Package: tgml (via r-universe)

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Type Package

Title Tree Guided Machine Learning for Personalized Predictions and Precision Diagnostics

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Description Generalization of the classification and regression tree (CART) model that partitions subjects into terminal nodes and tailors machine learning model to each terminal node.

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Depends R (>= 4.5.0), glmnet, randomForest, e1071, pROC, stats, graphics

NeedsCompilation no

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tgml *Tree Guided Machine Learning*

Description

Generalized classification and tree model that assigns the most effective predictive model to each terminal node.

Usage

```
tgml(y,x,z,ynew,xnew,znew,MLlist,eval,cut,max_depth,min_sample,verbose)
```

Arguments

y	Response vector. If a factor codied as 0 or 1, classification is assumed. Otherwise, regression is assumed.
x	Data.frame or matrix of predictors that is used to estimate a tree structure.
z	Data.frame or matrix of predictors that is used in terminal node specific ML models.
ynew	Response vector for the test set corresponding to y (default ynew=NULL).
xnew	Data.frame or matrix for the test set corresponding to x (default xnew=NULL).
znew	Data.frame or matrix for the test set corresponding to z (default znew=NULL).
MLlist	Candidate predictive models that can be assigned to each terminal node (default MLlist=c("lasso","rf","svm")). Any other predictive models can be included. See the details below.
eval	Criterion for splitting trees: "mse" (mean squared error), "bs", or "auc" (area under the ROC curve). Default: eval=NULL, then "mse" for continuous y and "bs" for binary y.
cut	Number of percentile-based candidate cutoff values for each x[,j], j=1,2,.... (default cut=10). This is only used when x[,j] has the unique values more than cut.
max_depth	Maximum depth of trees. (default max_depth=4).
min_sample	The number of minimum sample size per each node, i.e., length(y)>min_sample if y is continuous and min(length(y==1),length(y==0))>min_sample (default min_sample=20).
verbose	Show progress messages if verbose=TRUE.

Details

The tgml function uses recursive partitioning to simultaneously identify subgroups and subgroup-specific predictive models. Specifically, the data (y,x,z) are randomly split into training and validation sets. At each candidate split, predictive models specified in MLlist are fitted using the training set, and the optimal split is selected based on the validation MSE or BS.

Ideally, two distinct sets of predictors are available: x and z (e.g., clinical variables and biomarkers), where x is used to construct the tree splits and z is used for terminal-node-specific predictive models. When such a separation is not feasible, individualized prediction of y given x is also allowed by using the same variable x for both roles, for example:

tgml(y = y, x = x, z = x, ynew = ynew, xnew = xnew, znew = xnew).

Regarding node numbering, each internal node s has left and right child nodes indexed as 2s and 2s+1, respectively. The root node is indexed as node 1; nodes 2 and 3 are the left and right children of node 1; nodes 4 and 5 are the left and right children of node 2; and so on.

Currently, terminal-node-specfic predictive models include lasso(), randomForest(), and svm(..., kernel = "radial") from the R packages cv.glmnet, randomForest, and e1071, respectively. Additional models can be flexibly incorporated; see Example 3 below for an illustration.

Value

An object of class tgml, which is a list with the following components:

`terminal`	Terminal node numbers.
`internal`	Internal node numbers.
`splitVariable`	splitVariable[k] (i.e., x[,k]) is used to split the internal node k.
`cutoff`	cutoff[k] is the cutoff value to split the internal node k.
`selML`	selML[k] is ML model assigned to the terminal node t.
`fitML`	fitML[[t]] is the fitted ML model at the terminal node t.
`y_hat`	Estimated y (or estimated probability) on the training set (y,x,z) if y is continuous (or binary).
`node_hat`	Estimated node on the training set.
`mse`	Training MSE.
`bs`	Training Brier Score.
`roc`	Training ROC curve.
`auc`	Training AUC.
`y_hat_new`	Estimated y (or estimated probability) on the test set (ynew,xnew,znew) if y is continuous (or binary).
`node_hat_new`	Estimated node on the test set.
`mse_new`	Test MSE.
`bs_new`	Test Brier Score.
`roc_new`	Test ROC curve.
`auc_new`	Test AUC.

Author(s)

Yunro Chung [aut, cre]

References

Nishtha Shah, Hassan Ghasemzadeh and Yunro Chung, Treed-guided machine learning for precision diagnostics and subgroup-specific biomarker discovery (in preperation)

Examples

```
set.seed(99)
###
#1. continuous y
###
n=200*2 #n=200 & 200 for training & test sets

x=matrix(rnorm(n*10),n,10) #10 predictors
z=matrix(rnorm(n*10),n,10) #10 biomarkers

xcut=median(x[,1])
subgr=1*(x[,1]<xcut)+2*(x[,1]>=xcut) #2 subgroups

lp=rep(NA,n)
for(i in 1:n)
  lp[i]=1+3*z[i,subgr[i]]
y=lp+rnorm(n,0,1)

idx.nex=sample(1:n,n*1/2,replace=FALSE)
ynew=y[idx.nex]
xnew=x[idx.nex,]
znew=z[idx.nex,]

y=y[-idx.nex]
x=x[-idx.nex,]
z=z[-idx.nex,]

fit1=tgml(y,x,z,ynew=ynew,xnew=xnew,znew=znew)
fit1$mse_new
plot(fit1$y_hat_new~ynew,ylab="Predicted y",xlab="ynew")
abline(a=0,b=1)

###
#2. binary y
###
x=matrix(rnorm(n*10),n,10) #10 predictors
z=matrix(rnorm(n*10),n,10) #10 biomarkers

xcut=median(x[,1])
subgr=1*(x[,1]<xcut)+2*(x[,1]>=xcut) #2 subgroups

lp=rep(NA,n)
for(i in 1:n)
  lp[i]=1+3*z[i,subgr[i]]
prob=1/(1+exp(-lp))
y=rbinom(n,1,prob)
y=as.factor(y)

idx.nex=sample(1:n,n*1/2,replace=FALSE)
ynew=y[idx.nex]
xnew=x[idx.nex,]
znew=z[idx.nex,]
```

```
y=y[-idx.nex]
x=x[-idx.nex,]
z=z[-idx.nex,]

fit2=tgml(y,x,z,ynew=ynew,xnew=xnew,znew=znew)
fit2$auc_new
plot(fit2$roc_new)

###
#3. add new ML models
#   1) write two functions:
#      c_xx & c_xx_predict if y is continuous or
#      b_xx & b_xx.predict if y is binary
#   2) update MLlist that includes xx, not c_xx nor b_xx.
#   3) run tgml using updated MLlist.
#   The below is an example of adding ridge regression.
###
#3.1. ridge regression for continuous y.
c_ridge=function(y,x){
  x=data.matrix(x)
  fit=NULL
  suppressWarnings(try(fit<-glmnet::cv.glmnet(x,y,alpha=0),silent=TRUE))
  return(fit)
}
c_ridge_predict=function(fit,xnew){
  y.hat=rep(NA,nrow(xnew))
  if(!is.null(fit)){
    xnew=data.matrix(xnew)
    y.hat=as.numeric(predict(fit,newx=xnew,s="lambda.min",type="response"))
  }
  return(y.hat)
}

#3.2. ridge regression for binary y.
b_ridge=function(y,x){
  x=data.matrix(x)
  fit=NULL
 suppressWarnings(try(fit<-glmnet::cv.glmnet(x,y,alpha=1,family="binomial"),silent=TRUE))
  return(fit)
}
b_ridge_predict=function(fit,xnew){
  y.hat=rep(NA,nrow(xnew))
  if(!is.null(fit)){
    xnew=data.matrix(xnew)
    y.hat=as.numeric(predict(fit,newx=xnew,s="lambda.min",type="response"))
  }
  return(y.hat)
}

#3.3. update MLlist
MLlist=c("lasso","ridge")
fit3=tgml(y,x,z,ynew=ynew,xnew=xnew,znew=znew,MLlist=MLlist)
```

```
fit3$auc_new
plot(fit3$roc_new)
```

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