

Package ‘pencal’

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Title Penalized Regression Calibration (PRC)

Version 1.1.0

Description Computes penalized regression calibration (PRC), a statistical method that allows to predict survival from high-dimensional longitudinal predictors. PRC is described in Signorelli et al. (2021, <[doi:10.1002/sim.9178](https://doi.org/10.1002/sim.9178)>).

License GPL-3

URL <https://mirkosignorelli.github.io/r>

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Imports doParallel, glmnet, foreach, nlme, survival, MASS, stats, survcomp, survivalROC, dplyr, Matrix, magic, lamm

Suggests survminer, ptmixed, knitr, rmarkdown

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fitted_prclmm	<i>A fitted PRC LMM</i>
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Description

This list contains a fitted PRC LMM, where the CBOCP is computed using 50 cluster bootstrap samples. It is used to reduce the computing time in the example of the function `performance_prc`

Usage

```
data(fitted_prclmm)
```

Format

A list comprising step 2 and step 3 as obtained during the estimation of a PRC LMM

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*. DOI: 10.1002/sim.9178

See Also

[performance_prc](#)

Examples

```
data(fitted_prclmm)
ls(fitted_prclmm)
```

fitted_prcmlpmm	<i>A fitted PRC MLPMM</i>
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Description

This list contains a fitted PRC MLPMM. It is used to reduce the computing time in the example of the function `survpred_prcmlpmm`

Usage

```
data(fitted_prcmlmm)
```

Format

A list comprising step 2 and step 3 as obtained during the estimation of a PRC MLPMM

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

See Also

[survpred_prcmlpmm](#)

Examples

```
data(fitted_prcmlpmm)
ls(fitted_prcmlpmm)
```

fit_lmms	<i>Step 1 of PRC-LMM (estimation of the linear mixed models)</i>
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Description

This function performs the first step for the estimation of the PRC-LMM model proposed in Signorelli et al. (2021)

Usage

```
fit_lmms(y.names, fixefs, ranefs, long.data, surv.data, t.from.base,
         n.boots = 0, n.cores = 1, verbose = TRUE)
```

Arguments

<code>y.names</code>	character vector with the names of the response variables which the LMMs have to be fitted to
<code>fixefs</code>	fixed effects formula for the model, example: <code>~ time</code>
<code>ranefs</code>	random effects formula for the model, specified using the representation of random effect structures of the R package <code>nlme</code>
<code>long.data</code>	a data frame with the longitudinal predictors, comprehensive of a variable called <code>id</code> with the subject ids
<code>surv.data</code>	a data frame with the survival data and (if relevant) additional baseline covariates. <code>surv.data</code> should at least contain a subject id (called <code>id</code>), the time to event outcome (<code>time</code>), and binary event variable (<code>event</code>)
<code>t.from.base</code>	name of the variable containing time from baseline in <code>long.data</code>
<code>n.boots</code>	number of bootstrap samples to be used in the cluster bootstrap optimism correction procedure (CBOCP). If 0, no bootstrapping is performed
<code>n.cores</code>	number of cores to use to parallelize the computation of the CBOCP procedure. If <code>n.cores = 1</code> (default), no parallelization is done. Pro tip: you can use <code>parallel::detectCores()</code> to check how many cores are available on your computer
<code>verbose</code>	if TRUE (default and recommended value), information on the ongoing computations is printed in the console

Value

A list containing the following objects:

- `call.info`: a list containing the following function call information: `call`, `y.names`, `fixefs`, `ranefs`;
- `lmm.fits.orig`: a list with the LMMs fitted on the original dataset (it should comprise as many LMMs as the elements of `y.names` are);
- `df.sanitized`: a sanitized version of the supplied `long.data` dataframe, without the longitudinal measurements that are taken after the event or after censoring;
- `n.boots`: number of bootstrap samples;
- `boot.ids`: a list with the ids of bootstrapped subjects (when `n.boots > 0`);
- `lmm.fits.boot`: a list of lists, which contains the LMMs fitted on each bootstrapped datasets (when `n.boots > 0`).

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

See Also

[simulate_prclmm_data](#), [summarize_lmms](#) (step 2), [fit_prclmm](#) (step 3), [performance_prc](#)

Examples

```
# generate example data
set.seed(1234)
p = 4 # number of longitudinal predictors
simdata = simulate_prclmm_data(n = 100, p = p, p.relev = 2,
                              seed = 123, t.values = c(0, 0.2, 0.5, 1, 1.5, 2))

# specify options for cluster bootstrap optimism correction
# procedure and for parallel computing
do.bootstrap = FALSE
# IMPORTANT: set do.bootstrap = TRUE to compute the optimism correction!
n.boots = ifelse(do.bootstrap, 100, 0)
parallelize = FALSE
# IMPORTANT: set parallelize = TRUE to speed computations up!
if (!parallelize) n.cores = 1
if (parallelize) {
  # identify number of available cores on your machine
  n.cores = parallel::detectCores()
  if (is.na(n.cores)) n.cores = 1
}

# step 1 of PRC-LMM: estimate the LMMS
y.names = paste('marker', 1:p, sep = '')
step1 = fit_lmms(y.names = y.names,
                 fixeFs = ~ age, ranefs = ~ age | id,
                 long.data = simdata$long.data,
                 surv.data = simdata$surv.data,
                 t.from.base = t.from.base,
                 n.boots = n.boots, n.cores = n.cores)
```

fit_mlpmms

Step 1 of PRC-MLPMM (estimation of the linear mixed models)

Description

This function performs the first step for the estimation of the PRC-MLPMM model proposed in Signorelli et al. (2021)

Usage

```
fit_mlpmmms(y.names, fixefs, ranef.time, randint.items = TRUE, long.data,
  surv.data, t.from.base, n.boots = 0, n.cores = 1, verbose = TRUE,
  maxiter = 100, conv = rep(0.001, 3), lcmm.warnings = FALSE)
```

Arguments

<code>y.names</code>	a list with the names of the response variables which the MLPMMs have to be fitted to. Each element in the list contains all the items used to reconstruct a latent biological process of interest
<code>fixefs</code>	a fixed effects formula for the model, where the time variable (specified also in <code>ranef.time</code>) is included as first element and within the function <code>contrast()</code> . Examples: <code>~ contrast(age)</code> , <code>~ contrast(age) + group + treatment</code>
<code>ranef.time</code>	a character with the name of the time variable for which to include a shared random slope
<code>randint.items</code>	logical: should item-specific random intercepts be included in the MLCMMs? Default is TRUE. It can also be a vector, with different values for different elements of <code>y.names</code>
<code>long.data</code>	a data frame with the longitudinal predictors, comprehensive of a variable called <code>id</code> with the subject ids
<code>surv.data</code>	a data frame with the survival data and (if relevant) additional baseline covariates. <code>surv.data</code> should at least contain a subject id (called <code>id</code>), the time to event outcome (<code>time</code>), and binary event variable (<code>event</code>)
<code>t.from.base</code>	name of the variable containing time from baseline in <code>long.data</code>
<code>n.boots</code>	number of bootstrap samples to be used in the cluster bootstrap optimism correction procedure (CBOCP). If 0, no bootstrapping is performed
<code>n.cores</code>	number of cores to use to parallelize the computation of the CBOCP procedure. If <code>n.cores = 1</code> (default), no parallelization is done. Pro tip: you can use <code>parallel::detectCores()</code> to check how many cores are available on your computer
<code>verbose</code>	if TRUE (default and recommended value), information on the ongoing computations is printed in the console
<code>maxiter</code>	maximum number of iterations to use when calling the function <code>multlcmm</code> . Default is 100
<code>conv</code>	a vector containing the three convergence criteria (<code>convB</code> , <code>convL</code> and <code>convG</code>) to use when calling the function <code>multlcmm</code> . Default is <code>c(1e-3, 1e-3, 1e-3)</code>
<code>lcmm.warnings</code>	logical. If TRUE, a warning is printed every time the (strict) convergence criteria of the <code>multlcmm</code> function are not met. Default is FALSE

Details

This function is essentially a wrapper of the `multlcmm` function that has the goal of simplifying the estimation of several MLPMMs. In general, ensuring convergence of the algorithm implemented in `multlcmm` is sometimes difficult, and it is hard to write a function that can automatically solve these convergence problems. `fit_mlpmmms` returns a warning when estimation did not converge for one

or more MLPMMs. If this happens, try to change the convergence criteria in `conv` or the relevant `randint.items` value. If doing this doesn't solve the problem, it is recommended to re-estimate the specific MLPMMs for which estimation didn't converge directly with `multlcm`, trying to manually solve the convergence issues

Value

A list containing the following objects:

- `call.info`: a list containing the following function call information: `call`, `y.names`, `fixefs`, `ranef.time`, `randint.items`;
- `mlpmm.fits.orig`: a list with the MLPMMs fitted on the original dataset (it should comprise as many MLPMMs as the elements of `y.names` are);
- `df.sanitized`: a sanitized version of the supplied `long.data` dataframe, without the longitudinal measurements that are taken after the event or after censoring;
- `n.boots`: number of bootstrap samples;
- `boot.ids`: a list with the ids of bootstrapped subjects (when `n.boots > 0`);
- `mlpmm.fits.boot`: a list of lists, which contains the MLPMMs fitted on each bootstrapped datasets (when `n.boots > 0`).

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

See Also

[simulate_prcmlpmm_data](#), [summarize_mlpmm](#) (step 2), [fit_prcmlpmm](#) (step 3), [performance_prc](#)

Examples

```
# generate example data
set.seed(123)
n.items = c(4,2,2,3,4,2)
simdata = simulate_prcmlpmm_data(n = 100, p = length(n.items),
                                p.relev = 3, n.items = n.items,
                                type = 'u+b', seed = 1)

# specify options for cluster bootstrap optimism correction
# procedure and for parallel computing
do.bootstrap = FALSE
# IMPORTANT: set do.bootstrap = TRUE to compute the optimism correction!
```

```

n.boots = ifelse(do.bootstrap, 100, 0)
parallelize = TRUE
# IMPORTANT: set parallelize = TRUE to speed computations up!
if (!parallelize) n.cores = 1
if (parallelize) {
  # identify number of available cores on your machine
  n.cores = parallel::detectCores()
  if (is.na(n.cores)) n.cores = 1
}

# step 1 of PRC-MLPMM: estimate the MLPMMs
y.names = vector('list', length(n.items))
for (i in 1:length(n.items)) {
  y.names[[i]] = paste('marker', i, '_', 1:n.items[i], sep = '')
}

step1 = fit_mlpmm(y.names, fixefs = ~ contrast(age),
                 ranef.time = age, randint.items = TRUE,
                 long.data = simdata$long.data,
                 surv.data = simdata$surv.data,
                 t.from.base = t.from.base,
                 n.boots = n.boots, n.cores = n.cores)

```

fit_prclmm

Step 3 of PRC-LMM (estimation of the penalized Cox model(s))

Description

This function performs the third step for the estimation of the PRC-LMM model proposed in Signorelli et al. (2021)

Usage

```

fit_prclmm(object, surv.data, baseline.covs = NULL, penalty = "ridge",
           standardize = TRUE, pfac.base.covs = 0, n.alpha.elnet = 11,
           n.folds.elnet = 5, n.cores = 1, verbose = TRUE)

```

Arguments

object	the output of step 2 of the PRC-LMM procedure, as produced by the summarize_lmms function
surv.data	a data frame with the survival data and (if relevant) additional baseline covariates. <code>surv.data</code> should at least contain a subject id (called <code>id</code>), the time to event outcome (<code>time</code>), and binary event variable (<code>event</code>)
baseline.covs	a formula specifying the variables (e.g., baseline age) in <code>surv.data</code> that should be included as baseline covariates in the penalized Cox model. Example: <code>baseline.covs = '~ baseline.age'</code> . Default is <code>NULL</code>

penalty	the type of penalty function used for regularization. Default is 'ridge', other possible values are 'elasticnet' and 'lasso'
standardize	logical argument: should the predicted random effects be standardized when included in the penalized Cox model? Default is TRUE
pfac.base.covs	a single value, or a vector of values, indicating whether the baseline covariates (if any) should be penalized (1) or not (0). Default is pfac.base.covs = 0 (no penalization of all baseline covariates)
n.alpha.elnet	number of alpha values for the two-dimensional grid of tuning parameters in elasticnet. Only relevant if penalty = 'elasticnet'. Default is 11, so that the resulting alpha grid is c(1, 0.9, 0.8, ..., 0.1, 0)
n.folds.elnet	number of folds to be used for the selection of the tuning parameter in elasticnet. Only relevant if penalty = 'elasticnet'. Default is 5
n.cores	number of cores to use to parallelize the computation of the cluster bootstrap optimism correction procedure. If ncores = 1 (default), no parallelization is done. Pro tip: you can use <code>parallel::detectCores()</code> to check how many cores are available on your computer
verbose	if TRUE (default and recommended value), information on the ongoing computations is printed in the console

Value

A list containing the following objects:

- `call`: the function call
- `pcox.orig`: the penalized Cox model fitted on the original dataset;
- `surv.data`: the supplied survival data (ordered by subject id)
- `n.boots`: number of bootstrap samples;
- `boot.ids`: a list with the ids of bootstrapped subjects (when `n.boots > 0`);
- `pcox.boot`: a list where each element is a fitted penalized Cox model for a given bootstrap sample (when `n.boots > 0`).

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

See Also

[fit_lmms](#) (step 1), [summarize_lmms](#) (step 2), [performance_prc](#)

Examples

```

# generate example data
set.seed(1234)
p = 4 # number of longitudinal predictors
simdata = simulate_prcmlmm_data(n = 100, p = p, p.relev = 2,
                               seed = 123, t.values = c(0, 0.2, 0.5, 1, 1.5, 2))

# specify options for cluster bootstrap optimism correction
# procedure and for parallel computing
do.bootstrap = FALSE
# IMPORTANT: set do.bootstrap = TRUE to compute the optimism correction!
n.boots = ifelse(do.bootstrap, 100, 0)
parallelize = FALSE
# IMPORTANT: set parallelize = TRUE to speed computations up!
if (!parallelize) n.cores = 1
if (parallelize) {
  # identify number of available cores on your machine
  n.cores = parallel::detectCores()
  if (is.na(n.cores)) n.cores = 1
}

# step 1 of PRC-LMM: estimate the LMMs
y.names = paste('marker', 1:p, sep = '')
step1 = fit_lmms(y.names = y.names,
                fixeFs = ~ age, ranefs = ~ age | id,
                long.data = simdata$long.data,
                surv.data = simdata$surv.data,
                t.from.base = t.from.base,
                n.boots = n.boots, n.cores = n.cores)

# step 2 of PRC-LMM: compute the summaries
# of the longitudinal outcomes
step2 = summarize_lmms(object = step1, n.cores = n.cores)

# step 3 of PRC-LMM: fit the penalized Cox models
step3 = fit_prcmlmm(object = step2, surv.data = simdata$surv.data,
                   baseline.covs = ~ baseline.age,
                   penalty = 'ridge', n.cores = n.cores)

```

fit_prcmlpmm

Step 3 of PRC-MLPMM (estimation of the penalized Cox model(s))

Description

This function performs the third step for the estimation of the PRC-MLPMM model proposed in Signorelli et al. (2021)

Usage

```
fit_prcmlpmm(object, surv.data, baseline.covs = NULL, include.b0s = TRUE,
  penalty = "ridge", standardize = TRUE, pfac.base.covs = 0,
  n.alpha.elnet = 11, n.folds.elnet = 5, n.cores = 1, verbose = TRUE)
```

Arguments

<code>object</code>	the output of step 2 of the PRC-MLPMM procedure, as produced by the <code>summarize_mlpmms</code> function
<code>surv.data</code>	a data frame with the survival data and (if relevant) additional baseline covariates. <code>surv.data</code> should at least contain a subject id (called <code>id</code>), the time to event outcome (<code>time</code>), and binary event variable (<code>event</code>)
<code>baseline.covs</code>	a formula specifying the variables (e.g., baseline age) in <code>surv.data</code> that should be included as baseline covariates in the penalized Cox model. Example: <code>baseline.covs = '~ baseline.age'</code> . Default is <code>NULL</code>
<code>include.b0s</code>	logical. If <code>TRUE</code> , the PRC-MLPMM(U+B) model is estimated; if <code>FALSE</code> , the PRC-MLPMM(U) model is estimated. See Signorelli et al. (2021) for details
<code>penalty</code>	the type of penalty function used for regularization. Default is <code>'ridge'</code> , other possible values are <code>'elasticnet'</code> and <code>'lasso'</code>
<code>standardize</code>	logical argument: should the predicted random effects be standardized when included in the penalized Cox model? Default is <code>TRUE</code>
<code>pfac.base.covs</code>	a single value, or a vector of values, indicating whether the baseline covariates (if any) should be penalized (1) or not (0). Default is <code>pfac.base.covs = 0</code> (no penalization of all baseline covariates)
<code>n.alpha.elnet</code>	number of alpha values for the two-dimensional grid of tuning parameters in elasticnet. Only relevant if <code>penalty = 'elasticnet'</code> . Default is 11, so that the resulting alpha grid is <code>c(1, 0.9, 0.8, ..., 0.1, 0)</code>
<code>n.folds.elnet</code>	number of folds to be used for the selection of the tuning parameter in elasticnet. Only relevant if <code>penalty = 'elasticnet'</code> . Default is 5
<code>n.cores</code>	number of cores to use to parallelize the computation of the cluster bootstrap optimism correction procedure. If <code>ncores = 1</code> (default), no parallelization is done. Pro tip: you can use <code>parallel::detectCores()</code> to check how many cores are available on your computer
<code>verbose</code>	if <code>TRUE</code> (default and recommended value), information on the ongoing computations is printed in the console

Value

A list containing the following objects:

- `call`: the function call
- `pcox.orig`: the penalized Cox model fitted on the original dataset;
- `surv.data`: the supplied survival data (ordered by subject id)
- `n.boots`: number of bootstrap samples;
- `boot.ids`: a list with the ids of bootstrapped subjects (when `n.boots > 0`);

- `pcox.boot`: a list where each element is a fitted penalized Cox model for a given bootstrap sample (when `n.boots > 0`).

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

See Also

[fit_mlpmm](#) (step 1), [summarize_mlpmm](#) (step 2), [performance_prc](#)

Examples

```
# generate example data
set.seed(123)
n.items = c(4,2,2,3,4,2)
simdata = simulate_prcmlpmm_data(n = 100, p = length(n.items),
                                p.relev = 3, n.items = n.items,
                                type = 'u+b', seed = 1)

# specify options for cluster bootstrap optimism correction
# procedure and for parallel computing
do.bootstrap = FALSE
# IMPORTANT: set do.bootstrap = TRUE to compute the optimism correction!
n.boots = ifelse(do.bootstrap, 100, 0)
parallelize = TRUE
# IMPORTANT: set parallelize = TRUE to speed computations up!
if (!parallelize) n.cores = 1
if (parallelize) {
  # identify number of available cores on your machine
  n.cores = parallel::detectCores()
  if (is.na(n.cores)) n.cores = 1
}

# step 1 of PRC-MLPMM: estimate the MLPMMs
y.names = vector('list', length(n.items))
for (i in 1:length(n.items)) {
  y.names[[i]] = paste('marker', i, '_', 1:n.items[i], sep = '')
}

step1 = fit_mlpmm(y.names, fixefs = ~ contrast(age),
                 ranef.time = age, randint.items = TRUE,
                 long.data = simdata$long.data,
                 surv.data = simdata$surv.data,
```

```

t.from.base = t.from.base,
n.boots = n.boots, n.cores = n.cores)

# step 2 of PRC-MLPMM: compute the summaries
step2 = summarize_mlpmm(object = step1, n.cores = n.cores)

# step 3 of PRC-LMM: fit the penalized Cox models
step3 = fit_prcmlpmm(object = step2, surv.data = simdata$surv.data,
                     baseline.covs = ~ baseline.age,
                     include.b0s = TRUE,
                     penalty = 'ridge', n.cores = n.cores)

```

pencox_baseline

*Estimation of a penalized Cox model with baseline covariates onlu***Description**

This function estimates a penalized Cox model where only baseline covariates are included as predictors, and then computes a bootstrap optimism correction procedure that is used to validate the predictive performance of the model

Usage

```

pencox_baseline(data, formula, penalty = "ridge", standardize = TRUE,
                penalty.factor = 1, n.alpha.elnet = 11, n.folds.elnet = 5,
                n.boots = 0, n.cores = 1, verbose = TRUE)

```

Arguments

data	a data frame with one row for each subject. It should at least contain a subject id (called id), the time to event outcome (time), and the binary censoring indicator (event), plus at least one covariate to be included in the linear predictor
formula	a formula specifying the variables in data to include as predictors in the penalized Cox model
penalty	the type of penalty function used for regularization. Default is 'ridge', other possible values are 'elasticnet' and 'lasso'
standardize	logical argument: should the predicted random effects be standardized when included in the penalized Cox model? Default is TRUE
penalty.factor	a single value, or a vector of values, indicating whether the covariates (if any) should be penalized (1) or not (0). Default is penalty.factor = 1
n.alpha.elnet	number of alpha values for the two-dimensional grid of tuning parameteres in elasticnet. Only relevant if penalty = 'elasticnet'. Default is 11, so that the resulting alpha grid is c(1, 0.9, 0.8, ..., 0.1, 0)
n.folds.elnet	number of folds to be used for the selection of the tuning parameter in elasticnet. Only relevant if penalty = 'elasticnet'. Default is 5

n.boots	number of bootstrap samples to be used in the bootstrap optimism correction procedure. If 0, no bootstrapping is performed
n.cores	number of cores to use to parallelize the computation of the bootstrap optimism correction procedure. If ncores = 1 (default), no parallelization is done. Pro tip: you can use <code>parallel::detectCores()</code> to check how many cores are available on your computer
verbose	if TRUE (default and recommended value), information on the ongoing computations is printed in the console

Value

A list containing the following objects:

- `call`: the function call
- `pcox.orig`: the penalized Cox model fitted on the original dataset;
- `surv.data`: a data frame with the survival data
- `X.orig`: a data frame with the design matrix used to estimate the Cox model
- `n.boots`: number of bootstrap samples;
- `boot.ids`: a list with the ids of bootstrapped subjects (when `n.boots > 0`);
- `pcox.boot`: a list where each element is a fitted penalized Cox model for a given bootstrap sample (when `n.boots > 0`).

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

See Also

[fit_prclmm](#), [fit_prcmlpmm](#)

Examples

```
# generate example data
set.seed(1234)
p = 4 # number of longitudinal predictors
simdata = simulate_prclmm_data(n = 100, p = p, p.relev = 2,
                              seed = 123, t.values = c(0, 0.2, 0.5, 1, 1.5, 2))
#create dataframe with baseline measurements only
baseline.visits = simdata$long.data[which(!duplicated(simdata$long.data$id)),]
df = cbind(simdata$surv.data, baseline.visits)
df = df[, -c(5:7)]
```

```

do.bootstrap = FALSE
# IMPORTANT: set do.bootstrap = TRUE to compute the optimism correction!
n.boots = ifelse(do.bootstrap, 100, 0)
parallelize = FALSE
# IMPORTANT: set parallelize = TRUE to speed computations up!
if (!parallelize) n.cores = 1
if (parallelize) {
  # identify number of available cores on your machine
  n.cores = parallel::detectCores()
  if (is.na(n.cores)) n.cores = 1
}

form = as.formula(~ baseline.age + marker1 + marker2
                  + marker3 + marker4)
base.pcox = pencox_baseline(data = df,
                           formula = form,
                           n.boots = n.boots, n.cores = n.cores)
ls(base.pcox)

```

performance_pencox_baseline

Predictive performance of the penalized Cox model with baseline covariates

Description

This function computes the naive and optimism-corrected measures of performance (C index and time-dependent AUC) for a penalized Cox model with baseline covariates as presented in Signorelli et al. (2021). The optimism correction is a bootstrap optimism correction procedure

Usage

```
performance_pencox_baseline(fitted_pencox, times = 1, n.cores = 1,
                           verbose = TRUE)
```

Arguments

fitted_pencox	the output of pencox_baseline
times	numeric vector with the time points at which to estimate the time-dependent AUC
n.cores	number of cores to use to parallelize the computation of the CBOCP procedure. If ncores = 1 (default), no parallelization is done. Pro tip: you can use <code>parallel::detectCores()</code> to check how many cores are available on your computer
verbose	if TRUE (default and recommended value), information on the ongoing computations is printed in the console

Value

A list containing the following objects:

- call: the function call;
- concordance: a data frame with the naive and optimism-corrected estimates of the concordance (C) index;
- tdAUC: a data frame with the naive and optimism-corrected estimates of the time-dependent AUC at the desired time points.

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

See Also

[pencox_baseline](#)

Examples

```
# generate example data
set.seed(1234)
p = 4 # number of longitudinal predictors
simdata = simulate_prclmm_data(n = 100, p = p, p.relev = 2,
                              seed = 123, t.values = c(0, 0.2, 0.5, 1, 1.5, 2))
# create dataframe with baseline measurements only
baseline.visits = simdata$long.data[which(!duplicated(simdata$long.data$id)),]
df = cbind(simdata$surv.data, baseline.visits)
df = df[, -c(5:7)]

do.bootstrap = FALSE
# IMPORTANT: set do.bootstrap = TRUE to compute the optimism correction!
n.boots = ifelse(do.bootstrap, 100, 0)
parallelize = FALSE
# IMPORTANT: set parallelize = TRUE to speed computations up!
if (!parallelize) n.cores = 1
if (parallelize) {
  # identify number of available cores on your machine
  n.cores = parallel::detectCores()
  if (is.na(n.cores)) n.cores = 1
}

form = as.formula(~ baseline.age + marker1 + marker2
                  + marker3 + marker4)
base.pcox = pencox_baseline(data = df,
```



```

        formula = form,
        n.boots = n.boots, n.cores = n.cores)
ls(base.pcox)

# compute the performance measures
perf = performance_pencox_baseline(fitted_pencox = base.pcox,
    times = c(0.5, 1, 1.5, 2), n.cores = n.cores)

# concordance index:
perf$concordance
# time-dependent AUC:
perf$tdAUC

```

performance_prc

Predictive performance of the PRC-LMM and PRC-MLPMM models

Description

This function computes the naive and optimism-corrected measures of performance (C index and time-dependent AUC) for the PRC models proposed in Signorelli et al. (2021). The optimism correction is computed based on a cluster bootstrap optimism correction procedure (CBOCP)

Usage

```
performance_prc(step2, step3, times = 1, n.cores = 1, verbose = TRUE)
```

Arguments

step2	the output of either summarize_lmms or summarize_mlpms (step 2 of the estimation of PRC)
step3	the output of fit_prclmm or fit_prcmlpmm (step 3 of PRC)
times	numeric vector with the time points at which to estimate the time-dependent AUC
n.cores	number of cores to use to parallelize the computation of the CBOCP procedure. If ncores = 1 (default), no parallelization is done. Pro tip: you can use <code>parallel::detectCores()</code> to check how many cores are available on your computer
verbose	if TRUE (default and recommended value), information on the ongoing computations is printed in the console

Value

A list containing the following objects:

- `call`: the function call;
- `concordance`: a data frame with the naive and optimism-corrected estimates of the concordance (C) index;
- `tdAUC`: a data frame with the naive and optimism-corrected estimates of the time-dependent AUC at the desired time points.

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

See Also

for the PRC-LMM model: `fit_lmms` (step 1), `summarize_lmms` (step 2) and `fit_prclmm` (step 3);
for the PRC-MLPMM model: `fit_mlpmm` (step 1), `summarize_mlpmm` (step 2) and `fit_prclpmm` (step 3).

Examples

```
data(fitted_prclmm)

parallelize = FALSE
# IMPORTANT: set parallelize = TRUE to speed computations up!
if (!parallelize) n.cores = 1
if (parallelize) {
  # identify number of available cores on your machine
  n.cores = parallel::detectCores()
  if (is.na(n.cores)) n.cores = 1
}

# compute the performance measures
perf = performance_prc(fitted_prclmm$step2, fitted_prclmm$step3,
  times = c(0.5, 1, 1.5, 2), n.cores = n.cores)

# concordance index:
perf$concordance
# time-dependent AUC:
perf$tdAUC
```

simulate_prclmm_data *Simulate data that can be used to fit the PRC-LMM model*

Description

This function allows to simulate a survival outcome from longitudinal predictors. Specifically, the longitudinal predictors are simulated from linear mixed models (LMMs), and the survival outcome from a Weibull model where the time to event depends on the random effects from the LMMs. It is an implementation of the simulation method used in Signorelli et al. (2021)

Usage

```
simulate_prclmm_data(n = 100, p = 10, p.relev = 4, lambda = 0.2,  
  nu = 2, seed = 1, base.age.range = c(3, 5), cens.range = c(0.5, 10),  
  t.values = c(0, 0.5, 1, 2))
```

Arguments

n	sample size
p	number of longitudinal outcomes
p.relev	number of longitudinal outcomes that are associated with the survival outcome (min: 1, max: p)
lambda	Weibull location parameter, positive
nu	Weibull scale parameter, positive
seed	random seed (defaults to 1)
base.age.range	range for age at baseline (set it equal to c(0, 0) if you want all subjects to enter the study at the same age)
cens.range	range for censoring times
t.values	vector specifying the time points at which longitudinal measurements are collected (NB: for simplicity, this function assumes a balanced designed; however, pencial is designed to work both with balanced and with unbalanced designs!)

Value

A list containing the following elements:

- a dataframe `long.data` with data on the longitudinal predictors, comprehensive of a subject id (`id`), baseline age (`base.age`), time from baseline (`t.from.base`) and the longitudinal biomarkers;
- a dataframe `surv.data` with the survival data: a subject id (`id`), baseline age (`baseline.age`), the time to event outcome (`time`) and a binary vector (`event`) that is 1 if the event is observed, and 0 in case of right-censoring;
- `perc.cens` the proportion of censored individuals in the simulated dataset.

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

Examples

```
# generate example data
simdata = simulate_prcmlmm_data(n = 20, p = 10,
                               p.relev = 4, seed = 1)
# view the longitudinal markers:
library(ptmixed)
make.spaghetti(x = age, y = marker1,
              id = id, group = id,
              data = simdata$long.data,
              legend.inset = - 1)
# proportion of censored subjects
simdata$censoring.prop
# visualize KM estimate of survival
library(survival)
surv.obj = Surv(time = simdata$surv.data$time,
                event = simdata$surv.data$event)
kaplan <- survfit(surv.obj ~ 1,
                 type="kaplan-meier")
plot(kaplan)
```

simulate_prcmlpmm_data

Simulate data that can be used to fit the PRC-LMM model

Description

This function allows to simulate a survival outcome from longitudinal predictors. Specifically, the longitudinal predictors are simulated from multivariate latent process mixed models (MLPMMs), and the survival outcome from a Weibull model where the time to event depends on the random effects from the MLPMMs. It is an implementation of the simulation method used in Signorelli et al. (2021)

Usage

```
simulate_prcmlpmm_data(n = 100, p = 5, p.relev = 2, n.items = c(3, 2,
  3, 4, 1), type = "u", lambda = 0.2, nu = 2, seed = 1,
  base.age.range = c(3, 5), cens.range = c(0.5, 10), t.values = c(0, 0.5,
  1, 2))
```

Arguments

n	sample size
p	number of longitudinal latent processes
p.relev	number of latent processes that are associated with the survival outcome (min: 1, max: p)
n.items	number of items that are observed for each latent process of interest. It must be either a scalar, or a vector of length p

type	the type of relation between the longitudinal outcomes and survival time. Two values can be used: 'u' refers to the PRC-MLPMM(U) model, and 'u+b' to the PRC-MLPMM(U+B) model presented in Section 2.3 of Signorelli et al. (2021). See the article for the mathematical details
lambda	Weibull location parameter, positive
nu	Weibull scale parameter, positive
seed	random seed (defaults to 1)
base.age.range	range for age at baseline (set it equal to c(0, 0) if you want all subjects to enter the study at the same age)
cens.range	range for censoring times
t.values	vector specifying the time points at which longitudinal measurements are collected (NB: for simplicity, this function assumes a balanced designed; however, pncal is designed to work both with balanced and with unbalanced designs!)

Value

A list containing the following elements:

- a dataframe `long.data` with data on the longitudinal predictors, comprehensive of a subject id (`id`), baseline age (`base.age`), time from baseline (`t.from.base`) and the longitudinal biomarkers;
- a dataframe `surv.data` with the survival data: a subject id (`id`), baseline age (`baseline.age`), the time to event outcome (`time`) and a binary vector (`event`) that is 1 if the event is observed, and 0 in case of right-censoring;
- `perc.cens` the proportion of censored individuals in the simulated dataset.

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

Examples

```
# generate example data
simdata = simulate_prcmlpmm_data(n = 40, p = 6,
                                p.relev = 3, n.items = c(3,4,2,5,4,2),
                                type = 'u+b', seed = 1)

# names of the longitudinal outcomes:
names(simdata$long.data)
# markerx_y is the y-th item for latent process (LP) x
# we have 6 latent processes of interest, and for LP1
```

```
# we measure 3 items, for LP2 4, for LP3 2 items, and so on

# visualize trajectories of marker1_1
library(ptmixed)
make.spaghetti(x = age, y = marker1_1,
              id = id, group = id,
              data = simdata$long.data,
              legend.inset = - 1)

# proportion of censored subjects
simdata$censoring.prop
# visualize KM estimate of survival
library(survival)
surv.obj = Surv(time = simdata$surv.data$time,
               event = simdata$surv.data$event)
kaplan <- survfit(surv.obj ~ 1,
                 type="kaplan-meier")
plot(kaplan)
```

simulate_t_weibull *Generate survival data from a Weibull model*

Description

This function implements the algorithm proposed by Bender et al. (2005) to simulate survival times from a Weibull model

Usage

```
simulate_t_weibull(n, lambda, nu, X, beta, seed = 1)
```

Arguments

n	sample size
lambda	Weibull location parameter, positive
nu	Weibull scale parameter, positive
X	design matrix (n rows, p columns)
beta	p-dimensional vector of regression coefficients associated to X
seed	random seed (defaults to 1)

Value

A vector of survival times

Author(s)

Mirko Signorelli

References

Bender, R., Augustin, T., & Blettner, M. (2005). Generating survival times to simulate Cox proportional hazards models. *Statistics in medicine*, 24(11), 1713-1723.

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

Examples

```
# generate example data
set.seed(1)
n = 50
X = cbind(matrix(1, n, 1),
           matrix(rnorm(n*9, sd = 0.7), n, 9))
beta = rnorm(10, sd = 0.7)
times = simulate_t_weibull(n = n, lambda = 1, nu = 2,
                           X = X, beta = beta)
hist(times, 20)
```

summarize_lmms	<i>Step 2 of PRC-LMM (computation of the predicted random effects)</i>
----------------	--

Description

This function performs the second step for the estimation of the PRC-LMM model proposed in Signorelli et al. (2021)

Usage

```
summarize_lmms(object, n.cores = 1, verbose = TRUE)
```

Arguments

object	a list of objects as produced by fit_lmms
n.cores	number of cores to use to parallelize the computation of the cluster bootstrap optimism correction procedure. If ncores = 1 (default), no parallelization is done. Pro tip: you can use <code>parallel::detectCores()</code> to check how many cores are available on your computer
verbose	if TRUE (default and recommended value), information on the ongoing computations is printed in the console

Value

A list containing the following objects:

- `call`: the function call
- `ranef.orig`: a matrix with the predicted random effects computed for the original data;
- `n.boots`: number of bootstrap samples;
- `boot.ids`: a list with the ids of bootstrapped subjects (when `n.boots > 0`);
- `ranef.boot.train`: a list where each element is a matrix that contains the predicted random effects for each bootstrap sample (when `n.boots > 0`);
- `ranef.boot.valid`: a list where each element is a matrix that contains the predicted random effects on the original data, based on the lmms fitted on the cluster bootstrap samples (when `n.boots > 0`);

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

See Also

[fit_lmms](#) (step 1), [fit_prclmm](#) (step 3), [performance_prc](#)

Examples

```
# generate example data
set.seed(1234)
p = 4 # number of longitudinal predictors
simdata = simulate_prclmm_data(n = 100, p = p, p.relev = 2,
                              seed = 123, t.values = c(0, 0.2, 0.5, 1, 1.5, 2))

# specify options for cluster bootstrap optimism correction
# procedure and for parallel computing
do.bootstrap = FALSE
# IMPORTANT: set do.bootstrap = TRUE to compute the optimism correction!
n.boots = ifelse(do.bootstrap, 100, 0)
parallelize = FALSE
# IMPORTANT: set parallelize = TRUE to speed computations up!
if (!parallelize) n.cores = 1
if (parallelize) {
  # identify number of available cores on your machine
  n.cores = parallel::detectCores()
  if (is.na(n.cores)) n.cores = 1
}
```



```

# step 1 of PRC-LMM: estimate the LMMs
y.names = paste('marker', 1:p, sep = '')
step1 = fit_lmms(y.names = y.names,
                 fixeefs = ~ age, ranefs = ~ age | id,
                 long.data = simdata$long.data,
                 surv.data = simdata$surv.data,
                 t.from.base = t.from.base,
                 n.boots = n.boots, n.cores = n.cores)

# step 2 of PRC-LMM: compute the summaries
# of the longitudinal outcomes
step2 = summarize_lmms(object = step1, n.cores = n.cores)

```

summarize_mlpmmms *Step 2 of PRC-MLPMM (computation of the predicted random effects)*

Description

This function performs the second step for the estimation of the PRC-MLPMM model proposed in Signorelli et al. (2021)

Usage

```
summarize_mlpmmms(object, n.cores = 1, verbose = TRUE)
```

Arguments

object	a list of objects as produced by <code>fit_mlpmmms</code>
n.cores	number of cores to use to parallelize the computation of the cluster bootstrap optimism correction procedure. If <code>ncores = 1</code> (default), no parallelization is done. Pro tip: you can use <code>parallel::detectCores()</code> to check how many cores are available on your computer
verbose	if TRUE (default and recommended value), information on the ongoing computations is printed in the console

Value

A list containing the following objects:

- `call`: the function call
- `ranef.orig`: a matrix with the predicted random effects computed for the original data;
- `n.boots`: number of bootstrap samples;
- `boot.ids`: a list with the ids of bootstrapped subjects (when `n.boots > 0`);
- `ranef.boot.train`: a list where each element is a matrix that contains the predicted random effects for each bootstrap sample (when `n.boots > 0`);
- `ranef.boot.valid`: a list where each element is a matrix that contains the predicted random effects on the original data, based on the `mlpmmms` fitted on the cluster bootstrap samples (when `n.boots > 0`);

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

See Also

[fit_mlpmms](#) (step 1), [fit_prcmlpmm](#) (step 3), [performance_prc](#)

Examples

```
# generate example data
set.seed(123)
n.items = c(4,2,2,3,4,2)
simdata = simulate_prcmlpmm_data(n = 100, p = length(n.items),
                                p.relev = 3, n.items = n.items,
                                type = 'u+b', seed = 1)

# specify options for cluster bootstrap optimism correction
# procedure and for parallel computing
do.bootstrap = FALSE
# IMPORTANT: set do.bootstrap = TRUE to compute the optimism correction!
n.boots = ifelse(do.bootstrap, 100, 0)
parallelize = TRUE
# IMPORTANT: set parallelize = TRUE to speed computations up!
if (!parallelize) n.cores = 1
if (parallelize) {
  # identify number of available cores on your machine
  n.cores = parallel::detectCores()
  if (is.na(n.cores)) n.cores = 1
}

# step 1 of PRC-MLPMM: estimate the MLPMMs
y.names = vector('list', length(n.items))
for (i in 1:length(n.items)) {
  y.names[[i]] = paste('marker', i, '_', 1:n.items[i], sep = '')
}

step1 = fit_mlpmms(y.names, fixefs = ~ contrast(age),
                  ranef.time = age, randint.items = TRUE,
                  long.data = simdata$long.data,
                  surv.data = simdata$surv.data,
                  t.from.base = t.from.base,
                  n.boots = n.boots, n.cores = n.cores)

# step 2 of PRC-MLPMM: compute the summaries
```

```
step2 = summarize_mlpmms(object = step1, n.cores = n.cores)
```

survpred_prclmm	<i>Compute the predicted survival probabilities obtained from the PRC models</i>
-----------------	--

Description

This function computes the predictive survival probabilities for the for the PRC-LMM model proposed in Signorelli et al. (2021)

Usage

```
survpred_prclmm(step1, step2, step3, times = 1, new.longdata = NULL,
  new.basecovs = NULL, keep.ranef = FALSE)
```

Arguments

step1	the output of <code>fit_lmms</code> (step 1 of the estimation of PRC-LMM)
step2	the output of <code>summarize_lmms</code> (step 2 of the estimation of PRC-LMM)
step3	the output of <code>fit_prclmm</code> (step 3 of the estimation of PRC-LMM)
times	numeric vector with the time points at which to estimate the time-dependent AUC
new.longdata	longitudinal data if you want to compute predictions for new subjects on which the model was not trained. It should comprise an identifier variable called 'id'. Default is <code>new.longdata = NULL</code>
new.basecovs	a dataframe with baseline covariates for the new subjects for which predictions are to be computed. It should comprise an identifier variable called 'id'. Only needed if baseline covariates were included in step 3 and <code>new.longdata</code> is specified. Default is <code>new.basecovs = NULL</code>
keep.ranef	should a data frame with the predicted random effects be included in the output? Default is <code>FALSE</code>

Value

A list containing the function call (`call`), a data frame with the predicted survival probabilities computed at the supplied time points (`predicted_survival`), and if `keep.ranef = TRUE` also the predicted random effects `predicted_ranefs`.

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

See Also

[fit_lmms](#) (step 1), [summarize_lmms](#) (step 2) and [fit_prclmm](#) (step 3)

Examples

```
# generate example data
set.seed(1234)
p = 4 # number of longitudinal predictors
simdata = simulate_prclmm_data(n = 100, p = p, p.relev = 2,
                              seed = 123, t.values = c(0, 0.2, 0.5, 1, 1.5, 2))

# step 1 of PRC-LMM: estimate the LMMs
y.names = paste('marker', 1:p, sep = '')
step1 = fit_lmms(y.names = y.names,
                fixefs = ~ age, ranefs = ~ age | id,
                long.data = simdata$long.data,
                surv.data = simdata$surv.data,
                t.from.base = t.from.base,
                n.boots = 0)

# step 2 of PRC-LMM: compute the summaries
# of the longitudinal outcomes
step2 = summarize_lmms(object = step1)

# step 3 of PRC-LMM: fit the penalized Cox models
step3 = fit_prclmm(object = step2, surv.data = simdata$surv.data,
                  baseline.covs = ~ baseline.age,
                  penalty = 'ridge')

# predict survival probabilities at times 1, 2, 3
surv.probs = survpred_prclmm(step1, step2, step3, times = 1:3)
head(surv.probs$predicted_survival)

# predict survival probabilities for new subjects:
temp = simulate_prclmm_data(n = 10, p = p, p.relev = 2,
                          seed = 321, t.values = c(0, 0.2, 0.5, 1, 1.5, 2))
new.longdata = temp$long.data
new.basecovs = temp$surv.data[, 1:2]
surv.probs.new = survpred_prclmm(step1, step2, step3,
                                times = 1:3,
                                new.longdata = new.longdata,
                                new.basecovs = new.basecovs)
head(surv.probs.new$predicted_survival)
```

survpred_prcmlpmm	<i>Compute the predicted survival probabilities obtained from the PRC models</i>
-------------------	--

Description

This function computes the predictive survival probabilities for the for the PRC-MLPMM(U) and PRC-MLPMM(U+B) models proposed in Signorelli et al. (2021)

Usage

```
survpred_prcmlpmm(step2, step3, times = 1)
```

Arguments

step2	the output of summarize_mlpmms (step 2 of the estimation of PRC-MLPMM)
step3	the output of fit_prcmlpmm (step 3 of the estimation of PRC-MLPMM)
times	numeric vector with the time points at which to estimate the time-dependent AUC

Value

A data frame with the predicted survival probabilities computed at the supplied time points

Author(s)

Mirko Signorelli

References

Signorelli, M., Spitali, P., Al-Khalili Szigyarto, C, The MARK-MD Consortium, Tsonaka, R. (2021). Penalized regression calibration: a method for the prediction of survival outcomes using complex longitudinal and high-dimensional data. *Statistics in Medicine*, 40 (27), 6178-6196. DOI: 10.1002/sim.9178

See Also

[fit_mlpmms](#) (step 1), [summarize_mlpmms](#) (step 2) and [fit_prcmlpmm](#) (step 3).

Examples

```
data(fitted_prcmlpmm)

# predict survival probabilities at times 1, 2, 3
surv.probs = survpred_prcmlpmm(fitted_prcmlpmm$step2,
                               fitted_prcmlpmm$step3, times = 1:3)
ls(surv.probs)
head(surv.probs$predicted_survival)
```

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