Package ‘adapt4pv’

May 30, 2023

Type Package
Title Adaptive Approaches for Signal Detection in Pharmacovigilance
Version 0.2-3
Depends R (>= 3.6.0), Matrix (>= 1.0-6), glmnet (>= 3.0-2)
Imports speedglm, xgboost, doParallel, foreach
License GPL-2
Encoding UTF-8
LazyData true
RoxygenNote 7.0.2
Author Emeline Courtois [cre], Ismaïl Ahmed [aut], Hervé Perdry [ctb]
Maintainer Emeline Courtois <courtoise@iarc.who.int>
NeedsCompilation no
Repository CRAN
Date/Publication 2023-05-30 10:50:13 UTC

R topics documented:

adapt4pv-package ................................................. 2
adapt_bic .......................................................... 2
adapt_cisl .......................................................... 4
adapt_cv ............................................................ 6
adapt_univ .......................................................... 8
cisl ................................................................. 10
data_PV ............................................................. 12
est_ps_bic .......................................................... 13
est_ps_hdps ......................................................... 14
adapt_bic

Description

This package fits adaptive lasso approaches in high dimension for signal detection in pharmacovigilance. In addition to classical implementations found in the literature, we implemented two approaches particularly appropriate to variable selections framework, which is the one that stands in pharmacovigilance. We also supply in this package signal detection approaches based on lasso regression and propensity score in high dimension.

Author(s)

Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

adapt_bic

Description

Fit a first lasso regression and use Bayesian Information Criterion to determine adaptive weights (see lasso_bic function for more details), then run an adaptive lasso with this penalty weighting. BIC is used for the adaptive lasso for variable selection. Can deal with very large sparse data matrices. Intended for binary response only (option family = "binomial" is forced). Depends on the glmnet and relax.glmnet function from the package glmnet.

Usage

adapt_bic(x, y, gamma = 1, maxp = 50, path = TRUE, betaPos = TRUE, ...)

adapt4pv-package

Adaptive approaches for signal detection in PharmacoVigilance
**adapt_bic**

**Arguments**

- **x**
  Input matrix, of dimension `nobs x nvars`. Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package `Matrix`).

- **y**
  Binary response variable, numeric.

- **gamma**
  Tuning parameter to defined the penalty weights. See details below. Default is set to 1.

- **maxp**
  A limit on how many relaxed coefficients are allowed. Default is 50, in `glmnet` option default is 'n-3', where 'n' is the sample size.

- **path**
  Since `glmnet` does not do stepsize optimization, the Newton algorithm can get stuck and not converge, especially with relaxed fits. With `path=TRUE`, each relaxed fit on a particular set of variables is computed pathwise using the original sequence of lambda values (with a zero attached to the end). Default is `path=TRUE`.

- **betaPos**
  Should the covariates selected by the procedure be positively associated with the outcome? Default is `TRUE`.

- **...**
  Other arguments that can be passed to `glmnet` from package `glmnet` other than `penalty.factor`, `family`, `maxp` and `path`.

**Details**

The adaptive weight for a given covariate `i` is defined by

\[ w_i = \frac{1}{|\beta_i^{BIC}|^\gamma} \]

where `\beta_i^{BIC}` is the NON PENALIZED regression coefficient associated to covariate `i` obtained with lasso-bic.

**Value**

An object with S3 class "adaptive".

- **aws**
  Numeric vector of penalty weights derived from lasso-bic. Length equal to `nvars`.

- **criterion**
  Character, indicates which criterion is used with the adaptive lasso for variable selection. For `adapt_bic` function, criterion is "bic".

- **beta**
  Numeric vector of regression coefficients in the adaptive lasso. If `criterion = "cv"` the regression coefficients are PENALIZED, if `criterion = "bic"` the regression coefficients are UNPENALIZED. Length equal to `nvars`. Could be NA if adaptive weights are all equal to infinity.

- **selected_variables**
  Character vector, names of variable(s) selected with this adaptive approach. If `betaPos = TRUE`, this set is the covariates with a positive regression coefficient in `beta`. Else this set is the covariates with a non null regression coefficient in `beta`. Covariates are ordering according to the `p-values` (two-sided if `betaPos = FALSE`, one-sided if `betaPos = TRUE`) in the classical multiple logistic regression model that minimizes the BIC in the adaptive lasso.
adapt_cisl

Author(s)

Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

Examples

set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
ab <- adapt_bic(x = drugs, y = ae, maxp = 50)

Description

Compute the CISL procedure (see cis1 for more details) to determine adaptive penalty weights, then run an adaptive lasso with this penalty weighting. BIC is used for the adaptive lasso for variable selection. Can deal with very large sparse data matrices. Intended for binary response only (option family = "binomial" is forced). Depends on the glmnet function from the package glmnet.

Usage

adapt_cisl(
x,
y,
cisl_nB = 100,
cisl_dfmax = 50,
cisl_nlambda = 250,
cisl_ncore = 1,
maxp = 50,
path = TRUE,
betaPos = TRUE,
...
)

Arguments

x Input matrix, of dimension nobs x nvars. Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package Matrix).
y Binary response variable, numeric.
cisl_nB nB option in cis1 function. Default is 100.
The CISL procedure is first implemented with its default value except for dfmax and nlambda through parameters cisl_dfmax and cisl_nlambda. In addition, the betaPos parameter is set to FALSE in cisl. For each covariate $i$, cisl_nB values of the CISL quantity $\tau_i$ are estimated. The adaptive weight for a given covariate $i$ is defined by

$$w_i = 1 - 1/cisl_nB \sum_{b=1,...,cisl_nB} 1[\tau_i^b > 0]$$

If $\tau_i$ is the null vector, the associated adaptive weights in infinity. If $\tau_i$ is always positive, rather than “forcing” the variable into the model, we set the corresponding adaptive weight to $1/cisl_nB$.

Value
An object with S3 class "adaptive".

aws  Numeric vector of penalty weights derived from CISL. Length equal to nvars.
criterion Character, indicates which criterion is used with the adaptive lasso for variable selection. For adapt_cisl function, criterion is "bic".
beta  Numeric vector of regression coefficients in the adaptive lasso. If criterion = "cv" the regression coefficients are PENALIZED, if criterion = "bic" the regression coefficients are UNPENALIZED. Length equal to nvars. Could be NA if adaptive weights are all equal to infinity.
selected_variables Character vector, names of variable(s) selected with this adaptive approach. If betaPos = TRUE, this set is the covariates with a positive regression coefficient in beta. Else this set is the covariates with a non null regression coefficient in beta. Covariates are ordering according to the p-values (two-sided if betaPos = FALSE, one-sided if betaPos = TRUE) in the classical multiple logistic regression model that minimizes the BIC in the adaptive lasso.
adapt_cv

fit an adaptive lasso with adaptive weights derived from lasso-cv

Description

Fit a first lasso regression with cross-validation to determine adaptive weights. Run a cross-validation to determine an optimal lambda. Two options for implementing cross-validation for the adaptive lasso are possible through the type_cv parameter (see below). Can deal with very large sparse data matrices. Intended for binary response only (option family = "binomial" is forced). The cross-validation criterion used is deviance. Depends on the cv.glmnet function from the package glmnet.

Usage

adapt_cv(
  x,
  y,
  gamma = 1,
  nfolds = 5,
  foldid = NULL,
  type_cv = "proper",
  betaPos = TRUE,
  ...
)

Arguments

x Input matrix, of dimension nobs x nvars. Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package Matrix).

y Binary response variable, numeric.
adapt_cv

gamma  Tuning parameter to defined the penalty weights. See details below. Default is set to 1.
nfolds  Number of folds - default is 5. Although nfolds can be as large as the sample size (leave-one-out CV), it is not recommended for large datasets. Smallest value allowable is nfolds=3.
foldid  An optional vector of values between 1 and nfolds identifying what fold each observation is in. If supplied, nfolds can be missing.
type_cv  Character, indicates which implementation of cross-validation is performed for the adaptive lasso: a "naive" one, where adaptive weights obtained on the full data are used, and a "proper" one, where adaptive weights are calculated for each training sets. Could be either "naive" or "proper". Default is "proper".
betaPos  Should the covariates selected by the procedure be positively associated with the outcome? Default is TRUE.

...  Other arguments that can be passed to glmnet from package glmnet other than nfolds, foldid, penalty.factor, standardize, intercept and family.

Details

The adaptive weight for a given covariate i is defined by

\[ w_i = \frac{1}{\|\beta_{CV}^i \|^\gamma} \]

where \( \beta_{CV}^i \) is the PENALIZED regression coefficient associated to covariate i obtained with cross-validation.

Value

An object with S3 class "adaptive".

aws  Numeric vector of penalty weights derived from cross-validation. Length equal to nvars.
criterion  Character, indicates which criterion is used with the adaptive lasso for variable selection. For adapt_cv function, criterion is "cv".
beta  Numeric vector of regression coefficients in the adaptive lasso. If criterion = "cv" the regression coefficients are PENALIZED, if criterion = "bic" the regression coefficients are UNPENALIZED. Length equal to nvars. Could be NA if adaptive weights are all equal to infinity.

selected_variables  Character vector, names of variable(s) selected with this adaptive approach. If betaPos = TRUE, this set is the covariates with a positive regression coefficient in beta. Else this set is the covariates with a non null regression coefficient in beta. Covariates are ordering according to magnitude of their regression coefficients absolute value in the adaptive lasso.

Author(s)

Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>
adapt_univ

fit an adaptive lasso with adaptive weights derived from univariate coefficients

Description

Compute odd-ratios between each covariate of \( x \) and \( y \) then derived adaptive weights to incorporate in an adaptive lasso. BIC or cross-validation could either be used for the adaptive lasso for variable selection. Two options for implementing cross-validation for the adaptive lasso are possible through the type_cv parameter (see bellow). Can deal with very large sparse data matrices. Intended for binary response only (option family = "binomial" is forced). The cross-validation criterion used is deviance. Depends on the glmnet and relax.glmnet function from the package glmnet.

Usage

\[
\text{adapt_univ}(x, y, \\
gamma = 1, \\
criterion = "bic", \\
maxp = 50, \\
path = TRUE, \\
nfolds = 5, \\
foldid = NULL, \\
type_cv = "proper", \\
betaPos = TRUE, \\
...)
\]

Arguments

- \( x \)
  - Input matrix, of dimension \( \text{nobs} \times \text{nvars} \). Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package Matrix).
- \( y \)
  - Binary response variable, numeric.
- \( gamma \)
  - Tunning parameter to defined the penalty weights. See details below. Default is set to 1.
criterion  Character, indicates which criterion is used with the adaptive lasso for variable selection. Could be either "bic" or "cv". Default is "bic"

maxp  Used only if criterion = "bic", ignored if criterion = "cv". A limit on how many relaxed coefficients are allowed. Default is 50, in glmnet option default is 'n-3', where 'n' is the sample size.

path  Used only if criterion = "bic", ignored if criterion = "cv". Since glmnet does not do stepsize optimization, the Newton algorithm can get stuck and not converge, especially with relaxed fits. With path=TRUE, each relaxed fit on a particular set of variables is computed pathwise using the original sequence of lambda values (with a zero attached to the end). Default is path=TRUE.

nfolds  Used only if criterion = "cv", ignored if criterion = "bic". Number of folds - default is 5. Although nfolds can be as large as the sample size (leave-one-out CV), it is not recommended for large datasets. Smallest value allowable is nfolds=3.

foldid  Used only if criterion = "cv", ignored if criterion = "bic". An optional vector of values between 1 and nfolds identifying what fold each observation is in. If supplied, nfolds can be missing.

type_cv  Used only if criterion = "cv", ignored if criterion = "bic". Character, indicates which implementation of cross-validation is performed for the adaptive lasso: a "naive" one, where adaptive weights obtained on the full data are used, and a "proper" one, where adaptive weights are calculated for each training sets. Could be either "naive" or "proper". Default is "proper".

betaPos  Should the covariates selected by the procedure be positively associated with the outcome? Default is TRUE.

...  Other arguments that can be passed to glmnet from package glmnet other than family, maxp, standardize, intercept

Details

The adaptive weight for a given covariate i is defined by

\[ w_i = \frac{1}{|\beta_i^{univ}|^\gamma} \]

where \( \beta_i^{univ} = \log(OR_i) \), with \( OR_i \) is the odd-ratio associated to covariate \( i \) with the outcome.

Value

An object with S3 class "adaptive".

aws  Numeric vector of penalty weights derived from odds-ratios. Length equal to nvars.

criterion  Character, same as input. Could be either "bic" or "cv".

beta  Numeric vector of regression coefficients in the adaptive lasso. If criterion = "cv" the regression coefficients are PENALIZED, if criterion = "bic" the regression coefficients are UNPENALIZED. Length equal to nvars. Could be NA if adaptive weights are all equal to infinity.
selected_variables
Character vector, names of variable(s) selected with this adaptive approach. If `betaPos = TRUE`, this set is the covariates with a positive regression coefficient in `beta`. Else this set is the covariates with a non null regression coefficient in `beta`. If `criterion = "bic"`, covariates are ordering according to magnitude of their regression coefficients absolute value in the adaptive lasso. If `criterion = "bic"`, covariates are ordering according to the p-values (two-sided if `betaPos = FALSE`, one-sided if `betaPos = TRUE`) in the classical multiple logistic regression model that minimizes the BIC in the adaptive lasso.

Author(s)
Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

Examples

```r
set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
au <- adapt_univ(x = drugs, y = ae, criterion = "cv", nFolds = 3)
```

Description
Implementation of CISM and the stability selection according to subsampling options.

Usage
```r
cisl(
  x,
  y,
  r = 4,
  nB = 100,
  dfmax = 50,
  nlambda = 250,
  nMin = 0,
  replace = TRUE,
  betaPos = TRUE,
  ncore = 1
)
```
Arguments

x Input matrix, of dimension nobs x nvars. Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package Matrix).

y Binary response variable, numeric.

r Number of control in the CISL sampling. Default is 4. See details below for other implementations.

nB Number of sub-samples. Default is 100.

dfmax Corresponds to the maximum size of the models visited with the lasso (E in the paper). Default is 50.

nlambda Number of lambda values as is glmnet documentation. Default is 250.

nMin Minimum number of events for a covariate to be considered. Default is 0, all the covariates from x are considered.

replace Should sampling be with replacement? Default is TRUE.

betaPos If betaPos=TRUE, variable selection is based on positive regression coefficient. Else, variable selection is based on non-zero regression coefficient. Default is TRUE.

ncore The number of calcul units used for parallel computing. This has to be set to 1 if the parallel package is not available. Default is 1. WARNING: parallel computing is not supported for windows machines!

Details

CISL is a variation of the stability method adapted to characteristics of pharmacovigilance databases. Tuning $r = 4$ and replace = TRUE are used to implement our CISL sampling. For instance, $r = NULL$ and replace = FALSE can be used to implement the $\frac{n}{2}$ sampling in Stability Selection.

Value

An object with S3 class "cisl".

prob Matrix of dimension nvars x nB. Quantity compute by CISL for each covariate, for each subsample.

q05 5 % quantile of the CISL quantity for each covariates. Numeric, length equal to nvars.

q10 10 % quantile of the CISL quantity for each covariates. Numeric, length equal to nvars.

q15 15 % quantile of the CISL quantity for each covariates. Numeric, length equal to nvars.

q20 20 % quantile of the CISL quantity for each covariates. Numeric, length equal to nvars.

Author(s)

Ismail Ahmed
References


Examples

```r
set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
lcisl <- cisl(x = drugs, y = ae, nB = 50)
```

---

**data_PV**

*Simulated data for the adapt4pv package*

**Description**

Simple simulated data, used to demonstrate the features of functions from adapt4cv package.

**Format**

- X large sparse and binary matrix with 117160 rows and 300 columns. Drug matrix exposure: each row corresponds to an individual and each column corresponds to a drug.
- Y large sparse and binary vector of length 117160. Indicator of the presence/absence of an adverse event for each individual. Only the first 30 drugs (out of the 300) are associated with the outcome.

**Examples**

```r
data(ExamplePvData)
```
**est_ps_bic**

**propensity score estimation in high dimension with automated covariates selection using lasso-bic**

---

### Description

Estimate a propensity score to a given drug exposure by (i) selecting among other drug covariates in \( x \) which ones to include in the PS estimation model automatically using lasso-bic approach, (ii) estimating a score using a classical logistic regression with the afore selected covariates. Internal function, not supposed to be used directly.

### Usage

```r
est_ps_bic(idx_expo, x, penalty = rep(1, nvars - 1), ...)
```

### Arguments

- `idx_expo`: Index of the column in \( x \) that corresponds to the drug covariate for which we aim at estimating the PS.
- `x`: Input matrix, of dimension \( \text{nobs} \times \text{nvars} \). Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package Matrix).
- `penalty`: TEST OPTION penalty weights in the variable selection to include in the PS.
- `...`: Other arguments that can be passed to `glmnet` from package `glmnet` other than `penalty.factor`, `family`, `maxp` and `path`.

### Details

`betaPos` option of `lasso_bic` function is set to `FALSE` and `maxp` is set to 20. For optimal storage, the returned elements `indicator_expo` and `score` are Matrix with \( \text{ncol} = 1 \).

### Value

An object with S3 class "ps", "bic".

- `expo_name`: Character, name of the drug exposure for which the PS was estimated. Correspond to `colnames(x)[idx_expo]`
- `indicator_expo`: One-column Matrix object. Indicator of the drug exposure for which the PS was estimated. Defined by `x[, idx_expo]`.
- `score_variables`: Character vector, names of covariates(s) selected with the lasso-bic approach to include in the PS estimation model. Could be empty.
- `score`: One-column Matrix object, the estimated score.
Author(s)

Emeline Courtois

Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

Examples

```
set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
psb2 <- est_ps_bic(idx_expo = 2, x = drugs)
psb2$score_variables #selected variables to include in the PS model of drug_2
```

Description

Estimate a propensity score to a given drug exposure by (i) selecting among other drug covariates in \( x \) which ones to include in the PS estimation model automatically using hdPS algorithm, (ii) estimating a score using a classical logistic regression with the afore selected covariates. Internal function, not supposed to be used directly.

Usage

```
est_ps_hdps(idx_expo, x, y, keep_total = 20)
```

Arguments

- **idx_expo**: Index of the column in \( x \) that corresponds to the drug covariate for which we aim at estimating the PS.
- **x**: Input matrix, of dimension \( \text{nobs} \times \text{nvars} \). Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package Matrix).
- **y**: Binary response variable, numeric.
- **keep_total**: number of covariates to include in the PS estimation model according to the hdps algorithm ordering. Default is 20.

Details

Compared to the situation of the classic use of hdps (i) there is only one dimension (the co-exposition matrix) (ii) no need to expand covariates since they are already binary. In other words, in our situation hdps consists in the "prioritize covariates" step from the original algorithm, using Bross formula. We consider the correction on the interpretation on this formula made by Richard Wyss (drug epi).
est_ps_xgb

Value

An object with S3 class "ps", "hdps".

expo_name Character, name of the drug exposure for which the PS was estimated. Correspond to colnames(x)[idx_expo]

indicator_expo One-column Matrix object. Indicator of the drug exposure for which the PS was estimated. Defined by x[, idx_expo].

score_variables Character vector, names of covariates(s) selected with the hdPS algorithm to include in the PS estimation model. Could be empty.

score One-column Matrix object, the estimated score.

Author(s)

Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

References


Examples

set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
pshdps2 <- est_ps_hdps(idx_expo = 2, x = drugs, y = ae, keep_total = 10)
pshdps2$score_variables #selected variables to include in the PS model of drug_2

---

est_ps_xgb propensity score estimation in high dimension using gradient tree boosting

Description

Estimate a propensity score to a given drug exposure (treatment) with extreme gradient boosting. Depends on xgboost package. Internal function, not supposed to be used directly.
Usage

```r
est_ps_xgb(
  idx_expo,
  x,
  parameters = list(eta = 0.1, max_depth = 6, objective = "binary:logistic", nthread = 1),
  nrounds = 200,
  ...
)
```

Arguments

- **idx_expo**: Index of the column in `x` that corresponds to the drug covariate for which we aim at estimating the PS.
- **x**: Input matrix, of dimension nobs x nvars. Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package Matrix).
- **parameters**: correspond to `params` in `xgb.train` function. The complete list of parameters is available at [http://xgboost.readthedocs.io/en/latest/parameter.html](http://xgboost.readthedocs.io/en/latest/parameter.html). Default is a list with `eta=0.1` (learning rate), `max_depth = 6` (maximum length of a tree), `objective = "binary:logistic"` and `nthread = 1` (number of threads for parallelization).
- **nrounds**: Maximum number of boosting iterations. Default is 200.
- **...**: Other arguments that can be passed to `xgb.train` function.

Value

An object with S3 class "ps", "xgb".

- **expo_name**: Character, name of the drug exposure for which the PS was estimated. Correspond to `colnames(x)[idx_expo]`.
- **indicator_expo**: One-column Matrix object. Indicator of the drug exposure for which the PS was estimated. Defined by `x[, idx_expo]`.
- **score_variables**: Character vector, names of covariates(s) used in a at list one tree in the gradient tree boosting algorithm. Obtained with `xgb.importance` function from xgboost package.
- **score**: One-column Matrix object, the estimated score.

Author(s)

Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>
lasso_bic

Examples

```r
set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
psxgb2 <- est_ps_xgb(idx_expo = 2, x = drugs, nrounds = 100)
psxgb2$score_variables # selected variables to include in the PS model of drug_2
```

### Description

Fit a lasso regression and use the Bayesian Information Criterion (BIC) to select a subset of selected covariates. Can deal with very large sparse data matrices. Intended for binary response only (option family = "binomial" is forced). Depends on the glmnet and relax.glmnet functions from the package glmnet.

### Usage

```r
lasso_bic(x, y, maxp = 50, path = TRUE, betaPos = TRUE, ...)
```

### Arguments

- **x**: Input matrix, of dimension nobs x nvars. Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package Matrix).
- **y**: Binary response variable, numeric.
- **maxp**: A limit on how many relaxed coefficients are allowed. Default is 50, in glmnet option default is 'n-3', where 'n' is the sample size.
- **path**: Since glmnet does not do stepsize optimization, the Newton algorithm can get stuck and not converge, especially with relaxed fits. With path=TRUE, each relaxed fit on a particular set of variables is computed pathwise using the original sequence of lambda values (with a zero attached to the end). Default is path=TRUE.
- **betaPos**: Should the covariates selected by the procedure be positively associated with the outcome? Default is TRUE.
- **...**: Other arguments that can be passed to glmnet from package glmnet other than family, maxp and path.
Details

For each tested penalisation parameter $\lambda$, a standard version of the BIC is implemented.

$$BIC_\lambda = -2l_\lambda + df(\lambda) \times \ln(N)$$

where $l_\lambda$ is the log-likelihood of the non-penalized multiple logistic regression model that includes the set of covariates with a non-zero coefficient in the penalised regression coefficient vector associated to $\lambda$, and $df(\lambda)$ is the number of covariates with a non-zero coefficient in the penalised regression coefficient vector associated to $\lambda$. The optimal set of covariates according to this approach is the one associated with the classical multiple logistic regression model which minimizes the BIC.

Value

An object with S3 class "log.lasso".

beta
Numeric vector of regression coefficients in the lasso. In lasso_bic function, the regression coefficients are UNPENALIZED. Length equal to nvars.

selected_variables
Character vector, names of variable(s) selected with the lasso-bic approach. If betaPos = TRUE, this set is the covariates with a positive regression coefficient in beta. Else this set is the covariates with a non null regression coefficient in beta. Covariates are ordering according to the p-values (two-sided if betaPos = FALSE, one-sided if betaPos = TRUE) in the classical multiple logistic regression model that minimizes the BIC.

Author(s)

Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

Examples

```r
set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
lb <- lasso_bic(x = drugs, y = ae, maxp = 20)
```

Description

Fit a first cross-validation on lasso regression and return selected covariates. Can deal with very large sparse data matrices. Intended for binary response only (option family = "binomial" is forced). Depends on the cv.glmnet function from the package glmnet.
Usage

lasso_cv(x, y, nfolds = 5, foldid = NULL, betaPos = TRUE, ...)

Arguments

x
Input matrix, of dimension nobs x nvars. Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package Matrix).

y
Binary response variable, numeric.

nfolds
Number of folds - default is 5. Although nfolds can be as large as the sample size (leave-one-out CV), it is not recommended for large datasets. Smallest value allowable is nfolds=3.

foldid
An optional vector of values between 1 and nfolds identifying what fold each observation is in. If supplied, nfolds can be missing.

betaPos
Should the covariates selected by the procedure be positively associated with the outcome ? Default is TRUE.

...
Other arguments that can be passed to cv.glmnet from package glmnet other than nfolds, foldid, and family.

Value

An object with S3 class "log.lasso".

beta
Numeric vector of regression coefficients in the lasso. In lasso_cv function, the regression coefficients are PENALIZED. Length equal to nvars.

selected_variables
Character vector, names of variable(s) selected with the lasso-cv approach. If betaPos = TRUE, this set is the covariates with a positive regression coefficient in beta. Else this set is the covariates with a non null regression coefficient in beta. Covariates are ordering according to magnitude of their regression coefficients absolute value.

Author(s)

Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

Examples

set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
lcv <- lasso_cv(x = drugs, y = ae, nfolds = 3)
lasso_perm

*fit a lasso regression and use standard permutation of the outcome for variable selection*

**Description**

Performed K lasso logistic regression with K different permuted version of the outcome. For each of the lasso regression, the $\lambda_{\text{max}}$ (i.e. the smaller $\lambda$ such as all penalized regression coefficients are shrunk to zero) is obtained. The median value of these K $\lambda_{\text{max}}$ is used to for variable selection in the lasso regression with the non-permuted outcome. Depends on the glmnet function from the package glmnet.

**Usage**

```r
lasso_perm(x, y, K = 20, keep = NULL, betaPos = TRUE, ncore = 1, ...)
```

**Arguments**

- `x`  
  Input matrix, of dimension nobs x nvars. Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package Matrix).

- `y`  
  Binary response variable, numeric.

- `K`  
  Number of permutations of y. Default is 20.

- `keep`  
  Do some variables of x have to be permuted in the same way as y? Default is NULL, means no. If yes, must be a vector of covariates indices. TEST OPTION

- `betaPos`  
  Should the covariates selected by the procedure be positively associated with the outcome? Default is TRUE.

- `ncore`  
  The number of calcul units used for parallel computing. Default is 1, no parallelization is implemented.

- `...`  
  Other arguments that can be passed to glmnet from package glmnet other than family.

**Details**

The selected $\lambda$ with this approach is defined as the closest $\lambda$ from the median value of the K $\lambda_{\text{max}}$ obtained with permutation of the outcome.

**Value**

An object with S3 class "log.lasso".

- `beta`  
  Numeric vector of regression coefficients in the lasso In lasso_perm function, the regression coefficients are PENALIZED. Length equal to nvars.
ps_adjust

selected_variables
Character vector, names of variable(s) selected with the lasso-perm approach. If betaPos = TRUE, this set is the covariates with a positive regression coefficient in beta. Else this set is the covariates with a non null regression coefficient in beta. Covariates are ordering according to magnitude of their regression coefficients absolute value.

Author(s)
Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

References

Examples

set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
lp <- lasso_perm(x = drugs, y = ae, K = 10)

ps_adjust

adjusment on propensity score

Description
Implement the adjustment on propensity score for all the drug exposures of the input drug matrix x which have more than a given number of co-occurrence with the outcome. The binary outcome is regressed on a drug exposure and its estimated PS, for each drug exposure considered after filtering. With this approach, a p-value is obtained for each drug and a variable selection is performed over the corrected for multiple comparisons p-values.

Usage

ps_adjust(
  x,
  y,
  n_min = 3,
  betaPos = TRUE,
  est_type = "bic",
)
Arguments

- **x**: Input matrix, of dimension `nobs x nvars`. Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package Matrix).
- **y**: Binary response variable, numeric.
- **n_min**: Numeric, Minimal number of co-occurrence between a drug covariate and the outcome `y` to estimate its score. See details belows. Default is 3.
- **betaPos**: Should the covariates selected by the procedure be positively associated with the outcome? Default is TRUE.
- **est_type**: Character, indicates which approach is used to estimate the PS. Could be either "bic", "hdps" or "xgb". Default is "bic".
- **threshold**: Threshold for the p-values. Default is 0.05.
- **ncore**: The number of calcul units used for parallel computing. Default is 1, no parallelization is implemented.

Details

The PS could be estimated in different ways: using lasso-bic approach, the hdps algorithm or gradient tree boosting. The scores are estimated using the default parameter values of `est_ps_bic`, `est_ps_hdps` and `est_ps_xgb` functions (see documentation for details). We apply the same filter and the same multiple testing correction as in the paper (UPCOMING REFERENCE). first, PS are estimated only for drug covariates which have more than `n_min` co-occurrence with the outcome `y`. Adjustment on the PS is performed for these covariates and one sided or two-sided (depend on `betaPos` parameter) p-values are obtained. The p-values of the covariates not retained after filtering are set to 1. All these p-values are then adjusted for multiple comparison with the Benjamini-Yekutieli correction. COULD BE VERY LONG. Since this approach (i) estimate a score for several drug covariates and (ii) perform an adjustment on these scores, parallelization is highly recommanded.

Value

An object with S3 class "ps", "adjust", "*", where "*" is "bic", "hdps" or "xgb" according on how the score were estimated.

- **estimates**: Regression coefficients associated with the drug covariates. Numeric, length equal to the number of selected variables with this approach. Some elements could be NA if (i) the corresponding covariate was filtered out, (ii) adjustment model did not converge. Trying to estimate the score in a different way could help, but it’s not insured.
- **corrected_pvals**: One sided p-values if `betaPos` = TRUE, two-sided p-values if `betaPos` = FALSE adjusted for multiple testing. Numeric, length equal to `nvars`.

```r
threshold = 0.05,
ncore = 1
)
```
selected_variables

Character vector, names of variable(s) selected with the ps-adjust approach. If betaPos = TRUE, this set is the covariates with a corrected one-sided p-value lower than threshold. Else this set is the covariates with a corrected two-sided p-value lower than threshold. Covariates are ordering according to their corrected p-value.

Author(s)

Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

References


Examples

set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
adjps <- ps_adjust(x = drugs, y = ae, n_min = 10)

Description

Implement the adjustment on propensity score for one drug exposure. The binary outcome is regressed on the drug exposure of interest and its estimated PS. Internal function, not supposed to be used directly.

Usage

ps_adjust_one(ps_est, y)

Arguments

An object of class "ps", "*" where "*" is "bic", "hdps" or "xgb" according on how the score was estimated, respective outputs of internal functions est_ps_bic, est_ps_hdps, est_ps_xgb. It is a list with the following elements: * score_type: character, name of the drug exposure for which the PS was estimated. * indicator_expo: indicator of the drugs exposure for which the
PS was estimated. One-column Matrix object. * score_variables: Character vector, names of covariate(s) selected to include in the PS estimation model. Could be empty. *score: One-column Matrix object, the estimated score.

Details

The PS could be estimated in different ways: using lasso-bic approach, the hdPS algorithm or gradient tree boosting using functions est_ps_bic, est_ps_hdps and est_ps_xgb respectively.

Value

An object with S3 class "ps", "adjust"

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>expo_name</td>
<td>Character, name of the drug exposure for which the PS was estimated.</td>
</tr>
<tr>
<td>estimate</td>
<td>Regression coefficient associated with the drug exposure in adjustment on PS.</td>
</tr>
<tr>
<td>pval_1sided</td>
<td>One sided p-value associated with the drug exposure in adjustment on PS.</td>
</tr>
<tr>
<td>pval_2sided</td>
<td>Two sided p-value associated with the drug exposure in adjustment on PS.</td>
</tr>
</tbody>
</table>

Could return NA if the adjustment on the PS did not converge.

Author(s)

Emeline Courtois

Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

Examples

```r
set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
pshdps2 <- est_ps_hdps(idx_expo = 2, x = drugs, y = ae, keep_total = 10)
adjs2 <- ps_adjust_one(ps_est = pshdps2, y = ae)
adjs2$estimate #estimated strength of association between drug_2 and the outcome by PS adjustment
```

Description

Implement the weighting on propensity score with Matching Weights (MW) or the Inverse Probability of Treatment Weighting (IPTW) for all the drug exposures of the input drug matrix `x` which have more than a given number of co-occurrence with the outcome. The binary outcome is regressed on a drug exposure through a classical weighted regression, for each drug exposure considered after filtering. With this approach, a p-value is obtained for each drug and a variable selection is performed over the corrected for multiple comparisons p-values.
ps_pond

Usage

ps_pond(
  x,
  y,
  n_min = 3,
  betaPos = TRUE,
  weights_type = c("mw", "iptw"),
  truncation = FALSE,
  q = 0.025,
  est_type = "bic",
  threshold = 0.05,
  ncore = 1
)

Arguments

x  Input matrix, of dimension nobs x nvars. Each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package Matrix).

y  Binary response variable, numeric.

n_min  Numeric. Minimal number of co-occurrence between a drug covariate and the outcome y to estimate its score. See details belows. Default is 3.

betaPos  Should the covariates selected by the procedure be positively associated with the outcome ? Default is TRUE.

weights_type  Character. Indicates which type of weighting is implemented. Could be either "mw" or "iptw".

truncation  Boolean, should we do weight truncation? Default is FALSE.

q  If truncation is TRUE, quantile value for weight truncation. Ignored if truncation is FALSE. Default is 2.5 %.

est_type  Character, indicates which approach is used to estimate the propensity score. Could be either "bic", "hdps" or "xgb". Default is "bic".

threshold  Threshold for the p-values. Default is 0.05.

ncore  The number of calcul units used for parallel computing. Default is 1, no parallelization is implemented.

Details

The MW are defined by

\[ mw_i = \min(PS_i, 1 - PS_i)/(expo_i \times PS_i + (1 - expo_i) \times (1 - PS_i)) \]

and weights from IPTW by

\[ iptw_i = expo_i/PS_i + (1 - expo_i)/(1 - PS_i) \]

where \( expo_i \) is the drug exposure indicator. The PS could be estimated in different ways: using lasso-bic approach, the hdps algorithm or gradient tree boosting. The scores are estimated using the
default parameter values of est_ps_bic, est_ps_hdps and est_ps_xgb functions (see documentation for details). We apply the same filter and the same multiple testing correction as in the paper.

UPCOMING REFERENCE: first, PS are estimated only for drug covariates which have more than \( n_{\text{min}} \) co-occurrence with the outcome \( y \). Adjustment on the PS is performed for these covariates and one sided or two-sided (depend on betaPos parameter) p-values are obtained. The p-values of the covariates not retained after filtering are set to 1. All these p-values are then adjusted for multiple comparison with the Benjamini-Yekutieli correction. COULD BE VERY LONG. Since this approach (i) estimate a score for several drug covariates and (ii) perform an adjustment on these scores, parallelization is highly recommended.

**Value**

An object with S3 class "ps", "*", "**", where "*" is "mw" or "iptw", same as the input parameter weights_type, and "**" is "bic", "hdps" or "xgb" according on how the score was estimated.

estimates Regression coefficients associated with the drug covariates. Numeric, length equal to the number of selected variables with this approach. Some elements could be NA if (i) the corresponding covariate was filtered out, (ii) weighted regression did not converge. Trying to estimate the score in a different way could help, but it’s not insured.

corrected_pvals One sided p-values if betaPos = TRUE, two-sided p-values if betaPos = FALSE adjusted for multiple testing. Numeric, length equal to nvars.

selected_variables Character vector, names of variable(s) selected with the weighting on PS based approach. If betaPos = TRUE, this set is the covariates with a corrected one-sided p-value lower than threshold. Else this set is the covariates with a corrected two-sided p-value lower than threshold. Covariates are ordering according to their corrected p-value.

**Author(s)**

Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

**References**


**Examples**

```r
set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
pondps <- ps_pond(x = drugs, y = ae, n_min = 10, weights_type = "iptw")
```
ps_pond_one

**Description**

Implement the weighting on propensity score with Matching Weights (MW) or the Inverse Probability of Treatment Weighting (IPTW) for one drug exposure. The binary outcome is regressed on the drug exposure of interest through a classical weighted regression. Internal function, not supposed to be used directly.

**Usage**

```
ps_pond_one(
  ps_est,
  y,
  weights_type = c("mw", "iptw"),
  truncation = FALSE,
  q = 0.025
)
```

**Arguments**

- `ps_est`:
  An object of class "ps", "*" where "*" is "bic", "hdps" or "xgb" according on how the score was estimated, respective outputs of internal functions `est_ps_bic`, `est_ps_hdps`, `est_ps_xgb`. It is a list with the following elements:
  - `score_type`: character, name of the drug exposure for which the PS was estimated.
  - `indicator_expo`: indicator of the drugs exposure for which the PS was estimated. One-column Matrix object.
  - `score_variables`: Character vector, names of covariate(s) selected to include in the PS estimation model. Could be empty.
  - `score`: One-column Matrix object, the estimated score.

- `y`:
  Binary response variable, numeric.

- `weights_type`:
  Character. Indicates which type of weighting is implemented. Could be either "mw" or "iptw".

- `truncation`:
  Boolean, should we do weight truncation? Default is FALSE.

- `q`:
  If truncation is TRUE, quantile value for weight truncation. Ignored if truncation is FALSE. Default is 2.5%.

**Details**

The MW are defined by

\[ mw_i = \min(PS_i, 1 - PS_i)/[(expo_i) * PS_i + (1 - expo_i) * (1 - PS_i)] \]

and weights from IPTW by

\[ iptw_i = expo_i/PS_i + (1 - expo_i)/(1 - PS_i) \]
where \( \text{expo}_i \) is the drug exposure indicator. The PS could be estimated in different ways: using lasso-bic approach, the hdPS algorithm or gradient tree boosting using functions `est_ps_bic`, `est_ps_hdps` and `est_ps_xgb` respectively.

**Value**

An object with S3 class "ps","*", where "*" is "mw" or "iptw", same as the input parameter `weights_type`

- `expo_name` Character, name of the drug exposure for which the PS was estimated.
- `estimate` Regression coefficient associated with the drug exposure in adjustment on PS.
- `pval_1sided` One sided p-value associated with the drug exposure in adjustment on PS.
- `pval_2sided` Two sided p-value associated with the drug exposure in adjustment on PS.

Could return NA if the adjustment on the PS did not converge.

**Author(s)**

Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

**Examples**

```r
set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
phdps2 <- est_ps_hdps(idx_expo = 2, x = drugs, y = ae, keep_total = 10)
pondps2 <- ps_pond_one(ps_est = phdps2, y = ae, weights_type = "iptw")
pondps2$estimate #estimated strength of association between drug_2 and the outcome by PS weighting
```

**Description**

Return the Sensitivity and the False Discovery Rate of an approach implemented by the main functions of adapt4pv package.

**Usage**

```r
summary_stat(object, true_pos, q = 10)
```
Arguments

object     An object of class "log.lasso", "cisl", "adaptive" and "+", "ps", "+*" where "+*" is either "adjust", "iptw" or "mw" and "+**" is either "bic", "hdps" or "xgb".
true_pos   Character vector, names of the true positives controls
q          Quantile value for variable selection with an object of class "cisl". Possible values are 5, 10, 15, 20. Default is 10

Value

A data frame which details for the signal detection method implemented in object: its number of generated signals, its sensitivity and its false discovery rate.

Author(s)

Emeline Courtois
Maintainer: Emeline Courtois <emeline.courtois@inserm.fr>

Examples

set.seed(15)
drugs <- matrix(rbinom(100*20, 1, 0.2), nrow = 100, ncol = 20)
colnames(drugs) <- paste0("drugs",1:ncol(drugs))
ae <- rbinom(100, 1, 0.3)
lcv <- lasso_cv(x = drugs, y = ae, nfolds = 3)
summary_stat(object = lcv, true_pos = colnames(drugs)[1:10])
# the data are not simulated in such a way that there are true positives
Index

* datasets
  data_PV, 12
adapt4pv-package, 2
adapt_bic, 2
adapt_cisl, 4
adapt_cv, 6
adapt_univ, 8
cisl, 10
data_PV, 12
est_ps_bic, 13
est_ps_hdps, 14
est_ps_xgb, 15
lasso_bic, 17
lasso_cv, 18
lasso_perm, 20
ps_adjust, 21
ps_adjust_one, 23
ps_pond, 24
ps_pond_one, 27
summary_stat, 28
X (data_PV), 12
Y (data_PV), 12