Package 'JMbayes2'

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Type Package

Title Extended Joint Models for Longitudinal and Time-to-Event Data

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BugReports https://github.com/drizopoulos/JMbayes2/issues

Description Fit joint models for longitudinal and time-to-event data under the Bayesian approach. Multiple longitudinal outcomes of mixed type (continuous/categorical) and multiple event times (competing risks and multi-state processes) are accommodated. Rizopoulos (2012, ISBN:9781439872864).

Suggests lattice, knitr, rmarkdown, pkgdown

Encoding UTF-8

Depends survival, nlme, GLMMadaptive, splines

Imports coda, Rcpp, parallel, matrixStats, ggplot2, gridExtra

LinkingTo Rcpp, RcppArmadillo

LazyLoad yes

LazyData yes

License GPL (>= 3)

URL https://drizopoulos.github.io/JMbayes2/,
https://github.com/drizopoulos/JMbayes2

NeedsCompilation yes

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Repository CRAN

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R topics documented:

`aids` *Didanosine versus Zalcitabine in HIV Patients*

Description

A randomized clinical trial in which both longitudinal and survival data were collected to compare the efficacy and safety of two antiretroviral drugs in treating patients who had failed or were intolerant of zidovudine (AZT) therapy.

Format

A data frame with 1408 observations on the following 9 variables.

`patient` patients identifier; in total there are 467 patients.

`Time` the time to death or censoring.

`death` a numeric vector with 0 denoting censoring and 1 death.

`CD4` the CD4 cells count.

`obstime` the time points at which the CD4 cells count was recorded.

`drug` a factor with levels `ddC` denoting zalcitabine and `ddI` denoting didanosine.

`gender` a factor with levels `female` and `male`.

`prevOI` a factor with levels `AIDS` denoting previous opportunistic infection (AIDS diagnosis) at study entry, and `noAIDS` denoting no previous infection.

`AZT` a factor with levels `intolerance` and `failure` denoting AZT intolerance and AZT failure, respectively.

Note

The data frame `aids.id` contains the first CD4 cell count measurement for each patient. This data frame is used to fit the survival model.

References

Goldman, A., Carlin, B., Crane, L., Launer, C., Korvick, J., Deyton, L. and Abrams, D. (1996) Response of CD4+ and clinical consequences to treatment using ddI or ddC in patients with advanced HIV infection. *Journal of Acquired Immune Deficiency Syndromes and Human Retrovirology* **11**, 161–169.

Guo, X. and Carlin, B. (2004) Separate and joint modeling of longitudinal and event time data using standard computer packages. *The American Statistician* **58**, 16–24.

`crLong` *Transform Competing Risks Data in Long Format*

Description

In a competing risks setting this function expands the data frame with a single row per subject to a data frame in the long format in which each subject has as many rows as the number of competing events.

Usage

```
crLong(data, statusVar, censLevel,
    nameStrata = "strata", nameStatus = "status2")
```

Arguments

`data`	the data frame containing the competing risk data with a single row per subject.
`statusVar`	a character string denoting the name of the variable in `data` that identifies the status variable which equals 1 if the subject had any of the competing events and 0 otherwise.
`censLevel`	a character string or a scalar denoting the censoring level in the `statusVar` variable of `data`.
`nameStrata`	a character string denoting the variable that will be added in the long version of `data` denoting the various causes of event.
`nameStatus`	a character string denoting the variable that will be added in the long version of `data` denoting if the subject experience any of the competing events.

Value

A data frame in the long format with multiple rows per subject.

Author(s)

Dimitris Rizopoulos <d.rizopoulos@erasmusmc.nl>

References

Rizopoulos, D. (2012) *Joint Models for Longitudinal and Time-to-Event Data: with Applications in R*. Boca Raton: Chapman and Hall/CRC.

Putter, H., Fiocco, M., and Geskus, R. (2007). Tutorial in biostatistics: Competing risks and multi-state models. *Statistics in Medicine* **26**, 2389–2430.

Examples

```
head(crLong(pbc2.id, "status", "alive"))
```

---

jm *Joint Models for Longitudinal and Time-to-Event Data*

Description

Fits multivariate joint models for longitudinal and time-to-event data.

Usage

```
jm(Surv_object, Mixed_objects, time_var, functional_forms = NULL,
  data_Surv = NULL, id_var = NULL, priors = NULL, control = NULL, ...)

value(x)
slope(x)
area(x)

tv(x, knots = NULL, ord = 2L)
```

Arguments

`Surv_object` an object:

- of class 'coxph' fitted by function `coxph()` from package **survival**, or
- of class 'survreg' fitted by function `survreg()` from package **survival**.

`Mixed_objects` a `list` of objects or a single object. Objects may be:

- of class 'lme' fitted by function `lme()` from package **nlme**, or
- of class 'MixMod' fitted by function `mixed_model()` from package **GLMMadaptive**.

`time_var` a `character` string indicating the time variable in the mixed-effects model(s).

`functional_forms`
a `list` of formulas. Each formula corresponds to one longitudinal outcome and specifies the association structure between that outcome and the survival submodel as well as any interaction terms between the components of the longitudinal outcome and the survival submodel. See **Examples**.

data_Surv the data.frame used to fit the Cox/AFT survival submodel.

id_var a character string indicating the id variable in the survival submodel.

priors a named list of user-specified prior parameters:

- mean_betas_HC the prior mean vector of the normal prior for the regression coefficients of the covariates of the longitudinal model(s), which were hierarchically centered.
- Tau_betas_HC the prior precision matrix of the normal prior for the regression coefficients of the longitudinal model(s), which were hierarchically centered.
- mean_betas_nHC a list of the prior mean vector(s) of the normal prior(s) for the regression coefficients of the covariates of the longitudinal model(s), which were not hierarchically centered.
- Tau_betas_nHC a list of the prior precision matrix(ces) of the normal prior(s) for the regression coefficients of the longitudinal model(s), which were not Hierarchically Centered.
- mean_bs_gammas the prior mean vector of the normal prior for the B-splines coefficients used to approximate the baseline hazard.
- Tau_bs_gammas the prior precision matrix of the normal prior for the B-splines coefficients used to approximate the baseline hazard.
- A_tau_bs_gammas the prior shape parameter of the gamma prior for the precision parameter of the penalty term for the B-splines coefficients for the baseline hazard.
- B_tau_bs_gammas the prior rate parameter of the gamma prior for the precision parameter of the penalty term for the B-splines coefficients for the baseline hazard.
- rank_Tau_bs_gammas the prior rank parameter for the precision matrix of the normal prior for the B-splines coefficients used to approximate the baseline hazard.
- mean_gammas the prior mean vector of the normal prior for the regression coefficients of baseline covariates.
- Tau_gammas the prior precision matrix of the normal prior for the regression coefficients of baseline covariates.
- penalty_gammas a character string with value 'none', 'ridge', or 'horseshoe' indicating whether the coefficients of the baseline covariates included in the survival submodel should not be shrunk, shrank using ridge prior, or shrank using horseshoe prior, respectively.
- A_lambda_gammas the prior shape parameter of the gamma prior for the precision parameter of the local penalty term for the baseline regression coefficients. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.
- B_lambda_gammas the prior rate parameter of the gamma prior for the precision parameter of the local penalty term for the baseline regression coefficients. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.
- A_tau_gammas the prior shape parameter of the gamma prior for the precision parameter of the global penalty term for the baseline regression coefficients.

Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.

B_tau_gammas the prior rate parameter of the gamma prior for the precision parameter of the global penalty term for the baseline regression coefficients. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.

A_nu_gammas the prior shape parameter of the gamma prior for the variance hyperparameter for the precision parameter of the local penalty term for the baseline regression coefficients. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.

B_nu_gammas the prior rate parameter of the gamma prior for the variance hyperparameter for the precision parameter of the local penalty term for the baseline regression coefficients. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.

A_xi_gammas the prior shape parameter of the gamma prior for the variance hyperparameter for the precision parameter of the global penalty term for the baseline regression coefficients. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.

B_xi_gammas the prior rate parameter of the gamma prior for the variance hyperparameter for the precision parameter of the global penalty term for the baseline regression coefficients. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.

mean_alphas the prior mean vector of the normal prior for the association parameter(s).

Tau_alphas the prior mean vector of the normal prior for the association parameter(s).

penalty_alphas a character string with value 'none', 'ridge', 'horseshoe' indicating whether the coefficients association parameters should not be shrunk, shrank using ridge prior, or shrank using horseshoe prior, respectively.

A_lambda_alphas the prior shape parameter of the gamma prior for the precision parameter of the local penalty term for the association parameters. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.

B_lambda_alphas the prior rate parameter of the gamma prior for the precision parameter of the local penalty term for the association parameters. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.

A_tau_alphas the prior shape parameter of the gamma prior for the precision parameter of the global penalty term for the association parameters. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.

B_tau_alphas the prior rate parameter of the gamma prior for the precision parameter of the global penalty term for the association parameters. Only relevant when penalty_gammas = 'ridge' or penalty_gammas = 'horseshoe'.

A_nu_alphas the prior shape parameter of the gamma prior for the variance hyperparameter for the precision parameter of the local penalty term for the association parameters. Only relevant when penalty_gammas = 'ridge', or penalty_gammas = 'horseshoe'.

B_nu_alphas the prior rate parameter of the gamma prior for the variance hyperparameter for the precision parameter of the local penalty term for the association parameters. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.

A_xi_alphas the prior shape parameter of the gamma prior for the variance hyperparameter for the precision parameter of the global penalty term for the association parameters. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.

B_xi_alphas the prior rate parameter of the gamma prior for the variance hyperparameter for the precision parameter of the global penalty term for the association parameters. Only relevant when penalty_gammas = 'ridge' or when penalty_gammas = 'horseshoe'.

gamma_prior_D_sds logical; if TRUE, a gamma prior will be used for the standard deviations of the D matrix (variance-covariance matrix of the random effects). Defaults to TRUE

D_sds_df the prior degrees of freedom parameter for the half-t prior for the standard deviations of the D matrix (variance-covariance matrix of the random effects).

D_sds_sigma the prior sigma parameter vector for the half-t prior for the standard deviations of the D matrix (variance-covariance matrix of the random effects).

D_sds_shape the prior shape parameter for the gamma prior for the standard deviations of the D matrix (variance-covariance matrix of the random effects).

D_sds_mean the prior mean parameter vector for the gamma prior for the standard deviations of the D matrix (variance-covariance matrix of the random effects).

D_L_etaLKJ the prior eta parameter for the LKJ prior for the correlation matrix of the random effects.

sigmas_df the prior degrees of freedom parameter for the half-t prior for the error term(s).

sigmas_sigma the prior sigma parameter for the half-t prior for the error term(s).

control a list of control values with components:

GK_k the number of quadrature points for the Gauss Kronrod rule; options 15 and 7.

Bsplines_degree the degree of the splines in each basis; default quadratic splines.

base_hazard_segments the number of segments to split the follow-up period. Defaults to 10.

diff the order of the difference used in the penalty matrix for the B-splines for h_0. Defaults to 2.

n_chains an integer specifying the number of chains for the MCMC. Defaults to 1.

n_burnin an integer specifying the number of burn-in iterations. Defaults to 500.

n_iter an integer specifying the number of total iterations per chain. Defaults to 3500.

seed the seed used in the sampling procedures. Defaults to 123.

MALA a logical; if TRUE, the MALA algorithm is used when updating the elements of the Cholesky factor of the D matrix. Defaults to FALSE.

save_random_effects a logical; if TRUE, the full MCMC results of the random effects will be saved and returned with the jm object. Defaults to FALSE.

cores an integer specifying the number of cores to use. Defaults to the available cores minus one.

x a numeric input variable.

knots a numeric vector of knots.

ord an integer denoting the order of the spline.

... arguments passed to control.

Details

The mathematical details regarding the definition of the multivariate joint model, and the capabilities of the package can be found in the vignette in the doc directory.

Value

A list of class jm with components:

mcmc a list of the MCMC samples for each parameter.

acc_rates a list of the acceptance rates for each parameter.

logLik a matrix of dimensions [((n_iter -n_burnin)/n_thin)*n_thin, number of individuals], with element [i, j] being the conditional log-Likelihood value of the i^{th} iteration for the j^{th} individual.

mlogLik a matrix of dimensions [((n_iter -n_burnin)/n_thin)*n_thin, number of individuals], with element [i, j] being the marginal log-Likelihood value of the i^{th} iteration for the j^{th} individual.

running_time an object of class proc_time with the time used to run jm.

statistics a list with posterior estimates of the parameters (means, medians, standard deviations, standard errors, effective sample sizes, tail probabilities, upper and lower bounds of credible intervals, etc.).

fit_stats a list of lists with fit statistics (DIC, pD, LPML, CPO, WAIC) for both conditional and marginal formulations.

model_data a list of data used to fit the model.

model_info a list of components of the fit useful to other functions.

initial_values a list with the initial values of the parameters.

control a copy of the control values used to fit the model.

priors a copy of the priors used to fit the model.

call the matched call.

Author(s)

Dimitris Rizopoulos <d.rizopoulos@erasmusmc.nl>

See Also

methods.jm, coda_methods.jm

Examples

```
##############################################################################

#############################################
# Univariate joint model for serum bilirubin #
# 1 continuous outcome                      #
#############################################

# [1] Fit the mixed model using lme().
fm1 <- lme(fixed = log(serBilir) ~ year * sex + I(year^2) +
           age + prothrombin, random =  ~ year | id, data = pbc2)

# [2] Fit a Cox model, specifying the baseline covariates to be included in the
# joint model.
fCox1 <- coxph(Surv(years, status2) ~ drug + age, data = pbc2.id)

# [3] The basic joint model is fitted using a call to jm() i.e.,
joint_model_fit_1 <- jm(fCox1, fm1, time_var = "year", n_chains = 1L)
summary(joint_model_fit_1)
traceplot(joint_model_fit_1)

##############################################################################

#############################################################################
# Multivariate joint model for serum bilirubin, hepatomegaly and ascites #
# 1 continuous outcome, 2 categorical outcomes                           #
#############################################################################

# [1] Fit the mixed-effects models using lme() for continuous
# outcomes and mixed_model() for categorical outcomes.
fm1 <- lme(fixed = log(serBilir) ~ year * sex,
           random = ~ year | id, data = pbc2)

fm2 <- mixed_model(hepatomegaly ~ sex + age + year, data = pbc2,
                   random = ~ year | id, family = binomial())

fm3 <- mixed_model(ascites ~ year + age, data = pbc2,
                   random = ~ year | id, family = binomial())

# [2] Save all the fitted mixed-effects models in a list.
Mixed <- list(fm1, fm2, fm3)

# [3] Fit a Cox model, specifying the baseline covariates to be included in the
```

```
# joint model.
fCox1 <- coxph(Surv(years, status2) ~ drug + age, data = pbc2.id)

# [4] The joint model is fitted using a call to jm() i.e.,
joint_model_fit_2 <- jm(fCox1, Mixed, time_var = "year", n_chains = 1L)
summary(joint_model_fit_2)
traceplot(joint_model_fit_2)

################################################################################

######################
# Slope & Area Terms #
######################

# We extend model 'joint_model_fit_2' by including the value and slope term for
# bilirubin, the area term for hepatomegaly (in the log-odds scale), and the
# value and area term for spiders (in the log-odds scale).
# To include these terms into the model, we specify the 'functional_forms'
# argument. This should be a list of right side formulas. Each component of the
# list should have as name the name of the corresponding outcome variable. In
# the right side formula we specify the functional form of the association using
# functions 'value()', 'slope()' and 'area()'.
# Notes: (1) For terms not specified in the 'functional_forms' list, the default
# value functional form is used.

# [1] Fit the mixed-effects models using lme() for continuous outcomes
# and mixed_model() for categorical outcomes.
fm1 <- lme(fixed = log(serBilir) ~ year * sex, random = ~ year | id, data = pbc2)

fm2 <- mixed_model(hepatomegaly ~ sex + age + year, data = pbc2,
                   random = ~ year | id, family = binomial())

fm3 <- mixed_model(ascites ~ year + age, data = pbc2,
                   random = ~ year | id, family = binomial())

# [2] Save all the fitted mixed-effects models in a list.
Mixed <- list(fm1, fm2, fm3)

# [3] Fit a Cox model, specifying the baseline covariates to be included in the
# joint model.
fCox1 <- coxph(Surv(years, status2) ~ drug + age, data = pbc2.id)

# [4] Specify the list of formulas to be passed to the functional_forms argument
# of jm().
fForms <- list("log(serBilir)" = ~ value(log(serBilir)) + slope(log(serBilir)),
               "hepatomegaly" = ~ area(hepatomegaly),
               "ascites" = ~ value(ascites) + area(ascites))

# [5] The joint model is fitted using a call to jm() and passing the list
# to the functional_forms argument.
joint_model_fit_2 <- jm(fCox1, Mixed, time_var = "year",
                        functional_forms = fForms, n_chains = 1L)
summary(joint_model_fit_2)
```

jm coda Methods *Various Methods for Functions from the* coda *Package*

Description

Methods for an object of class "jm" for diagnostic functions.

Usage

```
traceplot(object, ...)

## S3 method for class 'jm'
traceplot(object,
  parm = c("all", "betas", "sigmas", "D", "bs_gammas",
           "tau_bs_gammas", "gammas", "alphas"), ...)

ggtraceplot(object, ...)

## S3 method for class 'jm'
ggtraceplot(object,
  parm = c("all", "betas", "sigmas", "D", "bs_gammas",
           "tau_bs_gammas", "gammas", "alphas"),
  size = 1, alpha = 0.8,
  theme = c('standard', 'catalog', 'metro',
                'pastel', 'beach', 'moonlight', 'goo', 'sunset'),
  grid = FALSE, gridrows = 3, gridcols = 1, ...)

gelman_diag(object, ...)

## S3 method for class 'jm'
gelman_diag(object,
  parm = c("all", "betas", "sigmas", "D", "bs_gammas",
           "tau_bs_gammas", "gammas", "alphas"), ...)

densplot(object, ...)

## S3 method for class 'jm'
densplot(object,
  parm = c("all", "betas", "sigmas", "D", "bs_gammas",
           "tau_bs_gammas", "gammas", "alphas"), ...)

ggdensityplot(object, ...)
```

```
## S3 method for class 'jm'
ggdensityplot(object,
  parm = c("all", "betas", "sigmas", "D", "bs_gammas",
           "tau_bs_gammas", "gammas", "alphas"),
  size = 1, alpha = 0.6,
  theme = c('standard', 'catalog', 'metro', 'pastel',
                'beach', 'moonlight', 'goo', 'sunset'),
  grid = FALSE, gridrows = 3, gridcols = 1, ...)

cumuplot(object, ...)

## S3 method for class 'jm'
cumuplot(object,
  parm = c("all", "betas", "sigmas", "D", "bs_gammas",
           "tau_bs_gammas", "gammas", "alphas"), ...)
```

Arguments

`object`	an object inheriting from class `"jm"`.
`parm`	a character string specifying which parameters of the joint model to plot. Possible options are `'all'`, `'betas'`, `'alphas'`, `'sigmas'`, `'D'`, `'bs_gammas'`, `'tau_bs_gammas'`, or `'gammas'`.
`size`	the width of the traceplot line in mm. Defaults to 1.
`alpha`	the opacity level of the traceplot line. Defaults to 0.8.
`theme`	a character string specifying the color theme to be used. Possible options are `'standard'`, `'catalog'`, `'metro'`, `'pastel'`, `'beach'`, `'moonlight'`, `'goo'`, or `'sunset'`.
`grid`	logical; defaults to `FALSE`. If `TRUE`, the plots are returned in grids split over multiple pages. For more details see the documentation for `gridExtra::marrangeGrob()`.
`gridrows`	number of rows per page for the grid. Only relevant when using `grid = TRUE`. Defaults to 3.
`gridcols`	number of columns per page for the grid. Only relevant when using `grid = TRUE`. Defaults to 1.
`...`	further arguments passed to the corresponding function from the **coda** package.

Value

`traceplot()` Plots the evolution of the estimated parameter vs. iterations in a fitted joint model.

`ggtraceplot()` Plots the evolution of the estimated parameter vs. iterations in a fitted joint model using **ggplot2**.

`gelman_diag()` Calculates the potential scale reduction factor for the estimated parameters in a fitted joint model, together with the upper confidence limits.

densplot() Plots the density estimate for the estimated parameters in a fitted joint model.

ggdensityplot() Plots the evolution of the estimated parameter vs. iterations in a fitted joint model using **ggplot2**.

cumuplot() Plots the evolution of the sample quantiles vs. iterations in a fitted joint model.

Author(s)

Dimitris Rizopoulos <d.rizopoulos@erasmusmc.nl>

See Also

jm

Examples

```
# linear mixed model fits
fit_lme1 <- lme(log(serBilir) ~ year:sex + age,
                random = ~ year | id, data = pbc2)

fit_lme2 <- lme(prothrombin ~ sex,
                random = ~ year | id, data = pbc2)

# cox model fit
fit_cox <- coxph(Surv(years, status2) ~ age, data = pbc2.id)

# joint model fit
fit_jm <- jm(fit_cox, list(fit_lme1, fit_lme2), time_var = "year", n_chains = 1L)

# trace plot for the fixed effects in the linear mixed submodels
traceplot(fit_jm, parm = "betas")

# density plot for the fixed effects in the linear mixed submodels
densplot(fit_jm, parm = "betas")

# cumulative quantile plot for the fixed effects in the linear mixed submodels
cumuplot(fit_jm, parm = "betas")

# trace plot for the fixed effects in the linear mixed submodels
ggtraceplot(fit_jm, parm = "betas")
ggtraceplot(fit_jm, parm = "betas", grid = TRUE)

# trace plot for the fixed effects in the linear mixed submodels
ggdensityplot(fit_jm, parm = "betas")
ggdensityplot(fit_jm, parm = "betas", grid = TRUE)
```

jm Methods *Various Methods for Standard Generics*

Description

Methods for object of class "jm" for standard generic functions.

Usage

```
coef(object, ...)

## S3 method for class 'jm'
coef(object, ...)

fixef(object, ...)

## S3 method for class 'jm'
fixef(object, outcome = Inf, ...)

ranef(object, ...)

## S3 method for class 'jm'
ranef(object, outcome = Inf, post_vars = FALSE, ...)

terms(x, ...)

## S3 method for class 'jm'
terms(x, process = c("longitudinal", "event"),
                      type = c("fixed", "random"), ...)

model.frame(formula, ...)

## S3 method for class 'jm'
model.frame(formula, process = c("longitudinal", "event"),
                            type = c("fixed", "random"), ...)

model.matrix(object, ...)

## S3 method for class 'jm'
model.matrix(object, ...)

family(object, ...)

## S3 method for class 'jm'
family(object, ...)
```

```
compare_jm(..., type = c("marginal", "conditional"),
  order = c("WAIC", "DIC", "LPML", "none"))
```

Arguments

`object, x, formula`
: object inheriting from class `"jm"`.

`outcome`
: the index of the linear mixed submodel to extract the estimated fixed effects. If greater than the total number of submodels, extracts from all of them.

`post_vars`
: logical; if `TRUE`, returns the variance of the posterior distribution.

`process`
: which submodel(s) to extract the terms:

  - if `"longitudinal"`, the linear mixed model(s), or
  - if `"survival"`, the survival model.

`type`
: in `terms()` and `model.frame()`, which effects to select in the longitudinal process:

  - if `"fixed"`, the fixed-effects, or
  - if `"random"`, the random-efects.

  in `compare_jm()`, which log-likelihood function use to calculate the criteria:

  - if `"marginal"`, the marginal log-likelihood, or
  - if `"conditional"`, the conditional log-likelihood.

`...`
: further arguments; currently, none is used.
  in `compare_jm()`, a series of `jm` objects.

`order`
: which criteria use to sort the models in the output.

Details

`coef()` Extracts estimated fixed effects for the event process from a fitted joint model.

`fixef()` Extracts estimated fixed effects for the longitudinal processes from a fitted joint model.

`ranef()` Extracts estimated random effects from a fitted joint model.

`terms()` Extracts the terms object(s) from a fitted joint model.

`model.frame()` Creates the model frame from a fitted joint model.

`model.matrix()` Creates the design matrices for linear mixed submodels from a fitted joint model.

`family()` Extracts the error distribution and link function used in the linear mixed submodel(s) from a fitted joint model.

`compare_jm()` Compares two or more fitted joint models using the criteria WAIC, DIC, and LPML.

Value

`coef()` a list with the elements:

- `gammas`: estimated baseline fixed effects, and
- `association`: estimated association parameters.

`fixef()` a numeric vector of the estimated fixed effects for the `outcome` selected. If the `outcome` is greater than the number of linear mixed submodels, it returns a list of numeric vectors for all outcomes.

`ranef()` a numeric matrix with rows denoting the individuals and columns the random effects. If `postVar = TRUE`, the numeric matrix has the extra attribute "postVar".

`terms()` if `process = "longitudinal"`, a list of the terms object(s) for the linear mixed model(s).
if `process = "event"`, the terms object for the survival model.

`model.frame()` if `process = "longitudinal"`, a list of the model frames used in the linear mixed model(s).
if `process = "event"`, the model frame used in the survival model.

`model.matrix()` a list of the design matrix(ces) for the linear mixed submodel(s).

`family()` a list of `family` objects.

`compare_jm()` a list with the elements:

- `table`: a table with the criteria calculated for each joint model, and
- `type`: the log-likelihood function used to calculate the criteria.

Author(s)

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See Also

`jm`

Examples

```
# linear mixed model fits
fit_lme1 <- lme(log(serBilir) ~ year:sex + age,
                random = ~ year | id, data = pbc2)

fit_lme2 <- lme(prothrombin ~ sex,
                random = ~ year | id, data = pbc2)

# cox model fit
fit_cox <- coxph(Surv(years, status2) ~ age, data = pbc2.id)

# joint model fit
fit_jm <- jm(fit_cox, list(fit_lme1, fit_lme2), time_var = "year", n_chains = 1L)

# coef(): fixed effects for the event process
```

```
coef(fit_jm)

# fixef(): fixed effects for the first linear mixed submodel
fixef(fit_jm, outcome = 1)

# ranef(): random effects from all linear mixed submodels
head(ranef(fit_jm))

# terms(): random effects terms for the first linear mixed submodel
terms(fit_jm, process = "longitudinal", type = "random")[[1]]

# mode.frame(): model frame for the fixed effects in the second
# linear mixed submodel
head(model.frame(fit_jm, process = "longitudinal", type = "fixed")[[2]])

# model.matrix(): fixed effects design matrix for the first linear
# mixed submodel
head(model.matrix(fit_jm)[[1]])

# family(): family objects from both linear mixed submodels
family(fit_jm)

# compare_jm(): compare two fitted joint models
fit_lme1b <- lme(log(serBilir) ~ 1,
                 random = ~ year | id, data = pbc2)

fit_jm2 <- jm(fit_cox, list(fit_lme1b, fit_lme2), time_var = "year", n_chains = 1L)

compare_jm(fit_jm, fit_jm2)
```

JMbayes2 *Extended Joint Models for Longitudinal and Time-to-Event Data*

Description

Fit joint models for longitudinal and time-to-event data under the Bayesian approach. Multiple longitudinal outcomes of mixed type (continuous/categorical) and multiple event times (competing risks and multi-state processes) are accommodated.

Details

Package:	JMbayes2
Type:	Package
Version:	0.1-3
Date:	2021-01-18
License:	GPL (>=3)

This package fits joint models for longitudinal and time-to-event data. It can accommodate multiple longitudinal outcomes of different type (e.g., continuous, dichotomous, ordinal, counts), and assuming different distributions, i.e., Gaussian, Student's-t, Gamma, Beta, unit Lindley, censored Normal, Binomial, Poisson, Negative Binomial, and Beta-Binomial. For the event time process, right, left and interval censored data can be handled, while competing risks and multi-sate processes are also covered.

JMbayes2 fits joint models using Markov chain Monte Carlo algorithms implemented in C++. The package also offers several utility functions that can extract useful information from fitted joint models. The most important of those are included in the **See also** Section below.

Author(s)

Dimitris Rizopoulos, Grigorios Papageorgiou, Pedro Miranda Afonso

Maintainer: Dimitris Rizopoulos <d.rizopoulos@erasmusmc.nl>

References

Rizopoulos, D. (2012). Joint Models for Longitudinal and Time-to-Event Data With Applications in R. Boca Raton: Chapman & Hall/CRC.

See Also

`jm`, `methods.jm`, `coda_methods.jm`

`pbc2` *Mayo Clinic Primary Biliary Cirrhosis Data*

Description

Follow up of 312 randomised patients with primary biliary cirrhosis, a rare autoimmune liver disease, at Mayo Clinic.

Format

A data frame with 1945 observations on the following 20 variables.

`id` patients identifier; in total there are 312 patients.

`years` number of years between registration and the earlier of death, transplantion, or study analysis time.

`status` a factor with levels `alive`, `transplanted` and `dead`.

`drug` a factor with levels `placebo` and `D-penicil`.

`age` at registration in years.

`sex` a factor with levels `male` and `female`.

`year` number of years between enrollment and this visit date, remaining values on the line of data refer to this visit.

`ascites` a factor with levels `No` and `Yes`.

`hepatomegaly` a factor with levels `No` and `Yes`.

`spiders` a factor with levels `No` and `Yes`.

`edema` a factor with levels `No edema` (i.e., no edema and no diuretic therapy for edema), `edema no diuretics` (i.e., edema present without diuretics, or edema resolved by diuretics), and `edema despite diuretics` (i.e., edema despite diuretic therapy).

`serBilir` serum bilirubin in mg/dl.

`serChol` serum cholesterol in mg/dl.

`albumin` albumin in g/dl.

`alkaline` alkaline phosphatase in U/liter.

`SGOT` SGOT in U/ml.

`platelets` platelets per cubic ml / 1000.

`prothrombin` prothrombin time in seconds.

`histologic` histologic stage of disease.

`status2` a numeric vector with the value 1 denoting if the patient was dead, and 0 if the patient was alive or transplanted.

Note

The data frame `pbc2.id` contains the first measurement for each patient. This data frame is used to fit the survival model.

References

Fleming, T. and Harrington, D. (1991) *Counting Processes and Survival Analysis*. Wiley, New York.

Therneau, T. and Grambsch, P. (2000) *Modeling Survival Data: Extending the Cox Model*. Springer-Verlag, New York.

`prothro` *Prednisone versus Placebo in Liver Cirrhosis Patients*

Description

A randomized trial on 488 liver cirrhosis patients.

Format

Two data frames with the following variables.

`id` patients identifier; in total there are 467 patients.

`pro` prothrobin measurements.

`time` for data frame `prothro` the time points at which the prothrobin measurements were taken; for data frame `prothros` the time to death or censoring.

`death` a numeric vector with 0 denoting censoring and 1 death.

`treat` randomized treatment; a factor with levels "placebo" and "prednisone".

Source

http://www.gllamm.org/books/readme.html#14.6.

References

Andersen, P. K., Borgan, O., Gill, R. D. and Keiding, N. (1993). *Statistical Models Based on Counting Processes*. New York: Springer.

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