580Project

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```r
# include packages
library(fastDummies)
library(caret)
```

```
## Loading required package: ggplot2

## Loading required package: lattice
```

```r
library(ggplot2)
library(ggrepel)
library(corrplot)
```

```
## corrplot 0.95 loaded
```

```r
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v lubridate 1.9.4     v tibble    3.2.1
## v purrr     1.0.4     v tidyr     1.3.1

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## x purrr::lift()   masks caret::lift()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```r
library(randomForest)
```

```
## randomForest 4.7-1.2
## Type rfNews() to see new features/changes/bug fixes.
##
## Attaching package: 'randomForest'
##
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
##
## The following object is masked from 'package:ggplot2':
##
##     margin
```

```
library(nnet)
library(rpart)
library(rpart.plot)
library(xgboost)
```

```
##
## Attaching package: 'xgboost'
##
## The following object is masked from 'package:dplyr':
##
##     slice
```

```
library(MASS)
```

```
##
## Attaching package: 'MASS'
##
## The following object is masked from 'package:dplyr':
##
##     select
```

```
library(pROC)
```

```
## Type 'citation("pROC")' for a citation.
##
## Attaching package: 'pROC'
##
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```
library(vcdExtra)
```

```
## Loading required package: vcd
## Loading required package: grid
## Loading required package: gnm
##
## Attaching package: 'gnm'
##
## The following object is masked from 'package:lattice':
##
##     barley
##
##
## Attaching package: 'vcdExtra'
##
```

```
## The following object is masked from 'package:dplyr':
##
##     summarise
```

```r
library(vcd)
library(rpart)
library(rattle)
```

```
## Loading required package: bitops
## Rattle: A free graphical interface for data science with R.
## Version 5.5.1 Copyright (c) 2006-2021 Togaware Pty Ltd.
## Type 'rattle()' to shake, rattle, and roll your data.
##
## Attaching package: 'rattle'
##
## The following object is masked from 'package:xgboost':
##
##     xgboost
##
## The following object is masked from 'package:randomForest':
##
##     importance
```

```r
library(partykit)
```

```
## Loading required package: libcoin
## Loading required package: mvtnorm
##
## Attaching package: 'mvtnorm'
##
## The following object is masked from 'package:gnm':
##
##     Mult
```

```r
library(NeuralNetTools) # for neural net plots
```

```r
# read train.data
train.data <- read.csv("train.csv",
                       header = T,
                       na.strings = " ?")

# remove NA
train.data <- na.omit(train.data)

# remove empty space in front of each char cell
# factorize char columns

# remove fnlwgt
train.data <- subset(train.data, select = -c(fnlwgt))

train.data[] <- lapply(train.data,
                       function(x) {
```

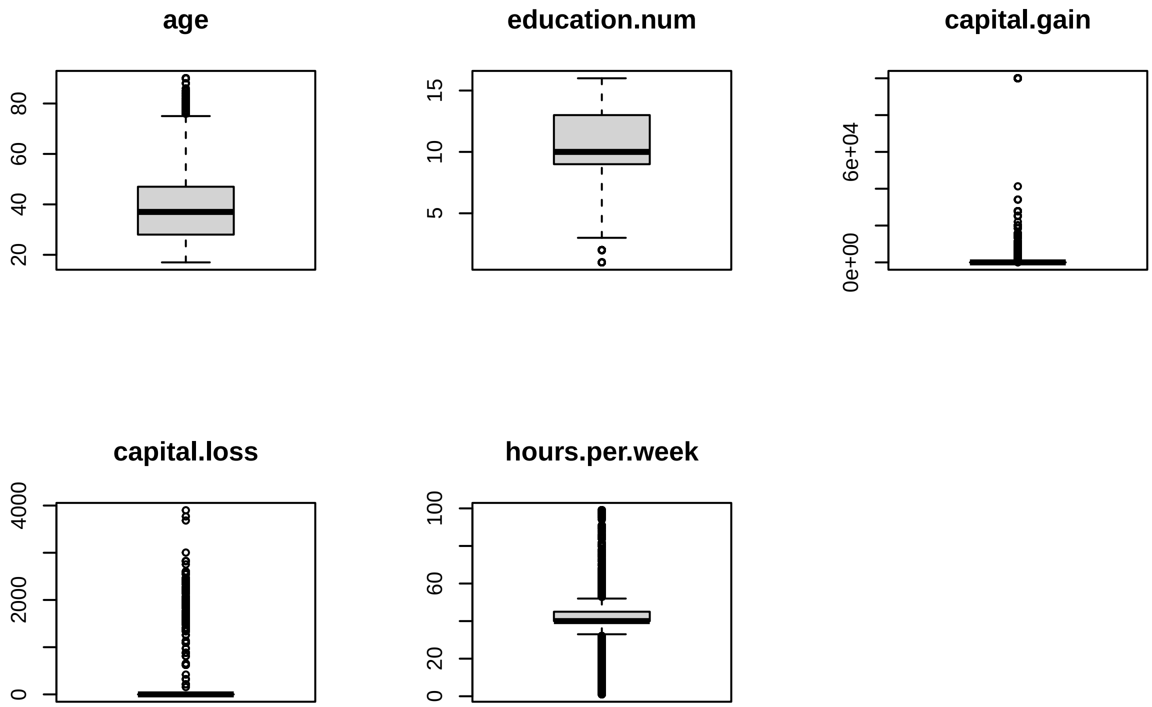
```
                          if(is.character(x))
                            as.factor(trimws(x))
                          else x
                        })

# View(train.data)
# str(train.data)
```

```
# read test data
test.data <-read.csv("test.csv",
                     header = T,
                     na.strings = " ?")

# remove NA
test.data <- na.omit(test.data)

# remove fnlwgt
test.data <- subset(test.data, select = -c(fnlwgt))

# remove empty space in front of each char cell
test.data[] <- lapply(test.data,
                       function(x) {
                         if(is.character(x))
                           as.factor(trimws(x))
                         else x
                       })
test.data$native.country <- factor(test.data$native.country,
                                    levels = levels(train.data$native.country))

# View(test.data)
# str(test.data)
```

variable selection, identify important features

outliers

```
# Start with box plots to visualize which variables have outliers
numeric_vars <- names(train.data)[sapply(train.data, is.numeric)]
numeric_data <- train.data[, numeric_vars]

par(mfrow = c(2,3))
for(n in numeric_vars) {
  boxplot(train.data[[n]], main = n)
}

par(mfrow = c(1,1))
```



Capital gain and loss are highly skewed variables with many 0s, treat as binary?

Age has a decent amount of observations >=80, far from the average

Education.num seems clean

fnlwgt might not have any interpretable meaning, drop?

hours.per.week is centered around 40, but with considerable values <20 and >60, what is reasonable?

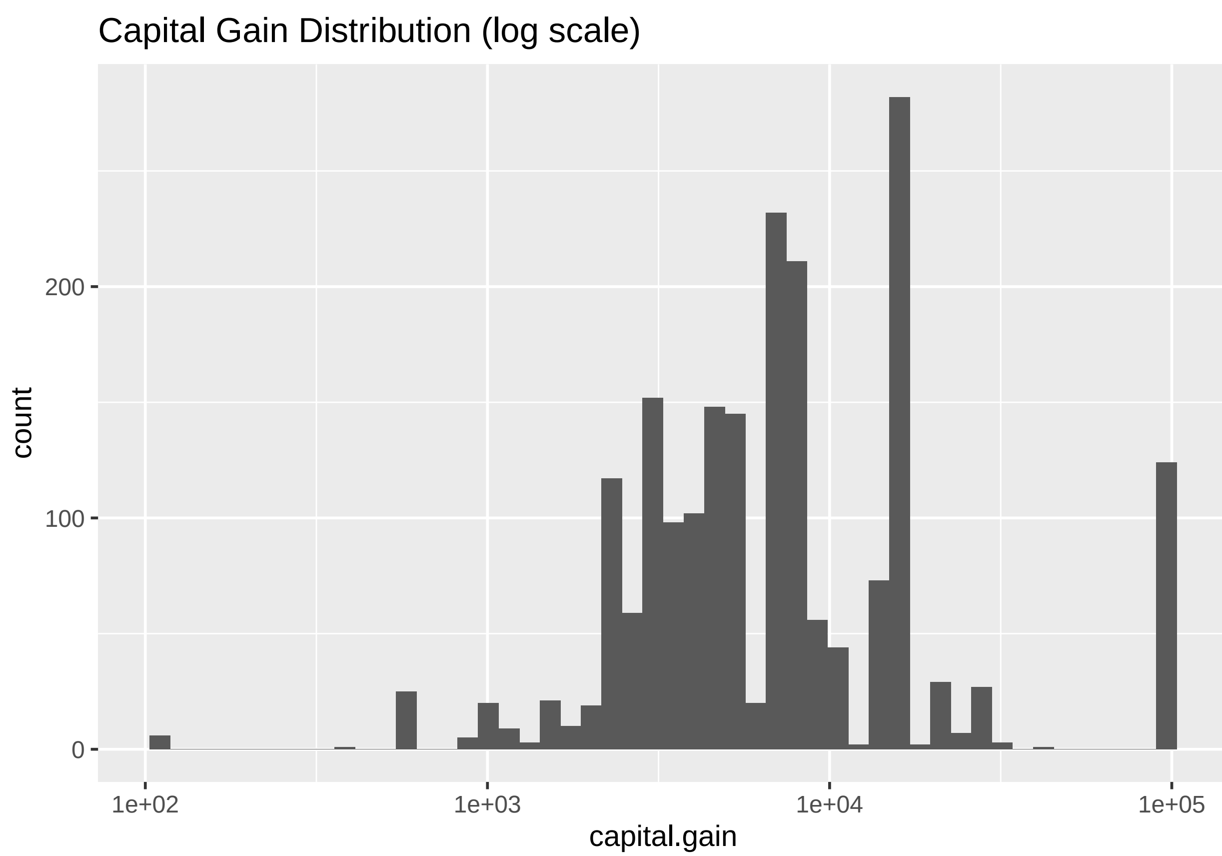
```r
# z-score method

z.scores <- scale(numeric_data)

outlier.indices <- which(apply(abs(z.scores), 1, function(x) any(x>3)))
outliers <- numeric_data[outlier.indices, ]
str(outliers)
```

```
## 'data.frame':    1809 obs. of  5 variables:
##  $ age           : int  37 43 39 45 47 79 48 20 24 45 ...
##  $ education.num : int  10 7 9 13 15 10 16 10 9 11 ...
##  $ capital.gain  : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ capital.loss  : int  0 2042 0 1408 1902 0 1902 1719 1762 1564 ...
##  $ hours.per.week: int  80 40 80 40 60 20 60 28 40 40 ...
```

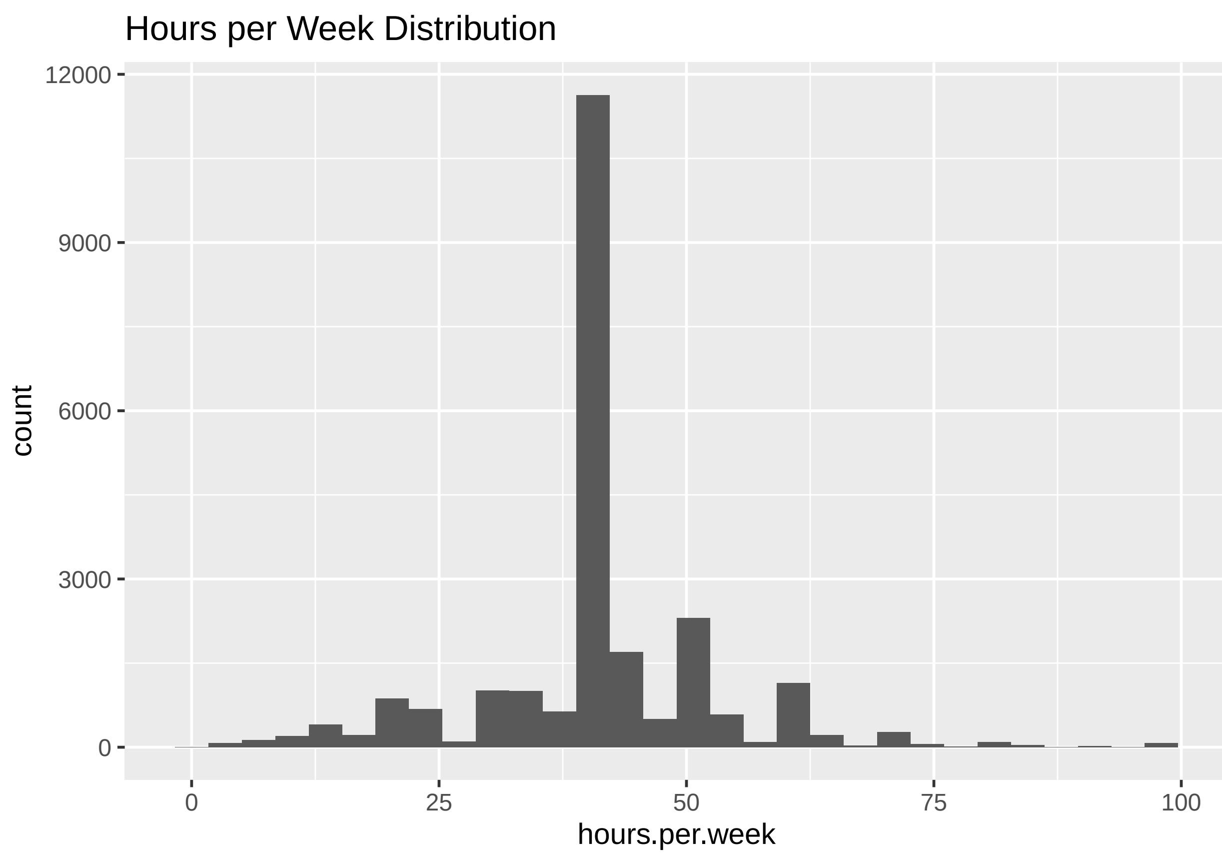
```r
rm(z.scores, outlier.indices, outliers)
```

```r
# look at distributions of some vars

ggplot(train.data, aes(x = capital.gain)) +
  geom_histogram(bins = 50) +
  scale_x_log10() +
  ggtitle("Capital Gain Distribution (log scale)")
```

```
## Warning in scale_x_log10(): log-10 transformation introduced infinite values.

## Warning: Removed 22094 rows containing non-finite outside the scale range
## (`stat_bin()`).
```




```r
ggplot(train.data, aes(x = hours.per.week)) +
  geom_histogram(bins = 30) +
  ggtitle("Hours per Week Distribution")
```



If keeping capital.gain, maybe remove values <1000 or >50000 Consider trimming hours per week of values <20 or >60, there are not many

Multivariate outliers

```
numeric_data <- na.omit(train.data[, numeric_vars])

dists <- mahalanobis(numeric_data, colMeans(numeric_data), cov(numeric_data))
threshold <- qchisq(0.975, df = length(numeric_vars))

mv.outliers <- numeric_data[which(dists > threshold), ]
str(mv.outliers)
```

```
## 'data.frame':    1773 obs. of  5 variables:
##  $ age           : int  43 47 79 48 20 24 45 64 27 51 ...
##  $ education.num : int  7 15 10 16 10 9 11 7 9 10 ...
##  $ capital.gain  : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ capital.loss  : int  2042 1902 0 1902 1719 1762 1564 2179 1980 1977 ...
##  $ hours.per.week: int  40 60 20 60 28 40 40 40 40 40 ...
```

```
rm(numeric_data, dists, threshold, mv.outliers)
```

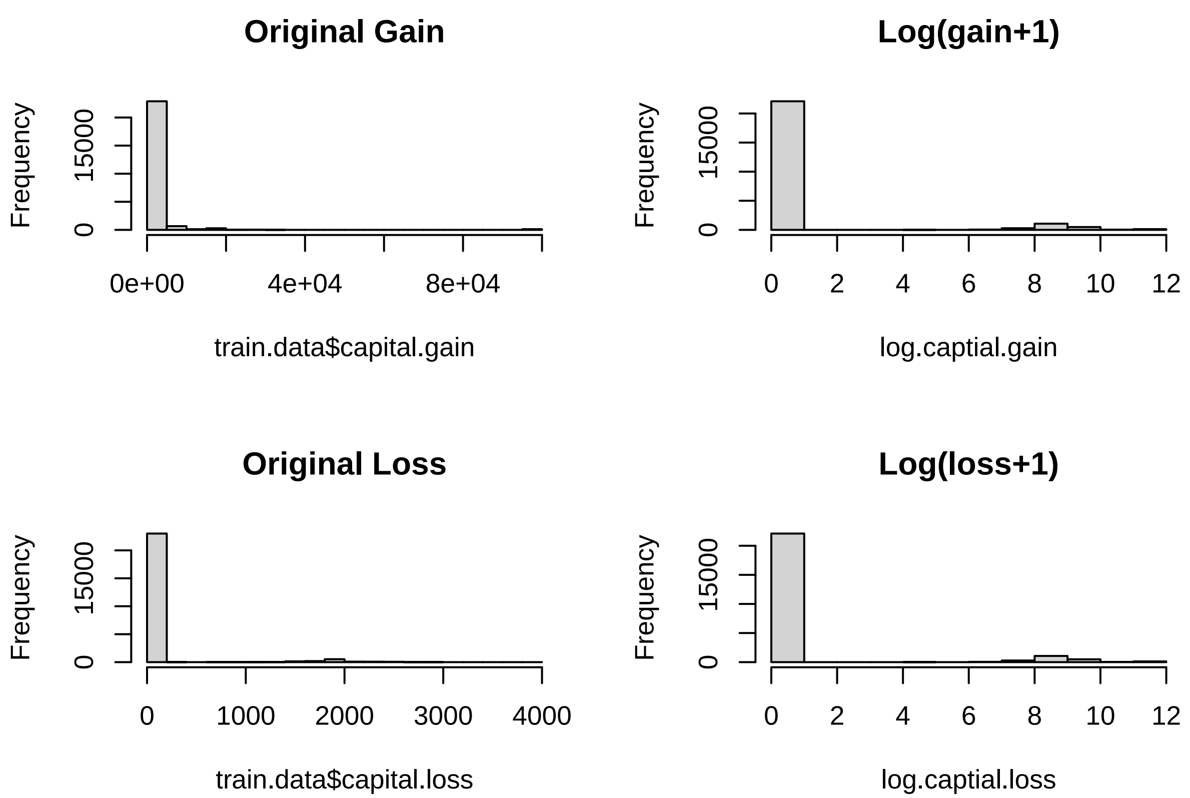
IQR method to remove outliers for column hours.per.week –> lowered model accuracy, withdraw

```
# Q1 <- quantile(train.data$hours.per.week, 0.25, na.rm = TRUE)
# Q3 <- quantile(train.data$hours.per.week, 0.75, na.rm = TRUE)
```

```r
# IQR <- Q3 - Q1

# lower <- Q1 - 1.5 * IQR
# upper <- Q3 + 1.5 * IQR

# train.data <- train.data[train.data$hours.per.week >= lower & train.data$hours.per.week <= upper, ]
```

Testing log transform – Doesn't seem to help

```r
log.captial.gain <- log(train.data$capital.gain + 1)
log.captial.loss <- log(train.data$capital.gain + 1)

par(mfrow = c(2,2))
hist(train.data$capital.gain, main = "Original Gain")
hist(log.captial.gain, main = "Log(gain+1)")
hist(train.data$capital.loss, main = "Original Loss")
hist(log.captial.loss, main = "Log(loss+1)")
```




```r
par(mfrow = c(1,1))

rm(log.captial.gain, log.captial.loss)
```

Use binary flags instead

```r
has.gain <- as.factor(ifelse(train.data$capital.gain > 0, 1, 0))
has.loss <- as.factor(ifelse(train.data$capital.loss > 0, 1, 0))

test.has.gain <- as.factor(ifelse(test.data$capital.gain > 0, 1, 0))
test.has.loss <- as.factor(ifelse(test.data$capital.loss > 0, 1, 0))
```

correlation analysis

```r
# Subset only numeric predictors
numeric_vars <- names(train.data)[sapply(train.data, is.numeric)]
numeric_data <- train.data[, numeric_vars]

# Compute correlation matrix
cor_matrix <- cor(numeric_data)
cor_matrix
```

```
##                       age education.num capital.gain capital.loss
## age            1.00000000    0.03781210   0.08064292   0.05948878
## education.num  0.03781210    1.00000000   0.12437130   0.08487161
## capital.gain   0.08064292    0.12437130   1.00000000  -0.03230727
## capital.loss   0.05948878    0.08487161  -0.03230727   1.00000000
## hours.per.week 0.09908376    0.14973533   0.08135083   0.05005427
##                hours.per.week
## age                0.09908376
## education.num      0.14973533
## capital.gain       0.08135083
## capital.loss       0.05005427
## hours.per.week     1.00000000
```

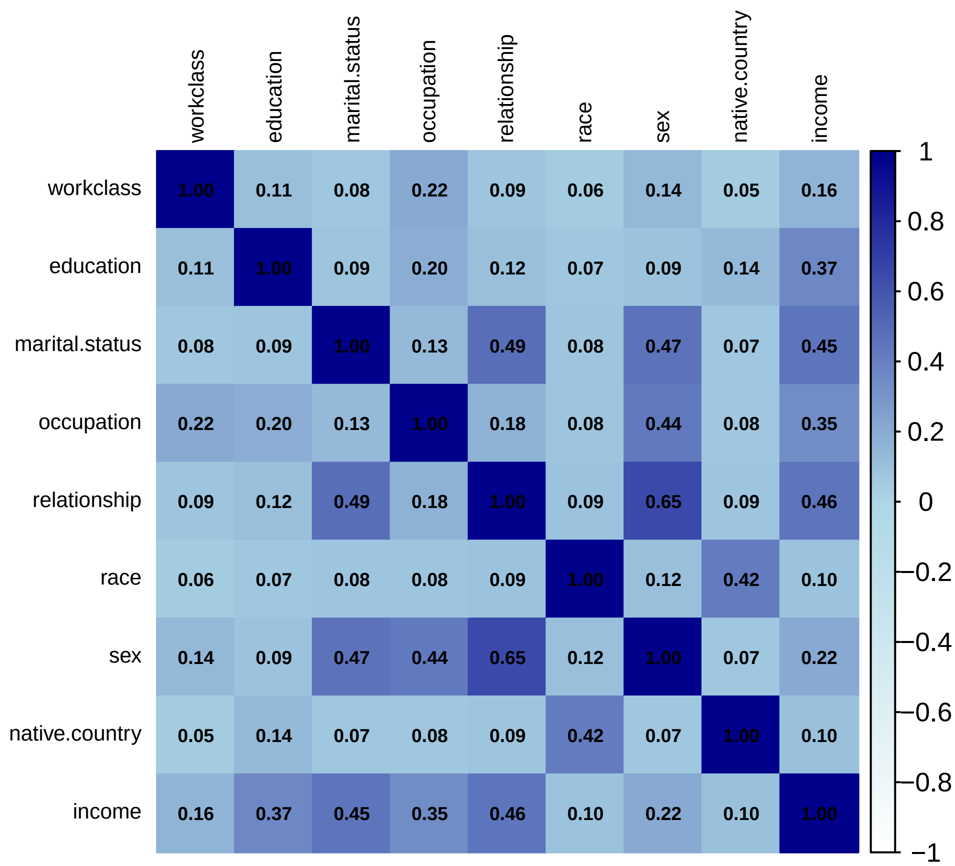
```r
# Display heat map
# Display heat map
corrplot(cor_matrix,
         method = "color",
         col = colorRampPalette(c("white", "lightpink", "deeppink4"))(10),
         tl.col = "black",
         tl.cex = 0.9,
         addCoef.col = "black",
         number.cex = 0.7)
```


```r
# no strong linear dependencies among numeric predictors (all |r| < 0.15),
# so no further variable removal due to multicollinearity is needed

rm(numeric_vars, numeric_data, cor_matrix)
```

Correlation Matrix for Categorical Variables (just testing this out):

```r
# Select categorical columns
cat_vars <- train.data[, sapply(train.data, is.factor)]

# Function to compute Cramér's V matrix
cramers_v_matrix <- function(df) {
  vars <- names(df)
  mat <- matrix(NA, ncol = length(vars), nrow = length(vars),
                dimnames = list(vars, vars))
  for (i in vars) {
    for (j in vars) {
      tbl <- table(df[[i]], df[[j]])
      mat[i, j] <- assocstats(tbl)$cramer
    }
  }
  return(as.data.frame(mat))
}

cramers_v_df <- cramers_v_matrix(cat_vars)
```

```r
cramer_mat <- as.matrix(cramers_v_df)
corrplot(cramer_mat,
         method = "color",
         col = colorRampPalette(c("white", "lightblue", "darkblue"))(200),
         type = "full",
         tl.col = "black",
         tl.cex = 0.7,
         na.label = " ",
         addCoef.col = "black",
         number.cex = 0.6)
```




```r
rm(cat_vars, cramers_v_df, cramer_mat)
```

Variance Thresholding

```r
# get all numeric features
numeric.data <- train.data[, sapply(train.data, is.numeric)]

# look for numbers of columns with variance near 0
nzv <- nearZeroVar(numeric.data)

# display low variance columns
head(numeric.data[, nzv], 2)
```

```
##   capital.gain capital.loss
```

```
## 1             0             0
## 2             0             0
```

```
### NOTE: ### 'capital.gain'& 'capital.loss' are mostly 0's but have some very large values.
# They are classic long-tailed features, KEEP them for now.
```

tree-based models (CART, RF, XGBoost) –> dataset 1

```
# -> use education(categorical, factorized)
# -> no scaling
# -> no dummy encoding

### NOTE: ### Tree-based models can natively handle categorical variables (factors).
# So keep 'education' factor var, remove 'education.num'.
# No scaling or dummy encoding is needed for these models.

train.data.1 <- subset(train.data, select = -c(education.num))
test.data.1 <- subset(test.data, select = -c(education.num))
# identical(names(train.data.1), names(test.data.1))        # true
```

Linear/Logistic/NN/KNN –> dataset 2

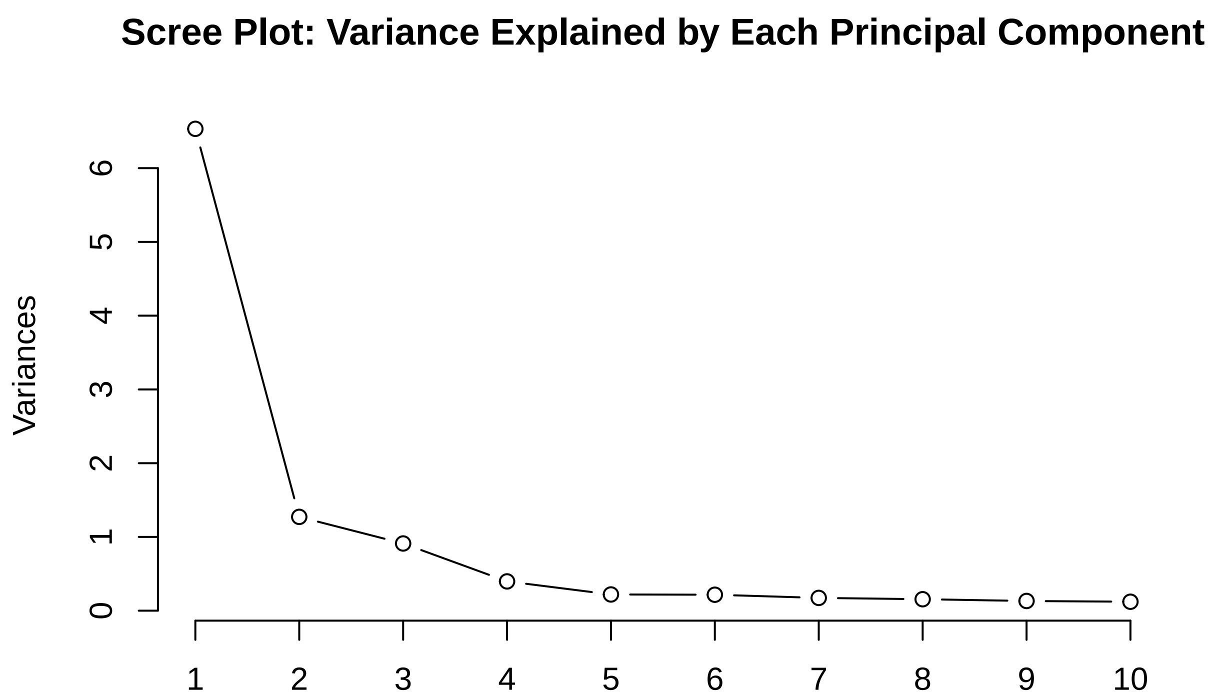
```
# -> use education.num(numeric, original)
# -> scaling
# -> dummy encode all categorical variables


### preprocess train.data
train.data.2 <- subset(train.data, select = -c(education))
train.data.2$capital.gain <- has.gain
train.data.2$capital.loss <- has.loss

# obtain numeric & categorical column names
num_cols <- names(train.data.2)[sapply(train.data.2, is.numeric)]
num_cols <- num_cols[num_cols != "education.num"]
### education.num is treated as an ordinal categorical variable (1-16), so we do not scale it.

cat_cols <- names(train.data.2)[sapply(train.data.2, is.factor)]
cat_cols <- setdiff(cat_cols, "income")  # exclude target

# scale numeric data
scaled_data <- scale(train.data.2[, num_cols])
train.data.2[, num_cols] <- scaled_data

# obtain means & stds for KNN
means <- attr(scaled_data, "scaled:center")
sds   <- attr(scaled_data, "scaled:scale")

# dummy encode all categorical variables
### note: it is normal that there are more columns being created ###
```

```r
train.data.2 <- dummy_cols(
  train.data.2,
  select_columns = cat_cols,
  remove_first_dummy = TRUE,
  remove_selected_columns = TRUE
)

# ------------------------------------------------------------------------------

### preprocess test.data in the same way
test.data.2 <- subset(test.data, select = -c(education))

# num_cols are the same

test.data.2$capital.gain <- test.has.gain
test.data.2$capital.loss <- test.has.loss

# scale test data using means & stds from the train data
test.data.2[, num_cols] <- sweep(test.data.2[, num_cols], 2, means, "-")
test.data.2[, num_cols] <- sweep(test.data.2[, num_cols], 2, sds, "/")

# dummy encode all categorical variables
test.data.2 <- dummy_cols(
  test.data.2,
  select_columns = cat_cols,
  remove_first_dummy = TRUE,
  remove_selected_columns = TRUE
)

# check missing columns
# setdiff(names(train.data.2), names(test.data.2))

### NOTE: ### level "Holand-Netherlands" appeared in the training set but
# not in the test set, so dummy encoding did not create this column in the test data.
# We manually add the missing dummy variable and set it to 0 for all rows.
test.data.2[["native.country_Holand-Netherlands"]] <- 0


### NOTE: ### check if column names of train and test datasets are identical.
# model prediction requires the exact same column order, so align test.data
# columns to match train.data.

# identical(names(train.data.2), names(test.data.2))      # false
test.data.2 <- test.data.2[, names(train.data.2)]

# ------------------------------------------------------------------------------

# testing: variance thresholding for preprocessed train.data.2

# get all numeric features
numeric.data <- train.data.2[, sapply(train.data.2, is.numeric)]

# look for numbers of columns with variance near 0
```

```r
nzv <- nearZeroVar(numeric.data)

# obtain low variance columns, except for "capital.loss", "capital.gain"
low.var.cols <- names(numeric.data[, nzv])
low.var.cols <- setdiff(low.var.cols, c("capital.loss", "capital.gain"))
# low.var.cols

# remove them from train.data.2 & test.data.2
train.data.2 <- train.data.2[, !(names(train.data.2) %in% low.var.cols)]
test.data.2 <- test.data.2[, !(names(test.data.2) %in% low.var.cols)]

# check if columns are in identical order
# identical(names(train.data.2), names(test.data.2))    --> true

# ------------------------------------------------------------------------------

# remove temp variables
rm(scaled_data, low.var.cols, nzv)
```

PCA test for variable importance, only on train.data.2

```r
# reason: all vars are numeric, either dummy or continuous, and is standardized
# for building Linear/Logistic/NN/KNN models

# obtain new numeric features (after all the processes above)
numeric.data <- train.data.2[, sapply(train.data.2, is.numeric)]

# get pca result
pca_result <- prcomp(numeric.data, center = TRUE, scale. = FALSE)
# summary(pca_result)

# ------------------------------------------------------------------------------

plot(pca_result, type = "l", main = "Scree Plot: Variance Explained by Each Principal Component")
```




```
# first principal component (PC1) explains a significantly larger portion of the variance
```

```
# check variable loading of PC 1,2,3, 4
# they explain most of the variance before the scree plot flattens.
loadings <- round(pca_result$rotation[, 1:4], 3)

# get all vars with loadings < 0.01 (low contribution)
low.contrib.vars <- rownames(loadings)[apply(abs(loadings) < 0.01, 1, all)]

cat("Low-contribution variables (loading < 0.01 across PC1-PC4):\n")
```

```
## Low-contribution variables (loading < 0.01 across PC1-PC4):
```

```
print(low.contrib.vars)
```

```
## character(0)
```

```
# remove vars with low contribution (loading near 0)
# to reduce dimensionality without significant information loss
train.data.2 <- train.data.2[, !(names(train.data.2) %in% low.contrib.vars)]
test.data.2  <- test.data.2[, !(names(test.data.2) %in% low.contrib.vars)]

# ------------------------------------------------------------------------------
```

```r
# check if columns are in identical order
identical(names(train.data.2), names(test.data.2))
```

```
## [1] TRUE
```

```r
dim(train.data.2)
```

```
## [1] 24147    24
```

```r
dim(test.data.2)
```

```
## [1] 6015   24
```

```r
# --------------------------------------------------------------------------------
# new pca result
pca_result <- prcomp(train.data.2[, sapply(train.data.2, is.numeric)],
                     center = TRUE,
                     scale. = FALSE)


# remove temp variables
rm(numeric.data, loadings, low.contrib.vars)
```

Optional: PCA datasets for modeling(if implementing)

```r
# -> remove all categorical variables
# -> scaling
# train.data.3 <- train.data[, sapply(train.data, is.numeric)]
# train.data.3 <- scale(train.data.3)
```

*** remember to optimize model parameters***

model 1: multiple linear model

```r
### while testing, do not only run this code chunk,
###clear the environment & run from the beginning

# Convert income column to **numeric**
train.data.2$income <- as.numeric(ifelse(train.data.2$income == ">50K",1,0))
test.data.2$income <- as.numeric(ifelse(test.data.2$income == ">50K",1,0))

# --------------------------------------------------------------------------------

#fit mlr
mlr_model <- lm(income ~ ., data = train.data.2)
#prediction
pred_mlr <- predict(mlr_model, test.data.2)
```

```r
# find y and y_hat
y <- test.data.2$income
yhat <- pred_mlr

# ------------------------------------------------------------------------------
# Predict class
yhat_binary <- ifelse(pred_mlr > 0.5, 1, 0)

# MSE
mse_mlr <- mean((y - yhat)^2)
print(paste("MLR MSE:", mse_mlr))
```

```
## [1] "MLR MSE: 0.122564581358856"
```

```r
# Accuracy
accuracy_mlr <- mean(y == yhat_binary)
print(paste("MLR Accuracy:", accuracy_mlr))
```

```
## [1] "MLR Accuracy: 0.828927680798005"
```

```r
cat("\n")
```

```r
# ------------------------------------------------------------------------------
cm_mlr <- confusionMatrix(factor(yhat_binary), factor(y), positive = "1")
cm_mlr
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction    0    1
##          0 4210  711
##          1  318  776
##
##                Accuracy : 0.8289
##                  95% CI : (0.8192, 0.8384)
##     No Information Rate : 0.7528
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.4956
##
##  Mcnemar's Test P-Value : < 2.2e-16
##
##             Sensitivity : 0.5219
##             Specificity : 0.9298
##          Pos Pred Value : 0.7093
##          Neg Pred Value : 0.8555
##              Prevalence : 0.2472
##          Detection Rate : 0.1290
##    Detection Prevalence : 0.1819
##       Balanced Accuracy : 0.7258
##
##        'Positive' Class : 1
##
```

```r
# remove temp variables
rm(y, yhat, yhat_binary, mse_mlr, accuracy_mlr, pred_mlr)
```

model 2: logistic model

```r
# build full model
lr_model0 <- glm(income~. , data = train.data.2, family = binomial)
# summary(lr_model0)
# race, sex_Male, occupation_Craft-repair seemed to be not significant

# step-wise variable selection, both direction
suppressWarnings({
  lr_model <- stepAIC(lr_model0, k = log(nrow(train.data.2)), trace = 0, direction = "both")
})
summary(lr_model)
```

```
##
## Call:
## glm(formula = income ~ age + education.num + hours.per.week +
##     `workclass_Self-emp-not-inc` + `marital.status_Married-civ-spouse` +
##     `marital.status_Never-married` + `occupation_Craft-repair` +
##     `occupation_Exec-managerial` + `occupation_Other-service` +
##     `occupation_Prof-specialty` + occupation_Sales + `relationship_Own-child` +
##     relationship_Unmarried + capital.gain_1 + `native.country_United-States`,
##     family = binomial, data = train.data.2)
##
## Coefficients:
##                                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)                         -6.36559    0.14854 -42.856  < 2e-16 ***
## age                                  0.34803    0.02291  15.191  < 2e-16 ***
## education.num                        0.31585    0.01008  31.333  < 2e-16 ***
## hours.per.week                       0.33426    0.02086  16.024  < 2e-16 ***
## `workclass_Self-emp-not-inc`        -0.53817    0.06528  -8.244  < 2e-16 ***
## `marital.status_Married-civ-spouse`  1.99706    0.06765  29.519  < 2e-16 ***
## `marital.status_Never-married`      -0.40956    0.08638  -4.741 2.13e-06 ***
## `occupation_Craft-repair`            0.20050    0.05933   3.380 0.000726 ***
## `occupation_Exec-managerial`         0.92491    0.05833  15.857  < 2e-16 ***
## `occupation_Other-service`          -0.76667    0.11448  -6.697 2.12e-11 ***
## `occupation_Prof-specialty`          0.59283    0.06476   9.154  < 2e-16 ***
## occupation_Sales                     0.44105    0.06390   6.902 5.13e-12 ***
## `relationship_Own-child`            -1.14661    0.15152  -7.567 3.81e-14 ***
## relationship_Unmarried              -0.46675    0.10433  -4.474 7.68e-06 ***
## capital.gain_1                       1.54901    0.06218  24.910  < 2e-16 ***
## `native.country_United-States`       0.31710    0.07620   4.161 3.16e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 27123  on 24146  degrees of freedom
## Residual deviance: 16931  on 24131  degrees of freedom
```

```
## AIC: 16963
##
## Number of Fisher Scoring iterations: 7
```

```
# predict test data, obtain confusion matrix
probs <- lr_model %>% predict(newdata = test.data.2, type = "response")
pred.income <- ifelse(probs > 0.5,  1, 0)

confusionMatrix(factor(pred.income), factor(test.data.2$income), positive = "1")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction    0    1
##          0 4173  657
##          1  355  830
##
##                Accuracy : 0.8318
##                  95% CI : (0.8221, 0.8411)
##     No Information Rate : 0.7528
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.5149
##
##  Mcnemar's Test P-Value : < 2.2e-16
##
##             Sensitivity : 0.5582
##             Specificity : 0.9216
##          Pos Pred Value : 0.7004
##          Neg Pred Value : 0.8640
##              Prevalence : 0.2472
##          Detection Rate : 0.1380
##    Detection Prevalence : 0.1970
##       Balanced Accuracy : 0.7399
##
##        'Positive' Class : 1
##
```

```
y_true <- test.data.2$income
y_pred <- pred.income
y_prob <- probs

# AUC
roc_obj <- roc(y_true, y_prob)
```

```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```

```
auc_val <- auc(roc_obj)
cat("AUC:", auc_val, "\n")
```

```
## AUC: 0.882659
```

```r
# precision
precision <- posPredValue(factor(y_pred), factor(y_true), positive = "1")
cat("precision:", precision, "\n")
```

```
## precision: 0.7004219
```

```r
# F1 score
recall <- sensitivity(factor(y_pred), factor(y_true), positive = "1")
cat("recall/sensitivity:", recall, "\n")
```

```
## recall/sensitivity: 0.5581708
```

```r
f1_score <- 2 * precision * recall / (precision + recall)
cat("F1 Score:", f1_score, "\n")
```

```
## F1 Score: 0.6212575
```

```r
rm(y_true, y_pred, y_prob, roc_obj, probs, pred.income)
```

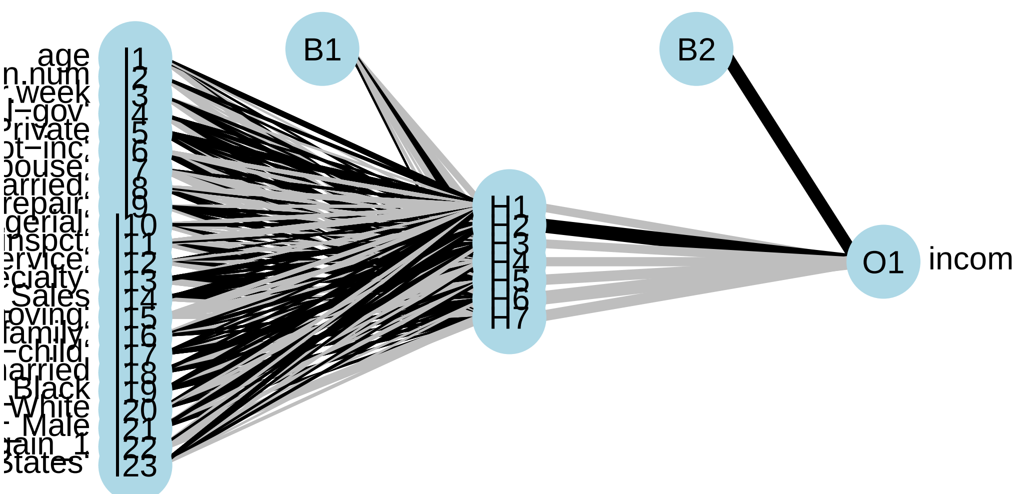
model 3: NN model

After fitting neural network model with reduced features, I found that full model without any feature selection has the highest accuracy.

```r
#***NOTE*** We commented this chunk out after getting the bestTune results since
# it takes at least 30 min to run while knitting


# Find the best parameter for size and decay
# grid_full <- expand.grid(size = c(5, 7, 9, 11), decay = c(0.0001, 0.001, 0.01, 0.05, 0.1, 0.2))

# convert training target to factor
# train.data.2$income <- as.factor(train.data.2$income)
#
#
# set.seed(123)
# nn_model_full_tuned <- train(
#   income ~ .,
#   data = train.data.2,
#   method = "nnet",
#   tuneGrid = grid_full,
#   trControl = trainControl(method = "cv", number = 10),
#   maxit = 300,
#   trace = FALSE
# )

# View best parameters
# nn_model_full_tuned$bestTune
```

```r
# nn_model_full_tuned$results[order(-nn_model_full_tuned$results$Accuracy), ]

# size = 7
# decay = 0.2
```

```r
# Neural Network Full Model (includes all predictors) from nnet package
train.data.2$income <- factor(train.data.2$income, levels = c("0", "1"))
test.data.2$income <- factor(test.data.2$income, levels = c("0", "1"))

# build model
set.seed(123)
nn_model_full <- nnet(
  income ~ .,
  data = train.data.2,
  size = 7,
  decay = 0.2,
  maxit = 300,
  trace = FALSE
)
# plot full model
plotnet(nn_model_full)
```




```r
# predictions
nn_pred_full <- predict(nn_model_full, newdata = test.data.2, type = "class")
nn_pred_full <- factor(nn_pred_full, levels = c("0", "1"))
```

```r
# confusion matrix
cm_full <- confusionMatrix(data = nn_pred_full,reference = test.data.2$income,
            positive = "1")
cm_full
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction    0    1
##          0 4163  600
##          1  365  887
##
##                Accuracy : 0.8396
##                  95% CI : (0.83, 0.8488)
##     No Information Rate : 0.7528
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.5448
##
##  Mcnemar's Test P-Value : 4.969e-14
##
##             Sensitivity : 0.5965
##             Specificity : 0.9194
##          Pos Pred Value : 0.7085
##          Neg Pred Value : 0.8740
##              Prevalence : 0.2472
##          Detection Rate : 0.1475
##    Detection Prevalence : 0.2081
##       Balanced Accuracy : 0.7579
##
##        'Positive' Class : 1
##
```

```r
# Accuracy : 0.8396
# Sensitivity : 0.5965
# Specificity : 0.9194
```

```r
# Neural Network from caret package
# set.seed(123)

# build model
# nn_model_full <- train(
#   income ~ .,
#   data = train.data.2,
#   method = "nnet",
#   tuneGrid = data.frame(size = 7, decay = 0.2),
#   maxit = 300,
#   trace = FALSE
# )

# predictions
# nn_pred_full <- predict(nn_model_full, newdata = test.data.2, type = "raw")
```

```r
# nn_pred_full <- factor(nn_pred_full, levels = c("0", "1"))

# confusion matrix
# cm_full <- confusionMatrix(
#   data = nn_pred_full,
#   reference = test.data.2$income,
#   positive = "1"
# )
# cm_full

# Accuracy : 0.8394
# Sensitivity : 0.6005
# Specificity : 0.9178
```

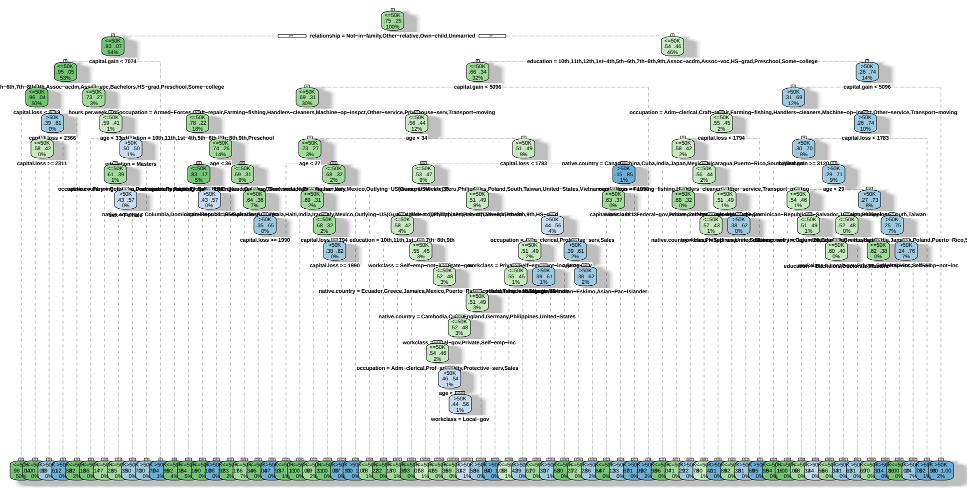
model 4: CART model

```r
# feature selection
cart_model <- rpart(income ~ ., data = train.data.1, control=rpart.control(cp=0), method = "class")
importance <- as.data.frame(cart_model$variable.importance)
print(importance)
```

```
##                cart_model$variable.importance
## relationship                        1931.53200
## marital.status                      1868.25395
## education                           1011.32541
## occupation                           938.38895
## capital.gain                         906.68851
## age                                  852.52286
## sex                                  648.35841
## hours.per.week                       499.97596
## capital.loss                         258.30455
## workclass                            156.18319
## native.country                       138.78359
## race                                  38.63108
```

```r
# prune
# printcp(modelCART)

best_cp <- cart_model$cptable[which.min(cart_model$cptable[,"xerror"]),"CP"]
pruned_model <- prune(cart_model, cp = best_cp)

fancyRpartPlot(pruned_model)
```

```
## Warning: labs do not fit even at cex 0.15, there may be some overplotting
```



Rattle 2025−Apr−25 13:18:08 zianshang

```r
# helper function - compare model performances
comparemodels <- function(model1, model2, test_data, target_col) {
  preds1 <- predict(model1, test_data, type = "class")
  preds2 <- predict(model2, test_data, type = "class")

  actuals <- test_data[[target_col]]

  cm1 <- confusionMatrix(preds1, actuals, positive = levels(actuals)[2])
  cm2 <- confusionMatrix(preds2, actuals, positive = levels(actuals)[2])

  metrics <- data.frame(
    Model = c("Model 1", "Model 2"),
    Accuracy = c(cm1$overall["Accuracy"], cm2$overall["Accuracy"]),
    Sensitivity = c(cm1$byClass["Sensitivity"], cm2$byClass["Sensitivity"]),
    Specificity = c(cm1$byClass["Specificity"], cm2$byClass["Specificity"])
  )
  return(metrics)
}

comparemodels(cart_model, pruned_model, test.data.1, 'income')
```

```
##     Model  Accuracy Sensitivity Specificity
## 1 Model 1 0.8412303   0.6274378   0.9114399
## 2 Model 2 0.8543641   0.5938130   0.9399293
```

```r
# pruned model is better, now lets remove unimportant variables
test.data.1a <- subset(test.data.1, select = -c(race, native.country))
train.data.1a <- subset(train.data.1, select = -c(race, native.country))

cart_model_a <- rpart(income ~ ., data = train.data.1a, control=rpart.control(cp=0), method = "class")
best_cp <- cart_model_a$cptable[which.min(cart_model$cptable[,"xerror"]),"CP"]
pruned_model_a <- prune(cart_model_a, cp = best_cp)
comparemodels(cart_model_a, pruned_model_a, test.data.1, 'income')
```

```
##     Model  Accuracy Sensitivity Specificity
## 1 Model 1 0.8433915   0.6314728   0.9129859
## 2 Model 2 0.8568579   0.5965030   0.9423587
```

```r
# -----------------------------------------------------------------------------

preds <- predict(pruned_model_a, test.data.1, type = "class")
confusionMatrix(preds, test.data.1$income, positive = ">50K")
```

```
## Confusion Matrix and Statistics
##
##             Reference
## Prediction <=50K >50K
##      <=50K  4267  600
##      >50K    261  887
##
##                Accuracy : 0.8569
##                  95% CI : (0.8478, 0.8656)
##     No Information Rate : 0.7528
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.5835
##
##  Mcnemar's Test P-Value : < 2.2e-16
##
##             Sensitivity : 0.5965
##             Specificity : 0.9424
##          Pos Pred Value : 0.7726
##          Neg Pred Value : 0.8767
##              Prevalence : 0.2472
##          Detection Rate : 0.1475
##    Detection Prevalence : 0.1909
##       Balanced Accuracy : 0.7694
##
##        'Positive' Class : >50K
##
```

```r
# -----------------------------------------------------------------------------

rm(test.data.1a, train.data.1a)
```

model 5: random forest model

```
# Fitting Random Forest Model before feature selection:
set.seed(123)
rf_model <- randomForest(income ~ ., data = train.data.1, importance = TRUE, ntree = 500)

# Predictions on training data
test_preds <- predict(rf_model, newdata = test.data.1)

# Confusion matrix
cm <- confusionMatrix(test_preds, test.data.1$income, positive = ">50K")
cm
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction <=50K >50K
##      <=50K  4207  504
##      >50K    321  983
##
##                Accuracy : 0.8628
##                  95% CI : (0.8539, 0.8714)
##     No Information Rate : 0.7528
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.6156
##
##  Mcnemar's Test P-Value : 2.352e-10
##
##             Sensitivity : 0.6611
##             Specificity : 0.9291
##          Pos Pred Value : 0.7538
##          Neg Pred Value : 0.8930
##              Prevalence : 0.2472
##          Detection Rate : 0.1634
##    Detection Prevalence : 0.2168
##       Balanced Accuracy : 0.7951
##
##        'Positive' Class : >50K
##
```

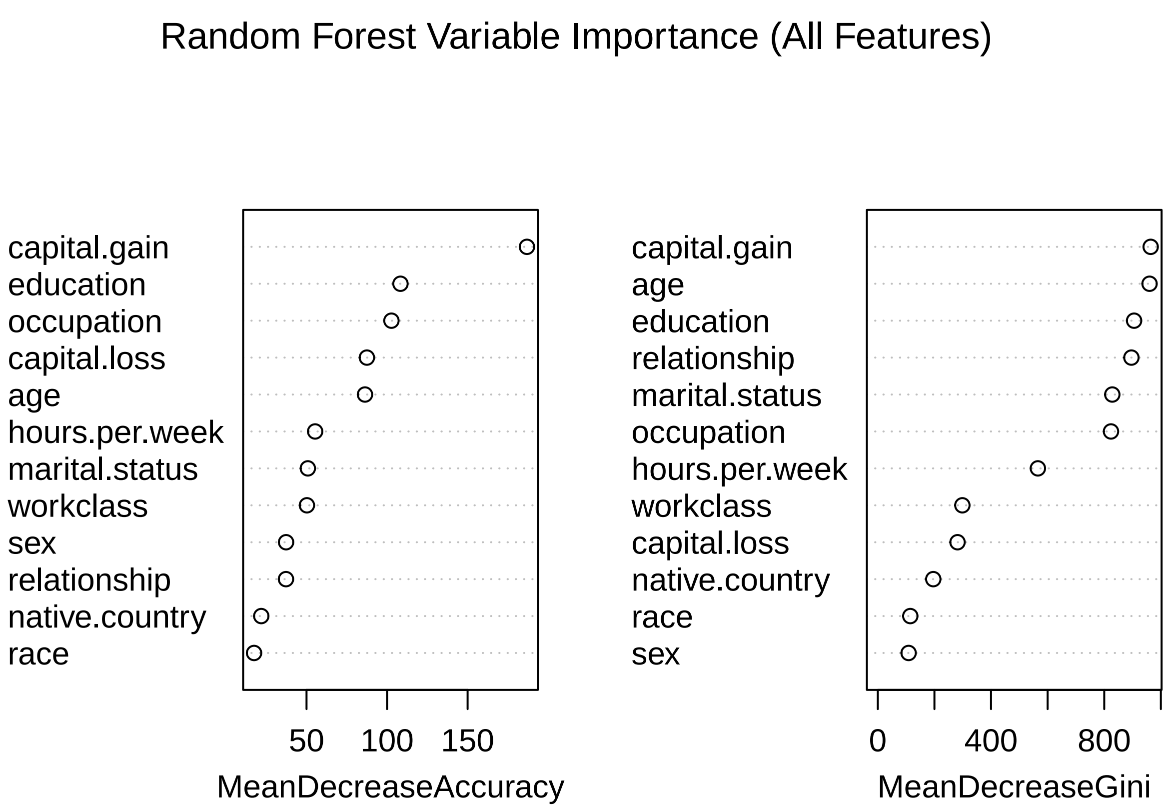
Feature importance scores using random forest:

```
# Extract importance scores
importance_df <- as.data.frame(rf_model$importance)

# Add variable names as columns
importance_df$Variable <- rownames(importance_df)

# Reorder columns
importance_df <- importance_df[, c("Variable", "MeanDecreaseAccuracy", "MeanDecreaseGini")]
```

```r
# Sort by MeanDecreaseGini (most commonly used)
importance_df <- importance_df[order(-importance_df$MeanDecreaseGini), ]
importance_df
```

```
##                     Variable MeanDecreaseAccuracy MeanDecreaseGini
## capital.gain     capital.gain          0.038796788         964.0763
## age                       age          0.018801182         960.0870
## education           education          0.029168280         905.4104
## relationship     relationship          0.041906098         895.9086
## marital.status marital.status          0.047587706         828.3922
## occupation         occupation          0.027308810         823.8177
## hours.per.week hours.per.week          0.009858466         565.5229
## workclass           workclass          0.005912831         298.7715
## capital.loss     capital.loss          0.008538429         281.7051
## native.country native.country          0.001699666         196.0093
## race                     race          0.001136251         114.8469
## sex                       sex          0.006968736         108.8781
```

```r
# Plot variable importance
varImpPlot(rf_model,
           main = "Random Forest Variable Importance (All Features)")
```



Random Forest with Reduced Features: –> don't need anymore

```
# train.rf.reduced <- subset(train.data.1, select = -c(sex))
#
# set.seed(123)
# rf_reduced <- randomForest(income ~ .,
#                            data = train.rf.reduced,
#                           ntree = 500,
#                           importance = TRUE)
#
# rf_reduced$importance
#
# # Plot variable importance
# varImpPlot(rf_reduced,
#            main = "Random Forest Variable Importance (Reduced Features)")
```

Confusion Matrix for RF w/ reduced features:

```
# test.rf.reduced <- subset(test.data.1, select = -c(sex))
#
# preds_reduced <- predict(rf_reduced, newdata = test.rf.reduced)
#
# cm <- confusionMatrix(preds_reduced, test.data.1$income, positive = ">50K")
# cm

# Accuracy : 0.862
# Sensitivity : 0.6604
# Specificity : 0.9282
```

model 6: extra model, XgBoost classification

```


# if testing this code chunk, run train.data.1 first

train.data.1$income <- factor(ifelse(train.data.1$income == ">50K", 1, 0))
test.data.1$income <- factor(ifelse(test.data.1$income == ">50K", 1, 0))

# Convert to Matrix
train.dummy <- model.matrix(income ~ . - 1, data = train.data.1)
test.dummy <- model.matrix(income ~ . - 1, data = test.data.1)

# Extract Label
train.label <- as.numeric(as.character(train.data.1$income))
test.label <- as.numeric(as.character(test.data.1$income))

# Convert to xgboost matrix format
dtrain <- xgb.DMatrix(data = train.dummy, label = train.label)
dtest <- xgb.DMatrix(data = test.dummy, label = test.label)

# Set XGBoost parameters for binary classification
params <- list(
  booster = "gbtree",
  objective = "binary:logistic",
```

```r
  eval_metric = "auc",
  eta = 0.1,
  max_depth = 6,
  subsample = 0.8,
  colsample_bytree = 0.8
)

# ---------------------------------------------------------------------------

# Train
set.seed(123)
xgb_model <- xgb.train(
  params = params,
  data = dtrain,
  nrounds = 100,
  watchlist = list(train = dtrain, test = dtest),
  verbose = 0,
  early_stopping_rounds = 10
)

# ---------------------------------------------------------------------------

# Prediction
xgb_probs <- predict(xgb_model, dtest)
# Convert probabilities to binary
xgb_pred <- ifelse(xgb_probs > 0.5, 1, 0)


# Confusion Matrix
cm_xgb <- confusionMatrix(factor(xgb_pred), factor(test.label), positive = "1")
cm_xgb
```

Without Dealing with Imbalance

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction    0    1
##          0 4275  537
##          1  253  950
##
##                Accuracy : 0.8687
##                  95% CI : (0.8599, 0.8771)
##     No Information Rate : 0.7528
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.6229
##
##  Mcnemar's Test P-Value : < 2.2e-16
##
##             Sensitivity : 0.6389
##             Specificity : 0.9441
##          Pos Pred Value : 0.7897
```

```
##          Neg Pred Value : 0.8884
##              Prevalence : 0.2472
##          Detection Rate : 0.1579
##    Detection Prevalence : 0.2000
##       Balanced Accuracy : 0.7915
##
##        'Positive' Class : 1
##
```

```r
# check for data imbalance
table(train.data$income)
```

With Dealing with Imbalance

```
##
## <=50K  >50K
## 18126  6021
```

```r
prop.table(table(train.data$income))
```

```
##
##     <=50K      >50K
## 0.7506523 0.2493477
```

```r
# somewhat imbalanced

### ***if model predicts income>50K poorly, try handle imbalance***
```

```r
# if testing this code chunk, run train.data.1 first

# Set XGBoost parameters for binary classification

# Calculate the weight
neg <- sum(train.label == 0)
pos <- sum(train.label == 1)
scale_weight <- neg / pos

params <- list(
  booster = "gbtree",
  objective = "binary:logistic",
  eval_metric = "auc",
  eta = 0.1,
  max_depth = 6,
  subsample = 0.8,
  colsample_bytree = 0.8,
  scale_pos_weight = scale_weight
)

# ------------------------------------------------------------------------------
```

```r
# Train
set.seed(123)
xgb_model <- xgb.train(
  params = params,
  data = dtrain,
  nrounds = 100,
  watchlist = list(train = dtrain, test = dtest),
  verbose = 0,
  early_stopping_rounds = 10
)

# -------------------------------------------------------------------------------

# Prediction
xgb_probs <- predict(xgb_model, dtest)
# Convert probabilities to binary
xgb_pred <- ifelse(xgb_probs > 0.5, 1, 0)


# Confusion Matrix
cm_xgb <- confusionMatrix(factor(xgb_pred), factor(test.label), positive = "1")
cm_xgb
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction    0    1
##          0 3681  212
##          1  847 1275
##
##                Accuracy : 0.8239
##                  95% CI : (0.8141, 0.8335)
##     No Information Rate : 0.7528
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.5863
##
##  Mcnemar's Test P-Value : < 2.2e-16
##
##             Sensitivity : 0.8574
##             Specificity : 0.8129
##          Pos Pred Value : 0.6008
##          Neg Pred Value : 0.9455
##              Prevalence : 0.2472
##          Detection Rate : 0.2120
##    Detection Prevalence : 0.3528
##       Balanced Accuracy : 0.8352
##
##        'Positive' Class : 1
##
```

```r
# Remove Temporary Variables
rm(
```

```
  train.dummy,
  test.dummy,
  train.label,
  test.label,
  dtrain,
  dtest,
  params,
  xgb_probs,
  xgb_pred,
  neg,
  pos,
  scale_weight
  )
```