Package 'BPHO' documentation

of

April 2, 2008

Version 1.2-4

Title Bayesian Prediction with High-order Interactions

Author Longhai Li <longhai@math.usask.ca>

Maintainer Longhai Li <longhai@math.usask.ca>

Depends R (>= 2.5.1)

Description This software is used in two situations. The first is to predict the next outcome based on the previous states of a discrete sequence. The second is to classify a discrete response based on a number of discrete covariates. In both situations, we use Bayesian logistic regression models that consider the high-order interactions. The time arising from using high-order interactions is reduced greatly by our compression technique that represents a group of original parameters as a single one in MCMC step. In this version, we use log-normal prior for the hyperparameters. When it is used for the second situation — classification, we consider the full set of interaction patterns up to a specified order.

License GPL (>=2)

URL http://www.r-project.org, http://math.usask.ca/~longhai

R topics documented:

---

comp_train_pred   *User-level functions for compressing parameters, training the models*
                         with MCMC, and making predictions for test cases

---

Description

The function `comp_train_pred` can be used for three tasks: compressing parameter, training
the models with MCMC, and making prediction for test cases. When **new_compression=1**,
it compresses parameters based on training cases and the information about parameter compres-
sion is written to the binary file `ptn_file`. When **new_compression=0**, it uses the exist-
ing `ptn_file`. When **iters_mc > 0**, it trains the models with Markov chain Monte Carlo
and the Markov chain iterations are written to the binary file `mc_file`. The methods of writing
to and reading from the files `ptn_file` and `mc_file` can be found from the documentations
compression and training. When **iters_pred > 0**, it predicts the responses of test
cases and the result is written to the file `pred_file` and also returned as a value of this function.

The function `cv_comp_train_pred` is a short-cut function for performing cross-validation with
the function `comp_train_pred`.

The argument `is_sequence=1` indicates that a sequence prediction model is fitted to the data,
and `is_sequence=1` indicates that a general classification model based on discrete predictor
variables is fitted.

Usage

```
comp_train_pred(
################## specify data information  ####################
test_x,train_x,train_y,no_cls=c(),nos_fth=c(),
################## specify for compression ######################
is_sequence=1,order,ptn_file=".ptn.log",new_compression=1,do_comp=1,
##################### specify for priors  ######################
alpha=1,log_sigma_widths=c(),log_sigma_modes=c(),
################# specify for mc sampling ######################
mc_file=".mc.log",start_over=FALSE,iters_mc=200,iters_bt=10,
iters_sgm=50,w_bt=5,w_sgm=1,m_bt=20,m_sgm=20,ini_log_sigmas=c(),
################## specify for prediction ######################
pred_file=c(),iter_b = 100,forward = 1,iters_pred = 100)

cv_comp_train_pred(
###################### Specify data,order,no_fold ################
no_fold=10,train_x,train_y,no_cls=c(),nos_fth=c(),
#################### specify for compressing####################
is_sequence=1,order,ptn_file=".ptn.log",new_compression=1,do_comp=1,
#################### specify for priors  ######################
alpha=1,log_sigma_widths=c(),log_sigma_modes=c(),
################ specify for mc sampling ######################
mc_file=".mc.log",iters_mc=200,iters_bt=10,iters_sgm=50,
w_bt=5,w_sgm=1,m_bt=20,m_sgm=20,ini_log_sigmas=c(),
```

```
################## specify for prediction ######################
pred_file = c(),iter_b = 100,forward = 1,iters_pred = 100)
```

Arguments

test_x
: Discrete features (also called inputs,covariates,independent variables, explanatory variables, predictor variables) of test data on which the predictions are based. The row is subject and the columns are inputs, which are coded with 1,2,..., with 0 reserved to represent that this input is not considered in a pattern. When the sequence prediction models are fitted, it is assumed that the first column is the state closest to the response. For example, a sequence 'x1,x2,x3,x4' is saved in test_x as 'x4,x3,x2,x1', for predicting the response 'x5'.

train_x
: Discrete features of training data of the same format as test_x.

train_y
: Discrete response of training data, a vector with length equal to the row of train_x. Assumed to be coded with 1,2,... no_cls .

no_cls
: the number of possibilities (classes) of the response, default to the maximum value in train_y.

nos_fth
: a vector, with each element storing the number of possibilities (classes) of each feature, default to the maximum value of each feature.

is_sequence
: is_sequence=1 indicates that sequence prediction models are fitted to the data, and is_sequence=0 indicates that general classification models based on discrete predictor variables are fitted.

no_fold
: Number of folders in cross-validation.

order
: the order of interactions considered, default to the total number of features, i.e. ncol(train_x).

ptn_file
: a character string, the name of the binary file to which the compression result is written. The method of writing to and reading from ptn_file can be found from the documentation for compression.

new_compression
: new_compression=1 indicates removing the old file ptn_file if it exists and doing the compression once again. new_compression=0 indicates using the old file ptn_file without doing compression once again. Note that when new_compression=0, the specification related to training cases does not take effect.

do_comp
: do_comp=1 indicates doing compression, and do_comp=0 indicates using original parametrization. This is used only to make comparison. In practice, we definitely recommend using our compression technique to reduce the number of parameters.

alpha
: alpha=1 indicates that Cauchy prior is used, alpha=2 indicates that Gaussian prior is used.

log_sigma_widths, log_sigma_modes
: two vectors of length order+1, which are interpreted as follows: the Gaussian distribution with location log_sigma_modes[o] and standard deviation log_sigma_widths[o] is the prior for 'log(sigmas[o])', which is the hyperparameter (width parameter of Gaussian distribution or Cauchy distribution) for the regression coefficients (i.e. 'beta's) associated with the interactions of order 'o'.

mc_file   A character string, the name of the binary file to which Markov chain is written.
                 The method of writing to and reading from mc_file can be found from the
                 documentation for training.

start_over   start_over=TRUE indicates that the existing file mc_file is deleted before
                 a Markov chain sampling starts, otherwise the Markov chain will continue from
                 the last iteration stored in mc_file.

iters_mc,iters_bt,iters_sgm
                 iters_mc iterations of super-transition will be run. Each super-transition
                 consists of iters_bt iterations of updating 'beta's, and for each updating
                 of 'beta's, the hyperparameters 'log(sigma)'s are updated iters_sgm times.
                 When iters_mc=0, no Markov chain sampling will be run and other argu-
                 ments related to Markov chain sampling take no effect.

w_bt,w_sgm, m_bt,m_sgm
                 w_bt is the amount of stepping-out in updating 'beta' with slice sampling,
                 m_bt is the maximum number of stepping-out in slice sampling for updating
                 'beta'. w_sgm and m_sgm are intepreted similarly for sampling for 'log(sigma)'.

ini_log_sigmas
                 Initial values of 'log(sigma)', default to log_sigma_modes.

pred_file   A character string, the name of the file to which the prediction result is written.
                 If pred_file=c(), the prediction result is printed out on screen (or sent to
                 standard output).

iter_b, forward, iters_pred
                 Starting from iter_b, one of every forward Markov chain samples, with the
                 number of total samples being <= iters_pred and the maximum usable in
                 the file mc_file, is used to make prediction.

Value

times   The time in second for, as this order, compressing parameters, training the
                 model, predicting for test cases

pred_result   a data frame with first no_cls columns being the predictive probability and the
                 next column being the predicted response value is returned.

files   Three character strings: the 1st is the name of the file storing compression
                 information, the 2nd is the name of the file storing Markov chain, and the
                 3rd one is the name of the file containing the detailed prediction result, i.e.,
                 pred_result

Author(s)

Longhai Li, http://math.usask.ca/~longhai

References

http://math.usask.ca/~longhai/doc/seqpred/seqpred.abstract.html

See Also

gendata,compression,training,prediction

Examples

```
##  loading package
##  library("BPHO",lib.loc="~/rlib")

#####################################################################
########The following are demonstrations of using the whole package
#####################################################################

## generate data from a hidden Markov model
data_hmm <- gen_hmm(n=200,p=10,no_h=8,no_o=2,
                    prob_h_stay=0.8,prob_o_stay=0.8)

## compressing parameters, training model, making prediction
comp_train_pred(
        ################## specify data information  ###############
        test_x=data_hmm$X[1:100,],train_x=data_hmm$X[-(1:100),],
        train_y=data_hmm$y[-(1:100)],no_cls=2,nos_fth=rep(2,10),
        ################## specify for compression ################
        is_sequence=1,order=4,ptn_file=".ptn_file.log",
        new_compression=1,do_comp=1,
        ###################### specify for priors  ################
        alpha=1,log_sigma_widths=c(),log_sigma_modes=c(),
        ################# specify for mc sampling #################
        mc_file=".mc_file.log",start_over=TRUE,iters_mc=100,
        iters_bt=1,iters_sgm=2,w_bt=5,w_sgm=1,
        m_bt=20,m_sgm=20,ini_log_sigmas=c(),
        ################## specify for prediction #################
        pred_file=".pred_file.csv",iter_b = 10,forward = 1,
        iters_pred = 90)

## display summary information about compression
display_ptn(ptn_file=".ptn_file.log")

## display the pattern information for group 1 and group 2
display_ptn(ptn_file=".ptn_file.log",gid=c(1,2))

## display the general information of Markov chain sampling
display_mc(mc_file=".mc_file.log")

## read Markov chain values of log-likelihood from  ".mc_file.log"
read_mc(mc_file=".mc_file.log",group="lprobs",ix=0,
        iter_b=0,forward=1,n=100)

## particularly read `betas' by specifying the group and class id
read_betas(mc_file=".mc_file.log",ix_g=5,ix_cls=2,
           iter_b=0,forward=1,n=100)

## display the information on the pattern related to a `beta'
display_a_beta(mc_file=".mc_file.log",
               ptn_file=".ptn_file.log",id_beta=5)

## calculate the medians of samples of each 'beta'
```

```
calc_medians_betas(mc_file=".mc_file.log",iter_b=10,forward=1,n=90)

## evaluate prediction with true values of the response
evaluate_prediction(
        test_y=data_hmm$y[1:100],
        pred_result=read.csv(".pred_file.csv"),
        file_eval_details="eval_details")

#perform cross-validation with training data only
cv_comp_train_pred(
        ################## specify data information  ################
        no_fold=2,train_x=data_hmm$X[-(1:100),],
        train_y=data_hmm$y[-(1:100)],no_cls=2,nos_fth=rep(2,10),
        ################## specify for compression ##################
        is_sequence=1,order=4,ptn_file=".ptn_file.log",
        new_compression=1,do_comp=1,
        ###################### specify for priors  ##################
        alpha=1,log_sigma_widths=c(),log_sigma_modes=c(),
        ################## specify for mc sampling ##################
        mc_file=".mc_file.log",iters_mc=100,
        iters_bt=1,iters_sgm=2,w_bt=5,w_sgm=1,
        m_bt=20,m_sgm=20,ini_log_sigmas=c(),
        ################## specify for prediction ##################
        pred_file=".pred_file.csv",iter_b = 10,forward = 1,
        iters_pred = 90)

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

## generating a classification data
data_class <- gen_bin_ho(n=400,p=3,order=3,alpha=1,
                sigmas=c(0.3,0.2,0.1),nos_features=c(4,4,4),beta0=0)

## compressing parameters, training model, making prediction
comp_train_pred(
        ################## specify data information  ################
        test_x=data_class$X[1:100,],train_x=data_class$X[-(1:100),],
        train_y=data_class$y[-(1:100)],no_cls=2,nos_fth=rep(4,3),
        ################## specify for compression ##################
        is_sequence=0,order=3,ptn_file=".ptn_file.log",
        new_compression=1,do_comp=1,
        ###################### specify for priors  ##################
        alpha=1,log_sigma_widths=c(),log_sigma_modes=c(),
        ################# specify for mc sampling ##################
        mc_file=".mc_file.log",start_over=TRUE,iters_mc=500,
        iters_bt=1,iters_sgm=5,w_bt=5,w_sgm=0.5,
        m_bt=20,m_sgm=20,ini_log_sigmas=c(),
        ################## specify for prediction ##################
        pred_file=".pred_file.csv",iter_b = 100,forward = 1,
        iters_pred = 400)

## display summary information about compression
display_ptn(ptn_file=".ptn_file.log")
```

```
## display the pattern information for group 1 and group 2
display_ptn(ptn_file=".ptn_file.log",gid=c(1,2))

## display the general information of Markov chain sampling
display_mc(mc_file=".mc_file.log")

## read Markov chain values of log-likelihood from ".mc_file.log"
read_mc(mc_file=".mc_file.log",group="lprobs",ix=0,
        iter_b=0,forward=1,n=100)

## particularly read `betas' by specifying the group and class id
read_betas(mc_file=".mc_file.log",ix_g=5,ix_cls=2,
           iter_b=0,forward=1,n=500)

## display the information on the pattern related to a `beta'
display_a_beta(mc_file=".mc_file.log",ptn_file=".ptn_file.log",
               id_beta=5)

## calculate the medians of samples of each 'beta'
calc_medians_betas(mc_file=".mc_file.log",iter_b=100,forward=1,n=400)

## evaluate prediction with true values of the response
evaluate_prediction(
        test_y=data_class$y[1:100],
        pred_result=read.csv(".pred_file.csv"),
        file_eval_details="eval_details")
```

---

compression   *Functions related to parameter compression*

Description

The function compress groups the patterns in a way such that the interaction patterns in a group
are expressed by the same training cases. In training the models with MCMC, we need to use
only one parameter for each group, which represents the sum of all the parameters in this group.
The original parameters are seemly compressed. A large amount of training time is saved by this
compression techniques.

The result of this grouping is saved in a binary file in a way such that it can be retrieved as a linked
list in C, with each node consisting of a description (an integer vector of fixed length) of the group
of patterns and the indice (an integer vector of varying length, with 0 for the first training case) of
training cases expressing this group of patterns. This file is needed to train the models with MCMC
and to predict the responses of test cases using the function comp_train_pred.

The function display_ptn displays the summary information about this compression, such as
the number of groups and total number of patterns expressed by the training cases. When gids is
nonempty, it also displays the detailed information about the groups specified by gids, such as the
pattern description and the indice of training cases associated with this group.

Usage

```
compress(features,nos_fth=c(),no_cases_ign=0,
         ptn_file=".ptn_file.log",quiet=1,
         do_comp=1,sequence=1,order=ncol(features))
display_ptn(ptn_file, gids=c())
```

Arguments

features
: Discrete features (also called features,covariates,independent variables, explanatory variables, predictor variables) of training data on which the predictions are based. The row is subject and the columns are inputs, which are coded with 1,2,..., with 0 reserved to represent that this input is not considered in a pattern. When the sequence prediction models are fitted, it is assumed that the first column is the state closest to the response. For example, a sequence 'x1,x2,x3,x4' is saved in `test_x` as 'x4,x3,x2,x1', for predicting the response 'x5'.

nos_fth
: a vector, with each element storing the number of possibilities (classes) of each feature, default to the maximum value of each feature.

order
: the order of interactions considered, default to the total number of features, i.e. `ncol(features)`.

ptn_file
: a character string, the name of the binary file to which the compression result is written.

do_comp
: `do_comp=1` indicates doing compression, and `do_comp=0` indicates using original parametrization. This is used only to make comparison. In practice, we definitely recommend using our compression technique to reduce the number of parameters.

sequence
: `sequence=1` indicates that sequence prediction models are fitted to the data, and `sequence=0` indicates that general classification models based on discrete predictor variables are fitted.

gids
: an integer vector, containing the indice of groups whose information you want to display, with 0 for the first group.

no_cases_ign
: When the number of training cases for a pattern is no more than `no_cases_ign`, this pattern will be ignored, default to 0, i.e. considering all interactions. So far there is no other justification to set it a value greater than 0, except that it can reduce the number of groups.

quiet
: If `quiet=0`, some messages during compression are printed on screen for monitor the compression, if `quiet=1` the function works silently.

Value

The function `compress` returns no value. Instead, it saves the result of compression in the file `ptn_file`.

The function `display_ptn` returns a vector of 6 numbers. Their meanings are as follows: `is.sequence` – indictor whether a sequence model is fitted,`order` – the maximum order of interactions considered, `#groups` – the number of groups found, `#patterns` – the number of interaction patterns expressed by the training cases,`#cases` – the number of training cases, `#features` – the number of features.

When `gids` is nonempty, it also displays the details about the queried groups. The information printed on screen for each group is read as follows. Under **superpatterns**, it displays a compact description of the pattern group, which is in a special format defined in the references associated with this software. Under **expression**, it displays the indice of training cases that express this group of patterns. Under **sigmas**, it displays the number of patterns with a certain order, starting from order 0. This information is needed to compute the width parameter of the regression coeficient associated with this group from the values of hyperparameters 'sigma's.

See Also

[comp_train_pred](), [training](), [prediction]()

Examples

```
## generate features
features <- gen_X(50,5,2)

## compressing the parameter based on 'features'
compress(features,nos_fth=rep(2,5),no_cases_ign=0,
        ptn_file=".ptn_file.log",quiet=1,do_comp=1,
        sequence=1,order=4)

## display the summary information in the file ".ptn_file.log"
display_ptn(".ptn_file.log")

## display the information for group #2 and #3
display_ptn(".ptn_file.log",gids=c(2,3))
```

---

training	*Functions related to Markov chain sampling*

Description

The models are trained with Markov chain Monte Carlo (MCMC) methods. Slice sampling is used to update 'beta's, the regression coefficients for groups, and Metropolis sampling with Gaussian proposal is used to update 'log(sigma)', where 'sigma' is the width parameter of the prior for 'beta'.

The function `training` carries out the Markov chain sampling, saving the Markov chain samples in a binary file `mc_file`.

The function `display_mc` displays the summary information in the file `mc_file`.

The function `read_mc` reads the Markov chain samples from the file `mc_file` at given iterations.

The function `read_betas` is based on the function `read_mc`. It specifically reads the 'beta' for given group and class identities.

The function `display_a_beta` displays both the pattern information for the group associated with the 'beta' specified by `id_beta`, and also return the full Markov chain samples of this 'beta'.

The function `calc_medians_betas` returns the medians of the Markov chain samples for all 'beta's at specified iterations. This function is for discovering important interaction patterns. An interaction pattern with large absolute medians is highly suspected to be an important pattern for predicting the response.

Usage

```
display_mc(mc_file)
read_mc (mc_file,group,ix, iter_b=0,forward=1,n=c(),quiet=1)
read_betas (mc_file,ix_g,ix_cls,iter_b=0,forward=1,n=c(),quiet=1)
display_a_beta(mc_file,ptn_file, id_beta)
calc_medians_betas(mc_file,iter_b,forward,n)
training(mc_file,ptn_file, train_y,no_cls,
         alpha,log_sigma_widths,log_sigma_modes,ini_log_sigmas,
         iters_mc,iters_bt,iters_sgm,
         w_bt,w_sgm,m_bt,m_sgm)
```

Arguments

`mc_file`	A character string, the name of the binary file to which Markov chain is written.
`group`	A character string giving the group name of values.
	It can be one of 'lprobs',lsigmas','betas', 'evals'.
	Group 'lprobs' contains: the values of log probabilities of data given the values of 'beta's (identified by `ix=0`), the value of log prior of 'beta's given 'sigma's (identified by `ix=1`), the value of log prior of 'log(sigma)'s (identified by `ix=2`), and the value of log posterior (identified by `ix=3`), which is the sum of the previous three values.
	Group 'lsigmas' contains: the values of hyperparameters 'log(sigma)', with `ix` indicating the order, starting from 0.
	Group 'betas' contains: the values of 'betas', with `ix` indicating the index of 'beta'. The 'beta's in each iteration is placed as that the `no_cls` values of 'beta's for pattern group 'i' are followed by the next `no_cls` values for pattern group 'i+1'. The smallest index is 0.
	Group 'evals' contains: the average times of evaluating the posterior distribution in updating each 'beta' using slice sampling (identified by `ix=0`), and the average rejection rate of updating each 'log(sigma)' with Metropolis sampling (identified by `ix=1`).
`ix`	index of parameters inside each group, as discussed for `group` above.
`ix_g`	index of pattern group, starting from 0.
`ix_cls`	index of class, ranging from **1** to **no_cls**.
`id_beta`	index of 'beta', starting from 0.
`iter_b, forward, n`	
	Starting from `iter_b`, one of every `forward` Markov chain samples, with the number of total samples being `<=` n and the maximum usable in the file `mc_file`, is read.

train_y   Discrete response of training data. Assumed to be coded with 1,2,... no_cls.

no_cls   the number of possibilities (classes) of the response, default to the maximum
               value in train_y.

alpha   alpha=1 indicates that Cauchy prior is used, alpha=2 indicates that Gaus-
               sian prior is used.

log_sigma_widths, log_sigma_modes
               two vectors of length order+1, which are interpreted as follows: the Gaus-
               sian distribution with location log_sigma_modes[o] and standard devia-
               tion log_sigma_widths[o] is the prior for 'log(sigmas[o])', which is the
               hyperparameter (width parameter of Gaussian distribution or Cauchy distribu-
               tion) for the regression coefficients (i.e. 'beta's) associated with the interactions
               of order 'o'.

ptn_file   a character string, the name of the binary file where the compression result is
               saved. The method of writing to and reading from ptn_file can be found
               from the documentation for compression.

iters_mc,iters_bt,iters_sgm
               iters_mc iterations of super-transition will be run. Each super-transition
               consists of iters_bt iterations of updating 'beta's, and for each updating
               of 'beta's, the hyperparameters 'log(sigma)'s are updated iters_sgm times.
               When iters_mc=0, no Markov chain sampling will be run and other argu-
               ments related to Markov chain sampling take no effect.

w_bt,w_sgm, m_bt,m_sgm
               w_bt is the amount of stepping-out in updating 'beta' with slice sampling,
               m_bt is the maximum number of stepping-out in slice sampling for updating
               'beta'. w_sgm and m_sgm are intepreted similarly for sampling for 'log(sigma)'.

ini_log_sigmas
               Initial values of 'log(sigma)', default to log_sigma_mode.

quiet   quiet=1 suppresses the messages printed during reading the file mc_file.

Value

               The function display_mc returns a vector with names as
               #iters,#class,#groups,order,alpha.

               The function read_mc returns the Markov chain samples for a variable at spec-
               ified iterations.

               The function read_betas returns the Markov chain samples for a 'beta' at
               specified iterations.

               The function display_a_beta displays the pattern group information for
               the group associated with the queried 'beta', and also returns the Markov chain
               samples of this 'beta'. The method of reading the on-screen messages about a
               pattern group is documented in compression.

               The function calc_medians_betas returns the medians of Markov chain
               samples of all 'beta's at given iterations.

               The function training returns no value. Instead, the Markov chain samples
               are written to the binary file mc_file.

See Also

comp_train_pred,compression,prediction

Examples

```
## examples are given in comp_train_pred.
```

---

prediction	*Functions related to prediction*

Description

The function `predict_bpho` predicts the response of test cases.

The function `evaluate_prediction` evaluates the performance of the prediction in terms of average minus log probabilities and error rate. The function `split_cauchy` draws samples from a Cauchy distribution of two variables constraint to that their sum is fixed.

Usage

```
predict_bpho(test_x,no_cls,mc_file,ptn_file,iter_b,forward,
             iters_pred)
evaluate_prediction(test_y,pred_result,file_eval_details=c())
split_cauchy(n,s, sigma1,sigmasum,debug=1)
```

Arguments

`test_x`	Discrete features (also called inputs,covariates,independent variables, explanatory variables, predictor variables) of test data on which the predictions are based. The row is subject and the columns are inputs, which are coded with 1,2,..., with 0 reserved to represent that this input is not considered in a pattern. When the sequence prediction models are fitted, it is assumed that the first column is the state closest to the response. For example, a sequence 'x1,x2,x3,x4' is saved in `test_x` as 'x4,x3,x2,x1', for predicting the response 'x5'.
`test_y`	Discrete responses of test data, a vector with length equal to the row of `test_x`. Assumed to be coded with 1,2,... `no_cls`.
`no_cls`	the number of possibilities (classes) of the response.
`ptn_file`	a character string, the name of the binary file to which the compression result is saved. The method of writing to and reading from `ptn_file` can be found from the documentation compression.
`mc_file`	A character string, the name of the binary file to which Markov chain is written. The method of writing to and reading from `mc_file` can be found from the documentation training.
`iter_b, forward, iters_pred`	Starting from `iter_b`, one of every `forward` Markov chain samples, with the number of total samples being `<=` `iters_pred` and the maximum usable in the file `mc_file`, is used to make prediction.

pred_result   the value returned from the function `predict_bpho`.

file_eval_details

               the details of evaluation is sent to the file `file_eval_details`.

n   number of samples one wishes to obtain.

s   sum of two Cauchy random variables.

sigma1   scale parameter for the first Cauchy random variable.

sigmasum   the sum of scale parameters for two Cauchy random variables.

debug   indicator whether you are debugging the C program.

Value

The function `predict_bpho` returns a data frame, with the first `no_cls` columns storing the predictive probabilities for each class, and the last column is the guess for the response by choosing the label of the class with largest predictive probability.

The function `evaluate_prediction` returns the following values:

eval_details   a data frame. The first column is the true response, the second is the guessed value by taking the label of class with largest predictive probability, the third is indicator whether a wrong decision is make, the last column is the predictive probability at the true class.

error_rate   the proportion of wrong prediction.

amll   the average of minus log probabilities at true class, i.e. the average of the logarithms of the last column of `eval_details`.

The function `split_cauchy` returns a vector of `n` random numbers.

See Also

[comp_train_pred](#),[compression](#),[training](#)

Examples

```
## the function `predict_bpho' is demonstrated with the function
## `comp_train_pred' which calls `predict_bpho' inside.

## examples of 'evaluate_prediction' can be found from
## the documentation for comp_train_pred.

## testing the function split_cauchy
split_cauchy(100,10,1,5)
```

---

gendata   *Functions for generating data sets*

Description

`gen_hmm` generates sequences using hidden Markov models. `gen_bin_ho` generates general discrete data using logistic models, with high-order interactions considered; the response is binary. `text_to_number` converts an English text file into sequence of 1 (special symbols such as space, symbol),2 (vowl),3 (consonant).

Usage

```
gen_hmm(n,p,no_h,no_o,prob_h_stay, prob_o_stay)
gen_bin_ho(n,p,order,alpha,sigmas,nos_features,beta0)
text_to_number(p,file)
gen_X(n,p,K)
```

Arguments

`n`	number of cases.
`p`	number of features, or length of sequence.
`K`	number of possibilities for each feature.
`no_h`	number of states of hidden Markov chain.
`no_o`	number of states of output in hidden Markov model.
`prob_h_stay`	In simulating the hidden Markov chain, a chain will stay in its previous state with probability `prob_h_stay`, and move to other states with some minor probabilities adding up to `1-prob_h_stay`.
`prob_o_stay`	In simulating the output state of hidden Markov model, the "output" is equal to ("hidden state" mod `no_o`)+1 with probability `prob_o_stay` and equally likely other states.
`order`	the order of interactions considered in simulating data from general classification models.
`alpha`	`alpha=2` indicates that Gaussian distributions are used to generate the "beta"s and `alpha=1` indicates that Cauchy distributions are used.
`sigmas`	hyperparameters in generating "beta"s, a vector of length `order`.
`nos_features`	number of states for each feature, i.e., the number of possibilities for each feature. A vector of length `p`.
`beta0`	intercept of linear function in generating classification data.
`file`	name of the file containing text file, a character string.

Value

X	values of predictors, a matrix. Each row is a case. For sequence, the data for each case (a row) is placed in the reverse order of time. For example, sequence "x1,x2,x3" is represented with a row of X: x3,x2,x1. The values of predictor X are coded by 1,2,3,...,nos_features. The function gen_X generates only this matrix.
y	values of the response, a vector, coded by 1,2,...
betas	a matrix of two columns saving the values of "betas" used in generating classification data. The first column is the absolute identity of this beta, and the 2nd column is the value. The total number of "betas" is saved in no_betas.

See Also

comp_train_pred

Examples

```
data_hmm <- gen_hmm(100,10,8,2,0.8,0.8)
data_bin_ho <- gen_bin_ho(100,3,2,1,c(5,2),c(3,3,3),0)
X <- gen_X(100,5,3)
```

Index