

Package ‘CondIndTests’

November 12, 2019

Type Package

Title Nonlinear Conditional Independence Tests

Version 0.1.5

Date 2019-11-11

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Depends R (>= 3.1.0)

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Description Code for a variety of nonlinear conditional independence tests:
Kernel conditional independence test (Zhang et al., UAI 2011, <arXiv:1202.3775>),
Residual Prediction test (based on Shah and Buehlmann, <arXiv:1511.03334>),
Invariant environment prediction,
Invariant target prediction,
Invariant residual distribution test,
Invariant conditional quantile prediction (all from Heinze-Deml et al., <arXiv:1706.08576>).

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LazyData TRUE

Imports methods, randomForest, quantregForest, lawstat, RPtests,
caTools, mgcv, MASS, kernlab, pracma, mize

URL <https://github.com/christinaheinze/nonlinearICP-and-CondIndTests>

BugReports <https://github.com/christinaheinze/nonlinearICP-and-CondIndTests/issues>

RoxygenNote 6.1.1

Suggests testthat

NeedsCompilation no

Repository CRAN

Date/Publication 2019-11-12 06:50:21 UTC

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CondIndTest	<i>Wrapper function for conditional independence tests.</i>
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Description

Tests the null hypothesis that Y and E are independent given X.

Usage

```
CondIndTest(Y, E, X, method = "KCI", alpha = 0.05,
  parsMethod = list(), verbose = FALSE)
```

Arguments

Y	An n-dimensional vector or a matrix or dataframe with n rows and p columns.
E	An n-dimensional vector or a matrix or dataframe with n rows and p columns.
X	An n-dimensional vector or a matrix or dataframe with n rows and p columns.
method	The conditional independence test to use, can be one of "KCI", "InvariantConditionalQuantilePrediction", "InvariantEnvironmentPrediction", "InvariantResidualDistributionTest", "InvariantTargetPrediction", "ResidualPredictionTest".
alpha	Significance level. Defaults to 0.05.
parsMethod	Named list to pass options to method.
verbose	If TRUE, intermediate output is provided. Defaults to FALSE.

Value

A list with the p-value of the test (pvalue) and possibly additional entries, depending on the output of the chosen conditional independence test in method.

References

Please cite C. Heinze-Deml, J. Peters and N. Meinshausen: "Invariant Causal Prediction for Nonlinear Models", [arXiv:1706.08576](https://arxiv.org/abs/1706.08576) and the corresponding reference for the conditional independence test.

Examples

```
# Example 1
set.seed(1)
n <- 100
Z <- rnorm(n)
X <- 4 + 2 * Z + rnorm(n)
Y <- 3 * X^2 + Z + rnorm(n)
test1 <- CondIndTest(X,Y,Z, method = "KCI")
cat("These data come from a distribution, for which X and Y are NOT
cond. ind. given Z.")
cat(paste("The p-value of the test is: ", test1$pvalue))

# Example 2
set.seed(1)
Z <- rnorm(n)
X <- 4 + 2 * Z + rnorm(n)
Y <- 3 + Z + rnorm(n)
test2 <- CondIndTest(X,Y,Z, method = "KCI")
cat("The data come from a distribution, for which X and Y are cond.
ind. given Z.")
cat(paste("The p-value of the test is: ", test2$pvalue))
```

fishersTestExceedance *Fishers test to test whether the exceedance of the conditional quantiles is independent of the categorical variable E.*

Description

Used as a subroutine in InvariantConditionalQuantilePrediction to test whether the exceedance of the conditional quantiles is independent of the categorical variable E.

Usage

```
fishersTestExceedance(Y, predicted, E, verbose)
```

Arguments

Y	An n-dimensional vector.
predicted	A matrix with n rows. The columns contain predictions for different conditional quantiles of Y X.
E	An n-dimensional vector. E needs to be a factor.
verbose	Set to TRUE if output should be printed.

Value

A list with the p-value for the test.

fTestTargetY	<i>F-test for a nested model comparison.</i>
--------------	--

Description

Used as a subroutine in InvariantTargetPrediction to test whether out-of-sample prediction performance is better when using X and E as predictors for Y, compared to using X only.

Usage

```
fTestTargetY(Y, predictedOnlyX, predictedXE, verbose, ...)
```

Arguments

Y	An n-dimensional vector.
predictedOnlyX	Predictions for Y based on predictors in X only.
predictedXE	Predictions for Y based on predictors in X and E.
verbose	Set to TRUE if output should be printed.
...	The dimensions of X (df) and E (dimE) need to be passed via the ... argument to allow for coherent interface of fTestTargetY and wilcoxTestTargetY.

Value

A list with the p-value for the test.

InvariantConditionalQuantilePrediction	<i>Invariant conditional quantile prediction.</i>
--	---

Description

Tests the null hypothesis that Y and E are independent given X.

Usage

```
InvariantConditionalQuantilePrediction(Y, E, X, alpha = 0.05,
  verbose = FALSE, test = fishersTestExceedance,
  mtry = sqrt(NCOL(X)), ntree = 100, nodesize = 5, maxnodes = NULL,
  quantiles = c(0.1, 0.5, 0.9), returnModel = FALSE)
```

Arguments

Y	An n-dimensional vector.
E	An n-dimensional vector. If <code>test = fishersTestExceedance</code> , E needs to be a factor.
X	A matrix or dataframe with n rows and p columns.
alpha	Significance level. Defaults to 0.05.
verbose	If TRUE, intermediate output is provided. Defaults to FALSE.
test	Unconditional independence test that tests whether exceedance is independent of E. Defaults to <code>fishersTestExceedance</code> .
mtry	Random forest parameter: Number of variables randomly sampled as candidates at each split. Defaults to <code>sqrt(NCOL(X))</code> .
ntree	Random forest parameter: Number of trees to grow. Defaults to 100.
nodesize	Random forest parameter: Minimum size of terminal nodes. Defaults to 5.
maxnodes	Random forest parameter: Maximum number of terminal nodes trees in the forest can have. Defaults to NULL.
quantiles	Quantiles for which to test independence between exceedance and E. Defaults to <code>c(0.1, 0.5, 0.9)</code> .
returnModel	If TRUE, the fitted quantile regression forest model will be returned. Defaults to FALSE.

Value

A list with the following entries:

- `pvalue` The p-value for the null hypothesis that Y and E are independent given X.
- `model` The fitted quantile regression forest model if `returnModel = TRUE`.

Examples

```
# Example 1
n <- 1000
E <- rbinom(n, size = 1, prob = 0.2)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * (X)^2 + rnorm(n)
InvariantConditionalQuantilePrediction(Y, as.factor(E), X)

# Example 2
E <- rbinom(n, size = 1, prob = 0.2)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * E + rnorm(n)
InvariantConditionalQuantilePrediction(Y, as.factor(E), X)
```

 InvariantEnvironmentPrediction

Invariant environment prediction.

Description

Tests the null hypothesis that Y and E are independent given X.

Usage

```
InvariantEnvironmentPrediction(Y, E, X, alpha = 0.05, verbose = FALSE,
  trainTestSplitFunc = caTools::sample.split,
  argsTrainTestSplitFunc = list(Y = E, SplitRatio = 0.8),
  test = propTestTargetE, mtry = sqrt(NCOL(X)), ntree = 100,
  nodesize = 5, maxnodes = NULL, permute = TRUE,
  returnModel = FALSE)
```

Arguments

Y	An n-dimensional vector.
E	An n-dimensional vector. If test = propTestTargetE, E needs to be a factor.
X	A matrix or dataframe with n rows and p columns.
alpha	Significance level. Defaults to 0.05.
verbose	If TRUE, intermediate output is provided. Defaults to FALSE.
trainTestSplitFunc	Function to split sample. Defaults to stratified sampling using <code>caTools::sample.split</code> , assuming E is a factor.
argsTrainTestSplitFunc	Arguments for sampling splitting function.
test	Unconditional independence test that tests whether the out-of-sample prediction accuracy is the same when using X only vs. X and Y as predictors for E. Defaults to propTestTargetE.
mtry	Random forest parameter: Number of variables randomly sampled as candidates at each split. Defaults to <code>sqrt(NCOL(X))</code> .
ntree	Random forest parameter: Number of trees to grow. Defaults to 100.
nodesize	Random forest parameter: Minimum size of terminal nodes. Defaults to 5.
maxnodes	Random forest parameter: Maximum number of terminal nodes trees in the forest can have. Defaults to NULL.
permute	Random forest parameter: If TRUE, model that would use X only for predicting Y also includes a random permutation of E. Defaults to TRUE.
returnModel	If TRUE, the fitted quantile regression forest model will be returned. Defaults to FALSE.

Value

A list with the following entries:

- `pvalue` The p-value for the null hypothesis that Y and E are independent given X.
- `model` The fitted models if `returnModel = TRUE`.

Examples

```
# Example 1
n <- 1000
E <- rbinom(n, size = 1, prob = 0.2)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * (X)^2 + rnorm(n)
InvariantEnvironmentPrediction(Y, as.factor(E), X)

# Example 2
E <- rbinom(n, size = 1, prob = 0.2)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * E + rnorm(n)
InvariantEnvironmentPrediction(Y, as.factor(E), X)

# Example 3
E <- rnorm(n)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * (X)^2 + rnorm(n)
InvariantEnvironmentPrediction(Y, E, X, test = wilcoxTestTargetY)
InvariantEnvironmentPrediction(Y, X, E, test = wilcoxTestTargetY)
```

InvariantResidualDistributionTest

Invariant residual distribution test.

Description

Tests the null hypothesis that Y and E are independent given X.

Usage

```
InvariantResidualDistributionTest(Y, E, X, alpha = 0.05,
  verbose = FALSE, fitWithGam = TRUE,
  test = leveneAndWilcoxResidualDistributions, colNameNoSmooth = NULL,
  mtry = sqrt(NCOL(X)), ntree = 100, nodesize = 5, maxnodes = NULL,
  returnModel = FALSE)
```

Arguments

Y	An n-dimensional vector.
E	An n-dimensional vector. E needs to be a factor.
X	A matrix or dataframe with n rows and p columns.
alpha	Significance level. Defaults to 0.05.
verbose	If TRUE, intermediate output is provided. Defaults to FALSE.
fitWithGam	If TRUE, a GAM is used for the nonlinear regression, else a random forest is used. Defaults to TRUE.
test	Unconditional independence test that tests whether residual distribution is invariant across different levels of E. Defaults to <code>leveneAndWilcoxResidDistributions</code> .
colNameNoSmooth	Gam parameter: Name of variables that should enter linearly into the model. Defaults to NULL.
mtry	Random forest parameter: Number of variables randomly sampled as candidates at each split. Defaults to <code>sqrt(NCOL(X))</code> .
ntree	Random forest parameter: Number of trees to grow. Defaults to 100.
nodesize	Random forest parameter: Minimum size of terminal nodes. Defaults to 5.
maxnodes	Random forest parameter: Maximum number of terminal nodes trees in the forest can have. Defaults to NULL.
returnModel	If TRUE, the fitted quantile regression forest model will be returned. Defaults to FALSE.

Value

A list with the following entries:

- `pvalue` The p-value for the null hypothesis that Y and E are independent given X.
- `model` The fitted model if `returnModel = TRUE`.

Examples

```
# Example 1
n <- 1000
E <- rbinom(n, size = 1, prob = 0.2)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * (X)^2 + rnorm(n)
InvariantResidualDistributionTest(Y, as.factor(E), X)
InvariantResidualDistributionTest(Y, as.factor(E), X, test = ksResidualDistributions)

# Example 2
E <- rbinom(n, size = 1, prob = 0.2)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * E + rnorm(n)
InvariantResidualDistributionTest(Y, as.factor(E), X)
InvariantResidualDistributionTest(Y, as.factor(E), X, test = ksResidualDistributions)
```

InvariantTargetPrediction

Invariant target prediction.

Description

Tests the null hypothesis that Y and E are independent given X.

Usage

```
InvariantTargetPrediction(Y, E, X, alpha = 0.05, verbose = FALSE,
  fitWithGam = TRUE, trainTestSplitFunc = caTools::sample.split,
  argsTrainTestSplitFunc = NULL, test = fTestTargetY,
  colNameNoSmooth = NULL, mtry = sqrt(NCOL(X)), ntree = 100,
  nodesize = 5, maxnodes = NULL, permute = TRUE,
  returnModel = FALSE)
```

Arguments

Y	An n-dimensional vector.
E	An n-dimensional vector or an nxq dimensional matrix or dataframe.
X	A matrix or dataframe with n rows and p columns.
alpha	Significance level. Defaults to 0.05.
verbose	If TRUE, intermediate output is provided. Defaults to FALSE.
fitWithGam	If TRUE, a GAM is used for the nonlinear regression, else a random forest is used. Defaults to TRUE.
trainTestSplitFunc	Function to split sample. Defaults to stratified sampling using <code>caTools::sample.split</code> , assuming E is a factor.
argsTrainTestSplitFunc	Arguments for sampling splitting function.
test	Unconditional independence test that tests whether the out-of-sample prediction accuracy is the same when using X only vs. X and E as predictors for Y. Defaults to <code>fTestTargetY</code> .
colNameNoSmooth	Gam parameter: Name of variables that should enter linearly into the model. Defaults to NULL.
mtry	Random forest parameter: Number of variables randomly sampled as candidates at each split. Defaults to <code>sqrt(NCOL(X))</code> .
ntree	Random forest parameter: Number of trees to grow. Defaults to 100.
nodesize	Random forest parameter: Minimum size of terminal nodes. Defaults to 5.
maxnodes	Random forest parameter: Maximum number of terminal nodes trees in the forest can have. Defaults to NULL.

permute	Random forest parameter: If TRUE, model that would use X only for predicting Y also includes a random permutation of E. Defaults to TRUE.
returnModel	If TRUE, the fitted quantile regression forest model will be returned. Defaults to FALSE.

Value

A list with the following entries:

- pvalue The p-value for the null hypothesis that Y and E are independent given X.
- model The fitted models if returnModel = TRUE.

Examples

```
# Example 1
n <- 1000
E <- rbinom(n, size = 1, prob = 0.2)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * (X)^2 + rnorm(n)
InvariantTargetPrediction(Y, as.factor(E), X)
InvariantTargetPrediction(Y, as.factor(E), X, test = wilcoxTestTargetY)

# Example 2
E <- rbinom(n, size = 1, prob = 0.2)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * E + rnorm(n)
InvariantTargetPrediction(Y, as.factor(E), X)
InvariantTargetPrediction(Y, as.factor(E), X, test = wilcoxTestTargetY)

# Example 3
E <- rnorm(n)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * (X)^2 + rnorm(n)
InvariantTargetPrediction(Y, E, X)
InvariantTargetPrediction(Y, X, E)
InvariantTargetPrediction(Y, E, X, test = wilcoxTestTargetY)
InvariantTargetPrediction(Y, X, E, test = wilcoxTestTargetY)
```

Description

Tests the null hypothesis that Y and E are independent given X. The distribution of the test statistic under the null hypothesis equals an infinite weighted sum of chi squared variables. This distribution can either be approximated by a gamma distribution or by a Monte Carlo approach. This version includes an implementation of choosing the hyperparameters by Gaussian Process regression.

Usage

```
KCI(Y, E, X, width = 0, alpha = 0.05, unbiased = FALSE,
    gammaApprox = TRUE, GP = TRUE, nRepBs = 5000, lambda = 0.001,
    thresh = 1e-05, numEig = NROW(Y), verbose = FALSE)
```

Arguments

Y	A vector of length n or a matrix or dataframe with n rows and p columns.
E	A vector of length n or a matrix or dataframe with n rows and p columns.
X	A matrix or dataframe with n rows and p columns.
width	Kernel width; if it is set to zero, the width is chosen automatically (default: 0).
alpha	Significance level (default: 0.05).
unbiased	A boolean variable that indicates whether a bias correction should be applied (default: FALSE).
gammaApprox	A boolean variable that indicates whether the null distribution is approximated by a Gamma distribution. If it is FALSE, a Monte Carlo approach is used (default: TRUE).
GP	Flag whether to use Gaussian Process regression to choose the hyperparameters
nRepBs	Number of draws for the Monte Carlo approach (default: 500).
lambda	Regularization parameter (default: 1e-03).
thresh	Threshold for eigenvalues. Whenever eigenvalues are computed, they are set to zero if they are smaller than thresh times the maximum eigenvalue (default: 1e-05).
numEig	Number of eigenvalues computed (only relevant for computing the distribution under the hypothesis of conditional independence) (default: length(Y)).
verbose	If TRUE, intermediate output is provided. (default: FALSE).

Value

A list with the following entries:

- `testStatistic` the statistic $\text{Tr}(K_{\cdot}(\text{ddot}(Y)|X) * K_{\cdot}(E|X))$
- `criticalValue` the critical point at the p-value equal to alpha; obtained by a Monte Carlo approach if `gammaApprox = FALSE`, otherwise obtained by Gamma approximation.
- `pvalue` The p-value for the null hypothesis that Y and E are independent given X. It is obtained by a Monte Carlo approach if `gammaApprox = FALSE`, otherwise obtained by Gamma approximation.

Examples

```
# Example 1
n <- 100
E <- rnorm(n)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * (X)^2 + rnorm(n)
```

KCI(Y, E, X)
KCI(Y, X, E)

ksResidualDistributions

Kolmogorov-Smirnov test to compare residual distributions

Description

Used as a subroutine in InvariantResidualDistributionTest to test whether residual distribution remains invariant across different levels of E.

Usage

ksResidualDistributions(Y, predicted, E, verbose)

Arguments

Y	An n-dimensional vector.
predicted	An n-dimensional vector of predictions for Y.
E	An n-dimensional vector. E needs to be a factor.
verbose	Set to TRUE if output should be printed.

Value

A list with the p-value for the test.

leveneAndWilcoxResidualDistributions

Levene and wilcoxon test to compare first and second moments of residual distributions

Description

Used as a subroutine in InvariantResidualDistributionTest to test whether residual distribution remains invariant across different levels of E.

Usage

leveneAndWilcoxResidualDistributions(Y, predicted, E, verbose)

Arguments

- Y An n-dimensional vector.
- predicted An n-dimensional vector of predictions for Y.
- E An n-dimensional vector. E needs to be a factor.
- verbose Set to TRUE if output should be printed.

Value

A list with the p-value for the test.

propTestTargetE *Proportion test to compare two misclassification rates.*

Description

Used as a subroutine in `InvariantEnvironmentPrediction` to test whether out-of-sample performance is better when using X and Y as predictors for E, compared to using X only.

Usage

```
propTestTargetE(E, predictedOnlyX, predictedXY, verbose)
```

Arguments

- E An n-dimensional vector.
- predictedOnlyX Predictions for E based on predictors in X only.
- predictedXY Predictions for E based on predictors in X and Y.
- verbose Set to TRUE if output should be printed.

Value

A list with the p-value for the test.

 ResidualPredictionTest

Residual prediction test.

Description

Tests the null hypothesis that Y and E are independent given X.

Usage

```
ResidualPredictionTest(Y, E, X, alpha = 0.05, verbose = FALSE,
  degree = 4, basis = c("nystrom", "nystrom_poly", "fourier",
    "polynomial", "provided")[1], resid_type = "OLS", XBasis = NULL,
  noiseMat = NULL, getnoiseFct = function(n, ...) { rnorm(n) },
  argsGetNoiseFct = NULL, nSim = 100, funcOfRes = function(x) {
    abs(x) }, useX = TRUE, returnXBasis = FALSE,
  nSub = ceiling(NROW(X)/4), ntree = 100, nodesize = 5,
  maxnodes = NULL)
```

Arguments

Y	An n-dimensional vector.
E	An n-dimensional vector or an nxq dimensional matrix or dataframe.
X	A matrix or dataframe with n rows and p columns.
alpha	Significance level. Defaults to 0.05.
verbose	If TRUE, intermediate output is provided. Defaults to FALSE.
degree	Degree of polynomial to use if basis="polynomial" or basis="nystrom_poly". Defaults to 4.
basis	Can be one of "nystrom", "nystrom_poly", "fourier", "polynomial", "provided". Defaults to "nystrom".
resid_type	Can be "Lasso" or "OLS". Defaults to "OLS".
XBasis	Basis if basis="provided". Defaults to NULL.
noiseMat	Matrix with simulated noise. Defaults to NULL in which case the simulation is performed inside the function.
getnoiseFct	Function to use to generate the noise matrix. Defaults to function(n, ...){rnorm(n)}.
argsGetNoiseFct	Arguments for getnoiseFct. Defaults to NULL.
nSim	Number of simulations to use. Defaults to 100.
funcOfRes	Function of residuals to use in addition to predicting the conditional mean. Defaults to function(x){abs(x)}.
useX	Set to TRUE if the predictors in X should also be used when predicting the scaled residuals with E. Defaults to TRUE.

returnXBasis	Set to TRUE if basis expansion should be returned. Defaults to FALSE.
nSub	Number of random features to use if basis is one of "nystrom", "nystrom_poly" or "fourier". Defaults to ceiling(NROW(X)/4).
ntree	Random forest parameter: Number of trees to grow. Defaults to 500.
nodesize	Random forest parameter: Minimum size of terminal nodes. Defaults to 5.
maxnodes	Random forest parameter: Maximum number of terminal nodes trees in the forest can have. Defaults to NULL.

Value

A list with the following entries:

- pvalue The p-value for the null hypothesis that Y and E are independent given X.
- XBasis Basis expansion if returnXBasis was set to TRUE.
- fctBasisExpansion Function used to create basis expansion if basis is not "provided".

Examples

```
# Example 1
n <- 100
E <- rbinom(n, size = 1, prob = 0.2)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * (X)^2 + rnorm(n)
ResidualPredictionTest(Y, as.factor(E), X)

# Example 2
E <- rbinom(n, size = 1, prob = 0.2)
X <- 4 + 2 * E + rnorm(n)
Y <- 3 * E + rnorm(n)
ResidualPredictionTest(Y, as.factor(E), X)

# not run:
# # Example 3
# E <- rnorm(n)
# X <- 4 + 2 * E + rnorm(n)
# Y <- 3 * (X)^2 + rnorm(n)
# ResidualPredictionTest(Y, E, X)
# ResidualPredictionTest(Y, X, E)
```

wilcoxTestTargetY *Wilcoxon test to compare two mean squared error rates.*

Description

Used as a subroutine in InvariantTargetPrediction to test whether out-of-sample performance is better when using X and E as predictors for Y, compared to using X only.

Usage

```
wilcoxTestTargetY(Y, predictedOnlyX, predictedXE, verbose, ...)
```

Arguments

Y	An n-dimensional vector.
predictedOnlyX	Predictions for Y based on predictors in X only.
predictedXE	Predictions for Y based on predictors in X and E.
verbose	Set to TRUE if output should be printed.
...	Argument to allow for coherent interface of <code>fTestTargetY</code> and <code>wilcoxTestTargetY</code> .

Value

A list with the p-value for the test.

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