

Package: HDJM (via r-universe)

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Type Package

Title Penalized High-Dimensional Joint Model

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Description Joint models have been widely used to study the associations between longitudinal biomarkers and a survival outcome. However, existing joint models only consider one or a few longitudinal biomarkers and cannot deal with high-dimensional longitudinal biomarkers. This package can be used to fit our recently developed penalized joint model that can handle high-dimensional longitudinal biomarkers. Specifically, an adaptive lasso penalty is imposed on the parameters for the effects of the longitudinal biomarkers on the survival outcome, which allows for variable selection. Also, our algorithm is computationally efficient, which is based on the Gaussian variational approximation method.

Depends R (>= 3.6.0)

Imports Rcpp (>= 1.0.0), survival(>= 3.2), statmod(>= 1.4)

LinkingTo Rcpp, RcppArmadillo, RcppEnsmallen

License GPL-2

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control_list	<i>control_list</i>
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Description

This list contains a list of parameters specifying the joint model.

Details

- ID_name the variable name for the patient ID in both longitudinal data and survival data.
- item_name the variable name for the longitudinal outcomes in the longitudinal data.
- value_name the variable name for the longitudinal measurements in the longitudinal data.
- time_name the variable name for the measurement timepoints in the longitudinal data.
- fix_cov a set of variables names indicating the covariates of fixed-effects in the longitudinal submodel. If NULL, not baseline covariates are included.
- random_cov a set of variables names indicating the covariates of random-effects in the longitudinal submodel. If NULL, not baseline covariates are included.
- FUN a function specifying the time-related basis functions in the longitudinal submodel.
- ran_time_ind a vector of integers specifying which time-related basis functions are also included with random-effects in the longitudinal submodel.
- surv_time_name the variable name for the survival time in the survival data.
- surv_status_name the variable name for the censoring indicator in the survival data.
- surv_cov a set of variables names specifying the baseline covariates in the survival submodel.
- n_points an integer indicating the numebr of nodes being used in the Gaussian quadrature.

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`HDJM_fit`*The function to fit penalized HDJM.*

Description

The function is used to fit the penalized HDJM with adaptive lasso penalty.

Usage

```
HDJM_fit(  
  LongData = NULL,  
  SurvData = NULL,  
  marker.name = NULL,  
  control_list = NULL,  
  nlam = 50,  
  ridge = 0,  
  pmax = 10,  
  min_ratio = 0.01,  
  maxiter = 100,  
  eps = 1e-04,  
  UseSurvN = FALSE  
)
```

Arguments

<code>LongData</code>	a data frame containing the longitudinal data (see LongData).
<code>SurvData</code>	a data frame containing the survival data (see SurvData).
<code>marker.name</code>	a vector indicating which set of longitudinal biomarkers to be analyzed. If <code>NULL</code> , all biomarkers in <code>LongData</code> will be used.
<code>control_list</code>	a list of parameters specifying the joint model (see control_list).
<code>nlam</code>	number of tuning parameters.
<code>ridge</code>	ridge penalty.
<code>pmax</code>	the maximum of biomarkers being selected. The algorithm will stop early if the maximum has been reached.
<code>min_ratio</code>	the ratio between the largest possible penalty and the smallest penalty to tune.
<code>maxiter</code>	the maximum number of iterations.
<code>eps</code>	threshold for convergence.
<code>UseSurvN</code>	a logical variable indicating whether the effective sample size (i.e., the number of events) should be used in calculating BIC.

Value

return a list with the following objects.

marker.name	the names for biomarkers being analyzed.
alpha	the estimates for the effects of biomarkers in the survival submodel.
weib	the estimates for the Weibull baseline hazard in the survival submodel.
gamma	the estimates for the effects of baseline covariates in the survival submodel.
beta	the estimates for the fixed-effects in the longitudinal submodel.
sig2	the estimates for the noise variances in the longitudinal submodel.
Sigma	the estimates for the covariance matrices of the random effects in the longitudinal submodel.

References

Jiehuan Sun and Sanjib Basu. "Penalized Joint Models of High-Dimensional Longitudinal Biomarkers and A Survival Outcome".

Examples

```
data(HDJMdata)
flex_time_fun <- function(x=NULL){
  xx = matrix(x, ncol = 1)
  colnames(xx) = c("year_1")
  xx
}
ran_time_ind = 1 ## random time-trend effects
control_list = list(
  ID_name = "ID", item_name = "item",
  value_name = "value", time_name = "years",
  fix_cov = NULL, random_cov = NULL,
  FUN = flex_time_fun, ran_time_ind=ran_time_ind,
  surv_time_name = "ftime", surv_status_name = "fstat",
  surv_cov = "x", n_points = 5
)

## takes about one minute.
res = HDJM_fit(LongData=LongData, SurvData=SurvData,
               control_list=control_list)
```

LongData

Simulated Longitudinal Data

Description

This dataset contains longitudinal outcomes.

Usage

```
data(HDJMdata)
```

Format

A data frame with 48700 rows and 4 variables

Details

- ID patient ID
- item types of longitudinal outcome
- years measurement timepoints
- value measurements

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SurvData

Simulated Survival Data

Description

This dataset contains survival outcome.

Usage

```
data(HDJMdata)
```

Format

A data frame with 100 rows and 4 variables

Details

- ID patient ID
- fstat censoring indicator
- ftime survival time
- x baseline covariates

Author(s)

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