Project 3 - Example Main Script

Yuting Ma, Tian Zheng with updates by Cindy Rush

February 2, 2018

In your final Project 2 repo, there should be an R markdown file called `main.Rmd` that organizes **all computational steps** for evaluating your proposed image classification framework.

This file is meant to be a template for evaluating models used for image analysis (and could be generalized for any predictive modeling). You should update it according to your models/codes but your final document should have precisely the same structure.

```
if(!require("EBImage")){
  source("https://bioconductor.org/biocLite.R")
  biocLite("EBImage")
}
```

```
## Loading required package: EBImage
```

```
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
```

```
library("EBImage")
library("gbm")
```

Step 0: Specify directories.

We first set the working directory to the location of this .Rmd file (it should be in a project folder). Then we specify our training and testing data. If you do not have an independent test set, you need to create your own testing data by random subsampling from the training data (we haven't done this here), and in order to obain reproducible results, you should use `set.seed()` whenever randomization is used.

```
setwd("Spring2018/Project_Starter_Codes/Project2-PredictiveModelling/doc")
# Replace the above with your own path or manually set it in RStudio to where this rmd file is located.
```

Now we provide directories for teh raw images. Here we assume the training set and test set are in different subfolders.

```
experiment_dir <- "../data/zipcode/" # This will be modified for different data sets.
img_train_dir  <- paste(experiment_dir, "train/", sep="")
img_test_dir   <- paste(experiment_dir, "test/", sep="")
```

Step 1: Set up controls for model evaluation.

In this step, we have a set of controls for the model evaluation. The code in the rest of the document runs (or not) according to our choices here.

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

```
run.cv            <- TRUE # run cross-validation on the training set
K                 <- 5    # 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. In this example, we use GBM with different `depth`. In the following code chunk, we list, in a vector, setups (in this case, `depth`) corresponding to model parameters that we will compare. In your project, you will likely be comparing different classifiers than the one considered here and therefore will need to expand this code. You could, for example, assign them numerical IDs and labels specific to your project.

```
model_values <- seq(3, 11, 2)
model_labels <- paste("GBM with depth =", model_values)
```

Step 2: Import training images class labels.

For the example of zip code digits, we code digit 9 as "1" and digit 7 as "0" for binary classification.

```
label_train <- read.table(paste(experiment_dir, "train_label.txt", sep = ""), header = F)
label_train <- as.numeric(unlist(label_train) == "9")
```

Step 3: Construct visual features

For this simple example, we use the row averages of raw pixel values as the visual features. Note that this strategy **only** works for images with the same number of rows. For some other image datasets, the feature function should be able to handle heterogeneous input images. Save the constructed features to the output subfolder.

`feature.R` should be the wrapper for all your feature engineering functions and options. The function `feature( )` should have options that correspond to different scenarios for your project and produces an R object that contains features that are required by all the models you are going to evaluate later.

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

tm_feature_train <- NA
if(run.feature.train){
  tm_feature_train <- system.time(dat_train <- feature(img_train_dir, "train",
                                                       data_name = "zip", export = TRUE))
}

tm_feature_test <- NA
if(run.feature.test){
  tm_feature_test <- system.time(dat_test <- feature(img_test_dir, "test",
```

```
                                                    data_name = "zip", export = TRUE))
}

#save(dat_train, file = "../output/feature_train.RData")
#save(dat_test, file = "../output/feature_test.RData")
```

Step 4: Train a classification model with training images (and the visual features constructed above)

Call the train model and test model from library.

`train.R` and `test.R` should be wrappers for all your model training steps and your classification/prediction steps. + `train.R` + Input: a path that points to the training set features. + Input: an R object of training sample labels. + Output: an RData file that contains trained classifiers in the forms of R objects: models/settings/links to external trained configurations. + `test.R` + Input: a path that points to the test set features. + Input: an R object that contains a trained classifier. + Output: an R object of class label predictions on the test set. If there are multiple classifiers under evaluation, there should be multiple sets of label predictions.

```
source("../lib/train.R")
source("../lib/test.R")
```

Model selection with cross-validation

- Do model selection. Here we choose between model parameters, in this case the interaction depth for GBM.

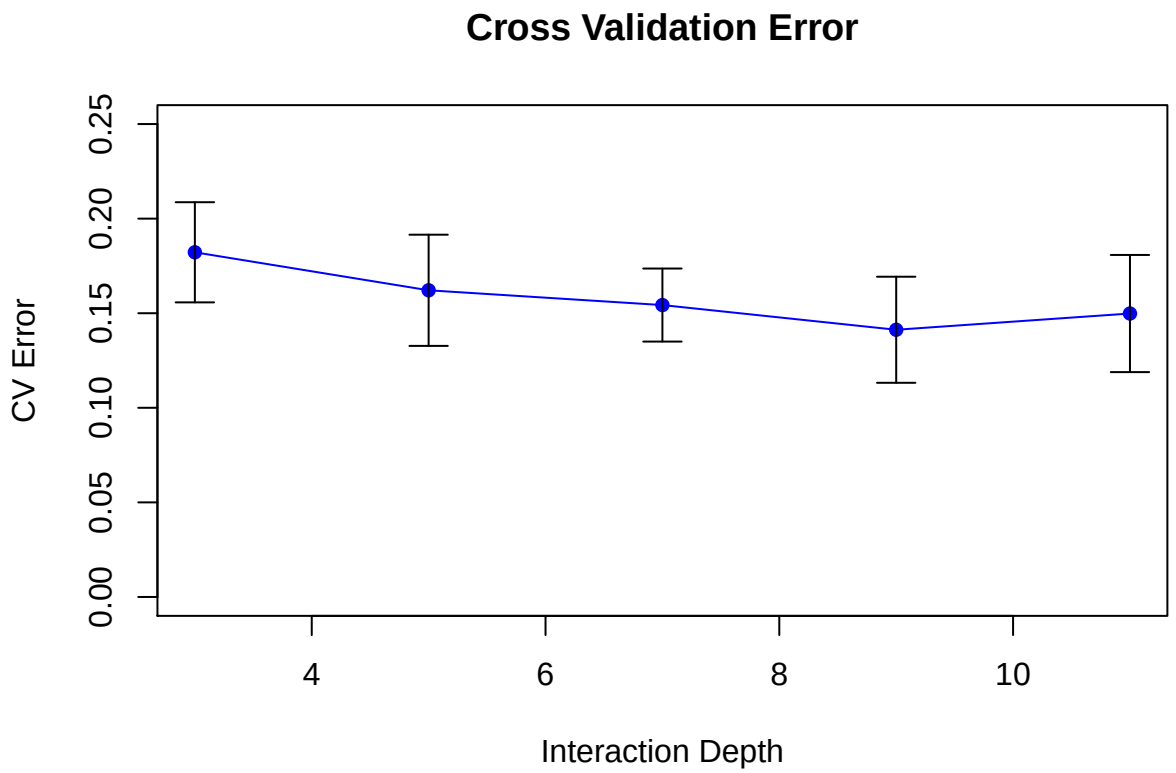
```
source("../lib/cross_validation.R")

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/err_cv.RData")
}
```

```
## k= 1
## k= 2
## k= 3
## k= 4
## k= 5
```

- Visualize the cross-validation results.

```
if(run.cv){
  load("../output/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, 0.25))
  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 (in this case, 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 = "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/fit_train.RData")
```

Step 5: Make prediction

Feed the final training model with the test data. (Note that for this to truly be 'test' data, it should have had no part of the training procedure used above.)

```
tm_test <- NA
if(run.test){
  load(file = paste0("../output/feature_", "zip", "_", "test", ".RData"))
  load(file = "../output/fit_train.RData")
  tm_test <- system.time(pred_test <- test(fit_train, dat_test))
  save(pred_test, file = "../output/pred_test.RData")
}
```

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 constructing training features=", tm_feature_train[1], "s \n")
```

```
## Time for constructing training features= 0.51 s
```

```
cat("Time for constructing testing features=", tm_feature_test[1], "s \n")
```

```
## Time for constructing testing features= 0.118 s
```

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

```
## Time for training model= 3.664 s
```

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

```
## Time for making prediction= 0.021 s
```