Package 'jmBIG'

November 3, 2026

Type Package

Title Joint Longitudinal and Survival Model for Big Data

Version 0.1.4

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Description Provides analysis tools for big data where the sample size is very large. It offers a suite of functions for fitting and predicting joint models, which allow for the simultaneous analysis of longitudinal and time-to-event data. This statistical methodology is particularly useful in medical research where there is often interest in understanding the relationship between a longitudinal biomarker and a clinical outcome, such as survival or disease progression. This can be particularly useful in a clinical setting where it is important to be able to predict how a patient's health status may change over time. Overall, this package provides a comprehensive set of tools for joint modeling of BIG data obtained as survival and longitudinal outcomes with both Bayesian and non-Bayesian approaches. Its versatility and flexibility make it a valuable resource for researchers in many different fields, particularly in the medical and health sciences.

Imports JMbayes2,joineRML,rstanarm,FastJM (>= 1.7.0),dplyr,nlme,survival,ggplot2

License GPL-3

Encoding UTF-8

LazyData true

Depends R (>= 2.10)

RoxygenNote 7.3.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-11-03 11:00:02 UTC

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`cisurvfitJMCS` *Bootstrapped CI using* `FastJM`

Description

Bootstrapped CI for predicted survival probability

Usage

```
cisurvfitJMCS(object)
```

Arguments

`object`	a `survfitJMCS` object

Value

Bootstrap CI for the survival probability and other relevant information for predicted survival plot

Examples

```
##
library(survival)
library(dplyr)
jmcs1<-jmcsBig(dtlong=data.frame(long2),
dtsurv = data.frame(surv2),
longm=y~ x7+visit,
survm=Surv(time,status)~x1+visit,
rd= ~ visit|id,
samplesize=200,id='id')
mod2<-jmcs1
P2<-survfitJMCS(model<-mod2,ids<-c(5),u<-seq(surv2[surv2$id==5,]$time,
surv2[surv2$id==5,]$time+10,0.2),obs.time='time')
bootci<-cisurvfitJMCS(P2)
print(bootci)
##
```

`jmbayesBig` *Joint model for BIG data using JMbayes2*

Description

function for joint model in BIG DATA using `JMbayes2`

Usage

```
jmbayesBig(
  dtlong,
  dtsurv,
  longm,
  survm,
  samplesize = 50,
  rd,
  timeVar,
  nchain = 1,
  id,
  niter = 2000,
  nburnin = 1000
)
```

Arguments

`dtlong`	longitudinal dataset, which contains id,visit time,longitudinal measurements along with various covariates
`dtsurv`	survival dataset corresponding to the longitudinal dataset, with survival status and survival time

longm	fixed effect model for longitudinal response
survm	survival model
samplesize	sample size to divide the Big data
rd	random effect model part
timeVar	time variable in longitudinal model, included in the longitudinal data
nchain	number of chain for MCMC
id	name of id column in longitudinal dataset
niter	number of iteration for MCMC chain
nburnin	number of burnin sample for MCMC chain

Value

returns a list containing various output which are useful for prediction.

Author(s)

Atanu Bhattacharjee, Bhrigu Kumar Rajbongshi and Gajendra Kumar Vishwakarma

References

Rizopoulos, D., G. Papageorgiou, and P. Miranda Afonso. "JMbayes2: extended joint models for longitudinal and time-to-event data." R package version 0.2-4 (2022).

See Also

jmcsBig,jmstanBig,joinRMLBig

Examples

```
##
library(survival)
library(nlme)
library(dplyr)
fit5<-jmbayesBig(dtlong=long2,dtsurv = surv2,longm=y~ x7+visit,survm=Surv(time,status)~x1+visit,
rd= ~ visit|id,timeVar='visit',nchain=1,samplesize=200,id='id')
ydt<-long2%>%filter(id%in%c(900))
cdt<-surv2[,'id']%>%filter(id%in%c(900))
newdata<-full_join(ydt,cdt,by='id')
P2<-predJMbayes(model<-fit5,ids<-c(900),newdata=newdata,process = 'event')
plot(P2$p1[[1]])
##
```

jmcsBig *Joint model for BIG data using FastJM*

Description

function for joint model in BIG DATA using `FastJM`

Usage

```
jmcsBig(dtlong, dtsurv, longm, survm, samplesize = 50, rd, id)
```

Arguments

`dtlong`	longitudinal dataset, which contains id,visit time,longitudinal measurements along with various covariates
`dtsurv`	survival dataset corresponding to the longitudinal dataset, with survival status and survival time
`longm`	model for longitudinal response
`survm`	survival model
`samplesize`	sample size to divide the Big data
`rd`	random effect part
`id`	name of id column in longitudinal dataset

Value

returns a list containing various output which are useful for prediction.

Author(s)

Atanu Bhattacharjee, Bhrigu Kumar Rajbongshi and Gajendra Kumar Vishwakarma

References

Li, Shanpeng, et al. "Efficient Algorithms and Implementation of a Semiparametric Joint Model for Longitudinal and Competing Risk Data: With Applications to Massive Biobank Data." Computational and Mathematical Methods in Medicine 2022 (2022).

See Also

jmbayesBig,jmstanBig,joinRMLBig

Examples

```
##
library(survival)
library(dplyr)
fit2<-jmcsBig(dtlong=data.frame(long2),dtsurv = data.frame(surv2),
longm=y~ x7+visit,survm=Surv(time,status)~x1+visit,rd= ~ visit|id,samplesize=200,id='id')
print(fit2)
##
```

`jmstanBig` *Joint model for BIG data using rstanarm*

Description

function for joint model in BIG DATA using `rstanarm` package

Usage

```
jmstanBig(
  dtlong,
  dtsurv,
  longm,
  survm,
  samplesize = 50,
  time_var,
  id,
  nchain = 1,
  refresh = 2000
)
```

Arguments

`dtlong`	longitudinal dataset, which contains id,visit time,longitudinal measurements along with various covariates
`dtsurv`	survival dataset corresponding to the longitudinal dataset, with survival status and survival time
`longm`	model for longitudinal response
`survm`	survival model
`samplesize`	sample size to divide the Big data
`time_var`	time variable in longitudinal model, included in the longitudinal data
`id`	name of id column in longitudinal dataset
`nchain`	number of chain for MCMC
`refresh`	refresh rate for MCMC chain

Value

returns a list containing various output which are useful for prediction.

Author(s)

Atanu Bhattacharjee, Bhrigu Kumar Rajbongshi and Gajendra Kumar Vishwakarma

References

Goodrich, B., et al. "rstanarm: Bayesian applied regression modeling via Stan. R package version 2.17. 4." Online< http://mc-stan. org (2018).

See Also

jmbayesBig,jmcsBig,joinRMLBig

Examples

```
##
library(survival)
library(dplyr)
fit3<-jmstanBig(dtlong=long2,dtsurv = surv2,longm=y~ x7+visit+(1|id),
survm=Surv(time,status)~x1+visit,samplesize=200,time_var='visit',id='id')
P2<-postTraj(model<-fit3,m<-1,ids<-c(1,2,100))
pp1<-plot(P2$p1[[1]],plot_observed = TRUE)
pp2<-plot(P2$p1[[2]],plot_observed = TRUE)
pp3<-plot(P2$p1[[3]],plot_observed = TRUE)
##
```

---

joinRMLBig *Joint model for BIG data using joineRML*

Description

function for joint model in BIG DATA using `joineRML`

Usage

```
joinRMLBig(dtlong, dtsurv, longm, survm, samplesize = 50, rd, timeVar, id)
```

Arguments

dtlong	longitudinal dataset, which contains id,visit time,longitudinal measurements along with various covariates
dtsurv	survival dataset corresponding to the longitudinal dataset, with survival status and survival time
longm	model for longitudinal response
survm	survival model
samplesize	random effect part
rd	random effect part
timeVar	time variable in longitudinal model, included in the longitudinal data
id	name of id column in longitudinal dataset

Value

returns a list containing various output which are useful for prediction.

Author(s)

Atanu Bhattacharjee, Bhrigu Kumar Rajbongshi and Gajendra Kumar Vishwakarma

References

Hickey, Graeme L., et al. "joineRML: a joint model and software package for time-to-event and multivariate longitudinal outcomes." BMC medical research methodology 18 (2018): 1-14.

See Also

jmbayesBig,jmstanBig,jmcsBig

Examples

```
##
library(survival)
library(dplyr)
fit4<-joinRMLBig(dtlong=long2,dtsurv = surv2,longm=y~ x7+visit,survm=Surv(time,status)~x1+visit,
rd=~ visit|id,timeVar='visit',samplesize=200,id='id')
P2<-predJRML(model<-fit4,ids<-c(10),dtlong=long2,dtsurv=surv2)
pp1<-plot(P2$plong[[1]])
pp1<-plot(P2$psurv[[1]])
##
```

long2 *longitudinal data*

Description

A longitudinal dataset with single marker , with different numeric and categorical covariate

Usage

```
data(long2)
```

Format

a tibble of 13 columns and 5639 observations,

id id value for subjects

status survival status

time survival time

y longitudinal marker

visit visit time of longitudinal measurements

x1,x2,...,x7 different numeric and categorical variable

longsurv *longitudinal- survival dataset*

Description

A longitudinal dataset with single marker , with different numeric and categorical covariate

Usage

```
data(longsurv)
```

Format

a tibble of 13 columns and 5639 observations,

id id value for subjects

status survival status

time survival time

y longitudinal marker

visit visit time of longitudinal measurements

x1,x2,...,x7 different numeric and categorical variable

plot_cisurvfitJMCS *Plot for* cisurvfitJMCS *object*

Description

prediction of survival probability and longitudinal marker using FastJM for BIG data

Usage

```
plot_cisurvfitJMCS(object)
```

Arguments

object	fitted survfitJMCS object

Value

Plot for predicted survival probability

Examples

```
##
library(survival)
library(dplyr)
jmcs1<-jmcsBig(dtlong=data.frame(long2),
dtsurv = data.frame(surv2),
longm=y~ x7+visit,
survm=Surv(time,status)~x1+visit,
rd= ~ visit|id,
samplesize=200,id='id')
mod2<-jmcs1
P2<-survfitJMCS(model<-mod2,ids<-c(5),u<-seq(surv2[surv2$id==5,]$time,
surv2[surv2$id==5,]$time+10,0.2),obs.time='time')
P3<-cisurvfitJMCS(P2)
plot_cisurvfitJMCS(P3)
##
```

postSurvfit *Prediction using* rstanarm

Description

posterior survival probability estimates from rstanarm for BIG data

Usage

```
postSurvfit(model, ids, ...)
```

Arguments

model	fitted model
ids	value of id
...	other parameter option, see posterior_survfit

Value

list of predicted value for the given id

Examples

```
##
library(survival)
library(dplyr)
jmstan<-jmstanBig(dtlong=long2,
         dtsurv = surv2,
         longm=y~ x7+visit+(1|id),
         survm=Surv(time,status)~x1+visit,
         samplesize=200,
         time_var='visit',id='id')
mod1<-jmstan
P2<-postSurvfit(model<-mod1,ids<-c(1,2,210))
pp1<-plot(P2$p1[[1]])
pp1
pp2<-plot(P2$p1[[2]])
pp2
pp3<-plot(P2$p1[[3]])
pp3
 ##
```

---

postTraj *Prediction using* rstanarm

Description

prediction of the posterior trajectory for longitudinal marker while using rstanarm for Big data

Usage

```
postTraj(model, m, ids, ...)
```

Arguments

model	fitted model object
m	m for posterior_traj function
ids	value of id
...	other parameter option, see posterior_traj

Value

list of predicted values for the given id

Examples

```
##
library(survival)
library(dplyr)
fit6<-jmstanBig(dtlong=long2,dtsurv = surv2,longm=y~ x7+visit+(1|id),
         survm=Surv(time,status)~x1+visit,samplesize=200,time_var='visit',id='id')
P2<-postTraj(model<-fit6,m<-1,ids<-c(1,2,100))
pp1<-plot(P2$p1[[1]],plot_observed = TRUE)
pp2<-plot(P2$p1[[2]],plot_observed = TRUE)
pp3<-plot(P2$p1[[3]],plot_observed = TRUE)
##
```

---

predJMbayes *Prediction using* JMbayes2

Description

prediction of survival probability and longitudinal marker using `jmBayes2` for BIG data

Usage

```
predJMbayes(model, ids, process = "longitudinal", newdata, ...)
```

Arguments

`model`	fitted model object
`ids`	value of id
`process`	see `jm`
`newdata`	dataset having covariate information for the ids mentioned above.
`...`	other parameter options, see `predict.jm`

Value

list of predicted value for the given id

Examples

```
##
library(survival)
library(nlme)
library(dplyr)
jmcs1<-jmbayesBig(dtlong=long2,
dtsurv = surv2 ,
longm=y~ x7+visit,
survm=Surv(time,status)~x1+visit,
rd= ~ visit|id,
timeVar='visit',
nchain=1,
samplesize=200,
id='id')
mod3<-jmcs1
ydt<-long2%>%filter(id%in%c(900))
names(ydt)
cdt<-surv2[,'id']%>%filter(id%in%c(900))
names(cdt)
newdata<-full_join(ydt,cdt,by='id')
P2<-predJMbayes(model<-mod3,ids<-c(900),newdata=newdata,process = 'event')
plot(P2$p1[[1]])

##
```

---

predJRML *Prediction using* joineRML

Description

prediction of survival probability and longitudinal marker using joineRML for BIG data

Usage

```
predJRML(model, ids, dtlong, dtsurv, ...)
```

Arguments

model	fitted model object
ids	value of id
dtlong	longitudinal data
dtsurv	survival data
...	other parameter options, see dynSurv

Value

list of predicted values for the given id

Examples

```
##
library(survival)
library(dplyr)
jmcs1<-joinRMLBig(dtlong=long2,
dtsurv = surv2,
longm=y~ x7+visit,
survm=Surv(time,status)~x1+visit,
rd=~ visit|id,
timeVar='visit',
samplesize=200,
id='id')
mod4<-jmcs1
P2<-predJRML(model<-mod4,ids<-c(10),dtlong=long2,dtsurv=surv2)
plot(P2$plong[[1]])
plot(P2$psurv[[1]])
##
```

---

print.jmbayesBig *print.jmbayesBig*

Description

print method for class 'jmbayesBig'

Usage

```
## S3 method for class 'jmbayesBig'
print(x, ...)
```

Arguments

x	fitted object
...	others

Value

prints table containing various parameter estimates, SE, P- value for both survival and longitudinal submodel, if the model is bayesian it includes their credible interval too.

Examples

```
##
library(survival)
library(dplyr)

################################
mod3<-jmbayesBig(dtlong=long2,
dtsurv = surv2 ,
longm=y~ x7+visit,
survm=Surv(time,status)~x1+visit,
rd= ~ visit|id,
timeVar='visit',
nchain=1,
samplesize=200,
id='id')
print(mod3)
```

`print.jmcsBig` *print.jmcsBig*

Description

print method for class 'jmcsBig'

Usage

```
## S3 method for class 'jmcsBig'
print(x, ...)
```

Arguments

`x`	fitted object
`...`	others

Value

prints table containing various parameter estimates, SE, P- value for both survival and longitudinal submodel, if the model is bayesian it includes their credible interval too.

Examples

```
##
library(survival)
library(dplyr)
################################
mod2<-jmcsBig(dtlong=data.frame(long2),
dtsurv = data.frame(surv2),
longm=y~ x7+visit,
```

```
survm=Surv(time,status)~x1+visit,
rd= ~ visit|id,
samplesize=200,id='id')
print(mod2)
```

`print.jmstanBig` *print.jmstanBig*

Description

print method for class 'jmstanBig'

Usage

```
## S3 method for class 'jmstanBig'
print(x, ...)
```

Arguments

`x`	fitted object
`...`	others

Value

prints table containing various parameter estimates, SE, P- value for both survival and longitudinal submodel, if the model is bayesian it includes their credible interval too.

Examples

```
##
library(survival)
library(dplyr)
mod1<-jmstanBig(dtlong=long2,
         dtsurv = surv2,
         longm=y~ x7+visit+(1|id),
         survm=Surv(time,status)~x1+visit,
         samplesize=200,
         time_var='visit',id='id')
print(mod1)
```

print.joinRMLBig *print.joinRMLBig*

Description

print method for class 'joinRMLBig'

Usage

```
## S3 method for class 'joinRMLBig'
print(x, ...)
```

Arguments

x	fitted object
...	others

Value

prints table containing various parameter estimates, SE, P- value for both survival and longitudinal submodel, if the model is bayesian it includes their credible interval too.

Examples

```
##
library(survival)
library(dplyr)
mod4<-joinRMLBig(dtlong=long2,
dtsurv = surv2,
longm=y~ x7+visit,
survm=Surv(time,status)~x1+visit,
rd=~ visit|id,
timeVar='visit',
samplesize=200,
id='id')
print(mod4)
```

surv2 *survival data*

Description

A survival dataset related the long2 dataset, with different numeric and categorical covariate

Usage

```
data(surv2)
```

Format

a tibble of 13 columns and 1000 observations,

id id value for subjects

status survival status

time survival time

visit visit time of longitudinal measurements

x1,x2,...,x7 different numeric and categorical variable

---

survfitJMCS *Prediction using* FastJM

Description

prediction of survival probability using FastJM for BIG data

Usage

```
survfitJMCS(model, ids, u, method = "GH", obs.time)
```

Arguments

model	fitted model object
ids	value of id
u	see survfitJM
method	options are 'Laplace','GH'
obs.time	vector which represents time variable in the longitudinal data

Value

list of predicted value for the given id along with other information relevant for survival probability confidence plot

Examples

```
##
library(survival)
library(dplyr)
jmcs1<-jmcsBig(dtlong=data.frame(long2),
dtsurv = data.frame(surv2),
longm=y~ x7+visit,
survm=Surv(time,status)~x1+visit,
rd= ~ visit|id,
samplesize=200,id='id')
mod2<-jmcs1
P2<-survfitJMCS(model<-mod2,ids<-c(5),u<-seq(surv2[surv2$id==5,]$time,
surv2[surv2$id==5,]$time+10,0.2),obs.time='time')
print(P2)
##
```

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