE,
  eps_l = 0.5,
  eps_r = 0.5
)
```

Arguments

thin	Thinning period.
Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
prior	Indicator of prior (1: Jeffreys, 2: Type I Ind. Jeffreys, 3: Ind. Jeffreys).
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.LM

LN <- MCMC_LN(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
              Cens = cancer[, 2], X = cancer[, 3:11])
LN.LML <- LML_LN(thin = 20, Time = cancer[, 1], Cens = cancer[, 2],
                         X = cancer[, 3:11], chain = LN)
```

LML_LST *Log-marginal Likelihood estimator for the log-student's t model*

Description

Log-marginal Likelihood estimator for the log-student's t model

Usage

```
LML_LST(
  thin,
  Time,
  Cens,
  X,
  chain,
  Q = 1,
```

```
  prior = 2,
  set = TRUE,
  eps_l = 0.5,
  eps_r = 0.5
)
```

Arguments

thin	Thinning period.
Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
chain	MCMC chains generated by a BASSLINE MCMC function
Q	Update period for the λ_i's
prior	Indicator of prior (1: Jeffreys, 2: Type I Ind. Jeffreys, 3: Ind. Jeffreys).
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LST <- MCMC_LST(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                Cens = cancer[, 2], X = cancer[, 3:11])

LST.LML <- LML_LST(thin = 20, Time = cancer[, 1], Cens = cancer[, 2],
                   X = cancer[, 3:11], chain = LST)
```

MCMC_LEP *MCMC algorithm for the log-exponential power model*

Description

Adaptive Metropolis-within-Gibbs algorithm with univariate Gaussian random walk proposals for the log-exponential model

Usage

```
MCMC_LEP(
  N,
  thin,
  burn,
  Time,
  Cens,
  X,
  beta0 = NULL,
  sigma20 = NULL,
  alpha0 = NULL,
  prior = 2,
  set = TRUE,
  eps_l = 0.5,
  eps_r = 0.5,
  ar = 0.44
)
```

Arguments

N	Total number of iterations. Must be a multiple of thin.
thin	Thinning period.
burn	Burn-in period. Must be a multiple of thin.
Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
beta0	Starting values for β. If not provided, they will be randomly generated from a normal distribution.
sigma20	Starting value for σ^2. If not provided, it will be randomly generated from a gamma distribution.
alpha0	Starting value for α. If not provided, then it will be randomly generated from a uniform distribution.
prior	Indicator of prior (1: Jeffreys, 2: Type I Ind. Jeffreys, 3: Ind. Jeffreys).
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)
ar	Optimal acceptance rate for the adaptive Metropolis-Hastings updates

Value

A matrix with $N/thin + 1$ rows. The columns are the MCMC chains for β (k columns), σ^2 (1 column), θ (1 column, if appropriate), u (n columns, not provided for log-normal model), $\log(t)$ (n columns, simulated via data augmentation) and the logarithm of the adaptive variances (the number varies among models). The latter allows the user to evaluate if the adaptive variances have been stabilized.

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations (especially for the log-exponential power model).

LEP <- MCMC_LEP(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                Cens = cancer[, 2], X = cancer[, 3:11])
```

MCMC_LLAP *MCMC algorithm for the log-Laplace model*

Description

Adaptive Metropolis-within-Gibbs algorithm with univariate Gaussian random walk proposals for the log-Laplace model

Usage

```
MCMC_LLAP(
  N,
  thin,
  burn,
  Time,
  Cens,
  X,
  Q = 1,
  beta0 = NULL,
  sigma20 = NULL,
  prior = 2,
  set = TRUE,
  eps_l = 0.5,
  eps_r = 0.5
)
```

Arguments

N	Total number of iterations. Must be a multiple of thin.
thin	Thinning period.
burn	Burn-in period. Must be a multiple of thin.
Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
Q	Update period for the λ_i's
beta0	Starting values for β. If not provided, they will be randomly generated from a normal distribution.
sigma20	Starting value for σ^2. If not provided, it will be randomly generated from a gamma distribution.
prior	Indicator of prior (1: Jeffreys, 2: Type I Ind. Jeffreys, 3: Ind. Jeffreys).
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Value

A matrix with $N/thin + 1$ rows. The columns are the MCMC chains for β (k columns), σ^2 (1 column), θ (1 column, if appropriate), λ (n columns, not provided for log-normal model), $\log(t)$ (n columns, simulated via data augmentation) and the logarithm of the adaptive variances (the number varies among models). The latter allows the user to evaluate if the adaptive variances have been stabilized.

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LLAP <- MCMC_LLAP(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                  Cens = cancer[, 2], X = cancer[, 3:11])
```

MCMC_LLOG *MCMC algorithm for the log-logistic model*

Description

Adaptive Metropolis-within-Gibbs algorithm with univariate Gaussian random walk proposals for the log-logistic model

Usage

```
MCMC_LLOG(
  N,
  thin,
  burn,
  Time,
  Cens,
  X,
  Q = 10,
  beta0 = NULL,
  sigma20 = NULL,
  prior = 2,
  set = TRUE,
  eps_l = 0.5,
  eps_r = 0.5,
  N.AKS = 3
)
```

Arguments

N	Total number of iterations. Must be a multiple of thin.
thin	Thinning period.
burn	Burn-in period. Must be a multiple of thin.
Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
Q	Update period for the λ_i's
beta0	Starting values for β. If not provided, they will be randomly generated from a normal distribution.
sigma20	Starting value for σ^2. If not provided, it will be randomly generated from a gamma distribution.
prior	Indicator of prior (1: Jeffreys, 2: Type I Ind. Jeffreys, 3: Ind. Jeffreys).

set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)
N.AKS	Maximum number of terms of the Kolmogorov-Smirnov density used for the rejection sampling when updating mixing parameters (default value: 3)

Value

A matrix with $N/thin + 1$ rows. The columns are the MCMC chains for β (k columns), σ^2 (1 column), θ (1 column, if appropriate), λ (n columns, not provided for log-normal model), $\log(t)$ (n columns, simulated via data augmentation) and the logarithm of the adaptive variances (the number varies among models). The latter allows the user to evaluate if the adaptive variances have been stabilized.

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LLOG <- MCMC_LLOG(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                  Cens = cancer[, 2], X = cancer[, 3:11])
```

MCMC_LN *MCMC algorithm for the log-normal model*

Description

Adaptive Metropolis-within-Gibbs algorithm with univariate Gaussian random walk proposals for the log-normal model (no mixture)

Usage

```
MCMC_LN(
  N,
  thin,
  burn,
  Time,
  Cens,
  X,
  beta0 = NULL,
```

```
  sigma20 = NULL,
  prior = 2,
  set = TRUE,
  eps_l = 0.5,
  eps_r = 0.5
)
```

Arguments

N	Total number of iterations. Must be a multiple of thin.
thin	Thinning period.
burn	Burn-in period. Must be a multiple of thin.
Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
beta0	Starting values for β. If not provided, they will be randomly generated from a normal distribution.
sigma20	Starting value for σ^2. If not provided, it will be randomly generated from a gamma distribution.
prior	Indicator of prior (1: Jeffreys, 2: Type I Ind. Jeffreys, 3: Ind. Jeffreys).
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)

Value

A matrix with $(N - burn)/thin + 1$ rows. The columns are the MCMC chains for β (k columns), σ^2 (1 column), θ (1 column, if appropriate), $\log(t)$ (n columns, simulated via data augmentation) and the logarithm of the adaptive variances (the number varies among models). The latter allows the user to evaluate if the adaptive variances have been stabilized.

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LN <- MCMC_LN(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
              Cens = cancer[, 2], X = cancer[, 3:11])
```

MCMC_LST *MCMC algorithm for the log-student's t model*

Description

Adaptive Metropolis-within-Gibbs algorithm with univariate Gaussian random walk proposals for the log-student's T model (no mixture)

Usage

```
MCMC_LST(
  N,
  thin,
  burn,
  Time,
  Cens,
  X,
  Q = 1,
  beta0 = NULL,
  sigma20 = NULL,
  nu0 = NULL,
  prior = 2,
  set = TRUE,
  eps_l = 0.5,
  eps_r = 0.5,
  ar = 0.44
)
```

Arguments

N	Total number of iterations. Must be a multiple of thin.
thin	Thinning period.
burn	Burn-in period. Must be a multiple of thin.
Time	Vector containing the survival times.
Cens	Censoring indication (1: observed, 0: right-censored).
X	Design matrix with dimensions n x k where n is the number of observations and k is the number of covariates (including the intercept).
Q	Update period for the λ_i's
beta0	Starting values for β. If not provided, they will be randomly generated from a normal distribution.
sigma20	Starting value for σ^2. If not provided, it will be randomly generated from a gamma distribution.
nu0	Starting value for v. If not provided, then it will be randomly generated from a gamma distribution.

prior	Indicator of prior (1: Jeffreys, 2: Type I Ind. Jeffreys, 3: Ind. Jeffreys).
set	Indicator for the use of set observations (1: set observations, 0: point observations). The former is strongly recommended over the latter as point observations cause problems in the context of Bayesian inference (due to continuous sampling models assigning zero probability to a point).
eps_l	Lower imprecision (ϵ_l) for set observations (default value: 0.5).
eps_r	Upper imprecision (ϵ_r) for set observations (default value: 0.5)
ar	Optimal acceptance rate for the adaptive Metropolis-Hastings updates

Value

A matrix with $N/thin + 1$ rows. The columns are the MCMC chains for β (k columns), σ^2 (1 column), θ (1 column, if appropriate), λ (n columns, not provided for log-normal model), $\log(t)$ (n columns, simulated via data augmentation) and the logarithm of the adaptive variances (the number varies among models). The latter allows the user to evaluate if the adaptive variances have been stabilized.

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LST <- MCMC_LST(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
                Cens = cancer[, 2], X = cancer[, 3:11])
```

Trace_plot *Produce a trace plot of a variable's MCMC chain*

Description

Plots the chain across (non-discarded) iterations for a specified observation

Usage

```
Trace_plot(variable = NULL, chain = NULL)
```

Arguments

variable	Indicates the index of the variable
chain	MCMC chains generated by a BASSLINE MCMC function

Value

A ggplot2 object

Examples

```
library(BASSLINE)

# Please note: N=1000 is not enough to reach convergence.
# This is only an illustration. Run longer chains for more accurate
# estimations.

LN <- MCMC_LN(N = 1000, thin = 20, burn = 40, Time = cancer[, 1],
              Cens = cancer[, 2], X = cancer[, 3:11])
Trace_plot(1, LN)
```

Index