Package ‘PUlasso’

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Type Package

Title High-Dimensional Variable Selection with Presence-Only Data

Version 3.2.3

Date 2019-4-25

Description Efficient algorithm for solving PU (Positive and Unlabeled) problem in low or high
dimensional setting with lasso or group lasso penalty. The algorithm uses Maximization-
Minorization and (block) coordinate descent. Sparse calculation and parallel computing are sup-

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Imports Rcpp (>= 0.12.8), methods, Matrix, doParallel, foreach, ggplot2

Depends R(>= 2.10)

LinkingTo Rcpp, RcppEigen, Matrix

RoxygenNote 6.1.1

Suggests testthat, knitr, rmarkdown

VignetteBuilder knitr


BugReports https://github.com/hsong1/PUlasso/issues

NeedsCompilation yes

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Description


Details

Main functions: grpPUlasso, cv.grpPUlasso, coef, predict

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See Also

Useful links:

- Report bugs at [https://github.com/hsong1/PULasso/issues](https://github.com/hsong1/PULasso/issues)

Examples

data("simulPU")
fit<grpPUlasso(X=simulPU$x,z=simulPU$z,py1=simulPU$truePY1)
## Not run:
cvfit=cv.grpPUlasso(X=simulPU$x,z=simulPU$z,py1=simulPU$truePY1)

## End(Not run)
coef(fit,lambda=fit$lambda[10])
predict(fit,newdata = head(simulPU$x), lambda = fit$lambda[10], type = "response")
cv.grpPUlasso

Cross-validation for PUlasso

Description

Do a n-fold cross-validation for PUlasso.

Usage

```r
cv.grpPUlasso(x, z, py1, initial_coef = NULL, group = 1:p,
penalty = NULL, lambda = NULL, nlambda = 100,
lambdaMinRatio = ifelse(N < p, 0.05, 0.005), maxit = ifelse(method ==
"CD", 1000, N * 10), weights = NULL, eps = 1e-04, inner_eps = 0.01,
verbose = FALSE, stepSize = NULL, stepSizeAdjustment = NULL,
batchSize = 1, updateFrequency = N, samplingProbabilities = NULL,
method = c("CD", "GD", "SGD", "SVRG", "SAG"), nfolds = 10,
fitInd = 1:nfolds, nCores = 1, trace = c("none", "param", "fVal",
"all"))
```

Arguments

- **x**: Input matrix; each row is an observation. Can be a matrix or a sparse matrix.
- **z**: Response vector representing whether an observation is labeled or unlabeled.
- **py1**: True prevalence Pr(Y=1)
- **initial_coef**: A vector representing an initial point where we start PUlasso algorithm from.
- **group**: A vector representing grouping of the coefficients. For the least ambiguity, it is recommended if group is provided in the form of vector of consecutive ascending integers.
- **penalty**: penalty to be applied to the model. Default is sqrt(group size) for each of the group.
- **lambda**: A user supplied sequence of lambda values. If unspecified, the function automatically generates its own lambda sequence based on nlambda and lambdaMinRatio.
- **nlambda**: The number of lambda values.
- **lambdaMinRatio**: Smallest value for lambda, as a fraction of lambda.max which leads to the intercept only model.
- **maxit**: Maximum number of iterations.
- **weights**: observation weights. Default is 1 for each observation.
- **eps**: Convergence threshold for the outer loop. The algorithm iterates until the maximum change in coefficients is less than eps in the outer loop.
- **inner_eps**: Convergence threshold for the inner loop. The algorithm iterates until the maximum change in coefficients is less than eps in the inner loop.
- **verbose**: A logical value. if TRUE, the function prints out the fitting process.
stepSize  A step size for gradient-based optimization. If NULL, a step size is taken to be 
stepSizeAdj/mean(Li) where Li is a Lipschitz constant for ith sample 

stepSizeAdjustment  
A step size adjustment. By default, adjustment is 1 for GD and SGD, 1/8 for 
SVRG and 1/16 for SAG.

batchSize  A batch size. Default is 1.

updateFrequency  
An update frequency of full gradient for method == "SVRG"

samplingProbabilities  
sampling probabilities for each of samples for stochastic gradient-based opti-
mization. If NULL, each sample is chosen proportionally to Li.

method  Optimization method. Default is Coordinate Descent. CD for Coordinate De-
scent, GD for Gradient Descent, SGD for Stochastic Gradient Descent, SVRG 
for Stochastic Variance Reduction Gradient, SAG for Stochastic Averaging Gra-
dient.

nfolds  Number of cross-validation folds to be created.

fitInd  A vector of indices of cross-validation models which will be fitted. Default is to 
fit the model for each of the cross-validation fold.

nCores  Number of threads to be used for parallel computing. If nCores=0, it is set to be 
(the number of processors available-1) . Default value is 1.

trace  An option for saving intermediate quantities when fitting a full dataset.

Value

cvm  Mean cross-validation error

cvstdev  Estimate of standard error of cvm

cvcoef  Coefficients for each of the fitted CV models

cvstdcoef  Coefficients in a standardized scale for each of the fitted CV models

lambda  The actual sequence of lambda values used.

lambda.min  Value of lambda that gives minimum cvm.

lambda.1se  The largest value of lambda such that the error is within 1 standard error of the minimum 
cvm.

PUfit  A fitted PUfit object for the full data

Examples

data("simulPU")
fit<-cv.grpPUlasso(X=simulPU$X,z=simulPU$z,py1=simulPU$truePY1)
**deviances**

**Description**

Calculate deviances at provided coefficients

**Usage**

deviances(X, z, py1, coefMat, weights = NULL)

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>X</td>
<td>Input matrix</td>
</tr>
<tr>
<td>z</td>
<td>Response vector</td>
</tr>
<tr>
<td>py1</td>
<td>True prevalence Pr(Y=1)</td>
</tr>
<tr>
<td>coefMat</td>
<td>A coefficient matrix whose column corresponds to a set of coefficients</td>
</tr>
<tr>
<td>weights</td>
<td>Observation weights. Default is 1 for each observation.</td>
</tr>
</tbody>
</table>

**Value**

deviances

**Examples**

data("simulPU")
coef0<-replicate(2,runif(ncol(simulPU$X)+1))
deviances(simulPU$X,simulPU$z,py1=simulPU$truePY1,coefMat = coef0)

---

**grppUlasso**

Solve PU problem with lasso or group lasso penalty.

**Description**

Fit a model using PUlasso algorithm over a regularization path. The regularization path is computed at a grid of values for the regularization parameter lambda.

**Usage**

groupUlasso(X, z, py1, initial_coef = NULL, group = 1:ncol(X),
penalty = NULL, lambda = NULL, nlambda = 100,
lambdaMinRatio = ifelse(N < p, 0.05, 0.005), maxit = ifelse(method == "CD", 1000, N * 10), maxit_inner = 1e+05, weights = NULL,
eps = 1e-04, inner_eps = 0.01, verbose = FALSE, stepSize = NULL,
stepSizeAdjustment = NULL, batchSize = 1, updateFrequency = N,
samplingProbabilities = NULL, method = c("CD", "GD", "SGD", "SVRG", "SAG"), trace = c("none", "param", "fVal", "all"))
Arguments

X  Input matrix; each row is an observation. Can be a matrix or a sparse matrix.
z  Response vector representing whether an observation is labeled or unlabeled.
py1  True prevalence Pr(Y=1)
initial_coef  A vector representing an initial point where we start PUlasso algorithm from.
group  A vector representing grouping of the coefficients. For the least ambiguity, it is recommended if group is provided in the form of vector of consecutive ascending integers.
penalty  penalty to be applied to the model. Default is sqrt(group size) for each of the group.
lambda  A user supplied sequence of lambda values. If unspecified, the function automatically generates its own lambda sequence based on nlambda and lambdaMinRatio.
nlambda  The number of lambda values.
lambdaMinRatio  Smallest value for lambda, as a fraction of lambda.max which leads to the intercept only model.
maxit  Maximum number of iterations.
maxit_inner  Maximum number of iterations for a quadratic sub-problem for CD.
weights  observation weights. Default is 1 for each observation.
eps  Convergence threshold for the outer loop. The algorithm iterates until the maximum change in coefficients is less than eps in the outer loop.
inner_eps  Convergence threshold for the inner loop. The algorithm iterates until the maximum change in coefficients is less than eps in the inner loop.
verbose  A logical value. if TRUE, the function prints out the fitting process.
stepSize  A step size for gradient-based optimization. if NULL, a step size is taken to be stepSizeAdj/mean(Li) where Li is a Lipschitz constant for ith sample
stepSizeAdjustment  A step size adjustment. By default, adjustment is 1 for GD and SGD, 1/8 for SVRG and 1/16 for SAG.
batchSize  A batch size. Default is 1.
updateFrequency  An update frequency of full gradient for method =="SVRG"
samplingProbabilities  sampling probabilities for each of samples for stochastic gradient-based optimization. if NULL, each sample is chosen proportionally to Li.
trace  An option for saving intermediate quantities. All intermediate standardized-scale parameter estimates(trace=="param"), objective function values at each iteration(trace=="fVal"), or both(trace=="all") are saved in optResult. Since this is computationally very heavy, it should be only used for decently small-sized dataset and small maxit. A default is "none".
Value

coeff A p by length(lambda) matrix of coefficients
std_coef A p by length(lambda) matrix of coefficients in a standardized scale
lambda The actual sequence of lambda values used.
nullDev Null deviance defined to be 2*(logLik_sat -logLik_null)
deviance Deviance defined to be 2*(logLik_sat -logLik(model))

optResult A list containing the result of the optimization. fValues, subGradients contain objective function values and subgradient vectors at each lambda value. If trace = TRUE, corresponding intermediate quantities are saved as well.

iters Number of iterations(EM updates) if method = "CD". Number of steps taken otherwise.

Examples

data("simulPU")
fit<-grpPUlasso(X=simulPU$x,z=simulPU$z,py1=simulPU$truePY1)

Description

A simulated data for the illustration. Covariates $x_i$ are drawn from $N(\mu, I_{5 \times 5})$ or $N(-\mu, I_{5 \times 5})$ with probability 0.5. To make the first two variables active, $\mu = [\mu_1, \ldots, \mu_2, 0, 0, 0]^T, \theta = [\theta_0, \ldots, \theta_2, 0, 0, 0]^T$ and we set $\mu_i = 1.5, \theta_i \sim Uniform[0.5, 1]$ Responses $y_i$ is simulated via $P_\theta(y = 1|x) = 1/\exp(-\theta^T x)$. 1000 observations are sampled from the sub-population of positives($y=1$) and labeled, and another 1000 observations are sampled from the original population and unlabeled.

Usage

simulPU

Format

A list containing model matrix X, true response y, labeled/unlabeled response vector z, and a true positive probability truePY1.
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