baseline_main

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```
print(R.version)
##
                  x86 64-w64-mingw32
## platform
## arch
                  x86_64
## os
                 mingw32
## system
                 x86 64, mingw32
## status
## major
## minor
                 4.2
## year
                  2017
## month
                  09
## day
                  28
## svn rev
               73368
## language
                  R
## version.string R version 3.4.2 (2017-09-28)
## nickname
                  Short Summer
if(!require("gbm")){
  install.packages("gbm")
}
## Loading required package: gbm
## Loading required package: survival
## Loading required package: lattice
## Loading required package: splines
## Loading required package: parallel
## Loaded gbm 2.1.3
```

```
if(!require("dplyr")){
  install.packages("dplyr")
}
## Loading required package: dplyr
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
   The following objects are masked from 'package:base':
##
       intersect, setdiff, setequal, union
##
library(gbm)
library(dplyr)
```

Step 0: set seed.

In order to obain reproducible results, set.seed() whenever randomization is used.

```
set.seed(1)
```

Step 1: set up controls for evaluation experiments.

In this chunk, ,we have a set of controls for the evaluation experiments.

- (T/F) cross-validation on the training set
- (number) K, the number of CV folds
- (T/F) process features for training set
- (T/F) run evaluation on an independent test set
- (T/F) process features for test set

```
run.cv=TRUE # run cross-validation on the training set
K <- 3 # number of CV folds
#run.feature.train=TRUE # process features for training set
run.test=TRUE # run evaluation on an independent test set
#run.feature.test=TRUE # process features for test set</pre>
```

Using cross-validation or independent test set evaluation, we compare the performance of different classifiers or classifiers with different specifications. In this example, we use GBM with different depth. In the following chunk, we list, in a vector, setups (in this case, depth) corresponding to models that we will compare. In your project, you maybe comparing very different classifiers. You can assign them numerical IDs and labels specific to your project.

```
model_values <- seq(3, 11, 4)
model_labels = paste("GBM with depth =", model_values)</pre>
```

Read in data

```
# lables(0 for muffin, 1 for chicken, 2 for dog)
labels <- read.csv("../data/label_train.csv", header=TRUE)
colnames(labels)[2] <- "labels"</pre>
```

```
sift_data <- read.csv("../data/sift_train.csv",header=TRUE, stringsAsFactors = FALSE)</pre>
```

divide into training and sampling data set

```
sampling <- sample(seq(1:3000),3000*0.25) %>% sort()
label_test <- labels[sampling,-1]
label_train <- labels[-sampling,-1]
dat_test <- sift_data[sampling,-1]
dat_train <- sift_data[-sampling,-1]</pre>
```

load train and test method

```
source("../lib/baseline_train.R")
source("../lib/baseline_test.R")
```

Model selection with cross-validation

 Do model selection by choosing among different values of training model parameters, that is, the interaction depth for GBM in this example.

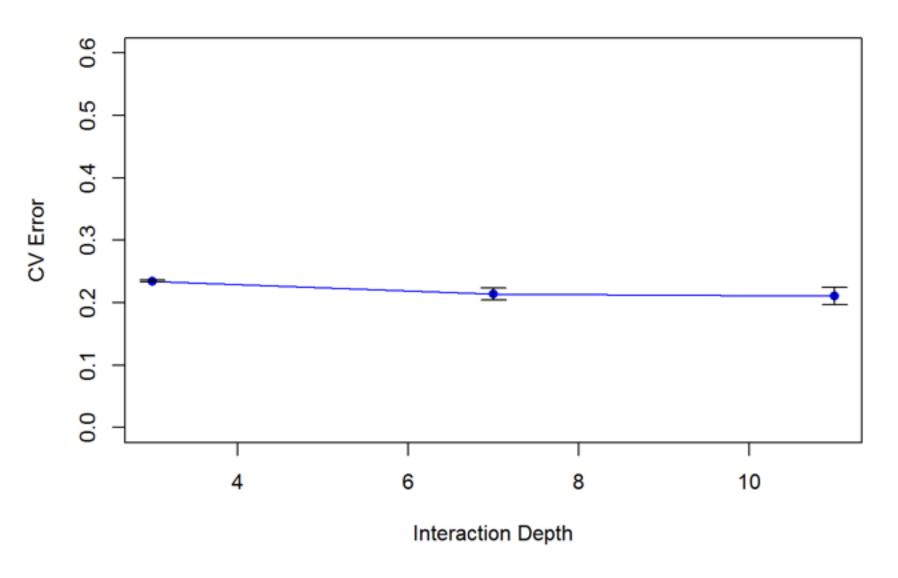
```
source("../lib/baseline_cv.R")

if(run.cv){
    err_cv <- array(dim=c(length(model_values), 2))
    for(k in 1:length(model_values)){
        cat("k=", k, "\n")
        err_cv[k,] <- cv.function(dat_train, label_train, model_values[k], K)
    }
    save(err_cv, file="../output/baseline_err_cv.RData")
}</pre>
```

```
## k= 1
## k= 2
## k= 3
```

Visualize cross-validation results.

Cross Validation Error



• Choose the "best"" parameter value

```
model_best=model_values[1]
if(run.cv){
  model_best <- model_values[which.min(err_cv[,1])]
}
par_best <- list(depth=model_best)</pre>
```

 Train the model with the entire training set using the selected model (model parameter) via crossvalidation.

```
tm_train=NA
tm_train <- system.time(fit_train <- train(dat_train, label_train, par_best))</pre>
```

```
## Warning in gbm.fit(x = dat_train, y = label_train, n.trees = 1000,
## distribution = "multinomial", : variable 1012: V1012 has no variation.
```

```
## Warning in gbm.fit(x = dat_train, y = label_train, n.trees = 1000,
## distribution = "multinomial", : variable 2688: V2688 has no variation.
```

```
## Warning in gbm.perf(fit_gbm, method = "OOB", plot.it = FALSE): OOB
## generally underestimates the optimal number of iterations although
## predictive performance is reasonably competitive. Using cv.folds>0 when
## calling gbm usually results in improved predictive performance.
```

```
save(fit_train, file="../output/baseline_fit_train.RData")
```

Step 5: Make prediction

Feed the final training model with the completely holdout testing data.

```
tm_test=NA
if(run.test){
  load(file="../output/baseline_fit_train.RData")
  tm_test <- system.time(pred_test <- test(fit_train, dat_test))
  save(pred_test, file="../output/baseline_pred_test.RData")
}</pre>
```

Calculate the prediction rate

```
load(file="../output/baseline_pred_test.RData")
correct_rate <- mean(pred_test == label_test)
cat("Correct rate for prediction = ", correct_rate[1], "\n")</pre>
```

```
## Correct rate for prediction = 0.7546667
```

Summarize Running Time

Prediction performance matters, so does the running times for constructing features and for training the model, especially when the computation resource is limited.

```
cat("Time for training model=", tm_train[1], "s \n")

## Time for training model= 2775.39 s

cat("Time for making prediction=", tm_test[1], "s \n")
```

```
## Time for making prediction= 0.11 s
```