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CS 498 AM1

Homework 1

Part 1:

1A: 0.75817

1B: 0.74575

1D: 0.77386

```r
# 1. Find p(y) aka prior
prior_0 <- 0
count_0 <- 0
for (i in 1:n_row) {
  if (lbs[i] == 0)
    count_0 <- count_0 + 1
}
prior_0 <- count_0/n_row
prior_1 <- 1 - prior_0

# 2. Find p(x|y) aka likelyhood
normal_param_0 <- matrix(ncol = n_col - 1, nrow = 2)
normal_param_1 <- matrix(ncol = n_col - 1, nrow = 2)
for (i in 1:(n_col - 1) ) {
  feat_0 <- matrix(ncol = 1, nrow = count_0)
  feat_1 <- matrix(ncol = 1, nrow = n_row - count_0)
  n_0 <- 1
  n_1 <- 1
  for (j in 1:n_row) {
    entry = d_train[j, i]
    if (lbs[j] == 0) {
      feat_0[n_0] <- entry
      n_0 <- n_0 + 1
    } else {
      feat_1[n_1] <- entry
      n_1 <- n_1 + 1
    }
  }
  normal_param_0[1, i] <- mean(feat_0)
  normal_param_0[2, i] <- sqrt(var(feat_0))
  normal_param_1[1, i] <- mean(feat_1)
  normal_param_1[2, i] <- sqrt(var(feat_1))
}

# 3.Test
n_row_test <- n_row_total - n_row
predicts <- matrix(ncol = 1, nrow = n_row_test)
for (i in 1:n_row_test) {
  prob_0 <- log(prior_0)
  prob_1 <- log(prior_1)
  for (j in 1:(n_col - 1)) {
    entry <- d_test[i, j]
    prob_0 <- prob_0 + dnorm(entry, mean = normal_param_0[1, j], sd = normal_param_0[2, j], log = TRUE)
    prob_1 <- prob_1 + dnorm(entry, mean = normal_param_1[1, j], sd = normal_param_1[2, j], log = TRUE)
  }
  if (prob_1 > prob_0) {
    predicts[i, 1] <- 1
  } else {
    predicts[i, 1] <- 0
  }
```

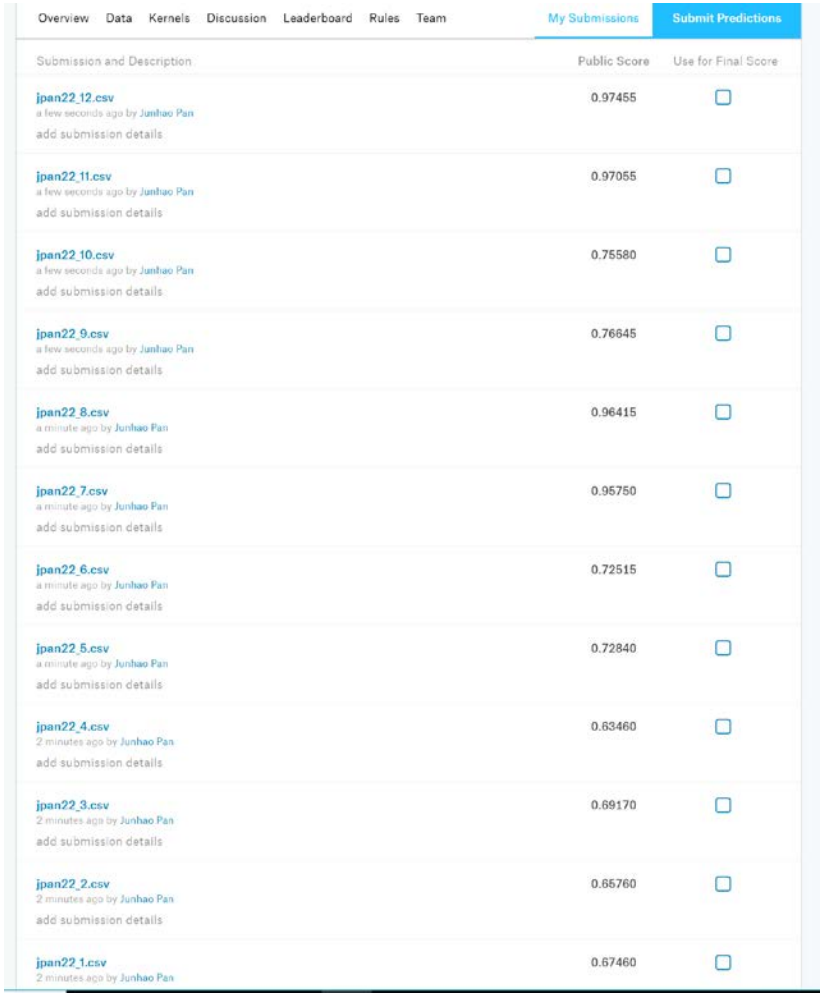
P1A

P1B is roughly the same with substitution of NA

```r
library(caret)

d_train_all <- read.csv("pima-indians-diabetes.csv")
n_col_total <- ncol(d_train_all)
n_row_total <- nrow(d_train_all)

accuracy <- matrix(ncol = 1, nrow = 10)

for (t in 1:10) {

  train_idx <- createDataPartition(d_train_all$X1, p = 0.8, list = FALSE, times = 1)

  d_test <- d_train_all[-train_idx,]
  d_train <- d_train_all[train_idx,]

  n_col <- ncol(d_train)
  n_row <- nrow(d_train)

  lbs <- d_train[, 9]

  svm <- svmlight(d_train[, 1:8], d_train[, 9], pathsvm = ".")
  pred <- predict(svm, d_test[, 1:8])

  correct_count <- 0
  for (i in 1:n_row_test) {
    if (pred[1] == d_test[i, 9])
      correct_count <- correct_count + 1
  }
  accuracy[t, 1] <- correct_count/n_row_test
}

final_accuracy = mean(accuracy)
```

P1D with SVM Light

Gaussian untouched	0.6746
Gaussian stretched	0.6576
Bernoulli untouched	0.6917
Bernoulli stretched	0.6346
10 trees 4 depth untouched	0.7284
10 trees 4 depth stretched	0.72515
10 trees 16 depth untouched	0.9575
10 trees 16 depth stretched	0.96415
32 trees 4 depth untouched	0.76645
32 trees 4 depth stretched	0.7558
32 trees 16 depth untouched	0.97055
32 trees 16 depth stretched	0.97455



```r
library(caret)
library(EBImage)

thres <- 200

d_test_all <- read.csv("test.csv", header = FALSE)
d_train_all <- read.csv("train.csv")
d_val_all <- read.csv("val.csv")

source("util.R")

d_train_fit_all <- read.csv("d_train_fit.csv")
d_val_fit_all <- read.csv("d_val_fit.csv")
d_test_fit_all <- read.csv("d_test_fit.csv")

d_train_fit_all <- d_train_fit_all[, 2:ncol(d_train_fit_all)]
d_val_fit_all <- d_val_fit_all[, 2:ncol(d_val_fit_all)]
d_test_fit_all <- d_test_fit_all[, 2:ncol(d_test_fit_all)]


d_train <- d_train_all[, 2:ncol(d_train_all)]
d_val <- d_val_all[,]
d_test <- d_test_all[,]

d_train_fit <- d_train_fit_all[,]
d_val_fit <- d_val_fit_all[,]
d_test_fit <- d_test_fit_all[,]
```

```r
rb_train <- function(data_t, data_v, data_tt, n_tree, n_level, code) {

    x <- data_t[, 2:ncol(data_t)]
    y <- as.factor(data_t[, 1])
    rb <- Rborist(x, y, nTree = n_tree, nLevel = n_level)
    z <- data_v[, 2:ncol(data_v)]
    true <- as.factor(data_v[, 1])
    pred <- predict(rb, z)
    pred_tt <- predict(rb, data_tt)
    y_pred <- pred$yPred - 1
    y_pred_tt <- pred_tt$yPred - 1
    # y_pred_r <- round(y_pred, digits = 0)

    test_csv <- matrix(y_pred_tt, nrow = length(y_pred_tt), ncol = 1)
    file_str <- paste("jpan22_", code, ".csv", sep = "")
    write.csv(test_csv, file = file_str)

    correct <- 0
    confusion <- matrix(0L, nrow = 10, ncol = 10)
    for (i in 1:length(true)) {
        lb <- data_v[i, 1]
        pd <- y_pred[i]
        confusion[lb, pd] <- confusion[lb, pd] + 1
        if (pd == lb) {
            correct <- correct + 1
        }
    }
    accuracy <- correct/length(true)

    ret <- list(confusion, accuracy)
    return (ret)
}
```

```r
pred <- function (data, priors, params, thres) {
    means <- matrix(unlist(params[1]), ncol = ncol(data), byrow = TRUE)
    stddv <- matrix(unlist(params[2]), ncol = ncol(data), byrow = TRUE)
    bern1 <- matrix(unlist(params[3]), ncol = ncol(data), byrow = TRUE)

    predicts_norm <- matrix(0L, nrow = nrow(data), ncol = 1)
    predicts_bern <- matrix(0L, nrow = nrow(data), ncol = 1)
    for (i in 1:nrow(data)) {
        probs_norm <- matrix(0L, nrow = 10, ncol = 1)
        probs_bern <- matrix(0L, nrow = 10, ncol = 1)
        for (j in 1:10) {
            probs_norm[j] <- log(priors[j])
            probs_bern[j] <- log(priors[j])
        }
        for (j in 3:ncol(data)) {
            entry <- data[i, j-1]
            for (k in 1:10) {
                if (means[k, j] != 0)
                    probs_norm[k] <- probs_norm[k] + dnorm(entry, mean = means[k, j], sd = stddv[k, j], log = TRUE)
                if (entry > thres)
                    probs_bern[k] <- probs_bern[k] + log(bern1[k, j])
            }
        }
        idx_norm <- arrayInd(which.max(probs_norm), dim(probs_norm))
        idx_bern <- arrayInd(which.max(probs_bern), dim(probs_bern))
        predicts_norm[i] <- idx_norm[, 1] - 1
        predicts_bern[i] <- idx_bern[, 1] - 1
    }
    ret = list(predicts_norm, predicts_bern)
    return (ret)
}
```

```r
train <- function(data, counts, thres) {
    n_row <- nrow(data)
    n_col <- ncol(data)

    means <- matrix(0L, nrow = 10, ncol = n_col)
    stddv <- matrix(0L, nrow = 10, ncol = n_col)
    bern1 <- matrix(0L, nrow = 10, ncol = n_col)

    for (i in 3:n_col) {
        # First dimension for normal, second for bern
        feat_0 <- matrix(0L, nrow = counts[1], ncol = 2)
        feat_1 <- matrix(0L, nrow = counts[2], ncol = 2)
        feat_2 <- matrix(0L, nrow = counts[3], ncol = 2)
        feat_3 <- matrix(0L, nrow = counts[4], ncol = 2)
        feat_4 <- matrix(0L, nrow = counts[5], ncol = 2)
        feat_5 <- matrix(0L, nrow = counts[6], ncol = 2)
        feat_6 <- matrix(0L, nrow = counts[7], ncol = 2)
        feat_7 <- matrix(0L, nrow = counts[8], ncol = 2)
        feat_8 <- matrix(0L, nrow = counts[9], ncol = 2)
        feat_9 <- matrix(0L, nrow = counts[10], ncol = 2)
        nums <- matrix(0L, nrow = 10, ncol = 1)
        for (j in 1:n_row) {
            entry = data[j, i]
            # if (entry > thres)
            #     entry = entry + 500
            if (lbs[j] == 0) {
                nums[1] <- nums[1] + 1
                n <- nums[1]
                if (entry > thres) {
                    feat_0[n, 1] <- entry
                    feat_0[n, 2] <- 1
                }
            } else if (lbs[j] == 1) {
                nums[2] <- nums[2] + 1
                n <- nums[2]
                if (entry > thres) {
                    feat_1[n, 1] <- entry
                    feat_1[n, 2] <- 1
                }
            } else if (lbs[j] == 2) {
                nums[3] <- nums[3] + 1
                n <- nums[3]
                if (entry > thres) {
                    feat_2[n, 1] <- entry
                    feat_2[n, 2] <- 1
                }
            } else if (lbs[j] == 3) {
                nums[4] <- nums[4] + 1
                n <- nums[4]
                if (entry > thres) {
```