Package ‘JMbdirect’

March 11, 2025

Type Package

Title Joint Model for Longitudinal and Multiple Time to Events Data

Version 0.1.0

Imports JMbayes2,joineRML,FastJM,rstanarm,dplyr,jmBIG

Maintainer Atanu Bhattacharjee <`atanustat@gmail.com`>

Description Provides model fitting, prediction, and plotting for joint models of longitudinal and multiple time-to-event data, including methods from Rizopoulos (2012) <doi:10.1201/b12208>. Useful for handling complex survival and longitudinal data in clinical research.

License GPL-3

Encoding UTF-8

LazyData true

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

RoxygenNote 7.3.2

Depends R (>= 2.10)

NeedsCompilation no

Repository CRAN

Date/Publication 2025-03-11 17:00:15 UTC

Contents

`bootciJMCS` *Function for bootstrapped confidence interval*

Description

Function for bootstrapped confidence interval

Usage

```
bootciJMCS(object, future_time)
```

Arguments

`object`	fitted model
`future_time`	time sequence at which estimates are required

Value

Returns bootstraped confidence interval for model fitted through FastJM

`jmbB` *Joint model for Bidirectional survival data using* `JMbayes2`

Description

The function fits joint model for survival data with two events. It utilizes the JMbayes2 package for obtaining the model parameter estimates.

Usage

```
jmbB(
  dtlong,
  dtsurv,
  longm,
  survm,
  rd,
  timeVar,
  id,
  samplesize = NULL,
  BIGdata = FALSE,
  niter = 200,
  nburnin = 100,
  nchain = 1
)
```

Arguments

`dtlong`	longitudinal data
`dtsurv`	survival data with two event status along with event time
`longm`	longitudinal model e.g. list(serBilir~drug * year,serBilir ~ drug * year)
`survm`	survival model e.g. list(Surv(years,status2)~drug,Surv(time_2,status_2)~drug+age)
`rd`	random effect component e.g. list(~yearlid,~yearlid)
`timeVar`	time variable
`id`	ID variable
`samplesize`	samplesize for bigdata
`BIGdata`	logical argument TRUE or FALSE
`niter`	number if iteration
`nburnin`	number of sample to burn
`nchain`	number of MCMC chain

Value

Estimated model parameters of Joint model with bidirectional survival data

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).

Bhattacharjee, A., Rajbongshi, B. K., & Vishwakarma, G. K. (2024). jmBIG: enhancing dynamic risk prediction and personalized medicine through joint modeling of longitudinal and survival data in big routinely collected data. BMC Medical Research Methodology, 24(1), 172.

Examples

```
library(JMbayes2)
st_pbcid<-function(){
  new_pbcid<-pbc2.id
  new_pbcid$time_2<-rexp(n=nrow(pbc2.id),1/10)
  cen_time<-runif(nrow(pbc2.id),min(new_pbcid$time_2),max(new_pbcid$time_2))
  status_2<-ifelse(new_pbcid$time_2<cen_time,1,0)
  new_pbcid$status_2<-status_2
  new_pbcid$time_2<-ifelse(new_pbcid$time_2<cen_time,new_pbcid$time_2,cen_time)
 new_pbcid$time_2<-ifelse(new_pbcid$time_2<new_pbcid$years,new_pbcid$years,new_pbcid$time_2)
  new_pbcid
}
new_pbc2id<-st_pbcid()
pbc2$status_2<-rep(new_pbc2id$status_2,times=data.frame(table(pbc2$id))$Freq)
pbc2$time_2<-rep(new_pbc2id$time_2,times=data.frame(table(pbc2$id))$Freq)
pbc2_new<-pbc2[pbc2$id%in%c(1:100),]
new_pbc2id<-new_pbc2id[new_pbc2id$id%in%c(1:100),]
model_jmbBdirect<-jmbB(dtlong=pbc2_new,dtsurv =new_pbc2id,
                       longm=list(serBilir~drug*year,serBilir~drug*year),
                    survm=list(Surv(years,status2)~drug,Surv(time_2,status_2)~drug+age),
                       rd=list(~year|id,~year|id),
                       id='id',timeVar ='year')
model_jmbBdirect
```

`jmcsB` *Joint model for Bidirectional survival data using* `FastJM`

Description

The function fits joint model for survival data with two events. It utilizes the FastJM package for obtaining the model parameter estimates.

Usage

```
jmcsB(
  dtlong,
  dtsurv,
  longm,
  survm,
  rd,
  id,
  timeVar,
  BIGdata = FALSE,
  samplesize = 200
)
```

Arguments

`dtlong`	longitudinal data
`dtsurv`	survival data with two event status along with event time
`longm`	longitudinal model e.g. list(serBilir~drug * year,serBilir ~ drug * year)
`survm`	survival model e.g. list(Surv(years,status2)~drug,Surv(time_2,status_2)~drug+age)
`rd`	random effect component e.g. list(~year|id,~year|id)
`id`	ID variable
`timeVar`	time variable
`BIGdata`	logical argument TRUE or FALSE
`samplesize`	samplesize for bigdata

Value

Estimated model parameters of Joint model with bidirectional survival data

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).

Bhattacharjee, A., Rajbongshi, B. K., & Vishwakarma, G. K. (2024). jmBIG: enhancing dynamic risk prediction and personalized medicine through joint modeling of longitudinal and survival data in big routinely collected data. BMC Medical Research Methodology, 24(1), 172.

Examples

```
library(FastJM)
library(JMbayes2)
st_pbcid<-function(){
  new_pbcid<-pbc2.id
  new_pbcid$time_2<-rexp(n=nrow(pbc2.id),1/10)
  cen_time<-runif(nrow(pbc2.id),min(new_pbcid$time_2),max(new_pbcid$time_2))
  status_2<-ifelse(new_pbcid$time_2<cen_time,1,0)
  new_pbcid$status_2<-status_2
  new_pbcid$time_2<-ifelse(new_pbcid$time_2<cen_time,new_pbcid$time_2,cen_time)
 new_pbcid$time_2<-ifelse(new_pbcid$time_2<new_pbcid$years,new_pbcid$years,new_pbcid$time_2)
  new_pbcid
}
new_pbc2id<-st_pbcid()
pbc2$status_2<-rep(new_pbc2id$status_2,times=data.frame(table(pbc2$id))$Freq)
pbc2$time_2<-rep(new_pbc2id$time_2,times=data.frame(table(pbc2$id))$Freq)
pbc2_new<-pbc2[pbc2$id%in%c(1:50),]
new_pbc2id<-new_pbc2id[new_pbc2id$id%in%c(1:50),]
```

```
model_jmcs<-jmcsB(dtlong=pbc2_new,dtsurv=new_pbc2id,
                  longm=list(serBilir~drug*year,
                             serBilir~drug*year),
                  survm=list(Surv(years,status2)~drug,
                             Surv(time_2,status_2)~drug+age),
                  rd=list(~1|id,~1|id),
                  id='id',timeVar='year')
model_jmcs
```

`jmrmlB` *Joint model for Bidirectional survival data using* `joineRML`

Description

The function fits joint model for survival data with two events. It utilizes the joineRML package for obtaining the model parameter estimates.

Usage

```
jmrmlB(
  dtlong,
  dtsurv,
  longm,
  survm,
  rd,
  timeVar,
  id,
  samplesize = 200,
  BIGdata = FALSE
)
```

Arguments

`dtlong`	longitudinal data
`dtsurv`	survival data with two event status along with event time
`longm`	longitudinal model e.g. list(serBilir~drug * year,serBilir ~ drug * year)
`survm`	survival model e.g. list(Surv(years,status2)~drug,Surv(time_2,status_2)~drug+age)
`rd`	random effect component e.g. list(~year|id,~year|id)
`timeVar`	time variable
`id`	ID variable
`samplesize`	samplesize for bigdata
`BIGdata`	logical argument TRUE or FALSE

Value

Estimated model parameters of Joint model with bidirectional survival data

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.

Bhattacharjee, A., Rajbongshi, B. K., & Vishwakarma, G. K. (2024). jmBIG: enhancing dynamic risk prediction and personalized medicine through joint modeling of longitudinal and survival data in big routinely collected data. BMC Medical Research Methodology, 24(1), 172.

Examples

```
##
library(JMbayes2)
library(joineRML)
jmrmlBModel<-jmrmlB(dtlong=new_long2[new_long2$id%in%c(1:80),],
                  dtsurv=new_surv2[new_surv2$id%in%c(1:80),],
              longm=list(y~x7+visit,y~x7+visit),survm=list(Surv(time,status)~x1+visit,
                 Surv(time_2,status_2)~x1+visit),rd=list(~visit|id,~visit|id),id='id',
                  timeVar='visit',samplesize=40,BIGdata=TRUE)
jmrmlBModel
##
```

`jmstB` *Joint model for Bidirectional survival data using* `rstanarm`

Description

The function fits joint model for survival data with two events. It utilizes the rstanarm package for obtaining the model parameter estimates.

Usage

```
jmstB(
  dtlong,
  dtsurv,
  longm,
  survm,
  timeVar,
  id,
  nchain = 1,
  refresh = 1000,
  BIGdata = FALSE,
  samplesize = 200
)
```

Arguments

`dtlong`	longitudinal data
`dtsurv`	survival data with two event status along with event time
`longm`	longitudinal model e.g. list(serBilir~drug * year+(year|id),serBilir ~ drug * year+(year|id))
`survm`	survival model e.g. list(Surv(years,status2)~drug,Surv(time_2,status_2)~drug+age)
`timeVar`	time variable
`id`	ID variable
`nchain`	number of MCMC chain
`refresh`	number of refresh sample
`BIGdata`	logical argument TRUE or FALSE
`samplesize`	samplesize for bigdata

Value

Estimated model parameters of Joint model with bidirectional survival data

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).

Bhattacharjee, A., Rajbongshi, B. K., & Vishwakarma, G. K. (2024). jmBIG: enhancing dynamic risk prediction and personalized medicine through joint modeling of longitudinal and survival data in big routinely collected data. BMC Medical Research Methodology, 24(1), 172.

Examples

```
 ##
library(JMbayes2)
library(rstanarm)
st_pbcid<-function(){
  new_pbcid<-pbc2.id
  new_pbcid$time_2<-rexp(n=nrow(pbc2.id),1/10)
  cen_time<-runif(nrow(pbc2.id),min(new_pbcid$time_2),max(new_pbcid$time_2))
  status_2<-ifelse(new_pbcid$time_2<cen_time,1,0)
  new_pbcid$status_2<-status_2
  new_pbcid$time_2<-ifelse(new_pbcid$time_2<cen_time,new_pbcid$time_2,cen_time)
  new_pbcid$time_2<-ifelse(new_pbcid$time_2<new_pbcid$years,new_pbcid$years,
                            new_pbcid$time_2)
  new_pbcid
}
new_pbc2id<-st_pbcid()
pbc2$status_2<-rep(new_pbc2id$status_2,times=data.frame(table(pbc2$id))$Freq)
```

```
pbc2$time_2<-rep(new_pbc2id$time_2,times=data.frame(table(pbc2$id))$Freq)
pbc2_new<-pbc2[pbc2$id%in%c(1:50),]
new_pbc2id<-new_pbc2id[new_pbc2id$id%in%c(1:50),]
model_jmstBdirect<-jmstB(
  dtlong=pbc2_new,
  dtsurv = new_pbc2id,
  longm=list(serBilir~drug*year+(year|id),albumin~drug+year+(year|id)),
  survm=list(Surv(years,status2)~drug,Surv(time_2,status_2)~drug),
  timeVar="year",
  id='id',
  refresh=400,
  nchain=1)
model_jmstBdirect
##
```

`new_long2` *longitudinal- survival dataset*

Description

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

Usage

`data(new_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

`new_surv2` *survival data*

Description

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

Usage

```
data(new_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

`plot.jmbB` *Prediction plot from* `jmbB()`

Description

Prediction plot from `jmbB()`

Usage

```
## S3 method for class 'jmbB'
plot(x, y, ...)
```

Arguments

`x`	fitted model
`y`	newdata
`...`	others

Value

Returns prediction plot for the newdata using the model fitted through `jmbB()`.

Note

In the example code we use newdata as the data for ID 2 in the PBC2 dataset, it has follow up information till 8.832. Now suppose we want to look at the survival of ID 2 under joint model 1 after time 4 and for joint model 2 after time 9. For that we created the newdata as if the individual is followed till for a time period less than min(4,9).

Examples

```
##
library(JMbayes2)
st_pbcid<-function(){
  new_pbcid<-pbc2.id
  new_pbcid$time_2<-rexp(n=nrow(pbc2.id),1/10)
  cen_time<-runif(nrow(pbc2.id),min(new_pbcid$time_2),max(new_pbcid$time_2))
  status_2<-ifelse(new_pbcid$time_2<cen_time,1,0)
  new_pbcid$status_2<-status_2
  new_pbcid$time_2<-ifelse(new_pbcid$time_2<cen_time,new_pbcid$time_2,cen_time)
 new_pbcid$time_2<-ifelse(new_pbcid$time_2<new_pbcid$years,new_pbcid$years,new_pbcid$time_2)
  new_pbcid
}
new_pbc2id<-st_pbcid()
pbc2$status_2<-rep(new_pbc2id$status_2,times=data.frame(table(pbc2$id))$Freq)
pbc2$time_2<-rep(new_pbc2id$time_2,times=data.frame(table(pbc2$id))$Freq)
pbc2_new<-pbc2[pbc2$id%in%c(1:100),]
new_pbc2id<-new_pbc2id[new_pbc2id$id%in%c(1:100),]
model_jmbBdirect<-jmbB(dtlong=pbc2_new,dtsurv = new_pbc2id,
                       longm=list(serBilir ~ drug*year,serBilir ~ drug*year),
                       survm=list(Surv(years,status2) ~ drug,
                                  Surv(time_2,status_2) ~ drug+age),
                       rd=list(~year|id,~year|id),
                       id='id',timeVar ='year')

t0<-4
nd <- pbc2[pbc2$id %in% c(2), ]
nd<-nd[nd$year<t0,]
nd$status2<-0
nd$years<-t0
nd$time_2<-9
nd$status_2<-0
plot(model_jmbBdirect,nd)
nd <- pbc2[pbc2$id %in% c(2), ]
nd<-nd[nd$year<12,]
nd$status2<-0
nd$years<-12
nd$time_2<-9
nd$status_2<-0
plot(model_jmbBdirect,nd)
##
```

`plot.jmcsB` *Prediction plot from* `jmcsB()`

Description

Prediction plot from `jmcsB()`

Usage

```
## S3 method for class 'jmcsB'
plot(x, y, ...)
```

Arguments

`x`	fitted model object
`y`	newdata longitudinal
`...`	other

Value

Returns prediction plot for the newdata using the model fitted through `jmcsB()`

Note

In the example code we use newdata as the data for ID 2 in the PBC2 dataset, it has follow up information till 8.832. Now suppose we want to look at the survival of ID 2 under joint model 1 after time 4 and for joint model 2 after time 9. For that we created the newdata as if the individual is followed till for a time period less than min(4,9).

Examples

```
 library(JMbayes2)
 library(FastJM)
  st_pbcid<-function(){
  new_pbcid<-pbc2.id
  new_pbcid$time_2<-rexp(n=nrow(pbc2.id),1/10)
  cen_time<-runif(nrow(pbc2.id),min(new_pbcid$time_2),max(new_pbcid$time_2))
  status_2<-ifelse(new_pbcid$time_2<cen_time,1,0)
  new_pbcid$status_2<-status_2
  new_pbcid$time_2<-ifelse(new_pbcid$time_2<cen_time,new_pbcid$time_2,cen_time)
 new_pbcid$time_2<-ifelse(new_pbcid$time_2<new_pbcid$years,new_pbcid$years,new_pbcid$time_2)
  new_pbcid}
new_pbc2id<-st_pbcid()
pbc2$status_2<-rep(new_pbc2id$status_2,times=data.frame(table(pbc2$id))$Freq)
pbc2$time_2<-rep(new_pbc2id$time_2,times=data.frame(table(pbc2$id))$Freq)
pbc2_new<-pbc2[pbc2$id%in%c(1:50),]
new_pbc2id<-new_pbc2id[new_pbc2id$id%in%c(1:50),]
model_jmcs<-jmcsB(dtlong=pbc2_new,dtsurv = new_pbc2id,
```

```
                    longm=list(serBilir~drug*year,
                               serBilir~drug*year),
                    survm=list(Surv(years,status2)~drug,
                               Surv(time_2,status_2)~drug+age),
                    rd=list(~1|id,~1|id),
                    id='id',timeVar='year')

t0<-4
nd<-pbc2[pbc2$id %in% c(2),]
nd<-nd[nd$year<t0,]
nd$status2<-0
nd$years<-t0
nd$time_2<-9
nd$status_2<-0
plot(x=model_jmcs,y=nd)
##
```

`plot.jmrmlB` *Prediction plot from* `jmrmlB()`

Description

Prediction plot from `jmrmlB()`

Usage

```
## S3 method for class 'jmrmlB'
plot(x, y, ...)
```

Arguments

`x`	fitted model object
`y`	newdata
`...`	others

Value

Returns prediction plot for the newdata using the model fitted through `jmrmlB()`.

Note

In the example code we use newdata as the data for ID 2 in the PBC2 dataset, it has follow up information till 8.832. Now suppose we want to look at the survival of ID 2 under joint model 1 after time 4 and for joint model 2 after time 9. For that we created the newdata as if the individual is followed till for a time period less than min(4,9).

Examples

```
##
library(JMbayes2)
library(joineRML)
jmrmlBModel<-jmrmlB(dtlong=new_long2[new_long2$id<=400,],
                    dtsurv=new_surv2[new_surv2$id<=400,],
                    longm=list(y~x7+visit,y~x7+visit),
                    survm=list(Surv(time,status)~x1+visit,
                               Surv(time_2,status_2)~x1+visit),
                    rd=list(~visit|id,~visit|id),
                    id='id',
                    timeVar='visit',
                    samplesize=200,
                    BIGdata=TRUE)
t0<-6
ndBIG<-new_long2[new_long2$id==10,]
ndBIG<-ndBIG[ndBIG$visit<t0,]
ndBIG$status<-0
ndBIG$time<-t0
ndBIG$time_2<-10
ndBIG$status_2<-0
plot(jmrmlBModel,ndBIG)
##
```

`plot.jmstB` *Prediction plot from* `jmstB()`

Description

Prediction plot from `jmstB()`

Usage

```
## S3 method for class 'jmstB'
plot(x, y, ...)
```

Arguments

`x`	fitted model object
`y`	newdata
`...`	others

Value

Returns prediction plot for the newdata using the model fitted through `jmstB()`.

Note

In the example code we use newdata as the data for ID 2 in the PBC2 dataset, it has follow up information till 8.832. Now suppose we want to look at the survival of ID 2 under joint model 1 after time 4 and for joint model 2 after time 9. For that we created the newdata as if the individual is followed till for a time period less than min(4,9).

Examples

```
##
library(JMbayes2)
library(rstanarm)
st_pbcid<-function(){
  new_pbcid<-pbc2.id
  new_pbcid$time_2<-rexp(n=nrow(pbc2.id),1/10)
  cen_time<-runif(nrow(pbc2.id),min(new_pbcid$time_2),max(new_pbcid$time_2))
  status_2<-ifelse(new_pbcid$time_2<cen_time,1,0)
  new_pbcid$status_2<-status_2
  new_pbcid$time_2<-ifelse(new_pbcid$time_2<cen_time,new_pbcid$time_2,cen_time)
 new_pbcid$time_2<-ifelse(new_pbcid$time_2<new_pbcid$years,new_pbcid$years,new_pbcid$time_2)
  new_pbcid
}
new_pbc2id<-st_pbcid()
pbc2$status_2<-rep(new_pbc2id$status_2,times=data.frame(table(pbc2$id))$Freq)
pbc2$time_2<-rep(new_pbc2id$time_2,times=data.frame(table(pbc2$id))$Freq)
pbc2_new<-pbc2[pbc2$id%in%c(1:50),]
new_pbc2id<-new_pbc2id[new_pbc2id$id%in%c(1:50),]
model_jmstBdirect<-jmstB(
  dtlong=pbc2_new,
  dtsurv = new_pbc2id,
  longm=list(serBilir ~ drug * year+(year|id),albumin~drug+year+(year|id)),
  survm=list(Surv(years,status2) ~ drug,Surv(time_2,status_2) ~ drug),
  timeVar="year",
  id='id',
  refresh=400,
  nchain=1)
t0<-4
nd<-pbc2[pbc2$id %in% c(2), ]
nd<-nd[nd$year<t0,]
nd$status2<-0
nd$years<-t0
nd$time_2<-9
nd$status_2<-0
plot(x=model_jmstBdirect,y = nd)
##
```

`predict.jmbB` *predict.jmbB*

Description

predict.jmbB

Usage

```
## S3 method for class 'jmbB'
predict(object, newdata, ...)
```

Arguments

`object`	fitted model
`newdata`	newdata
`...`	others

Value

Survival Prediction for newdata from model fitted through `jmbB()`

`predict.jmcsB` *predict.jmcsB*

Description

predict.jmcsB

Usage

```
## S3 method for class 'jmcsB'
predict(object, newdata, ...)
```

Arguments

`object`	fitted model
`newdata`	newdata
`...`	others

Value

Survival Prediction for newdata from model fitted through `jmcsB()`

`predict.jmrmlB` *predict.jmrmlB*

Description

predict.jmrmlB

Usage

```
## S3 method for class 'jmrmlB'
predict(object, newdata, ...)
```

Arguments

`object`	fitted model
`newdata`	newdata
`...`	others

Value

Survival Prediction for newdata from model fitted through `jmrmlB()`

`predict.jmstB` *predict.jmstB*

Description

predict.jmstB

Usage

```
## S3 method for class 'jmstB'
predict(object, newdata, ...)
```

Arguments

`object`	fitted model
`newdata`	newdata
`...`	others

Value

Survival Prediction for newdata from model fitted through `jmstB()`

`print.jmbB` *print.*

Description

print method for class ’jmbB’

Usage

```
## S3 method for class 'jmbB'
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.

`print.jmcsB` *print.*

Description

print method for class ’jmcsB’

Usage

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

Arguments

`x`	fittedobject
`...`	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.

`print.jmrmlB` *print.*

Description

print method for class 'jmrmlB'

Usage

```
## S3 method for class 'jmrmlB'
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.

`print.jmstB` *print.*

Description

print method for class 'jmstB'

Usage

```
## S3 method for class 'jmstB'
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.

Index