Package ‘longit’

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Title High Dimensional Longitudinal Data Analysis Using MCMC

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Depends R (>= 2.10)

Imports AICcmodavg, missForest,R2jags,rjags,utils

LazyData Yes

LazyDataCompression xz

ByteCompile Yes

Description High dimensional longitudinal data analysis with Markov Chain Monte Carlo(MCMC). Currently support mixed effect regression with or without missing observations by considering covariance structures. It provides estimates by missing at random and missing not at random assumptions.
In this R package, we present Bayesian approaches that statisticians and clinical researchers can easily use. The functions' methodology is based on the book ``Bayesian Approaches in Oncology Using R and OpenBUGS'' by Bhattacharjee A (2020) <doi:10.1201/9780429329449-14>.

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Encoding UTF-8

NeedsCompilation no

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Repository CRAN

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Contents

`Bysmixed` *Bayesian mixed effect model with MCMC*

Description

Bayesian mixed effect model with random intercepts and random slopes. Fits using MCMC on longitudinal data set.

Usage

```
Bysmixed(m, n, t, group, chains, n.adapt, data)
```

Arguments

`m`	Starting number of column from where repeated observations begin
`n`	Ending number of columns till where the repeated observations ends
`t`	Timepoint information on which repeadted observations were taken
`group`	A categorical variable either 0 or 1. i.e. Gender - 1 male and 0 female
`chains`	Number of MCMC chains to be performed
`n.adapt`	Number of iterations to run in the JAGS adaptive phase.
`data`	High dimensional longitudinal data

Value

Gives posterior means, standard deviation.

Author(s)

Atanu Bhattacharjee, Akash Pawar and Bhrigu Kumar Rajbongshi

References

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

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., & Rubin, D. B. (2013). Bayesian data analysis. CRC press.

Fitzmaurice, G. M., Laird, N. M., & Ware, J. H. (2012). Applied longitudinal analysis (Vol. 998). John Wiley & Sons.

Examples

```
##
data(repdata)
Bysmixed(m=4,n=7,t="Age",group="Gender",chains=4,n.adapt=100,repdata)
##
```

`BysmxDIC` *Bayesian mixed effect model for high dimensional longitduinal data with deviance information criterion (DIC).*

Description

Bayesian mixed effect model with random intercept and slopes provides inference with deviance information criterion (DIC). Data longitudinally measured missing value and having batched information. Fits using MCMC on longitudinal data set

Usage

```
BysmxDIC(m, tmax, t, group, chains, iter, out, data)
```

Arguments

`m`	Starting number of column from where repeated observations begin
`tmax`	Ending number of columns till where the repeated observations ends
`t`	Timepoint information on which repeadted observations were taken
`group`	A categorical variable either 0 or 1. i.e. Gender - 1 male and 0 female
`chains`	Number of MCMC chains to be performed
`iter`	Number of iterations to be performed
`out`	DIC/HPD outcome
`data`	High dimensional longitudinal data

Value

Gives posterior means, standard deviation.

Author(s)

Atanu Bhattacharjee, Akash Pawar and Bhrigu Kumar Rajbongshi

References

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

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., & Rubin, D. B. (2013). Bayesian data analysis. CRC press.

Fitzmaurice, G. M., Laird, N. M., & Ware, J. H. (2012). Applied longitudinal analysis (Vol. 998). John Wiley & Sons.

Examples

```
##
data(msrep)
BysmxDIC(m=c(4,8,12),tmax=4,t="Age",group="Gender",chains=4,iter=1000,out="DIC",data=msrep)
##
```

`BysmxHPD` *Bayesian mixed effect model for high dimensional longitduinal data with highest posterior density interval (HPDI).*

Description

Bayesian mixed effect model with random intercept and slopes provides inference with highest posterior density interval (HPDI). Data longitudinally measured missing value and having batched information. Fits using MCMC on longitudinal data set

Usage

```
BysmxHPD(m, tmax, t, group, chains, iter, out, data)
```

Arguments

`m`	Starting number of column from where repeated observations begin
`tmax`	Ending number of columns till where the repeated observations ends
`t`	Timepoint information on which repeadted observations were taken
`group`	A categorical variable either 0 or 1. i.e. Gender - 1 male and 0 female
`chains`	Number of MCMC chains to be performed
`iter`	Number of iterations to be performed
`out`	DIC/HPD outcome
`data`	High dimensional longitudinal data

Value

Gives posterior means, standard deviation.

Author(s)

Atanu Bhattacharjee, Akash Pawar and Bhrigu Kumar Rajbongshi

References

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

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., & Rubin, D. B. (2013). Bayesian data analysis. CRC press.

Fitzmaurice, G. M., Laird, N. M., & Ware, J. H. (2012). Applied longitudinal analysis (Vol. 998). John Wiley & Sons.

Examples

```
##
data(msrep)
BysmxHPD(m=c(4,8,12),tmax=4,t="Age",group="Gender",chains=4,iter=1000,out="hpD",data=msrep)
##
```

`Bysmxms` *Bayesian mixed model with random intercepts and random slopes for high dimensional longitudinal data*

Description

Bayesian mixed effect model with random intercepts and slopes with longitudinally measured missing data. Fits using MCMC on longitudinal data set

Usage

```
Bysmxms(m, n, time, group, chains, n.adapt, data)
```

Arguments

`m`	Starting number of column from where repeated observations begin
`n`	Ending number of columns till where the repeated observations ends
`time`	Timepoint information on which repeadted observations were taken
`group`	A categorical variable either 0 or 1. i.e. Gender - 1 male and 0 female
`chains`	Number of MCMC chains to be performed
`n.adapt`	Number of iterations to run in the JAGS adaptive phase.
`data`	High dimensional longitudinal data

Value

Gives posterior means, standard deviation.

Author(s)

Atanu Bhattacharjee, Akash Pawar and Bhrigu Kumar Rajbongshi

References

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

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., & Rubin, D. B. (2013). Bayesian data analysis. CRC press.

Fitzmaurice, G. M., Laird, N. M., & Ware, J. H. (2012). Applied longitudinal analysis (Vol. 998). John Wiley & Sons.

Examples

```
##
data(mesrep)
Bysmxms(m=4,n=7,time="Age",group="Gender",chains=4,n.adapt=100,data=msrep)
##
```

`Bysmxmss` *Bayesian mixed model with random intercepts and random slopes for high dimensional longitudinal data with batch size.*

Description

Bayesian mixed effect model with random intercept and slopes. Data longitudinally measured missing value and having batched information. Fits using MCMC on longitudinal data set

Usage

```
Bysmxmss(m, tmax, timepoints, group, chains, iter, data)
```

Arguments

`m`	Starting number of column from where repeated observations begin
`tmax`	Maximum batch of visits considered as repeated measurements
`timepoints`	Timepoint information on which repeadted observations were taken
`group`	A categorical variable either 0 or 1. i.e. Gender - 1 male and 0 female
`chains`	Number of MCMC chains to be performed
`iter`	Number of iterations to be performed
`data`	High dimensional longitudinal data

Value

Gives posterior means, standard deviation.

Author(s)

Atanu Bhattacharjee and Akash Pawar

References

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

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., & Rubin, D. B. (2013). Bayesian data analysis. CRC press.

Fitzmaurice, G. M., Laird, N. M., & Ware, J. H. (2012). Applied longitudinal analysis (Vol. 998). John Wiley & Sons.

Examples

```
##
data(repdat)
```

`creg` *Bayesian multivariate regression with unstructured covariance matrix for high dimensional longitudinal data.*

Description

Multivariate Regression with unstructured covariance matrix in longitudinal datasetup with high dimensional.

Usage

```
creg(m, n, chains, n.adapt, data)
```

Arguments

`m`	Starting number of column from where repeated observations begin
`n`	Ending number of columns till where the repeated observations ends
`chains`	Number of MCMC chains to be performed
`n.adapt`	Number of iterations to be performed
`data`	High dimensional longitudinal data

Value

Results of posterior means and standard deviation.

Author(s)

Atanu Bhattacharjee, Akash Pawar and Bhrigu Kumar Rajbongshi

References

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

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., & Rubin, D. B. (2013). Bayesian data analysis. CRC press.

Fitzmaurice, G. M., Laird, N. M., & Ware, J. H. (2012). Applied longitudinal analysis (Vol. 998). John Wiley & Sons.

Examples

```
##
data(repdata)
creg(m=4,n=7,chains=4,n.adapt=100,data=repdata)
##
```

`gh` *gh*

Description

High dimensional data on three consecutive measurements for and treatment arm information column.

Usage

```
data(gh)
```

Format

A `tibble` with 4 columns which are :

y1 Observation on first timepoint

y2 Observation on second timepoint

y3 Observation on first timepoint

Treatment Treatment arm of the patient

`hdmarjg` *Missing at ranom by MCMC*

Description

Missing at ranom by MCMC

Usage

```
hdmarjg(m, n, treatment, n.chains, n.iter, dat)
```

Arguments

`m`	Starting column number of the Y observations
`n`	Ending column number of the Y observations
`treatment`	Variable/column name containing the Treatment observations
`n.chains`	Number of MCMC chains
`n.iter`	Number of MCMC iterations
`dat`	Data set containing treatment column and repeated observations arrange by columns observations

Value

A data table listing the posterior mean and sigma results

Author(s)

Atanu Bhattacharjee, Akash Pawar and Bhrigu Kumar Rajbongshi

References

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

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., & Rubin, D. B. (2013). Bayesian data analysis. CRC press.

Fitzmaurice, G. M., Laird, N. M., & Ware, J. H. (2012). Applied longitudinal analysis (Vol. 998). John Wiley & Sons.

Examples

```
##
data(gh)
hdmarjg(m=1,n=3,treatment="Treatment",n.chains=2,n.iter=10,dat=gh)
##
```

`hdmnarjg` *Missing not at random by MCMC*

Description

Missing not at random by MCMC

Usage

```
hdmnarjg(m, n, treatment, n.chains, n.iter, dat)
```

Arguments

`m`	Starting column number of repeated observations
`n`	Ending column number of the repeated observations
`treatment`	Variable/column name containing the Treatment observations
`n.chains`	Number of MCMC chains
`n.iter`	Number of MCMC iterations
`dat`	Data set containing treatment column and repeated observations

Value

Results containing a data table listing the means and sigma results

Author(s)

Atanu Bhattacharjee, Akash Pawar and Bhrigu Kumar Rajbongshi

References

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

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., & Rubin, D. B. (2013). Bayesian data analysis. CRC press.

Fitzmaurice, G. M., Laird, N. M., & Ware, J. H. (2012). Applied longitudinal analysis (Vol. 998). John Wiley & Sons.

Examples

```
##
data(gh)
hdmnarjg(m=1,n=3,treatment="Treatment",n.chains=2,n.iter=10,dat=gh)
##
```

`longitdata` *Repeatedly measured protein expression data*

Description

Longitudinal observation on single variable from different observations. Observations arranged in a column as the patient with corresponding column of ID.

Usage

```
data(longitdata)
```

Format

A `tibble` with 2 columns which are :

ID Patient ID

y Repeated observations on the patient arranged in a row as per a subject

---

`msrep` *longitudinal data*

Description

Longitudinal observation on single variable at different timepoints. Observations arranged in a column as the patient with corresponding column of ID.

Usage

```
data(msrep)
```

Format

A `tibble` with 7 columns which are :

Subject Patient ID

Gender Categorical numeric variable, 1 if Males and 0 if female

Age Time or age at which observations were taken from every subjects

x1,...,x4 Columns stating number of observations at age 18,10,12 and 14

`mvncovar1` *Bayesian multivariate regression with independent covariance matrix for high dimensional longitudinal data.*

Description

Multivariate Regression with independent covariance matrix in longitudinal datasetup with high dimensional.

Usage

```
mvncovar1(m, n, time, group, chains, iter, data)
```

Arguments

`m`	Starting number of column from where repeated observations begin
`n`	Ending number of columns till where the repeated observations ends
`time`	Timepoint information on which repeadted observations were taken
`group`	A categorical variable either 0 or 1. i.e. Gender - 1 male and 0 female
`chains`	Number of MCMC chains to be performed
`iter`	Number of iterations to be performed
`data`	High dimensional longitudinal data

Value

mvncovarout lists posterior omega and sigma values.

Author(s)

Atanu Bhattacharjee, Akash Pawar and Bhrigu Kumar Rajbongshi

References

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

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., & Rubin, D. B. (2013). Bayesian data analysis. CRC press.

Fitzmaurice, G. M., Laird, N. M., & Ware, J. H. (2012). Applied longitudinal analysis (Vol. 998). John Wiley & Sons.

Examples

```
##
data(repdata)
mvncovar1(m=4,n=7,time="Age",group="Gender",chains=10,iter=100,repdata)
##
```

`mvncovar2` *Bayesian multivariate normal regression with unstructured covariance matrix for high dimensional longitudinal data.*

Description

Multivariate normal regression with group covaraites and unstructured covariance matrix.

Usage

```
mvncovar2(m, n, time, group, chains, iter, data)
```

Arguments

`m`	Starting number of column from where repeated observations begin
`n`	Ending number of columns till where the repeated observations ends
`time`	Timepoint information on which repeadted observations were taken
`group`	A categorical variable either 0 or 1. i.e. Gender - 1 male and 0 female
`chains`	Number of MCMC chains to be performed
`iter`	Number of iterations to be performed
`data`	High dimensional longitudinal data

Value

mvncovarout

Author(s)

Atanu Bhattacharjee, Akash Pawar and Bhrigu Kumar Rajbongshi

References

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

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., & Rubin, D. B. (2013). Bayesian data analysis. CRC press.

Fitzmaurice, G. M., Laird, N. M., & Ware, J. H. (2012). Applied longitudinal analysis (Vol. 998). John Wiley & Sons.

Examples

```
##
data(repdata)
mvncovar2(m=4,n=7,time="Age",group="Gender",chains=4,iter=100,data=repdata)
##
```

`repdata` *longitudinal data*

Description

Longitudinal observation on single variable at different timepoints. Observations arranged in a column as the patient with corresponding column of ID.

Usage

```
data(repdata)
```

Format

A `tibble` with 7 columns which are :

Subject Patient ID

Gender Categorical numeric variable, 1 if Males and 0 if female

Age Time or age at which observations were taken from every subjects

x1,...,x4 Columns stating number of observations at age 18,10,12 and 14

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