Package 'joint.Cox'

September 17, 2019

Type Package

Title Joint Frailty-Copula Models for Tumour Progression and Death in Meta-Analysis

Version 3.6

Date 2019-9-17

Author Takeshi Emura

Maintainer Takeshi Emura <takeshiemura@gmail.com>

Description Perform likelihood estimation and dynamic prediction under joint frailty-copula models for tumour progression and death in meta-analysis. A penalized likelihood method is employed for estimating model parameters, where the baseline hazard functions are modeled by smoothing splines. The methods are applicable for meta-analytic data combining several studies. The methods can analyze data having information on both terminal event time (e.g., time-to-death) and non-terminal event time (e.g., time-to-tumour progression). See Emura et al. (2017) <doi:10.1177/0962280215604510> for likelihood estimation, and Emura et al. (2018) <doi:10.1177/0962280216688032> for dynamic prediction. More details on these methods can also be found in a book of Emura et al. (2019) <doi:10.1007/978-981-13-3516-7>. Survival data from ovarian cancer patients are also available.

License GPL-2

Depends survival

NeedsCompilation no

Repository CRAN

Date/Publication 2019-09-17 04:50:02 UTC

R topics documented:

`joint.Cox-package` *Joint Frailty-Copula Models for Tumour Progression and Death in Meta-Analysis*

Description

Perform likelihood estimation and dynamic prediction under joint frailty-copula models for tumour progression and death in meta-analysis. A penalized likelihood method is employed for estimating model parameters, where the baseline hazard functions are modeled by smoothing splines. The methods are applicable for meta-analytic data combining several studies. The methods can analyze data having information on both terminal event time (e.g., time-to-death) and non-terminal event time (e.g., time-to-tumour progression). See Emura et al. (2017) and Emura et al. (2018) for more details. More details on these methods can also be found in a book of Emura et al. (2019). Survival data from ovarian cancer patients are also available.

Details

Package:	joint.Cox
Type:	Package
Version:	3.6
Date:	2019-9-17
License:	GPL-2

Author(s)

Takeshi Emura Maintainer: Takeshi Emura <takeshiemura@gmail.com>

References

Emura T, Nakatochi M, Murotani K, Rondeau V (2017), A joint frailty-copula model between tumour progression and death for meta-analysis, Stat Methods Med Res 26(6): 2649-66

Emura T, Nakatochi M, Matsui S, Michimae H, Rondeau V (2018), Personalized dynamic prediction of death according to tumour progression and high-dimensional genetic factors: meta-analysis with a joint model, Stat Methods Med Res 27(9):2842-58

Emura T, Matsui S, Rondeau V (2019), Survival Analysis with Correlated Endpoints, Joint Frailty-Copula Models, JSS Research Series in Statistics, Springer

---

`cmprskCox.reg` *The Competing Risks Version of Penalized Likelihood Estimation under the Joint Cox Models Between Tumour Progression and Death for Meta-Analysis*

Description

Perform regression analyses under a copula-based joint Cox proportional hazards model between tumour progression and death for meta-analysis, which is proposed in Section 6.2 of Emura et al. (2017) and Section 5.1 of Emura et al. (2019-). This is the competing risks version of "joint.Cox.reg". To avoid the indentifiability problem, the copula parameter (theta) should be given by user, e.g., theta=2. The method is applicable for meta-analysis combining several studies or for cluster survival data.

Usage

```
cmprskCox.reg(t.event, event1, event2, Z1, Z2, group, theta, alpha = 1,
 kappa1 = c(seq(10, 1e+17, length = 30)), kappa2 = c(seq(10, 1e+17, length = 30)),
 LCV.plot = TRUE, Randomize_num = 10, Adj = 500,convergence.par=FALSE)
```

Arguments

`t.event`	a vector for event tims
`event1`	a vector for event-type 1 indicators (=1 with event; =0 without event)
`event2`	a vector for event-type 2 indicators (=1 with event; =0 without event)
`Z1`	a matrix for covariates associated with event-type 1; ncol(Z1)=the number of covariates
`Z2`	a matrix for covariates associated with event-type 2; ncol(Z2)=the number of covariates
`group`	a vector for a group identification number, like 1,2,3....
`theta`	A copula parameter under the Clayton copula (theta > 0)
`alpha`	A value related to the frailty (e.g., alpha=0 or =1); alpha=1 is default
`kappa1`	a vector for candidate smoothing parameters
`kappa2`	a vector for candidate smoothing parameters

LCV.plot	Plot the LCV curves if "TRUE"
Randomize_num	The number of randomizations for the ititial p0
Adj	Numerical adjustment to prevent overflow; Adj=500 is recommended
convergence.par	If TRUE, the converged estimate, gradient, and Hessian matrix are given (log-transformed)

Details

We employ "nlm" routine to maximize the penalized likelihood function with the initial value described in Emura et al. (2015). If "nlm" does not converge, then we randomize the initial value by adding uniform random variables (Hu and Emura, 2015).

Value

count	Count for event occurences
beta1	Regression coefficient for Z1
beta2	Regression coefficient for Z2
eta	Frailty parameter (variance)
theta	Copula parameter under the Clayton copula (fixed by user)
tau	Kendall's tau corresponding to the copula parameter
LCV1	Likelihood cross-validation for event-type 1
LCV2	Likelihood cross-validation for event-type 2
g	M-spline coefficients for event-type 1
h	M-spline coefficients for event-type 2
g_var	Variance of M-spline coefficients for event-type 1
h_var	Variance of M-spline coefficients for event-type 2
convergence	convergence results for maximizing penalized likelihood
convergence.parameters	converged estimate, gradient, and Hessian matrix (log-transformed)

Error

"Error in integrate(func1, 0.001, 10, stop.on.error = FALSE):non-finite function value", an error occurring when the penalized likelihood is maximizad by "nlm". The error may frequently occur during the iterations for maximizing the penalized likelihood, but is not crucial (can simply be ignored).

Warning

"NA/Inf replaced by maximum positive value", an error occurring when the penalized likelihood is maximizad by "nlm". The error frequently occurs during the iterations for maximizing the penalized likelihood, but is not crucial (can simply be ignored).

Author(s)

Takeshi Emura, Shih JH

References

Emura T, Nakatochi M, Murotani K, Rondeau V (2017), A joint frailty-copula model between tumour progression and death for meta-analysis, Stat Methods Med Res 26(6): 2649-66

Emura T, Shih JH, Ha ID, Wilke RA (2019-), Comparison between the marginal hazard models and sub-hazard models with an assumed copula, in revision

Hu YH, Emura T (2015), Maximum likelihood estimation for a special exponential family under random double-truncation, Computational Stat 30 (4): 1199-1229

Examples

```
data(dataOvarian)
t.event=dataOvarian$t.event
t.death=dataOvarian$t.death
event=dataOvarian$event
death=dataOvarian$death
non.event=which(event==1 & death==1 & t.event==t.death)
non.death=which(event==1 & death==1 & t.event<t.death)
event[non.event]=0 ## relapse before death
death[non.death]=0 ## death before relapse (tie is counted as death)
Z=as.matrix(dataOvarian$CXCL12)
group=dataOvarian$group
alpha_given=0
theta=2.35
kappa_grid=seq(10,1e+17,length = 30)

#set.seed(1)
#cmprskCox.reg(t.event=t.event,event1=event,event2=death,
#              Z1=Z,Z2=Z,group=group,theta=theta,alpha=alpha_given,
#              kappa1=kappa_grid,kappa2=kappa_grid,LCV.plot=TRUE,Adj=500)
```

`dataOvarian` *Meta-analytic data of ovarian cancer patients combining 4 independent studies.*

Description

Meta-analytic data for studying the CXCL12 gene expression as a predictive biomarker of survival in ovarian cancer. The dataset is a subset of the curated ovarian data of Ganzfried et al (2013). We prepared the dataset by using "patientselection.config" in "Curated ovarian data" around May 2015.

Usage

```
data("dataOvarian")
```

Format

A data frame with 1003 observations on the following 6 variables.

`t.event` : time to event in days

`event` : event indicator (1=recurrence, 0=no recurrence)

`t.death` : time to death in days

`death` : death indicator (1=death, 0=alive)

`group` : study ID; group=4, 8, 11, or 14

`CXCL12` : CXCL12 expression

Details

4 studies are combined (group=4, 8, 11, and 14). The numbers 4, 8, 11 and 14 corresponds to the IDs from the original data of Ganzfried et al. (2013).

Source

Ganzfried BF et al. (2013), Curated ovarian data: clinically annotated data for the ovarian cancer transcriptome, Database, Article ID bat013, doi:10.1093/database/bat013.

References

Ganzfried BF et al. (2013), Curated ovarian data: clinically annotated data for the ovarian cancer transcriptome, Database, Article ID bat013, doi:10.1093/database/bat013.

Examples

```
data(dataOvarian)
study4=dataOvarian[dataOvarian$group==4,] # extract one study
study4
```

`dataOvarian1` *Data on time-to-recurrence and 158 gene expressions for 912 ovarian cancer patients from 4 independent studies.*

Description

Meta-analytic data containing 158 gene expressions and time-to-relapse information for ovarian cancer patients. The data include time-to-recurrence, residual tumour size (>=1cm> vs. <1cm), and associated 158 gene expressions. The dataset is a subset of the curated ovarian data of Ganzfried et al (2013). We prepared the dataset by using "patientselection.config" in "Curated ovarian data" around October 2016.

Usage

```
data("dataOvarian1")
```

Format

A data frame with 912 observations on the following 162 variables.

`t.event` : time-to-recurrence in days

`event` : event indicator (1=recurrence, 0=no recurrence)

`group` : study ID; group=4, 9, 12, or 16

`debulk` : residual tumour size (>=1cm> vs. <1cm)

`ABI3BP` a numeric vector

`ADAM12` a numeric vector

`ADORA3` a numeric vector

`ANKRD27` a numeric vector

`AP2M1` a numeric vector

`AP3S1` a numeric vector

`ARHGAP28` a numeric vector

`ARHGAP29` a numeric vector

`ARTN` a numeric vector

`ASAP3` a numeric vector

`B4GALT5` a numeric vector

`BCAP31` a numeric vector

`BRD4` a numeric vector

`C1QTNF3` a numeric vector

`CALD1` a numeric vector

`CCNE1` a numeric vector

`CCNL1` a numeric vector

`CDC42` a numeric vector

`CDV3` a numeric vector

`CEBPB` a numeric vector

`CLIC4` a numeric vector

`COL10A1` a numeric vector

`COL11A1` a numeric vector

`COL16A1` a numeric vector

`COL3A1` a numeric vector

`COL5A1` a numeric vector

`COL5A2` a numeric vector

`COMP` a numeric vector

`CRISPLD2` a numeric vector

`CRYAB` a numeric vector

`CSE1L` a numeric vector

CTSK a numeric vector

CXCL12 a numeric vector

CYR61 a numeric vector

DCUN1D1 a numeric vector

DDX27 a numeric vector

DIAPH3 a numeric vector

DNAJB4 a numeric vector

DNAJC13 a numeric vector

DNAJC8 a numeric vector

DPYSL3 a numeric vector

DVL3 a numeric vector

EFNB2 a numeric vector

EIF3K a numeric vector

ELK1 a numeric vector

ENPP1 a numeric vector

EPYC a numeric vector

FABP4 a numeric vector

FAM69A a numeric vector

FAP a numeric vector

FERMT2 a numeric vector

FGF1 a numeric vector

FN1 a numeric vector

FOSL2 a numeric vector

FSTL1 a numeric vector

GABRG3 a numeric vector

GAS1 a numeric vector

GFRA1 a numeric vector

GFRA3 a numeric vector

GJC1 a numeric vector

GLIPR1 a numeric vector

GPATCH1 a numeric vector

HLTF a numeric vector

HP1BP3 a numeric vector

HSD17B6 a numeric vector

INHBA a numeric vector

ITGB1 a numeric vector

JUN a numeric vector

KIAA0226 a numeric vector

KIAA0355 a numeric vector

KIAA1598 a numeric vector

KIN a numeric vector

KLHL25 a numeric vector

KPNA6 a numeric vector

KRT7 a numeric vector

KRTAP5.8 a numeric vector

L2HGDH a numeric vector

LGALS1 a numeric vector

LOX a numeric vector

LPP a numeric vector

LUM a numeric vector

LUZP1 a numeric vector

MAP7D1 a numeric vector

MAPRE1 a numeric vector

MCL1 a numeric vector

MEOX2 a numeric vector

METTL9 a numeric vector

MFN1 a numeric vector

MICAL2 a numeric vector

MMP12 a numeric vector

MRPS22 a numeric vector

MXD1 a numeric vector

MXRA8 a numeric vector

N4BP2L2 a numeric vector

NCOA3 a numeric vector

NDRG3 a numeric vector

NINJ1 a numeric vector

NNMT a numeric vector

NOTCH2 a numeric vector

NPY a numeric vector

NTM a numeric vector

NUAK1 a numeric vector

OAT a numeric vector

OLFML2B a numeric vector

PARD3 a numeric vector

PCYT1A a numeric vector

PDE1A a numeric vector

PDGFD a numeric vector

PDPN a numeric vector

PGRMC1 a numeric vector

PLAU a numeric vector

PLOD2 a numeric vector

PLSCR4 a numeric vector

POSTN a numeric vector

PPIC a numeric vector

PRDM2 a numeric vector

PSMC4 a numeric vector

RAB22A a numeric vector

RAB31 a numeric vector

RAB32 a numeric vector

RARRES1 a numeric vector

RPS16 a numeric vector

SERPINE1 a numeric vector

SGK1 a numeric vector

SH3PXD2A a numeric vector

SKIL a numeric vector

SLC12A8 a numeric vector

SPARC a numeric vector

SPHK1 a numeric vector

STAU1 a numeric vector

SULF1 a numeric vector

SUPT5H a numeric vector

TAGLN a numeric vector

TBCB a numeric vector

TEAD1 a numeric vector

TESK1 a numeric vector

TGM5 a numeric vector

THEMIS2 a numeric vector

TIMP2 a numeric vector

TIMP3 a numeric vector

TJP1 a numeric vector

TP73.AS1 a numeric vector

TPM2 a numeric vector

TPM4 a numeric vector

TSC22D2 a numeric vector

TUBB2A a numeric vector

TUBB6 a numeric vector

TUFT1 a numeric vector

URI1 a numeric vector

USP48 a numeric vector

VCAN a numeric vector

VSIG4 a numeric vector

YWHAB a numeric vector

ZFP36 a numeric vector

ZFP36L2 a numeric vector

ZMYM1 a numeric vector

ZNF148 a numeric vector

ZNF79 a numeric vector

Details

4 studies are combined (group=4, 9, 12, and 16). The numbers 4, 9, 12 and 16 corresponds to the IDs from the original data of Ganzfried et al. (2013).

Source

Ganzfried BF et al. (2013), Curated ovarian data: clinically annotated data for the ovarian cancer transcriptome, Database, Article ID bat013, doi:10.1093/database/bat013.

References

Ganzfried BF et al. (2013), Curated ovarian data: clinically annotated data for the ovarian cancer transcriptome, Database, Article ID bat013, doi:10.1093/database/bat013.

Examples

```
data(dataOvarian1)
######## univariate Cox ##########
t.event=dataOvarian1$t.event
event=dataOvarian1$event
X.mat=dataOvarian1[,-c(1,2,3,4)] ## gene expression
Symbol=colnames(dataOvarian1)[-c(1,2,3,4)] ## gene symbol

p=ncol(X.mat)
P_value=coef=NULL
for(j in 1:p){
  res=summary(coxph(Surv(t.event,event)~X.mat[,j]))$coefficients
  P_value=c(P_value,res[5])
```

```
  coef=c(coef,res[1])
}
data.frame( gene=Symbol[order(P_value)], P=P_value[order(P_value)],
coef=round(coef[order(P_value)],3) )
```

`dataOvarian2` *Data on time-to-death and 128 gene expressions for 912 ovarian cancer patients from 4 independent studies.*

Description

Meta-analytic data containing 128 gene expressions and time-to-death information for ovarian cancer patients. The data include time-to-death, residual tumour size (>=1cm> vs. <1cm), and associated 128 gene expressions. The dataset is a subset of the curated ovarian data of Ganzfried et al (2013). We prepared the dataset by using "patientselection.config" in "Curated ovarian data" around October 2016.

Usage

```
data("dataOvarian2")
```

Format

A data frame with 912 observations on the following 132 variables.

`t.death` : time to death in days

`death` : death indicator (1=death, 0=alive)

`group` : study ID; group=4, 9, 12, or 16

`debulk` : residual tumour size (>=1cm> vs. <1cm)

`ANKRD27` a numeric vector

`AP3S1` a numeric vector

`APMAP` a numeric vector

`ARHGAP28` a numeric vector

`ASAP1` a numeric vector

`ASAP3` a numeric vector

`ASB7` a numeric vector

`B4GALT5` a numeric vector

`BYSL` a numeric vector

`C1QTNF3` a numeric vector

`CASP8` a numeric vector

`CCL18` a numeric vector

`CD79A` a numeric vector

`CDK19` a numeric vector

CLIC4 a numeric vector

COL11A1 a numeric vector

COL16A1 a numeric vector

COL3A1 a numeric vector

COL5A1 a numeric vector

COL5A2 a numeric vector

COMP a numeric vector

COX7A2P2 a numeric vector

CPNE1 a numeric vector

CRISPLD2 a numeric vector

CRYAB a numeric vector

CTNNBL1 a numeric vector

CXCL12 a numeric vector

CXCL9 a numeric vector

CYBRD1 a numeric vector

CYR61 a numeric vector

CYTH3 a numeric vector

DDX27 a numeric vector

DLGAP4 a numeric vector

DNAJC13 a numeric vector

DYNLRB1 a numeric vector

EFNB2 a numeric vector

EIF3K a numeric vector

ELN a numeric vector

EMP1 a numeric vector

ENPP1 a numeric vector

FABP4 a numeric vector

FAP a numeric vector

FBL a numeric vector

FGF1 a numeric vector

FOXN3 a numeric vector

FSTL1 a numeric vector

GABRG3 a numeric vector

GAS1 a numeric vector

GFRA1 a numeric vector

GJC1 a numeric vector

GPATCH1 a numeric vector

GZMB a numeric vector

HLA.DOB a numeric vector

HOXA5 a numeric vector

HP1BP3 a numeric vector

HSD17B6 a numeric vector

IL2RG a numeric vector

INHBA a numeric vector

ITGB1 a numeric vector

ITPKC a numeric vector

JAM2 a numeric vector

JUN a numeric vector

KCNH4 a numeric vector

KDELC1 a numeric vector

KIAA0355 a numeric vector

KIN a numeric vector

LEP a numeric vector

LOX a numeric vector

LPL a numeric vector

LSM14A a numeric vector

LUM a numeric vector

LUZP1 a numeric vector

MAPRE1 a numeric vector

MCL1 a numeric vector

MEOX2 a numeric vector

MMP12 a numeric vector

N4BP2L2 a numeric vector

NCOA3 a numeric vector

NCOA6 a numeric vector

NOTCH2NL a numeric vector

NR1H3 a numeric vector

NUAK1 a numeric vector

OAT a numeric vector

OMD a numeric vector

PAK4 a numeric vector

PCDH9 a numeric vector

PDP1 a numeric vector

PDPN a numeric vector

PHF20 a numeric vector
PLXNA1 a numeric vector
PSMC4 a numeric vector
PSMD8 a numeric vector
RAB13 a numeric vector
RAI14 a numeric vector
RARRES1 a numeric vector
RBM39 a numeric vector
RECQL a numeric vector
RIN2 a numeric vector
RND3 a numeric vector
RPS16 a numeric vector
SACS a numeric vector
SH3PXD2A a numeric vector
SKI a numeric vector
SLAMF7 a numeric vector
SLC37A4 a numeric vector
SMG5 a numeric vector
SOCS5 a numeric vector
SPARC a numeric vector
SSR4 a numeric vector
STAU1 a numeric vector
SUPT5H a numeric vector
TBCB a numeric vector
TBCC a numeric vector
TEAD1 a numeric vector
TESK1 a numeric vector
TIMP3 a numeric vector
TJP1 a numeric vector
TP53BP2 a numeric vector
TSPAN9 a numeric vector
TTI1 a numeric vector
TUBB2A a numeric vector
TUBB6 a numeric vector
URI1 a numeric vector
USP48 a numeric vector
YWHAB a numeric vector
ZFP36 a numeric vector
ZFP36L2 a numeric vector
ZNF148 a numeric vector

Details

4 studies are combined (group=4, 9, 12, and 16). The numbers 4, 9, 12 and 16 corresponds to the IDs from the original data of Ganzfried et al. (2013).

Source

Ganzfried BF et al. (2013), Curated ovarian data: clinically annotated data for the ovarian cancer transcriptome, Database, Article ID bat013, doi:10.1093/database/bat013.

References

Ganzfried BF et al. (2013), Curated ovarian data: clinically annotated data for the ovarian cancer transcriptome, Database, Article ID bat013, doi:10.1093/database/bat013.

Examples

```
data(dataOvarian2)
######## univariate Cox ##########
t.death=dataOvarian2$t.death
death=dataOvarian2$death
X.mat=dataOvarian2[,-c(1,2,3,4)] ## gene expression
Symbol=colnames(dataOvarian2)[-c(1,2,3,4)] ## gene symbol

p=ncol(X.mat)
P_value=coef=NULL
for(j in 1:p){
  res=summary(coxph(Surv(t.death,death)~X.mat[,j]))$coefficients
  P_value=c(P_value,res[5])
  coef=c(coef,res[1])
}
data.frame( gene=Symbol[order(P_value)], P=P_value[order(P_value)],
coef=round(coef[order(P_value)],3) )
```

F.KM *Prediction of death using the Kaplan-Meier estimator*

Description

Dynamic prediction of death using using the Kaplan-Meier estimator. Probability of death between t and t+w is calculated. The prediction probability is F(t,t+w)=1-S(t+w)/S(t), where S is the Kaplan-Meier estimator.

Usage

```
F.KM(time, widths, t.death, death)
```

Arguments

time	prediction time (=t)
widths	length of window (=w)
t.death	a vector object for overall survival (OS), i.e., time-to-death
death	a vector object for death indicator(=1 if death; =0 if not death)

Details

Prediction probability of death is calculated without covariates.

Value

time	t
widths	w
F	F(t,t+w)

Author(s)

Takeshi Emura

References

Emura T, Nakatochi M, Matsui S, Michimae H, Rondeau V (2018), Personalized dynamic prediction of death according to tumour progression and high-dimensional genetic factors: meta-analysis with a joint model, Stat Methods Med Res 27(9):2842-58

Examples

```
time=1
widths=c(0,0.5,1,1.5,2)
t.death=c(0.5,1,1.5,2,2.5,3)
death=c(1,1,1,1,1,1)
F.KM(time=time,width=widths,t.death=t.death,death=death)
```

F.prediction *Dynamic prediction of death*

Description

Dynamic prediction of death using a joint frailty-copula model. Probability of death between t and t+w is calculated given a tumour progression time X and covariates Z1 and Z2. If X<=t, the prediction probability is F(t,t+w|X=x, Z1, Z2). If X>t, the prediction probability is F(t,t+w|X>t, Z1, Z2). This function is a simpler version of F.windows. The guide for using this function shall be explained by Emura et al. (2019).

Usage

```
F.prediction(time, widths, X, Z1, Z2, beta1, beta2, eta, theta, alpha,
 g, h, xi1, xi3, Fplot = TRUE)
```

Arguments

time	prediction time (=t)
widths	length of window (=w)
X	time of tumour progression; if tumour progression does not occur before time t, one can set an arbitrary value X greater than t
Z1	a vector of covariates for progression
Z2	a vector of covariates for death
beta1	a vector of regression coefficients for progression
beta2	a vector of regression coefficients for death
eta	frailty variance
theta	copula parameter
alpha	parameter related to frailty; usually alpha=1
g	parameters related to the baseline hazard for progression
h	parameters related to the baseline hazard for death
xi1	lower bound for time-to-event
xi3	upper bound for time-to-death
Fplot	if FALSE, the plot is not shown

Details

Predicted probability of death is calculated given the event status (X<=t or X>t) and covariates (Z1 and Z2).

Value

time	t
widths	w
X	X
F	F(t,t+w|X=x, Z1, Z2) or F(t,t+w|X>t, Z1, Z2)

Author(s)

Takeshi Emura

References

Emura T, Nakatochi M, Matsui S, Michimae H, Rondeau V (2018), Personalized dynamic prediction of death according to tumour progression and high-dimensional genetic factors: meta-analysis with a joint model, Stat Methods Med Res 27(9):2842-58

Emura T, Michimae H, Matsui S (2019-), A clinician's guide for dynamic risk prediction of death using an R package joint.Cox, submitted for publication.

Examples

```
w=c(0,0.5,1,1.5,2)
par(mfrow=c(1,2))
F.prediction(time=1,X=0.8,widths=w,Z1=1,Z2=1,beta1=1,beta2=1,eta=0.5,theta=8,
         alpha=1,g=rep(1,5),h=rep(1,5),xi1=0,xi3=3)
F.prediction(time=1,X=1.5,widths=w,Z1=1,Z2=1,beta1=1,beta2=1,eta=0.5,theta=8,
         alpha=1,g=rep(1,5),h=rep(1,5),xi1=0,xi3=3)
```

`F.window` *Dynamic prediction of death under the joint frailty-copula model*

Description

Dynamic prediction of death using a joint frailty-copula model. Probability of death between t and t+w is calculated given a tumour progression time X and covariates Z1 and Z2. If X<=t, the prediction probability is F(t,t+w|X=x, Z1, Z2). If X>t, the prediction probability is F(t,t+w|X>t, Z1, Z2).

Usage

```
F.window(time, width, X, Z1, Z2, beta1, beta2, eta, theta, alpha,
 g, h, xi1, xi3, Fplot = TRUE)
```

Arguments

`time`	prediction time (=t)
`width`	length of window (=w)
`X`	time of tumour progression < time
`Z1`	a vector of covariates for progression
`Z2`	a vector of covariates for death
`beta1`	a vector of regression coefficients for progression
`beta2`	a vector of regression coefficients for death
`eta`	frailty variance
`theta`	copula parameter
`alpha`	parameter related to frailty; usually alpha=1
`g`	parameters related to the baseline hazard for progression
`h`	parameters related to the baseline hazard for death
`xi1`	lower bound for time to event
`xi3`	upper bound for time to death
`Fplot`	if FALSE, the plot is not shown

Details

Predicted probability of death is calculated given the event status (X<=t or X>t) and covariates (Z1 and Z2).

Value

time	t
width	w
X	X
F_event_at_X	F(t,t+w|X=x, Z1, Z2)
F_noevent	F(t,t+w|X>t, Z1, Z2)

Author(s)

Takeshi Emura

References

Emura T, Nakatochi M, Matsui S, Michimae H, Rondeau V (2018), Personalized dynamic prediction of death according to tumour progression and high-dimensional genetic factors: meta-analysis with a joint model, Stat Methods Med Res 27(9):2842-58

Examples

```
w=1
par(mfrow=c(1,2))
F.window(time=1,X=0.2,width=w,Z1=1,Z2=1,beta1=1,beta2=1,eta=0.5,theta=8,
         alpha=1,g=rep(1,5),h=rep(1,5),xi1=0,xi3=3)
F.window(time=1,X=0.8,width=w,Z1=1,Z2=1,beta1=1,beta2=1,eta=0.5,theta=8,
         alpha=1,g=rep(1,5),h=rep(1,5),xi1=0,xi3=3)
```

F.window.Weibull *Dynamic prediction of death under the joint frailty-copula model (the Weibull baseline hazard functions)*

Description

Dynamic prediction of death using a joint frailty-copula model. Probability of death between t and t+w is calculated given a tumour progression time X and covariates Z1 and Z2. If X<=t, the prediction probability is F(t,t+w|X=x, Z1, Z2). If X>t, the prediction probability is F(t,t+w|X>t, Z1, Z2).

Usage

```
F.window.Weibull(time, width, X, Z1, Z2, beta1, beta2, eta, theta, alpha,
                 scale1, shape1,scale2,shape2, xi1, xi3, Fplot = TRUE)
```

Arguments

time	prediction time (=t)
width	length of window (=w)
X	time of tumour progression < time
Z1	a vector of covariates for progression
Z2	a vector of covariates for death
beta1	a vector of regression coefficients for progression
beta2	a vector of regression coefficients for death
eta	frailty variance
theta	copula parameter
alpha	parameter related to frailty; usually alpha=1
scale1	scale parameter related to the baseline hazard for progression
shape1	shape parameter related to the baseline hazard for progression
scale2	scale parameter related to the baseline hazard for death
shape2	shape parameter related to the baseline hazard for death
xi1	lower bound for time to event
xi3	upper bound for time to death
Fplot	if FALSE, the plot is not shown

Details

Predicted probability of death is calculated given the event status (X<=t or X>t) and covariates (Z1 and Z2).

Value

time	t
width	w
X	X
F_event_at_X	F(t,t+w|X=x, Z1, Z2)
F_noevent	F(t,t+w|X>t, Z1, Z2)

Author(s)

Sayaka Shinohara, Takeshi Emura

References

Emura T, Nakatochi M, Matsui S, Michimae H, Rondeau V (2018), Personalized dynamic prediction of death according to tumour progression and high-dimensional genetic factors: meta-analysis with a joint model, Stat Methods Med Res 27(9):2842-58

Examples

```
w=1
par(mfrow=c(1,2))
F.window.Weibull(time=1,X=0.2,width=w,Z1=1,Z2=1,beta1=1,beta2=1,eta=0.5,theta=8,
                 alpha=1,scale1=1,shape1=1,scale2=1,shape2=1,xi1=0,xi3=3)
F.window.Weibull(time=1,X=0.8,width=w,Z1=1,Z2=1,beta1=1,beta2=1,eta=0.5,theta=8,
                 alpha=1,scale1=1,shape1=1,scale2=1,shape2=1,xi1=0,xi3=3)
```

F.windows *Dynamic prediction of death under the joint frailty-copula model*

Description

Dynamic prediction of death using a joint frailty-copula model. Probability of death between t and t+w is calculated given a tumour progression time X and covariates Z1 and Z2. If X<=t, the prediction probability is F(t,t+w|X=x, Z1, Z2). If X>t, the prediction probability is F(t,t+w|X>t, Z1, Z2). This is a vector version of F.window.

Usage

```
F.windows(time, widths, X, Z1, Z2, beta1, beta2, eta, theta, alpha,
 g, h, xi1, xi3, Fplot = TRUE)
```

Arguments

time	prediction time (=t)
widths	length of window (=w)
X	time of tumour progression < time
Z1	a vector of covariates for progression
Z2	a vector of covariates for death
beta1	regression coefficients for progression
beta2	regression coefficients for death
eta	frailty variance
theta	copula parameter
alpha	parameter related to frailty; usually alpha=1
g	parameters related to the baseline hazard for progression
h	parameters related to the baseline hazard for death
xi1	lower bound for time to event
xi3	upper bound for time to death
Fplot	if FALSE, the plot is not shown

Details

Predicted probability of death is calculated given the event status (X<=t or X>t) and covariates (Z1 and Z2).

Value

time	t
widths	w
X	X
F_event_at_X	F(t,t+w|X=x, Z1, Z2)
F_noevent	F(t,t+w|X>t, Z1, Z2)

Author(s)

Takeshi Emura

References

Emura T, Nakatochi M, Matsui S, Michimae H, Rondeau V (2018), Personalized dynamic prediction of death according to tumour progression and high-dimensional genetic factors: meta-analysis with a joint model, Stat Methods Med Res 27(9):2842-58

Examples

```
w=c(0,0.5,1,1.5,2)
par(mfrow=c(1,2))
F.windows(time=1,X=0.2,widths=w,Z1=1,Z2=1,beta1=1,beta2=1,eta=0.5,theta=8,
         alpha=1,g=rep(1,5),h=rep(1,5),xi1=0,xi3=3)
F.windows(time=1,X=0.8,widths=w,Z1=1,Z2=1,beta1=1,beta2=1,eta=0.5,theta=8,
         alpha=1,g=rep(1,5),h=rep(1,5),xi1=0,xi3=3)
```

F.windows.Weibull *Dynamic prediction of death under the joint frailty-copula model (the Weibull baseline hazard functions)*

Description

Dynamic prediction of death using a joint frailty-copula model. Probability of death between t and t+w is calculated given a tumour progression time X and covariates Z1 and Z2. If X<=t, the prediction probability is F(t,t+w|X=x, Z1, Z2). If X>t, the prediction probability is F(t,t+w|X>t, Z1, Z2). This is a vector version of F.window.Weibull.

Usage

```
F.windows.Weibull(time, widths, X, Z1, Z2, beta1, beta2, eta, theta, alpha,
                  scale1, shape1,scale2,shape2, xi1, xi3, Fplot = TRUE)
```

Arguments

time	prediction time (=t)
widths	length of window (=w)
X	time of tumour progression < time
Z1	a vector of covariates for progression
Z2	a vector of covariates for death
beta1	a vector of regression coefficients for progression
beta2	a vector of regression coefficients for death
eta	frailty variance
theta	copula parameter
alpha	parameter related to frailty; usually alpha=1
scale1	scale parameter related to the baseline hazard for progression
shape1	shape parameter related to the baseline hazard for progression
scale2	scale parameter related to the baseline hazard for death
shape2	shape parameter related to the baseline hazard for death
xi1	lower bound for time to event
xi3	upper bound for time to death
Fplot	if FALSE, the plot is not shown

Details

Predicted probability of death is calculated given the event status (X<=t or X>t) and covariates (Z1 and Z2).

Value

time	t
widths	w
X	X
F_event_at_X	F(t,t+w|X=x, Z1, Z2)
F_noevent	F(t,t+w|X>t, Z1, Z2)

Author(s)

Sayaka Shinohara, Takeshi Emura

References

Emura T, Nakatochi M, Matsui S, Michimae H, Rondeau V (2018), Personalized dynamic prediction of death according to tumour progression and high-dimensional genetic factors: meta-analysis with a joint model, Stat Methods Med Res 27(9):2842-58

Examples

```
w=c(0,0.5,1,1.5,2)
par(mfrow=c(1,2))
F.windows.Weibull(time=1,X=0.2,widths=w,Z1=1,Z2=1,beta1=1,beta2=1,eta=0.5,theta=8,
                  alpha=1,scale1=1,shape1=1,scale2=1,shape2=1,xi1=0,xi3=3)
F.windows.Weibull(time=1,X=0.8,widths=w,Z1=1,Z2=1,beta1=1,beta2=1,eta=0.5,theta=8,
                  alpha=1,scale1=1,shape1=1,scale2=1,shape2=1,xi1=0,xi3=3)
```

I.spline *I-Spline function*

Description

Calculate I-Spline bases (5 bases) suggested in Emura et al. (2015).

Usage

```
I.spline(time, xi1, xi3)
```

Arguments

time	a vector of times
xi1	lower bound of times
xi3	upper bound of times

Details

The "time" argument is a vector satisfying the contraints xi1<=time<=xi3. Otherwise, error messages will be produced.

Value

NULL	I-Spline bases (5 bases) evaluated at "time".

Author(s)

Takeshi Emura

References

Emura T, Chen YH (2018). Analysis of Survival Data with Dependent Censoring, Copula-Based Approaches, JSS Research Series in Statistics, Springer, Singapore.

Supplementary Material to: Emura T, Nakatochi M, Murotani K, Rondeau V (2017), A joint frailty-copula model between tumour progression and death for meta-analysis, Stat Methods Med Res 26(6): 2649-66

Examples

```
I.spline(c(1,1.5,2,2.5,3),xi1=1,xi3=3)
```

`jointCox.indep.reg` *Penalized Likelihood Estimation under the Joint Cox Models Between Tumour Progression and Death for Meta-Analysis*

Description

Perform regression analyses under a joint Cox proportional hazards model between tumour progression and death for meta-analysis, which is proposed by Rondeau et al. (2015). The method is applicable for meta-analysis combining several studies or for cluster survival data.

Usage

```
jointCox.indep.reg(t.event, event, t.death, death, Z1, Z2, group, alpha = 1,
 kappa1 = c(seq(10, 1e+17, length = 30)), kappa2 = c(seq(10, 1e+17, length = 30)),
 LCV.plot = TRUE,Randomize_num = 10, Adj = 500,convergence.par=FALSE)
```

Arguments

`t.event`	a vector for time-to-tumour progression (TTP)
`event`	a vector for progression indicator (=1 if progression; =0 if not progression)
`t.death`	a vector for overall survival (OS), i.e., time-to-death
`death`	a vector for death indicator(=1 if death; =0 if not death)
`Z1`	a matrix for covariates associated with TTP; ncol(Z1)=the number of covariates
`Z2`	a matrix for covariates associated with OS; ncol(Z2)=the number of covariates
`group`	a vector for group identification numbers, like 1,2,3....
`alpha`	A value related to the frailty (e.g., alpha=0 or =1); alpha=1 is default
`kappa1`	a vector for candidate smoothing parameters
`kappa2`	a vector for candidate smoothing parameters
`LCV.plot`	Plot the LCV curves if "TRUE"
`Randomize_num`	The number of randomizations for the ititial p0
`Adj`	Numerical adjustment to prevent overflow; Adj=500 is recommended
`convergence.par`	If TRUE, the converged estimate, gradient, and Hessian matrix are given (log-transformed)

Details

We employ "nlm" routine to maximize the penalized likelihood function with the initial value described in Emura et al. (2015). If "nlm" does not converge, then we randomize the initial value by adding uniform random variables (Hu and Emura, 2015).

Value

count	Count for event occurences
beta1	Regression coefficient for Z1
beta2	Regression coefficient for Z2
eta	Frailty parameter (variance)
LCV1	Likelihood cross-validation for TTP
LCV2	Likelihood cross-validation for OS
g	M-spline coefficients for TTP
h	M-spline coefficients for OS
g_var	Variance of M-spline coefficients for TTP
h_var	Variance of M-spline coefficients for OS
convergence	convergence results for maximizing penalized likelihood
convergence.parameters	converged estimate, gradient, and Hessian matrix (log-transformed)

Error

"Error in integrate(func1, 0.001, 10, stop.on.error = FALSE):non-finite function value", an error occurring when the penalized likelihood is maximizad by "nlm". The error may frequently occur during the iterations for maximizing the penalized likelihood, but is not crucial (can simply be ignored).

Warning

"NA/Inf replaced by maximum positive value", an error occurring when the penalized likelihood is maximizad by "nlm". The error frequently occurs during the iterations for maximizing the penalized likelihood, but is not crucial (can simply be ignored).

Author(s)

Takeshi Emura

References

Rondeau V, Pignon JP, Michiels S (2015). A joint model for dependence between clustered times to tumour progression and deaths: A meta-analysis of chemotherapy in head and neck cancer. Stat Methods Med Res 24(6):711-729.

Hu YH, Emura T (2015), Maximum likelihood estimation for a special exponential family under random double-truncation, Computational Statist 30(4): 1199-1229

Examples

```
############## Reproduce the results of Emura et al. (2015) #############
data(dataOvarian)
t.event=dataOvarian$t.event
event=dataOvarian$event
t.death=dataOvarian$t.death
death=dataOvarian$death
Z1=dataOvarian$CXCL12
group=dataOvarian$group
alpha_given=0
kappa_grid=seq(10,1e+17,length=30)
set.seed(1)
#jointCox.indep.reg(t.event=t.event,event=event,t.death=t.death,death=death,
#                 Z1=Z1,Z2=Z1,group=group,alpha=alpha_given,
#                 kappa1=kappa_grid,kappa2=kappa_grid,LCV.plot=TRUE,Adj=500)
```

`jointCox.reg` *Penalized Likelihood Estimation under the Joint Cox Models Between Tumour Progression and Death for Meta-Analysis*

Description

Perform regression analyses under a copula-based joint Cox proportional hazards model between tumour progression and death for meta-analysis, which is proposed by Emura et al. (2017). The methodological details can be found in Emura et al. (2019). The method is applicable for meta-analysis combining several studies or for cluster survival data.

Usage

```
jointCox.reg(t.event, event, t.death, death, Z1, Z2, group, alpha = 1,
 kappa1 = c(seq(10, 1e+17, length = 30)),kappa2 = c(seq(10, 1e+17, length = 30)),
 LCV.plot = TRUE, Randomize_num = 10,
 Adj = 500,convergence.par=FALSE)
```

Arguments

`t.event`	a vector for time-to-tumour progression (TTP)
`event`	a vector for progression indicator (=1 if progression; =0 if not progression)
`t.death`	a vector for overall survival (OS), i.e., time-to-death
`death`	a vector for death indicator(=1 if death; =0 if not death)
`Z1`	a matrix for covariates associated with TTP; ncol(Z1)=the number of covariates
`Z2`	a matrix for covariates associated with OS; ncol(Z2)=the number of covariates
`group`	a vector for group identification numbers, like 1,2,3....
`alpha`	A value related to the frailty (e.g., alpha=0 or =1); alpha=1 is default

kappa1	a vector for candidate smoothing parameters
kappa2	a vector for candidate smoothing parameters
LCV.plot	Plot the LCV curves if "TRUE"
Randomize_num	The number of randomizations for the ititial p0
Adj	Numerical adjustment to prevent overflow; Adj=500 is recommended
convergence.par	If TRUE, the converged estimate, gradient, and Hessian matrix are given (log-transformed)

Details

We employ "nlm" routine to maximize the penalized likelihood function with the initial value described in Emura et al. (2017). If "nlm" does not converge, then we randomize the initial value by adding uniform random variables (Hu and Emura, 2015).

Value

count	Count for event occurences
beta1	Regression coefficient for Z1
beta2	Regression coefficient for Z2
eta	Frailty parameter (variance)
theta	Copula parameter under the Clayton copula
tau	Kendall's tau corresponding to the copula parameter
LCV1	Likelihood cross-validation for TTP
LCV2	Likelihood cross-validation for OS
g	M-spline coefficients for TTP
h	M-spline coefficients for OS
g_var	Variance of M-spline coefficients for TTP
h_var	Variance of M-spline coefficients for OS
convergence	convergence results for maximizing penalized likelihood
convergence.parameters	converged estimate, gradient, and Hessian matrix (log-transformed)

Error

"Error in integrate(func1, 0.001, 10, stop.on.error = FALSE):non-finite function value", an error occurring when the penalized likelihood is maximizad by "nlm". The error may frequently occur during the iterations for maximizing the penalized likelihood, but is not crucial (can simply be ignored).

Warning

"NA/Inf replaced by maximum positive value", an error occurring when the penalized likelihood is maximizad by "nlm". The error frequently occurs during the iterations for maximizing the penalized likelihood, but is not crucial (can simply be ignored).

Author(s)

Takeshi Emura

References

Emura T, Nakatochi M, Murotani K, Rondeau V (2017), A joint frailty-copula model between tumour progression and death for meta-analysis, Stat Methods Med Res 26(6): 2649-66

Emura T, Matsui S, Rondeau V (2019), Survival Analysis with Correlated Endpoints; Joint Frailty-Copula Models, JSS Research Series in Statistics, Springer

Hu YH, Emura T (2015), Maximum likelihood estimation for a special exponential family under random double-truncation, Computational Stat 30 (4): 1199-1229

Examples

```
############## Reproduce the results of Emura et al. (2017) #############
data(data0varian)
t.event=data0varian$t.event
event=data0varian$event
t.death=data0varian$t.death
death=data0varian$death
Z1=data0varian$CXCL12
group=data0varian$group
alpha_given=0
kappa_grid=seq(10,1e+17,length=30)
set.seed(1)
#jointCox.reg(t.event=t.event,event=event,t.death=t.death,death=death,
#                 Z1=Z1,Z2=Z1,group=group,alpha=alpha_given,
#                 kappa1=kappa_grid,kappa2=kappa_grid,LCV.plot=TRUE,Adj=500)
```

`jointCox.reg1` *Penalized Likelihood Estimation under the Joint Cox Models Between Tumour Progression and Death for Meta-Analysis; Extension1*

Description

Perform regression analyses under a copula-based joint Cox proportional hazards model between tumour progression and death for meta-analysis, which is proposed by Emura et al. (201x). The method extends the joint frailty copula model of Emura et al. (2017). The method is applicable for meta-analysis combining several studies or for cluster survival data.

Usage

```
jointCox.reg1(t.event, event, t.death, death, Z1, Z2, Z12, group, alpha = 1,
 kappa1 = c(seq(10, 1e+17, length = 30)),kappa2 = c(seq(10, 1e+17, length = 30)),
 LCV.plot = TRUE, Randomize_num = 10,
 Adj = 500,convergence.par=FALSE)
```

Arguments

t.event	a vector for time-to-tumour progression (TTP)
event	a vector for progression indicator (=1 if progression; =0 if not progression)
t.death	a vector for overall survival (OS), i.e., time-to-death
death	a vector for death indicator(=1 if death; =0 if not death)
Z1	a matrix for covariates associated with TTP; ncol(Z1)=the number of covariates
Z2	a matrix for covariates associated with OS; ncol(Z2)=the number of covariates
Z12	a matrix for covariates associated with copula; ncol(Z12)=the number of covariates
group	a vector for group identification numbers, like 1,2,3....
alpha	A value related to the frailty (e.g., alpha=0 or =1); alpha=1 is default
kappa1	a vector for candidate smoothing parameters
kappa2	a vector for candidate smoothing parameters
LCV.plot	Plot the LCV curves if "TRUE"
Randomize_num	The number of randomizations for the ititial p0
Adj	Numerical adjustment to prevent overflow; Adj=500 is recommended
convergence.par	If TRUE, the converged estimate, gradient, and Hessian matrix are given (log-transformed)

Details

We employ "nlm" routine to maximize the penalized likelihood function with the initial value described in Emura et al. (2017). If "nlm" does not converge, then we randomize the initial value by adding uniform random variables (Hu and Emura, 2015).

Value

count	Count for event occurences
beta1	Regression coefficient for Z1
beta2	Regression coefficient for Z2
eta	Frailty parameter (variance)
theta	Baseline copula parameter under the Clayton copula
tau	Kendall's tau corresponding to the baseline copula parameter
beta12	Regression coefficient for a copula parameter
LCV1	Likelihood cross-validation for TTP
LCV2	Likelihood cross-validation for OS
g	M-spline coefficients for TTP
h	M-spline coefficients for OS
g_var	Variance of M-spline coefficients for TTP
h_var	Variance of M-spline coefficients for OS
convergence	convergence results for maximizing penalized likelihood
convergence.parameters	converged estimate, gradient, and Hessian matrix (log-transformed)

Error

"Error in integrate(func1, 0.001, 10, stop.on.error = FALSE):non-finite function value", an error occurring when the penalized likelihood is maximizad by "nlm". The error may frequently occur during the iterations for maximizing the penalized likelihood, but is not crucial (can simply be ignored).

Warning

"NA/Inf replaced by maximum positive value", an error occurring when the penalized likelihood is maximizad by "nlm". The error frequently occurs during the iterations for maximizing the penalized likelihood, but is not crucial (can simply be ignored).

Author(s)

Takeshi Emura

References

Emura T, Rondeau V (201x), Kendalls tau for individual-level surrogacy for failure time endpoints in meta-analysis (in preparation)

Emura T, Nakatochi M, Murotani K, Rondeau V (2017), A joint frailty-copula model between tumour progression and death for meta-analysis, Stat Methods Med Res 26(6): 2649-66

Hu YH, Emura T (2015), Maximum likelihood estimation for a special exponential family under random double-truncation, Computational Stat 30 (4): 1199-1229

Examples

```
##
```

---

jointCox.Weibull.reg *Weibull-based Likelihood Estimation under the Joint Cox Models Between Tumour Progression and Death for Meta-Analysis*

Description

Perform regression analyses under a copula-based joint Cox proportional hazards model between tumour progression and death for meta-analysis, which is proposed by Wu et al. (2019-).

Usage

```
jointCox.Weibull.reg(t.event, event, t.death, death, Z1, Z2, group, alpha = 1,
 Randomize_num = 10,Adj = 500,convergence.par=FALSE)
```

Arguments

t.event	a vector for time-to-tumour progression (TTP)
event	a vector for progression indicator (=1 if progression; =0 if not progression)
t.death	a vector for overall survival (OS), i.e., time-to-death
death	a vector for death indicator(=1 if death; =0 if not death)
Z1	a matrix for covariates associated with TTP; ncol(Z1)=the number of covariates
Z2	a matrix for covariates associated with OS; ncol(Z2)=the number of covariates
group	a vector for group identification numbers, like 1,2,3....
alpha	A value related to the frailty (e.g., alpha=0 or =1); alpha=1 is default
Randomize_num	The number of randomizations for the ititial p0
Adj	Numerical adjustment to prevent overflow; Adj=500 is recommended
convergence.par	If TRUE, the converged estimate, gradient, and Hessian matrix are given (log-transformed)

Details

We employ "nlm" routine to maximize the penalized likelihood function with the initial value described in Emura et al. (2017). If "nlm" does not converge, then we randomize the initial value by adding uniform random variables (Hu and Emura, 2015).

Value

count	Count for event occurences
beta1	Regression coefficient for Z1
beta2	Regression coefficient for Z2
eta	Frailty parameter (variance)
theta	Copula parameter under the Clayton copula
tau	Kendall's tau corresponding to the copula parameter
convergence	convergence results for maximizing penalized likelihood
convergence.parameters	converged estimate, gradient, and Hessian matrix (log-transformed)

Error

"Error in integrate(func1, 0.001, 10, stop.on.error = FALSE):non-finite function value", an error occurring when the penalized likelihood is maximizad by "nlm". The error may frequently occur during the iterations for maximizing the penalized likelihood, but is not crucial (can simply be ignored).

Warning

"NA/Inf replaced by maximum positive value", an error occurring when the penalized likelihood is maximizad by "nlm". The error frequently occurs during the iterations for maximizing the penalized likelihood, but is not crucial (can simply be ignored).

Author(s)

Takeshi Emura

References

Emura T, Nakatochi M, Murotani K, Rondeau V (2017), A joint frailty-copula model between tumour progression and death for meta-analysis, Stat Methods Med Res 26(6): 2649-66

Hu YH, Emura T (2015), Maximum likelihood estimation for a special exponential family under random double-truncation, Computational Stat 30 (4): 1199-1229

Examples

```
data(dataOvarian)
t.event=dataOvarian$t.event
event=dataOvarian$event
t.death=dataOvarian$t.death
death=dataOvarian$death
Z1=dataOvarian$CXCL12
group=dataOvarian$group
alpha_given=0
kappa_grid=seq(10,1e+17,length=30)

t.event[t.event == 0] = 1 ## data can not be zero ##
t.death[t.death == 0] = 1 ## data can not be zero ##

#set.seed(1)
#jointCox.Weibull.reg(t.event=t.event,event=event,t.death=t.death,death=death,
#                 Z1=Z1,Z2=Z1,group=group,alpha=alpha_given,Adj=500)
```

`M.spline` *M-Spline function*

Description

Calculate M-Spline bases (5 bases) suggested in Emura et al. (2015).

Usage

```
M.spline(time, xi1, xi3)
```

Arguments

`time`	a vector of times
`xi1`	lower bound of times
`xi3`	upper bound of times

Details

The "time" argument is a vector satisfying the contraints xi1<=time<=xi3. Otherwise, error messages will be produced.

Value

NULL	M-Spline bases (5 bases) evaluated at "time".

Author(s)

Takeshi Emura

References

Emura T, Chen YH (2018). Analysis of Survival Data with Dependent Censoring, Copula-Based Approaches, JSS Research Series in Statistics, Springer, Singapore.

Supplementary Material to: Emura T, Nakatochi M, Murotani K, Rondeau V (2017), A joint frailty-copula model between tumour progression and death for meta-analysis, Stat Methods Med Res 26(6): 2649-66

Examples

```
M.spline(c(1,1.5,2,2.5,3),xi1=1,xi3=3)
```

---

splineCox.reg *Fitting the Cox model with penalized splines using univariate survival data*

Description

Fitting the Cox model when the baseline hazard function is approximated by splines.

Usage

```
splineCox.reg(t.event, event, Z, xi1 = min(t.event), xi3 = max(t.event),
kappa = c(seq(10, 1e+17, length = 30)), LCV.plot = TRUE,p0=rep(0,5+p))
```

Arguments

t.event	a vector for time-to-event
event	a vector for event indicator (=1 event; =0 censoring)
Z	a matrix for covariates; nrow(Z)=sample size, ncol(Z)=the number of covariates
xi1	lower bound for the hazard function; the default is min(t.event)
xi3	upper bound for the hazard function; the default is max(t.event)
kappa	a vector for candidate smoothing parameters in LCV. Only positive values are allowed. Values too close to zero may yeild errors (see below).

LCV.plot	Plot the LCV curves if "TRUE"
p0	Initial values to maximize the penalized likelihood (5+p parameters; five M-spline coefficients and p regression coefficients)

Details

The definition of LCV is given in Emura et al. (2019). This is a subroutine used to compute the optimal smoothing parameter (kappa) in the penalized likelihood of Emura et al. (2017). The error message "Error in nlm(l.func, p = rep(0, 5 + p), hessian = TRUE):non-finite value supplied by 'nlm'" may imply that some candidate parameters for kappa are too close to zero; please exclude such values from kappa.

Value

beta	Regression coefficient for Z
h	M-spline coefficients
h_var	Variance of M-spline coefficients
kappa	smoothing parameter at the optimal LCV
DF	degree of freedom at the optimal LCV
LCV	the optimal LCV(=logL-DF)

Author(s)

Takeshi Emura

References

Emura T, Nakatochi M, Murotani K, Rondeau V (2017), A joint frailty-copula model between tumour progression and death for meta-analysis, Stat Methods Med Res 26(6): 2649-66

Emura T, Matsui S, Rondeau V (2019), Survival Analysis with Correlated Endpoint: Joint Frailty-copula models, JSS Research Series in Statistics, Springer

Emura T, Shih JH (2019-), R programs for semiparametric Cox regression with cubic M-spline (in preparation)

Examples

```
data(data0varian)
t.event=data0varian$t.event
event=data0varian$event
t.death=data0varian$t.death
death=data0varian$death
Z=data0varian$CXCL12
#splineCox.reg(t.event,event,Z,kappa=c(seq(10,1e+17,length=30)))
```

`Weibull.simu` *Simulating data from the Weibull joint frailty-copula model*

Description

Simulating data from the Weibull joint frailty-copula model.

Usage

```
Weibull.simu(G,N,scale1,scale2,shape1,shape2,beta1,beta2,
 eta,theta,alpha,beta12=0,C.max,Z.dist=runif,...)
```

Arguments

`G`	The number of studies or groups
`N`	The number of patients within each study
`scale1`	scale parameter related to the baseline hazard for progression
`scale2`	scale parameter related to the baseline hazard for death
`shape1`	shape parameter related to the baseline hazard for progression
`shape2`	shape parameter related to the baseline hazard for death
`beta1`	regression coefficients for progression
`beta2`	regression coefficients for death
`eta`	frailty variance
`theta`	copula parameter
`alpha`	parameter related to frailty; usually alpha=1
`beta12`	regression coefficients for copula
`C.max`	the upper bound for the censoring distribution
`Z.dist`	the distribution of a covariate Z
`...`	parameters for Z.dist

Details

To be discussed in the paper of Emura et al. (2019).

Value

`X`	: time to event
`D`	: time to death
`C`	: independent censoring time
`t.event`	: time to event (censored)
`event`	: event indicator (1=event, 0=no event)

t.death	: time to death (censored)
death	: death indicator (1=death, 0=alive)
group	: study ID (1~G)
Z	: covariate

Author(s)

Takeshi Emura

References

Wu BH, Michimae H, Emura T (2019), Meta-analysis of individual patient data with semi-competing risks under the Weibull joint frailty-copula model, in revision.

Examples

```
Weibull.simu(G=5,N=2,scale1=1,scale2=1,shape1=1,shape2=1,
        beta1=1,beta2=1,eta=0.5,theta=2,alpha=1,C.max=5)

Weibull.simu(G=5,N=2,scale1=1,scale2=1,shape1=1,shape2=1,
        beta1=1,beta2=1,eta=0.5,theta=2,alpha=1,C.max=5,Z.dist=rbinom,size=1,prob=0.5)
```

Index