

Package: predkmeans (via r-universe)

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Title Covariate Adaptive Clustering

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Author Joshua Keller

Maintainer Joshua Keller <joshua.keller@colostate.edu>

Description Implements the predictive k-means method for clustering observations, using a mixture of experts model to allow covariates to influence cluster centers. Motivated by air pollution epidemiology settings, where cluster membership needs to be predicted across space. Includes functions for predicting cluster membership using spatial splines and principal component analysis (PCA) scores using either multinomial logistic regression or support vector machines (SVMs). For method details see Keller et al. (2017) <doi:10.1214/16-AOAS992>.

Imports Rcpp (>= 0.11.5), maxLik, e1071, mgcv

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predkmeans-package	<i>Covariate Adaptive Clustering</i>
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Description

Clusters multivariate exposures, using a mixture of experts model to allow covariates to influence cluster centers. Motivated by air pollution epidemiology settings, where cluster membership needs to be predicted across space. Includes functions for predicting cluster membership using spatial splines and principal component analysis (PCA) scores using either multinomial logistic regression or support vector machines (SVMs). For method details see Keller et al. (2017) <doi:10.1214/16-AOAS992>

assignCluster	<i>Make Cluster Assignments</i>
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Description

Assigns observation to the nearest cluster center, using squared Euclidean distance.

Usage

```
assignCluster(X, centers)
```

Arguments

X	matrix of observations
centers	matrix of cluster centers

Value

A vector of cluster labels

Author(s)

Joshua Keller

Examples

```
X <- matrix(rnorm(100*5), nrow=100, ncol=5)
centers <- matrix(runif(3*5), nrow=3, ncol=5)

cl <- assignCluster(X, centers)
table(cl)
```

`createCVgroups`*Creating k-fold Cross-Validation Groups*

Description

Splits a vector of observation names or indices into a list of k groups, to be used as cross-validation (CV) test groups.

Usage

```
createCVgroups(x = NULL, n = length(x), k = 10, useNames = TRUE)
```

Arguments

<code>x</code>	vector of observation ID's (character or numeric) to split into cv groups.
<code>n</code>	number of observations to split into cv groups. Defaults to the length of <code>x</code> , but can also be provided instead of <code>x</code> .
<code>k</code>	number of cross-validation groups. Must be less than or equal to <code>n</code> .
<code>useNames</code>	logical indicator of whether the names of 'x' should be used to identify observations within cv groups.

Value

A list of length k giving the IDs of observations within each test group.

Author(s)

Joshua Keller

See Also

`predkmeansCVest` `predkmeansCVpred`

Examples

```
# 5-fold groups
cv5 <- createCVgroups(n=100, k=5)
cv5

# Leave-one-out
cvL00 <- createCVgroups(n=100, k=0)
cvL00
```

createPCAmodelmatrix *Create Principal Component Analysis (PCA) scores matrix*

Description

Wrapper function for creating PCA scores to be used in a regression analysis.

Usage

```
createPCAmodelmatrix(  
  data,  
  ncomps,  
  covarnames = colnames(data),  
  center = TRUE,  
  scale = TRUE,  
  matrixonly = TRUE  
)
```

Arguments

data	Matrix or data frame of data
ncomps	Number of PCA components to return.
covarnames	Names of variables or column numbers in data on which the PCA is to be run.
center	Logical indicator of whether data should be centered. Passed to prcomp .
scale	Logical indicator of whether data should be scaled. Passed to prcomp .
matrixonly	Logical indicator of whether only the model matrix should be returned, or the full output from prcomp .

Details

This is a wrapper around [prcomp](#), which does the necessary computation.

Value

If `matrixonly=TRUE`, a matrix of PCA scores. Otherwise a list containing two elements: `X`, a matrix of scores, and `pca`, the output from [prcomp](#).

Author(s)

Joshua Keller

See Also

[createTPRSmodelmatrix](#), [predkmeansCVest](#)

Examples

```
n <- 100
d <- 15
X <- matrix(rnorm(n*d), ncol=d, nrow=n)
X <- as.data.frame(X)
mx <- createPCAmatrix(data=X, ncomps=2)
```

createTPRSmodelmatrix *Create matrix of Thin-Plate Regression Splines (TPRS)*

Description

Wrapper function for creating a matrix of thin-plate regression splines (TPRS) to be used in a regression analysis.

Usage

```
createTPRSmodelmatrix(
  data,
  df = 5,
  covarnames = NULL,
  xname = "x",
  yname = "y",
  TPRSfx = TRUE,
  matrixonly = TRUE
)
```

Arguments

data	Matrix or data frame of data
df	Degrees of freedom for thinplate splines. This does not include an intercept, so the k argument of <code>s()</code> is $k = df + 1$.
covarnames	Names of other covariates to be included in the model matrix.
xname	Name of variable the provides the x-coordinate of location.
yname	Name of variable the provides the y-coordinate of location.
TPRSfx	Should the TPRS degrees of freedom be fixed. Passed as the <code>fx</code> argument to <code>s()</code> .
matrixonly	Logical indicator of whether only the model matrix should be returned, or the full output from <code>gam</code> .

Author(s)

Joshua Keller

See Also

[createPCAmatrix](#), [predkmeansCVest](#)

Examples

```
n <- 200
x <- runif(n=n, 0, 100)
y <- runif(n=n, 0, 100)
d <- data.frame(x=x, y=y)
mx <- createTPRSmatrix(data=d, df=5)
```

mlogit

Multinomial Logistic Regression

Description

Solves a multinomial logistic problem using Newton-Raphson method

Usage

```
mlogit(
  Y,
  X,
  beta = NULL,
  add.intercept = FALSE,
  betaOnly = FALSE,
  tol.zero = 1e-08,
  verbose = T,
  suppressFittedWarning = FALSE,
  maxNR.print.level = 0,
  iterlim = 150,
  checkY = TRUE
)
```

Arguments

- | | |
|------|---|
| Y | A matrix of the outcomes, with K columns for the K groups. Row sums of the matrix should be equal to one, but entries do not have to be 0/1 (but they should be positive). i.e. this is a matrix of hard or soft assignments to K categories. The first column is used as the reference category. |
| X | matrix of covariates for regression. Should have the same number of rows (observations) as Y. Coefficients for all parameters in X are computed for K-1 groups. The coefficients corresponding to the first column of Y are assumed to be zero. |
| beta | starting values for the optimization. Should be given as a matrix of column vectors, each vector a different starting value. If null, defaults to zeros. |

<code>add.intercept</code>	a logical indicator of whether an intercept column should be added to X
<code>betaOnly</code>	logical indicator of whether only the parameter estimates beta should be returned. Otherwise, beta is returned along with fitted objects. See Output.
<code>tol.zero</code>	the tolerance threshold for considering a fitted value as equal to zero. Used for warning about fitted values of 0/1. Is NOT part of the optimization control parameters.
<code>verbose</code>	logical indicator that controls whether text indicating progress is output to display
<code>suppressFittedWarning</code>	indicator of whether or not warnings about fitted values of 1 are returned
<code>maxNR.print.level</code>	numeric value giving the level of output produced by maxNR. see <code>?maxNR</code> for details. Defaults to 0.
<code>iterlim</code>	iteration limit for maxNR. Defaults to 150.
<code>checkY</code>	indicator for whether Y should be checked to be a valid assignment matrix. Set to FALSE if using decimal values in Y.

Details

The optimization is done using the `maxNR` function from the `maxLik` package. The log-likelihood function, along with its gradient and hessian, are implemented as C++ functions (via the `RcppArmadillo` package).

Value

A list containing the following:

<code>beta</code>	a $p \times K$ matrix of parameter estimates corresponding to the K columns of Y and p covariates in X
<code>fitted01</code>	indicator of whether fitted values of 1 were present.
<code>fitted</code>	the fitted probabilities
<code>res.best</code>	the best result from the maxNR fit
<code>status</code>	small data frame summarizing the status of the fits
<code>res.all</code>	a list containing the results from all maxNR fits

Author(s)

Joshua Keller

See Also

[predkmeans](#)

Examples

```

n <- 2000
X <- cbind(1,
           matrix(rnorm(2*n), nrow=n, ncol=2),
           rbinom(n, size=1, prob=0.3))
beta <- cbind(rep(0, 4),
              c(0.5, 1, 0, -1),
              c(0, 2, 2, 0))
probs <- exp(X %*% beta)
probs <- probs/rowSums(probs)
Y <- t(apply(probs, 1, function(p) rmultinom(1, 1, p)))
mfit <- mlogit(Y=Y, X=X, betaOnly=TRUE)
mfit

```

predictionMetrics *Measures of Prediction Performance*

Description

Computes several measures of performance for cluster label prediction.

Usage

```
predictionMetrics(centers, cluster.pred, X, labels = TRUE)
```

Arguments

centers	Matrix of Cluster centers
cluster.pred	Vector of predicted cluster membership. Should be integers or names corresponding to rows of centers.
X	Matrix of observations at prediction locations.
labels	Logical indicating whether cluster prediction and

Value

A list with the following elements:

MSPE	Mean squared prediction error. Sum of squared distances between observations and predicted cluster centers.
wSS	Within-cluster sum-of-squares. Sum of squared distances between observations at prediction locations and best (i.e. closest) cluster center.
MSME	Mean squared misclassification error. Sum of squared distances between predicted cluster center and best (i.e. closest) cluster center.
pred.acc	Proportion of cluster labels correctly predicted.
cluster.pred	Predicted cluster assignments (same as argument provided).
cluster.assign	Integer vector of 'best' cluster assignments (i.e. assignment to closest cluster center)

Author(s)

Joshua Keller

References

Keller, J.P., Drton, M., Larson, T., Kaufman, J.D., Sandler, D.P., and Szpiro, A.A. (2017). Covariate-adaptive clustering of exposures for air pollution epidemiology cohorts. *Annals of Applied Statistics*, 11(1):93–113.

See Also[predictML](#)**Examples**

```
n <- 100
d <- 5 # Dimension of exposure
K <- 3 # Number of clusters
X <- matrix(rnorm(n*d), ncol=d, nrow=n)
centers <- matrix(runif(d*K), nrow=K, ncol=d)
cluster_pred <- sample(1:K, size=n, replace=TRUE)
metrics <- predictionMetrics(centers, cluster_pred=cluster_pred, X=X)
metrics[c("MSPE", "wSS", "MSME", "pred.acc")]
```

predictML.predkmeans *Prediction of Cluster Membership*

Description

Predicts cluster membership using either multinomial logistic regression or SVMs.

Usage

```
## S3 method for class 'predkmeans'
predictML(
  object = NULL,
  centers = object$centers,
  K = nrow(centers),
  R,
  Rstar,
  Xstar = NULL,
  tr.assign = object$cluster,
  muStart = "random",
  maxitMlogit = 500,
  verbose = 1,
  nMlogitStarts = 1,
  mlogit.control = list(suppressFittedWarning = TRUE),
  ...
)
```

```

)

## S3 method for class 'predkmeans'
predictSVM(
  object = NULL,
  centers = object$centers,
  R,
  Rstar,
  K = nrow(centers),
  Xstar = NULL,
  tr.assign = object$cluster,
  svm.control = list(gamma = c(1/(2:1), 2), cost = seq(20, 100, by = 20)),
  ...
)

## S3 method for class 'predkmeans'
predictMixExp(object, R, Rstar = NULL, ...)

```

Arguments

<code>object</code>	A <code>predkmeans</code> object, from which the cluster centers will be extracted.
<code>centers</code>	Matrix of cluster centers, assumed to be K-by-p
<code>K</code>	Number of clusters
<code>R</code>	matrix of covariates for observations to be predicted at.
<code>Rstar</code>	matrix of covariates at training locations
<code>Xstar</code>	matrix of observation at training locations. Either this or <code>tr.assign</code> is required.
<code>tr.assign</code>	vector of cluster assignments at training locations. By default, extracted from <code>object</code> .
<code>muStart</code>	starting value for cluster centers in <code>mlogit</code> optimization (IDEA: change to pull from <code>predkmeans</code> object?). If not provided, starting values are selected randomly.
<code>maxitMlogit</code>	Maximum number of iterations for <code>mlogit</code> in prediction
<code>verbose</code>	integer indicating amount of output to be displayed
<code>nMlogitStarts</code>	number of <code>mlogit</code> starts to use in estimation of parameters
<code>mlogit.control</code>	list of control parameters to be passes to <code>mlogit</code>
<code>...</code>	Unused additional arguments
<code>svm.control</code>	list of options for <code>best.svm</code>

Details

Function for predicting cluster membership in clusters identified by k-means or predictive k-means using multinomial logistic regression or support vector machines (SVMs). For multinomial logistic regression, parameter estimation is handled by `mlogit`. The SVMs are fit using `best.svm` from `e1071` package.

Because this prediction includes return information about cluster assignment and prediction model parameters, this method is deliberately distinct from the generic predict functions.

The predictMixExp function provides predictions from the 'working' cluster assignments created as part of the mixture of experts algorithm from predkmeans.

Value

A list containing some or all of the following elements:

tr.assign	Cluster assignments at training locations
mlfit	A subset of the mlogit object returned by the function of that name
beta	Estimated model parameters
test.pred	Predicted cluster assignments at test locations

Author(s)

Joshua Keller

See Also

[mlogit](#), [predkmeans](#), [predictionMetrics](#)

Other methods for predkmeans objects: [relevel.predkmeans\(\)](#)

Examples

```
n <- 200
r1 <- rnorm(n)
r2 <- rnorm(n)
u1 <- rbinom(n, size=1,prob=0)
cluster <- ifelse(r1<0, ifelse(u1, "A", "B"), ifelse(r2<0, "C", "D"))
mu1 <- c(A=2, B=2, C=-2, D=-2)
mu2 <- c(A=1, B=-1, C=-1, D=-1)
x1 <- rnorm(n, mu1[cluster], 4)
x2 <- rnorm(n, mu2[cluster], 4)
R <- cbind(1, r1, r2)
X <- cbind(x1, x2)
pkm <- predkmeans(X=cbind(x1, x2), R=R, K=4)
n_pred <- 50
Rnew <- cbind(1, r1=rnorm(n_pred), r2=rnorm(n_pred))
pkmPred <- predictML(pkm, R=Rnew, Rstar=R)
pkmPred$test.pred
```

 predkmeans

Predictive K-means Clustering

Description

Uses a Mixture-of-experts algorithm to find cluster centers that are influenced by prediction covariates.

Usage

```

predkmeans(
  X,
  R,
  K,
  mu = NULL,
  muStart = c("kmeans", "random"),
  sigma2 = 0,
  sigma2fixed = FALSE,
  maxitEM = 100,
  tol = 1e-05,
  convEM = c("both", "mu", "gamma"),
  nStarts = 1,
  maxitMlogit = 500,
  verbose = 0,
  muRestart = 1000,
  returnAll = FALSE,
  ...
)

```

Arguments

X	An n by p matrix or data frame of data to be clustered.
R	Covariates used for clustering. Required unless doing k-means clustering (i.e. <code>sigma2=0</code> and <code>sigma2fixed=TRUE</code>).
K	Number of clusters
mu	starting values for cluster centers. If NULL (default), then value is chosen according to <code>muStart</code> .
muStart	Character string indicating how initial value of mu should be selected. Only used if <code>mu=NULL</code> . Possible values are "random" or "kmeans" (default).
sigma2	starting value of sigma2. If set to 0 and <code>sigma2fixed=TRUE</code> , the standard k-means is done instead of predictive k-means.
sigma2fixed	Logical indicating whether sigma2 should be held fixed. If FALSE, then sigma2 is estimated using Maximum Likelihood.
maxitEM	Maximum number of EM iterations for finding the Mixture of Experts solution. If doing regular k-means, this is passed as <code>iter.max</code> .

tol	convergence criterion
convEM	controls the measure of convergence for the EM algorithm. Should be one of "mu", "gamma", or "both". Defaults to "both." The EM algorithm stops when the Frobenius norm of the change in mu, the change in gamma, or the change in mu and the change in gamma is less than 'tol'.
nStarts	number of times to perform EM algorithm
maxitMlogit	Maximum number of iterations in the mlogit optimization (nested within EM algorithm)
verbose	numeric vector indicating how much output to produce
muRestart	Gives max number of attempts at picking starting values. Only used when muStart='random'. If selected starting values for mu are constant within each cluster, then the starting values are re-selected up to muRestart times.
returnAll	A list containing all nStarts solutions is included in the output.
...	Additional arguments passed to <code>mlogit</code>

Details

A thorough description of this method is provided in Keller et al. (2017). The algorithm for solving the mixture of Experts model is based upon the approach presented by Jordan and Jacobs (1994).

If `sigma2` is 0 and `sigma2fixed` is TRUE, then standard k-means clustering (using `kmeans`) is done instead.

Value

An object of class `predkmeans`, containing the following elements:

<code>res.best</code>	A list containing the results from the best-fitting solution to the Mixture of Experts problem: mu Maximum-likelihood estimate of intercepts from normal mixture model. These are the cluster centers. gamma Maximum-likelihood estimates of the mixture coefficients. sigma2 If <code>sigma2fixed=FALSE</code> , the maximum likelihood estimate of <code>sigma2</code> conv Indicator of convergence. objective Value of the log-likelihood. iter Number of iterations. mfit A subset of output from <code>mlogit</code> .
<code>center</code>	Matrix of cluster centers
<code>cluster</code>	Vector of cluster labels assigned to observations
<code>K</code>	Number of clusters
<code>sigma2</code>	Final value of σ^2 .
<code>wSS</code>	Mean within-cluster sum-of-squares
<code>sigma2fixed</code>	Logical indicator of whether <code>sigma2</code> was held fixed

Author(s)

Joshua Keller

References

- Keller, J.P., Drton, M., Larson, T., Kaufman, J.D., Sandler, D.P., and Szpiro, A.A. (2017). Covariate-adaptive clustering of exposures for air pollution epidemiology cohorts. *Annals of Applied Statistics*, 11(1):93–113.
- Jordan M. and Jacobs R. (1994). Hierarchical mixtures of experts and the EM algorithm. *Neural computation* 6(2), 181-214.

See Also

[predictML.predkmeans](#), [predkmeansCVest](#)

Examples

```
n <- 200
r1 <- rnorm(n)
r2 <- rnorm(n)
u1 <- rbinom(n, size=1,prob=0)
cluster <- ifelse(r1<0, ifelse(u1, "A", "B"), ifelse(r2<0, "C", "D"))
mu1 <- c(A=2, B=2, C=-2, D=-2)
mu2 <- c(A=1, B=-1, C=-1, D=-1)
x1 <- rnorm(n, mu1[cluster], 4)
x2 <- rnorm(n, mu2[cluster], 4)
R <- model.matrix(~r1 + r2)
X <- cbind(x1, x2)
pkm <- predkmeans(X=cbind(x1, x2), R=R, K=4)
summary(pkm)
```

predkmeansCVest

Cross-validation of Predictive K-means Clustering

Description

Performs cross-validation of predictive k-means clustering and cluster prediction.

Usage

```
predkmeansCVest(
  X,
  R,
  K,
  cv.groups = 10,
  sigma2 = 0,
  sigma2fixed = FALSE,
  scale = TRUE,
```

```

    covarnames = colnames(R),
    PCA = FALSE,
    PCAcontrol = list(covarnames = colnames(R), ncomps = 5),
    TPRS = FALSE,
    TPRScontrol = list(df = 5, xname = "x", yname = "y"),
    returnAll = FALSE,
    ...
)

predkmeansCVpred(
  object,
  X = object$X,
  R = object$R,
  method = c("ML", "MixExp", "SVM"),
  ...
)

```

Arguments

X	Outcome data
R	Covariates. Coerced to data frame.
K	Number of clusters
cv.groups	A list providing the cross-validation groups for splitting the data. groups for splitting the data. Alternatively, a single number giving the number of groups into which the data are randomly split. A value of '0' implies leave-one-out. Defaults to 10.
sigma2	starting value of sigma2. Setting sigma2=0 and sigma2fixed=TRUE results in regular k-means clustering.
sigma2fixed	Logical indicating whether sigma2 should be held fixed. If FALSE, then sigma2 is estimated using Maximum Likelihood.
scale	Should the outcomes be re-scaled within each training group?
covarnames	Names of covariates to be included directly.
PCA	Logical indicator for whether PCA components should be computed from R.
PCAcontrol	Arguments passed to createPCAmodelmatrix . This includes ncomps.
TPRS	Logical indicator for whether thin-plate regression splines should be created and added to covariates.
TPRScontrol	Arguments passed to createTPRSmodelmatrix . This includes df.
returnAll	A list containing all nStarts solutions is included in the output.
...	Additional arguments passed to either predkmeans or the prediction method.
object	A predkmeansCVest object.
method	Character string indicating which prediction method should be used. Options are ML, MixExp, and SVM. See predictML for more information.

Details

These wrappers are designed to simplify cross-validation of a dataset. For models including thin-plate regression splines (TPRS) or principal component analysis (PCA) scores, these functions will re-evaluate the TPRS basis or PCA decomposition on each training set.

Author(s)

Joshua Keller

See Also

[predkmeans](#), [createPCAmatrix](#), [createTPRSmatrix](#)

Examples

```
n <- 200
r1 <- rnorm(n)
r2 <- rnorm(n)
u1 <- rbinom(n, size=1,prob=0)
cluster <- ifelse(r1<0, ifelse(u1, "A", "B"), ifelse(r2<0, "C", "D"))
mu1 <- c(A=2, B=2, C=-2, D=-2)
mu2 <- c(A=1, B=-1, C=-1, D=-1)
x1 <- rnorm(n, mu1[cluster], 4)
x2 <- rnorm(n, mu2[cluster], 4)
R <- model.matrix(~r1 + r2)
X <- cbind(x1, x2)
pkmcv <- predkmeansCVest(X=cbind(x1, x2),
                        R=R, K=4, nStarts=4, cv.groups= 5,
                        TPRS=FALSE, PCA=FALSE, covarnames=colnames(R))

pkmcv
```

relevel.predkmeans *Re-order cluster labels*

Description

Function for re-ordering the order of clusters in a predkmeans object.

Usage

```
## S3 method for class 'predkmeans'
relevel(x, ref = NULL, order = NULL, ...)
```

Arguments

x	object of class predkmeans
ref	New reference group ("Cluster 1"). Only used if order is NULL.
order	New order of clusters.
...	Ignored additional arguments.

Details

The elements of the `order` argument should refer to the current position of clusters, with the position giving the new order. So `c(3, 1, 2)` moves 1 to 2, 2 to 3, and 3 to 1.

Author(s)

Joshua Keller

See Also

Other methods for `predkmeans` objects: [predictML.predkmeans\(\)](#)

Examples

```
n <- 200
r1 <- rnorm(n)
r2 <- rnorm(n)
u1 <- rbinom(n, size=1,prob=0)
cluster <- ifelse(r1<0, ifelse(u1, "A", "B"), ifelse(r2<0, "C", "D"))
mu1 <- c(A=2, B=2, C=-2, D=-2)
mu2 <- c(A=1, B=-1, C=-1, D=-1)
x1 <- rnorm(n, mu1[cluster], 4)
x2 <- rnorm(n, mu2[cluster], 4)
R <- model.matrix(~r1 + r2)
X <- cbind(x1, x2)
pkm <- predkmeans(X=cbind(x1, x2), R=R, K=4)
table(pkm$cluster)

# Move cluster '4' to be first
pkm2 <- relevel(pkm, ref=4)
table(pkm2$cluster)
# Re-order based upon number of observations in each cluster
pkm3 <- relevel(pkm, order=order(table(pkm$cluster), decreasing=TRUE))
table(pkm3$cluster)
```

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