Step 0: 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)

Install instruction: http://www.fftw.org/fftw3_doc/Installation-on-Unix.html (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 (https://github.com/tuttieee/lear-gist-python)

$ 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

Install instructions: 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)

Problems you might encounter when you install: https://stackoverflow.com/questions/36211018/clang-error-errorunsupported-option-fopenmp-on-mac-osx-el-capitan-buildin (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 model
filename = '../output/model_tuned.sav'
xgb_2 = pickle.load(open(filename, 'rb'))
```

In [5]:

```
start = time.time()
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)) ))

start = time.time()
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)) ))
```

```
Baseline: 
classification error=0.000000
Tuned: 
classification error=0.000000
```

In [ ]:

```
```

baseline_main

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2017/10/29

```
print(R.version)
```

```
##                _                           
## platform       x86_64-w64-mingw32          
## arch           x86_64                      
## os             mingw32                     
## system         x86_64, mingw32             
## status                                     
## major          3                           
## 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
```

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)
```

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)
```

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]
```

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.

```
# small range case !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
#dat_train <- sift_data[1:100,-1]
#label_train <- labels[1:100,-1]
#dat_test <- sift_data[101:200,-1]
#label_test <- labels[101:200,-1]
```

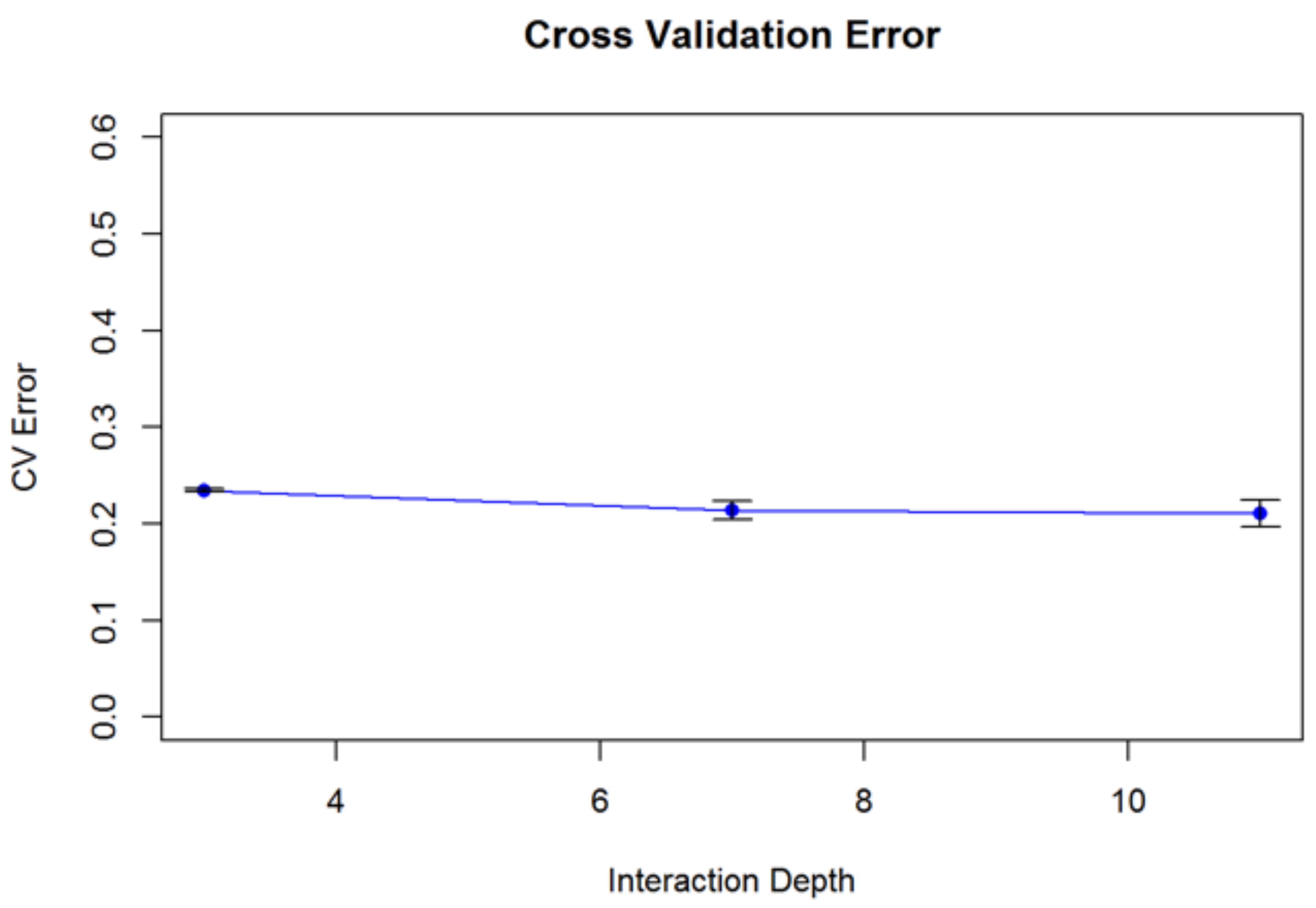
```
source("../lib/baseline_cv.R")

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
```

Visualize cross-validation results.

```
if(run.cv){
  load("../output/baseline_err_cv.RData")
  #pdf("../fig/cv_results.pdf", width=7, height=5)
  plot(model_values, err_cv[,1], xlab="Interaction Depth", ylab="CV Error",
       main="Cross Validation Error", type="n", ylim=c(0, 0.6))
  points(model_values, err_cv[,1], col="blue", pch=16)
  lines(model_values, err_cv[,1], col="blue")
  arrows(model_values, err_cv[,1]-err_cv[,2], model_values, err_cv[,1]+err_cv[,2],
        length=0.1, angle=90, code=3)
  #dev.off()
}
```



- 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)
```

- 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.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")
}
```

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")
```

```
## 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
```