Package: Sieve (via r-universe)

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Type Package

Title Nonparametric Estimation by the Method of Sieves

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Description Performs multivariate nonparametric regression/classification by the method of sieves (using orthogonal basis). The method is suitable for moderate high-dimensional features (dimension < 100). The l1-penalized sieve estimator, a nonparametric generalization of Lasso, is adaptive to the feature dimension with provable theoretical guarantees. We also include a nonparametric stochastic gradient descent estimator, Sieve-SGD, for online or large scale batch problems. Details of the methods can be found in: <doi:10.48550/arXiv.2206.02994> <doi:10.48550/arXiv.2104.00846><doi:10.48550/arXiv.2310.12140>.

License GPL-2

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`Sieve-package` *Nonparametric Estimation by the Method of Sieves*

Description

Performs multivariate nonparametric regression/classification by the method of sieves (using orthogonal basis). The method is suitable for moderate high-dimensional features (dimension < 100). The l1-penalized sieve estimator, a nonparametric generalization of Lasso, is adaptive to the feature dimension with provable theoretical guarantees. We also include a nonparametric stochastic gradient descent estimator, Sieve-SGD, for online or large scale batch problems. Details of the methods can be found in: <arXiv:2206.02994> <arXiv:2104.00846><arXiv:2310.12140>.

Details

The DESCRIPTION file:

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Index of help topics:

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create_index_matrix	Create the index matrix for multivariate regression
sieve.sgd.predict	Sieve-SGD makes prediction with new predictors.
sieve.sgd.preprocess	Preprocess the original data for sieve-SGD estimation.
sieve.sgd.solver	Fit sieve-SGD estimators, using progressive validation for hyperparameter tuning.
sieve_predict	Predict the outcome of interest for new samples
sieve_preprocess	Preprocess the original data for sieve estimation.
sieve_solver	Calculate the coefficients for the basis functions

~~ An overview of how to use the ~~ ~~ package, including the most ~~ ~~ important functions ~~

Author(s)

Tianyu Zhang

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References

Tianyu Zhang and Noah Simon (2022) <arXiv:2206.02994>

Examples

```
xdim <- 5
basisN <- 1000
type <- 'cosine'

#non-linear additive truth. Half of the features are truly associated with the outcome
TrainData <- GenSamples(s.size = 300, xdim = xdim,
            frho = 'additive', frho.para = xdim/2)

#noise-free testing samples
TestData <- GenSamples(s.size = 1e3, xdim = xdim, noise.para = 0,
            frho = 'additive', frho.para = xdim/2)

sieve.model <- sieve_preprocess(X = TrainData[,2:(xdim+1)],
            basisN = basisN, type = type, interaction_order = 2)

sieve.model <- sieve_solver(sieve.model, TrainData$Y, l1 = TRUE)

sieve_model_prediction <- sieve_predict(testX = TestData[,2:(xdim+1)],
                testY = TestData$Y, sieve.model)
```

clean_up_result *Clean up the fitted model*

Description

Clean up the fitted model

Usage

```
clean_up_result(sieve.model)
```

Arguments

sieve.model	a sieve sgd model.

Value

a processed sieve.model, adding function names and extract the best model

create_index_matrix *Create the index matrix for multivariate regression*

Description

Create the index matrix for multivariate regression

Usage

```
create_index_matrix(xdim, basisN = NULL, maxj = NULL, interaction_order = 5)
```

Arguments

xdim	a number. It specifies the predictors' dimension.
basisN	a number. The number of basis function to use.
maxj	a number. We use this to specify the largest row product in the index list.
interaction_order	a number The maximum order of interaction. 1 means additive model, 2 means including pairwise interaction terms, etc.

Value

a matrix. The first column is the product of the indices, the rest columns are the index vectors for constructing multivariate basis functions.

GenSamples *Generate some simulation/testing samples with nonlinear truth.*

Description

This function is used in several examples in the package.

Usage

```
GenSamples(
  s.size,
  xdim = 1,
  x.dis = "uniform",
  x.para = NULL,
  frho = "linear",
  frho.para = 100,
  y.type = "continuous",
  noise.dis = "normal",
  noise.para = 0.5
)
```

Arguments

s.size	a number. Sample size.
xdim	a number. Dimension of the feature vectors X.
x.dis	a string. It specifies the distribution of feature X. The default is uniform distribution over xdim-dimensional unit cube.
x.para	extra parameter to specify the feature distribution.
frho	a string. It specifies the true regression/log odds functions used to generate the data set. The default is a linear function.
frho.para	extra parameter to specify the true underlying regression/log odds function.
y.type	a string. Default is y.type = 'continuous', meaning the outcome is numerical and the problem is regression. Set it to y.type = 'binary' for binary outcome.
noise.dis	a string. For the distribution of the noise variable (under regression probelm settings). Default is Gaussian distribution.
noise.para	a number. It specifies the magnitude of the noise in regression settings.

Value

a data.frame. The variable Y is the outcome (either continuous or binary). Each of the rest of the variables corresponds to one dimension of the feature vector.

Examples

```
xdim <- 1 #1 dimensional feature
#generate 1000 training samples
TrainData <- GenSamples(s.size = 1000, xdim = xdim)
#generate some noise-free testing samples
TestData <- GenSamples(s.size = 1000, xdim = xdim, noise.para = 0)
```

`sieve.sgd.predict` *Sieve-SGD makes prediction with new predictors.*

Description

Sieve-SGD makes prediction with new predictors.

Usage

```
sieve.sgd.predict(sieve.model, X)
```

Arguments

`sieve.model`	a list initiated using sieve.sgd.preprocess and sieve.sgd.solver. Check the documentation of sieve.sgd.preprocess for more information.
`X`	a data frame containing prediction features/ independent variables.

Value

sieve.sgd.predict will update the given sieve.model input list.

`inf.list`	In each entry of the list inf.list, the array prdy is the predicted outcome under the given hyperparameter combination.

Examples

```
frho.para <- xdim <- 1 ##predictor dimension
frho <- 'additive' ###truth is a sum of absolute functions
type <- 'cosine' ###use cosine functions as the basis functions
#generate training data
TrainData <- GenSamples(s.size = 1e3, xdim = xdim,
                                frho.para = frho.para,
                                frho = frho, noise.para = 0.1)
#preprocess the model
sieve.model <- sieve.sgd.preprocess(X = TrainData[,2:(xdim+1)],
                                    type = type,
                                    s = c(1,2),
                                    r0 = c(0.5, 2, 4),
                                    J = c(1, 4, 8))

##train the model
sieve.model <- sieve.sgd.solver(sieve.model = sieve.model,
```

```
                                X = TrainData[,2:(xdim+1)],
                                Y  = TrainData[,1])
##generate new data
NewData <- GenSamples(s.size = 5e2, xdim = xdim,
                      frho.para = frho.para,
                      frho = frho, noise.para = 0.1)
sieve.model <- sieve.sgd.predict(sieve.model, X = NewData[, 2:(xdim+1)])
plot(NewData[, 2:(xdim+1)], sieve.model$best_model$prdy)
```

`sieve.sgd.preprocess` *Preprocess the original data for sieve-SGD estimation.*

Description

Preprocess the original data for sieve-SGD estimation.

Usage

```
sieve.sgd.preprocess(
  X,
  s = c(2),
  r0 = c(2),
  J = c(1),
  type = c("cosine"),
  interaction_order = c(3),
  omega = c(0.51),
  norm_feature = TRUE,
  norm_para = NULL,
  lower_q = 0.005,
  upper_q = 0.995
)
```

Arguments

`X`	a data frame containing prediction features/ independent variables. The (i,j)-th element is the j-th dimension of the i-th sample's feature vector. So the number of rows equals to the sample size and the number of columns equals to the feature/covariate dimension. If the complete data set is large, this can be a representative subset of it (ideally have more than 1000 samples).
`s`	numerical array. Smoothness parameter, a smaller s corresponds to a more flexible model. Default is 2. The elements of this array should take values greater than 0.5. The larger s is, the smoother we are assuming the truth to be.
`r0`	numerical array. Initial learning rate/step size, don't set it too large. The step size at each iteration will be r0*(sample size)^(-1/(2s+1)), which is slowly decaying.
`J`	numerical array. Initial number of basis functions, a larger J corresponds to a more flexible estimator The number of basis functions at each iteration will be J*(sample size)^(1/(2s+1)), which is slowly increasing. We recommend use

J that is at least the dimension of predictor, i.e. the column number of the X matrix.

`type` a string. It specifies what kind of basis functions are used. The default is (aperiodic) cosine basis functions ('cosine'), which is enough for generic usage.

`interaction_order` a number. It also controls the model complexity. 1 means fitting an additive model, 2 means fitting a model allows, 3 means interaction terms between 3 dimensions of the feature, etc. The default is 3. For large sample size, lower dimension problems, try a larger value (but need to be smaller than the dimension of original features); for smaller sample size and higher dimensional problems, try set it to a smaller value (1 or 2).

`omega` the rate of dimension-reduction parameter. Default is 0.51, usually do not need to change.

`norm_feature` a logical variable. Default is TRUE. It means sieve_preprocess will rescale the each dimension of features to 0 and 1. Only set to FALSE when user already manually rescale them between 0 and 1.

`norm_para` a matrix. It specifies how the features are normalized. For training data, use the default value NULL.

`lower_q` lower quantile used in normalization. Default is 0.01 (1% quantile).

`upper_q` upper quantile used in normalization. Default is 0.99 (99% quantile).

Value

A list containing the necessary information for next step model fitting. Typically, the list is used as the main input of sieve.sgd.solver.

`s.size.sofar` a number. Number of samples has been processed so far.

`type` a string. The type of basis funtion.

`hyper.para.list` a list of hyperparameters.

`index.matrix` a matrix. Identifies the multivariate basis functions used in fitting.

`index.row.prod` the index product for each basis function. It is used in calculating basis function - specific learning rates.

`inf.list` a list storing the fitted results. It has a length of "number of unique combinations of the hyperparameters". The component of inf.list is itself a list, it has a hyper.para.index domain to specify its corresponding hyperparameters (need to be used together with hyper.para.list). Its rolling.cv domain is the progressive validation statistics for hyperparameter tuning; beta.f is the regression coefficients for the first length(beta.f) basis functions, the rest of the basis have 0 coefficients.

`norm_para` a matrix. It records how each dimension of the feature/predictor is rescaled, which is useful when rescaling the testing sample's predictors.

Examples

```
xdim <- 1 #1 dimensional feature
#generate 1000 training samples
TrainData <- GenSamples(s.size = 1000, xdim = xdim)
sieve.model <- sieve.sgd.preprocess(X = TrainData[,2:(xdim+1)])
```

`sieve.sgd.solver` *Fit sieve-SGD estimators, using progressive validation for hyperparameter tuning.*

Description

Fit sieve-SGD estimators, using progressive validation for hyperparameter tuning.

Usage

```
sieve.sgd.solver(sieve.model, X, Y, cv_weight_rate = 1)
```

Arguments

`sieve.model`	a list initiated using sieve.sgd.preprocess. Check the documentation of sieve.sgd.preprocess for more information.
`X`	a data frame containing prediction features/ independent variables.
`Y`	training outcome.
`cv_weight_rate`	this governs the divergence rate of rolling validation statistics. Default is set to be 1 and in general does not need to be changed.

Value

A list. It contains the fitted regression coefficients and progressive validation statistics for each hyperparameter combination.

`s.size.sofar`	a number. Number of samples has been processed so far.
`type`	a string. The type of basis funtion.
`hyper.para.list`	a list of hyperparameters.
`index.matrix`	a matrix. Identifies the multivariate basis functions used in fitting.
`index.row.prod`	the index product for each basis function. It is used in calculating basis function - specific learning rates.
`inf.list`	a list storing the fitted results. It has a length of "number of unique combinations of the hyperparameters". The component of inf.list is itself a list, it has a hyper.para.index domain to specify its corresponding hyperparameters (need to be used together with hyper.para.list). Its rolling.cv domain is the progressive validation statistics for hyperparameter tuning; beta.f is the regression coefficients for the first length(beta.f) basis functions, the rest of the basis have 0 coefficients.
`norm_para`	a matrix. It records how each dimension of the feature/predictor is rescaled, which is useful when rescaling the testing sample's predictors.

Examples

```
frho.para <- xdim <- 1 ##predictor dimension
frho <- 'additive' ###truth is a sum of absolute functions
type <- 'cosine' ###use cosine functions as the basis functions
#generate training data
TrainData <- GenSamples(s.size = 1e3, xdim = xdim,
                                frho.para = frho.para,
                                frho = frho, noise.para = 0.1)
#preprocess the model
sieve.model <- sieve.sgd.preprocess(X = TrainData[,2:(xdim+1)],
                                    type = type,
                                    s = c(1,2),
                                    r0 = c(0.5, 2, 4),
                                    J = c(1, 4, 8))

##train the model
sieve.model <- sieve.sgd.solver(sieve.model = sieve.model,
                                X = TrainData[,2:(xdim+1)],
                                Y  = TrainData[,1])

##sieve-SGD can do multiple passes over the data, just like other SGD methods.
##usually a second pass can still improve the prediction accuracy
##watch out overfitting when performing multiple passes!
sieve.model <- sieve.sgd.solver(sieve.model = sieve.model,
                              X = TrainData[,2:(xdim+1)],
                              Y  = TrainData[,1])
```

`sieve_predict` *Predict the outcome of interest for new samples*

Description

Use the fitted sieve regression model from sieve_solver. It also returns the testing mean-squared errors.

Usage

```
sieve_predict(model, testX, testY = NULL)
```

Arguments

`model`	a list. Use the fitted model from sieve_solver.
`testX`	a data frame. Dimension equals to test sample size x feature diemnsion. Should be of a similar format as the training feature provided to sieve_preprocess.
`testY`	a vector. The outcome of testing samples (if known). Default is NULL. For regression problems, the algorithm also returns the testing mean-squared errors.

Value

a list.

predictY — a matrix. Dimension is test sample size (# of rows) x number of penalty hyperparameter lambda (# of columns). For regression problem, that is, when family = "gaussian", each entry is the estimated conditional mean (or predictor of outcome Y). For classification problems (family = "binomial"), each entry is the predicted probability of having Y = 1 (which class is defined as "class 1" depends on the training data labeling).

MSE — For regression problem, when testY is provided, the algorithm also calculates the mean-sqaured errors using testing data. Each entry of MSE correponds to one value of penalization hyperparameter lambda

Examples

```
xdim <- 1 #1 dimensional feature
#generate 1000 training samples
TrainData <- GenSamples(s.size = 1000, xdim = xdim)
#use 50 cosine basis functions
type <- 'cosine'
basisN <- 50
sieve.model <- sieve_preprocess(X = TrainData[,2:(xdim+1)],
                                basisN = basisN, type = type)
sieve.fit<- sieve_solver(model = sieve.model, Y = TrainData$Y)
#generate 1000 testing samples
TestData <- GenSamples(s.size = 1000, xdim = xdim)
sieve.prediction <- sieve_predict(model = sieve.fit,
                                  testX = TestData[,2:(xdim+1)],
                                  testY = TestData$Y)
###if the outcome is binary,
###need to solve a nonparametric logistic regression problem
xdim <- 1
TrainData <- GenSamples(s.size = 1e3, xdim = xdim, y.type = 'binary', frho = 'nonlinear_binary')
sieve.model <- sieve_preprocess(X = TrainData[,2:(xdim+1)],
                                basisN = basisN, type = type)
sieve.fit<- sieve_solver(model = sieve.model, Y = TrainData$Y,
                         family = 'binomial')

###the predicted value is conditional probability (of taking class 1).
TrainData <- GenSamples(s.size = 1e3, xdim = xdim, y.type = 'binary', frho = 'nonlinear_binary')
sieve.prediction <- sieve_predict(model = sieve.fit,
                                  testX = TestData[,2:(xdim+1)])
```

---

sieve_preprocess *Preprocess the original data for sieve estimation.*

Description

Generate the design matrix for the downstream lasso-type penalized model fitting.

Usage

```
sieve_preprocess(
  X,
  basisN = NULL,
  maxj = NULL,
  type = "cosine",
  interaction_order = 3,
  index_matrix = NULL,
  norm_feature = TRUE,
  norm_para = NULL
)
```

Arguments

X	a data frame containing original features. The (i,j)-th element is the j-th dimension of the i-th sample's feature vector. So the number of rows equals to the sample size and the number of columns equals to the feature dimension.
basisN	number of sieve basis function. It is in general larger than the dimension of the original feature. Default is 50*dimension of original feature. A larger value has a smaller approximation error but it is harder to estimate. The computational time/memory requirement should scale linearly to basisN.
maxj	a number. the maximum index product of the basis function. A larger value means more basisN. If basisN is already specified, do not need to provide value for this argument.
type	a string. It specifies what kind of basis functions are used. The default is (aperiodic) cosine basis functions, which is suitable for most purpose.
interaction_order	a number. It also controls the model complexity. 1 means fitting an additive model, 2 means fitting a model allows, 3 means interaction terms between 3 dimensions of the feature, etc. The default is 3. For large sample size, lower dimension problems, try a larger value (but need to be smaller than the dimension of original features); for smaller sample size and higher dimensional problems, try set it to a smaller value (1 or 2).
index_matrix	a matrix. provide a pre-generated index matrix. The default is NULL, meaning sieve_preprocess will generate one for the user.
norm_feature	a logical variable. Default is TRUE. It means sieve_preprocess will rescale the each dimension of features to 0 and 1. Only set to FALSE when user already manually rescale them between 0 and 1.
norm_para	a matrix. It specifies how the features are normalized. For training data, use the default value NULL.

Value

A list containing the necessary information for next step model fitting. Typically, the list is used as the main input of Sieve::sieve_solver.

Phi	a matrix. This is the design matrix directly used by the next step model fitting. The (i,j)-th element of this matrix is the evaluation of i-th sample's feature at the j-th basis function. The dimension of this matrix is sample size x basisN.
X	a matrix. This is the rescaled original feature/predictor matrix.
type	a string. The type of basis funtion.
index_matrix	a matrix. It specifies what are the product basis functions used when constructing the design matrix Phi. It has a dimension basisN x dimension of original features. There are at most interaction_order many non-1 elements in each row.
basisN	a number. Number of sieve basis functions.
norm_para	a matrix. It records how each dimension of the feature/predictor is rescaled, which is useful when rescaling the testing sample's predictors.

Examples

```
xdim <- 1 #1 dimensional feature
#generate 1000 training samples
TrainData <- GenSamples(s.size = 1000, xdim = xdim)
#use 50 cosine basis functions
type <- 'cosine'
basisN <- 50
sieve.model <- sieve_preprocess(X = TrainData[,2:(xdim+1)],
                                basisN = basisN, type = type)
#sieve.model$Phi #Phi is the design matrix

xdim <- 5 #1 dimensional feature
#generate 1000 training samples
#only the first two dimensions are truly associated with the outcome
TrainData <- GenSamples(s.size = 1000, xdim = xdim,
                              frho = 'additive', frho.para = 2)

#use 1000 basis functions
#each of them is a product of univariate cosine functions.
type <- 'cosine'
basisN <- 1000
sieve.model <- sieve_preprocess(X = TrainData[,2:(xdim+1)],
                                basisN = basisN, type = type)
#sieve.model$Phi #Phi is the design matrix

#fit a nonaprametric additive model by setting interaction_order = 1
sieve.model <- sieve_preprocess(X = TrainData[,2:(xdim+1)],
                                basisN = basisN, type = type,
                                interaction_order = 1)
#sieve.model$index_matrix #for each row, there is at most one entry >= 2.
#this means there are no basis functions varying in more than 2-dimensions
#that is, we are fitting additive models without interaction between features.
```

`sieve_solver` *Calculate the coefficients for the basis functions*

Description

This is the main function that performs sieve estimation. It calculate the coefficients by solving a penalized lasso type problem.

Usage

```
sieve_solver(
  model,
  Y,
  l1 = TRUE,
  family = "gaussian",
  lambda = NULL,
  nlambda = 100
)
```

Arguments

`model`	a list. Typically, it is the output of Sieve::sieve_preprocess.
`Y`	a vector. The outcome variable. The length of Y equals to the training sample size, which should also match the row number of X in model.
`l1`	a logical variable. TRUE means calculating the coefficients by sovling a l1-penalized empirical risk minimization problem. FALSE means solving a least-square problem. Default is TRUE.
`family`	a string. 'gaussian', mean-squared-error regression problem.
`lambda`	same as the lambda of glmnet::glmnet.
`nlambda`	a number. Number of penalization hyperparameter used when solving the lasso-type problem. Default is 100.

Value

a list. In addition to the preprocessing information, it also has the fitted value.

`Phi`	a matrix. This is the design matrix directly used by the next step model fitting. The (i,j)-th element of this matrix is the evaluation of i-th sample's feature at the j-th basis function. The dimension of this matrix is sample size x basisN.
`X`	a matrix. This is the rescaled original feature/predictor matrix.
`beta_hat`	a matrix. Dimension is basisN x nlambda. The j-th column corresponds to the fitted regression coeffcients using the j-th hyperparameter in lambda.
`type`	a string. The type of basis funtion.

index_matrix	a matrix. It specifies what are the product basis functions used when constructing the design matrix Phi. It has a dimension basisN x dimension of original features. There are at most interaction_order many non-1 elements in each row.
basisN	a number. Number of sieve basis functions.
norm_para	a matrix. It records how each dimension of the feature/predictor is rescaled, which is useful when rescaling the testing sample's predictors.
lambda	a vector. It records the penalization hyperparameter used when solving the lasso problems. Default has a length of 100, meaning the algorithm tried 100 different penalization hyperparameters.
family	a string. 'gaussian', continuous numerical outcome, regression probelm; 'binomial', binary outcome, classification problem.

Examples

```
xdim <- 1 #1 dimensional feature
#generate 1000 training samples
TrainData <- GenSamples(s.size = 1000, xdim = xdim)
#use 50 cosine basis functions
type <- 'cosine'
basisN <- 50
sieve.model <- sieve_preprocess(X = TrainData[,2:(xdim+1)],
                                basisN = basisN, type = type)
sieve.fit<- sieve_solver(model = sieve.model, Y = TrainData$Y)

###if the outcome is binary,
###need to solve a nonparametric logistic regression problem
xdim <- 1
TrainData <- GenSamples(s.size = 1e3, xdim = xdim, y.type = 'binary', frho = 'nonlinear_binary')
sieve.model <- sieve_preprocess(X = TrainData[,2:(xdim+1)],
                                basisN = basisN, type = type)
sieve.fit<- sieve_solver(model = sieve.model, Y = TrainData$Y,
                         family = 'binomial')
```

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