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| jointModel\_Subdistr\_Misc | R Documentation |

Joint modeling of longitudinal and competing-risks data using cumulative incidence functions under failure cause misclassification

**Description**

This function fits joint models of a normally distributed longitudinal marker and competing risk data using cumulative incidence functions under a proportional subdistribution hazard model. The true failure causes are assumed to be known only in a random sample of individuals who have failed from any event (double sampling). The fitting procedure is based on a hybrid MCMC algorithm.

**Usage**

jointModel\_Subdistr\_Misc (fitlme, fitCoxCause1, fitCoxCause2, prior, startingValues, nknotsCause1 = 3, nknotsCause2 = 3, scaleVarSurv = 1, iterMaxSurv\_1 = 1, iterMaxSurv\_2 = 1, DoubleSamplVar = "Robs", TrueStatusVar = "status", full.knotsCause1 = NULL, full.knotsCause2 = NULL, timeVar = "times", ndraw = 100, thin = 1, store.b = F, nburn = 0, useGauleg = T, Gauleg\_points = 30, tdf = 10)

**Arguments**

|  |  |
| --- | --- |
| fitlme | an object from the lme function (see also **Note**). |
| fitCoxCause1 | an object from the coxph function fitting proportional cause-specific hazards for cause 1. In the call to coxph(), you must specify the argument x = TRUE such that the design matrix is contained in the object fit. See **Examples**. |
| fitCoxCause2 | an object from the coxph function fitting proportional cause-specific hazards for cause 2. In the call to coxph(), you must specify the argument x = TRUE such that the design matrix is contained in the object fit. See **Examples**. |
| prior | a named list containing parameters for the prior distributions  Lc0: prior covariance matrix of the fixed effects  Lmu0: vector with the prior mean of the fixed effects  Smu0: vector with the prior mean of the combined survival parameters (cause 1 and cause 2). For each cause, the order is (1) parameters for baseline covariates (if any), (2) the association parameter, and (3) the B-spline parameters  Sc0: prior covariance matrix of the combined survival parameters (see above)  df: `degrees of freedom` for the inverse-Wishart prior distribution for the covariance matrix of the random effects  A: prior `guess` matrix for the inverse-Wishart prior distribution for the covariance matrix of the random effects.  lambda1: shape of the Gamma prior for the within-individual precision  lambda2: rate of the Gamma prior for the within-individual precision  a1: shape1 parameter of the Beta prior for , the probability of correctly classifying the cause 1  b1: shape2 parameter of the Beta prior for , the probability of correctly classifying the cause 1  a2: shape1 parameter of the Beta prior for , the probability of correctly classifying the cause 2  b2: shape2 parameter of the Beta prior for , the probability of correctly classifying the cause 2 |
| startingValues | a named list containing starting values for the parameters  Lbeta starting values for the fixed effects of the marker model  omega starting value for the within-individual precision  D starting values for the covariance matrix of the random effects |
| nknotsCause1 | number of internal knots for cubic B-splines of time approximating baseline CIF levels for cause 1 |
| nknotsCause2 | number of internal knots for cubic B-splines of time approximating baseline CIF levels for cause 2 |
| scaleVarSurv | scalar multiplied by the scale matrix of the multivariate student-t distribution used to propose a candidate value for the survival model parameters. |
| iterMaxSurv\_1 | number of BFGS iterations to find the posterior mode of the survival parameters for cause 1. The resulting value is used as the location parameter in the multivariate student-t distribution to propose a respective candidate value. |
| iterMaxSurv\_2 | number of BFGS iterations to find the posterior mode of the survival parameters for cause 2. The resulting value is used as the location parameter in the multivariate student-t distribution to propose a respective candidate value. |
| DoubleSamplVar | a character string indicating the binary variable in the survival dataset showing whether individuals are included in the double sampling (a subset of individuals with known failure causes). Equals 1 if individual is doubly sample and 0 otherwise. NA for right-censored individuals (double sampling was not intended). |
| TrueStatusVar | a character string indicating the variable with the true failure cause (1 or 2). NA if double sampling is not performed and 0 for right censoring. |
| full.knotsCause1 | vector with the full set of knots (i.e. including the Boundary.knots as well, see ?bs) of cubic B-splines of approximating baseline CIF levels for cause 1. nknotsCause1 should be NULL, otherwise, it is ignored. |
| full.knotsCause2 | vector with the full set of knots (i.e. including the Boundary.knots as well, see ?bs) of cubic B-splines of approximating baseline CIF levels for cause 2. nknotsCause2 should be NULL, otherwise, it is ignored. |
| timeVar | a character string indicating the time variable in the linear mixed model |
| ndraw | the number of MCMC draws recorded. |
| nburn | integer specifying how many iterations are to discard as burn-in. |
| thin | integer specifying the thinning of the chains. |
| store.b | logical, whether draws for the random effects are recorded. |
| useGauleg | logical, whether Gauss–Legendre quadrature is used to approximate the integral in the definition of the CIFs. If useGauleg=F, the 15-point Gauss-Kronrod rule is used. |
| Gauleg\_points | the number of Gauss–Legendre points. It is used if useGauleg=T, otherwise, it is ignored. |
| tdf | The degrees of freedom of the multivariate student-t distribution used to propose a candidate value for the survival model parameters. |

**Details**

Function jointModel\_Subdistr\_Misc can be used to jointly model a longitudinal marker and competing risks using cumulative incidence functions under a proportional substribution hazards model. For the longitudinal responses, the linear mixed model represented by fitlme is assumed

where and denote the fixed-effect and random-effect design matrices, respectively, as specified in the fitlme object. Also, is interpreted as the “true” marker value at . The objects fitCoxCause1 and fitCoxCause2 must represent cause-specific hazard Cox models with the observed failure causes (the observed failure causes must be included even for the doubly sampled individuals).

The baseline covariates in the competing risk models are specified through the fitCoxCause1 and fitCoxCause2 models. The model for the competing risks are

where is the association parameter relating the CIF to the “true” marker values. denote a cubic B-spline of time to approximate baseline CIF levels (see nknotsCause1 and nknotsCause2). The integral in the CIFs is approximated by either the Gauss–Legendre quadrature or the 15-point Gauss-Kronrod rule.

In the dataset provided by the fitCoxCause1, the doubly sampled individuals are indicated by DoubleSamplVar and the true failure causes by TrueStatusVar. The number or the position of the knots of the cubic B-splines are specified by nknotsCause1 and nknotsCause2 or full.knotsCause1 and full.knotsCause2. Misclassification is assumed to be nondifferential, i.e. there are two misclassification parameters, and , i.e. probabilities of correctly classifying the cause 1 and 2, respectively.

**Note**

1. The fitlme argument should represent a linear mixed model object with a general random-effects structure, i.e. only general positive definite structures for the covariance matrix of the random effects are allowed.

2. The fitlme object should not contain any within-group correlation structure (i.e., correlation argument of lme()) or within-group heteroscedasticity structure (i.e., weights argument of lme()).

3. It is assumed that the linear mixed effects model fitlme and the survival models fitCoxCause1 and fitCoxCause2 have been fitted to the same subjects. The data frames on which objects fitlme and fitCoxCause1 and fitCoxCause2 are should be sorted by the same numeric group variable (e.g. id=1,2,…). That is, it is assumed that the ordering of the subjects is the same for both fitlme and fitCoxCause1 and fitCoxCause2, i.e., that the first row in the data frame containing the event times corresponds to the first set of lines identified by the grouping variable in the data frame containing the repeated measurements, and so on.

### Examples

# Import functions for M1

source("SurvModel\_Subdistr.R")

source("JointModel\_Subdistr.R")

# Import functions for M2

source("SurvModel\_IncrCumInc.R")

source("JointModel\_IncrCumInc.R")

# List with the assumed prior distributions

prior = list()

prior$Lc0 = diag(4)\*100

prior$Lmu0 = rep(0,nrow(prior$Lc0))

prior$Smu0 = rep(0,17)

prior$Sc0 = diag(17)\*100

prior$df = 3

prior$A = 3\*diag(c(25,5,5))

prior$lambda1 = 0.01

prior$lambba2 = 0.01

prior$a1 = 1

prior$a2 = 1

prior$b1 = 1

prior$b2 = 1

# List with the initial values of the MCMC algorithm

startingValues = list()

startingValues$Lbeta = c(12.85,6.03,0.79,0.01)

startingValues$omega = 0.10

startingValues$D = matrix(c(25.26,-5.62,-2.44,-5.62,9.93,1.13,-2.44,1.13,0.85),nr = 3,nc = 3)

library(nlme)

library(survival)

library(Matrix)

library(cmprsk)

library(splines2)

library(numDeriv)

library(matrixcalc)

library(tmg)

library(restrictedMVN)

# Fitting the linear mixed model

fitlme = try(lme(sqcd4 ~ lspline(times,knots = c(1,5)),random = ~ lspline(times,knots = c(1,5))[,-3]|id,data = dataobs,method = "ML",

control = list(apVar = T,opt = "optim" , returnObject = F, maxIter = 100, msMaxIter = 100, niterEM = 150,msVerbose = T)),

silent = T)

summary(fitlme)

# Derivatives of the design matrices of the fixed and the random effects at the observed survival times

dataid = dataobs[dataobs$ord==1,]

# Fit the cox models

fitCoxCause1 = coxph(Surv(etimes,statusObs == 1) ~ group,data = dataid,x = T)

summary(fitCoxCause1)

fitCoxCause2 = coxph(Surv(etimes,statusObs == 2) ~ group,data = dataid,x = T)

summary(fitCoxCause2)

set.seed(15)

# Fit the SPM-1 model (subdistribution hazard)

fitProp\_Subd = try(jointModel\_Subdistr\_Misc(fitlme,fitCoxCause1,fitCoxCause2,prior,startingValues = startingValues,ndraw = 3500,thin = 3,nburn = 200,iterMaxSurv\_1 = 2,iterMaxSurv\_2 = 1,store.b = T,nknotsCause1 = 2,nknotsCause2 = 3,scaleVarSurv = 1,useGauleg = T,Gauleg\_points = 30),

silent = T)

round(fitProp\_Subd$summary$Longitudinal\_Process,3)

round(fitProp\_Subd$summary$sumSurvCause1,3)

round(fitProp\_Subd$summary$sumSurvCause2,3)

round(fitProp\_Subd$summary$sumMiscl,3)

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| DICSubdistr\_Misc | R Documentation |

Marginalized deviance information criterion

**Description**

This function computes the marginalized deviance information criterion for a jointModel\_Subdistr\_Misc object.

**Usage**

DICSubdistr\_Misc (fitProp, nMC = 100, thinDIC = 10)

**Arguments**

|  |  |
| --- | --- |
| fitProp | an object from the jointModel\_Subdistr\_Misc function (see also **Note**). |
| nMC | number of Monte Carlo samples to approximate the integral with respect to the random effects. |
| thinDIC | integer specifying the thinning of the chains. |

**Details**

This function computes the marginalized deviance information criterion (DIC) for a jointModel\_Subdistr\_Misc object. The posterior distributions of the parameters are extracted from jointModel\_Subdistr\_Misc, where option store.b = T must be specified. The survival likelihood takes misclassification of events into account, i.e

for the doubly sampled individuals

for the non-doubly sampled individuals who have failed from any event. For right-censored individuals, the contribution is equal to as right-censoring is assumed to be correctly classified.

**Note**

The option store.b = T must have been specified in the jointModel\_Subdistr\_Misc object in order for DICSubdistr\_Misc to work.

**Value**

A list with the following components

|  |  |
| --- | --- |
| eff | the effective sample size (posterior mean of posterior deviance minus the deviance at the posterior mean of the parameters) |
| dic | the marginalized deviance information criterion. |
| DevatPostMean | the deviance computed at the posterior mean of the parameters |
| PostDev | a posterior sample of the deviance of the model. |

### Examples

# Marginal DIC criterion

fitDICsubd = DICSubdistr\_Misc(fitProp\_Subd,nMC = 200,thinDIC = 7)

fitDICsubd$dic

fitDICsubd$eff

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| predictLatentStates\_Subdistr | R Documentation |

Population-averaged CIFs and marker states

**Description**

This function computes various additional population-averaged probabilities based on a jointModel\_Subdistr\_Misc object.

**Usage**

predictLatentStates\_Subdistr (fitProp, newdata1, newdata2, tt = seq(0, 10, by = 2), nMC = 1000, seed = 12, thin = 1, nburn = 200)

**Arguments**

|  |  |
| --- | --- |
| fitProp | an object from the jointModel\_Subdistr\_Misc function (see also **Note**). |
| newdata1 | a data.frame including specific values of the baseline covariates appearing in fitCoxCause1. |
| newdata2 | a data.frame including specific values of the baseline covariates appearing in fitCoxCause2. |
| tt | a vector of time points at which estimates are obtained. |
| nMC | number of Monte Carlo draws to approximate the integral with respect to the random effects |
| seed | the seed used in Monte Carlo integration |
| thin | integer specifying the thinning of the chains |
| nburn | burn-in used in Hamiltonian Monte Carlo to estimate population-averaged CIFs by latent marker states and latent marker state probabilities. |

**Details**

This function is currently problem-specific and should be used for investigational purposes only. Based on the posterior samples from jointModel\_Subdistr\_Misc, predictLatentStates\_Subdistr derives posterior samples for multistate probabilities defined jointly by marker and competing risk data.

* Population-averaged CIFs
* Population-averaged CIFs by baseline marker states
* Probabilities of being event-free and having “true” marker values in predefined intervals (latent marker states)
* Latent marker states by baseline marker states

Currently, only a lspline(tt,knots = c(1,5)) model for the marker evolution is allowed without further covariates. 7 marker states are currently allowed:

**Note**

Investigational use only; please use with caution. The names of the time variable and failure indicators used in fitCoxCause1 and fitCoxCause2 must appear in newdata1 and newdata2 assigning arbitrary values.

**Value**

A list with the following components

|  |  |
| --- | --- |
| sumCif1 | Posterior results (i.e mean, median, SD, 2.5% percentile and 97.5% percentile) for population-averaged cause 1. |
| sumCif2 | Posterior results for population-averaged cause 2. |
| sumS1 | Posterior results for the latent marker state 1. |
| sumS2 | Posterior results for the latent marker state 2. |
| sumS3 | Posterior results for the latent marker state 3. |
| sumS4 | Posterior results for the latent marker state 4 |
| sumS5 | Posterior results for the latent marker state 5 |
| sumS6 | Posterior results for the latent marker state 6 |
| sumS7 | Posterior results for the latent marker state 7 |
| sumCif1List | A list with posterior results for population-averaged CIF 1 by 7 baseline latent marker states. |
| sumCif2List | A list with posterior results for population-averaged CIF 2 by 7 baseline latent marker states. |
| sumS1List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 1. |
| sumS2List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 2. |
| sumS3List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 3. |
| sumS4List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 4. |
| sumS5List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 5. |
| sumS6List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 6. |
| sumS7List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 7. |

### Examples

newdata1 = data.frame(group = c(1),etimes = 0,statusObs = 0)

newdata2 = data.frame(group = c(1),etimes = 0,statusObs = 0)

tt = seq(0,10,by = 2)

fit1 = predictLatentStates\_Subdistr(fitProp\_Subd,newdata1,newdata2,tt = tt,nMC = 1000,thin = 10)

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| jointModel\_IncrCumInc\_Misc | R Documentation |

Joint modeling of longitudinal and competing-risks data using cumulative incidence functions under failure cause misclassification

**Description**

This function fits joint models of a normally distributed longitudinal marker and competing risk data using cumulative incidence functions under a class of generalized odds rate transformation models. The true failure causes are assumed to be known only in a random sample of individuals who have failed from any event (double sampling). The fitting procedure is based on a hybrid MCMC algorithm.

**Usage**

jointModel\_IncrCumInc\_Misc (fitlme, fitCoxCause1, fitCoxCause2, prior, startingValues, nknotsCause1 = 3, nknotsCause2 = 3, scaleVarSurv = 1, iterMaxSurv\_1 = 1, iterMaxSurv\_2 = 1, DoubleSamplVar = "Robs", TrueStatusVar = "status", full.knotsCause1 = NULL, full.knotsCause2 = NULL, timeVar = "times", alpha1 = 1, alpha2 = 1, ndraw = 100, thin = 1, store.b = F, nburn = 0, useGauleg = T, Gauleg\_points = 30, tdf = 10)

**Arguments**

|  |  |
| --- | --- |
| fitlme | an object from the lme function (see also **Note**). |
| fitCoxCause1 | an object from the coxph function fitting proportional cause-specific hazards for cause 1. In the call to coxph(), you must specify the argument x = TRUE such that the design matrix is contained in the object fit. See **Examples**. |
| fitCoxCause2 | an object from the coxph function fitting proportional cause-specific hazards for cause 2. In the call to coxph(), you must specify the argument x = TRUE such that the design matrix is contained in the object fit. See **Examples**. |
| prior | a named list containing parameters for the prior distributions  Lc0: prior covariance matrix of the fixed effects  Lmu0: vector with the prior mean of the fixed effects  Smu0: vector with the prior mean of the combined survival parameters (cause 1 and cause 2). For each cause, the order is (1) parameters for baseline covariates (if any), (2) the association parameter and (3) the B-spline parameters  Sc0: prior covariance matrix of the combined survival parameters (see above)  df: `degrees of freedom` for the inverse-Wishart prior distribution for the covariance matrix of the random effects  A: prior `guess` matrix for the inverse-Wishart prior distribution for the covariance matrix of the random effects.  lambda1: shape of the Gamma prior for the within-individual precision  lambda2: rate of the Gamma prior for the within-individual precision  a1: shape1 parameter of the Beta prior for , the probability of correctly classifying the cause 1  b1: shape2 parameter of the Beta prior for , the probability of correctly classifying the cause 1  a2: shape1 parameter of the Beta prior for , the probability of correctly classifying the cause 2  b2: shape2 parameter of the Beta prior for , the probability of correctly classifying the cause 2 |
| startingValues | a named list containing starting values for the parameters  Lbeta starting values for the fixed effects of the marker model  omega starting value for the within-individual precision  D starting values for the covariance matrix of the random effects |
| nknotsCause1 | number of internal knots for cubic B-splines of time approximating baseline CIF levels for cause 1 |
| nknotsCause2 | number of internal knots for cubic B-splines of time approximating baseline CIF levels for cause 2 |
| scaleVarSurv | scalar multiplied by the scale matrix of the multivariate student-t distribution used to propose a candidate value for the survival model parameters. |
| iterMaxSurv\_1 | number of BFGS iterations to find the posterior mode of the survival parameters for cause 1. The resulting value is used as the location parameter in the multivariate student-t distribution to propose a respective candidate value. |
| iterMaxSurv\_2 | number of BFGS iterations to find the posterior mode of the survival parameters for cause 2. The resulting value is used as the location parameter in the multivariate student-t distribution to propose a respective candidate value. |
| DoubleSamplVar | a character string indicating the binary variable in the survival dataset showing whether individuals are included in the double sampling (a subset of individuals with known failure causes). Equals 1 if individual is doubly sample and 0 otherwise. NA for right-censored individuals (double sampling was not intended). |
| TrueStatusVar | a character string indicating the variable with the true failure cause (1 or 2). NA if double sampling is not performed and 0 for right censoring. |
| full.knotsCause1 | vector with the full set of knots (i.e. including the Boundary.knots as well, see ?bs) of cubic B-splines of approximating baseline CIF levels for cause 1. nknotsCause1 should be NULL, otherwise, it is ignored. |
| full.knotsCause2 | vector with the full set of knots (i.e. including the Boundary.knots as well, see ?bs) of cubic B-splines of approximating baseline CIF levels for cause 2. nknotsCause2 should be NULL, otherwise, it is ignored. |
| timeVar | a character string indicating the time variable in the linear mixed model |
| alpha1 | the link function parameter for cause 1 (See **Details**) |
| alpha2 | the link function parameter for cause 2 (See **Details**) |
| ndraw | the number of MCMC draws recorded. |
| nburn | integer specifying how many iterations are to discard as burn-in. |
| thin | integer specifying the thinning of the chains. |
| store.b | logical, whether draws for the random effects are recorded. |
| useGauleg | logical, whether Gauss–Legendre quadrature is used to approximate the integral in the definition of the CIFs. If useGauleg=F, the 15-point Gauss-Kronrod rule is used. |
| Gauleg\_points | the number of Gauss–Legendre points. It is used if useGauleg=T, otherwise, it is ignored. |
| tdf | The degrees of freedom of the multivariate student-t distribution used to propose a candidate value for the survival model parameters. |

**Details**

Function jointModel\_IncrCumInc\_Misc can be used to jointly model a longitudinal marker and competing risks using cumulative incidence functions adopting a class of generalized odds rate transformation models. For the longitudinal responses, the linear mixed model represented by fitlme is assumed

where and denote the fixed-effect and random-effect design matrices, respectively, as specified in the fitlme object. Also, is interpreted as the “true” marker value at . The objects fitCoxCause1 and fitCoxCause2 must represent cause-specific hazard Cox models with the observed failure causes (the observed failure causes must be included even for the doubly sampled individuals).

The baseline covariates in the competing risk models are specified through the fitCoxCause1 and fitCoxCause2 models. The model for the competing risks are

where is the association parameter relating the CIF to the “true” marker values, denote a cubic B-spline of time to approximate baseline CIF levels (see nknotsCause1 and nknotsCause2) and are parameters of the generalized odds rate transformation (specified by the user). The integral in the CIFs is approximated by either the Gauss–Legendre quadrature or the 15-point Gauss-Kronrod rule.

In the dataset provided by the fitCoxCause1, the doubly sampled individuals are indicated by DoubleSamplVar and the true failure causes by TrueStatusVar. The number or the position of the knots of the cubic B-splines are specified by nknotsCause1 and nknotsCause2 or full.knotsCause1 and full.knotsCause2. Misclassification is assumed to be nondifferential, i.e. there are two misclassification parameters, and , i.e. probabilities of correctly classifying the cause 1 and 2, respectively.

**Note**

1. The fitlme argument should represent a linear mixed model object with a general random-effects structure, i.e. only general positive definite structures for the covariance matrix of the random effects are allowed.

2. The fitlme object should not contain any within-group correlation structure (i.e., correlation argument of lme()) or within-group heteroscedasticity structure (i.e., weights argument of lme()).

3. It is assumed that the linear mixed effects model fitlme and the survival models fitCoxCause1 and fitCoxCause2 have been fitted to the same subjects. The data frames on which objects fitlme and fitCoxCause1 and fitCoxCause2 are should be sorted by the same numeric group variable (e.g. id=1,2,…). That is, it is assumed that the ordering of the subjects is the same for both fitlme and fitCoxCause1 and fitCoxCause2, i.e., that the first row in the data frame containing the event times corresponds to the first set of lines identified by the grouping variable in the data frame containing the repeated measurements, and so on.

### Examples

set.seed(15)

# Fit the SPM-2 model

fitProp\_IncrCumInc = try(jointModel\_IncrCumInc\_Misc(fitlme,fitCoxCause1,fitCoxCause2,prior,startingValues = startingValues,ndraw = 3500,thin = 3,nburn = 200,alpha1 = 1,alpha2 = 1,iterMaxSurv\_1 = 2,iterMaxSurv\_2 = 1,store.b = T,nknotsCause1 = 2,nknotsCause2 = 3,scaleVarSurv = 1,useGauleg = T,Gauleg\_points = 30),silent = T)

round(fitProp\_IncrCumInc$summary$Longitudinal\_Process,3)

round(fitProp\_IncrCumInc$summary$sumSurvCause1,3)

round(fitProp\_IncrCumInc$summary$sumSurvCause2,3)

round(fitProp\_IncrCumInc$summary$sumMiscl,3)

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| DICIncrCumInc\_Misc | R Documentation |

Marginalized deviance information criterion

**Description**

This function computes the marginalized deviance information criterion for a jointModel\_IncrCumInc\_Misc object.

**Usage**

DICIncrCumInc\_Misc (fitProp, nMC = 100, thinDIC = 10)

**Arguments**

|  |  |
| --- | --- |
| fitProp | an object from the jointModel\_IncrCumInc\_Misc function (see also **Note**). |
| nMC | number of Monte Carlo samples to approximate the integral with respect to the random effects. |
| thinDIC | integer specifying the thinning of the chains. |

**Details**

This function computes the marginalized deviance information criterion (DIC) for a jointModel\_IncrCumInc\_Misc object. The posterior distributions of the parameters are extracted from jointModel\_IncrCumInc\_Misc, where option store.b = T must be specified. The survival likelihood takes misclassification of events into account, i.e

for the doubly sampled individuals

for the non-doubly sampled individuals who have failed from any event. For right-censored individuals, the contribution is equal to as right-censoring is assumed to be correctly classified.

**Note**

The option store.b = T must have been specified in the jointModel\_IncrCumInc\_Misc object in order for DICIncrCumInc\_Misc to work.

**Value**

A list with the following components

|  |  |
| --- | --- |
| eff | the effective sample size (posterior mean of posterior deviance minus the deviance at the posterior mean of the parameters) |
| dic | the marginalized deviance information criterion. |
| DevatPostMean | the deviance computed at the posterior mean of the parameters |
| PostDev | a posterior sample of the deviance of the model. |

### Examples

# Marginal DIC criterion

fitDICIncrCinc = DICIncrCumInc\_Misc(fitProp\_IncrCumInc,nMC = 200,thinDIC = 7)

fitDICIncrCinc$eff

fitDICIncrCinc$dic

|  |  |
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| predictLatentStates\_IncrCumInc | R Documentation |

Population-averaged CIFs and marker states

**Description**

This function computes various additional population-averaged probabilities based on a jointModel\_IncrCumInc\_Misc object.

**Usage**

predictLatentStates\_IncrCumInc (fitProp, newdata1, newdata2, tt = seq(0, 10, by = 2), nMC = 1000, seed = 12, thin = 1, nburn = 200)

**Arguments**

|  |  |
| --- | --- |
| fitProp | an object from the jointModel\_IncrCumInc\_Misc function (see also **Note**). |
| newdata1 | a data.frame including specific values of the baseline covariates appearing in fitCoxCause1. |
| newdata2 | a data.frame including specific values of the baseline covariates appearing in fitCoxCause2. |
| tt | a vector of time points at which estimates are obtained. |
| nMC | number of Monte Carlo draws to approximate the integral with respect to the random effects |
| seed | the seed used in Monte Carlo integration |
| thin | integer specifying the thinning of the chains |
| nburn | burn-in used in Hamiltonian Monte Carlo to estimate population-averaged CIFs by latent marker states and latent marker state probabilities. |

**Details**

This function is currently problem-specific and should be used for investigational purposes only. Based on the posterior samples from jointModel\_IncrCumInc\_Misc, predictLatentStates\_IncrCumInc derives posterior samples for multistate probabilities defined jointly by marker and competing risk data.

* Population-averaged CIFs
* Population-averaged CIFs by baseline marker states
* Probabilities of being event-free and having “true” marker values in predefined intervals (latent marker states)
* Latent marker states by baseline marker states

Currently, only a lspline(tt,knots = c(1,5)) model for the marker evolution is allowed without further covariates. 7 marker states are currently allowed:

**Note**

Investigational use only; please use with caution. The names of the time variable and failure indicators used in fitCoxCause1 and fitCoxCause2 must appear in newdata1 and newdata2 assigning arbitrary values.

**Value**

A list with the following components

|  |  |
| --- | --- |
| sumCif1 | Posterior results (i.e mean, median, SD, 2.5% percentile and 97.5% percentile) for population-averaged cause 1. |
| sumCif2 | Posterior results for population-averaged cause 2. |
| sumS1 | Posterior results for the latent marker state 1. |
| sumS2 | Posterior results for the latent marker state 2. |
| sumS3 | Posterior results for the latent marker state 3. |
| sumS4 | Posterior results for the latent marker state 4 |
| sumS5 | Posterior results for the latent marker state 5 |
| sumS6 | Posterior results for the latent marker state 6 |
| sumS7 | Posterior results for the latent marker state 7 |
| sumCif1List | A list with posterior results for population-averaged CIF 1 by 7 baseline latent marker states. |
| sumCif2List | A list with posterior results for population-averaged CIF 2 by 7 baseline latent marker states. |
| sumS1List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 1. |
| sumS2List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 2. |
| sumS3List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 3. |
| sumS4List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 4. |
| sumS5List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 5. |
| sumS6List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 6. |
| sumS7List | A list with posterior results for transition probabilities to the 7 latent marker states by baseline latent marker state 7. |

### Examples

newdata1 = data.frame(group = c(1),etimes = 0,statusObs = 0)

newdata2 = data.frame(group = c(1),etimes = 0,statusObs = 0)

fit1 = predictLatentStates\_IncrCumInc(fitProp\_IncrCumInc,newdata1,newdata2,tt = tt,nMC = 1000,thin = 10)