baseline main

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```
print(R.version)
##
                  x86 64-w64-mingw32
## platform
## arch
                  x86 64
                  mingw32
## os
                  x86_64, mingw32
## system
## status
## major
                  3
## minor
                  4.1
## year
                   2017
                  06
## month
## day
                  30
                  72865
## svn rev
## language
## version.string R version 3.4.1 (2017-06-30)
## nickname
                  Single Candle
if(!require("gbm")){
  install.packages("gbm")
library(gbm)
```

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) run evaluation on an independent test set

```
run.cv=TRUE # run cross-validation on the training set
K <- 3 # number of CV folds
run.test=TRUE # run evaluation on an independent test set
```

Step 2: perform model selection by 5 folds cross-validation

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

# prepare data
label_train <- labels[,-1]
dat_train <- sift_data[,-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.

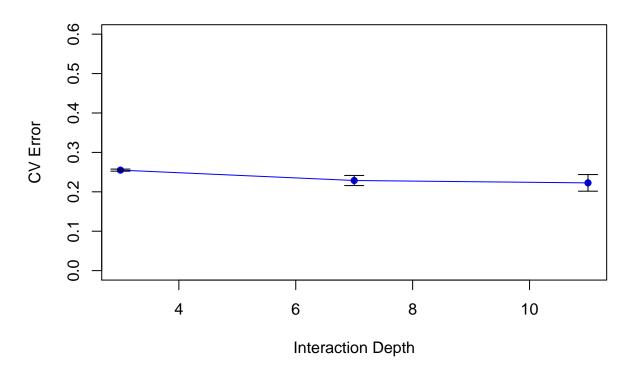
```
source("../lib/baseline_cv.R")

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")
}

## k= 1
## k= 2
## k= 3</pre>
```

Step 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)
cat(model_best)</pre>
```

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• Train the model with the entire training set using the selected model (model parameter) via cross-validation.

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

## Warning in gbm.perf(fit_gbm, method = "00B", plot.it = FALSE): 00B
## 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 4: Make prediction

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

```
{r} #dat_test <- read.csv("../data/sift_test.csv", header=TRUE)
#dat_test <- dat_test[,-1] #

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

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= 3944.14 s
#cat("Time for making prediction=", tm_test[1], "s \n")
```

Project 3 | Group 5

Step 0: Prepare Environment and Load Packages

Before you run next chunk, please follow the instructions to install all packages we need.

Pre-requirements:

numpy, random, pickle, time, xgboost, PIL, gist, csv, FFTW

(1) Install numpy, random, pickle

\$ pip install numpy

\$ pip install random

\$ pip install pickle

(2) Install FFTW

FFTW download: http://www.fftw.org (http://www.fftw.org (http://www.fftw.org (http://www.fftw.org)

Install instruction: http://www.fftw.org/fftw3 doc/Installation-on-Unix.html

\$./configure --enable-single --enable-shared

\$ make

\$ sudo make install

(3) Install gist

Download lear_gist: https://github.com/tuttieee/lear-gist-python (<a href="https://github.com/tut

\$ sudo python setup.py build_ext

\$ python setup.py install

If fftw3f is installed in non-standard path (for example, HOME/local), use -I and -L options:

\$ sudo python setup.py build_ext -I HOME/local/include -L HOME/local/lib

(4) Install xgboost

Instructions for Install XGBoost on Mac OSX:

https://www.ibm.com/developerworks/community/blogs/jfp/entry/Installing_XGBoost_on_Mac_OSX? lang=en

(https://www.ibm.com/developerworks/community/blogs/jfp/entry/Installing_XGBoost_on_Mac_OSX? lang=en)

You might encounter a problem when insert command "make -j4". Here is an efficeint way to solve the problem: https://stackoverflow.com/questions/36211018/clang-error-errorunsupported-option-fopenmp-on-mac-osx-el-capitan-buildin)

```
In [1]:
```

```
import GIST
import pandas as pd
import random
import pickle
import time
import xgboost
```

Step 1: Read Test Pictures Information

Before you run next chunk, please make sure you meet following requirements:

- (1) Make sure path variable is where you store all your test images
- (2) Make sure 5000 SIFT feature descriptors of your test images are stored in the data folder as feature_sift_test.csv
- (3) Make sure label of your test images are stored in the data folder as label_test.csv

```
In [2]:
```

```
path = "/Users/siyi/Documents/Study-Columbia/17FALL/GR5243-Applied-Data-Science/
Project3/training_set/images2"
GIST.feature_output(path)
gist_new = pd.read_csv('feature.csv', skiprows=1, header = None).iloc[:, 1:]
sift_new = pd.read_csv('../data/feature_sift_test.csv').iloc[:, 1:]
label_new = pd.read_csv('../data/label_test.csv').iloc[:, 1]
feature = pd.concat([sift_new, gist_new], axis=1)
feature.columns = ['x' + str(i+1) for i in range(5000)] + ['f' + str(i+1) for i
in range(960)]
```

Step 2: XGBoost Model

```
In [3]:
# require X test, y test
X test = feature
y_test = label_new
In [4]:
# load the baseline model
filename = '../output/model baseline.sav'
xgb 1 = pickle.load(open(filename, 'rb'))
# load the tuned xgboost model
filename = '../output/model tuned.sav'
xgb 2 = pickle.load(open(filename, 'rb'))
In [5]:
print("Baseline: ")
pred = xgb_1.predict(X test)
y label = y test.values
print ('classification error=%f' % (sum([pred[i] != y_label[i] for i in range(le
n(y label))]) / float(len(y label)) ))
print ('You can check training time in the file xgboost train.py.')
print("Tuned: ")
pred = xgb 2.predict(X test)
y label = y test.values
print ('classification error=%f' % (sum([pred[i] != y_label[i] for i in range(le
n(y label))]) / float(len(y label)) ))
print ('You can check training time in the file xgboost train.py.')
Baseline:
classification error=0.000000
You can check training time in the file xgboost train.py.
Tuned:
classification error=0.000000
You can check training time in the file xgboost train.py.
In [ ]:
```