

Package: gbm2sas (via r-universe)

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Type Package

Title Convert GBM Object Trees to SAS Code

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Description Writes SAS code to get predicted values from every tree of a gbm.object.

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Description

Writes SAS code to get predicted values from every tree of a gbm object.

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gbm2sas

Convert GBM Object Trees to SAS Code

Description

Writes SAS code to get predicted values for every tree of a gbm object. The predicted values are as reported by the gbm package function `pretty.gbm.tree`.

Usage

```
gbm2sas(  
  gbmobject,  
  data=NULL,  
  sasfile=NULL,  
  ntrees=NULL,  
  mysasdata="mysasdata",  
  treeval="treeval",  
  prefix="do_"  
)
```

Arguments

<code>gbmobject</code>	An object of type <code>gbm.object</code> .
<code>data</code>	Data used to fit <code>gbm.object</code> .
<code>sasfile</code>	Name of file to write the SAS code to.
<code>ntrees</code>	Optional number of trees to use in prediction. Default is the value <code>n.trees</code> from <code>gbmobject</code> .
<code>mysasdata</code>	Optional name of dataset operated on in the SAS code. Default is "mysasdata".
<code>treeval</code>	Optional name to use for the value from each gbm tree. These will have a number appended. Default variable names will be of the form "treeval1", "treeval2", etc. Set this to a different prefix to avoid overwriting SAS dataset values, if necessary.
<code>prefix</code>	Optional prefix to use for intermediate SAS program control variables. These will have a number appended. Default variable names will be of the form "do_1", "do_2", etc. Set this to a different prefix to avoid overwriting SAS dataset values, if necessary.

Value

`sasfile` SAS code will be written to `sasfile`.

Author(s)

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References

Package 'gbm'. Greg Ridgeway with contributions from others.

Examples

```

set.seed(18221)
# This example is taken from the gbm package documentation.
# create some data
N <- 1000
X1 <- runif(N)
X2 <- 2*runif(N)
X3 <- ordered(sample(letters[1:4],N,replace=TRUE),levels=letters[4:1])
X4 <- factor(sample(letters[1:6],N,replace=TRUE))
X5 <- factor(sample(letters[1:3],N,replace=TRUE))
X6 <- 3*runif(N)
mu <- c(-1,0,1,2)[as.numeric(X3)]

SNR <- 10 # signal-to-noise ratio
Y <- X1**1.5 + 2 * (X2**.5) + mu
sigma <- sqrt(var(Y)/SNR)
Y <- Y + rnorm(N,0,sigma)

# introduce some missing values
X1[sample(1:N,size=500)] <- NA
X4[sample(1:N,size=300)] <- NA

thedata <- data.frame(Y=Y,X1=X1,X2=X2,X3=X3,X4=X4,X5=X5,X6=X6)

# fit initial model
gbm1 <-
gbm(Y~X1+X2+X3+X4+X5+X6,
    data=thedata,
    var.monotone=c(0,0,0,0,0,0),
    distribution="gaussian",
    n.trees=1000,
    shrinkage=0.05,
    interaction.depth=3,
    bag.fraction = 0.5,
    train.fraction = 1,
    n.minobsinnode = 10,
    cv.folds = 3,
    keep.data=TRUE,
    verbose=FALSE,
    n.cores=1)

# We will pass a csv file to SAS, to demonstrate that the tree values from gbm2sas agree
# with R. Note that if train.fraction were <1 above, we would need to pass the
# analogous subsample to sas via the csv file below. Since the fraction used was 1,
# we pass the entire dataset "thedata" below.
best.iter<-gbm.perf(gbm1,method="cv",plot.it=FALSE) # find a good number of trees
fit_from_r<-predict(gbm1, n.trees=best.iter) # get fitted values from R
avgrresponse<-gbm1$initF # we will pass gbm1's intercept to SAS via the csv file

```

```

numtrees<-best.iter # we will pass the total number of trees to SAS via the csv file
fitdata<-cbind(thedata,avgresponse,numtrees,fit_from_r) # augment the training data
# Write the csv file. We require SAS's missing() function and R agree on what values
# are missing. Hence the "na" argument below, which assures SAS's proc import will
# assign missing values in agreement with what R considers a missing value.
write.table(fitdata,"checkdata.csv",
sep="," , quote=FALSE, row.names=FALSE, col.names=TRUE, na="")

# Now use gbm2sas
gbm2sas(
gbm1, # gbm object from above
data=thedata, # dataset used to fit model
sasfile="gbmforest.sas", # name to use for SAS code file
ntrees=best.iter, # number of trees
mysasdata="sasdataset", # name to use for dataset within SAS
treeval="treevalue", # name to use for value returned for each tree from pretty.gbm.tree
prefix="dobranch_" # variable name for controlling branching in SAS code
)

# SAS program to check R versus SAS fitted values
#proc import out=sasdataset
#   datafile= "checkdata.csv" /* file written by the R example code */
#   dbms=csv replace;
#   getnames=yes;
#run;
/* Below we assume the SAS missing() function and R agree on what values are missing.
The missing values were written by R to checkdata.csv such that proc import will
correctly assign a missing value to them. */
#
%include "gbmforest.sas"; /* SAS code written by gbm2sas */
#
#data sasdataset;
#set sasdataset;
#call symput('numtrees', numtrees); /* define macro variable holding ntrees */
#run;
#
#%macro checksascode(); /* macro to check SAS versus R */
#data sasdataset; set sasdataset;
#fit_from_sas=avgresponse; /* we need to start with the intercept from the gbm.object */
#%DO loop = 1 %TO &numtrees.;
#fit_from_sas=fit_from_sas+treevalue&loop.; /* add fitted value from each tree */
#%END;
/* find the discrepancy between R and SAS fitted values for this observation */
#diff=abs(fit_from_sas-fit_from_r);
#run;
#%mend checksascode;
#
#%checksascode() /* call the checking macro */
#
/* get worst discrepancy over all observations */
#proc sql; select max(diff) as max_discrepancy from sasdataset; quit;
#
# output from SAS

```

```
#max_discrepancy
#-----
#          7.33E-15

file.remove("checkdata.csv")
file.remove("gbmforest.sas")
```

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