Package: JMbdirect (via r-universe)

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Type Package

Title Joint Model for Longitudinal and Multiple Time to Events Data

Version 0.1.0

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

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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

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Depends R (>= 2.10)

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RemoteUrl https://github.com/cran/JMbdirect

RemoteRef HEAD

RemoteSha b24e8e5e8f439fed1b19a58598e1d49e3182df57

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(~year|id,~year|id)
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.

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