Package ‘jmBIG’

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Type Package

Title Joint Longitudinal and Survival Model for Big Data

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Maintainer Atanu Bhattacharjee <atanustat@gmail.com>

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,dplyr,nlme,survival

License GPL-3

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Author Atanu Bhattacharjee [aut, cre, ctb], Bhrigu Kumar Rajbongshi [aut, ctb], Gajendra K Vishwakarma [aut, ctb]

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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

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))
nnewdata<-full_join(ydt,cdt,by='id')
P2<predJMbayes(model<-fit5,ids<-c(900),newdata=newdata,process = 'event')
ppl<plot(P2$p1[[1]])
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


See Also

jmcbayesBig,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')
P2<-survfitJMCS(model<-fit2,ids<-c(400),estimator = 'median')
pl<-plot(P2$p1[[1]],estimator="both",include.y = TRUE)
##
---

**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

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)
##
```

Description
function for joint model in BIG DATA using joineRML

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

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


See Also

jmbayesBig, jmstanBig, jmcsBig

Examples

```r
##
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
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),
surv2m=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
##
### 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
```r
##
library(survival)
library(dplyr)
fit6<-jmstanBig(dtlong=long2,dtsurv = surv2,longm=y~ x7+visit+(1|id),
surv=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)
##
```

---

### 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

```r
##
library(survival)
library(nlme)
library(dplyr)
jmcs1<-jmBayesBig(dtlong=long2,
dtsurv = surv2,
longm=~ 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')
pp1<-plot(P2$p1[[1]])
pp1
##
```

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

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)
pp1<-plot(P2$plong[[1]])
pp1<-plot(P2$psurv[[1]])
##

print

description

print

Usage

print(object, ...)

print
print.jmbayesBig

Arguments

object  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)
fit7<-jmstanBig(dtlong=long2,dtsurv = surv2,longm=y~ x7+visit+(1|id),
survm=Surv(time,status)-x1+visit,samplesize=200,time_var='visit',id='id')

fit8<-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')

fit9<-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')

fit10<-joinRMLBig(dtlong=long2,dtsurv = surv2,
longm=y~ x7+visit,survm=Surv(time,status)-x1+visit,
rd= ~ visit|id,timeVar='visit',samplesize=200,id='id')
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

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

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

Description

print.jmcsBig

Usage

```r
## S3 method for class 'jmcsBig'
print(object, digits = 3, ...)
```

Arguments

- `object`: object
- `digits`: used for round the numeric values after decimal
- `...`: 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

```r
##
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)
```

Description

print.jmstanBig

Usage

```r
## S3 method for class 'jmstanBig'
print(object, digits = 3, ...)
```

Arguments

- `object` object
- `digits` used for round the numeric values after decimal
- `...` 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

```r
##
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(mod4)

Description

print.joinRMLBig

Usage

## S3 method for class 'joinRMLBig'
print(object, digits = 4, ...)

Arguments

  object object
  digits used for round the numeric values after decimal
    ... 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

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    survfitJMCS

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

Usage
survfitJMCS(model, ids, estimator, conf.int = TRUE, include.y = FALSE)

Arguments
model  fitted model object
ids    value of id
estimator see survfitjmcs
conf.int see survfitjmcs
include.y see survfitjmcs

Value
list of predicted value for the given id
Examples

```r
##
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(400), estimator = 'median')
pp1 <- plot(P2$p1[[1]], estimator = "both", include.y = TRUE)
pp1
##
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