Package 'JMcmprsk'

March 22, 2021

Type Package

Title Joint Models for Longitudinal and Competing Risks Data

Version 0.9.10

Date 2021-3-22

Author Hong Wang [aut, cre], Ning Li [ctb],Shanpeng Li[ctb] and Gang Li [ctb]

Maintainer Hong Wang <wh@csu.edu.cn>

Description Fit joint models of continuous or ordinal longitudinal data and time-to-event data with competing risks. For a detailed information, see Robert Elashoff, Gang Li and Ning Li (2016, ISBN:9781439807828); Robert M. Elashoff,Gang Li and Ning Li (200 0420.2007.00952.x> ; Ning Li, Robert Elashoff, Gang Li and Jeffrey Saver (2010) <doi:10.1002/sim.3798> .

License GPL (>= 2)

Imports Rcpp,MASS,stats,utils,statmod,pracma,reshape2,dplyr

LinkingTo Rcpp

SystemRequirements GNU GSL

NeedsCompilation yes

RoxygenNote 7.1.1

URL https://github.com/whcsu/JMcmprsk

BugReports https://github.com/whcsu/JMcmprsk/issues

Suggests knitr, rmarkdown

VignetteBuilder knitr

Encoding UTF-8

Depends R (>= 3.5.0)

Repository CRAN

Date/Publication 2021-03-22 08:30:02 UTC

R topics documented:

`coef.JMcmprsk` *Coefficients of longitudinal/survival sub-model*

Description

Joint modelling for longitutal and censored data with competing risks

Usage

```
## S3 method for class 'JMcmprsk'
coef(object, coeff = c("beta", "alpha", "gamma"), ...)
```

Arguments

`object`	The JMcmprsk object returned by either jmo or jmc function.
`coeff`	The coefficients returned by the JMcmprsk object.
`...`	further arguments passed to or from other methods.

Value

Return estimates fixed effects with variable names

See Also

`jmc`

jmc *An integrated function for reconstructing data and do the joint modelling*

Description

Reconstruct data into a regular longitudinal format as a refined dataset and do joint modelling for this refined data with continuous outcome.

Usage

```
jmc(
  long_data,
  surv_data,
  out,
  FE,
  RE,
  ID,
  cate = NULL,
  intcpt = 1,
  quad.points = 10,
  max.iter = 10000,
  quiet = TRUE,
  do.trace = FALSE
)
```

Arguments

long_data	Data matrix for longitudinal in long form. The time variable should be labeled 'time'.
surv_data	Data matrix for competing risks data. Each subject has one row of observation (as opposed to the long_data). First and second column should be the observed event time and censoring indicator, respectively. The coding for the censoring indicator is as follows: 0 - censored events, 1 - risk 1, 2 - risk 2. Two competing risks are assumed.
out	Column name for outcome variable in long_data.
FE	Vector of column names that correspond to the fixed effects in long_data. If missing, then all columns except for the outcome and ID columns will be considered.
RE	Types/Vector of random effects in long_data. The available type are "intercept", "linear", "quadratic" (time-related random effect specification) or other covariates in the input dataset. If specify other covariates, then they to be numerical vectors.
ID	Column name for subject ID number in long_data.
cate	Vector of categorical variables in long_data. Default is NULL.

intcpt	Specify either 0 or 1. Default is set as 1. 0 means no intercept in random effect.
quad.points	Number of quadrature points used in the EM procedure. Default is 20. Must be an even number. Larger values means higher accuracy but more time-consuming.
max.iter	Max iterations. Default is 10000.
quiet	Logical. Print progress of function. Default is TRUE.
do.trace	Logical. Print the parameter estimates during the iterations. Default is FALSE.

Value

Object of class JMcmprsk with elements

vcmatrix	The variance-covariance matrix for all the parameters. The parameters are in the order: β, σ^2, γ, ν, and Σ
betas	The point estimates of β.
se_betas	The standard error estimate of β.
gamma_matrix	The point estimate of γ.
se_gamma_matrix	The standard error estimate of γ.
v_estimate	The point estimate of ν.
se_v_estimate	The standard error estimate of ν.
sigma2_val	The point estimate of σ^2.
se_sigma2_val	The standard error estimate of σ^2.
sigma_matrix	The point estimate of Σ (only the upper triangle portion of the matrix is output).
se_sigma	The standard error estimate of Σ.The standard errors are given in this order: main diagonal, the second m
loglike	Log Likelihood.

See Also

jmc_0

Examples

```
require(JMcmprsk)
set.seed(123)
data(lung)
yread <- lung[, c(1,2:11)]
cread <- unique(lung[, c(1, 12, 13, 6:10)])

#Please note only those variables that will appear in the model can be included
res <- jmc(long_data = yread, surv_data = cread, out = "FVC",
           FE = c("time", "FVC0", "FIB0", "CYC", "FVC0.CYC",
                  "FIB0.CYC", "time.CYC"),
           RE = "linear", ID = "ID",cate = NULL, intcpt = 0,
           quad.points = 8, quiet = FALSE)


#make up two categorical variables and add them into yread
sex <- sample(c("Female", "Male"), nrow(cread), replace = TRUE)
race <- sample(c("White", "Black", "Asian", "Hispanic"),
```

```
               nrow(cread), replace = TRUE)
ID <- cread$ID
cate_var <- data.frame(ID, sex, race)
if (require(dplyr)) {
  yread <- dplyr::left_join(yread, cate_var, by = "ID")
}

# run jmc function again for yread file with two added categorical variables
res2 <- jmc(long_data = yread, surv_data = cread,
            out = "FVC", cate = c("sex", "race"),
            FE = c("time", "FVC0", "FIB0", "CYC", "FVC0.CYC",
                "FIB0.CYC", "time.CYC"),
            RE = "time", ID = "ID", intcpt = 0,
            quad.points = 8, quiet = FALSE)
res2
# Extract the parameter estimates of longitudinal sub-model fixed effects
 beta <- coef(res2, coeff = "beta")
 beta
## Linear hypothesis of testing all coefficients of beta's equal 0
 linearTest(res2, coeff="beta")
 ## Linear hypothesis of testing beta1=beta2
 ## create a linear contrast for beta1=beta2 (intercept not included in Lb)
 Lb <- matrix(c(1, -1, 0, 0, 0, 0, 0, 0, 0, 0, 0), ncol = length(beta)-1, nrow = 1)
 linearTest(res2, coeff="beta", Lb = Lb)
 # Extract the parameter estimates of survival sub-model fixed effects
 gamma <- coef(res2, coeff = "gamma")
 gamma
 ## Linear hypothesis of testing all coefficients of gamma's equal 0
 linearTest(res2, coeff="gamma")
 ## Linear hypothesis of testing gamma11=gamma21
 ##  (the coefficients of first covariate from
 ##    both risk functions are equal)
 Lg <- matrix(c(1, 0, 0, 0, 0, -1, 0, 0, 0, 0), ncol = length(gamma), nrow = 1)
 linearTest(res2, coeff="gamma", Lg = Lg)
 ## Extract the standard errors for the longitudinal portion
 summary(res2, coeff = "longitudinal", digits = 4)
 ## Extract the standard errors for the survival portion
 summary(res2, coeff = "survival", digits = 4)
```

---

jmc_0 *Joint Modelling for Continuous outcomes*

Description

Joint modeling of longitudinal continuous data and competing risks

Usage

```
jmc_0(
```

```
  p,
  yfile,
  cfile,
  mfile,
  point = 20,
  maxiterations = 1e+05,
  do.trace = FALSE,
  type_file = TRUE
)
```

Arguments

p	The dimension of fixed effects (include intercept) in yfile.
yfile	Y matrix for longitudinal measurements in long format. For example, for a subject with n measurements, there should be n rows for this subject. The # of rows in y matrix is the total number of measurements for all subjects in the study. The columns in Y should start with the longitudinal outcome (column 1), the covariates for the random effects, and then the covariates for the fixed effects.
cfile	C matrix for competing risks failure time data. Each subject has one data entry, so the number of rows equals to the number of subjects. The survival / censoring time is included in the first column, and the failure type coded as 0 (censored events), 1 (risk 1), or 2 (risk 2) is given in the second column. Two competing risks are assumed. The covariates are included in the third column and on.
mfile	M vector to indicate the number of longitudinal measurements per subject. The number of rows equals to the number of subjects.
point	Quadrature points used in the EM procedure.Default is 20.
maxiterations	Maximum values of iterations. Default is 100000.
do.trace	Print detailed information of each iteration. Default is false, i.e., not to print the iteration details.
type_file	Types of inputs. Default is true, i.e. data files with headers. If set to "F", inputs are changed to data matrixes or data.frames (with headers)

Value

Object of class `JMcmprsk` with elements

vcmatrix	The variance-covariance matrix for all the parameters. The parameters are in the order: β, σ^2, γ, ν, and Σ
betas	The point estimates of β.
se_betas	The standard error estimate of β.
gamma_matrix	The point estimate of γ.
se_gamma_matrix	The standard error estimate of γ.
v_estimate	The point estimate of ν.
se_v_estimate	The standard error estimate of ν.
sigma2_val	The point estimate of σ^2.
se_sigma2_val	The standard error estimate of σ^2.
sigma_matrix	The point estimate of Σ (only the upper triangle portion of the matrix is output).

se_sigma	The standard error estimate of Σ.The standard errors are given in this order: main diagonal, the second m
loglike	Log Likelihood.

References

- Elashoff, Robert M., Gang Li, and Ning Li. "A joint model for longitudinal measurements and survival data in the presence of multiple failure types." Biometrics 64.3 (2008): 762-771.

See Also

jmo

Examples

```
# A toy example on a dataset called from file paths
require(JMcmprsk)
set.seed(123)
yfile=system.file("extdata", "jmcsimy.txt", package = "JMcmprsk")
cfile=system.file("extdata", "jmcsimc.txt", package = "JMcmprsk")
mfile=system.file("extdata", "jmcsimm.txt", package = "JMcmprsk")
jmc_0fit = jmc_0(p=4, yfile, cfile, mfile, point=6, do.trace = FALSE)
## Not run:
# A toy example on data frames/matrices
require(JMcmprsk)
set.seed(123)
data(lung)
lungY <- lung[, c(2:11)]
lungC <- unique(lung[, c(1, 12, 13, 6:10)])
lungC <- lungC[, -1]
lungM <- data.frame(table(lung$ID))
lungM <- as.data.frame(lungM[, 2])
res1=jmc_0(p=8, lungY, lungC, lungM, point=20, do.trace = FALSE, type_file = FALSE)
res1

## End(Not run)
```

---

jmo *An integrated function for reconstructing data and do the joint modelling*

Description

Reconstruct data into a regular longitudinal format as a refined dataset and do joint modelling for this refined data with ordinal outcome.

Usage

```
jmo(
  long_data,
  surv_data,
  out,
  FE,
  RE,
  NP,
  ID,
  cate = NULL,
  intcpt = 1,
  quad.points = 20,
  max.iter = 10000,
  quiet = TRUE,
  do.trace = FALSE
)
```

Arguments

long_data	Data matrix for longitudinal in long format. The time variable should be labeled 'time'.
surv_data	Data matrix for competing risks data. Each subject has one row of observation (as opposed to the long_data). First and second column should be the observed event time and censoring indicator, respectively. The coding for the censoring indicator is as follows: 0 - censored events, 1 - risk 1, 2 - risk 2. Two competing risks are assumed.
out	Column name for outcome variable in long_data.
FE	Vector of column names that correspond to the fixed effects in long_data. If missing, then all columns except for the outcome and ID columns will be considered.
RE	Types/Vector of random effects in long_data. The available type are "intercept", "linear", "quadratic" (time-related random effect specification) or other covariates in the input dataset.
NP	Vector of column names that correspond to the non-proportional odds covariates. It won't run the model if NP is not specified.
ID	Column name for subject ID number in long_data.
cate	Vector of categorical variables in long_data.
intcpt	Specify either 0 or 1. Default is set as 1. 0 means no intercept in random effect.
quad.points	Number of quadrature points used in the EM procedure. Default is 20. Must be an even number. Larger values means higher accuracy but more time-consuming.
max.iter	Max iterations. Default is 10000.
quiet	Logical. Print progress of function. Default is TRUE.
do.trace	Logical. Print the parameter estimates during the iterations. Default is FALSE.

Value

Object of class `JMcmprsk` with elements

`vcmatrix`	The variance-covariance matrix for all the parameters. The parameters are in the order: β, σ^2, γ, ν, and Σ
`betas`	The point estimates of β.
`se_betas`	The standard error estimate of β.
`gamma_matrix`	The point estimate of γ.
`se_gamma_matrix`	The standard error estimate of γ.
`v_estimate`	The point estimate of ν.
`se_v_estimate`	The standard error estimate of ν.
`sigma2_val`	The point estimate of σ^2.
`se_sigma2_val`	The standard error estimate of σ^2.
`sigma_matrix`	The point estimate of Σ (only the upper triangle portion of the matrix is output).
`se_sigma`	The standard error estimate of Σ.The standard errors are given in this order: main diagonal, the second m
`loglike`	Log Likelihood.

See Also

`jmo_0`

Examples

```
require(JMcmprsk)
set.seed(123)
data(ninds)
yread <- ninds[, c(1, 2:14)]
cread <- ninds[, c(1, 15, 16, 6, 10:14)]
cread <- unique(cread)

# Please note only those variables that will appear in the model can be included
res1 <- jmo(yread, cread, out = "Y",
            FE = c("group", "time3", "time6", "time12", "mrkprior",
                   "smlves", "lvORcs", "smlves.group", "lvORcs.group"),
            cate = NULL,RE = "intercept", NP = c("smlves", "lvORcs"),
            ID = "ID",intcpt = 1, quad.points = 6,
            max.iter = 1000, quiet = FALSE, do.trace = FALSE)
 res1


## Not run:
#Create two categorical variables and add them into yread
ID <- cread$ID
set.seed(100)
sex <- sample(c("Female", "Male"), nrow(cread), replace = T)
race <- sample(c("White", "Black", "Asian", "Hispanic"), nrow(cread), replace = T)
cate_var <- data.frame(ID, sex, race)
if (require(dplyr)) {
  yread <- dplyr::left_join(yread, cate_var, by = "ID")
    }
```

```
  res2 <- jmo(yread, cread, out = "Y",
              FE = c("group", "time3", "time6", "time12", "mrkprior",
              "smlves", "lvORcs", "smlves.group", "lvORcs.group"), cate = c("race", "sex"),
         RE = "intercept", NP = c("smlves", "lvORcs", "race", "sex"), ID = "ID",intcpt = 1,
              quad.points = 20, max.iter = 10000, quiet = FALSE, do.trace = FALSE)
  res2

## End(Not run)
```

---

jmo_0 *Joint Modelling for Ordinal outcomes*

Description

Joint modeling of longitudinal ordinal data and competing risks

Usage

```
jmo_0(
  p,
  s,
  yfile,
  cfile,
  mfile,
  point = 20,
  maxiterations = 1e+05,
  do.trace = FALSE,
  type_file = TRUE
)
```

Arguments

p	The dimension of proportional odds covariates (not including intercept) in yfile.
s	The dimension of non-proportional odds covariates in yfile.
yfile	Y matrix for longitudinal measurements in long format. For example, for a subject with n measurements, there are n rows for this subject. The # of rows in y matrix is the total number of measurements for all subjects. The columns in Y are ordered this way: the longitudinal outcome (column 1), then the covariates for random effects, and lastly, the covariates for fixed effects (no intercept).
cfile	C matrix for competing risks failure time data. Each subject has one data entry, so the number of rows equals to the number of subjects. The survival / censoring time is included in the first column, and the failure type coded as 0 (censored events), 1 (risk 1), or 2 (risk 2) is given in the second column. Two competing risks are assumed. The covariates are included in the third column and on.

mfile	M vector to indicate the number of longitudinal measurements per subject. The number of rows equals to the number of subjects.
point	Quadrature points used in the EM procedure. Default is 20.
maxiterations	Maximum values of iterations. Default is 100000.
do.trace	Print detailed information of each iteration. Default is false, not to print the iteration details.
type_file	Types of inputs. Default is true, i.e. data files with headers. If set to "F", inputs are changed to data matrixes or data.frames (with headers)

Value

Object of class JMcmprsk with elements

vcmatrix	The variance-covariance matrix for all the parameters. The parameters are in the order: β, α, θ, γ, ν, and
betas	The point estimates of β.
se_betas	The standard error estimate of β.
alphamatrix	The point estimates of α.
se_alphas	The standard error estimate of α.
theta	The point estimates of θ.
se_theta	The standard error estimate of θ.
gamma_matrix	The point estimate of γ.
se_gamma_matrix	The standard error estimate of γ.
v_estimate	The point estimate of ν.
se_v_estimate	The standard error estimate of ν.
sigma_matrix	The point estimate of Σ (only the upper triangle portion of the matrix is output).
se_sigma	The standard error estimate of Σ.The standard errors are given in this order: main diagonal, the second m
loglike	Log Likelihood.

References

- Ning Li,Robert M. Elashoff,Gang Li and Jeffrey Saver. "Joint modeling of longitudinal ordinal data and competing risks survival times and analysis of the NINDS rt-PA stroke trial." Statistics in medicine 29.5 (2010): 546-557.

See Also

jmc_0

Examples

```
require(JMcmprsk)
set.seed(123)

# A toy example on a dataset called from file paths
yfn=system.file("extdata", "jmosimy.txt", package = "JMcmprsk")
cfn=system.file("extdata", "jmosimc.txt", package = "JMcmprsk")
mfn=system.file("extdata", "jmosimm.txt", package = "JMcmprsk")
fit <- jmo_0(p=3,s=1, yfn,cfn,mfn,point=6,do.trace = FALSE)
```

```
fit

## Not run:
# A toy example on a dataset called from data frame
data(ninds)
yread <- ninds[, c(2:14)]
mread <- as.data.frame(table(ninds$ID))
mread <- as.data.frame(mread[, 2])
cread <- ninds[, c(1, 15, 16, 6, 10:14)]
cread <- unique(cread)
cread <- cread[, -1]
jmofit=jmo_0(p=9,s=2, yread,cread,mread,point=6,do.trace = FALSE, type_file = FALSE)
jmofit

## End(Not run)
```

`linearTest` *Linear hypothesis testing of joint models*

Description

Joint modelling for longitutal and censored data with competing risks

Usage

```
linearTest(
  object,
  coeff = c("beta", "gamma", "alpha"),
  La = "identity",
  Lb = "identity",
  Lg = "identity",
  Ca = 0,
  Cb = 0,
  Cg = 0,
  digits = 4,
  ...
)
```

Arguments

`object`	The JMcmprsk object returned by either jmo or jmc function.
`coeff`	Types of coefficients selected for Wald. Note "alpha" is only avaiable to jmo type JMcmprsk object.
`La`	Linear contrast of the fixed effects of non-proportional odds covariates * (# of levels of the outcome - 2) in the longitudinal part. Default is "identity", i.e., all the fixed effects equal to zero. Otherwise, La must be a matrix.

Lb	Linear contrast of the fixed effects of proportional odds covariates in the longitudinal part. Default is "identity", i.e., all the fixed effects equal to zero. Otherwise, Lb must be a matrix.
Lg	Linear contrast of the fixed effects of covariates * # of competing risks in the survival part. Default is "identity", i.e., all the fixed effects equal to zero. Otherwise, Lg must be a matrix.
Ca	The hypothesized value of linear combination of the fixed effects of non-proportional odds covariates * (# of levels of the outcome - 2) in the longitudinal part. Default is 0. Otherwise, Ca must be a number / vector.
Cb	The hypothesized value of linear combination of the fixed effects of proportional odds covariates in the longitudinal part. Default is 0. Otherwise, Cb must be a number / vector.
Cg	The hypothesized value of linear combination of the fixed effects of covariates * # of competing risks in the survival part. Default is 0. Otherwise, Cg must be a number / vector.
digits	number of digits to be printed out.
...	further arguments passed to or from other methods.

Details

Wald test statistic is used for hypothesis testing on multiple parameters:

$H_0 : L\theta = C$ vs: $H_1 : L\theta \neq C$

The test statistic is:

$(L\hat{\theta} - C)'(L\hat{V}_\theta L)^{-1}(L\hat{\theta} - C) \sim \chi^2_q$,

where $\hat{V}_\theta$ is the estimate of covariance of the parameter θ and q is the rank of the linear contrast L.

Value

Return a Wald test statistic and the p value

beta	The Wald test for fixed effects for the longitutal part,i.e. β in jmo or jmc output.
gamma	The Wald test for fixed effects for the survival part,i.e. γ in jmo or jmc output.
alpha	The Wald test for non-proportional odds covariates,i.e. α in jmo output.

---

lung *Scleroderma lung study data*

Description

The lung data frame has 715 rows and 13 columns.

Usage

```
data(lung)
```

Format

A balanced data set with respect to the times at which observations recorded. The data consists of the following variables on each patient:

`ID` patient identifier.

`FVC` forced vital capacity (%) determined at 3-month intervals from the baseline.

`time_RE` time at visit at 3-month intervals.

`intercept` column of 1's for model setup.

`time` time at visit at 3-month intervals. Same as `time_RE`.

`FVC0` forced vital capacity (%) at baseline.

`FIB0` baseline lung fibrosis.

`CYC` treatment allocation. Coded as `1` = oral cyclophosphamide; `0` = placebo.

`FVC0.CYC` interaction term between `FVC0` and `CYC`.

`FIB0.CYC` interaction term between `FIB0` and `CYC`.

`time.CYC` interaction term between `time` and `CYC`.

`time.CYC` interaction term between `time` and `CYC`.

`surv` time to treatment failure or death.

`failure_type` treatment failure/death indicator. Coded as `0` = censored; `1` = death; `2` = treatment failure.

References

Elashoff, Robert M., Gang Li, and Ning Li. "A joint model for longitudinal measurements and survival data in the presence of multiple failure types." Biometrics 64.3 (2008): 762-771.

---

ninds *NINDS rt-PA stroke trial data*

Description

The `ninds` data frame has 1906 rows and 16 columns.

Usage

```
data(ninds)
```

Format

This data frame contains the following columns:

`ID` patient identifier.

`Y` Acute ischemic stroke in an ordinal scale. Coded as `1` = no symptoms or no significant disability despite symptoms; `2` = slight disability; `3` = moderate disability or moderately severe disability; `4` = severe disability or dead.

`intcpt_RE` a column of 1's for model setup as a random intercept covariate.

`smlves_NP` small vessel occlusive disease as a non-proportional odds covariate.

`lvORcs_NP` large vessel atherosclerosis / cardioembolic stroke as a non-proportional odds covariate.

`group` treatment group indicator.

`time3` dummy variable to indicate 3 months of follow-up.

`time6` dummy variable to indicate 6 months of follow-up.

`time12` dummy variable to indicate 12 months of follow-up.

`mrkprior` modified Rankin scale prior stroke onset.

`smlves` small vessel occlusive disease as a proportional odds covariate.

`lvORcs` large vessel atherosclerosis / cardioembolic stroke as a proportional odds covariate.

`smlves.group` interaction term between `smlves` and `group`.

`lvORcs.group` interaction term between `lvORcs` and `group`.

`surv` time to drop out or remaining in severe disability.

`comprisk` event indicator. Coded as `0` = censored; `1` = drop out; `2` = remaining in severe disability.

References

Li, Ning, et al. "Joint modeling of longitudinal ordinal data and competing risks survival times and analysis of the NINDS rt-PA stroke trial." Statistics in medicine 29.5 (2010): 546-557.

`print.JMcmprsk` *Print JMcmprsk*

Description

Print contents of JMcmprsk object.

Usage

```
## S3 method for class 'JMcmprsk'
print(x, digits = 4, ...)
```

Arguments

`x`	Object of class 'JMcmprsk'.
`digits`	The desired number of digits after the decimal point. Default is 4.
`...`	Further arguments passed to or from other methods.

Author(s)

Hong Wang

See Also

jmc

SimDataC *Data simulation of continuous outcomes and competing risks*

Description

Simulation of continuous longitudinal outcome and competing risks data Currently, only the simulation in Elashoff et al(2008) is implemented.

Usage

```
SimDataC(
  k_val,
  p1_val,
  p1a_val,
  p2_val,
  g_val,
  truebeta,
  truegamma,
  randeffect,
  yfn,
  cfn,
  mfn
)
```

Arguments

k_val	The number of subjects in study.
p1_val	The dimension of fixed effects in longitudinal measurements.
p1a_val	The dimension of random effects in longitudinal measurements.
p2_val	The dimension of fixed effects in competing risks failure time data.
g_val	The number of type of failure in competing risks data.
truebeta	True values for beta, the longitudinal coefficients.
truegamma	True values for gamma, the survival coefficients.
randeffect	True values for random effects in longitudinal and competing risks parts,namely in the order of σ,σ_b,ν_2,σ_u.
yfn	Filename of genereated Y matrix for longitudinal measurements in long format.
cfn	Filename of genereated C matrix for competing risks failure time data.
mfn	Filename of genereated M vector to indicate the number of longitudinal measurements per subject.

Value

Files with names yfn, cfn and mfn.

censoring_rate	Censoring rate of the survival data.
rate1	Censoring rate of competing risk 1.
rate2	Censoring rate of competing risk 2.
yfn	Filename of genereated Y matrix for longitudinal measurements.
cfn	Filename of genereated C matrix for competing risks failure time data.
mfn	Filename of genereated M vector to indicate the number of longitudinal measurements per subject.

References

- Elashoff, Robert M., Gang Li, and Ning Li. "A joint model for longitudinal measurements and survival data in the presence of multiple failure types." Biometrics 64.3 (2008): 762-771.

See Also

SimDataO

Examples

```
# A toy example testint data generations
require(JMcmprsk)
set.seed(123)
yfn=tempfile(pattern = "", fileext = ".txt")
cfn=tempfile(pattern = "", fileext = ".txt")
mfn=tempfile(pattern = "", fileext = ".txt")
k_val=30;p1_val=4;p1a_val=1; p2_val=2;g_val=2;
truebeta=c(10,-1,1.5,0.6);truegamma=c(0.8,-1,0.5,-1); randeffect=c(5,0.5,0.5,0.5);
#writing files
SimDataC(k_val, p1_val, p1a_val, p2_val, g_val,truebeta,
         truegamma, randeffect, yfn,  cfn,  mfn)

jmc_0(p=4,yfn,cfn,mfn,point=6)
```

SimDataO *Data simulation of ordinal outcomes and competing risks*

Description

Simulation of ordinal longitudinal outcome and competing risks data Currently, only the simulation in Li et al(2010) is implemented.

Usage

```
SimDataO(
  k_val,
  p1_val,
  p1a_val,
  p2_val,
  g_val,
  truebeta,
  truetheta,
  truegamma,
  randeffect,
  yfn,
  cfn,
  mfn
)
```

Arguments

k_val	The number of subjects in study.
p1_val	The dimension of fixed effects in longitudinal measurements.
p1a_val	The dimension of random effects in longitudinal measurements.
p2_val	The dimension of fixed effects in competing risks failure time data.
g_val	The number of type of failure in competing risks data.
truebeta	True values for beta, the longitudinal coefficients.
truetheta	True values for theta, subset of the non-proportional odds longitudinal coefficients.
truegamma	True values for gamma, the survival coefficients.
randeffect	True values for random effects in longitudinal and competing risks parts,namely in the order of σ_b,ν_2,σ_u.
yfn	Filename of genereated Y matrix for longitudinal measurements in long format.
cfn	Filename of genereated C matrix for competing risks failure time data.
mfn	Filename of genereated M vector to indicate the number of longitudinal measurements per subject.

Value

Files with names yfn, cfn and mfn.

censoring_rate	Censoring rate of the survival data.
rate1	Censoring rate of competing risk 1.
rate2	Censoring rate of competing risk 2.
yfn	Filename of genereated Y matrix for longitudinal measurements.
cfn	Filename of genereated C matrix for competing risks failure time data.
mfn	Filename of genereated M vector to indicate the number of longitudinal measurements per subject.

References

- Ning Li,Robert M. Elashoff,Gang Li and Jeffrey Saver. "Joint modeling of longitudinal ordinal data and competing risks survival times and analysis of the NINDS rt-PA stroke trial." Statistics in medicine 29.5 (2010): 546-557.

See Also

SimDataC

Examples

```
# A toy example testint data generations
require(JMcmprsk)
set.seed(123)
yfn=tempfile(pattern = "", fileext = ".txt")
cfn=tempfile(pattern = "", fileext = ".txt")
mfn=tempfile(pattern = "", fileext = ".txt")
 k_val=50;p1_val=3;p1a_val=1; p2_val=2;g_val=2;
truebeta=c(-1,1.5,0.8);truetheta=c(-0.5,1);truegamma=c(0.8,-1,0.5,-1); randeffect=c(1,0.5,0.5);
#writing files
SimDataO(k_val, p1_val, p1a_val, p2_val, g_val,
      truebeta, truetheta, truegamma, randeffect, yfn,  cfn,  mfn)

jmo_0(p=3,s=1, yfn,cfn,mfn,point=10,do.trace = TRUE)
```

`summary.JMcmprsk` *Extraction of standard error and 95% confidence interval of longitudinal/survival sub-model fixed effects*

Description

Joint modelling for longitutal and censored data with competing risks

Usage

```
## S3 method for class 'JMcmprsk'
summary(object, coeff = c("longitudinal", "survival"), digits = 4, ...)
```

Arguments

`object`	The JMcmprsk object returned by either jmo or jmc function.
`coeff`	The coefficients returned by the JMcmprsk object. Results of longitudinal/survival sub-model will be printed out when typing "longitudinal" or "survival".
`digits`	The number of digits to print out.
`...`	further arguments passed to or from other methods.

Value

Return standard errors of parameters with variable names

References

- Elashoff, Robert M., Gang Li, and Ning Li. "A joint model for longitudinal measurements and survival data in the presence of multiple failure types." Biometrics 64.3 (2008): 762-771.

See Also

jmc

Index