

Package ‘jmBIG’

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Type Package

Title Joint Longitudinal and Survival Model for Big Data

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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 JMbays2,joineRML,rstanarm,FastJM,dplyr,nlme,survival,ggplot2

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| | |
|---------------|-------------------------------------|
| cisurvfitJMCS | <i>Bootstrapped CI using FastJM</i> |
|---------------|-------------------------------------|

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, Bhriгу 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, Bhriku 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

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

Value

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

Author(s)

Atanu Bhattacharjee, Bhriku 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, Bhriгу 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]])
##
```

| | |
|-------------------------------|-------------------------|
| <code>print.jmbayesBig</code> | <i>print.jmbayesBig</i> |
|-------------------------------|-------------------------|

Description

print method for class 'jmbayesBig'

Usage

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

Arguments

| | |
|------------------|---------------|
| <code>x</code> | fitted object |
| <code>...</code> | 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 | <i>print.jmcsBig</i> |
|---------------|----------------------|

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 `survfitjmcs`

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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