Santander customer transaction prediction

Submitted by

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Contents

Chapter 1

Introduction

1.1 Problem Statement

At Santander, mission is to help people and businesses prosper. We are always looking for ways to help our customers understand their financial health and identify which products and services might help them achieve their monetary goals.

Our data science team is continually challenging our machine learning algorithms, working with the global data science community to make sure we can more accurately identify new ways to solve our most common challenge, binary classification problems such as: is a customer satisfied? Will a customer buy this product? Can a customer pay this loan?

In this challenge, we need to identify which customers will make a specific transaction in the future, irrespective of the amount of money transacted.

1.2 Data

In this project, our task is to build classification models which would be used to predict which customers will make a specific transaction in the future. Given below is a sample of the Santander customer transaction dataset:

TABLE 1.1: TRAIN DATASET (COLUMNS:1-202)

Out[2]:

	ID_code	target	var_0	var_1	var_2	var_3	var_4	var_5	var_6	var_7	...	var_190	var_191	var_192	var_193	var_194	var_195	var_196	var
0	train_0	0	8.9255	-6.7863	11.9081	5.0930	11.4607	-9.2834	5.1187	18.6266	...	4.4354	3.9642	3.1364	1.6910	18.5227	-2.3978	7.8784	8
1	train_1	0	11.5006	-4.1473	13.8588	5.3890	12.3622	7.0433	5.6208	16.5338	...	7.6421	7.7214	2.5837	10.9516	15.4305	2.0339	8.1267	8
2	train_2	0	8.6093	-2.7457	12.0805	7.8928	10.5825	-9.0837	6.9427	14.6155	...	2.9057	9.7905	1.6704	1.6858	21.6042	3.1417	-6.5213	8
3	train_3	0	11.0604	-2.1518	8.9522	7.1957	12.5846	-1.8361	5.8428	14.9250	...	4.4666	4.7433	0.7178	1.4214	23.0347	-1.2706	-2.9275	10
4	train_4	0	9.8369	-1.4834	12.8746	6.6375	12.2772	2.4486	5.9405	19.2514	...	-1.4905	9.5214	-0.1508	9.1942	13.2876	-1.5121	3.9267	9

5 rows × 202 columns

Table 1.2: Test Dataset (Columns: 1-201)

Out[9]:

	ID_code	var_0	var_1	var_2	var_3	var_4	var_5	var_6	var_7	var_8	...	var_190	var_191	var_192	var_193	var_194	var_195	var_196
0	test_0	11.0656	7.7798	12.9536	9.4292	11.4327	-2.3805	5.8493	18.2675	2.1337	...	-2.1556	11.8495	-1.4300	2.4508	13.7112	2.4669	4.3654
1	test_1	8.5304	1.2543	11.3047	5.1858	9.1974	-4.0117	6.0196	18.6316	-4.4131	...	10.6165	8.8349	0.9403	10.1282	15.5765	0.4773	-1.4852
2	test_2	5.4827	-10.3581	10.1407	7.0479	10.2628	9.8052	4.8950	20.2537	1.5233	...	-0.7484	10.9935	1.9803	2.1800	12.9813	2.1281	-7.1086
3	test_3	8.5374	-1.3222	12.0220	6.5749	8.8458	3.1744	4.9397	20.5660	3.3755	...	9.5702	9.0766	1.6580	3.5813	15.1874	3.1656	3.9567
4	test_4	11.7058	-0.1327	14.1295	7.7506	9.1035	-8.5848	6.8595	10.6048	2.9890	...	4.2259	9.1723	1.2835	3.3778	19.5542	-0.2860	-5.1612

5 rows × 201 columns

Table 1.3: Predictor Variables

SL.No.	Predictor
1	ID-code
2	var0
3	var1
4	var2
5	var3
6	var4
7	var5
….	.. …
	…..
….	……
….	……
….	…….
….	…….
….	…….
….	……..
202	var199

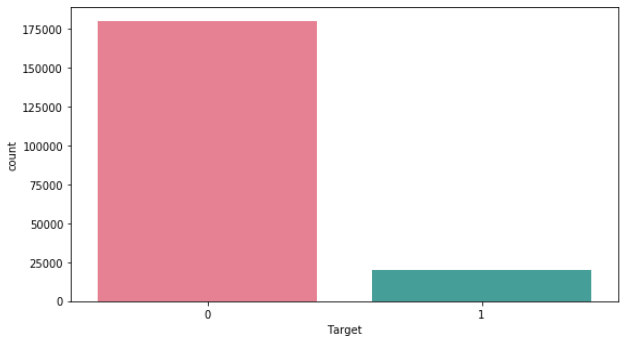
Chapter 2

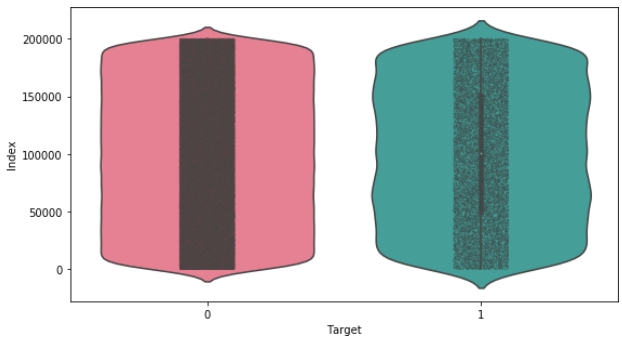
Methodology

2.1 Exploratory Data Analysis (EDA)

Exploratory data analysis is one of the most important steps in data mining in order to know features of data. It involves the loading dataset, target classes count, data cleaning, typecasting of attributes, missing value analysis, Attributes distributions and trends. So, we have to clean the data otherwise it will have impact on performance of the model. Now we are going to explain one by one as follows. In this EDA I explained with seaborn visualizations.

2.2.1 Target classes count





Take away:

- We have an unbalanced data, where 90% of the data is the number of customers those will not make a transaction and 10% of the data is those who will make a transaction.
- Look at the violin plots seems that there is no relationship between the targets with the index of the train data frame. This is more dominated by the zero targets then for the ones.
- Look at the jitter plots with violin plots. We can observe that targets look uniformly distributed over the index of the data frame.

2.2.2 Missing value Analysis

In this, we have to find out any missing values are present in dataset. If it's present then either delete or impute the values using mean, median and KNN imputation method. We have not found any missing values in both train and test data.

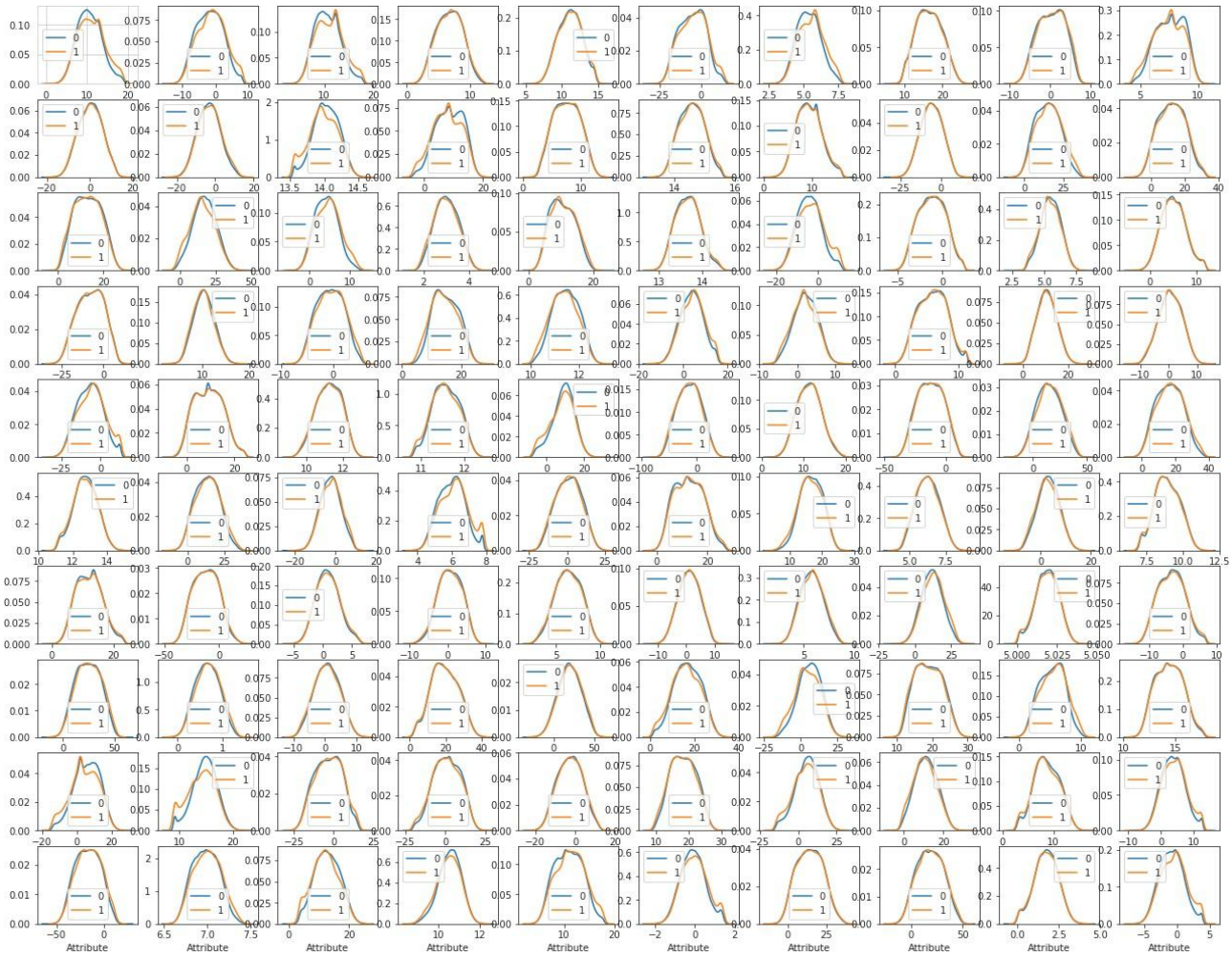
R and Python code as follows,

```
#Missing values in train and test data # R code
missing_val<-data.frame(missing_val=apply(train_df,2,function(x){sum(is.na(x))}))
missing_val<-sum(missing_val)
[1] 0
missing_val<-data.frame(missing_val=apply(test_df,2,function(x){sum(is.na(x))}))
missing_val<-sum(missing_val)
[1] 0


# Python code
train_missing=train_df.isnull().sum().sum()
```

2.1.1 Attributes distributions and trends

Distribution of train attributes

Let us look distribution of train attributes from var_0 to var_99

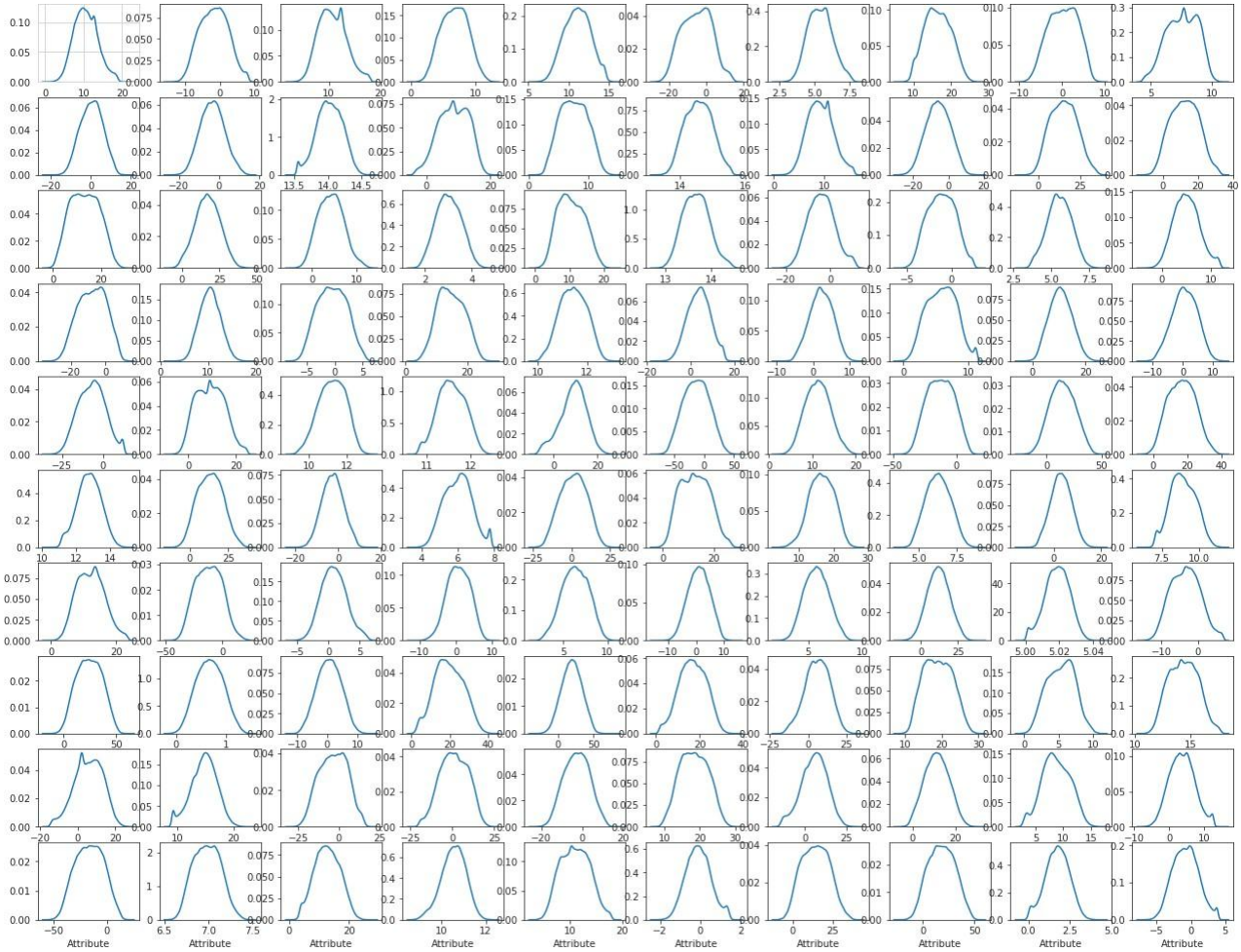


Take away:

- We can observe that there is a considerable number of features which are significantly have different distributions for two target variables. For example, like var_0, var_1, var_9, var_19, var_18 etc.
- We can observe that there is a considerable number of features which are significantly have same distributions for two target variables. For example like var_3, var_7, var_10, var_17, var_35 etc.

Distribution of test attributes

Let us look distribution of test attributes from var_0 to var_99

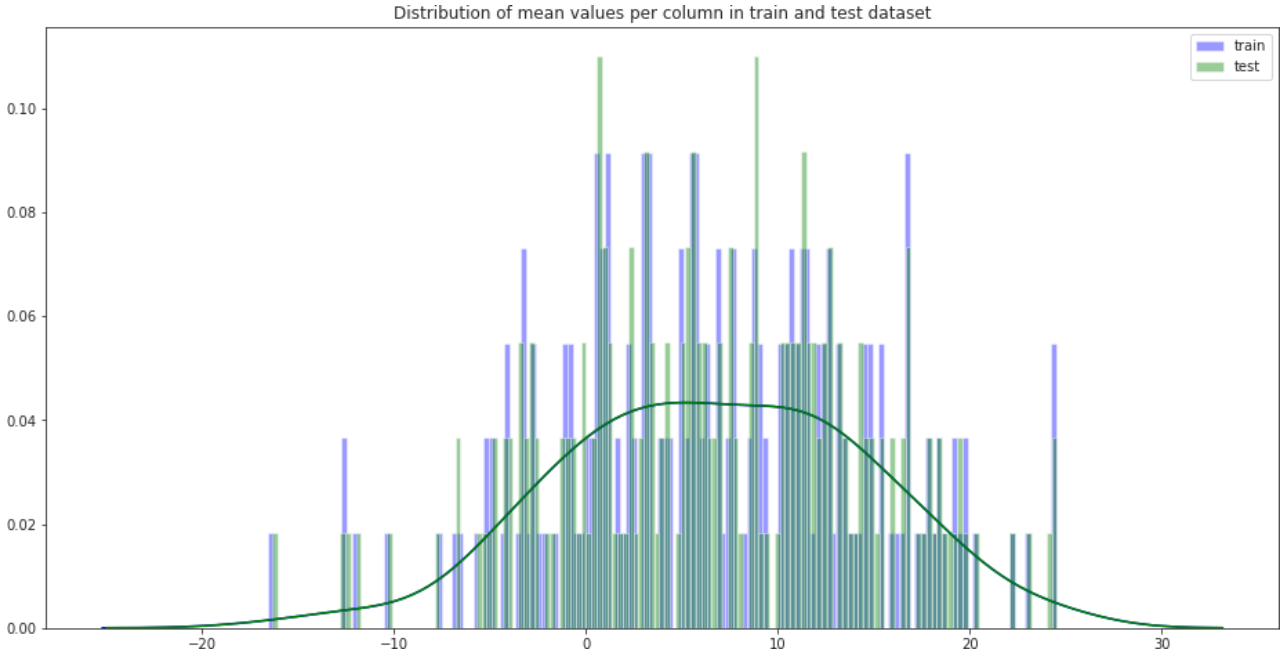


Take away:

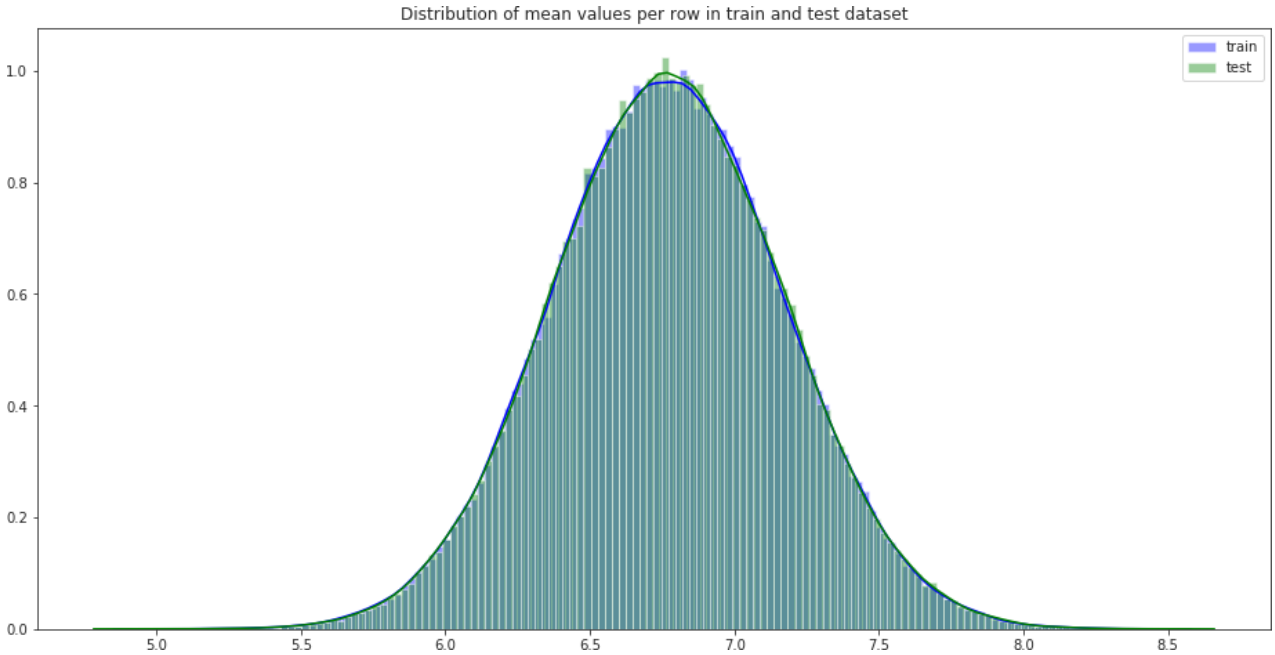
- We can observe that there is a considerable number of features which are significantly have different distributions. For example, like var_0, var_1, var_9, var_18 var_38 etc.
- We can observe that there is a considerable number of features which are significantly have same distributions. For example, like var_3, var_7, var_10, var_17, var_45, var_192 etc.

Distribution of mean values in both train and test dataset

Let us look distribution of mean values per column in train and test dataset

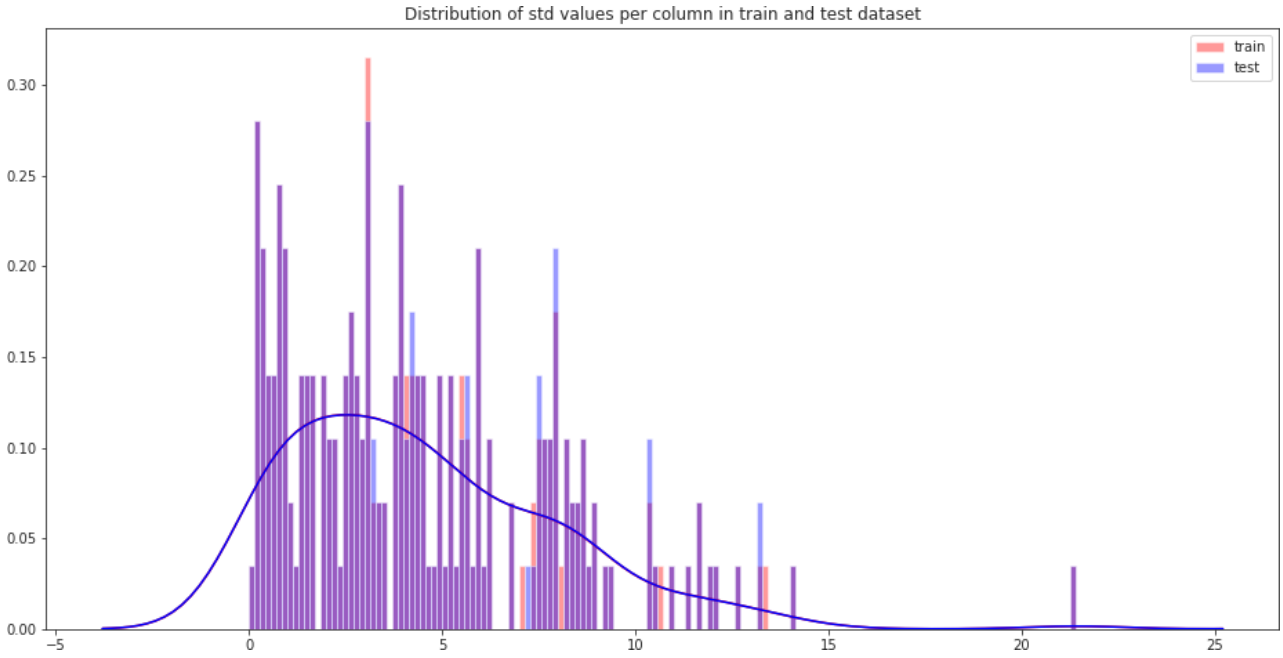


Let us look distribution of mean values per row in train and test dataset

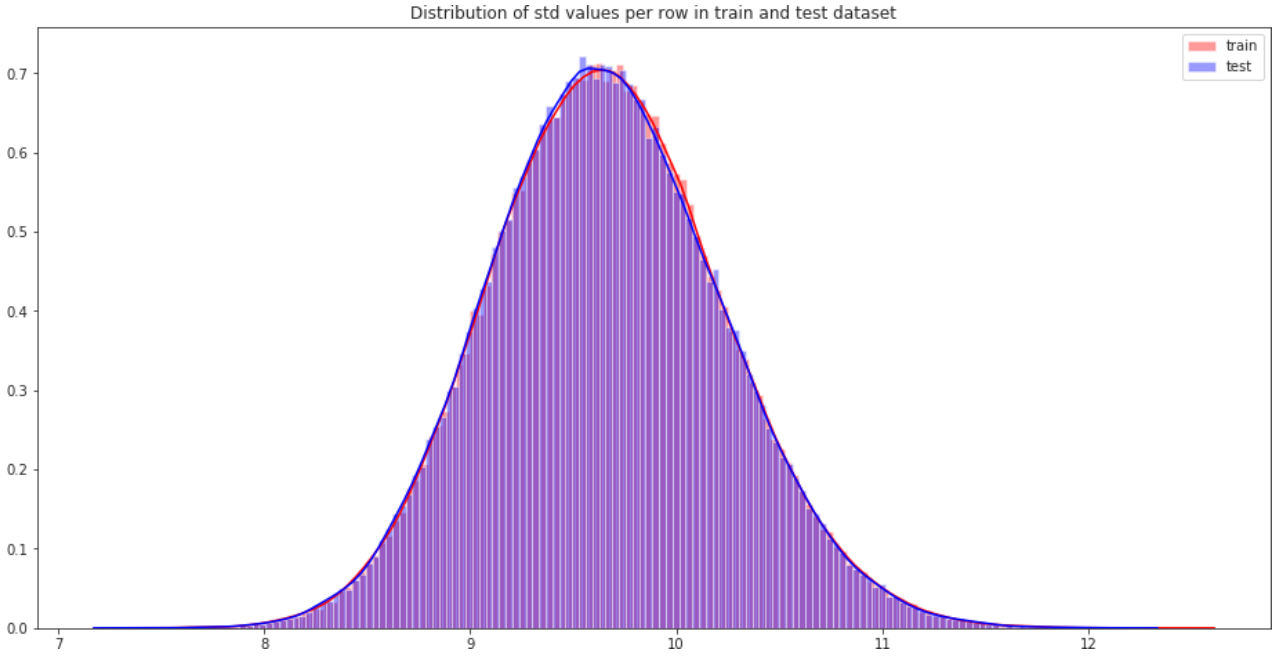


Distribution of standard deviation (std) values in train and test dataset

Let us look distribution of standard deviation (std) values per column in train and test dataset

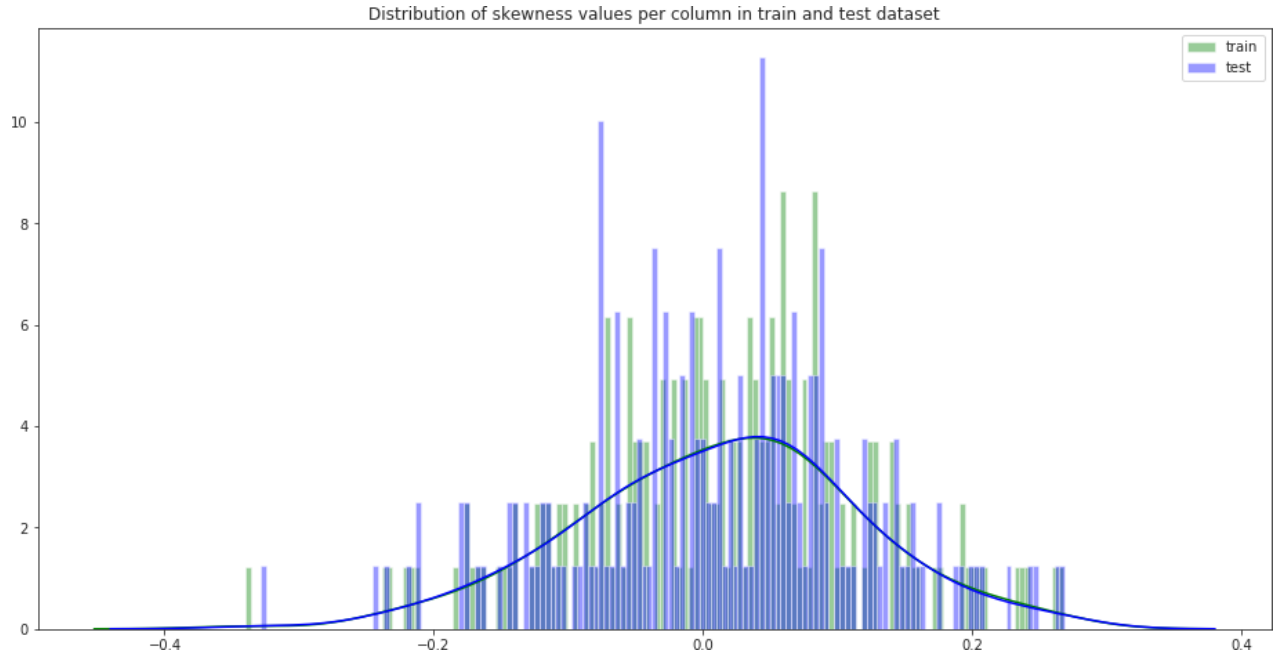


Let us look distribution of standard deviation (std) values per row in train and test dataset

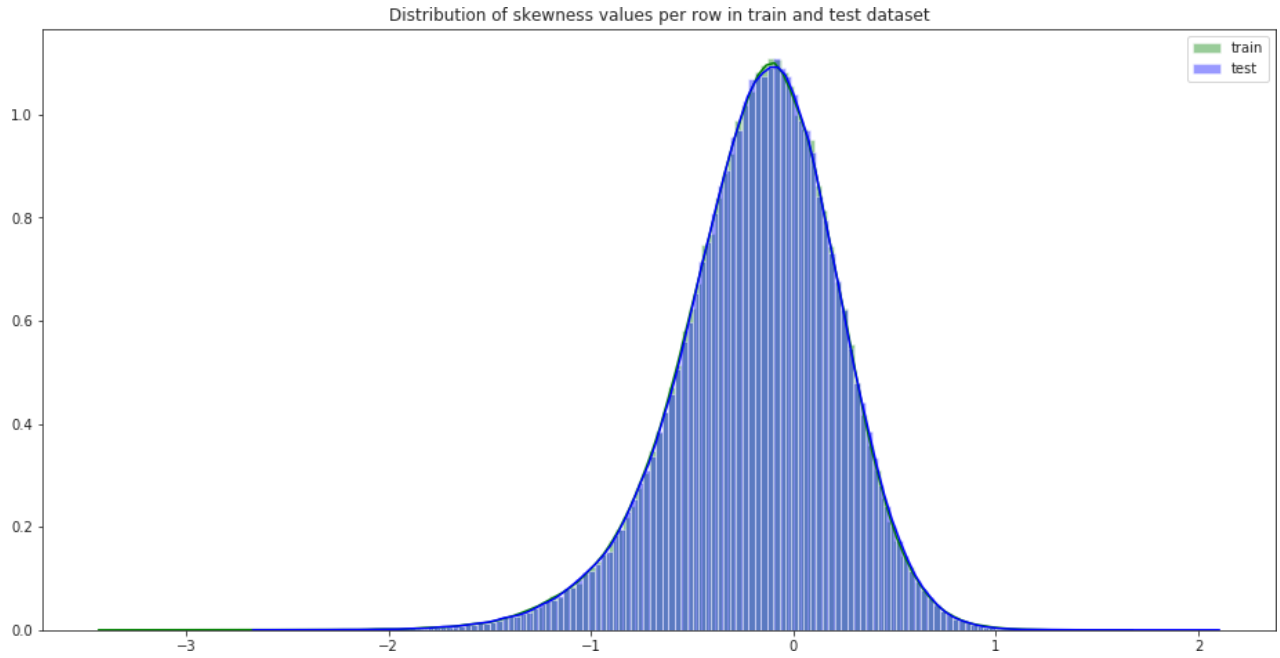


Distribution of skewness values in train and test dataset

Let us look distribution of skewness values per column in train and test dataset

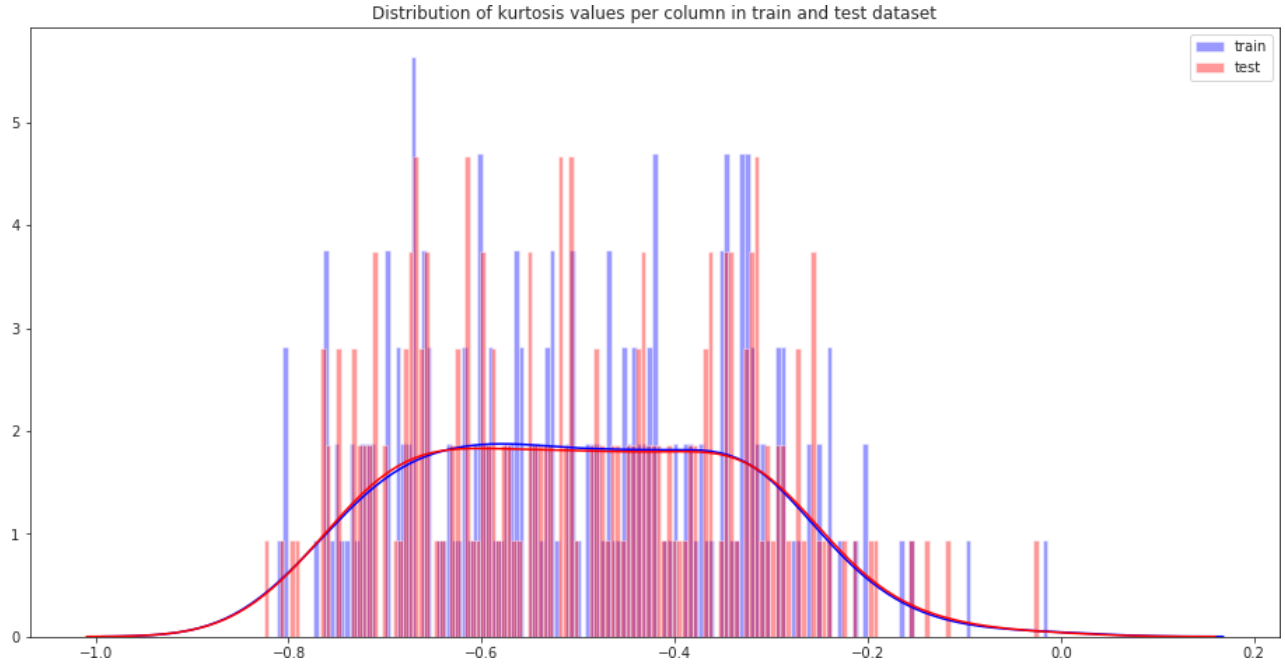


Let us look distribution of skewness per row in train and test dataset

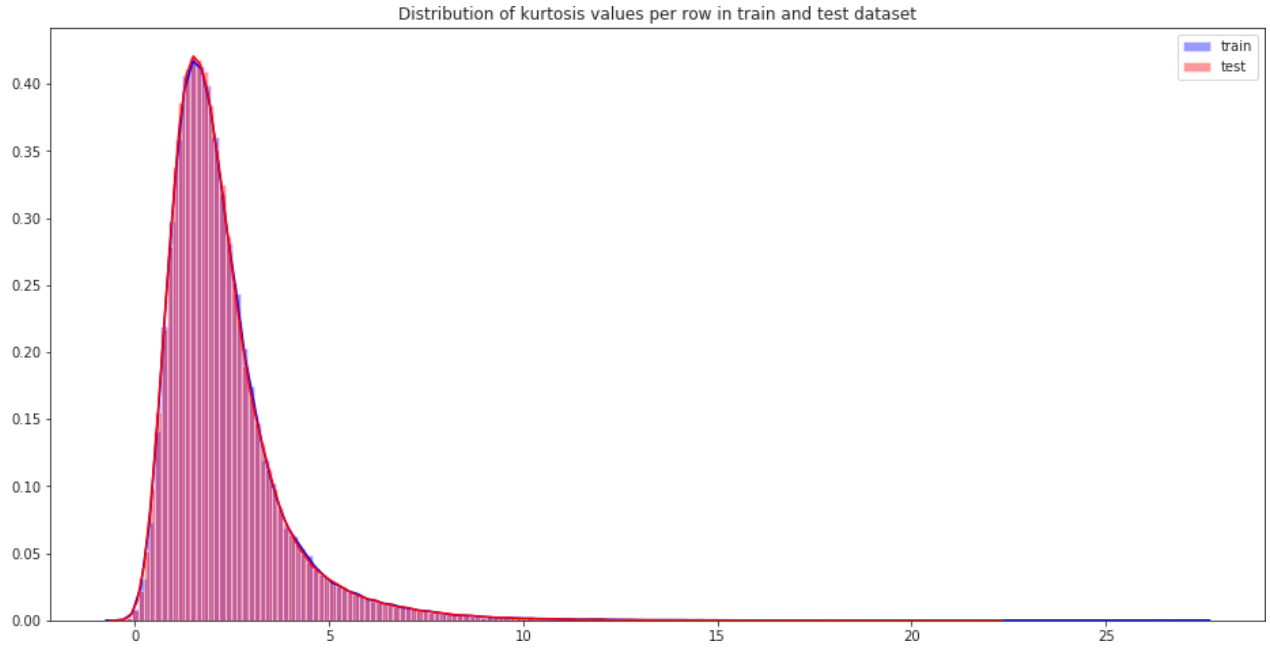


Distribution of kurtosis values in train and test dataset

Let us look distribution of kurtosis values per column in train and test dataset



Let us look distribution of kurtosis values per row in train and test dataset



2.1.2 Outlier analysis

In this project, we haven't performed outlier analysis due to the data is imbalanced and also not required for imbalanced data.

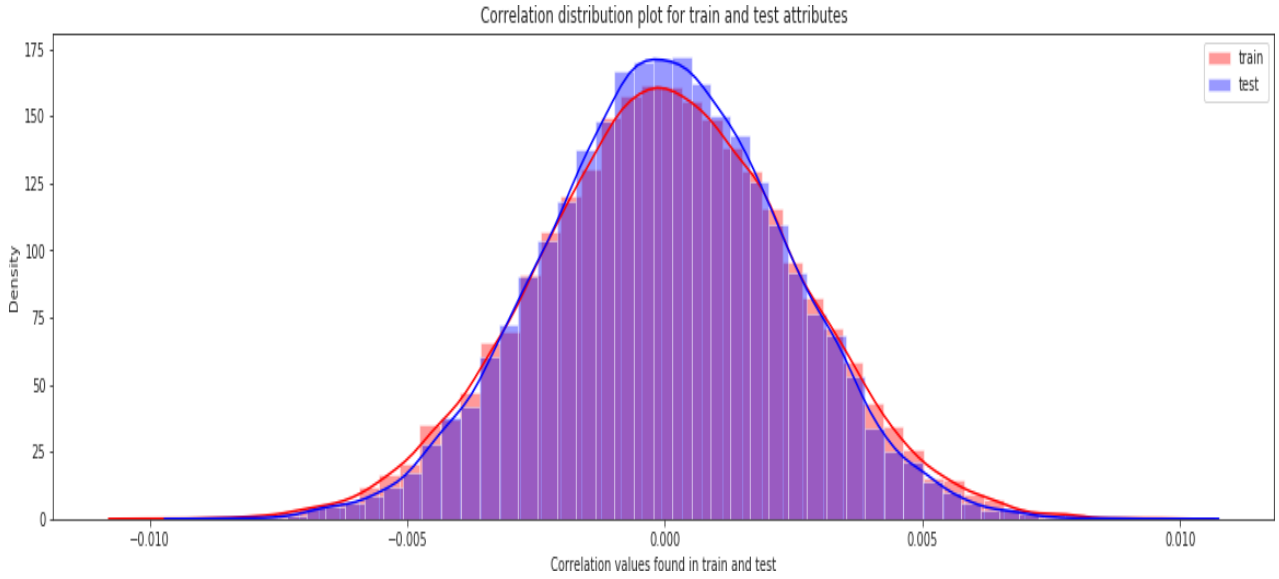
2.1.3 Feature Selection

Feature selection is very important for modelling the dataset. Every dataset has good and unwanted features. The unwanted features would affect on performance of model, so we have to delete those features. We have to select best features by using ANOVA, Chi-Square test and correlation matrix statistical techniques and so on. In this, we are selecting best features by using Correlation matrix.

Correlation matrix

Correlation matrix tells us about linear relationship between attributes and help us to build better models.

From correlation distribution plot, we can observe that correlation between both train and test attributes are very small. It means that all both train and test attributes are independent to each other.



2.1.4 Feature engineering

Let us do some feature engineering by using

- Permutation importance
- Partial dependence plots

Permutation importance

Permutation variable importance measure in a random forest for classification and regression. The variables which are mostly contributed to predict the model.

Python code

```
#training data X=train_df.drop(columns=['ID_code','target'],axis=1)
test=test_df.drop(columns=['ID_code'],axis=1) y=train_df['target']


#Split the training data X_train,X_valid,y_train,y_valid=train_test_split(X,y,random_state=42)


#Random forest classifier
rf_model=RandomForestClassifier(n_estimators=10,random_state=42) #fitting the
model

rf_model.fit(X_train,y_train)


#Let us calculate weights and show important features using eli5library. from eli5.sklearn import
PermutationImportance perm_imp=PermutationImportance(rf_model,random_state=42)

#fitting the model perm_imp.fit(X_valid,y_valid)
```

Weight	Feature
0.0004 ± 0.0002	var_81
0.0003 ± 0.0002	var_146
0.0003 ± 0.0002	var_109
0.0003 ± 0.0002	var_12
0.0002 ± 0.0001	var_110
0.0002 ± 0.0000	var_173
0.0002 ± 0.0001	var_174
0.0002 ± 0.0002	var_0
0.0002 ± 0.0002	var_26
0.0001 ± 0.0001	var_166
0.0001 ± 0.0001	var_169
0.0001 ± 0.0001	var_22
0.0001 ± 0.0001	var_99
0.0001 ± 0.0001	var_53
0.0001 ± 0.0001	var_8

R code

```
#Split the training data
train_index<-sample(1:nrow(train_df),0.75*nrow(train_df))
train_data<-train_df[train_index,]
valid_data<-train_df[-train_index,]


#Training the Random forest classifier
set.seed(2732)
train_data$target<-as.factor(train_data$target)
mtry<-floor(sqrt(200))
tuneGrid<-expand.grid(.mtry=mtry)
rf<-randomForest(target~.,train_data[,-c(1)],mtry=mtry,ntree=10,importance=TRUE)
```

Variable importance based on Mean Decrease Gini

	MeanDecreaseGini
var_0	178.19905
var_1	179.11005
var_2	186.08049
var_3	124.84417
var_4	115.25478
var_5	136.53634
var_6	193.64204
var_7	111.92811
var_8	109.93159
var_9	159.85075
var_10	117.02210

Take away:

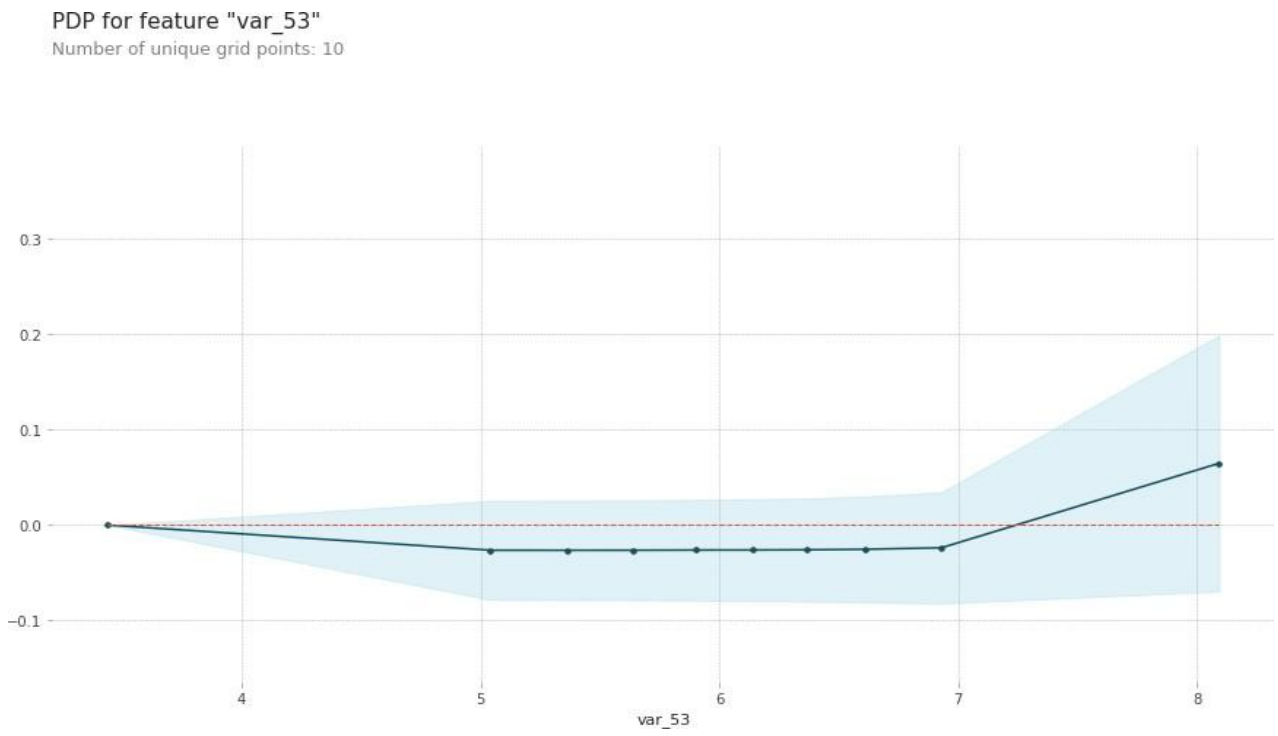
- We can observe that the top important features are var_12, var_26, var_22, var_174, var_198 and so on based on Mean decrease Gini.

Partial dependence plots

Partial dependence plot gives a graphical depiction of the marginal effect of a variable on the class probability or classification. While feature importance shows what variables most affect predictions, but partial dependence plots show how a feature affects predictions.

Python code

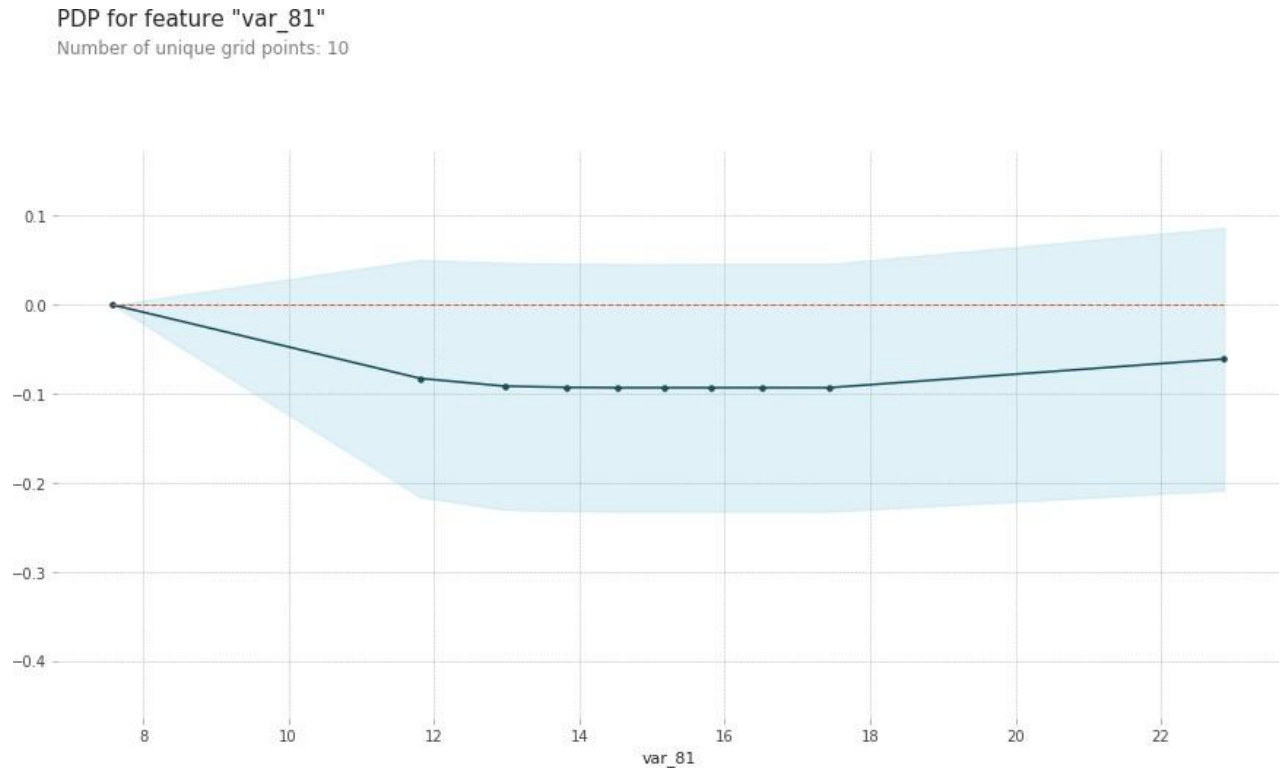
```
#Create the data we will plot 'var_53'
 features=[v for v in X_valid.columns if v not in ['ID_code','target']]
pdp_data=pdp.pdp_isolate(rf_model,dataset=X_valid,model_features=features,feature=
'var_53')
 #plot feature "var_53"
 pdp.pdp_plot(pdp_data,'var_53')
```



Take away:

- The y-axis does not show the predictor value instead how the value changing with the change in given predictor variable.
- The blue shaded area indicates the level of confidence of 'var_53'.
- On y-axis having a positive value means for that particular value of predictor variable it is less likely to predict the correct class and having a positive value means it has positive impact on predicting the correct class.

```
#Create the data we will plot 'var_81'
features=[v for v in X_valid.columns if v not in ['ID_code','target']]
pdp_data=pdp.pdp_isolate(rf_model,dataset=X_valid,model_features=features,feature='var_81')
#plot feature "var_81"
pdp.pdp_plot(pdp_data,'var_81')
```

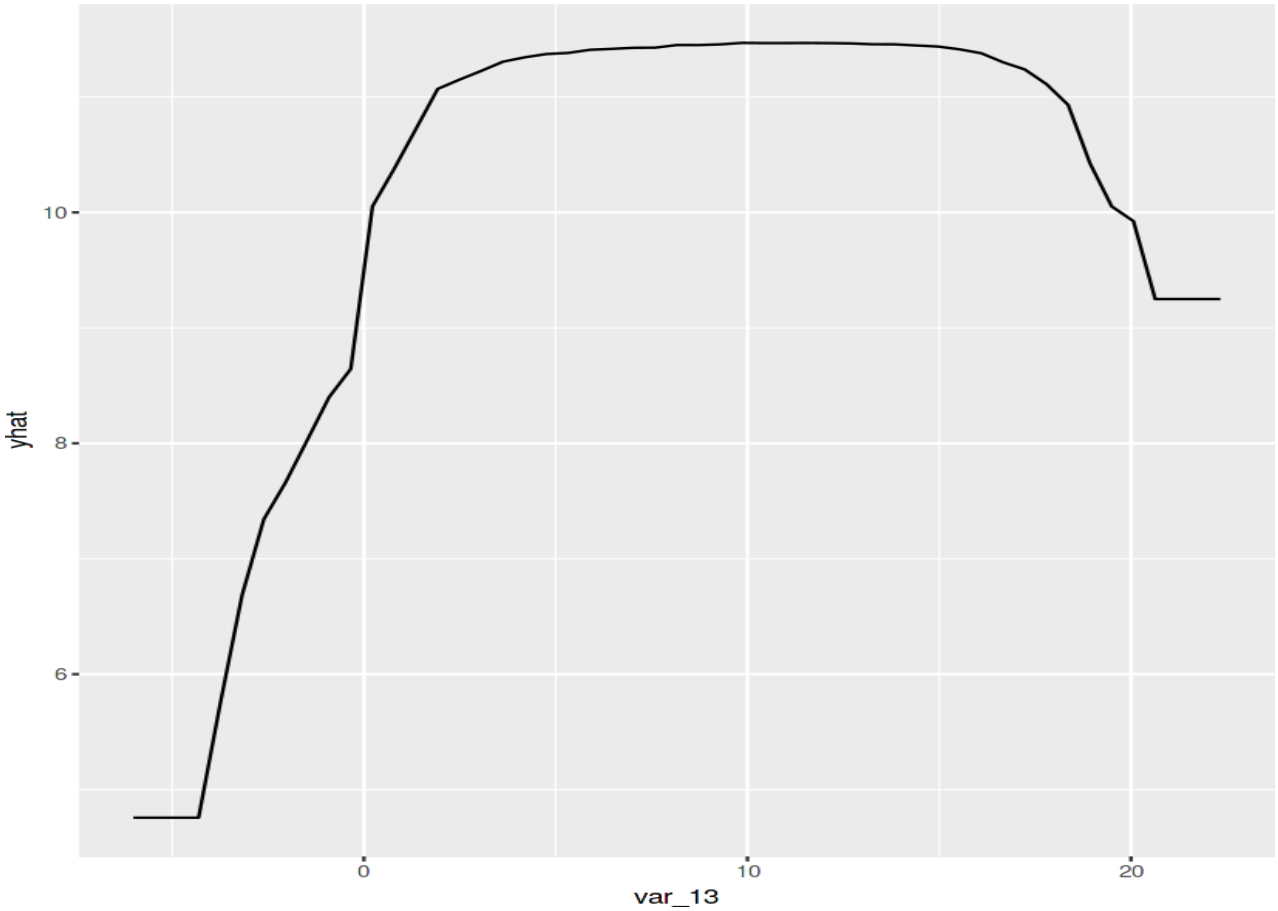


Take away:

- The y_axis does not show the predictor value instead how the value changing with the change in given predictor variable.
- The blue shaded area indicates the level of confidence of 'var_81'.
- On y-axis having a positive value means for that particular value of predictor variable it is less likely to predict the correct class and having a positive value means it has positive impact on predicting the correct class.

R code

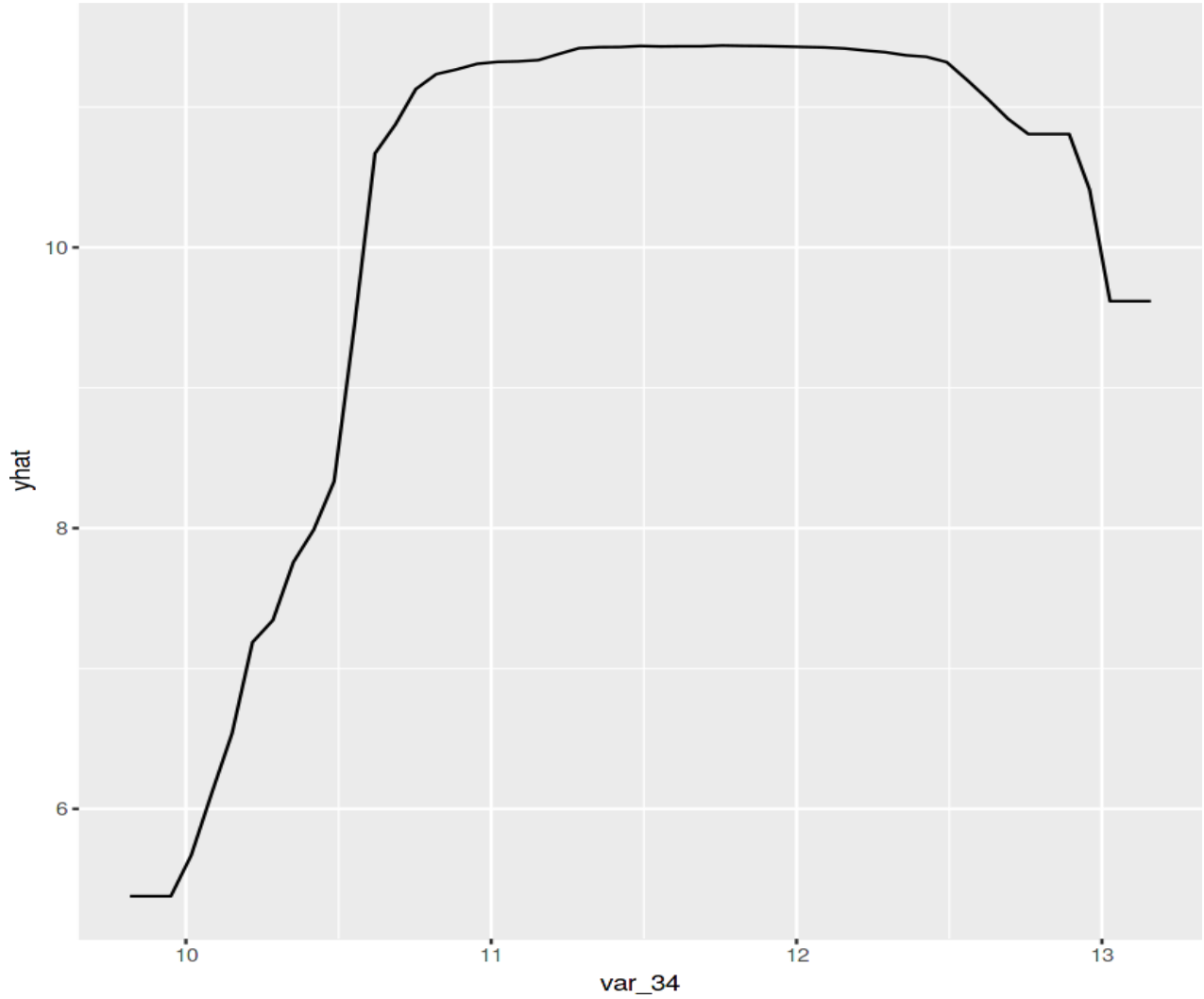
```
#We will plot "var_13"
par.var_13 <- partial(rf, pred.var = c("var_13"), chull = TRUE)
```



Take away:

- The y_axis does not show the predictor value instead how the value changing with the change in given predictor variable.
- The blue shaded area indicates the level of confidence of 'var_13'.
- On y-axis having a positive value means for that particular value of predictor variable it is less likely to predict the correct class and having a positive value means it has positive impact on predicting the correct class.

```
#We will plot "var_34"
 par.var_34 <- partial(rf, pred.var = c("var_34"), chull = TRUE)
```



Take away:

- The y_axis does not show the predictor value instead how the value changing with the change in given predictor variable.
- The blue shaded area indicates the level of confidence of 'var_34'.
- On y-axis having a positive value means for that particular value of predictor variable it is less likely to predict the correct class and having a positive value means it has positive impact on predicting the correct class.

2.1 Modeling

2.1.1 Model Selection

After all early stages of preprocessing, then model the data. So, we have to select best model for this project with the help of some metrics.

The dependent variable can fall in either of the four categories:

1. Nominal
2. Ordinal
3. Interval
4. Ratio

If the dependent variable is Nominal the only predictive analysis that we can perform is **Classification**, and if the dependent variable is Interval or Ratio like this project, the normal method is to do a **Regression** analysis, or classification after binning.

Handling of imbalance data

Now we are going to explore 5 different approaches for dealing with imbalanced datasets.

- Change the performance metric
- Oversample minority class
- Under sample majority class
- Synthetic Minority Oversampling Technique (SMOTE) in Python or Random Oversampling Examples (ROSE) in R
- Change the algorithm

We always start model building from the simplest to more complex.

2.1.2 Logistic Regression

We will use a Logistic Regression to predict the values of our target variable.

Python code

```
#Training dataset for modelling


#Training data
X=train_df.drop(['ID_code','target'],axis=1)
Y=train_df['target']


#StratifiedKFold cross validator
```

```
   y_train, y_valid=Y.iloc[train_index], Y.iloc[valid_index]


#Logistic regression model


lr_model=LogisticRegression(random_state=42)
#fitting the lr model
lr_model.fit(X_train,y_train)


#Accuracy of the model
lr=lr_model.score(X_train,y_train)
```

Accuracy of the model : **0.914**

```
#Cross validation prediction
cv_predict=cross_val_predict(lr_model,X_valid,y_valid,cv=5)
#Cross validation score
cv_score=cross_val_score(lr_model,X_valid,y_valid,cv=5)
print('cross_val_score :',np.average(cv_score))
```

R code

Glmnet is a package that fits a generalized linear model via penalized maximum likelihood.

```
#Split the data using CreateDataPartition
train.index<-createDataPartition(train_df$target,p=0.8,list=FALSE)
train.data<-train_df[train.index,]
valid.data<-train_df[-train.index,]


#Training dataset
X_t<-as.matrix(train.data[,-c(1,2)])
y_t<-as.matrix(train.data$target)


#validation dataset
X_v<-as.matrix(valid.data[,-c(1,2)])
y_v<-as.matrix(valid.data$target)


#test dataset
test<-as.matrix(test_df[,-c(1)])
```

```
 set.seed(8909)
 cv_lr <- cv.glmnet(X_t,y_t,family = "binomial", type.measure = "class")
#Plotting the missclassification error vs log(lambda) where lambda is
regularization parameter
 #Minimum lambda
 cv_lr$lambda.min
 #plot the auc score vs log(lambda)
 plot(cv_lr)


 #Model performance on validation dataset
 set.seed(5363)
 cv_predict.lr<-predict(cv_lr,X_v,s = "lambda.min", type = "class")


 #Confusion matrix
 set.seed(689)
 #actual target variable
 target<-valid.data$target
 #convert to factor
 target<-as.factor(target)
 #predicted target variable
 #convert to factor
 cv_predict.lr<-as.factor(cv_predict.lr)
 confusionMatrix(data=cv_predict.lr,reference=target)
```

Accuracy of the model is not the best metric to use when evaluating the imbalanced datasets as it may be misleading. So, we are going to change the performance metric.

Oversample minority class:

- It can be defined as adding more copies of minority class.
- It can be a good choice when we don't have a ton of data to work with.
- Drawback is that we are adding information. This may lead to overfitting and poor performance on test data.

Under sample majority class:

- It can be defined as removing some observations of the majority class.
- It can be a good choice when we have a ton of data -think millions of rows.
- Drawback is that we are removing information that may be valuable. This may leads to under fitting and poor performance on test data.

Both Oversampling and under sampling techniques have some drawbacks. So, we are not going to use these models for this problem and also we will use other best algorithms.

Synthetic Minority Oversampling Technique (SMOTE)

SMOTE uses a nearest neighbor's algorithm to generate new and synthetic data to use for training the model. In order to balance imbalanced data, we are going to use SMOTE sampling method.

Python code

```
from imblearn.over_sampling import SMOTE
#Synthetic Minority Oversampling Technique
sm = SMOTE(random_state=42, ratio=1.0)
#Generating synthetic data points

X_smote,y_smote=sm.fit_sample(X_train,y_train)
X_smote_v,y_smote_v=sm.fit_sample(X_valid,y_valid)


#Logistic regression model for SMOTE
smote=LogisticRegression(random_state=42)
#fitting the smote model
smote.fit(X_smote,y_smote)


smote_score=smote.score(X_smote,y_smote)
print('Accuracy of the smote_model :',smote_score)

Accuracy of the model : 0.798

#Cross validation prediction

cv_pred=cross_val_predict(smote,X_smote_v,y_smote_v,cv=5)

#Cross validation score
cv_score=cross_val_score(smote,X_smote_v,y_smote_v,cv=5)
print('cross_val_score :',np.average(cv_score))
```

R code

Random Oversampling Examples (ROSE)

It creates a sample of synthetic data by enlarging the features space of minority and majority class examples. In order to balance imbalanced data we are going to use SMOTE sampling method.

```
#Random Oversampling Examples(ROSE)
set.seed(699)

#train.data$target<-as.factor(train.data$target)

train.rose <- ROSE(target~., data =train.data[,-c(1)],seed=32)$data
table(train.rose$target)

valid.rose <- ROSE(target~., data =valid.data[,-c(1)],seed=42)$data
```

```
#Baseline logistic regression model
set.seed(462)

lr_rose <-glmnet(as.matrix(train.rose),as.matrix(train.rose$target),
family = "binomial")

summary(lr_rose)


#Cross validation prediction
set.seed(473)

cv_rose = cv.glmnet(as.matrix(valid.rose),as.matrix(valid.rose$target),
family = "binomial", type.measure = "class")


#Minimum lambda
cv_rose$lambda.min

#plot the auc score vs log(lambda)
plot(cv_rose)


#Model performance on validation dataset
set.seed(442)

cv_predict.rose<-predict(cv_rose,as.matrix(valid.rose),s = "lambda.min",
type = "class")

cv_predict.rose


#Confusion matrix
set.seed(478)

#actual target variable
target<-valid.rose$target
#convert to factor
target<-as.factor(target)

#predicted target variable
#convert to factor

cv_predict.rose<-as.factor(cv_predict.rose)
```

LightGBM

LightGBM is a gradient boosting framework that uses tree based learning algorithms. We are going to use LightGBM model.

Python code

Let us build LightGBM model

```
#Training the model
#training data
lgb_train=lgb.Dataset(X_train,label=y_train)
#validation data
lgb_valid=lgb.Dataset(X_valid,label=y_valid)

#Selecting best hyper parameters by tuning of different parameters

params={'boosting_type': 'gbdt',
         'max_depth' : -1, #no limit for max_depth if <0
         'objective': 'binary',
         'boost_from_average':False,
         'nthread': 8,
         'metric':'auc',
         'num_leaves': 100,
         'learning_rate': 0.03,
         'max_bin': 950,      #default 255
         'subsample_for_bin': 200,
         'subsample': 1,
         'subsample_freq': 1,
         'colsample_bytree': 0.8,
         'reg_alpha': 1.2, #L1 regularization(>0)
         'reg_lambda': 1.2,#L2 regularization(>0)
         'min_split_gain': 0.5, #>0
         'min_child_weight': 1,
         'min_child_samples': 5,
         'is_unbalance':True,
         }


num_rounds=3000
```

```
Training until validation scores don't improve for 5000 rounds.
[1000]  training's auc: 0.939079        valid_1's auc: 0.882655
[2000]  training's auc: 0.958502        valid_1's auc: 0.887842
[3000]  training's auc: 0.971937        valid_1's auc: 0.889724
[4000]  training's auc: 0.981492        valid_1's auc: 0.890474
[5000]  training's auc: 0.988242        valid_1's auc: 0.890772
[6000]  training's auc: 0.992813        valid_1's auc: 0.890549
[7000]  training's auc: 0.995775        valid_1's auc: 0.890488
[8000]  training's auc: 0.997627        valid_1's auc: 0.890549
[9000]  training's auc: 0.998739        valid_1's auc: 0.890309
[10000] training's auc: 0.999359        valid_1's auc: 0.889882
Did not meet early stopping. Best iteration is:
[10000] training's auc: 0.999359        valid_1's auc: 0.889882


<lightgbm.basic.Booster at 0x7f8b795edac8>
```

R code

```
#Convert data frame to matrix

X_train<-as.matrix(train_data[,-c(1,2)])
y_train<-as.matrix(train_data$target) X_valid<-
as.matrix(valid_data[,-c(1,2)]) y_valid<-
as.matrix(valid_data$target) test_data<-
as.matrix(test_df[,-c(1)])

#training data

lgb.train <- lgb.Dataset(data=X_train, label=y_train)
#Validation data

lgb.valid <- lgb.Dataset(data=X_valid,label=y_valid)

#Choosing parameters

lgb.grid = list(objective = "binary",
                metric = "auc",
                boost =”gbdt”

                min_sum_hessian_in_leaf = 1,

                feature_fraction = 0.7,

                bagging_fraction = 0.7,

                bagging_freq = 5,
                learning_rate=0.05,
                num_leaves=80,
```

```
num_threads=10,
min_data = 100,
max_bin = 200,
lambda_l1 = 8,
```

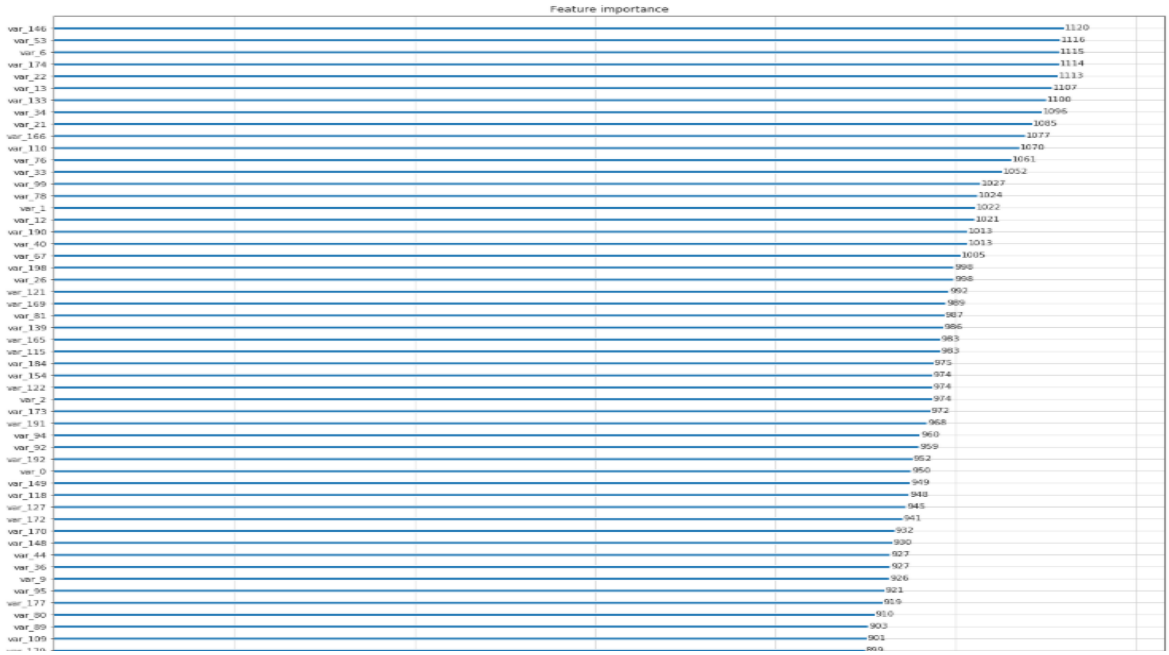
```
                lambda_l2 = 1.3,
                min_data_in_bin=150,
                min_gain_to_split = 20,
                min_data_in_leaf = 40,
                is_unbalance = TRUE)


lgbm.model <- lgb.train(params = lgb.grid, data = lgb.train, nrounds =10000,
```

```
[1]:    val1's auc:0.594625     val2's auc:0.586947
[1001]: val1's auc:0.922163     val2's auc:0.895506
[2001]: val1's auc:0.928038     val2's auc:0.898477
[3001]: val1's auc:0.929811     val2's auc:0.899515
[4001]: val1's auc:0.930609     val2's auc:0.899988
[5001]: val1's auc:0.931106     val2's auc:0.900336
[6001]: val1's auc:0.931368     val2's auc:0.900598
[7001]: val1's auc:0.931604     val2's auc:0.900685
[8001]: val1's auc:0.931813     val2's auc:0.900826
[9001]: val1's auc:0.931982     val2's auc:0.900869
[10000]:        val1's auc:0.93215      val2's auc:0.900892
```

Important features plot Python

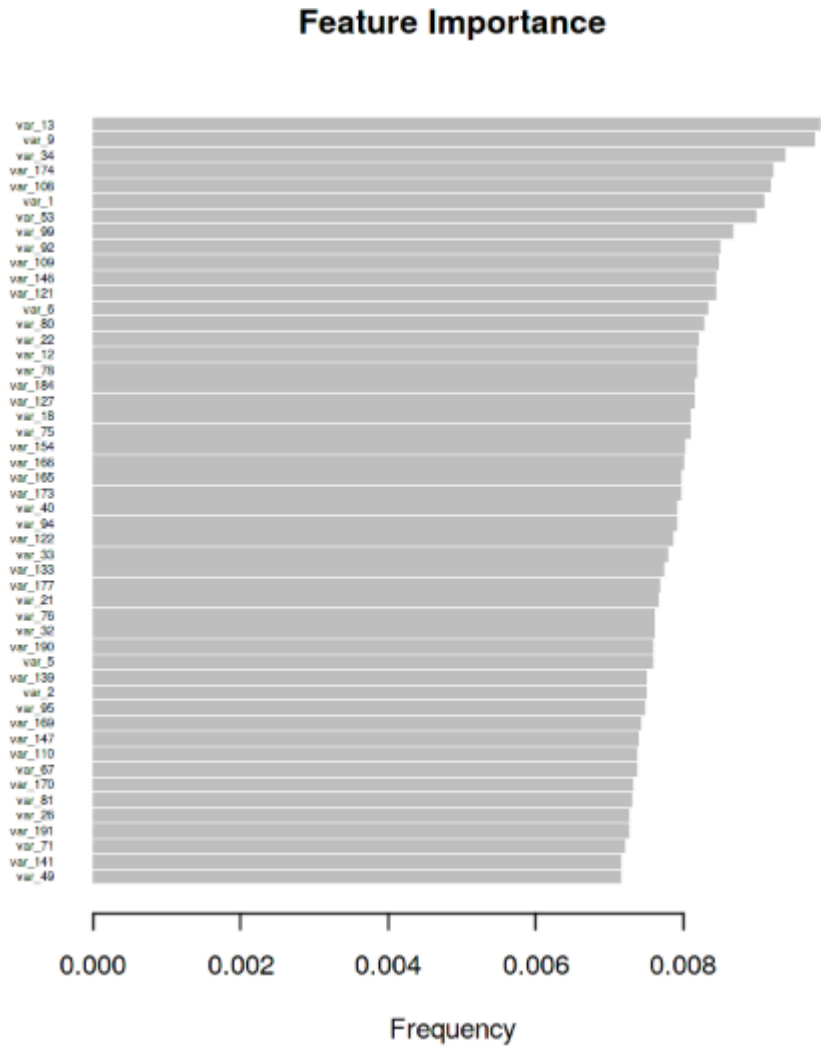
code

```
 #plot the important features
lgb.plot_importance(lgbm,max_num_features=150,importance_type="split",figsize=(20,
50))
```



R code

```
tree_imp <- lgb.importance(lgbm.model, percentage = TRUE)
lgb.plot.importance(tree_imp, top_n = 50, measure = "Gain")
```


Feature Importance
var_13
var_9
var_34
var_174
var_106
var_1
var_53
var_99
var_92
var_109
var_146
var_121
var_6
var_80
var_22
var_12
var_78
var_184
var_127
var_18
var_75
var_154
var_166
var_165
var_173
var_40
var_94
var_122
var_33
var_133
var_177
var_21
var_76
var_32
var_190
var_5
var_139
var_2
var_95
var_169
var_147
var_110
var_67
var_170
var_81
var_26
var_191
var_71
var_141
var_49
0.000
0.002
0.004
0.006
0.008
Frequency

Chapter 3

Conclusion

3.1 Model Evaluation

Now, we have three models for predicting the target variable, but we need to decide which model better for this project. There are many metrics used for model evaluation.

Classification accuracy may be misleading if we have an imbalanced dataset or if we have more than two classes in dataset.

For classification problems, the confusion matrix used for evaluation. But, in our case the data is imbalanced. So, roc_auc_score is used for evaluation.

In this project, we are using two metrics for model evaluation as follows,

Confusion Matrix: - It is a technique for summarizing the performance of a classification algorithm.

The number of correct predictions and incorrect predictions are summarized with count values and broken down by each class.

		Predicted class	
		P	*N*
Actual Class	*P*	True Positives (TP)	False Negatives (FN)
	N	False Positives (FP)	True Negatives (TN)

Accuracy: - The ratio of correct predictions to total predictions

$$\text{Accuracy} = \frac{TP+TN}{Total\ Predictions}$$

Misclassification error: - The ratio of incorrect predictions to total predictions

$$\text{Error rate} = \frac{FN+FP}{Total\ predictions}$$

Accuracy=1-Error rate

True Positive Rate (TPR) = $\frac{TP}{TP+FN}$ ↔ Recall

Precision = $\frac{TP}{TP+FP}$

True Negative Rate (TNR) = $\frac{TN}{TN+FP}$ ↔ Specificity

False Positive Rate (FPR) = $\frac{FP}{FP+TN}$

False Negative rate (FNR) = $\frac{FN}{FN+TP}$

F1 score :- Harmonic mean of precision and recall, used to indicate balance between them.

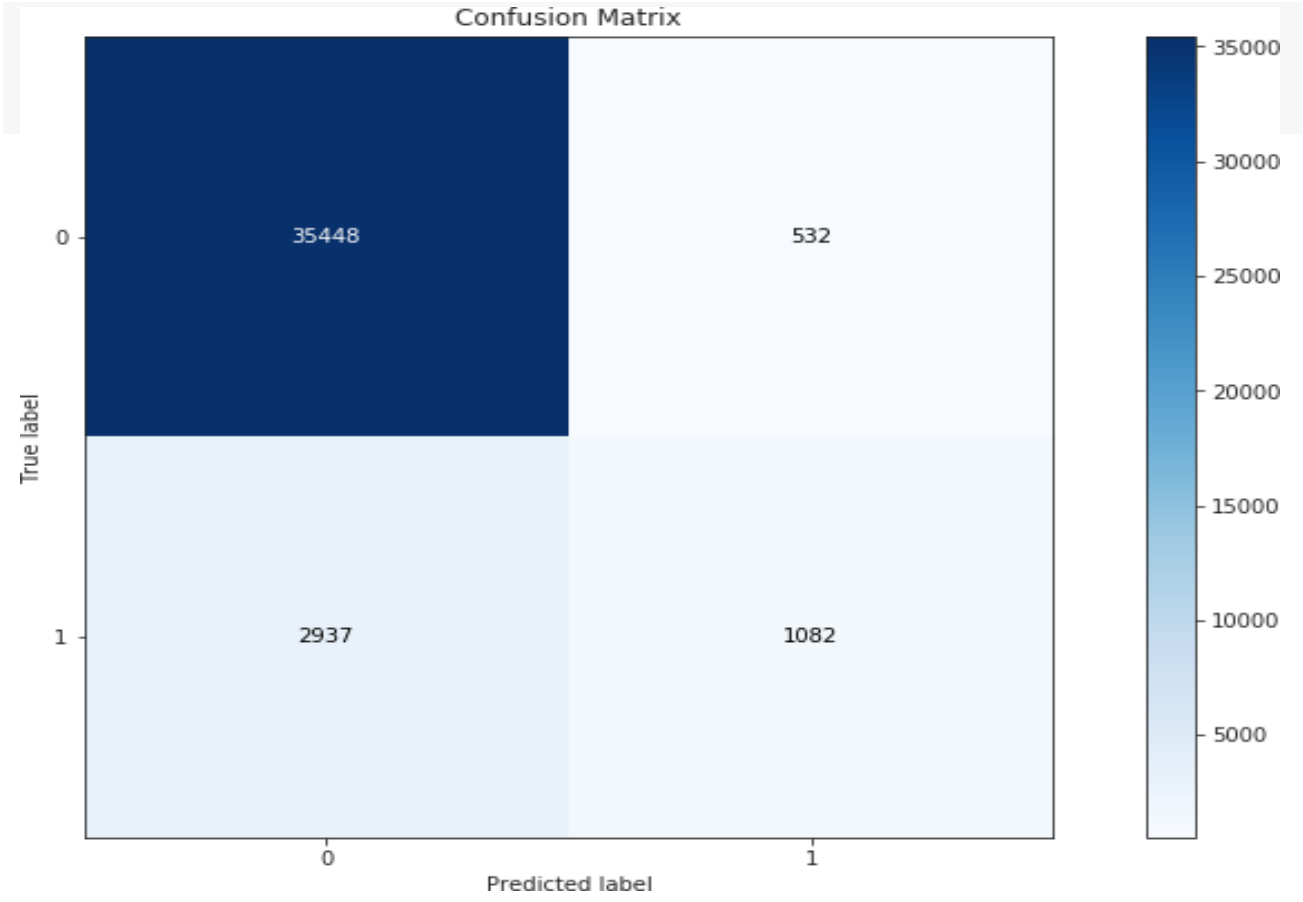
$$\text{F1 score} = 2*\frac{Precision*Recall}{Precision+Recall}$$

Receiver operating characteristics (ROC)_Area under curve(AUC) Score

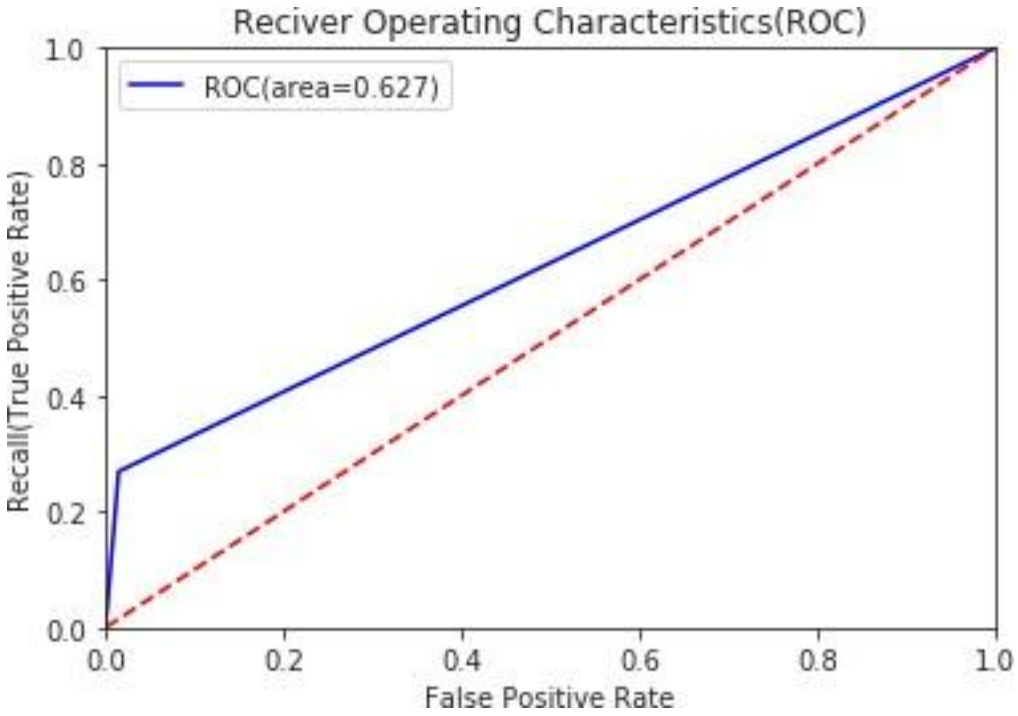
roc_auc_score :- It is a metric that computes the area under the Roc curve and also used metric for imbalanced data.

Roc curve is plotted true positive rate or Recall on y axis against false positive rate or specificity on x axis. The larger the area under the roc curve better the performance of the model.

Logistic Regression




```
#ROC_AUC curve


plt.figure()
false_positive_rate,recall,thresholds=roc_curve(y_valid,cv_predict)
roc_auc=auc(false_positive_rate,recall)
plt.title('Reciver Operating Characteristics(ROC)')
plt.plot(false_positive_rate,recall,'b',label='ROC(area=%0.3f)' %roc_auc)
plt.legend()
plt.plot([0,1],[0,1],'r--')
plt.xlim([0.0,1.0])
plt.ylim([0.0,1.0])
```



When we compare the roc_auc_score and cross validation score, conclude that model is not performing well on imbalanced data.

Classification report

```
#Classification report
scores=classification_report(y_valid,cv_predict)
print(scores)
```

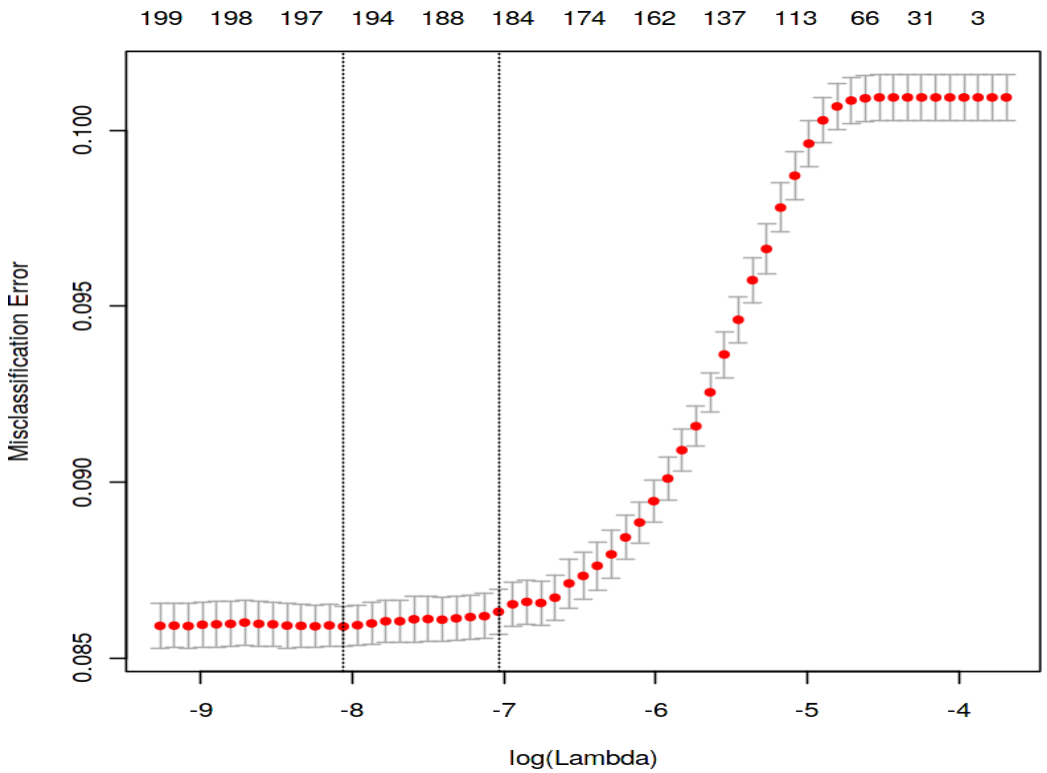
```
              precision    recall  f1-score   support

           0       0.92      0.99      0.95     35980
           1       0.67      0.27      0.38      4019

   micro avg       0.91      0.91      0.91     39999
   macro avg       0.80      0.63      0.67     39999
weighted avg       0.90      0.91      0.90     39999
```

We can observe that f1 score is high for number of customers those who will not make a transaction then who will make a transaction. So, we are going to change the algorithm.

R code

Logistic Regression

```
#Cross validation prediction
set.seed(8909)
cv_lr <- cv.glmnet(X_t,y_t,family = "binomial", type.measure = "class")


#Plotting misclassification error vs log(lambda)
#Minimum lambda-Regularization parameter
```



We can observed that miss classification error increases as increasing the log(Lambda).

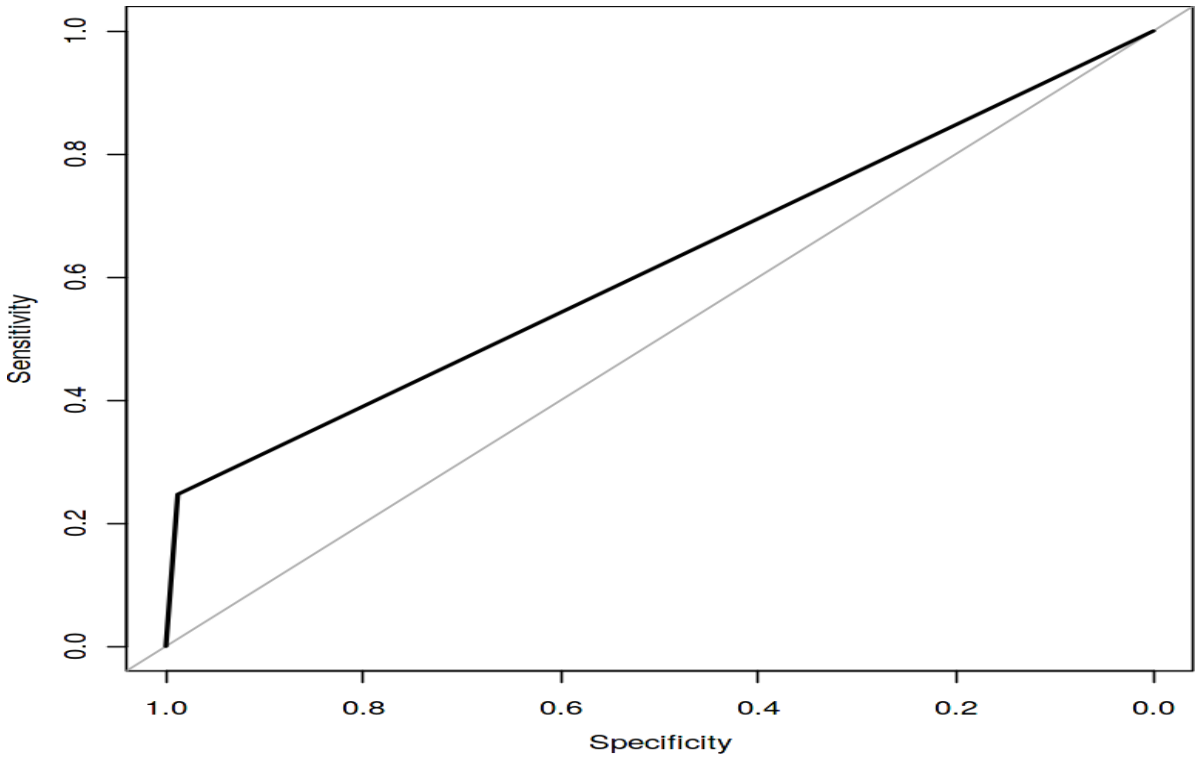
```
#Confusion matrix
set.seed(689)

#actual target variable
target<-valid.data$target
#convert to factor
target<-as.factor(target)

#predicted target variable
#convert to factor
```

```
Confusion Matrix and Statistics

          Reference
Prediction     1     2
         1 35618  2973
         2   434   975

               Accuracy : 0.9148
                 95% CI : (0.912, 0.9175)
    No Information Rate : 0.9013
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 0.3292

 Mcnemar's Test P-Value : < 2.2e-16

            Sensitivity : 0.9880
            Specificity : 0.2470
         Pos Pred Value : 0.9230
         Neg Pred Value : 0.6920
             Prevalence : 0.9013
         Detection Rate : 0.8904
   Detection Prevalence : 0.9648
      Balanced Accuracy : 0.6175

       'Positive' Class : 1
```

Reciever operating characteristics (ROC)-Area under curve (AUC) score and curve

```
#ROC_AUC score and curve
set.seed(892)
cv_predict.lr<-as.numeric(cv_predict.lr)
roc(data=valid.data[,-c(1,2)],response=target,predictor=cv_predict.lr,auc=TRUE,
```

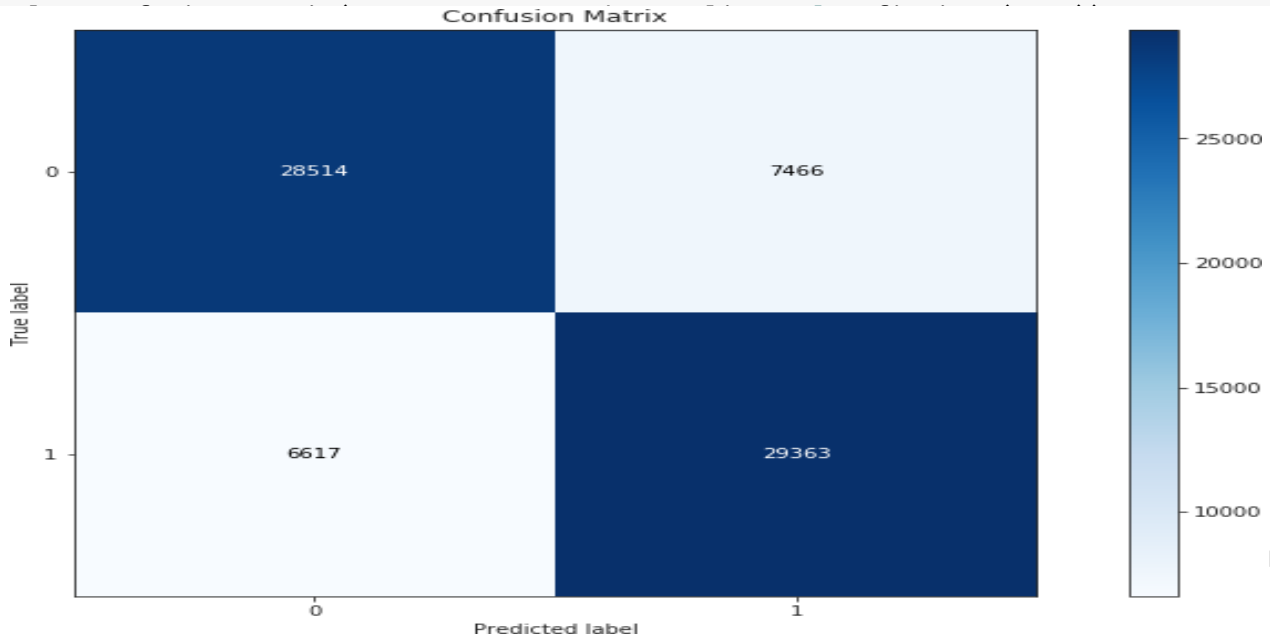
```
Call:
roc.default(response = target, predictor = cv_predict.lr, auc = TRUE,     plot = TRUE, data = v
alid.data[, -c(1, 2)])

Data: cv_predict.lr in 36052 controls (target 1) < 3948 cases (target 2).
Area under the curve: 0.6175
```



Python code

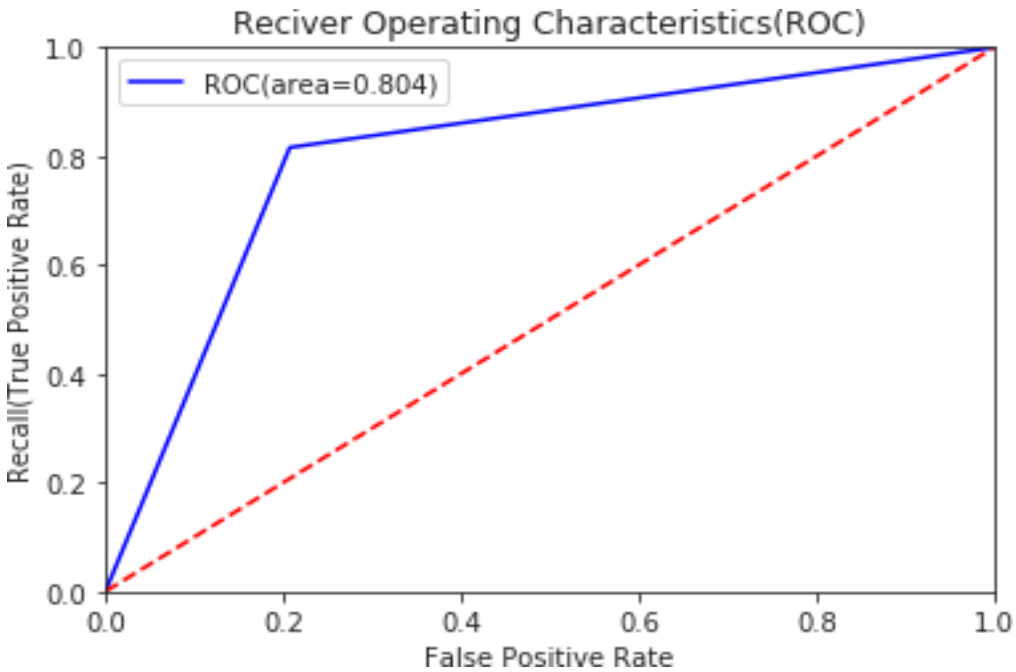
Synthetic Minority Oversampling Technique (SMOTE)

```
#Confusion matrix
cm=confusion_matrix(y_smote_v,cv_pred)
#Plot the confusion matrix
```



Reciever operating characteristics (ROC)-Area under curve (AUC) score and curve

```
#ROC_AUC curve
plt.figure()

false_positive_rate,recall,thresholds=roc_curve(y_smote_v,cv_pred)
roc_auc=auc(false_positive_rate,recall)

plt.title('Reciver Operating Characteristics(ROC)')
plt.plot(false_positive_rate,recall,'b',label='ROC(area=%0.3f)' %roc_auc)
plt.legend()

plt.plot([0,1],[0,1],'r--')

plt.xlim([0.0,1.0])

plt.ylim([0.0,1.0])
plt.ylabel('Recall(True Positive Rate)')
```



Classification report

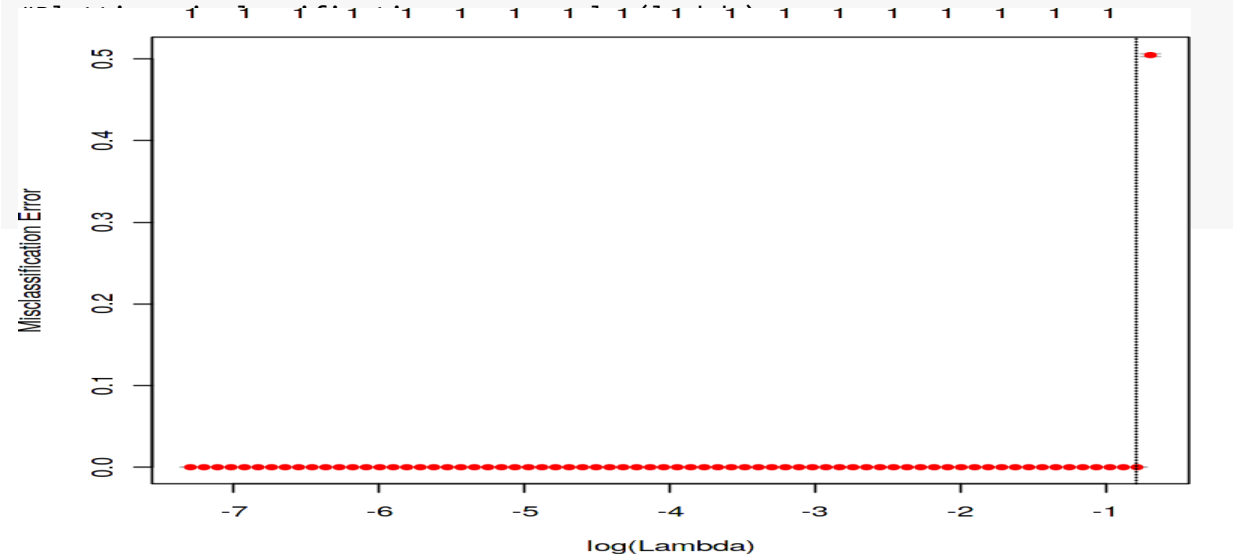
```
#Classification report
scores=classification_report(y_smote_v,cv_pred) print(scores)
```

	precision	recall	f1-score	support
0	0.81	0.79	0.80	35980
1	0.80	0.82	0.81	35980
micro avg	0.80	0.80	0.80	71960
macro avg	0.80	0.80	0.80	71960
weighted avg	0.80	0.80	0.80	71960

We can observe that smote model is performing well on imbalance data compare to baseline logistic regression.

R code

Random Oversampling Examples (ROSE)



```
#Confusion matrix
set.seed(478)

#actual target variable
target<-valid.rose$target
#convert to factor
target<-as.factor(target)

#predicted target variable
#convert to factor

cv_predict.rose<-as.factor(cv_predict.rose)
```

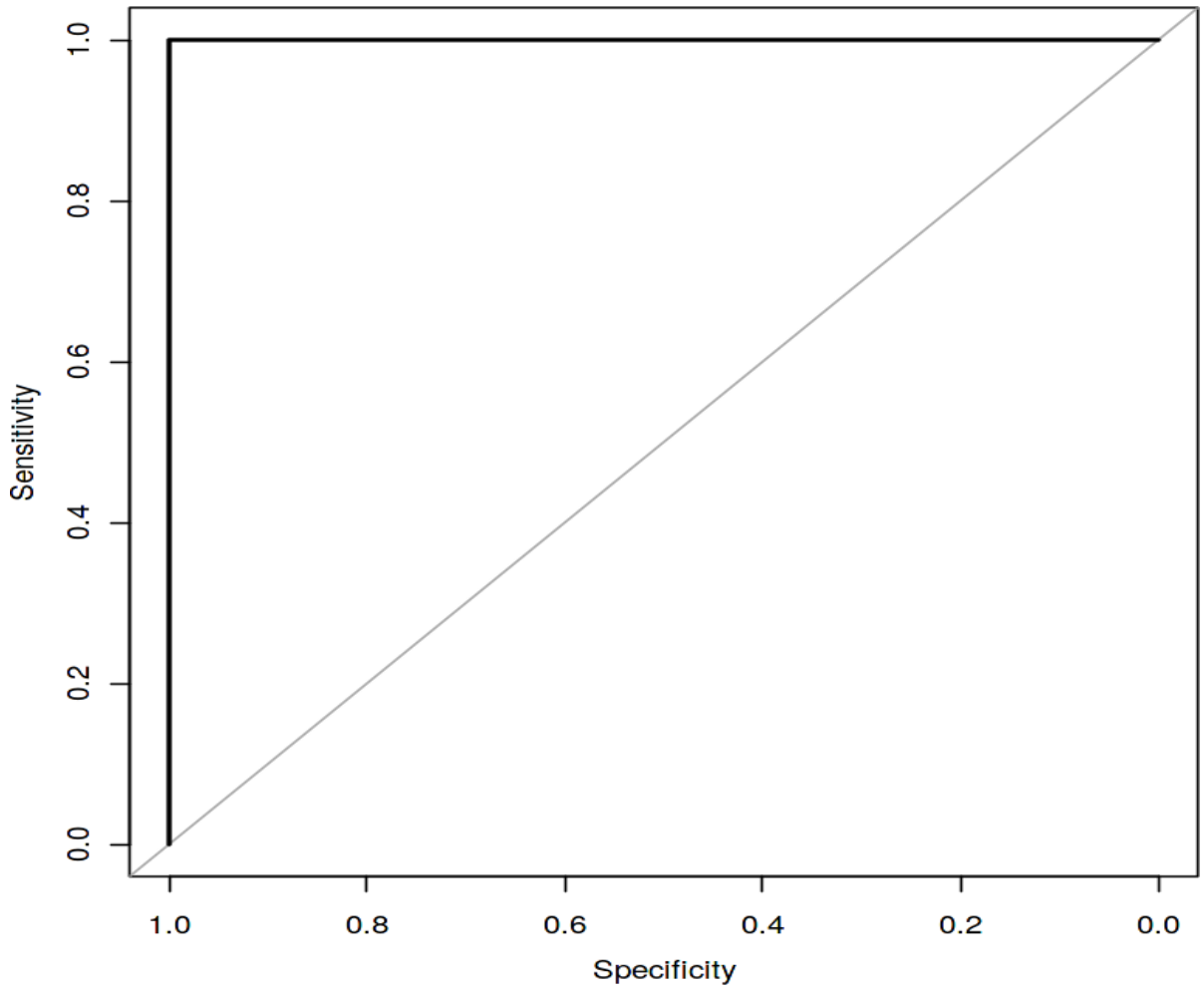
```
Confusion Matrix and Statistics

          Reference
Prediction     1     2
         1 20012     0
         2     0 19988

               Accuracy : 1
                 95% CI : (0.9999, 1)
    No Information Rate : 0.5003
    P-Value [Acc > NIR] : < 2.2e-16

                  Kappa : 1

 Mcnemar's Test P-Value : NA

            Sensitivity : 1.0000
            Specificity : 1.0000
         Pos Pred Value : 1.0000
         Neg Pred Value : 1.0000
             Prevalence : 0.5003
         Detection Rate : 0.5003
   Detection Prevalence : 0.5003
      Balanced Accuracy : 1.0000

       'Positive' Class : 1
```

Reciever operating characteristics (ROC)-Area under curve(AUC) score and curve

```
#ROC_AUC score and curve
set.seed(843)

#convert to numeric

cv_predict.rose<-as.numeric(cv_predict.rose)
```

```
 roc(data=valid.rose[,-c(1,2)],response=target,predictor=cv_predict.rose,auc=TR
UE,
```

```
Call:
roc.default(response = target, predictor = cv_predict.rose, auc = TRUE,     plot = TRUE, data =
valid.rose[, -c(1, 2)])

Data: cv_predict.rose in 20012 controls (target 1) < 19988 cases (target 2).
Area under the curve: 1
```



I tried different ways to get good accuracy like changing count of one target class variable. Finally got area under ROC curve is 1 but this may not be possible.

3.2 Model Selection

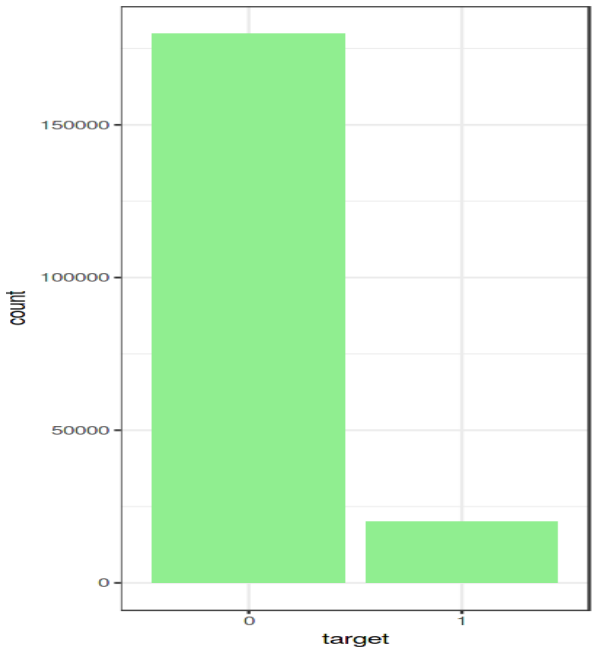
When we compare scores of areas under the ROC curve of all the models for an imbalanced data. We could conclude that below points as follow,

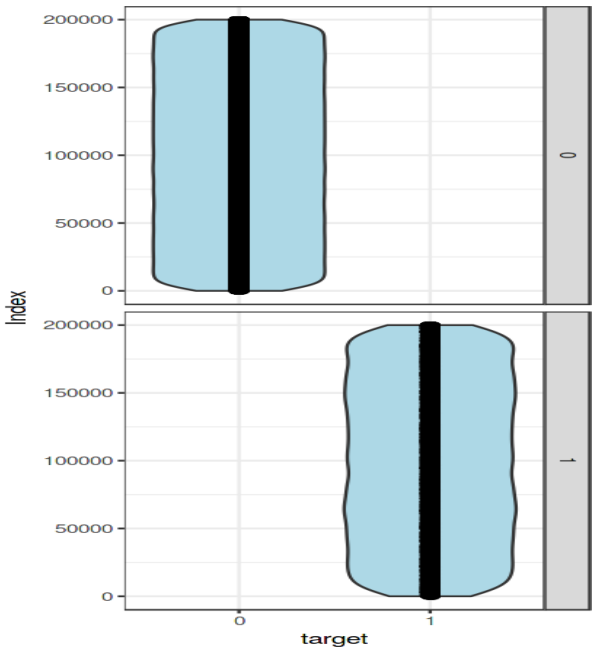
1. Logistic regression model is not performed well on imbalanced data.
2. We balance the imbalanced data using resampling techniques like SMOTE in python and ROSE in R.
3. Baseline logistic regression model is performed well on balanced data.
4. LightGBM model performed well on imbalanced data.

Finally, LightGBM is best choice for identifying which customers will make a specific transaction in the future, irrespective of the amount of money transacted.

Appendix A - Extra Figures

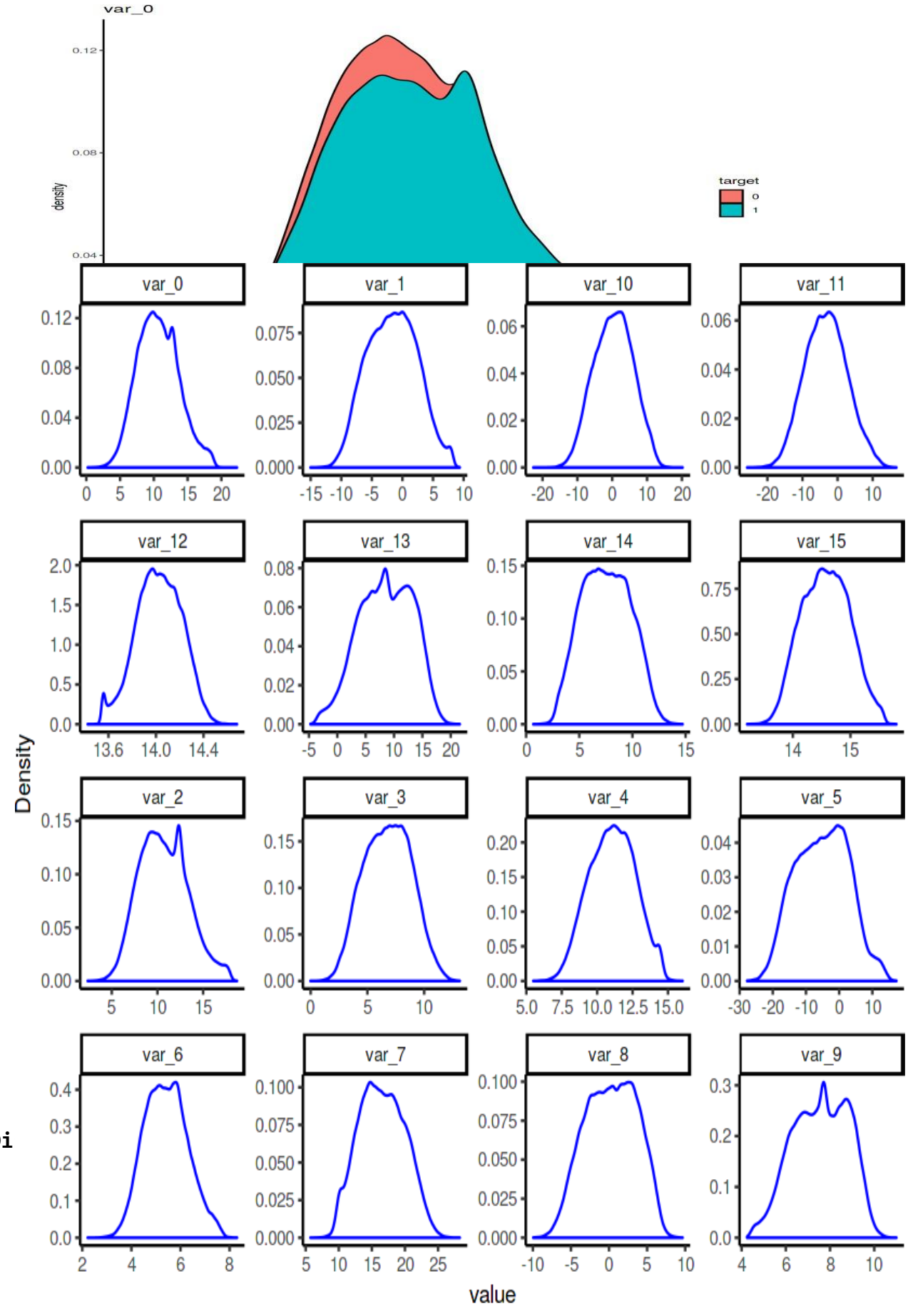
ggplot2 visualizations



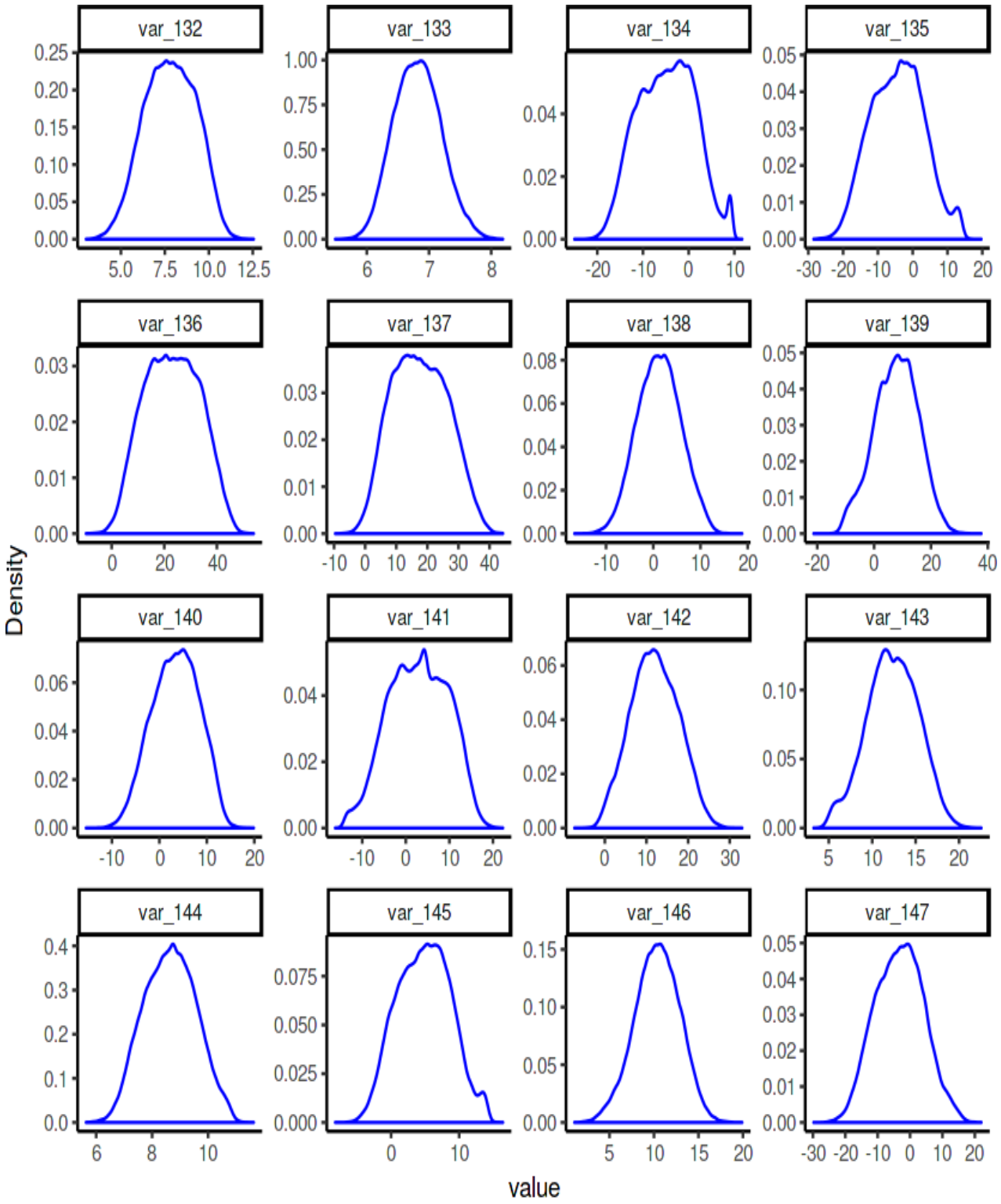


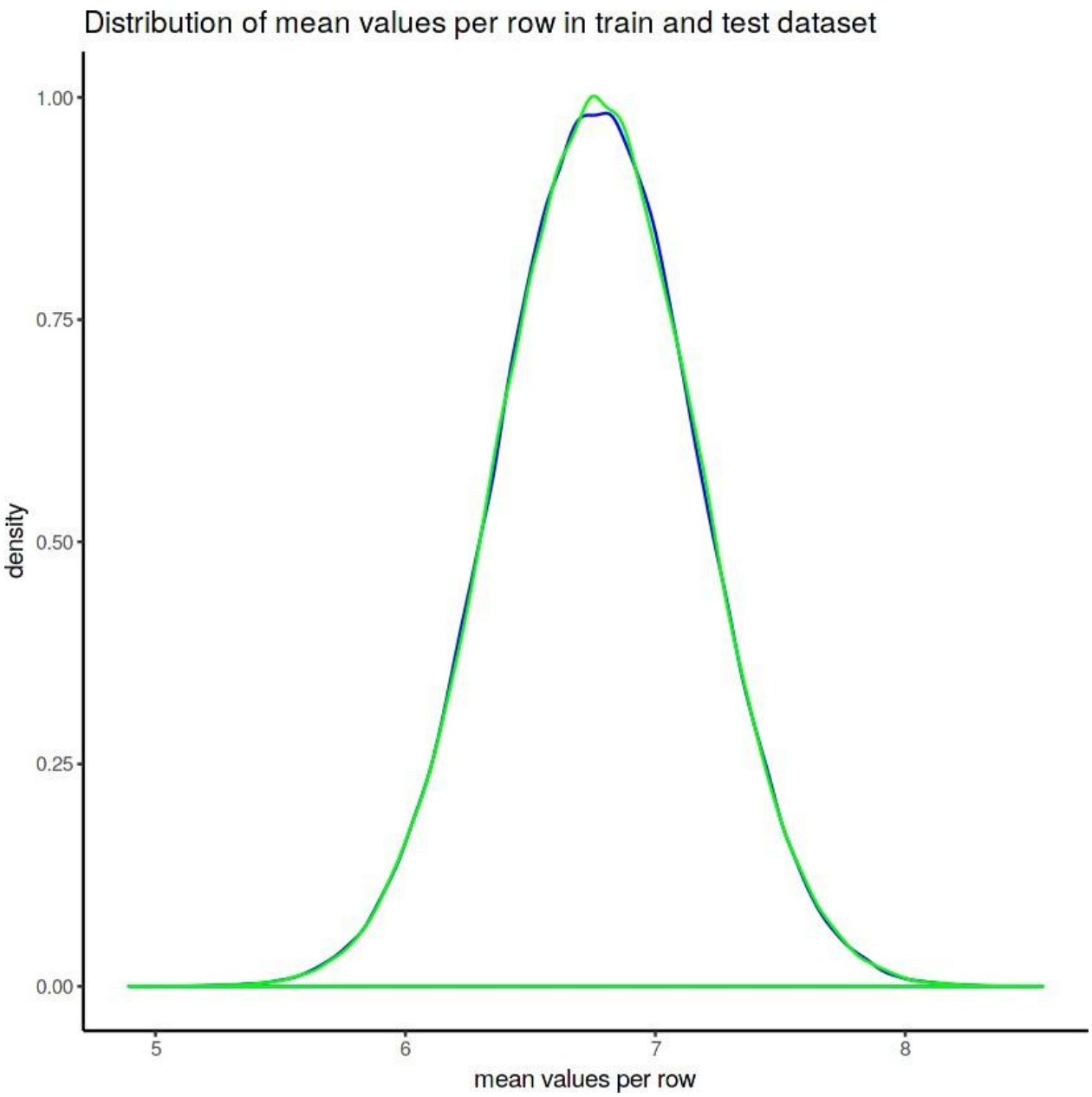
Target classes count

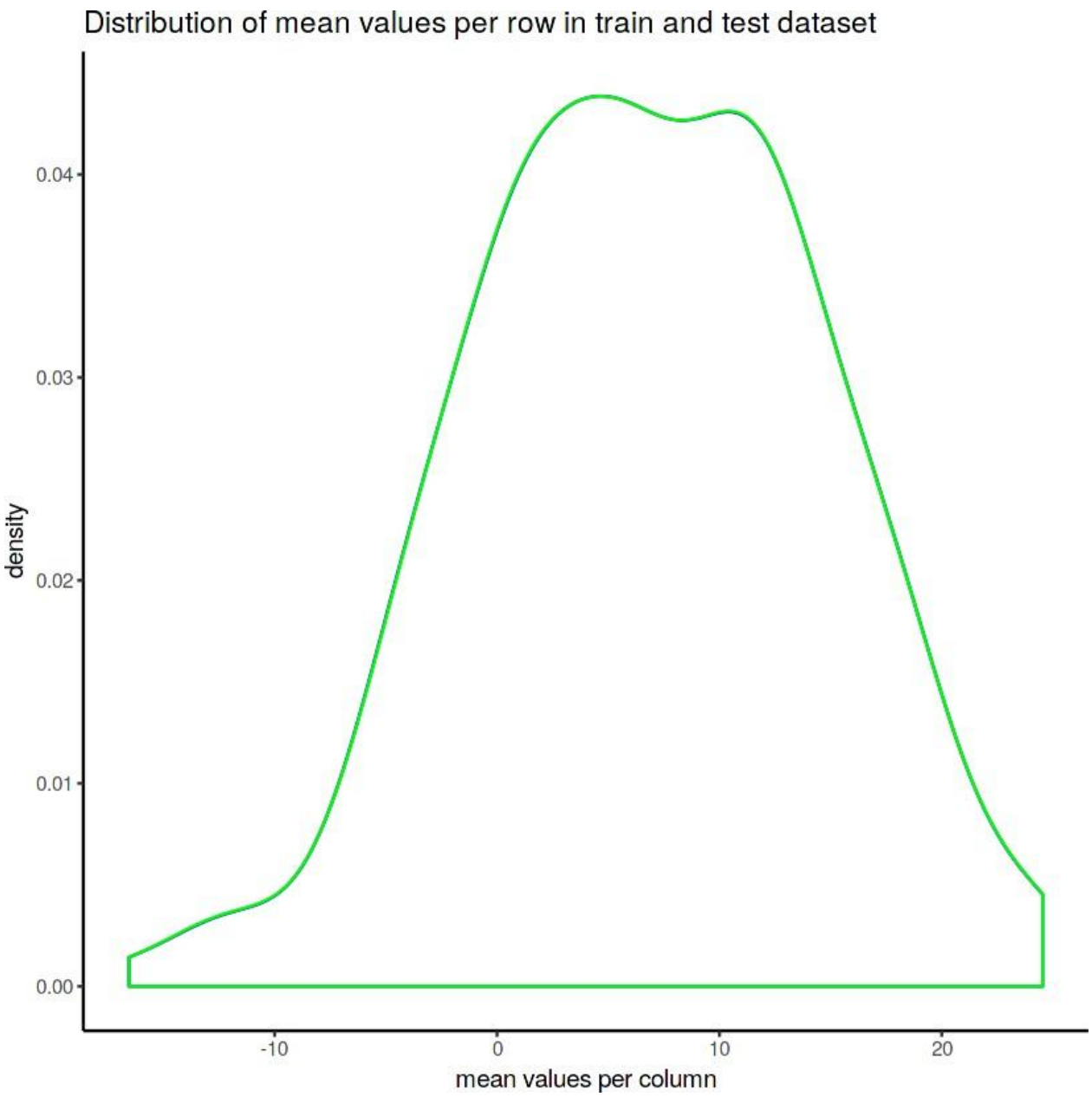
Distribution of train attributes

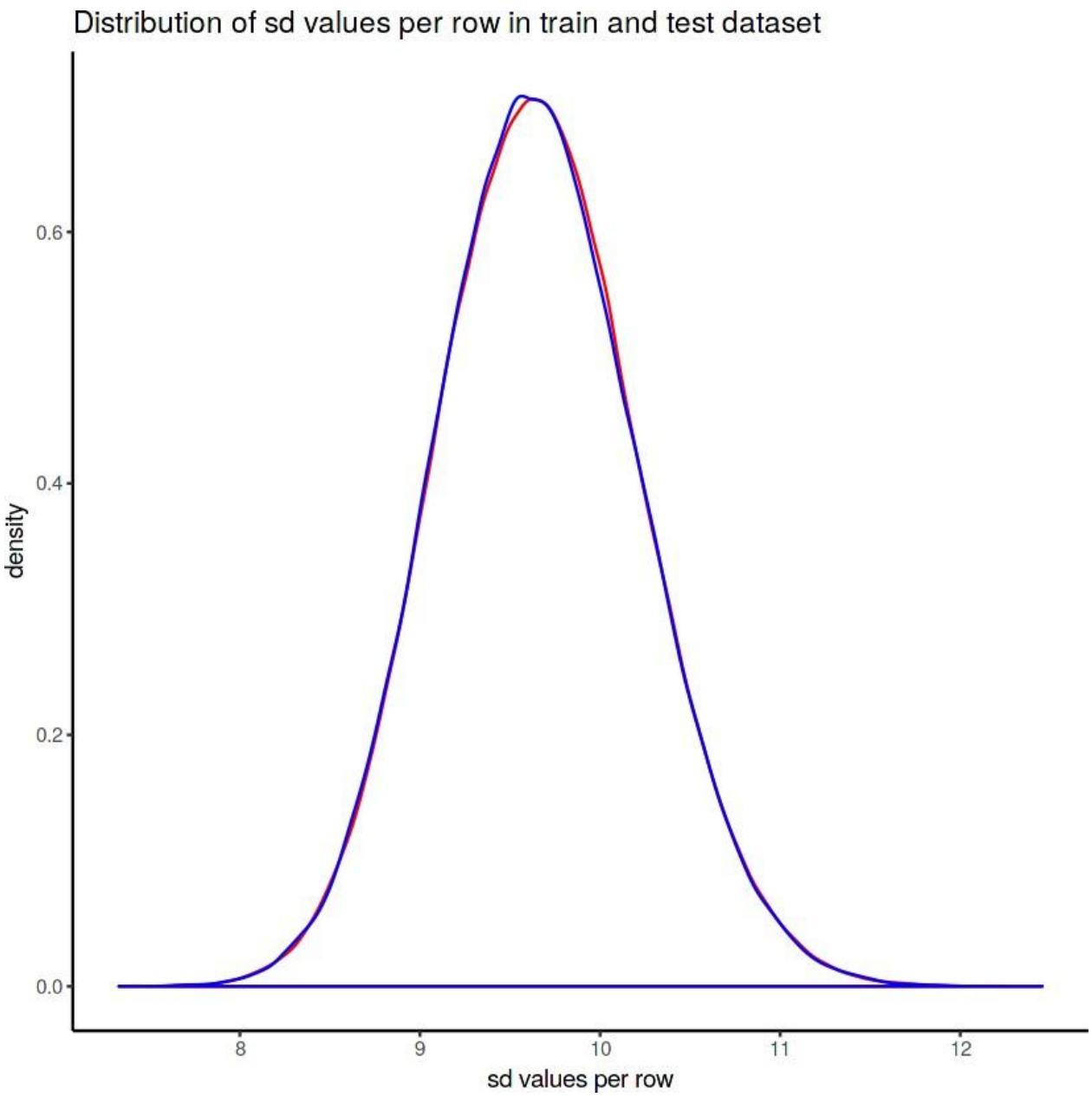

var_0
density
target
0
1
var_0
var_1
var_10
var_11
var_12
var_13
var_14
var_15
var_2
var_3
var_4
var_5
var_6
var_7
var_8
var_9
Density
value

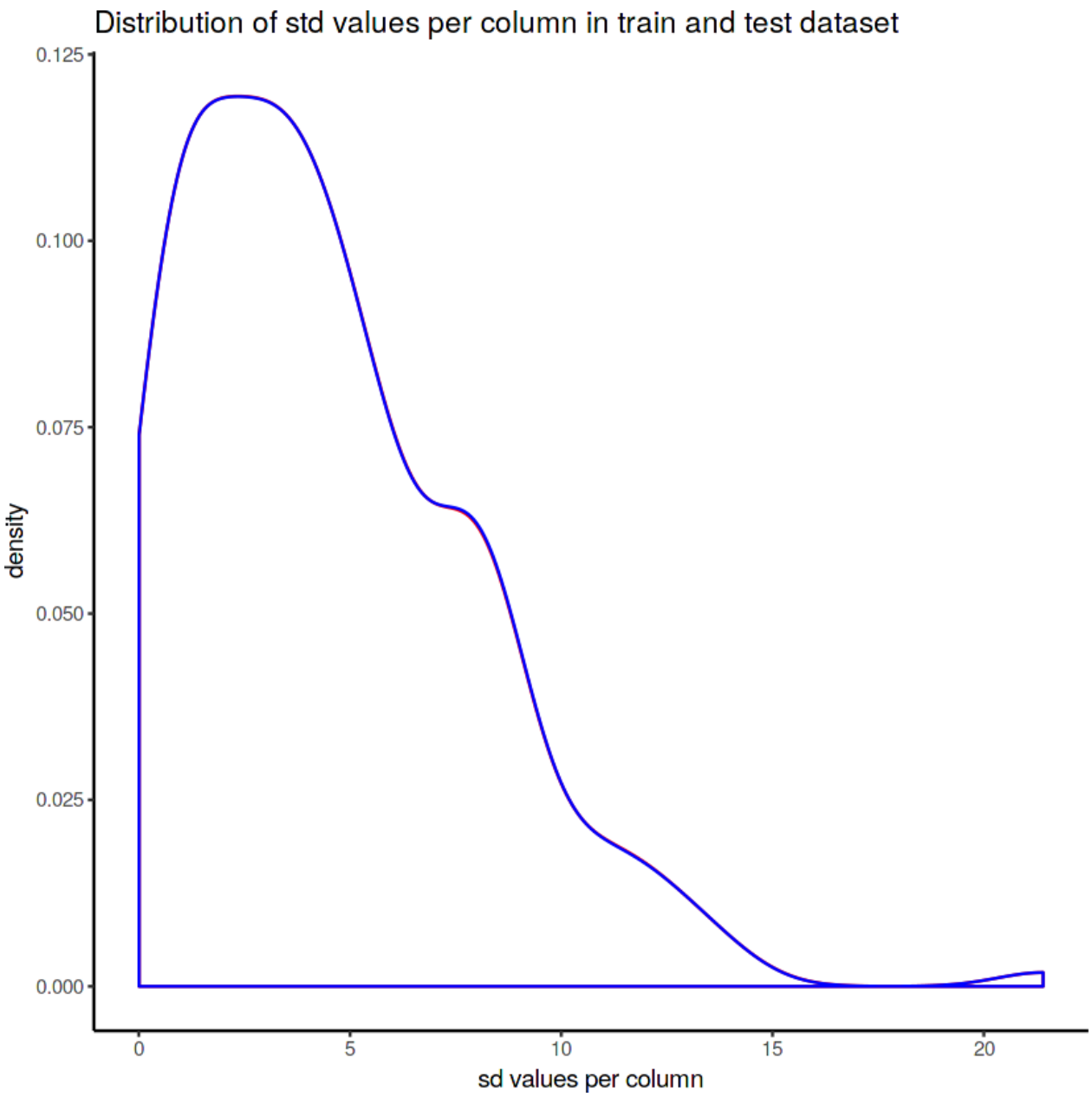
Di

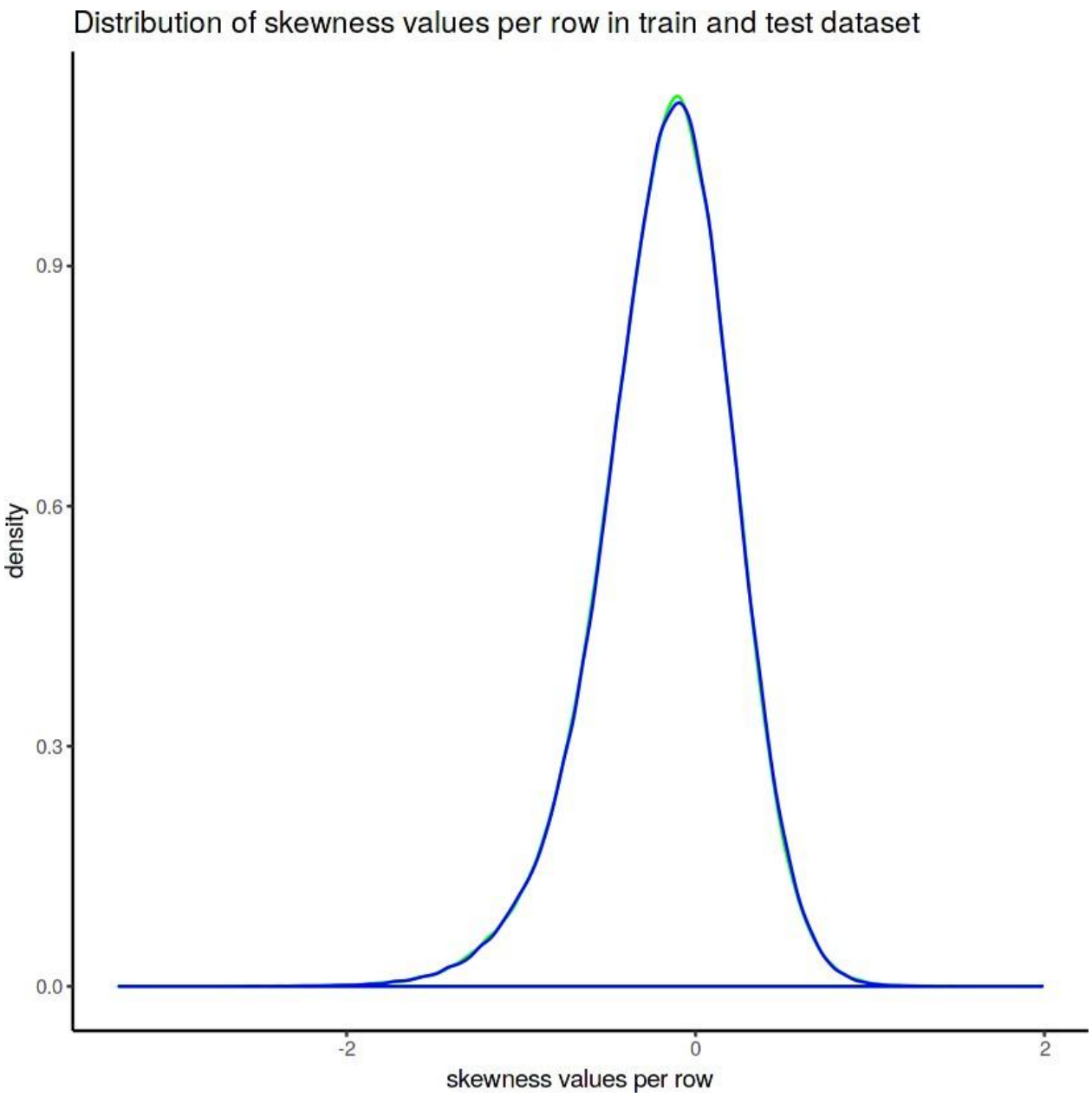

var_132
var_133
var_134
var_135
var_136
var_137
var_138
var_139
var_140
var_141
var_142
var_143
var_144
var_145
var_146
var_147
Density
value

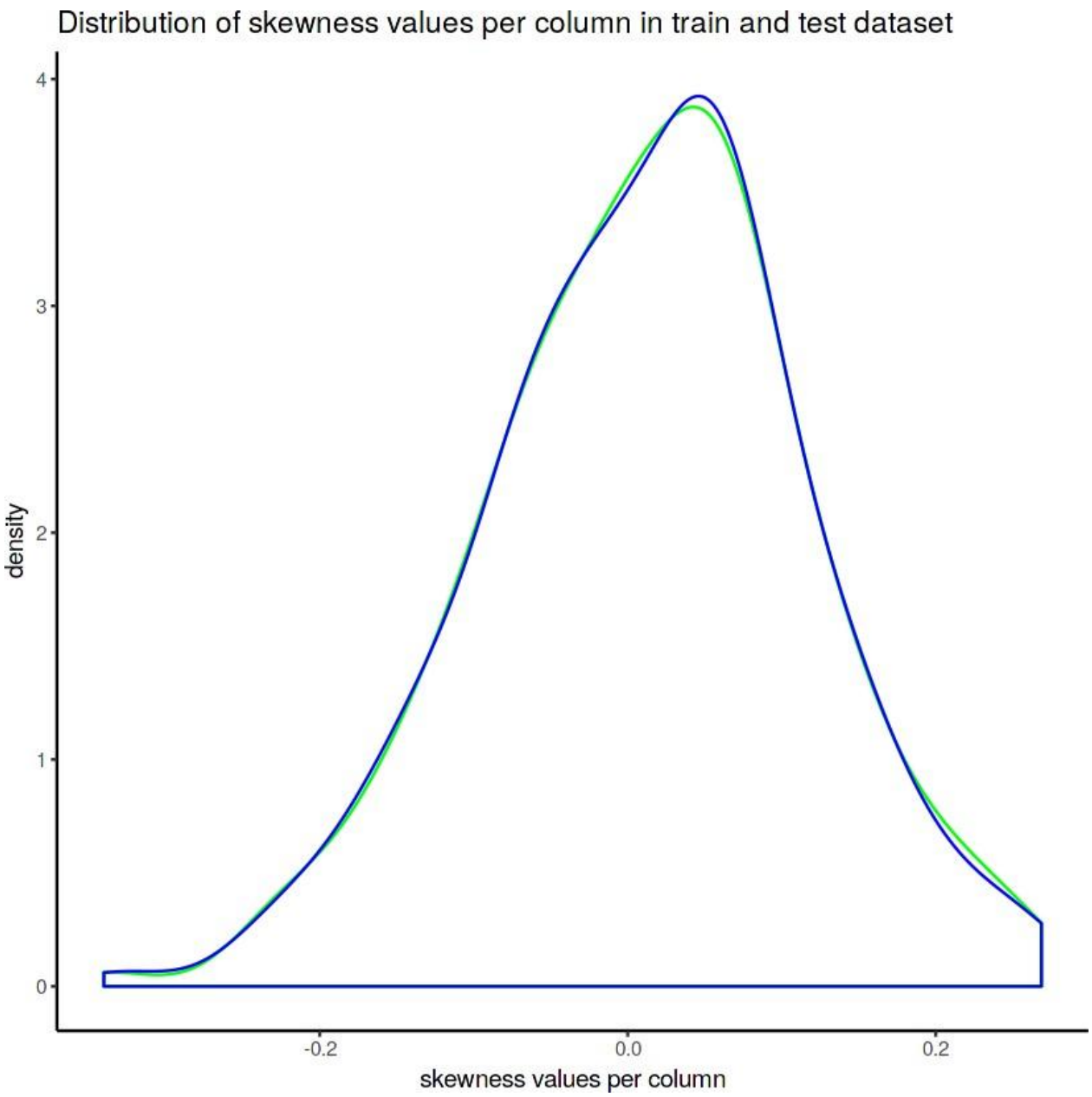

Distribution of mean values per row in train and test dataset
density
1.00
0.75
0.50
0.25
0.00
5
6
7
8
mean values per row

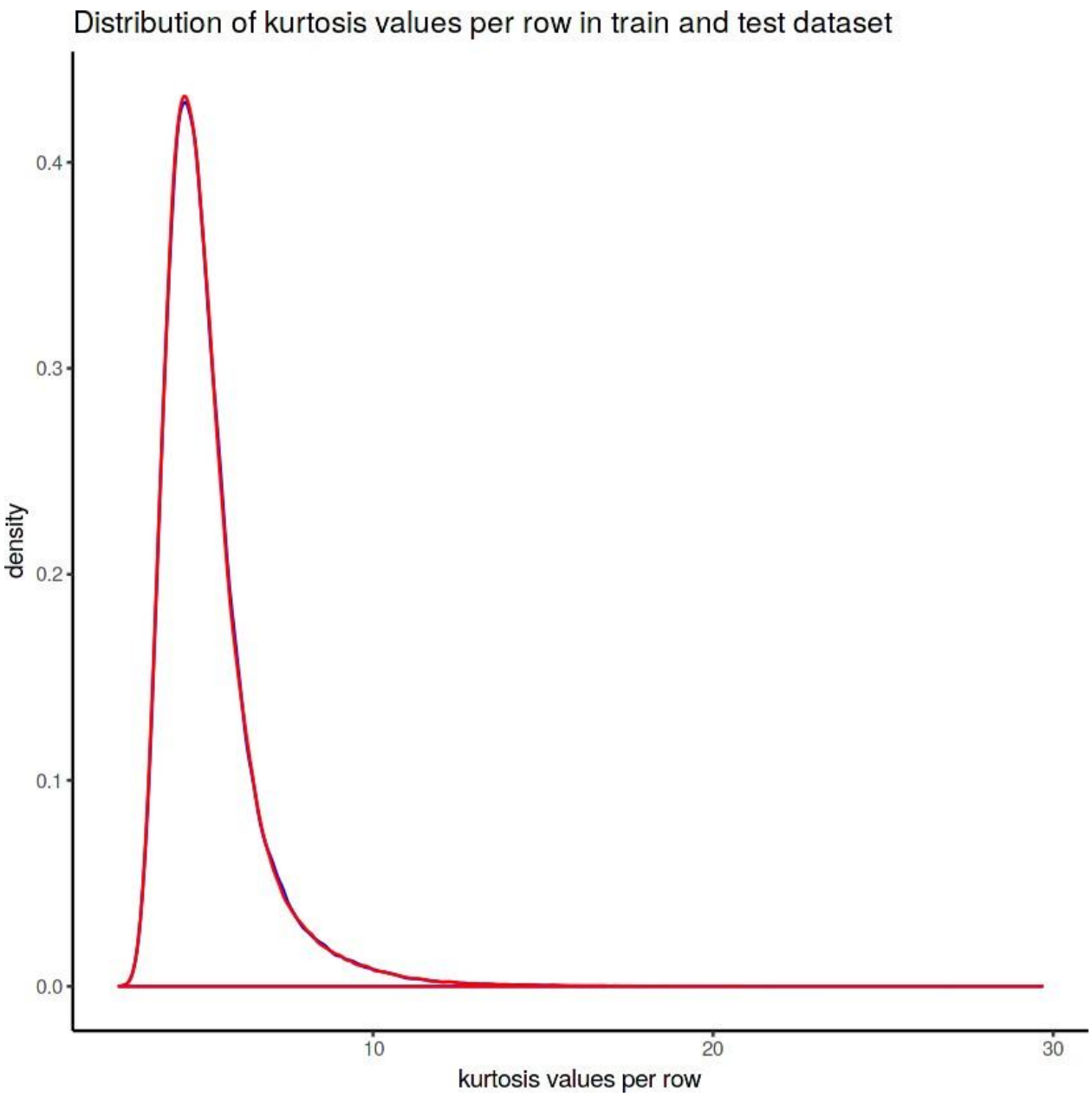

Distribution of mean values per row in train and test dataset
density
0.04
0.03
0.02
0.01
0.00
-10
0
10
20
mean values per column

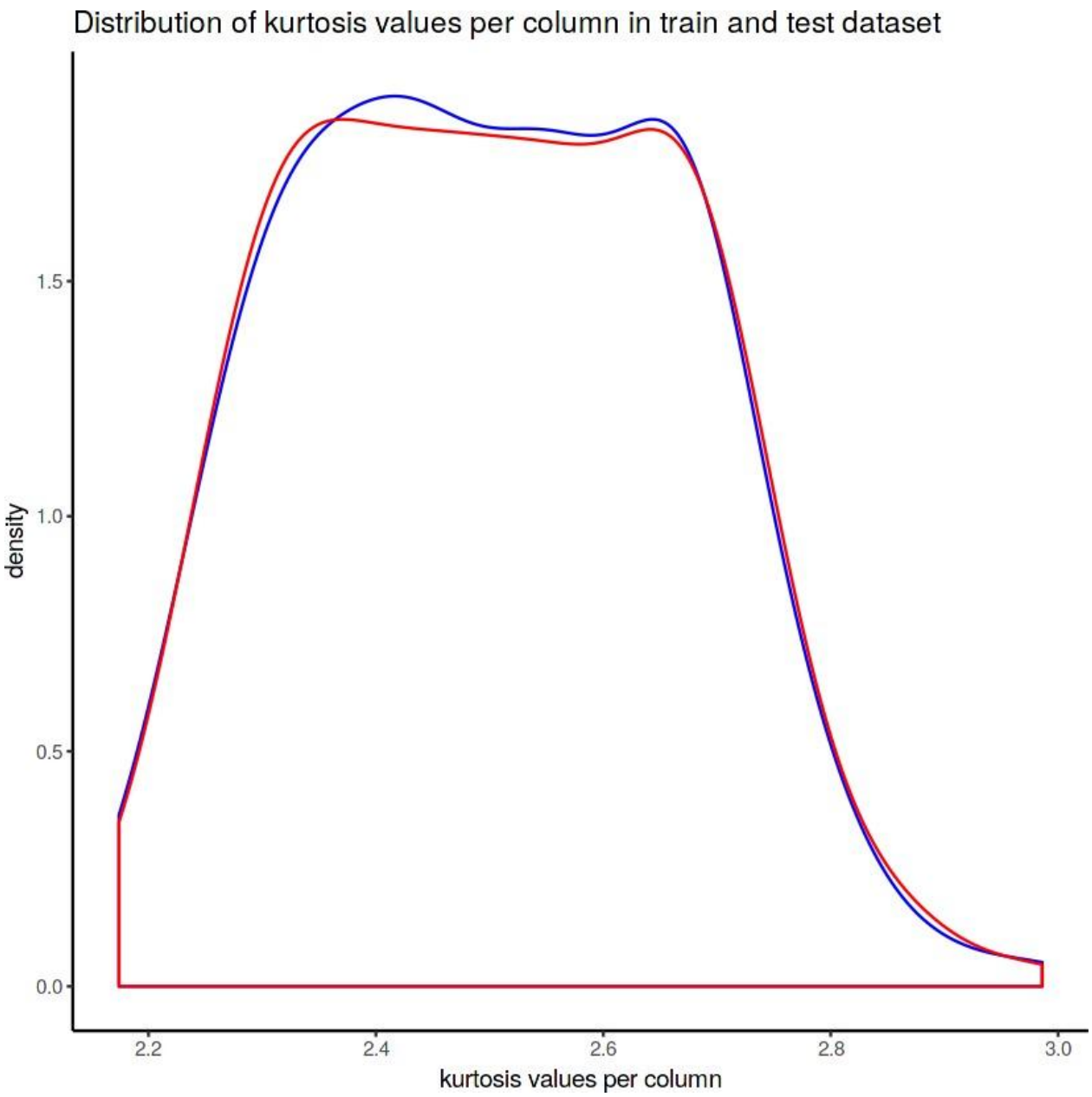

Distribution of sd values per row in train and test dataset
density
0.0
0.2
0.4
0.6
8
9
10
11
12
sd values per row


Distribution of std values per column in train and test dataset
0.125
0.100
0.075
0.050
0.025
0.000
density
0
5
10
15
20
sd values per column


Distribution of skewness values per row in train and test dataset
density
0.9
0.6
0.3
0.0
-2
0
2
skewness values per row


Distribution of skewness values per column in train and test dataset
density
4
3
2
1
0
-0.2
0.0
0.2
skewness values per column


Distribution of kurtosis values per row in train and test dataset
density
0.4
0.3
0.2
0.1
0.0
10
20
30
kurtosis values per row


Distribution of kurtosis values per column in train and test dataset
density
1.5
1.0
0.5
0.0
2.2
2.4
2.6
2.8
3.0
kurtosis values per column

Appendix B – Complete Python and R Code

Python Code

Exploratory Data Analysis

```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import RandomizedSearchCV
from sklearn.ensemble import RandomForestClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import train_test_split,cross_val_predict,cross_val_
score
from sklearn.metrics import roc_auc_score,confusion_matrix,make_scorer,classifica
tion_report,roc_curve,auc
from sklearn.model_selection import StratifiedKFold
from imblearn.over_sampling import SMOTE, RandomOverSampler
from imblearn.under_sampling import ClusterCentroids,NearMiss, RandomUnderSampler
import lightgbm as lgb
import eli5
from eli5.sklearn import PermutationImportance
from sklearn import tree
import graphviz
from pdpbox import pdp, get_dataset, info_plots
import scikitplot as skplt
from scikitplot.metrics import plot_confusion_matrix,plot_precision_recall_curve


from scipy.stats import randint as sp_randint
import warnings
warnings.filterwarnings('ignore')
random_state=42
np.random.seed(random_state)


#importing the train dataset
train_df=pd.read_csv('../input/train.csv')
train_df.head()
```

Target classes count

Distribution of train attributes

```
%%time
def plot_train_attribute_distribution(t0,t1,label1,label2,train_attributes):
    i=0
    sns.set_style('whitegrid')


    fig=plt.figure()
    ax=plt.subplots(10,10,figsize=(22,18))


    for attribute in train_attributes:
        i+=1
        plt.subplot(10,10,i)
        sns.distplot(t0[attribute],hist=False,label=label1)
        sns.distplot(t1[attribute],hist=False,label=label2)
        plt.legend()
        plt.xlabel('Attribute',)
        sns.set_style("ticks", {"xtick.major.size": 8, "ytick.major.size": 8})
    plt.show()


#importing the test dataset
test_df=pd.read_csv('../input/test.csv')
test_df.head()


#Shape of the test dataset
test_df.shape
```

Distribution of test attributes

```
def plot_test_attribute_distribution(test_attributes):
    i=0
    sns.set_style('whitegrid')


    fig=plt.figure()
    ax=plt.subplots(10,10,figsize=(22,18))


    for attribute in test_attributes:
        i+=1
        plt.subplot(10,10,i)
        sns.distplot(test_df[attribute],hist=False)
        plt.xlabel('Attribute',)
        sns.set_style("ticks", {"xtick.major.size": 8, "ytick.major.size": 8})
    plt.show()


#Let us see first 100 test attributes
```

Distribution of mean values in train and test dataset

```
%%time
#Distribution of mean values per column in train and test dataset
plt.figure(figsize=(16,8))
#train attributes
train_attributes=train_df.columns.values[2:202]
#test attributes
test_attributes=test_df.columns.values[1:201]
#Distribution plot for mean values per column in train attributes
sns.distplot(train_df[train_attributes].mean(axis=0),color='blue',kde=True,bins=150,label='train')
#Distribution plot for mean values per column in test attributes
sns.distplot(test_df[test_attributes].mean(axis=0),color='green',kde=True,bins=150,label='test')
```

```
#Distribution of mean values per row in train and test dataset
plt.figure(figsize=(16,8))
#Distribution plot for mean values per row in train attributes
sns.distplot(train_df[train_attributes].mean(axis=1),color='blue',kde=True,bins=150,label='train')
#Distribution plot for mean values per row in test attributes
sns.distplot(test_df[test_attributes].mean(axis=1),color='green',kde=True, bins=150, label='test')
plt.title('Distribution of mean values per row in train and test dataset')
```

Distribution of standard deviation (std) in train and test dataset

```
%%time
#Distribution of std values per column in train and test dataset
plt.figure(figsize=(16,8))
#train attributes
train_attributes=train_df.columns.values[2:202] #test
attributes test_attributes=test_df.columns.values[1:201]
#Distribution plot for std values per column in train attributes
sns.distplot(train_df[train_attributes].std(axis=0),color='red',kde=True, bins=150,label='train')
```

```
#Distribution plot for std values per column in test attributes
sns.distplot(test_df[test_attributes].std(axis=0),color='blue',kde=True,bins=150, label='test')
plt.title('Distribution of std values per column in train and test dataset') plt.legend()
plt.show()
#Distribution of std values per row in train and test dataset plt.figure(figsize=(16,8))
#Distribution plot for std values per row in train attributes
sns.distplot(train_df[train_attributes].std(axis=1),color='red',kde=True,bins=150
, label='train')
#Distribution plot for std values per row in test attributes
sns.distplot(test_df[test_attributes].std(axis=1),color='blue',kde=True, bins=150
,    label='test')
plt.title('Distribution of std values per row in train and test dataset') plt.legend()
```

Distribution of skewness in train and test dataset

```
%%time
#Distribution of skew values per column in train and test dataset
plt.figure(figsize=(16,8))
#train attributes
train_attributes=train_df.columns.values[2:202]
#test attributes
test_attributes=test_df.columns.values[1:201]
bins=150,label='train')
#Distribution plot for skew values per column in test attributes
sns.distplot(test_df[test_attributes].skew(axis=0),color='blue',kde=True,bins=150
,label='test')
plt.title('Distribution of skewness values per column in train and test dataset')
plt.legend()
plt.show()


#Distribution of skew values per row in train and test dataset
plt.figure(figsize=(16,8))
#Distribution plot for skew values per row in train attributes
sns.distplot(train_df[train_attributes].skew(axis=1),color='green',kde=True,
bins=150,label='train')
#Distribution plot for skew values per row in test attributes
```

Distribution of kurtosis values in train and test dataset

```
%%time
#Distribution of kurtosis values per column in train and test dataset plt.figure(figsize=(16,8))
#train attributes
train_attributes=train_df.columns.values[2:202] #test
attributes test_attributes=test_df.columns.values[1:201]
#Distribution plot for kurtosis values per column in train attributes
sns.distplot(train_df[train_attributes].kurtosis(axis=0),color='blue',kde=True, bins=150,label='train')
#Distribution plot for kurtosis values per column in test attributes
sns.distplot(test_df[test_attributes].kurtosis(axis=0),color='red',kde=True, bins=150,label='test')
plt.title('Distribution of kurtosis values per column in train and test dataset') plt.legend()
plt.show()


#Distribution of kutosis values per row in train and test dataset
plt.figure(figsize=(16,8))
#Distribution plot for kurtosis values per row in train attributes
sns.distplot(train_df[train_attributes].kurtosis(axis=1),color='blue',kde=True, bins=150,label='train')
#Distribution plot for kurtosis values per row in test attributes
sns.distplot(test_df[test_attributes].kurtosis(axis=1),color='red',kde=True, bins=150, label='test')
plt.title('Distribution of kurtosis values per row in train and test dataset') plt.legend()
plt.show()
```

Missing value analysis and Correlations

```
%%time
#Finding the missing values in train and test data
train_missing=train_df.isnull().sum().sum()
test_missing=test_df.isnull().sum().sum() print('Missing values
in train data :',train_missing) print('Missing values in test data
:',test_missing


%%time
#Correlations in train attributes train_attributes=train_df.columns.values[2:202]
```

```
train_correlations=train_df[train_attributes].corr().abs().unstack().sort_values(k
ind='quicksort').reset_index()
train_correlations=train_correlations[train_correlations['level_0']!=train_correla tions['level_1']]

print(train_correlations.head(10))
print(train_correlations.tail(10))


%%time

#Correlations in test attributes
test_attributes=test_df.columns.values[1:201]

test_correlations=test_df[test_attributes].corr().abs().unstack().sort_values(kind

='quicksort').reset_index()
test_correlations=test_correlations[test_correlations['level_0']!=test_correlation s['level_1']]

print(test_correlations.head(10))
print(test_correlations.tail(10))


#Correlation plot


%%time

#Correlations in train data
train_correlations=train_df[train_attributes].corr()
train_correlations=train_correlations.values.flatten()
train_correlations=train_correlations[train_correlations!=1]
test_correlations=test_df[test_attributes].corr() #Correlations in test
data test_correlations=test_correlations.values.flatten()
test_correlations=test_correlations[test_correlations!=1]


plt.figure(figsize=(20,5))

#Distribution plot for correlations in train data sns.distplot(train_correlations,
color="Red", label="train") #Distribution plot for correlations in test data
sns.distplot(test_correlations, color="Blue", label="test") plt.xlabel("Correlation
values found in train and test") plt.ylabel("Density")

plt.title("Correlation distribution plot for train and test attributes") plt.legend()
```

Feature engineering

```
#training data
X=train_df.drop(columns=['ID_code','target'],axis=1)
test=test_df.drop(columns=['ID_code'],axis=1)
y=train_df['target']
```

```
#Split the training data
X_train,X_valid,y_train,y_valid=train_test_split(X,y,random_state=42)


print('Shape of X_train :',X_train.shape)
print('Shape of X_valid :',X_valid.shape)
print('Shape of y_train :',y_train.shape)
print('Shape of y_valid :',y_valid.shape)


%%time

#Random forest classifier
rf_model=RandomForestClassifier(n_estimators=10,random_state=42) #fitting the
model

rf_model.fit(X_train,y_train)


#Permutation importance


%%time

from eli5.sklearn import PermutationImportance
perm_imp=PermutationImportance(rf_model,random_state=42) #fitting
the model

perm_imp.fit(X_valid,y_valid)


%%time

#Important features eli5.show_weights(perm_imp,feature_names=X_valid.columns.tolist(),top=200)


#partial dependence plots
```

```
%%time
#Create the data we will plot 'var_81'
features=[v for v in X_valid.columns if v not in ['ID_code','target']]
pdp_data=pdp.pdp_isolate(rf_model,dataset=X_valid,model_features=features,feature= 'var_81')
#plot feature "var_81"
pdp.pdp_plot(pdp_data,'var_81')
plt.show()


%%time
#Create the data we will plot
pdp_data=pdp.pdp_isolate(rf_model,dataset=X_valid,model_features=features,feature= '
var_109')
#plot feature "var_109"
pdp.pdp_plot(pdp_data,'var_109') plt.show()
```

Handling of imbalanced data

```
#Training data
X=train_df.drop(['ID_code','target'],axis=1)
Y=train_df['target']
#StratifiedKFold cross validator
cv=StratifiedKFold(n_splits=5,random_state=42,shuffle=True) for
train_index,valid_index in cv.split(X,Y):
    X_train, X_valid=X.iloc[train_index], X.iloc[valid_index] y_train,
    y_valid=Y.iloc[train_index], Y.iloc[valid_index]


print('Shape of X_train :',X_train.shape)
print('Shape of X_valid :',X_valid.shape)
print('Shape of y_train :',y_train.shape)
print('Shape of y_valid :',y_valid.shape)


%%time
#Logistic regression model
lr_model=LogisticRegression(random_state=42) #fitting
the lr model lr_model.fit(X_train,y_train)
```

```
#Accuracy of the model
lr_score=lr_model.score(X_train,y_train)
print('Accuracy of the lr_model :',lr_score)


%%time

#Cross validation prediction
cv_predict=cross_val_predict(lr_model,X_valid,y_valid,cv=5) #Cross
validation score cv_score=cross_val_score(lr_model,X_valid,y_valid,cv=5)
print('cross_val_score :',np.average(cv_score))


#Confusion matrix
cm=confusion_matrix(y_valid,cv_predict)
#Plot the confusion matrix

plot_confusion_matrix(y_valid,cv_predict,normalize=False,figsize=(15,8))


#ROC_AUC score
roc_score=roc_auc_score(y_valid,cv_predict)
print('ROC score :',roc_score)


#ROC_AUC
curve plt.figure()

false_positive_rate,recall,thresholds=roc_curve(y_valid,cv_predict)
roc_auc=auc(false_positive_rate,recall)

plt.title('Reciver Operating Characteristics(ROC)')
plt.plot(false_positive_rate,recall,'b',label='ROC(area=%0.3f)' %roc_auc) plt.legend()

plt.plot([0,1],[0,1],'r--')

plt.xlim([0.0,1.0])

plt.ylim([0.0,1.0]) plt.ylabel('Recall(True
Positive Rate)') plt.xlabel('False Positive Rate')

plt.show()
print('AUC:',roc_auc)


#Classification report
scores=classification_report(y_valid,cv_predict)
print(scores)
```

```
%%time

#Predicting the model
X_test=test_df.drop(['ID_code'],axis=1)
lr_pred=lr_model.predict(X_test)
print(lr_pred)


#Synthetic Minority Oversampling Technique sm
= SMOTE(random_state=42, ratio=1.0)
#Generating synthetic data points

X_smote,y_smote=sm.fit_sample(X_train,y_train)
X_smote_v,y_smote_v=sm.fit_sample(X_valid,y_valid)


#Logistic regression model for SMOTE
smote=LogisticRegression(random_state=42) #fitting the
smote model smote.fit(X_smote,y_smote)


#Accuracy of the model
smote_score=smote.score(X_smote,y_smote)
print('Accuracy of the smote_model :',smote_score)


#Cross validation prediction
cv_pred=cross_val_predict(smote,X_smote_v,y_smote_v,cv=5) #Cross
validation score
cv_score=cross_val_score(smote,X_smote_v,y_smote_v,cv=5)
print('cross_val_score :',np.average(cv_score))


#Confusion matrix
cm=confusion_matrix(y_smote_v,cv_pred)
#Plot the confusion matrix

plot_confusion_matrix(y_smote_v,cv_pred,normalize=False,figsize=(15,8))


#ROC_AUC score
roc_score=roc_auc_score(y_smote_v,cv_pred)
print('ROC score :',roc_score)
```

```
#ROC_AUC
curve plt.figure()

false_positive_rate,recall,thresholds=roc_curve(y_smote_v,cv_pred)
roc_auc=auc(false_positive_rate,recall)

plt.title('Reciver Operating Characteristics(ROC)')
plt.plot(false_positive_rate,recall,'b',label='ROC(area=%0.3f)' %roc_auc) plt.legend()

plt.plot([0,1],[0,1],'r--')

plt.xlim([0.0,1.0])

plt.ylim([0.0,1.0]) plt.ylabel('Recall(True
Positive Rate)')

plt.xlabel('False Positive Rate')
plt.show()

print('AUC:',roc_auc)


#Classification report
scores=classification_report(y_smote_v,cv_pred)
print(scores)


%%time

#Predicting the model
X_test=test_df.drop(['ID_code'],axis=1)
smote_pred=smote.predict(X_test)
print(smote_pred)


LightGBM


#Training the model
#training data

lgb_train=lgb.Dataset(X_train,label=y_train)
#validation data
lgb_valid=lgb.Dataset(X_valid,label=y_valid)


#Selecting best hyperparameters by tuning of different parameters
```

```
params={'boosting_type': 'gbdt',
              'max_depth' : -1, #no limit for max_depth if <0
              'objective': 'binary', 'boost_from_average':False,
              'nthread': 8,
              'metric':'auc',
              'num_leaves': 100,
              'learning_rate': 0.03,
              'max_bin': 950,              #default 255
              'subsample_for_bin': 200,
              'subsample': 1,
              'subsample_freq': 1,
              'colsample_bytree': 0.8,
              'reg_alpha':    1.2,    #L1     regularization(>0)
              'reg_lambda':    1.2,#L2     regularization(>0)
              'min_split_gain': 0.5, #>0
              'min_child_weight': 1,
              'min_child_samples': 5,
              'is_unbalance':True,
              }
num_rounds=3000
lgbm= lgb.train(params,lgb_train,num_rounds,valid_sets=[lgb_train,lgb_valid],
verbose_eval=100,early_stopping_rounds = 1000)


X_test=test_df.drop(['ID_code'],axis=1)
#predict the model
#probability predictions
lgbm_predict_prob=lgbm.predict(X_test,random_state=42,num_iteration=lgbm.best_iteration)
```

```
#Convert to binary output 1 or 0
lgbm_predict=np.where(lgbm_predict_prob>=0.5,1,0)
print(lgbm_predict_prob)
print(lgbm_predict)


#plot the important features
lgb.plot_importance(lgbm,max_num_features=150,importance_type="split",figsize=(20,
50))


#final submission
sub_df=pd.DataFrame({'ID_code':test_df['ID_code'].values})
sub_df['lgbm_predict_prob']=lgbm_predict_prob
sub_df['lgbm_predict']=lgbm_predict
```

R Code

Exploratory Data Analysis

```
#Load the libraries
library(tidyverse) library(moments)
library(DataExplorer) library(caret)
library(Matrix) library(mlbench)
library(caTools)
library(randomForest)
library(glmnet) library(mlr)
library(unbalanced) library(vita)
library(rBayesianOptimization)
library(lightgbm) library(boot)
library(pROC)
library(DMwR)
library(ROSE)
library(yardstick)


#loading the train data
train_df<-read.csv('../input/train.csv') head(train_df)


#Dimension of train data
dim(train_df)


#Summary of the dataset
str(train_df)
#convert to factor
train_df$target<-as.factor(train_df$target)
```

Target classes count in train data

```
require(gridExtra) #Count of
target classes
table(train_df$target)

#Percenatge counts of target classes
table(train_df$target)/length(train_df$target)*100 #Bar plot for count of
target classes

plot1<-ggplot(train_df,aes(target))+theme_bw()+geom_bar(stat='count',fill='lig htgreen')

#Violin with jitter plots for target classes

plot2<-ggplot(train_df,aes(y=target,x=1:nrow(train_df)))+theme_bw()+geom_violi n(fill='lightblue')+
facet_grid(train_df$target)+geom_jitter(width=0.02)+labs(y='Index') grid.arrange(plot1,plot2, ncol=2)
```

Distribution of train attributes

```
#loading test data
test_df<-read.csv('../input/test.csv') head(test_df)


#Dimension of test dataset dim(test_df)


#Distribution of test attributes from 2 to 101 plot_density(test_df[,c(2:101)],
ggtheme =theme_classic(), geom_density_args =list(color='blue'))


#Distribution of test attributes from 102 to 201 plot_density(test_df[,c(102:201)],
ggtheme = theme_classic(), geom_density_args = list(color='blue'))
```

Distribution of test attributes

Distribution of mean values in train and test dataset

```
#Applying the function to find mean values per row in train and test data. train_mean<-apply(train_df[,-
c(1,2)],MARGIN=1,FUN=mean)

test_mean<-apply(test_df[,-c(1)],MARGIN=1,FUN=mean) ggplot()+

#Distribution of mean values per row in train data geom_density(data=train_df[,-
c(1,2)],aes(x=train_mean),kernel='gaussian', show. legend=TRUE,color='blue')+theme_classic()+
```

```
#Distribution of mean values per row in test data geom_density(data=test_df[,-
c(1)],aes(x=test_mean),kernel='gaussian', show.legend=TRUE,color='green')+

labs(x='mean values per row',title="Distribution of mean values per row in train and test dataset")


#Applying the function to find mean values per column in train and test data. train_mean<-apply(train_df[,-
c(1,2)],MARGIN=2,FUN=mean)

test_mean<-apply(test_df[,-c(1)],MARGIN=2,FUN=mean) ggplot()+

#Distribution of mean values per column in train data
geom_density(aes(x=train_mean),kernel='gaussian',show.legend=TRUE, color='blue')+theme_classic()+

#Distribution of mean values per column in test data
geom_density(aes(x=test_mean),kernel='gaussian',show.legend=TRUE, color='green')+

labs(x='mean values per column',title="Distribution of mean values perrow in train and test
dataset")
```

Distribution of standard deviation in train and test dataset

```
#APPLYING THE FUNCTION TO FIND STANDARD DEVIATION VALUES PER ROW INTRAIN AND TEST DATA.
train_sd<-apply(train_df[,-c(1,2)],MARGIN=1,FUN=sd)
test_sd<-apply(test_df[,-c(1)],MARGIN=1,FUN=sd) ggplot()+

#Distribution of sd values per row in train data geom_density(data=train_df[,-
c(1,2)],aes(x=train_sd),kernel='gaussian', show.le
gend=TRUE,color='red')+theme_classic()+

#Distribution of mean values per row in test data geom_density(data=test_df[,-
c(1)],aes(x=test_sd),kernel='gaussian', show.legend=TRUE,color='blue')+

labs(x='sd values per row',title="Distribution of sd values per row in train and test
dataset")


#Applying the function to find sd values per column in train and test data. train_sd<-
apply(train_df[,-c(1,2)],MARGIN=2,FUN=sd)

test_sd<-apply(test_df[,-c(1)],MARGIN=2,FUN=sd)
ggplot()+

#Distribution of sd values per column in train data
geom_density(aes(x=train_sd),kernel='gaussian',show.legend=TRUE,color='red')+ theme_classic()+
```

```
#Distribution of sd values per column in test data
geom_density(aes(x=test_sd),kernel='gaussian',show.legend=TRUE,color='blue')+ labs(x='sd values per column',title="Distribution of std values per column in train and test dataset")
```

Distribution of skewness values in train and test dataset

```
#Applying the function to find skewness values per row in train and test data.
train_skew<-apply(train_df[,-c(1,2)],MARGIN=1,FUN=skewness) test_skew<-apply(test_df[,-c(1)],MARGIN=1,FUN=skewness) ggplot()+

#Distribution of skewness values per row in train data
geom_density(aes(x=train_skew),kernel='gaussian',show.legend=TRUE, color='green')+theme_classic()+

#Distribution of skewness values per column in test data
geom_density(aes(x=test_skew),kernel='gaussian',show.legend=TRUE, color='blue') +labs(x='skewness values per row',title="Distribution of skewness values per row in train and test dataset")


#Applying the function to find skewness values per column in train and test data.

train_skew<-apply(train_df[,-c(1,2)],MARGIN=2,FUN=skewness) test_skew<-apply(test_df[,-c(1)],MARGIN=2,FUN=skewness) ggplot()+

#Distribution of skewness values per column in train data
geom_density(aes(x=train_skew),kernel='gaussian',show.legend=TRUE, color='green')+theme_classic()+

#Distribution of skewness values per column in test data
geom_density(aes(x=test_skew),kernel='gaussian',show.legend=TRUE, color='blue')+labs(x='skewness values per column',title="Distribution of skewness values per column in train and test dataset")
```

Distribution of kurtosis values in train and test dataset

```
#Applying the function to find kurtosis values per row in train and test data. train_kurtosis<-apply(train_df[,-c(1,2)],MARGIN=1,FUN=kurtosis) test_kurtosis<-apply(test_df[,-c(1)],MARGIN=1,FUN=kurtosis)

ggplot()+

#Distribution of sd values per column in train data
geom_density(aes(x=train_kurtosis),kernel='gaussian',show.legend=TRUE, color='blue')+theme_classic()+

#Distribution of sd values per column in test data
geom_density(aes(x=test_kurtosis),kernel='gaussian',show.legend=TRUE, color='red')+labs(x='kurtosis values per row',title="Distribution of kurtosis values per row in train and test dataset")
```

#Applying the function to find kurtosis values per column in train and test data.

train_kurtosis<-apply(train_df[,-c(1,2)],MARGIN=2,FUN=kurtosis)
test_kurtosis<-apply(test_df[,-c(1)],MARGIN=2,FUN=kurtosis) ggplot()+

#Distribution of sd values per column in train data
geom_density(aes(x=train_kurtosis),kernel='gaussian',show.legend=TRUE,
color='blue')+theme_classic()+

#Distribution of sd values per column in test data
geom_density(aes(x=test_kurtosis),kernel='gaussian',show.legend=TRUE, color='red')+

labs(x='kurtosis values per column',title="Distribution of kurtosisvalues per column in train and test dataset")

Missing value analysis and Correlations

```
#Finding the missing values in train data missing_val<-
data.frame(missing_val=apply(train_df,2, function(x){sum(is.na(x))}))

missing_val<-sum(missing_val)
missing_val


#Finding the missing values in test data missing_val<-
data.frame(missing_val=apply(test_df,2, function(x){sum(is.na(x))}))

missing_val<-sum(missing_val)
missing_val


#Correlations in train data

train_df$target<-as.numeric(train_df$target)
train_correlations<-cor(train_df[,c(2:202)]) train_correlations


#Correlations in test data test_correlations<
```

Feature Engineering

```
#Split the training data
train_index<-sample(1:nrow(train_df),0.75*nrow(train_df)) train_data<-
train_df[train_index,]
valid_data<-train_df[-train_index,] dim(train_data)
dim(valid_data)


#Training the Random forest classifier set.seed(2732)
train_data$target<-as.factor(train_data$target) mtry<-
floor(sqrt(200))
tuneGrid<-expand.grid(.mtry=mtry)
rf<-randomForest(target~.,train_data[,-c(1)],mtry=mtry,ntree=10, importance=TRUE)


#Variable importance
VarImp<-importance(rf,type=2)
VarImp

#Partial dependence plot #We will
plot "var_81"
```

Handling of imbalanced data

```
#Confusion matrix set.seed(689)

#actual target variable target<-
valid.data$target #convert to factor
target<-as.factor(target) #predicted
target variable #convert to factor

cv_predict.lr<-as.factor(cv_predict.lr) confusionMatrix(data=cv_predict.lr,reference=target)



X_t<-as.matrix(train.data[-c(1,2)]) y_t<-
as.matrix(train.data$target) #validation dataset

X_v<-as.matrix(valid.data[-c(1,2)]) y_v<-
as.matrix(valid.data$target) #test data

test<-as.matrix(test_df[,-c(1)])


#Logistic regression model set.seed(667)

lr_model <-glmnet(X_t, y_t, family = "binomial") summary(lr_model)


#Cross validation prediction set.seed(8909)

cv_lr <- cv.glmnet(X_t,y_t,family = "binomial", type.measure = "class") cv_lr


#Minimum lambda
cv_lr$lambda.min

#plot the auc score vs log(lambda) plot(cv_lr)


#Model performance on validation dataset set.seed(5363)

cv_predict.lr<-predict(cv_lr,X_v,s = "lambda.min", type = "class") cv_predict.lr
```

```
#ROC_AUC score and curve
set.seed(892)
cv_predict.lr<-as.numeric(cv_predict.lr)
roc(data=valid.data[,-c(1,2)],response=target,predictor=cv_predict.lr, auc=TRUE,plot=TRUE)


#predict the model
set.seed(763)
lr_pred<-predict(lr_model,test,type='class') lr_pred


#Random Oversampling Examples(ROSE)
set.seed(699)
#train.data$target<-as.factor(train.data$target)
train.rose <- ROSE(target~., data=train.data[,-c(1)],seed=32)$data table(train.rose$target)
valid.rose <- ROSE(target~., data=valid.data[,-c(1)],seed=32)$data table(valid.rose$target)


#Logistic regression model set.seed(462)
lr_rose <-glmnet(as.matrix(train.rose),as.matrix(train.rose$target), family = "binomial")
summary(lr_rose)


#Cross validation prediction set.seed(473)
cv_rose = cv.glmnet(as.matrix(valid.rose),as.matrix(valid.rose$target), family =
"binomial", type.measure = "class")
cv_rose


#Minimum lambda
cv_rose$lambda.min
#plot the auc score vs log(lambda)
plot(cv_rose)


#Model performance on validation dataset set.seed(442)
cv_predict.rose<-predict(cv_rose,as.matrix(valid.rose),s ="lambda.min", type = "class")
```

```
cv_predict.rose


#Confusion matrix set.seed(478)

#actual target variable target<-
valid.rose$target #convert to
factor target<-as.factor(target)
#predicted target variable
#convert to factor

cv_predict.rose<-as.factor(cv_predict.rose) confusionMatrix(data=cv_predict.rose,reference=target)


#ROC_AUC score and curve
set.seed(843)

cv_predict.rose<-as.numeric(cv_predict.rose)

roc(data=valid.rose[,-c(1,2)],response=target,predictor=cv_predict.rose, auc=TRUE,plot=TRUE)


#predict the model
set.seed(6543)

rose_pred<-predict(lr_rose,test,type='class') rose_pred


#Convert data frame to matrix set.seed(5432)

X_train<-as.matrix(train.data[,-c(1,2)]) y_train<-
as.matrix(train.data$target) X_valid<-
as.matrix(valid.data[,-c(1,2)]) y_valid<-
as.matrix(valid.data$target) test_data<-
as.matrix(test_df[,-c(1)])


#training data

lgb.train <- lgb.Dataset(data=X_train, label=y_train) #Validation
data

lgb.valid <- lgb.Dataset(data=X_valid,label=y_valid)


set.seed(653)

lgb.grid = list(objective = "binary",
```

```
                metric = "auc", min_sum_hessian_in_leaf =
                1,
                feature_fraction = 0.7,
                bagging_fraction = 0.7,
                bagging_freq = 5,
                learning_rate=0.1,
                num_leaves=100,
                num_threads=8,
                min_data = 100,
                max_bin = 200,
                lambda_l1 = 8,
                lambda_l2 = 1.3, min_data_in_bin=150,
                min_gain_to_split = 20,
                min_data_in_leaf = 40,
                is_unbalance = TRUE)

set.seed(7663)

lgbm.model <- lgb.train(params = lgb.grid, data = lgb.train, nrounds =3000, eval_freq
=100,valids=list(val1=lgb.train,val2=lgb.valid), early_stopping_rounds = 1000)

#lgbm model performance on test data set.seed(6532)

lgbm_pred_prob <- predict(lgbm.model,test_data) print(lgbm_pred_prob)

#Convert to binary output (1 and 0) with threshold 0.5 lgbm_pred<-
ifelse(lgbm_pred_prob>0.5,1,0) print(lgbm_pred)


set.seed(6521)

tree_imp <- lgb.importance(lgbm.model, percentage = TRUE) lgb.plot.importance(tree_imp, top_n = 150,
measure = "Gain")


sub_df<-data.frame(ID_code=test_df$ID_code,lgb_predict_prob=lgbm_pred_prob, lgb
        _predict=lgbm_pred,smote_predict=smote_pred) write.csv(sub_df,'submission.CSV',row.names=F)
```

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