

# Package ‘SurvMChd’

May 23, 2021

**Title** High Dimensional Survival Data Analysis with Markov Chain Monte Carlo

**Version** 0.1.1

**Date** 2021-05-23

**Depends** R (>= 3.5.0)

**Imports** survival, utils, Rdpack (>= 0.7), readr, rjags, R2jags, tidyverse, icenReg, ICBayes, dplyr, rlang

**LazyData** Yes

**LazyDataCompression** xz

**ByteCompile** Yes

**Description** High dimensional survival data analysis with Markov Chain Monte Carlo(MCMC). Currently support frailty data analysis. Allows for Weibull and Exponential distribution. Includes function for interval censored data.

**License** GPL-3

**Encoding** UTF-8

**NeedsCompilation** no

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**RoxygenNote** 7.1.1.9000

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**Repository** CRAN

**Date/Publication** 2021-05-23 14:20:02 UTC

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fraidm	<i>Frailty with Discrete Mixture Model</i>
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## Description

Discrete mixture model with MCMC

## Usage

```
fraidm(m, n, Ins, Del, Time, T.min, chn, iter, data)
```

## Arguments

m	Starting column number form where study variables to be selected.
n	Ending column number till where study variables will get selected.
Ins	Variable name of Institute information.
Del	Variable name containing the event information.
Time	Variable name containing the time information.
T.min	Variable name containing the time of event information.
chn	Number of MCMC chains
iter	Define number of iterations as number.
data	High dimensional data, event information given as (delta=0 if alive, delta=1 if died). If patient is censored then t.min=duration of survival. If patient is died then t.min=0. If patient is died then t=duration of survival. If patient is alive then t=NA.

## Details

By given m and n, a total of 3 variables can be selected.

## Value

fraidmout - b[1] is the posterior estimate of the regression coefficient for first covariate.

b[2] is the posterior estimate of the regression coefficient for second covariate.

b[3] is the posterior estimate of the regression coefficient for third covariate.

omega[1] and omega[2] are frailty effects.

c[1] and c[2] are regression intercept and coefficients of covariates over mean effect.

## References

- Bhattacharjee, A. (2020). Bayesian Approaches in Oncology Using R and OpenBUGS. CRC Press.  
 Congdon, P. (2014). Applied bayesian modelling (Vol. 595). John Wiley & Sons.

## See Also

fraidpm frairand

## Examples

```
## Not run:
##
data(frailty)
fraidm(m=5,n=7,Ins="institute",Del="del",Time="timevar",T.min="time.min",chn=2,iter=6,data=frailty)
##

## End(Not run)
```

---

fraidpm	<i>Frailty with drichlet process mixture</i>
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## Description

Frailty analysis on high dimensional data by Drichlet process mixture.

## Usage

```
fraidpm(m, n, Ins, Del, Time, T.min, chn, iter, adapt, data)
```

## Arguments

m	Starting column number form where study variables to be selected.
n	Ending column number till where study variables will get selected.
Ins	Variable name of Institute information.
Del	Variable name containing the event information.
Time	Variable name containing the time information.
T.min	Variable name containing the time of event information.
chn	Number of MCMC chains.
iter	Define number of iterations as number.
adapt	Define number of adaptations as number.
data	High dimensional data, event information given as (delta=0 if alive, delta=1 if died). If patient is censored then t.min=duration of survival. If patient is died then t.min=0. If patient is died then t=duration of survival. If patient is alive then t=NA.

**Details**

By given  $m$  and  $n$ , a total of 3 variables can be selected.

**Value**

`fraidpmout omeg[i]` are frailty effects.

**Author(s)**

Atanu Bhattacharjee and Akash Pawar

**References**

Bhattacharjee, A. (2020). Bayesian Approaches in Oncology Using R and OpenBUGS. CRC Press.  
Congdon, P. (2014). Applied bayesian modelling (Vol. 595). John Wiley & Sons.

**See Also**

`fraidm frairand`

**Examples**

```
## Not run:  
##  
data(frailty)  
fraidpm(m=5,n=7,Ins="institute",Del="del",Time="timevar",T.min="time.min",chn=2,iter=6,  
adapt=100,data=frailty)  
##  
  
## End(Not run)
```

---

frailty

*Frailty in high dimensional survival data.*

---

**Description**

Data set listing institutional wise survival outcomes

Survival observations data for frailty model functions of `SurvIMChd`

**Usage**

```
data(frailty)
```

**Format**

A tibble with 7 columns and 272 rows which are :

**institute** Institute of the sample observations

**del** Numeric values 0 or 1 containing death/event information

**timevar** Survival duration

**time.min** Minimum survival

**female** Covariate\_1, gender variable indicating either a female or not

**ph.karno** Covariate\_2

**pat.karno** Covariate\_3

**Examples**

```
data(frailty)
```

---

frairand

*Frailty with random effects in high dimensional data with MCMC*


---

**Description**

Random effects frailty model

**Usage**

```
frairand(m, n, Ins, Del, Time, T.min, chn, iter, adapt, data)
```

**Arguments**

m	Starting column number form where study variables to be selected.
n	Ending column number till where study variables will get selected.
Ins	Variable name of Institute information.
Del	Variable name containing the event information.
Time	Variable name containing the time information.
T.min	Variable name containing the time of event information.
chn	Numner of MCMC chains.
iter	Define number of iterations as number.
adapt	Define number of adaptations as number.
data	High dimensional data having survival duration, event information and column of time for death cases.

**Details**

By given m and n, a total of 3 variables can be selected.

**Value**

frairandout omeg[i] are frailty effects.

**Author(s)**

Atanu Bhattacharjee and Akash Pawar

**References**

Tawiah, R., Yau, K. K., McLachlan, G. J., Chambers, S. K., & Ng, S. K. (2019). Multilevel model with random effects for clustered survival data with multiple failure outcomes. *Statistics in medicine*, **38**(6), 1036-1055.

**See Also**

fraidm afraidpm

**Examples**

```
## Not run:
##
data(frailty)
frairand(m=5,n=7,Ins="institute",Del="del",Time="timevar",T.min="time.min",chn=2,iter=6,
  adapt=100,data=frailty)
##

## End(Not run)
```

---

headneck

*High dimensional genomic data on head and neck cancer*

---

**Description**

Head and neck cancer data tibble on head and neck cancer patients for survexpMC and survweibMC functions.

**Usage**

```
data(headneck)
```

**Format**

A tibble with 13 columns which are :

**Subjects** Patients referred to as Subjects

**OS** Overall Survival

**Death** Death status for the particular subjects

**randgrp1** Arm of group assigned to subjects

**gender1** Demographic information of Subjects, i.e. Gender

**Stratum1** Stratum from where the sample is drawn

**prevoi** Categorical observation

**Covariate\_1** Continuous observations

**Covariate\_2** Continuous observations

**Covariate\_3** Continuous observations

**Covariate\_4** Continuous observations

**Covariate\_5** Continuous observations

**Covariate\_6** Continuous observations

### Examples

```
data(headneck)
```

---

hnscc	<i>hnscc Head and neck cancer data</i>
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---

### Description

High dimensional head and neck cancer gene expression data

### Usage

```
data(hnscc)
```

### Format

A dataframe with 565 rows and 104 variables

**ID** ID of subjects

**leftcensoring** Initial censoring time

**death** Survival event

**os** Duration of overall survival

**PFS** Duration of progression free survival

**Prog** Progression event

**GJB1,....,HMGCS2** High dimensional covariates

### Examples

```
data(hnscc)
```

---

`mcsurv`*Metronomic cancer data*

---

**Description**

Observations made tibble on the head and neck cancer patients. Data for survMC function from SurviMChd package.

**Usage**

```
data(mcsurv)
```

**Format**

A tibble with 15 columns which are :

**OS** Overall Survival

**Death** Death status

**t** Time at which event occurred

**x1** Variable measured on continuous scale

**x2** Variable measured on discrete scale

**x3** Variable measured on continuous scale

**x4** Variable measured on discrete scale

**x5** Variable measured on continuous scale

**Examples**

```
data(mcsurv)
```

---

`survexpMC`*Exponential survival analysis with MCMC*

---

**Description**

Survival analysis with exponential distribution by MCMC

**Usage**

```
survexpMC(m1, n1, m2, n2, chains, iter, data)
```



**Arguments**

m1	Starting column number from where variables of high dimensional data will be selected.
n1	Ending column number till where variables of high dimensional data will get selected.
m2	Starting column number from where demographic observations starts
n2	Ending column number of the demographic observations
chains	Number of MCMC chains
iter	Number of MCMC iterations
data	High dimensional data having survival duration as (OS), event information as Death (1 if died, or 0 if alive).

**Value**

survexpMCout A data set listing estimated posterior means and deviances

**Author(s)**

Atanu Bhattacharjee and Akash Pawar

**References**

Kumar, M., Sonker, P. K., Saroj, A., Jain, A., Bhattacharjee, A., & Saroj, R. K. (2020). Parametric survival analysis using R: Illustration with lung cancer data. *Cancer Reports*, **3(4)**, e1210.

**See Also**

survweibMC

**Examples**

```
## Not run:  
##  
data(headneck)  
survexpMC(m1=8,n1=12,m2=4,n2=7,chains=2,iter=10,data=headneck)  
##  
  
## End(Not run)
```

---

survintMC                      *High dimensional survival analysis with interval censored data by MCMC*

---

### Description

Performs survival analysis with MCMC on a data set by computing survival interval given left and right censoring time.

### Usage

```
survintMC(m, n, Leftcensor = NULL, OS, Death, iter, data)
```

### Arguments

m	Starting column number from where variables of high dimensional data will get selected.
n	Ending column number till where variables of high dimensional data will get selected.
Leftcensor	"Variable/column name" containing the left censoring information.
OS	"Variable/column name" containing survival duration event observations.
Death	"Variable/column name" containing the survival event information. i.e. Death
iter	Number of MCMC iterations.
data	High dimensional data containing the Left censoring, Right censoring, Status and DEG observations.

### Details

The survival columns of the data should be arranged as follows - leftcensoring The column containing the left censoring information, must be named as 'Leftcensor'. Rightcensor The column containing the right censoring information, must be named as 'Rightcensor' i.e. OS. Death The column containing the death and alive information, must be names as 'Status'.

### Value

survintMCout A table containing HR and CI for respective covariates.

### Author(s)

Atanu Bhattacharjee and Akash Pawar

### References

Bogaerts, K., Komarek, A., & Lesaffre, E. (2017). Survival analysis with interval-censored data: A practical approach with examples in R, SAS, and BUGS. CRC Press.

**See Also**

survMC

**Examples**

```
## Not run:
##
data(hnsc)
survintMC(m=7,n=11,Leftcensor="leftcensoring",OS="os",Death="death",iter=6,data=hnsc)
##

## End(Not run)
```

survMC

*Survival analysis using Cox Proportional Hazards with MCMC.***Description**

Performs survival analysis using Cox Proportional Hazards with MCMC.

**Usage**

```
survMC(m, n, Time, Event, chains, adapt, iter, data)
```

**Arguments**

m	Starting column number from where variables of high dimensional data will get selected.
n	Ending column number till where variables of high dimensional data will get selected.
Time	Variable/Column name containing the information on duration of survival
Event	Variable/Column name containing the information of survival event
chains	Number of chains to perform
adapt	Number of adaptations to perform
iter	Number of iterations to perform
data	High dimensional data having survival duration and event.

**Details**

The survival columns of the data should be arranged as follows - Death status=1 if died otherwise 0. OS Survival duration measured as 'OS' t.len Number of censored times

**Value**

Data set containing Posterior HR estimates, SD and quantiles.

**Author(s)**

Atanu Bhattacharjee and Akash Pawar

**References**

Bhattacharjee, A. (2020). Bayesian Approaches in Oncology Using R and OpenBUGS. CRC Press.

**See Also**

survintMC

**Examples**

```
## Not run:
##
data(mcsurv)
survMC(m=4,n=8,Time="OS",Event="Death",chains=2,adapt=100,iter=1000,data=mcsurv)
##

## End(Not run)
```

---

survMCmulti

*Survival analysis on multiple variables with MCMC*

---

**Description**

Performs survival analysis using Cox Proportional Hazards with MCMC with an option to input select multiple variables.

**Usage**

```
survMCmulti(
  var1 = NULL,
  var2 = NULL,
  var3 = NULL,
  var4 = NULL,
  var5 = NULL,
  Time,
  Event,
  chains,
  adapt,
  iter,
  data
)
```

**Arguments**

var1	Variable name (first one)
var2	Variable name (second one)
var3	Variable name (third one)
var4	Variable name (fourth one)
var5	Variable name (fifth one)
Time	Variable/Column name containing the information on duration of survival
Event	Variable/Column name containing the information of survival event
chains	Number of chains to perform
adapt	Number of chains to perform
iter	Number of iterations to perform
data	High dimensional data having survival duration and event.

**Details**

The survival columns of the data should be arranged as follows - Death Death status=1 if died otherwise 0. OS Survival duration measured as 'OS'

**Value**

Data set containing Posterior HR estimates, SD, quantiles and meandeviance.

**Author(s)**

Atanu Bhattacharjee and Akash Pawar

**References**

Bhattacharjee, A. (2020). Bayesian Approaches in Oncology Using R and OpenBUGS. CRC Press.

**See Also**

survintMC

**Examples**

```
## Not run:
##
data(mcsurv)
survMCmulti(var1="x1", var2=NULL, var3="x3", var4="x2",
            var5="x4", Time="OS", Event="Death", chains=2, adapt=100, iter=1000, data=mcsurv)
##

## End(Not run)
```

---

`survweibMC`*Weibull survival analysis with MCMC*

---

**Description**

Survival analysis with weibull distribution by MCMC

**Usage**

```
survweibMC(m1, n1, m2, n2, chains, iter, data)
```

**Arguments**

<code>m1</code>	Starting column number from where variables of high dimensional data will be selected.
<code>n1</code>	Ending column number till where variables of high dimensional data will get selected.
<code>m2</code>	Starting column number from where demographic observations starts
<code>n2</code>	Ending column number of the demographic observations
<code>chains</code>	Number of MCMC chains
<code>iter</code>	Number of MCMC iterations
<code>data</code>	High dimensional data having survival duration as (OS), event information as Death (1 if died, or 0 if alive).

**Value**

`beta1[1]` Posterior estimates of regression coefficients and deviance

**Author(s)**

Atanu Bhattacharjee and Akash Pawar

**References**

- Kumar, M., Sonker, P. K., Saroj, A., Jain, A., Bhattacharjee, A., & Saroj, R. K. (2020). Parametric survival analysis using R: Illustration with lung cancer data. *Cancer Reports*, **3(4)**, e1210.
- Khan, S. A. (2018). Exponentiated Weibull regression for time-to-event data. *Lifetime data analysis*, **24(2)**, 328-354.

**See Also**

`survexpMC`

**Examples**

```
## Not run:  
##  
data(headneck)  
survweibMC(m1=8,n1=12,m2=4,n2=7,chains=2,iter=10,data=headneck)  
##  
  
## End(Not run)
```

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