Santander customer transaction prediction

Submitted by

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Contents

1.Introduction

1.1. Background

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?

1.2. Problem statement

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

1.3. 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)

	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)

	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

2. Methodology

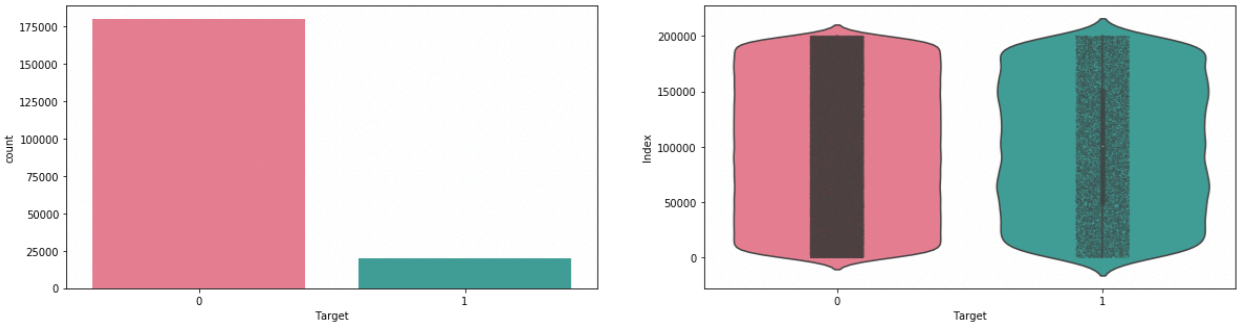
2.1. Exploratory Data Analysis (EDA)

Exploratory data analysis is one of the most important step 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 effect on performance of the model.

This is a binary classification problem under supervised machine learning algorithm. The task is to predict the value of target column in the test set

Now we are going to explain one by one as follows. In this EDA I explained with seaborn visualizations.

Target classes count



Observations:

- We have plotted countplot and violin plot for target variable.
- *seaborn.countplot* shows the counts of observations in each categorical bin using bars.

- *seaborn.violinplot* shows the distribution of quantitative data across several levels of one (or more) categorical variables such that those distributions can be compared.
- 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.
- Looking at the violin plots shows that there is no relationship between the target and the index of the train data frame. It is more dominated by the zero targets than for the ones.
- Looking at the jitter plots within the violin plots. We can observe that targets look uniformly distributed over the indexes of the data frame.

2.1.1. 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()
[1] 0
test_missing=test_df.isnull().sum().sum()
[1] 0
```

2.1.2. 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 observed 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 observed 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

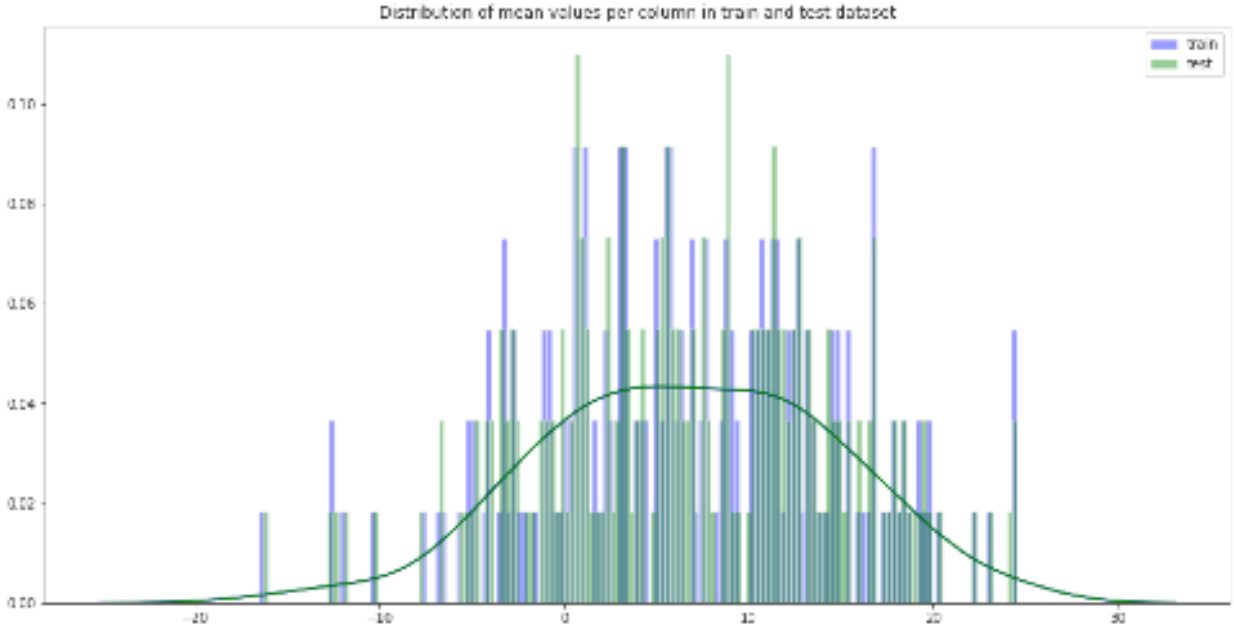
Let us look distribution of test attributes from var_0 to var_99

Take away:

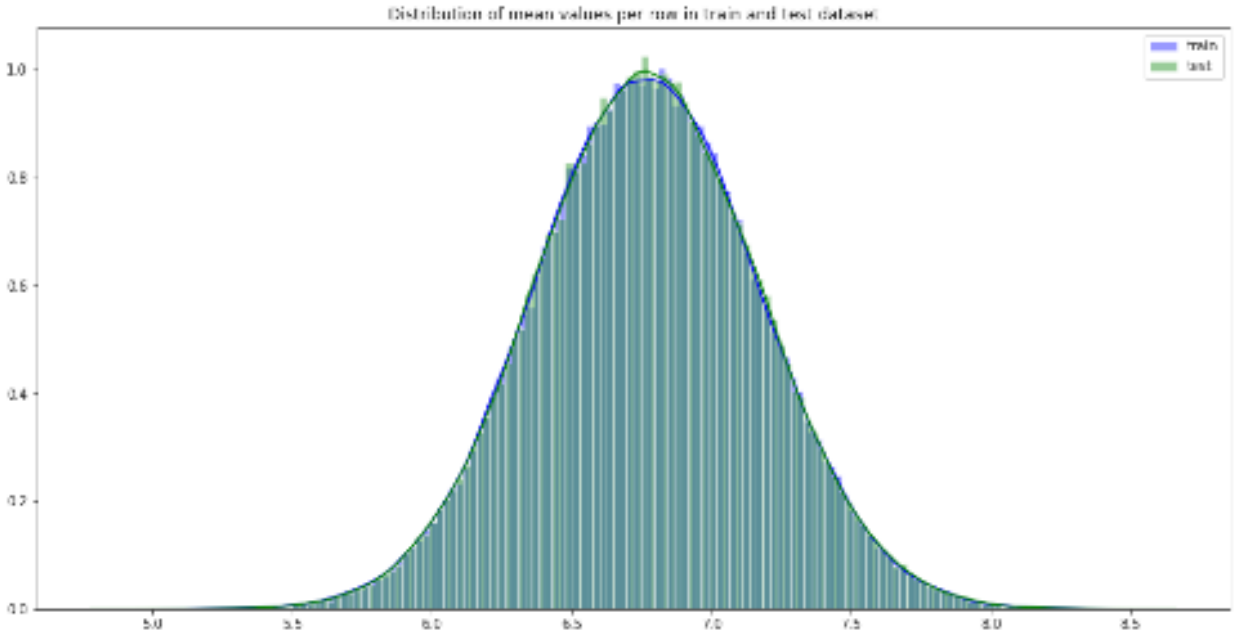
- We can observed that there is a considerable number of features which are significantly have different distributions. For example like var_0, var_1, var_9, var_18 var_38 etc.
- We can observed that there is a considerable number of features which are significantly have same distributions. For example 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

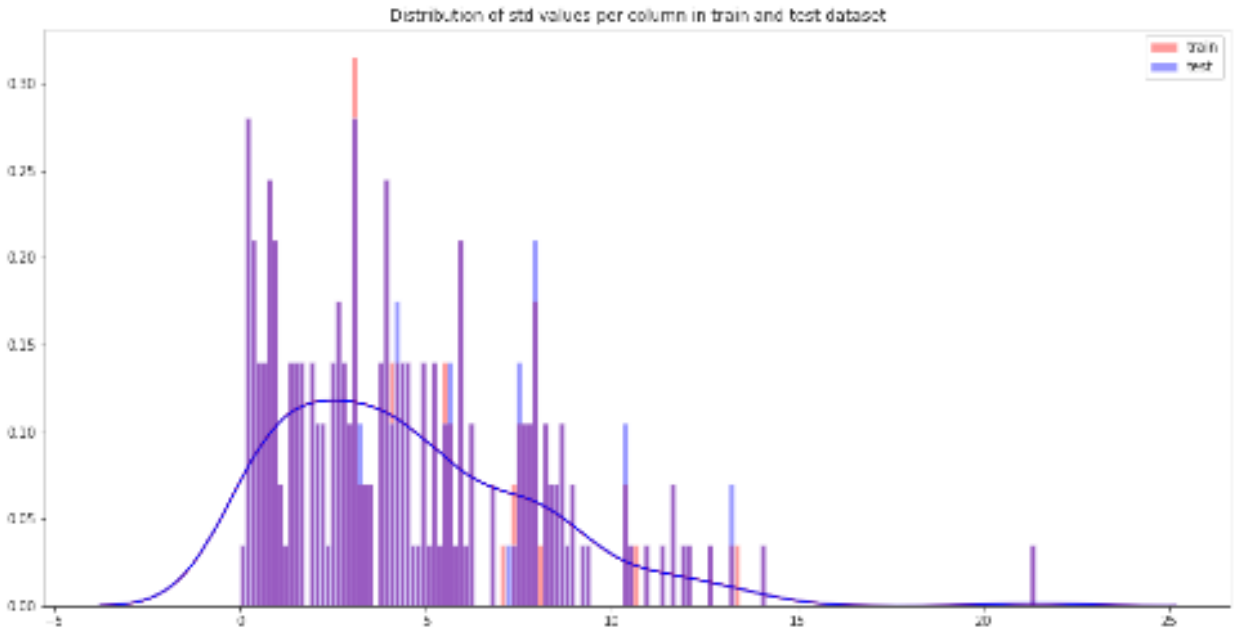


Let us look distribution of mean values per row in train and test dataset

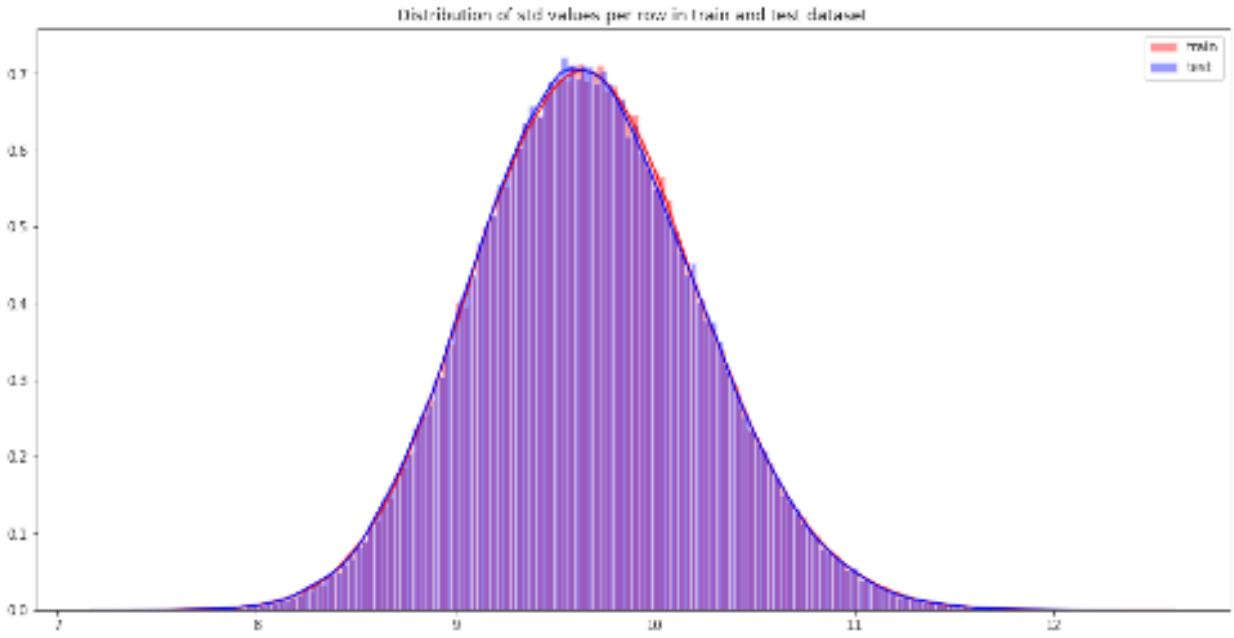


Distribution of standard deviation (std) values in train and test dataset

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

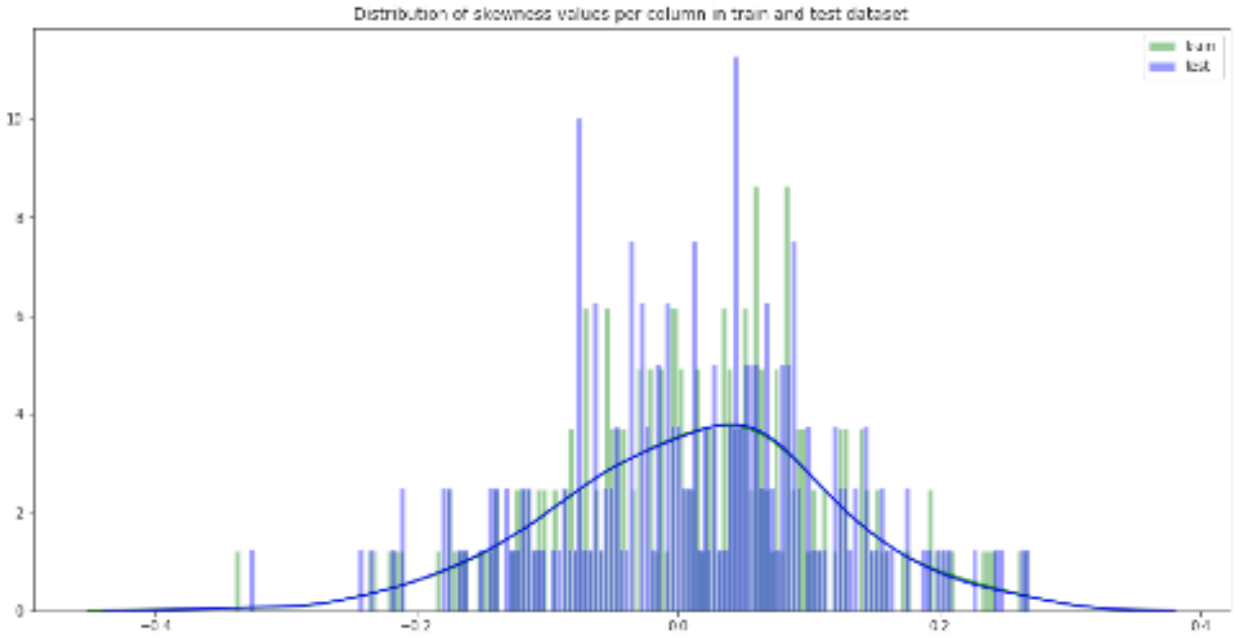


Let us look distribution of standard deviation (std) values per row in train and test dataset

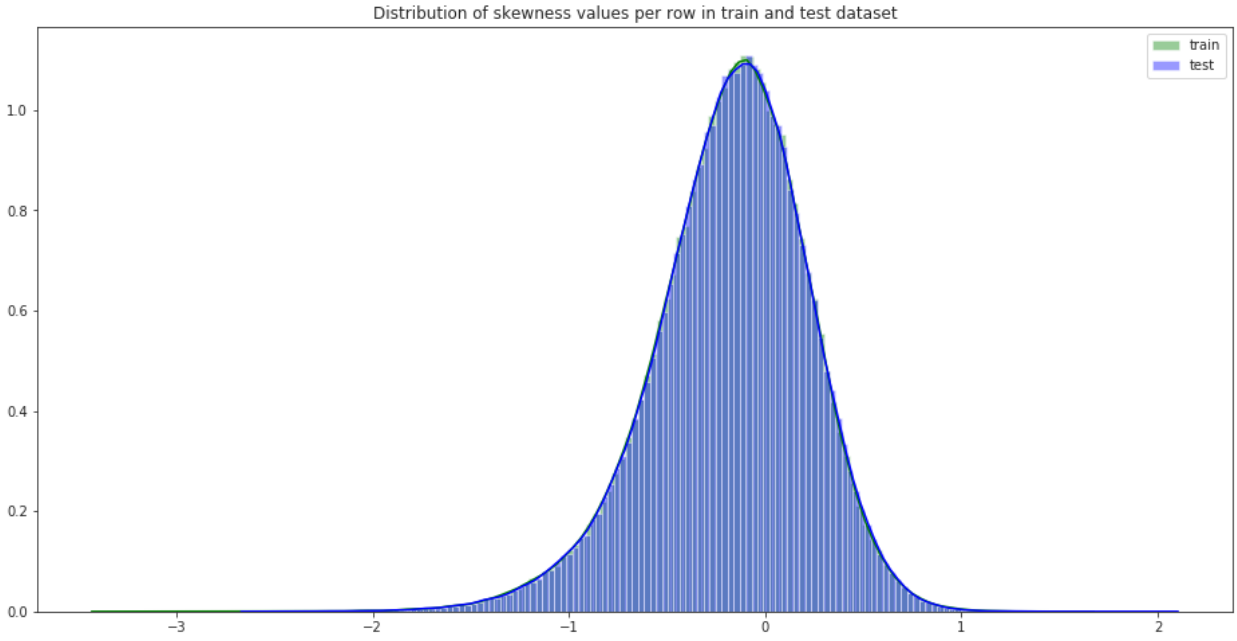


Distribution of skewness values in train and test dataset

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

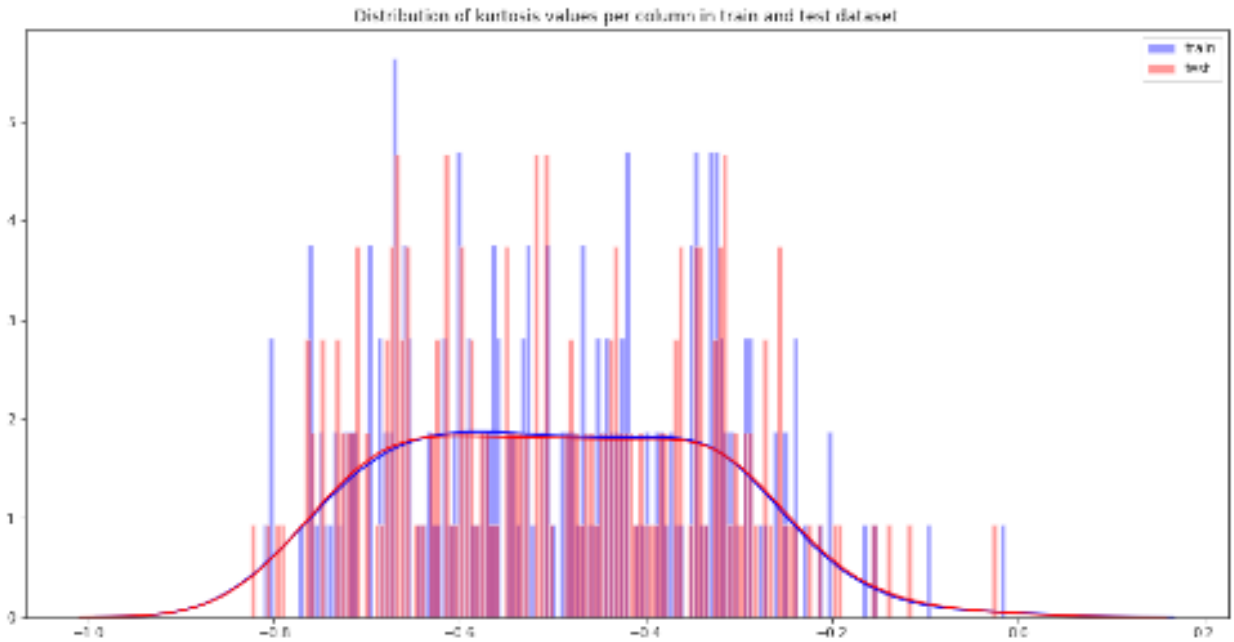


Let us look distribution of skewness per row in train and test dataset

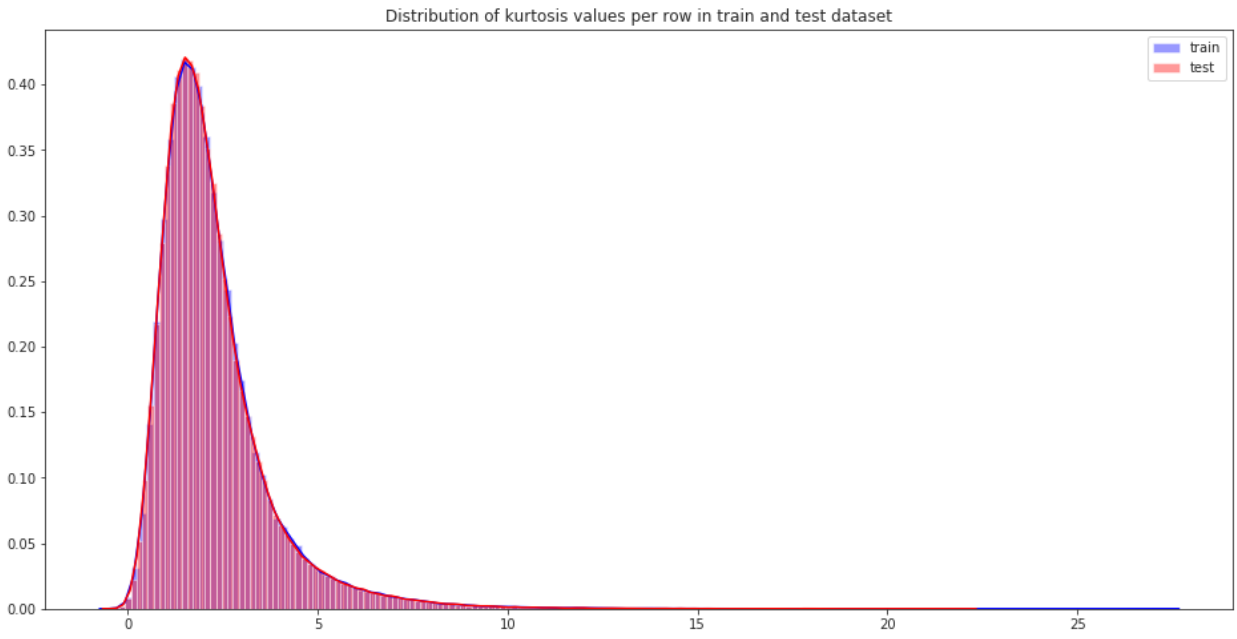


Distribution of kurtosis values in train and test dataset

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



2.1.3. Outlier Analysis

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

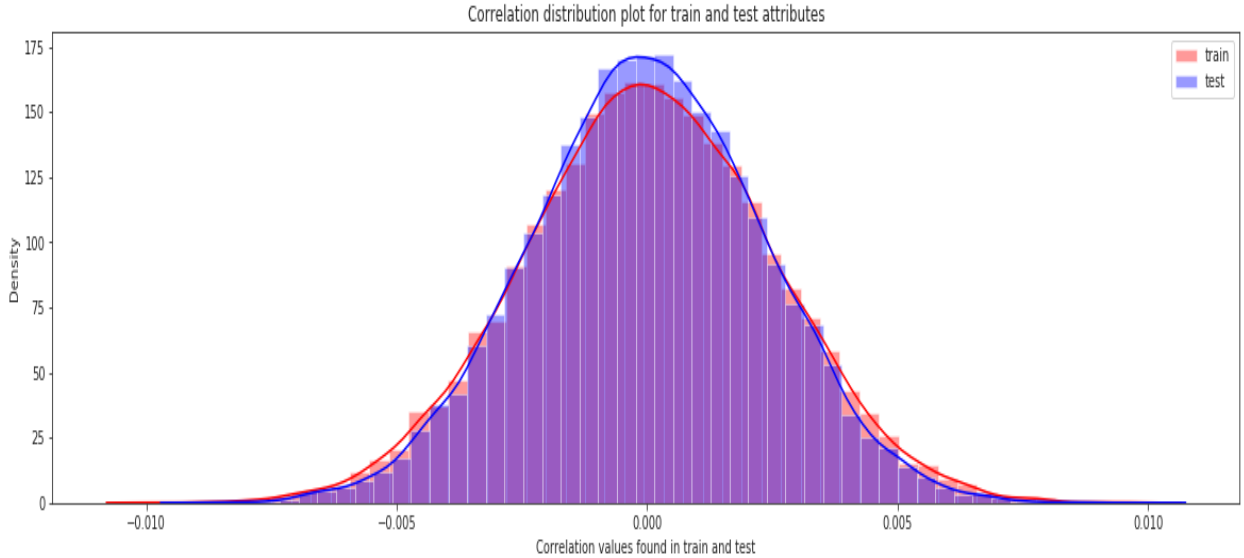
2.1.4. Feature Selection

Feature selection is very important for modelling the dataset. The every dataset have good and unwanted features. The unwanted features would effect 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 is tells about linear relationship between attributes and help us to build better models.

From correlation distribution plot, we can observed 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.



2.1.5. 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 eli5 library. from
eli5.sklearn import PermutationImportance
perm_imp=PermutationImportance(rf_model,random_state=42)
#fitting the model
perm_imp.fit(X_valid,y_valid)

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

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
VarImp<-importance(rf,type=2)
VarImp
```

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:

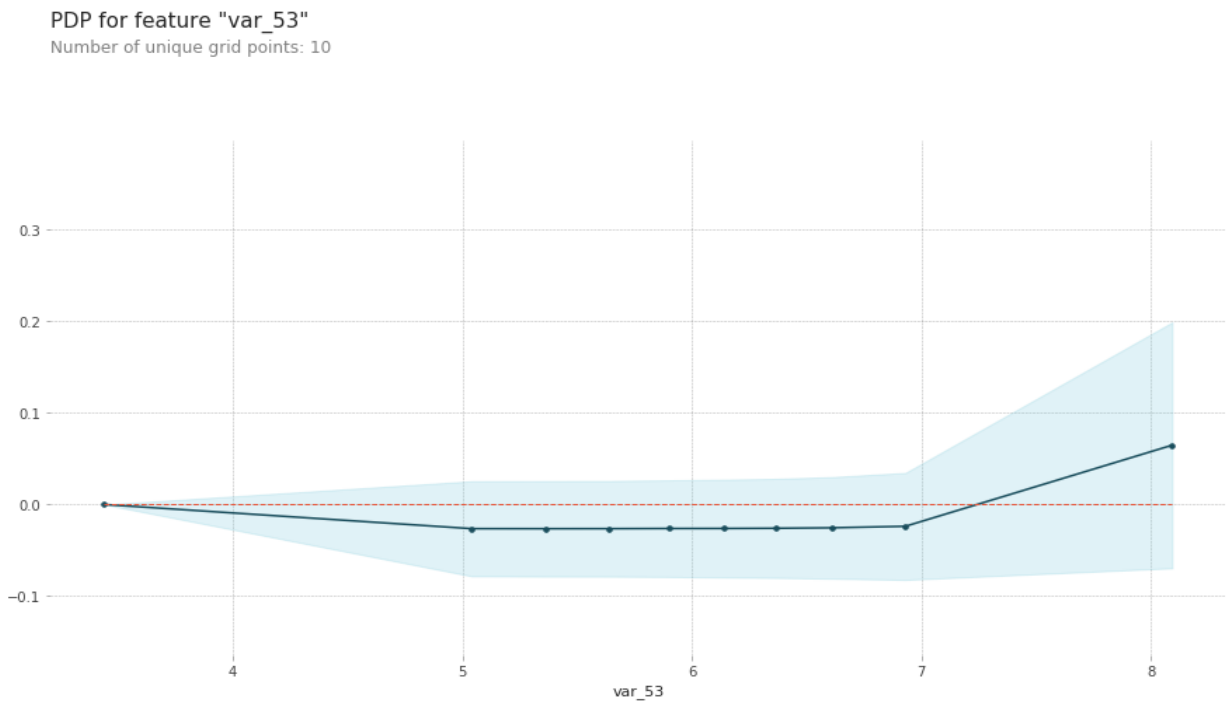
• We can observe that the top important features are var_12, var_26, var_22, var_174, var_198 and so on based on Mean decrease Gini.

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

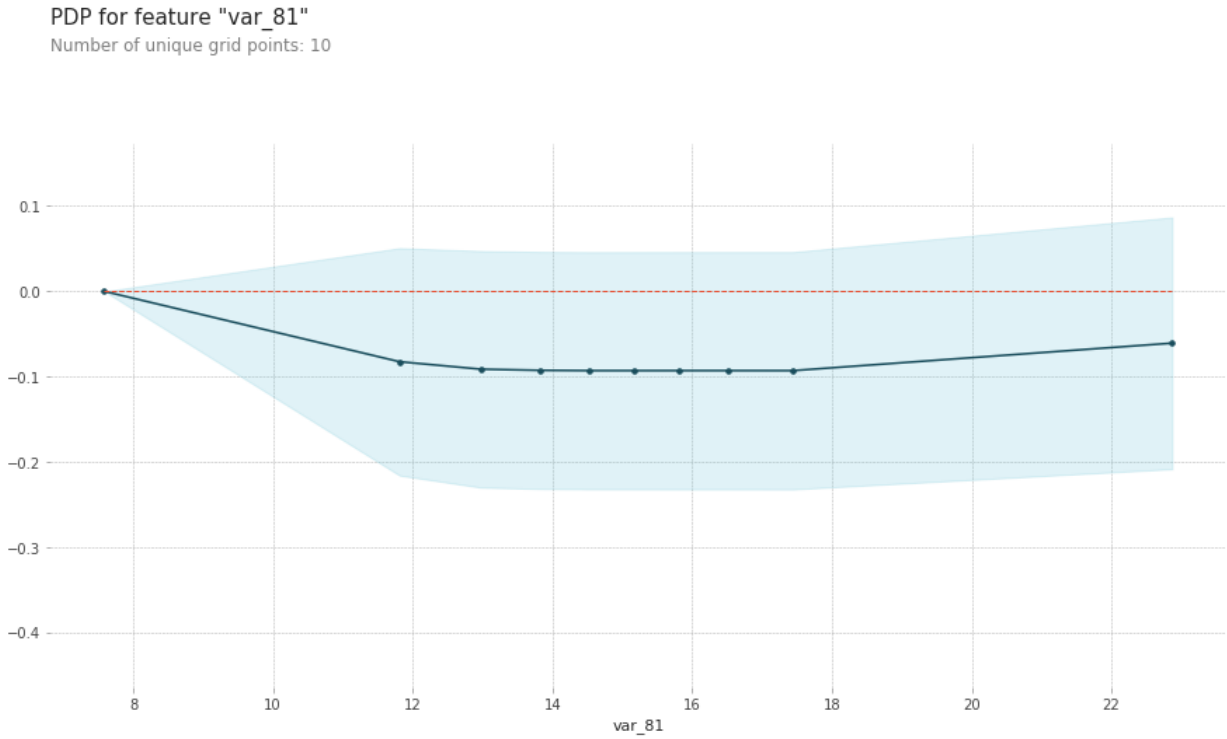
```
#Create the data we will plot 'var_53'
features=[v for v in X_valid.columns if v not in ['ID_code','target']]
pdp_data=pdp.pdp_isolate(rf_model,dataset=X_valid,model_features=features,
feature='var_53')#plot feature "var_53"
pdp.pdp_plot(pdp_data,'var_53')
plt.show()
```



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') plt.show()
```

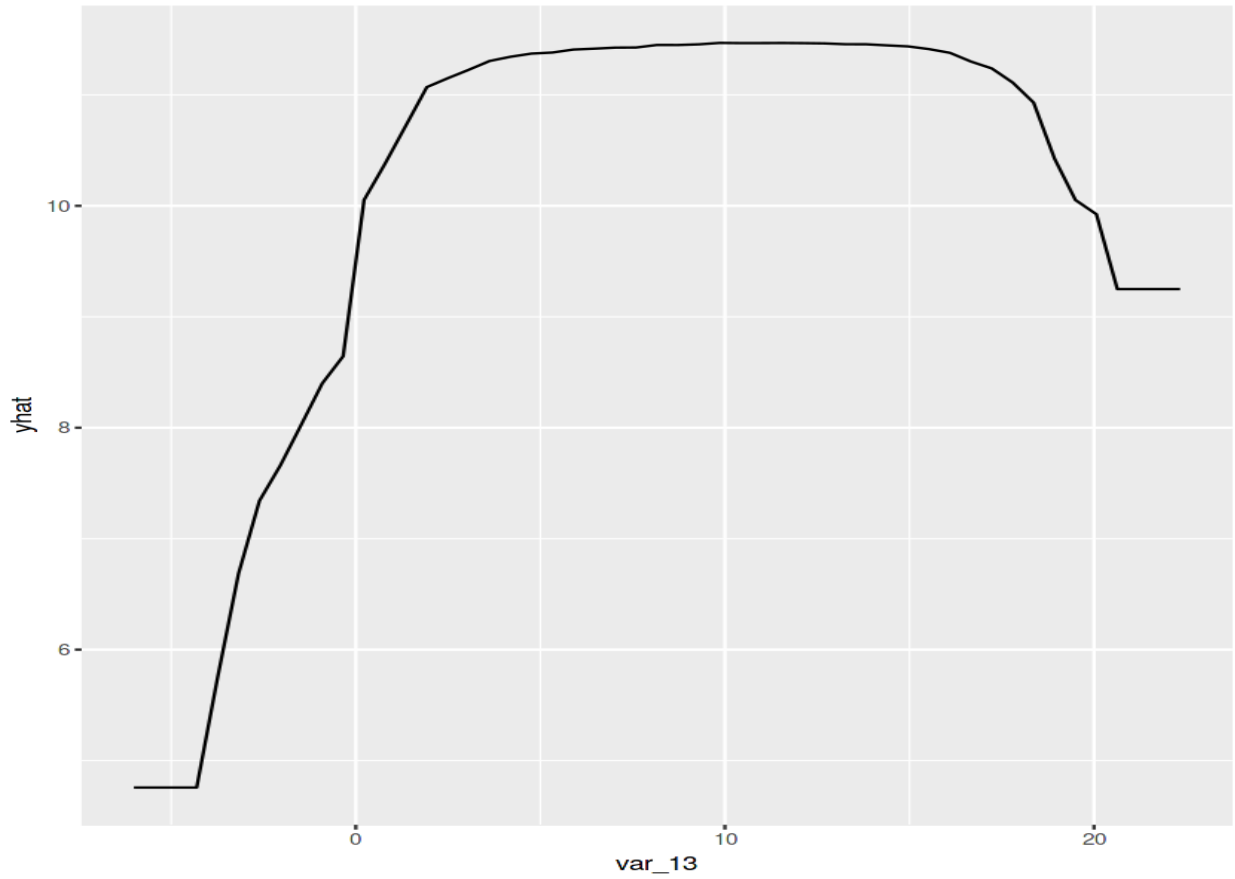


Take away:

- 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

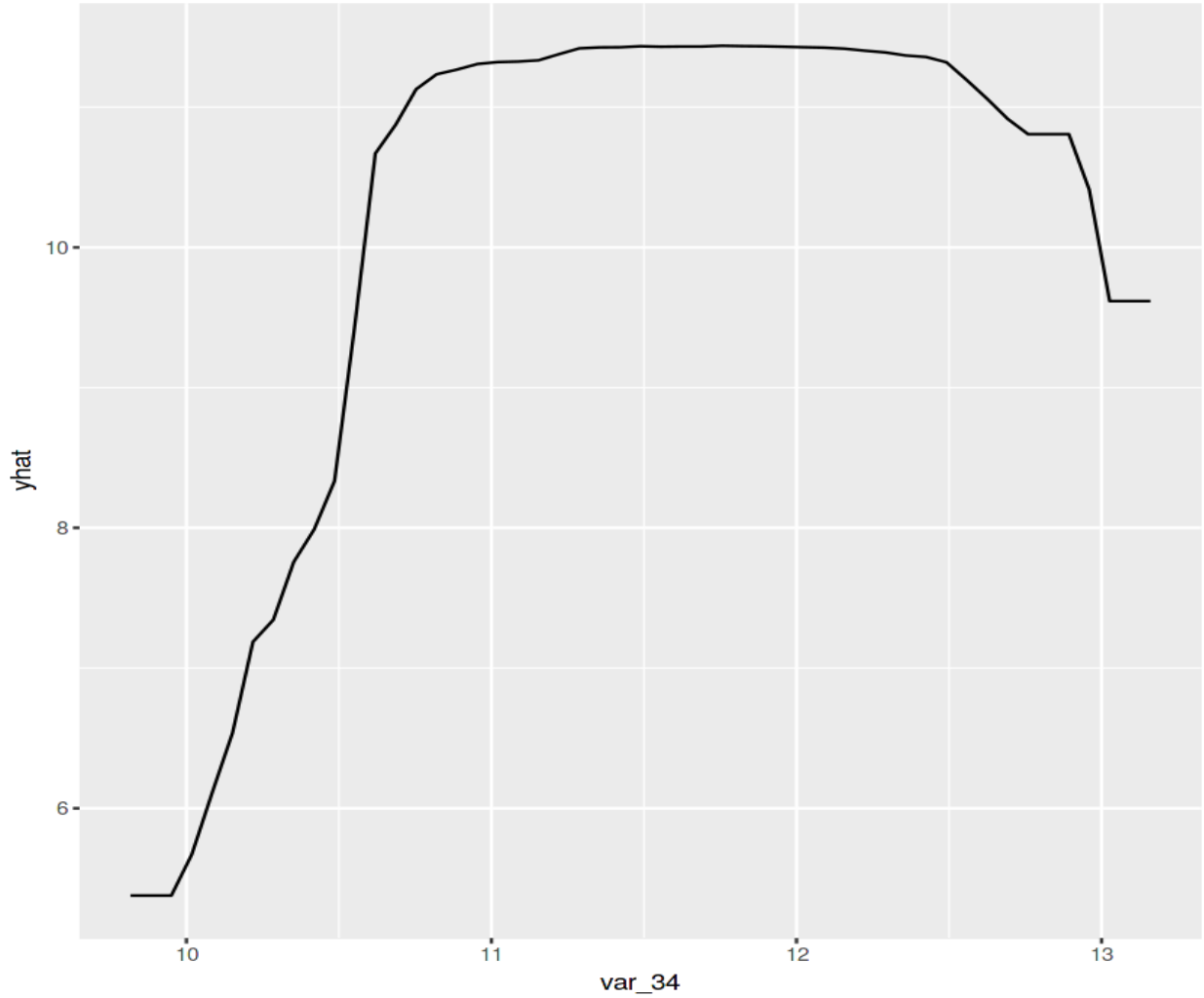
```
#We will plot "var_13"
par.var_13 <- partial(rf, pred.var = c("var_13"), chull = TRUE)
plot.var_13 <- autoplot(par.var_13, contour = TRUE)
```



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)
plot.var_34 <- autoplot(par.var_34, contour = 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.

2.2. Modelling

2.2.1. 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.

2.2.2. 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

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]


#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)

#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))

Cross_val_score : 0.9132

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

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)])

#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")
#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)
```

```
#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
lr_pred<-predict(lr_model,test_df[,-c(1)],type='class')
```

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 leads 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 don't have a ton of data to work with.
- Drawback is that we are adding information. This may leads to overfitting and poor performance on test data.

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

2.2.3. Synthetic Minority Oversampling Technique (SMOTE)

SMOTE uses a nearest neighbour'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))

cross_val_score : 0.80

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

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)$data
table(valid.rose$target)
```

```
#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)
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_df[,-c(1)],type='class')
```

2.2.4. 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
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)
```

```
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, eval_freq = 1000, valids = list(val1 = lgb.train, val2 =
lgb.valid), early_stopping_rounds = 5000)
```

```
[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
```

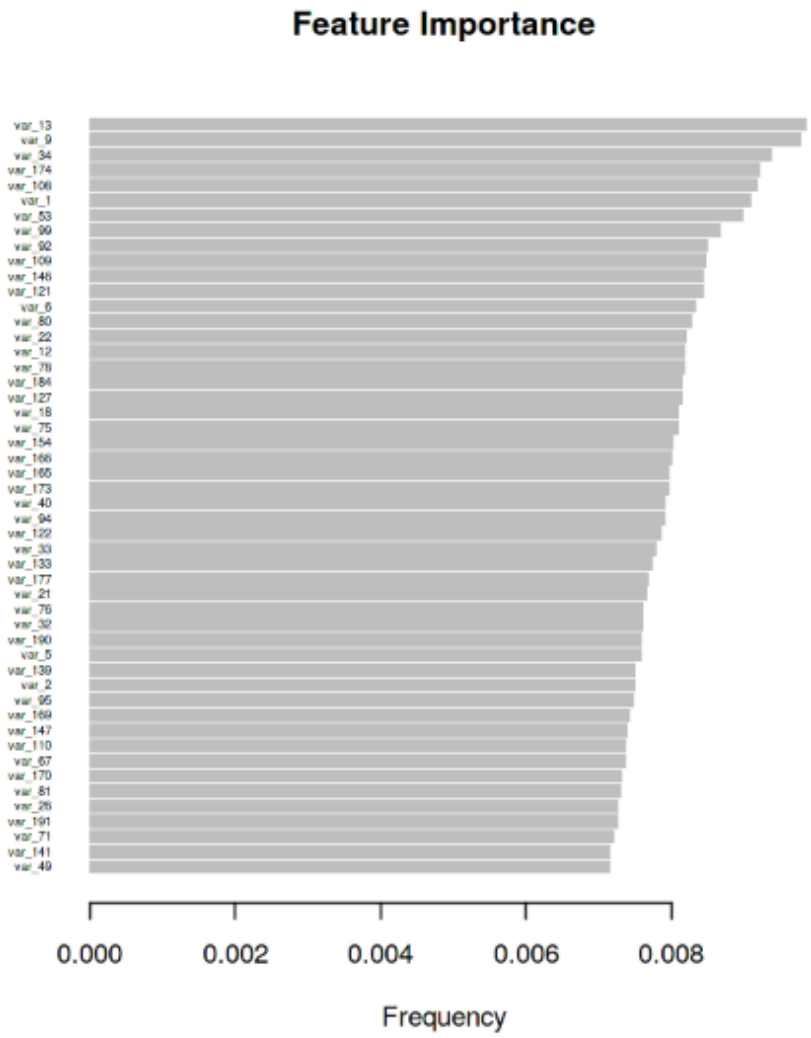
Important features plot

Python code

```
#plot the important features

lgb.plot_importance(lgbm,max_num_features=150,importance_type="split",figs
ize=(20, 50))
```

R code

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



3. Conclusion

3.1. Model Evaluation

Now, we have a 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

$$\text{True Positive Rate (TPR)} = \frac{TP}{TP+FN} \leftrightarrow \text{Recall}$$
$$\text{Precision} = \frac{TP}{TP+FP}$$
$$\text{True Negative Rate (TNR)} = \frac{TN}{TN+FP} \leftrightarrow \text{Specificity}$$
$$\text{False Positive Rate (FPR)} = \frac{FP}{FP+TN}$$
$$\text{False Negative rate (FNR)} = \frac{FN}{FN+TP}$$

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

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

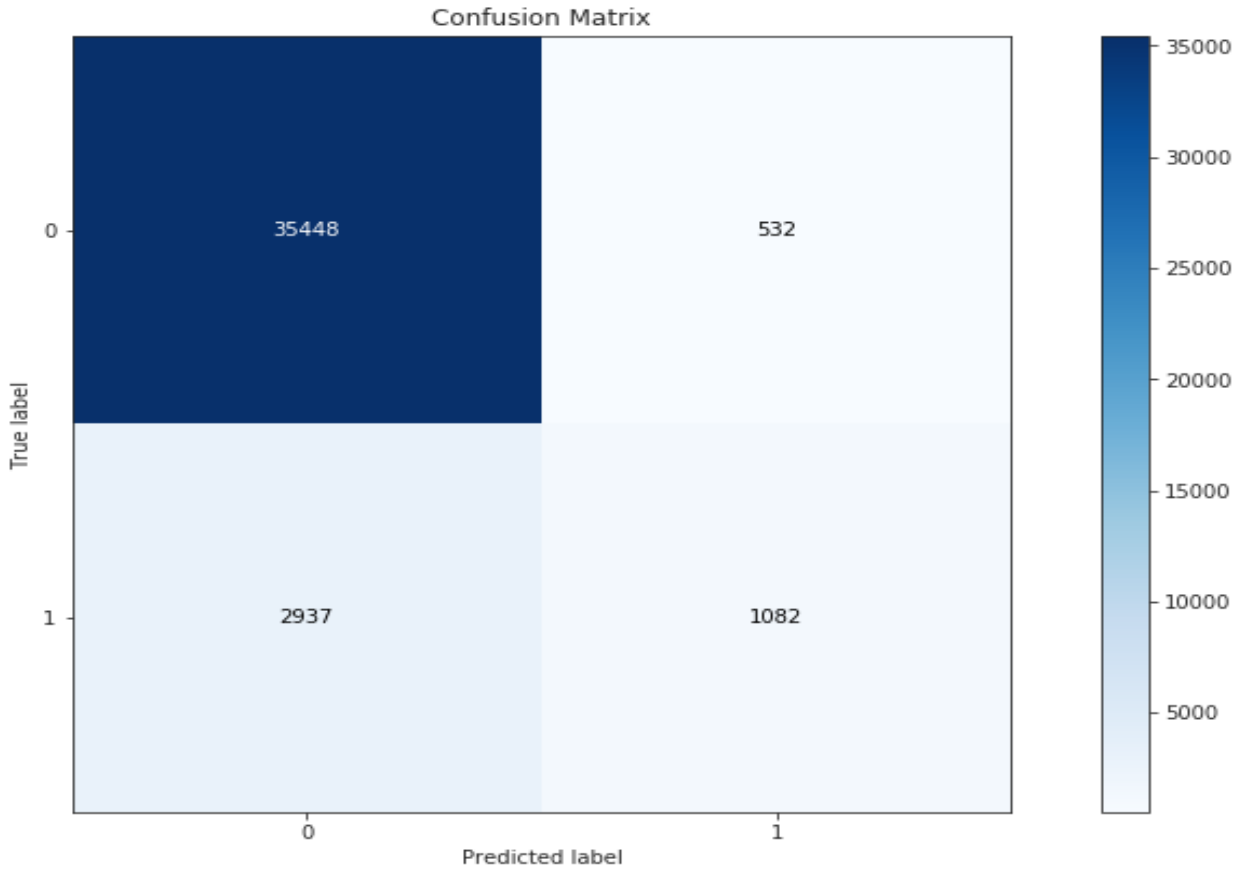
Receiver operating characteristics (ROC)_Area under curve(AUC) Score

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.

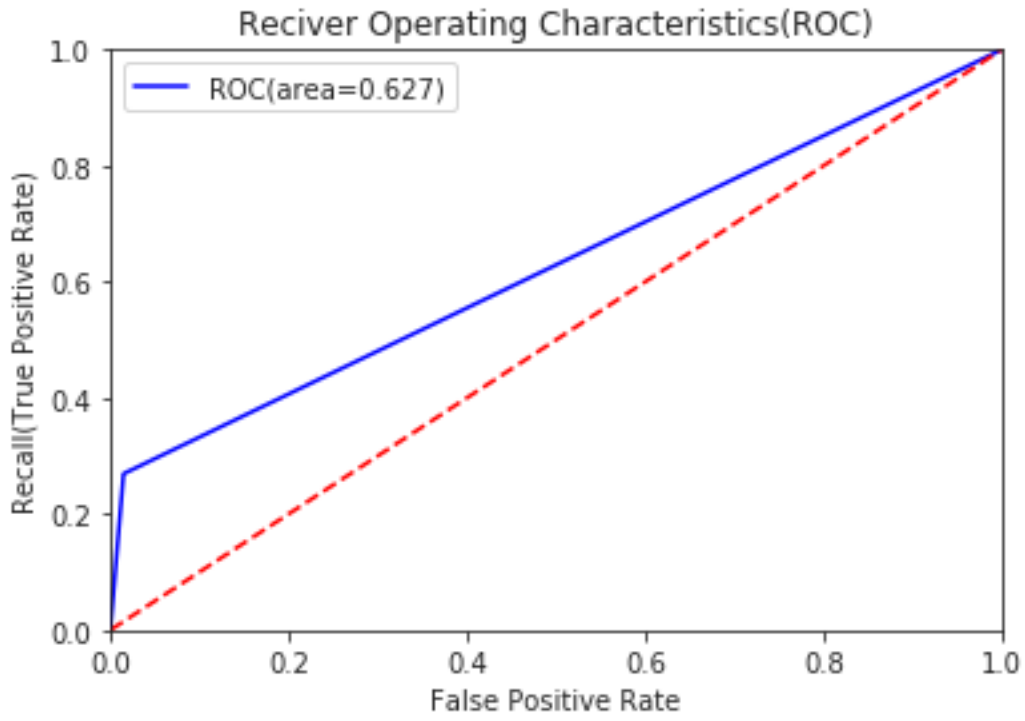
Logistic Regression

```
#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 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)
```



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

Classification report

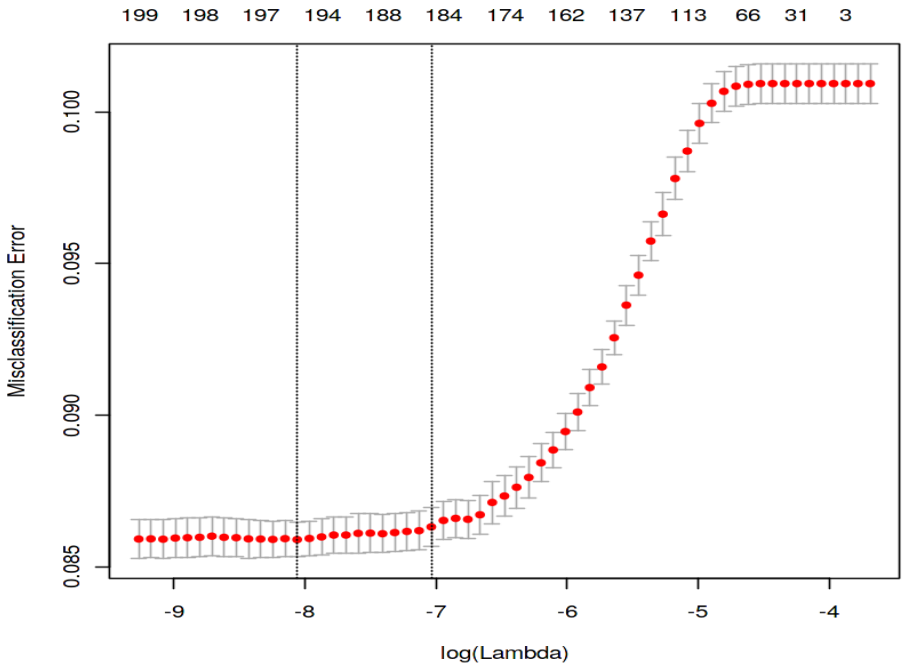
```
#Classification report
scores=classification_report(y_valid,cv_predict) print(scores)
```

```
              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 observed 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

cv_lr$lambda.min
#plot the auc score vs log(lambda)
plot(cv_lr)
```



We can observe 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 cv_predict.lr<-as.factor(cv_predict.lr)
confusionMatrix(data=cv_predict.lr,reference=target)
```

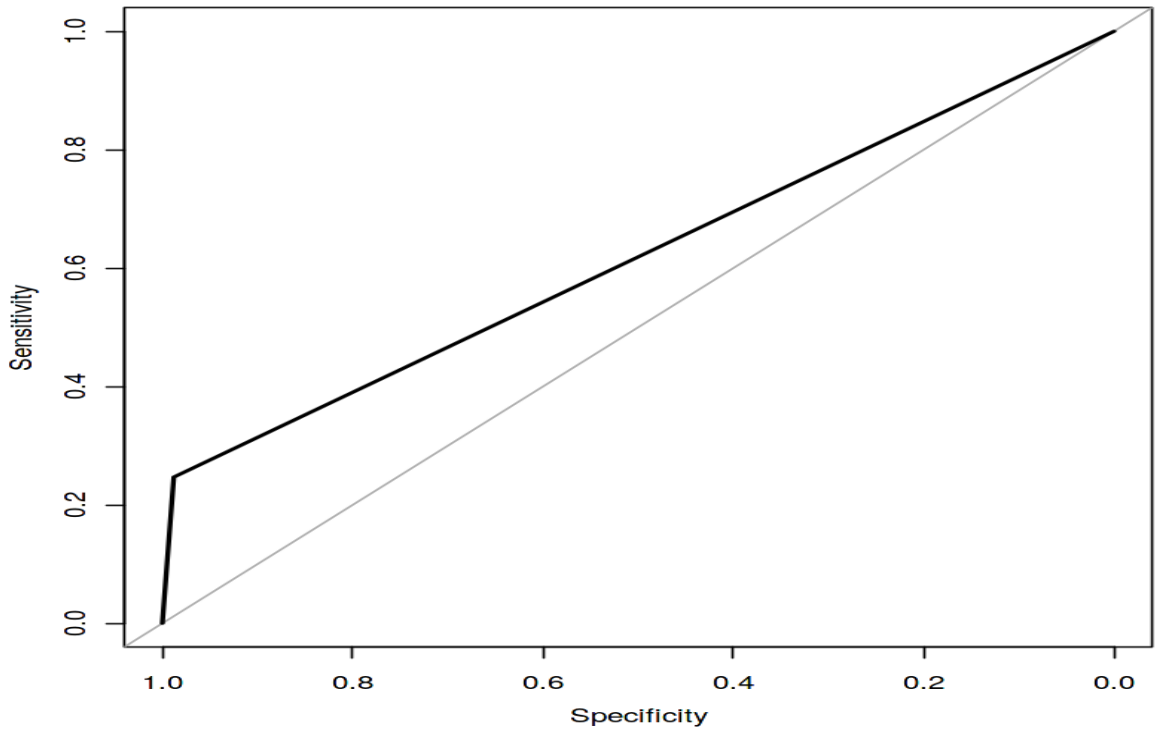
```
Confusion Matrix and Statistics

          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
```

Receiver 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, plot=TRUE)
```

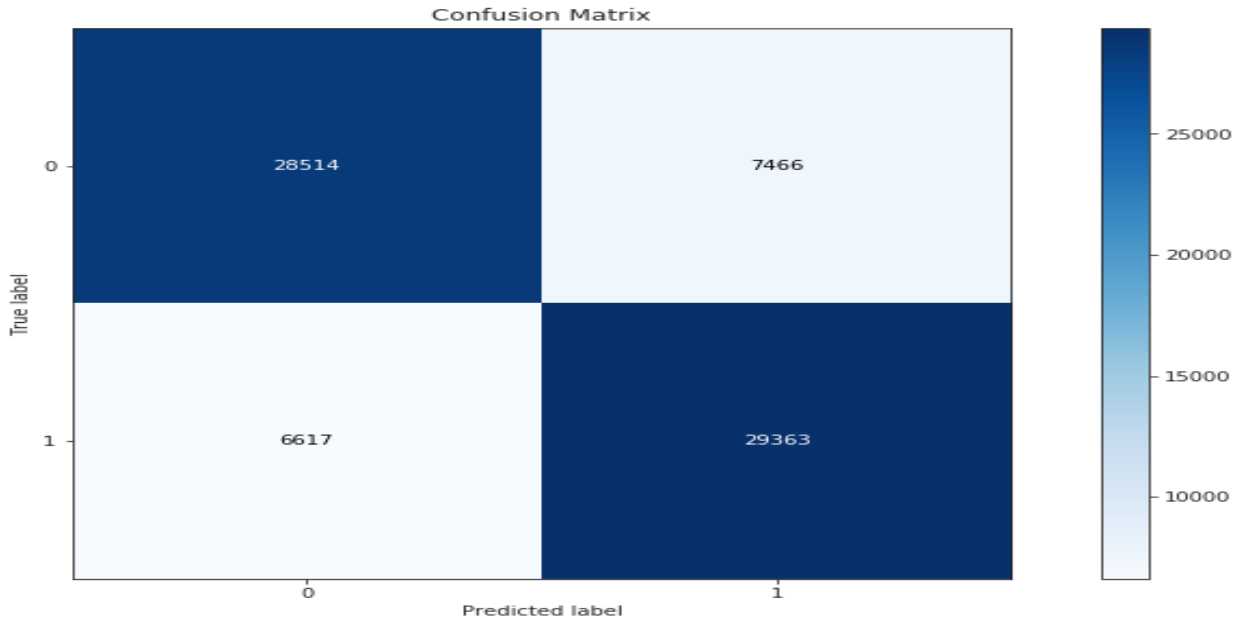
```
Call:
roc.default(response = target, predictor = cv_predict.lr, auc = TRUE,     plot = TRUE, data = valid.data[, -c(1, 2)])

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



Python code

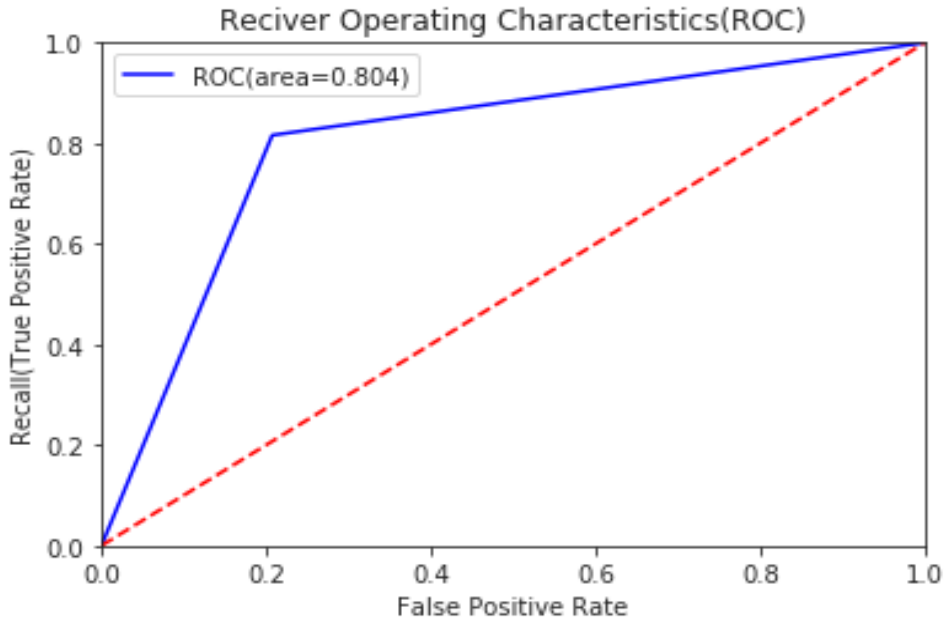
Synthetic Minority Oversampling Technique (SMOTE)

```
#Confusion matrix
cm=confusion_matrix(y_smote_v,cv_pred)
#Plot the confusion matrix
plot_confusion_matrix(y_smote_v,cv_pred,normalize=False,figsize=(15,8))
```



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)')
plt.xlabel('False Positive Rate') plt.show()
print('AUC:',roc_auc)
```



Classification report

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

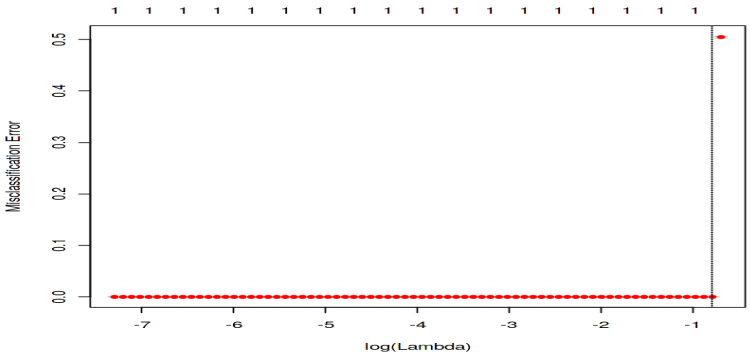
```
              precision    recall  f1-score   support

           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)

```
#Plotting misclassification error vs log(lambda) #lambda-Regularization
parameter
#Minimum lambda
cv_rose$lambda.min
#plot the auc score vs log(lambda) plot(cv_rose)
```



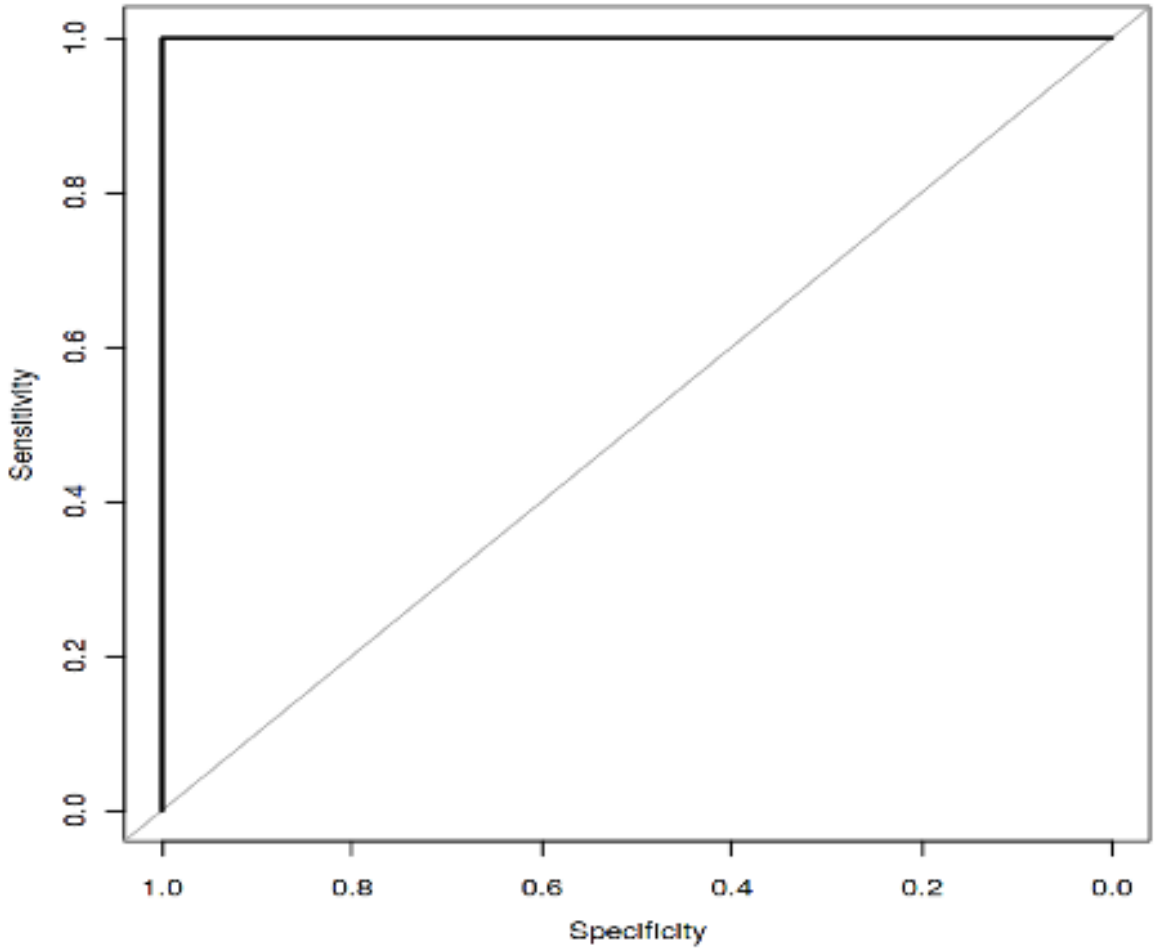

```
#Confusion matrix
set.seed(478)
#actual target variable
target<-valid.rose$target
#convert to factor
target<-as.factor(target)
#predicted target variable
#convert to factor cv_predict.rose<-as.factor(cv_predict.rose) #Confusion
matrix confusionMatrix(data=cv_predict.rose,reference=target)
```

```
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, plot=TRUE)
```

```
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 area under the ROC curve of all the models for an imbalanced data. We could conclude that below points as follow,

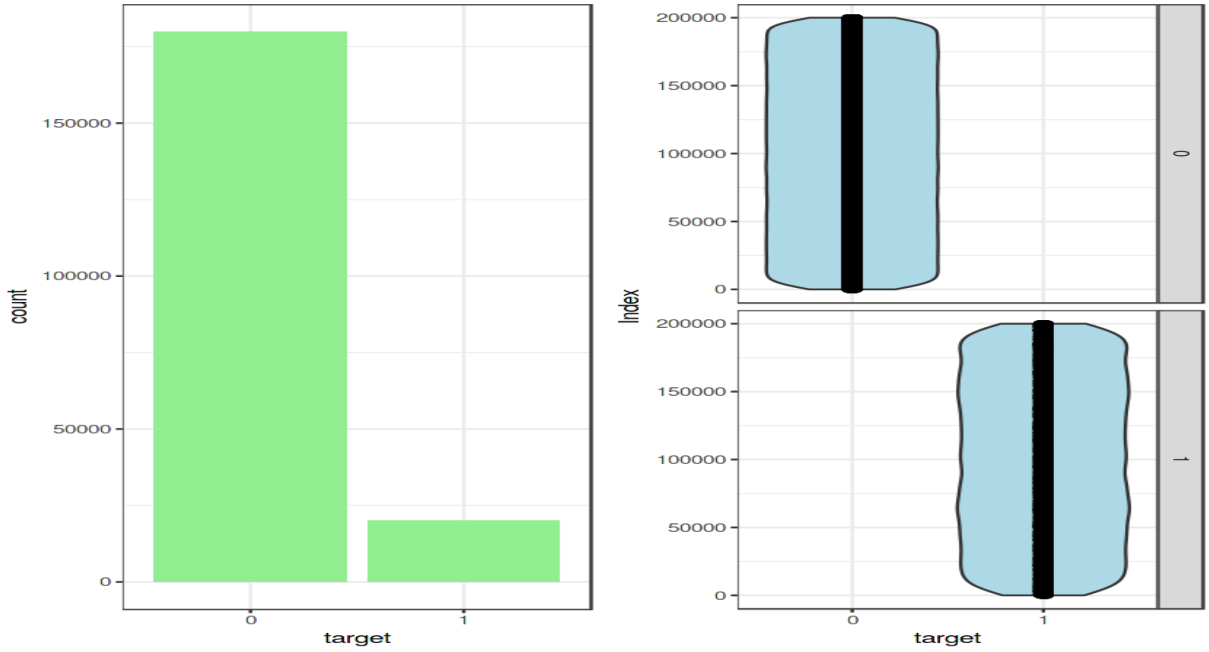
1. Logistic regression model is not performed well on imbalanced data.
2. We balance the imbalanced data using resampling techniques like SMOTE in python and ROSE in R.
3. Baseline logistic regression model is performed well on balanced data.
4. LightGBM model performed well on imbalanced data.

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

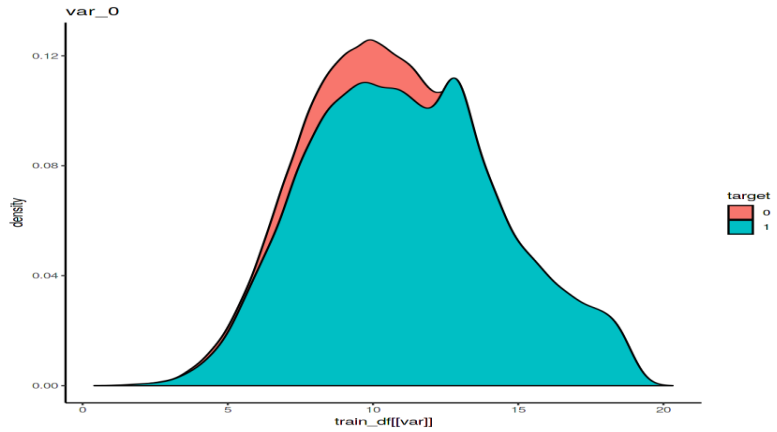
Appendix A - Extra Figures

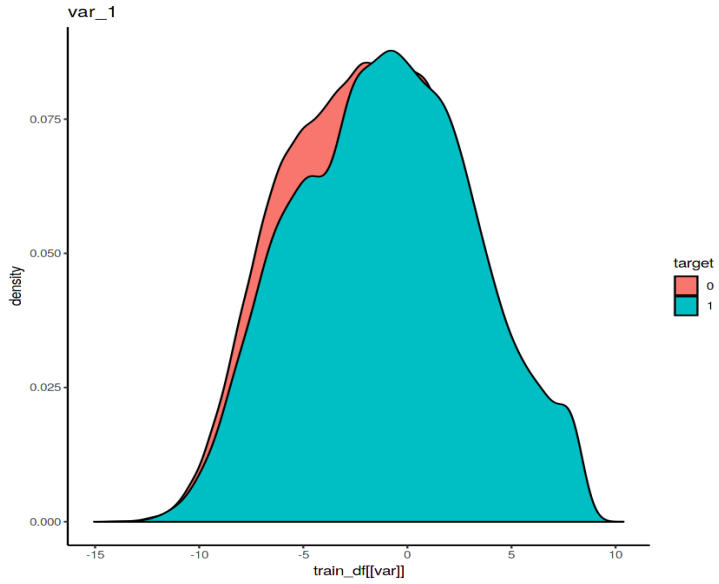
ggplot2 visualizations

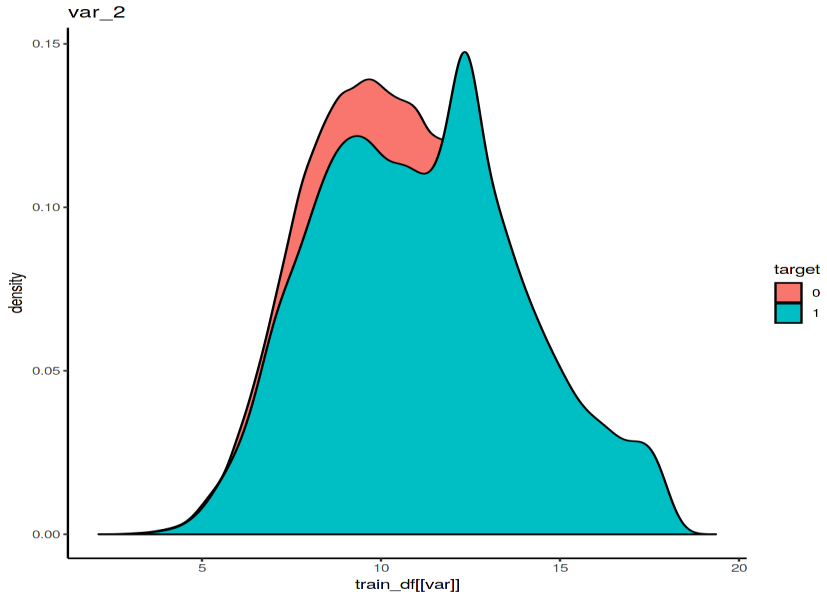
Target classes count



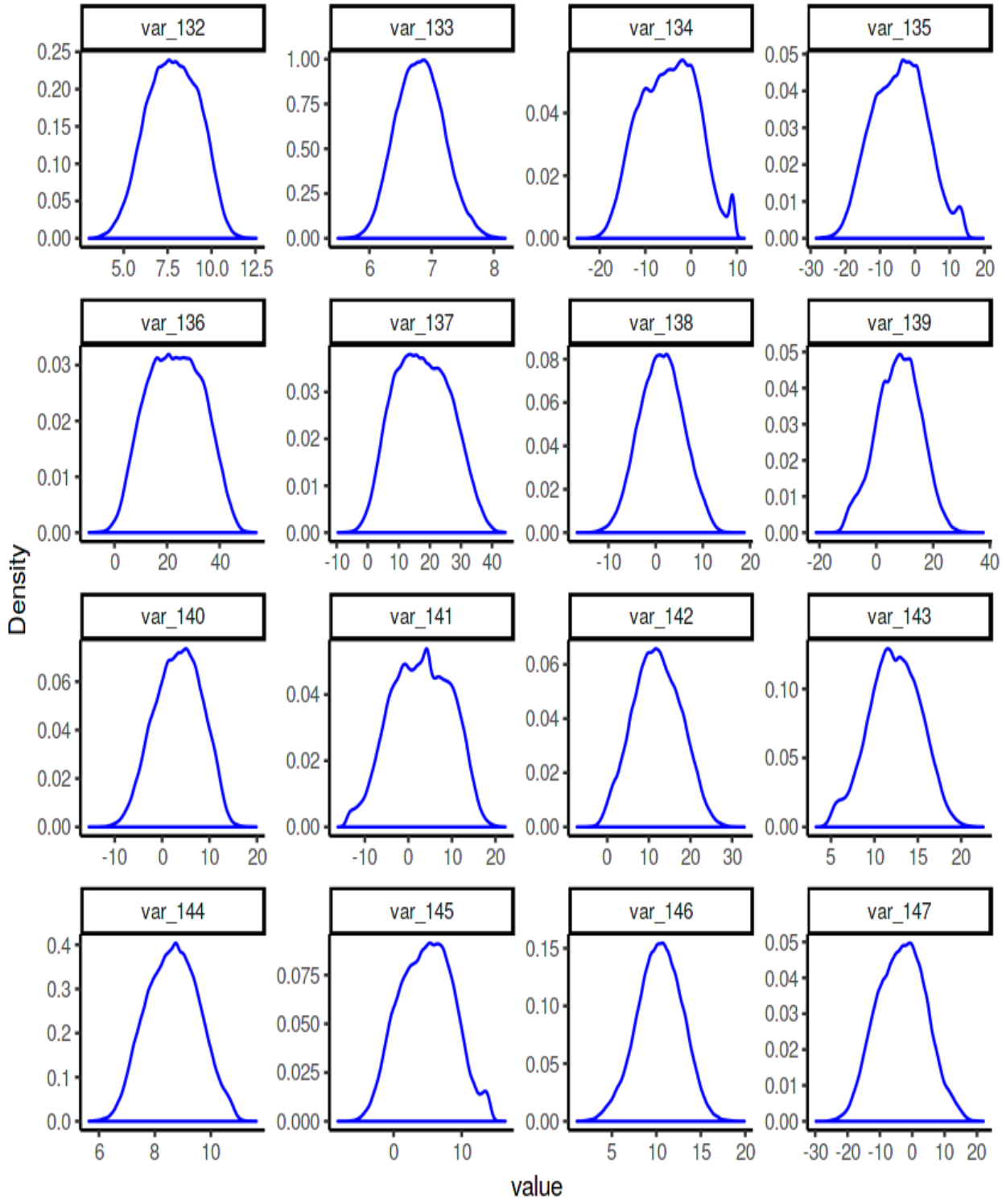
Distribution of train attributes

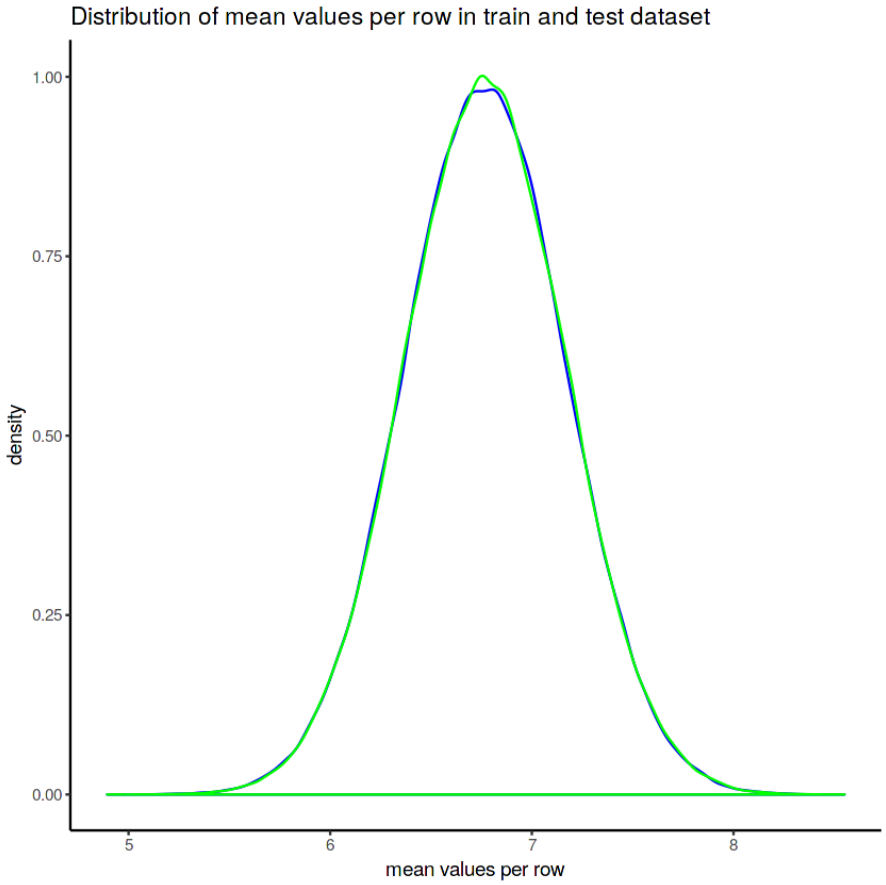


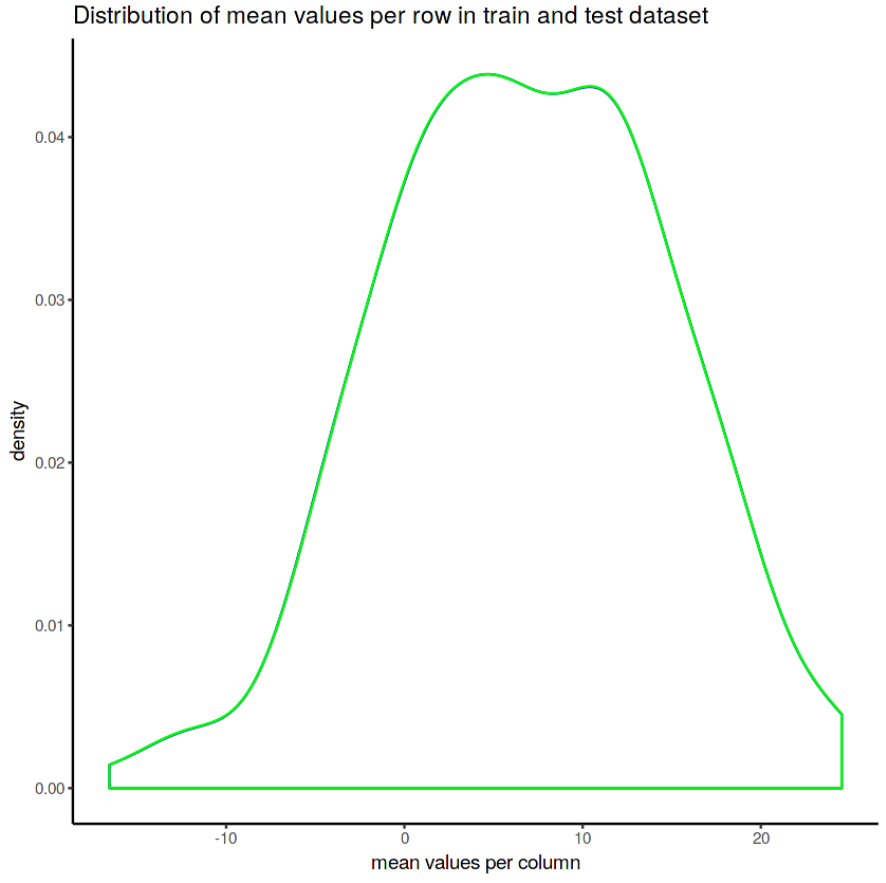


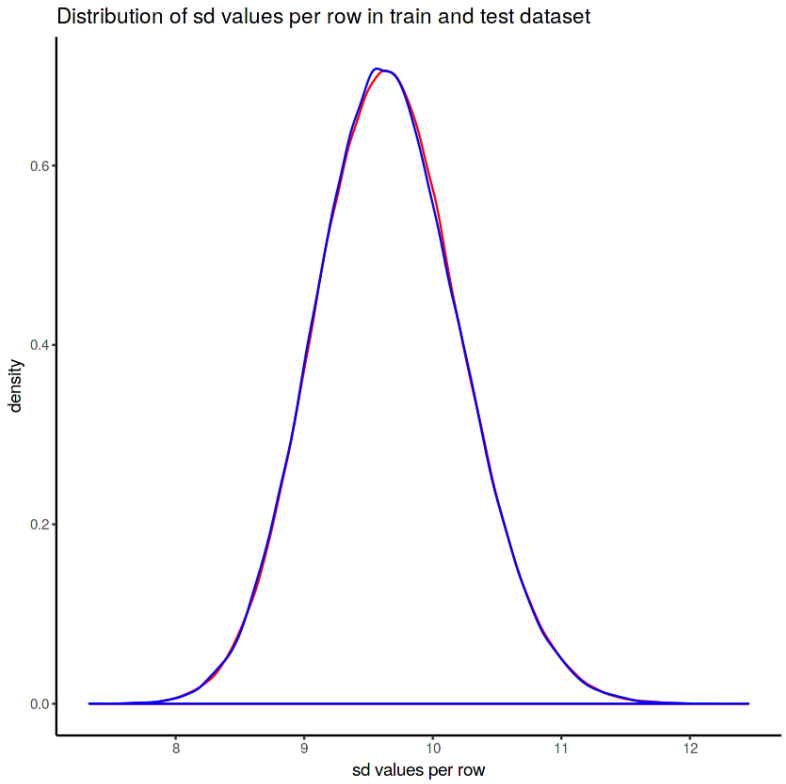


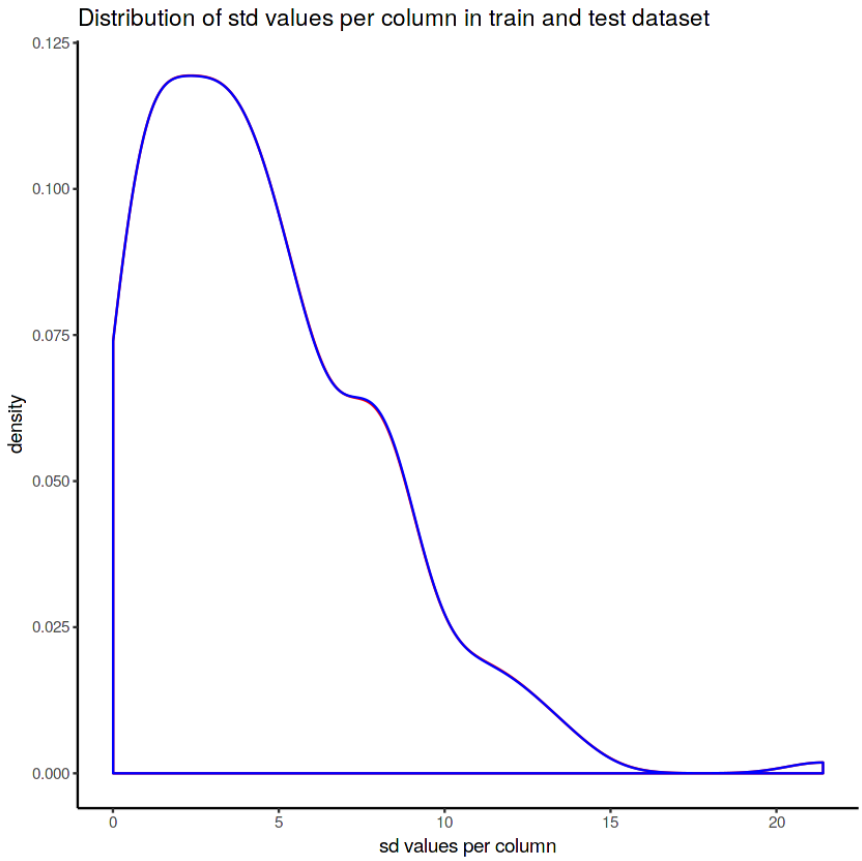
Distribution of test attribiutes

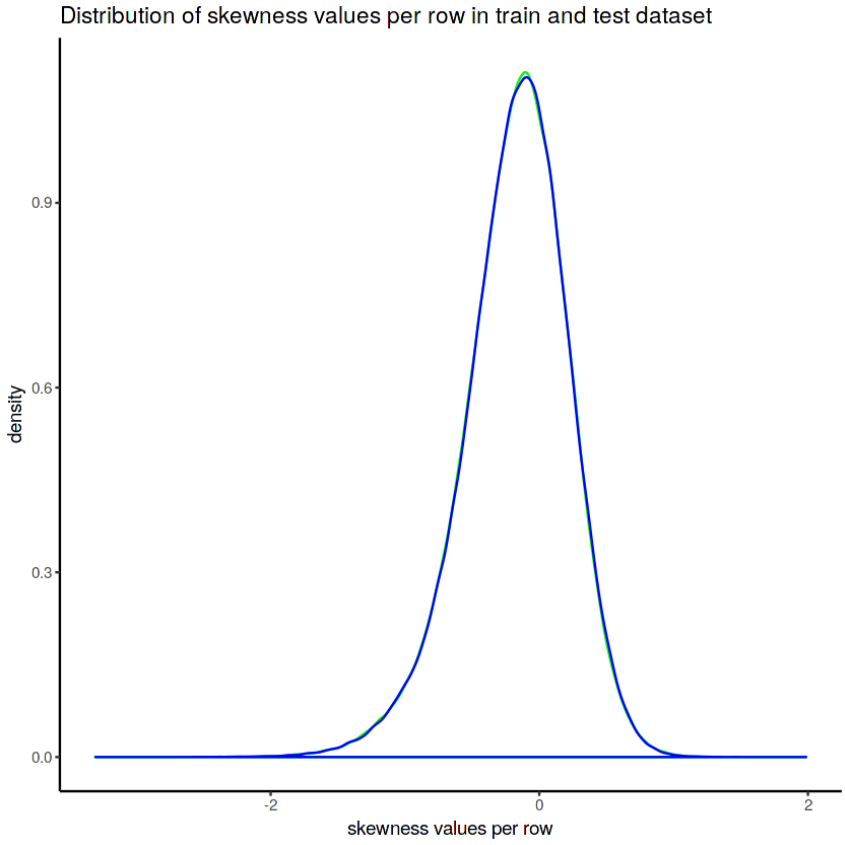


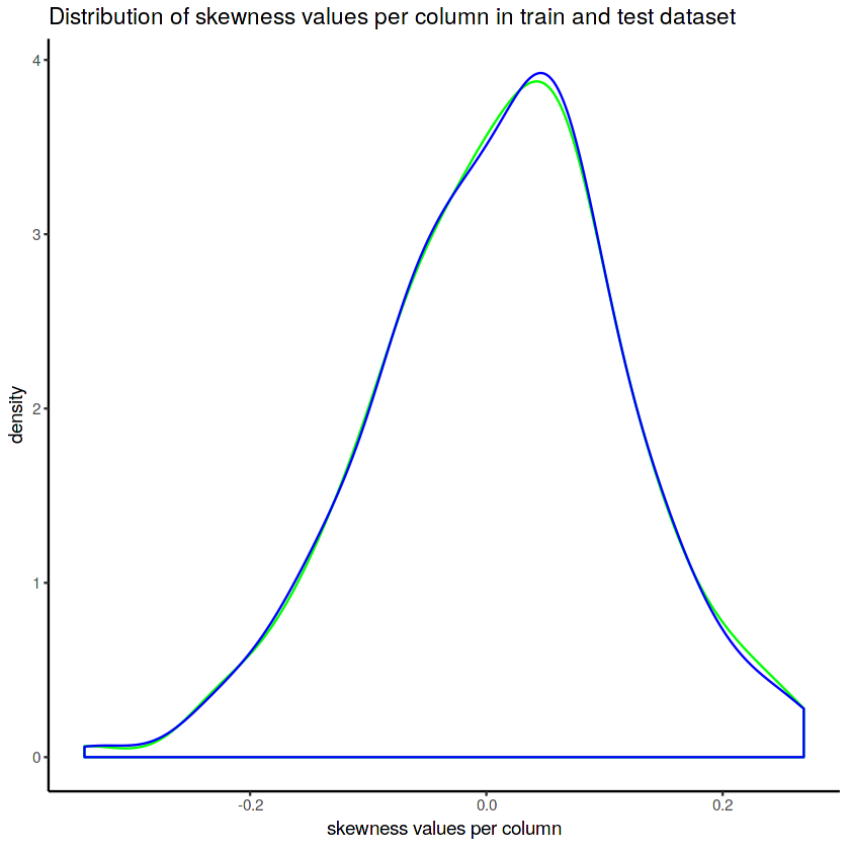

Distribution of mean values per row in train and test dataset
density
1.00
0.75
0.50
0.25
0.00
5
6
7
8
mean values per row

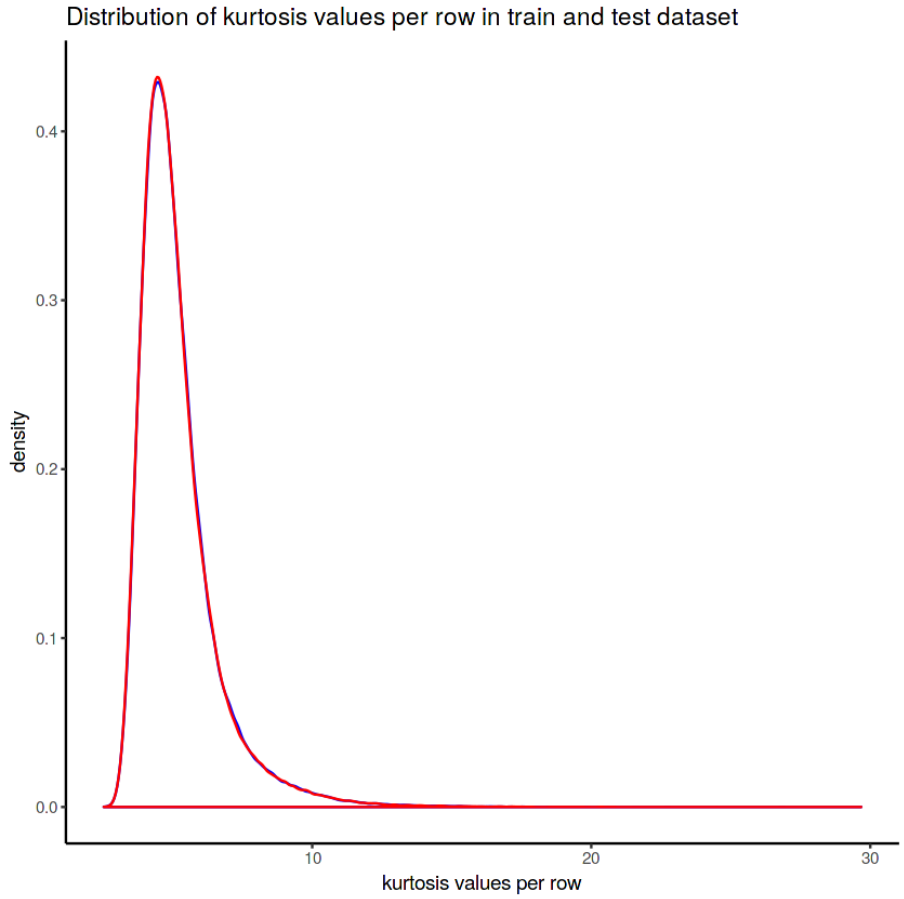

Distribution of mean values per row in train and test dataset
density
0.04
0.03
0.02
0.01
0.00
-10
0
10
20
mean values per column

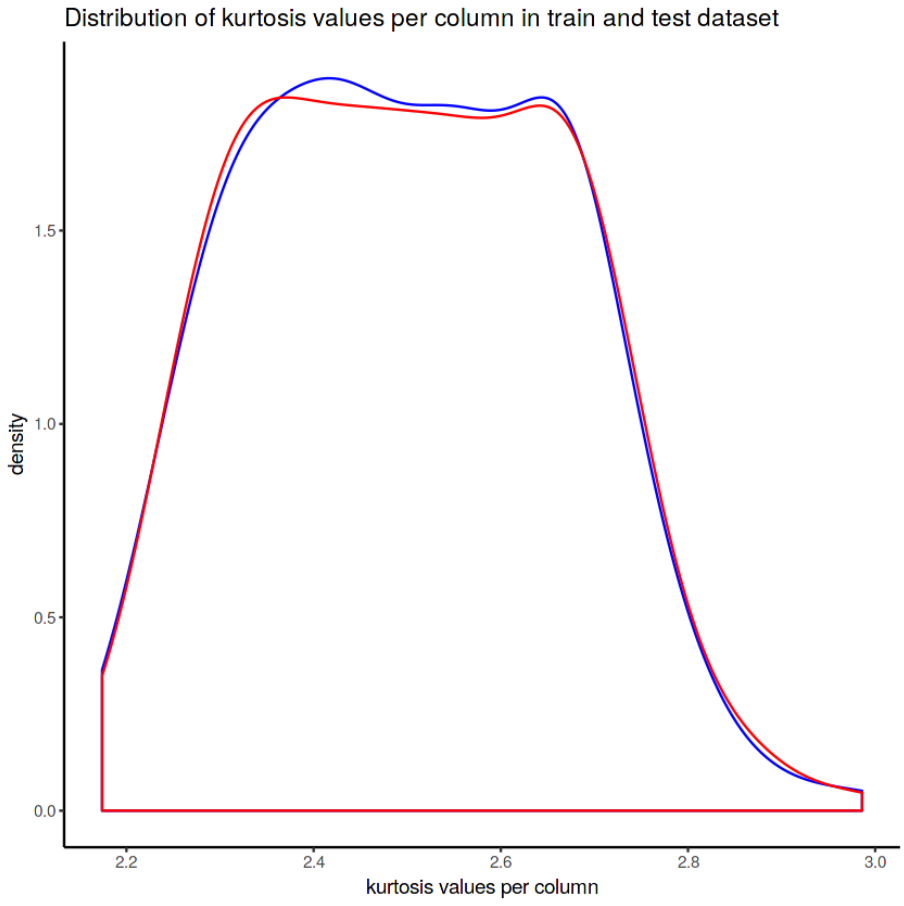

Distribution of sd values per row in train and test dataset
density
0.0
0.2
0.4
0.6
8
9
10
11
12
sd values per row


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


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


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

Importing libraries and Datasets

In [1]:

```
#Loading dataset and libraries
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,classification_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')
import os
print(os.listdir("./input"))
```

```
Using TensorFlow backend.
['test.csv', 'train.csv']
```

Importing the train dataset

In [2]:

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

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

Shape of the train dataset

In [3]:

```
#Shape of the train dataset
train_df.shape
```

Out[3]: (200000, 202)

In [4]:

```
#Summary of the dataset
train_df.describe()
```

Out[4]:

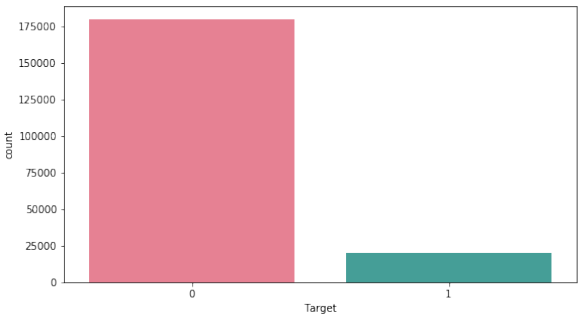
	target	var_0	var_1	var_2	var_3	var_4	var_5	var_6	var_7	var_
count	200000.000000	200000.000000	200000.000000	200000.000000	200000.000000	200000.000000	200000.000000	200000.000000	200000.000000	200000.00000
mean	0.100490	10.679914	-1.627622	10.715192	6.796529	11.078333	-5.065317	5.408949	16.545850	0.28416
std	0.300653	3.040051	4.050044	2.640894	2.043319	1.623150	7.863267	0.866607	3.418076	3.33263
min	0.000000	0.408400	-15.043400	2.117100	-0.040200	5.074800	-32.562600	2.347300	5.349700	-10.50550
25%	0.000000	8.453850	-4.740025	8.722475	5.254075	9.883175	-11.200350	4.767700	13.943800	-2.31780
50%	0.000000	10.524750	-1.608050	10.580000	6.825000	11.108250	-4.833150	5.385100	16.456800	0.39370
75%	0.000000	12.758200	1.358625	12.516700	8.324100	12.261125	0.924800	6.003000	19.102900	2.93790
max	1.000000	20.315000	10.376800	19.353000	13.188300	16.671400	17.251600	8.447700	27.691800	10.15130

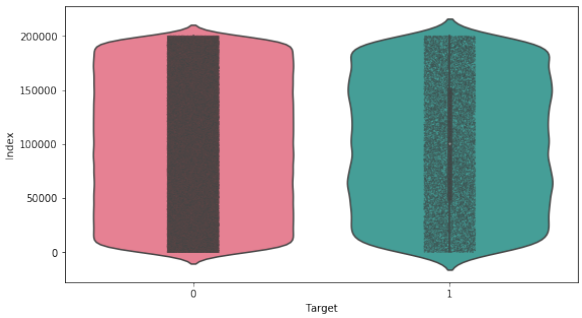
8 rows × 201 columns

Target classes count

In [5]:
```
#target classes count
target_class=train_df['target'].value_counts()
print('Count of target classes :\n',target_class)
#Percentage of target classes count
per_target_class=train_df['target'].value_counts()/len(train_df)*100
print('Percentage of count of target classes :\n', per_target_class)

#Countplot and violin plot for target classes
fig,ax=plt.subplots(1,2,figsize=(20,5))
sns.countplot(train_df.target.values,ax=ax[0],palette='husl')
sns.violinplot(x=train_df.target.values,y=train_df.index.values,ax=ax[1],palette='husl')
sns.stripplot(x=train_df.target.values,y=train_df.index.values,jitter=True,color='black',linewidth=0.5,size=0.5,alp
ax[0].set_xlabel('Target')
ax[1].set_xlabel('Target')
ax[1].set_ylabel('Index')

```

```
Count of target classes :
 0    179902
1     20098
Name: target, dtype: int64
Percentage of count of target classes :
 0    89.951
1    10.049
Name: target, dtype: float64
```





Observations:

- We have plotted countplot and violin plot for target variable.
- *seaborn.countplot* shows the counts of observations in each categorical bin using bars.
- *seaborn.violinplot* shows the distribution of quantitative data across several levels of one (or more) categorical variables such that those distributions can be compared.
- 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.
- Looking at the violin plots shows that there is no relationship between the target and the index of the train data frame. It is more dominated by the zero targets than for the ones.
- Looking at the jitter plots within the violin plots. We can observe that targets look uniformly distributed over the indexes of the data frame.

Let us look distribution of train attributes

In [8]:

```
# Distribution of train attributes
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()
#corresponding to negative class
t0=train_df[train_df.target.values==0]
#corresponding to positive class
t1=train_df[train_df.target.values==1]
#train attributes from 2 to 102
train_attributes=train_df.columns.values[2:102]
#plot distribution of train attributes
plot_train_attribute_distribution(t0,t1,'0','1',train_attributes)
#train attributes from 102 to 203
train_attributes=train_df.columns.values[102:203]
#plot distribution of train attributes
plot_train_attribute_distribution(t0,t1,'0','1',train_attributes)

```

Insights:

- We can observe that there are considerable number of features which significantly have different distributions as the target variables. For example like var_0,var_1,var_9,var_198 var_180 etc.
- We can observe that there are considerable number of features which significantly have same distributions as the target variables. For example like var_3,var_7,var_10,var_171,var_185 etc.

Importing the test dataset

In [9]:
```
#importing the test dataset
test_df=pd.read_csv('./input/test.csv')
test_df.head()
```

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

Shape of the test dataset

In [10]:
```
#Shape of the test dataset
test_df.shape

```

Out[10]: (200000, 201)

Let us look distribution of test attributes

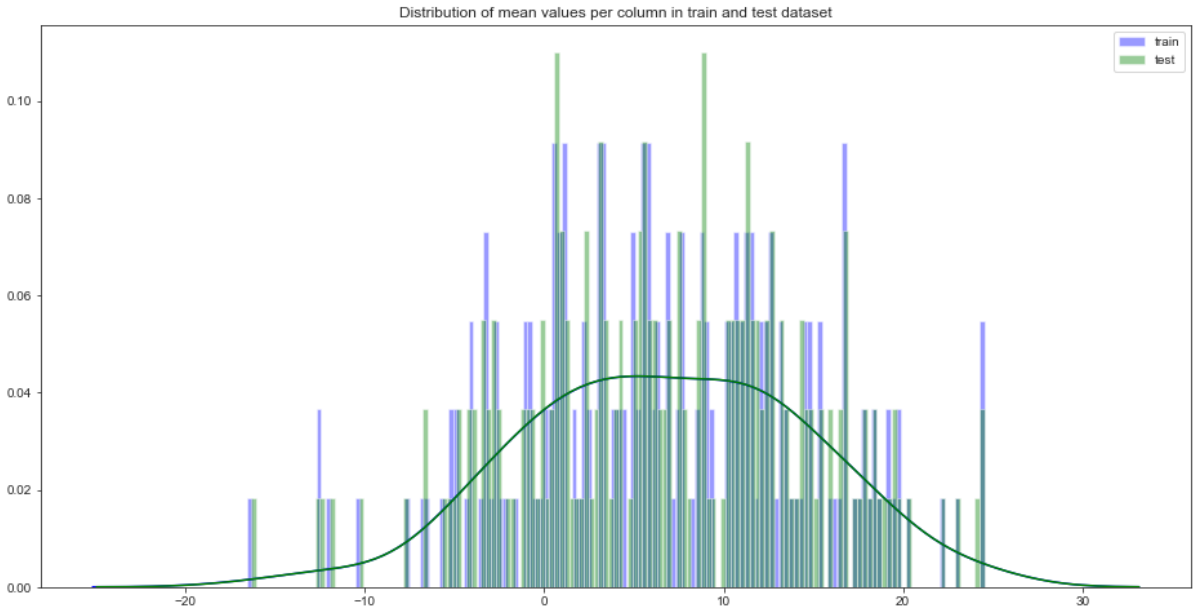
In [*]:
```
def plot_test_attribute_distribution(test_attributes):
    i=0
    sns.set_style('whitegrid')

    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()
#test attribiutes from 1 to 101
test_attributes=test_df.columns.values[1:101]
#plot distribution of test attributes
plot_test_attribute_distribution(test_attributes)

```

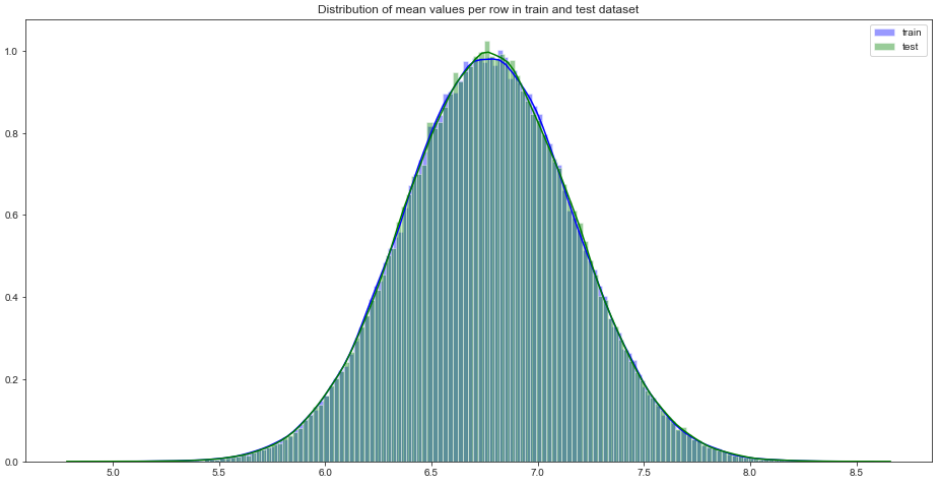
Insights:

- There are considerable number of features which are significantly have different distributions. For example like var_0,var_1,var_9,var_180 var_198 etc.
- There are considerable number of features which are significantly have same distributions. For example like var_3,var_7,var_10,var_171,var_185,var_192 etc.

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

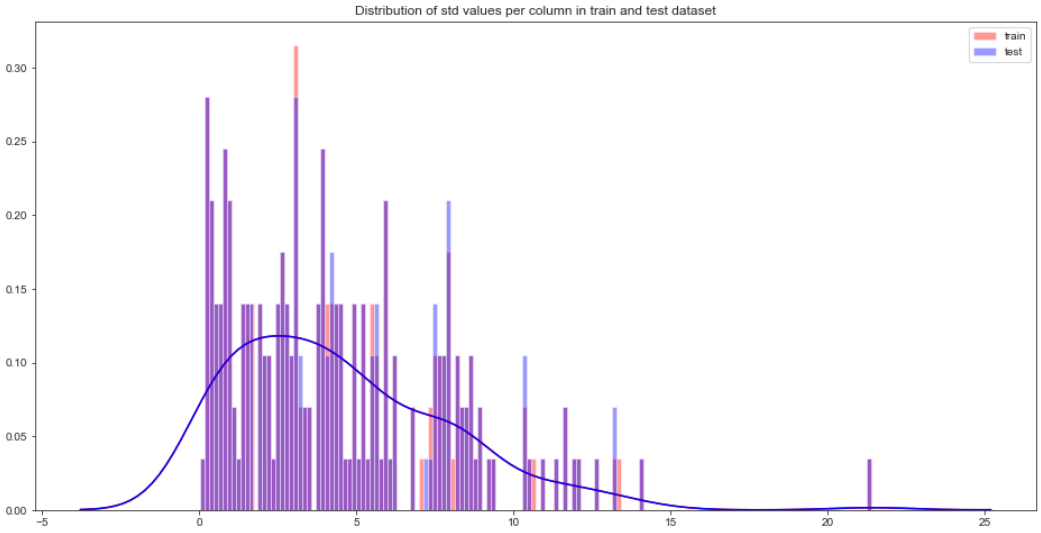
In [15]:
```
#Distribution of mean values per column in train and test dataset
plt.figure(figsize=(16,8))
#train attributes
train_attributes=train_df.columns.values[2:202]
#test attributes
test_attributes=test_df.columns.values[1:201]
#Distribution plot for mean values per column in train attributes
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')
plt.title('Distribution of mean values per column in train and test dataset')
plt.legend()
plt.show()

#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')
plt.legend()
plt.show()

```

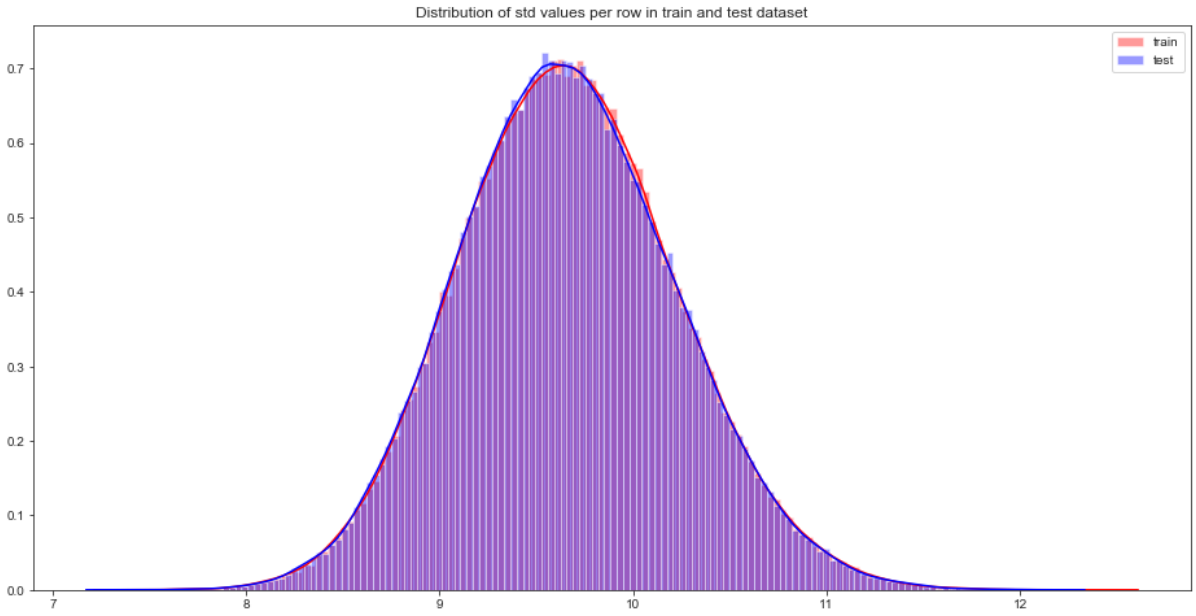




Let us look at the distribution of standard deviation (std) values per row and column in train and test dataset

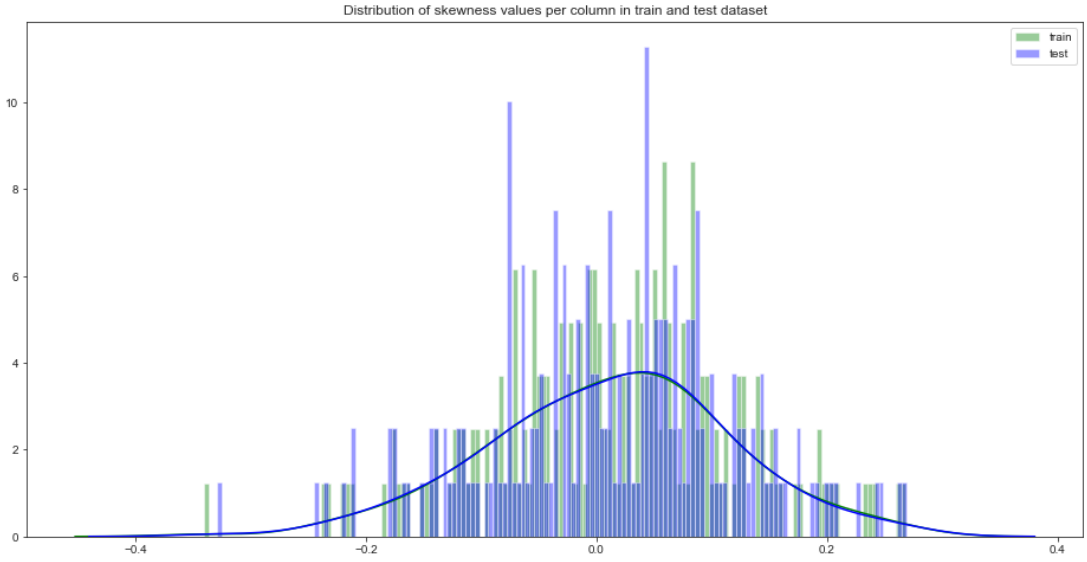
In [15]:
```
#Distribution of mean values per column in train and test dataset
plt.figure(figsize=(16,8))
#train attributes
train_attributes=train_df.columns.values[2:202]
#test attributes
test_attributes=test_df.columns.values[1:201]
#Distribution plot for mean values per column in train attributes
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')
plt.title('Distribution of mean values per column in train and test dataset')
plt.legend()
plt.show()

#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')
plt.legend()
plt.show()

```

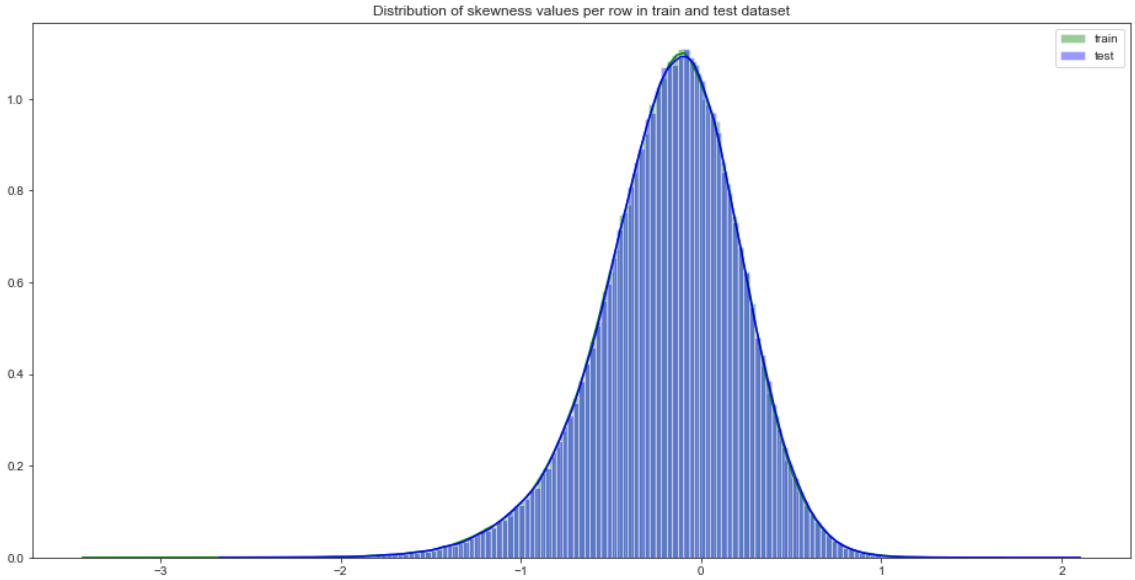




Let us look distribution of skewness per rows and columns in train and test dataset

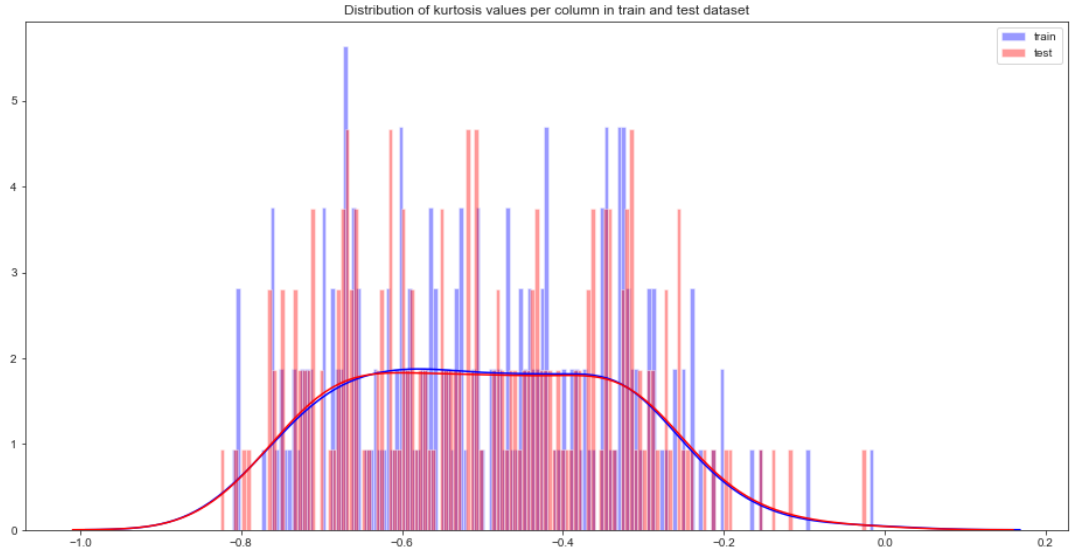
In [11]:
```
#Distribution of std values per column in train and test dataset
plt.figure(figsize=(16,8))
#train attributes
train_attributes=train_df.columns.values[2:202]
#test attributes
test_attributes=test_df.columns.values[1:201]
#Distribution plot for std values per column in train attributes
sns.distplot(train_df[train_attributes].std(axis=0),color='red',kde=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()
plt.show()

```

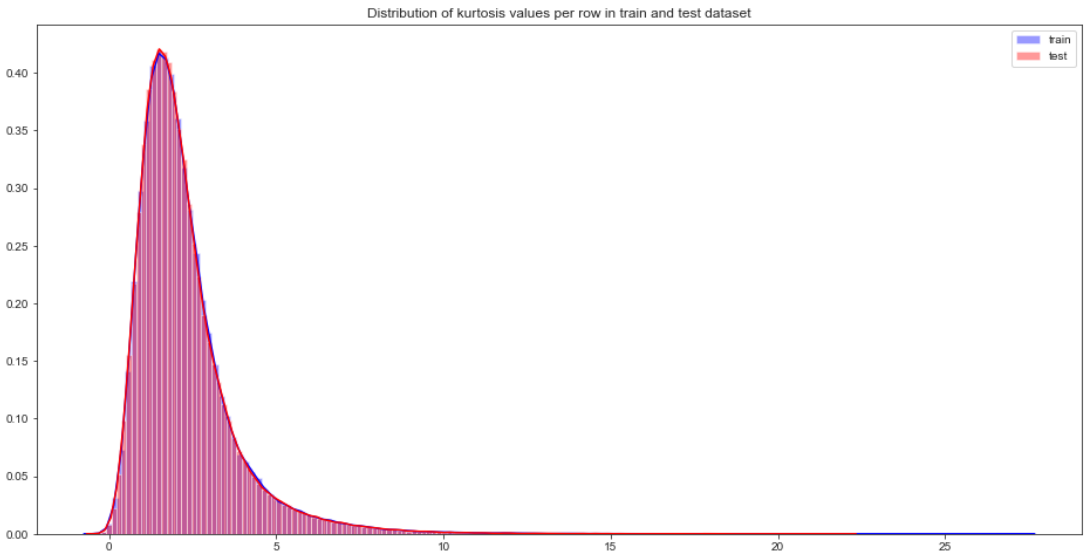




Let us look distribution of kurtosis values per rows and columns in train and test dataset

In [13]:
```
#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

In [14]:
```
#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)

```

```
Missing values in train data : 0
Missing values in test data : 0
```

No missing values are present in both train and test data.

Correlation between the attributes

In [15]:
```
#Correlations in train attributes
train_attributes=train_df.columns.values[2:202]
train_correlations=train_df[train_attributes].corr().abs().unstack().sort_values(kind='quicksort').reset_index()
train_correlations=train_correlations[train_correlations['level_0']!=train_correlations['level_1']]
print(train_correlations.head(10))
print(train_correlations.tail(10))

```

```
   level_0  level_1             0
0   var_75  var_191  2.703975e-08
1  var_191   var_75  2.703975e-08
2  var_173    var_6  5.942735e-08
3    var_6  var_173  5.942735e-08
4  var_126  var_109  1.313947e-07
5  var_109  var_126  1.313947e-07
6  var_144   var_27  1.772502e-07
7   var_27  var_144  1.772502e-07
8  var_177  var_100  3.116544e-07
9  var_100  var_177  3.116544e-07
       level_0  level_1         0
39790  var_183  var_189  0.009359
39791  var_189  var_183  0.009359
39792  var_174   var_81  0.009490
39793   var_81  var_174  0.009490
39794   var_81  var_165  0.009714
39795  var_165   var_81  0.009714
39796   var_53  var_148  0.009788
39797  var_148   var_53  0.009788
39798   var_26  var_139  0.009844
39799  var_139   var_26  0.009844
```

We can observe that the correlation between the train attributes is very small.

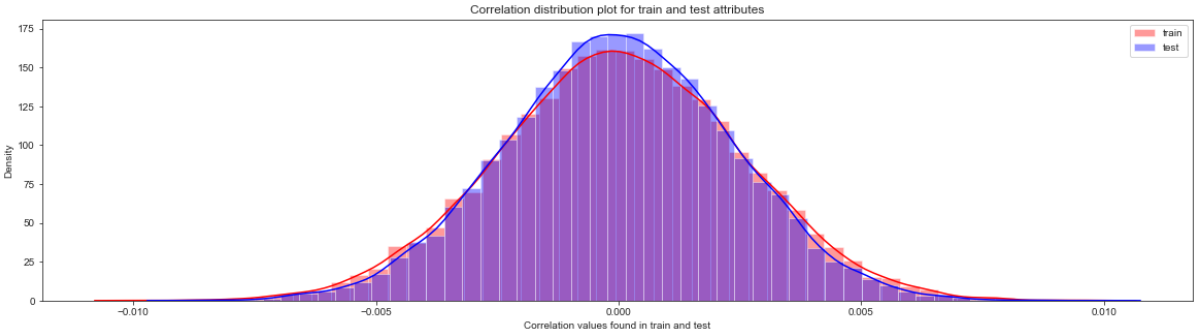
In [16]:
```
#Correlations in test attributes
test_attributes=test_df.columns.values[1:201]
test_correlations=test_df[test_attributes].corr().abs().unstack().sort_values(kind='quicksort').reset_index()
test_correlations=test_correlations[test_correlations['level_0']!=test_correlations['level_1']]
print(test_correlations.head(10))
print(test_correlations.tail(10))

```

```
   level_0  level_1             0
0  var_154  var_175  1.477268e-07
1  var_175  var_154  1.477268e-07
2  var_188  var_113  1.639749e-07
3  var_113  var_188  1.639749e-07
4  var_131    var_8  4.695407e-07
5    var_8  var_131  4.695407e-07
6   var_60  var_189  9.523709e-07
7  var_189   var_60  9.523709e-07
8  var_159   var_96  1.147835e-06
9   var_96  var_159  1.147835e-06
       level_0  level_1         0
39790  var_122  var_164  0.008513
39791  var_164  var_122  0.008513
39792  var_164    var_2  0.008614
39793    var_2  var_164  0.008614
39794   var_31  var_132  0.008714
39795  var_132   var_31  0.008714
39796   var_96  var_143  0.008829
39797  var_143   var_96  0.008829
39798  var_139   var_75  0.009868
39799   var_75  var_139  0.009868
```

We can observe that the correlation between the test attributes is very small.

Correlation plot for train and test data

In [17]:
```
#Correlations in train data
train_correlations=train_df[train_attributes].corr()
train_correlations=train_correlations.values.flatten()
train_correlations=train_correlations[train_correlations!=1]
#Correlations in test data
test_correlations=test_df[test_attributes].corr()
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()

```



We can observe from correlation distribution plot that the correlation between the train and test attributes is very very small, it means that features are independent each other.

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.

In [18]:
```
#training and testing data
X=train_df.drop(columns=['ID_code','target'],axis=1)
test=test_df.drop(columns=['ID_code'],axis=1)
y=train_df['target']

```

Let us build simple model to find features which are more important.

In [19]:
```
#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)

```

```
Shape of X_train : (150000, 200)
Shape of X_valid : (50000, 200)
Shape of y_train : (150000,)
Shape of y_valid : (50000,)
```

Random forest classifier

In [20]:
```
#Random forest classifier
rf_model=RandomForestClassifier(n_estimators=10,random_state=42)
#fitting the model
rf_model.fit(X_train,y_train)

```

Out[20]:
```
RandomForestClassifier(bootstrap=True, ccp_alpha=0.0, class_weight=None,
                       criterion='gini', max_depth=None, max_features='auto',
                       max_leaf_nodes=None, max_samples=None,
                       min_impurity_decrease=0.0, min_impurity_split=None,
                       min_samples_leaf=1, min_samples_split=2,
                       min_weight_fraction_leaf=0.0, n_estimators=10,
                       n_jobs=None, oob_score=False, random_state=42, verbose=0,
                       warm_start=False)
```

Let us calculate weights and show important features using eli5 library.

In [21]:
```
#Permutation importance
from eli5.sklearn import PermutationImportance
perm_imp=PermutationImportance(rf_model,random_state=42)
#fitting the model
perm_imp.fit(X_valid,y_valid)
```

Out[21]:
```
PermutationImportance(cv='prefit',
                      estimator=RandomForestClassifier(bootstrap=True,
                                                       ccp_alpha=0.0,
                                                       class_weight=None,
                                                       criterion='gini',
                                                       max_depth=None,
                                                       max_features='auto',
                                                       max_leaf_nodes=None,
                                                       max_samples=None,
                                                       min_impurity_decrease=0.0,
                                                       min_impurity_split=None,
                                                       min_samples_leaf=1,
                                                       min_samples_split=2,
                                                       min_weight_fraction_leaf=0.0,
                                                       n_estimators=10,
                                                       n_jobs=None,
                                                       oob_score=False,
                                                       random_state=42,
                                                       verbose=0,
                                                       warm_start=False),
                      n_iter=5, random_state=42, refit=True, scoring=None)
```

Let us see important features

In [22]:
```
#Important features
eli5.show_weights(perm_imp,feature_names=X_valid.columns.tolist(),top=200)

```

Out[22]:

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
0.0001 ± 0.0001	var_1
0.0001 ± 0.0000	var_37
0.0001 ± 0.0003	var_133
0.0001 ± 0.0000	var_152
0.0001 ± 0.0001	var_175
0.0001 ± 0.0001	var_88
0.0001 ± 0.0001	var_66

Take away:

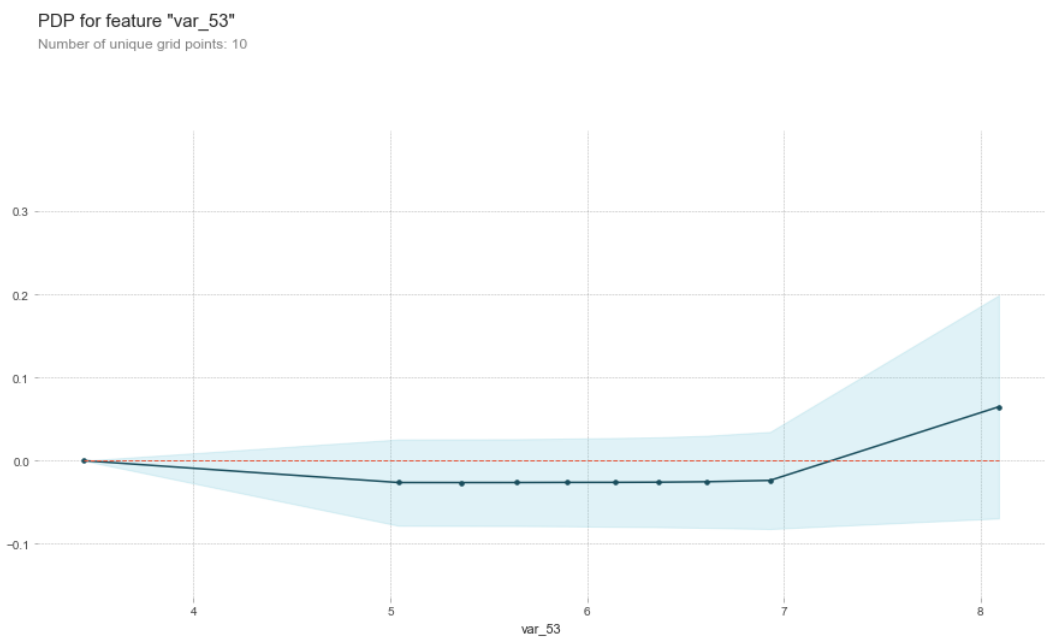
- Importance of the features decreases as we move down the top of the column.
- As we can see the features shown in green indicate that they have a positive impact on our prediction
- As we can see the features shown in white indicate that they have no effect on our prediction
- As we can see the features shown in red indicate that they have a negative impact on our prediction
- The most important feature is 'Var_81'

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.

Let us calculate partial dependence plots on random forest.

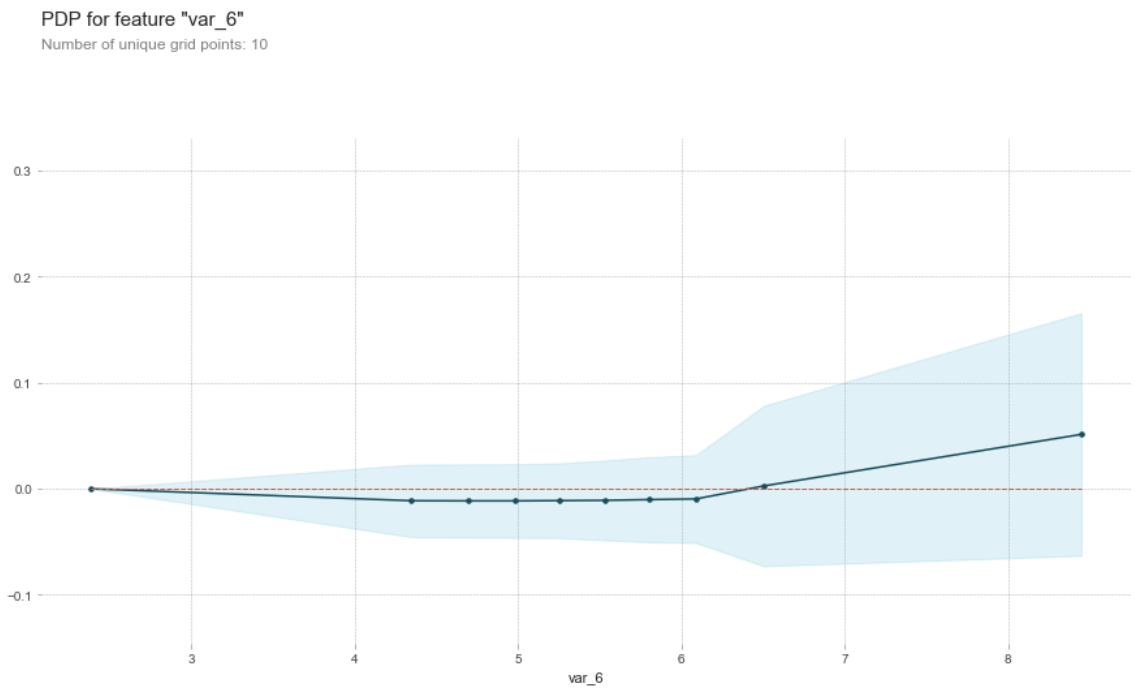
In [23]:
```
#Create the data we will plot 'var_53'
features=[v for v in X_valid.columns if v not in ['ID_code','target']]
pdp_data=pdp.pdp_isolate(rf_model,dataset=X_valid,model_features=features,feature='var_53')
#plot feature "var_53"
pdp.pdp_plot(pdp_data,'var_53')
plt.show()

```



Take aways:

- 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.

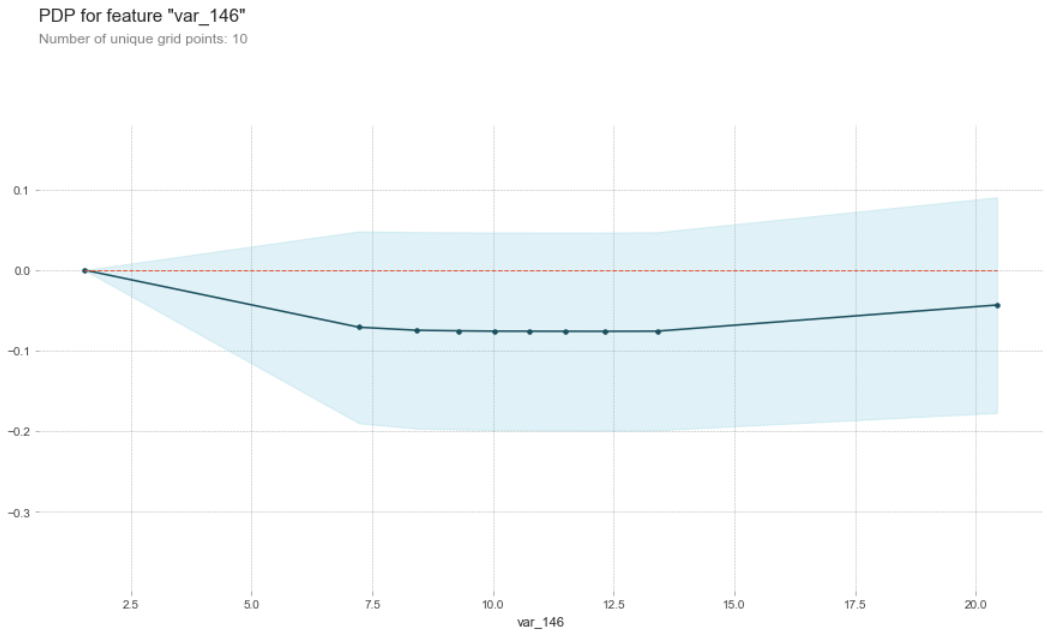
```
In [24]:
#Create the data we will plot
pdp_data=pdp.pdp_isolate(rf_model,dataset=X_valid,model_features=features,feature='var_6')
#plot feature "var_6"
pdp.pdp_plot(pdp_data,'var_6')
plt.show()
```



Take aways:

- 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_6'.
- 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.

```
In [25]:
#Create the data we will plot
pdp_data=pdp.pdp_isolate(rf_model,dataset=X_valid,model_features=features,feature='var_146')
#plot feature "var_146"
pdp.pdp_plot(pdp_data,'var_146')
plt.show()
```



Take aways:

- 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_146'.
- 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.

Handling of imbalanced data

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

- Change the performance metric
- Oversample minority class
- Undersample majority class
- Synthetic Minority Oversampling Technique(SMOTE)
- Change the algorithm

Now let us start with Simple Logistic regression model.

Split the train data using StratefiedKFold cross validator

In [26]:
```
#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)

```

```
Shape of X_train : (160000, 200)
Shape of X_valid : (40000, 200)
Shape of y_train : (160000,)
Shape of y_valid : (40000,)
```

Logistic Regression model

In [27]:
```
#Logistic regression model
lr_model=LogisticRegression(random_state=42)
#fitting the lr model
lr_model.fit(X_train,y_train)

```

Out[27]:
```
LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True,
                   intercept_scaling=1, l1_ratio=None, max_iter=100,
                   multi_class='auto', n_jobs=None, penalty='l2',
                   random_state=42, solver='lbfgs', tol=0.0001, verbose=0,
                   warm_start=False)
```

Accuracy of model

In [28]:
```
#Accuracy of the model
lr_score=lr_model.score(X_train,y_train)
print('Accuracy of the lr_model :',lr_score)

```

```
Accuracy of the lr_model : 0.91219375
```

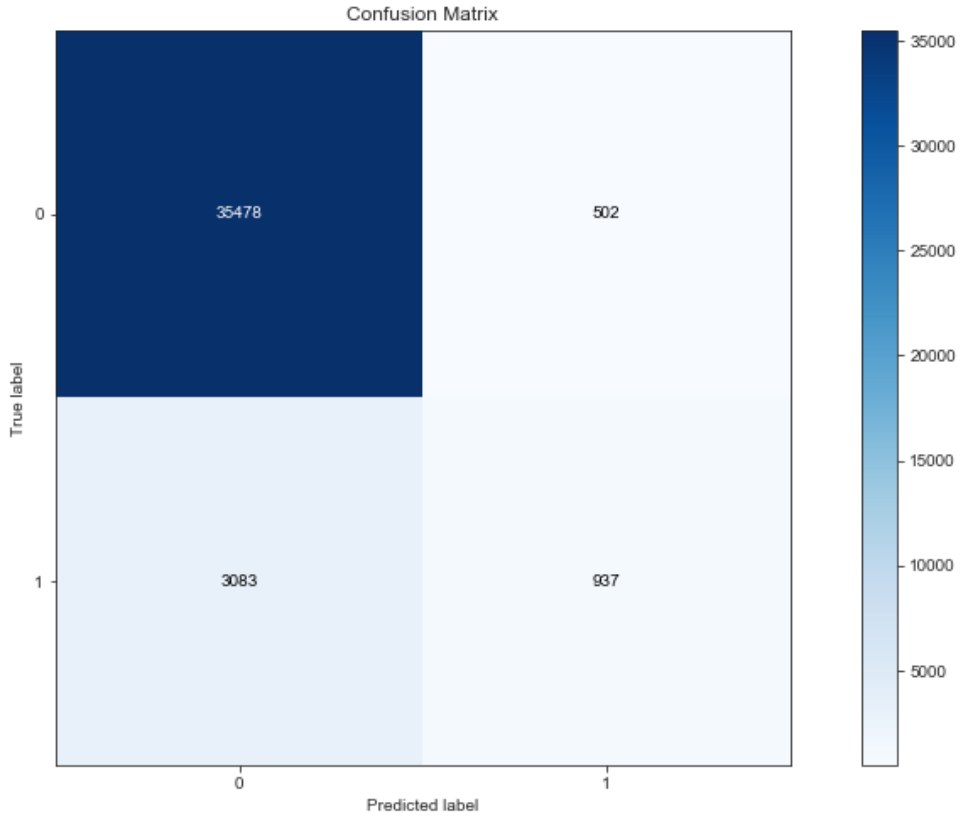
In [29]:
```
#Cross validation prediction
cv_predict=cross_val_predict(lr_model,X_valid,y_valid,cv=5)
#Cross validation score
cv_score=cross_val_score(lr_model,X_valid,y_valid,cv=5)
print('cross_val_score :',np.average(cv_score))

```

```
cross_val_score : 0.9103749999999999
```

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.

Confusion matrix

In [30]:
```
#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))

```

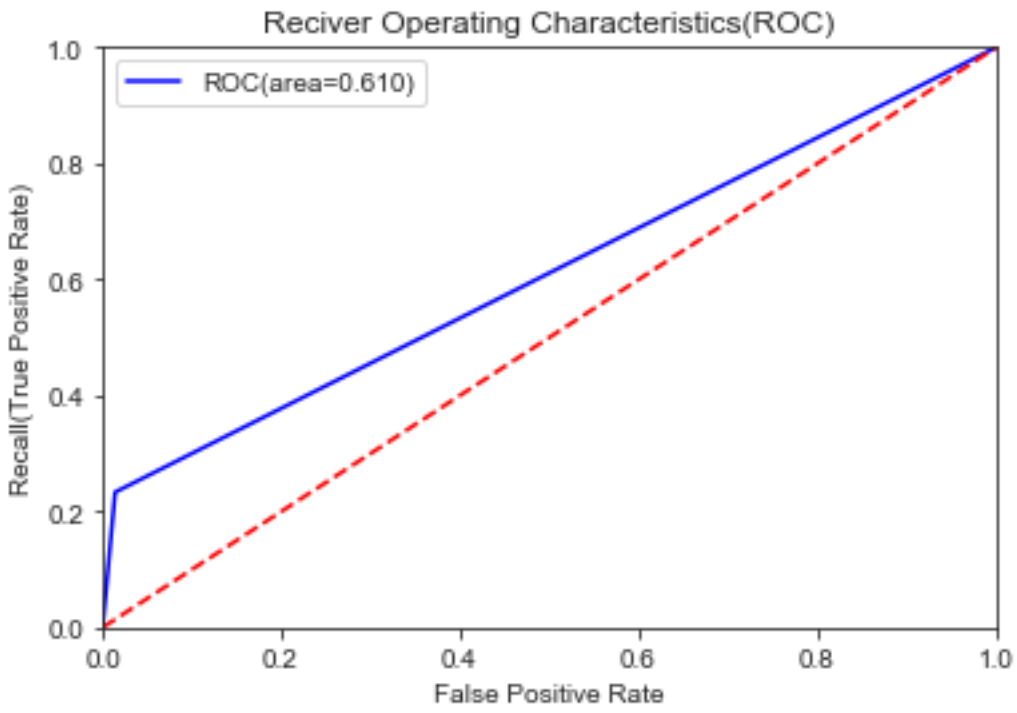


Reciever operating characteristics (ROC)-Area under curve(AUC) score and curve

In [31]:

```
#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)

```

ROC score : 0.609566190725085




```
AUC: 0.609566190725085
```

When we compare the roc_auc_score and model accuracy , model is not performing well on imbalanced data.

Classification report

```
In [32]:
#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	0.65	0.23	0.34	4020
accuracy			0.91	40000
macro avg	0.79	0.61	0.65	40000
weighted avg	0.89	0.91	0.89	40000

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

Model performance on test data

In [33]:
```
#Predicting the model
X_test=test_df.drop(['ID_code'],axis=1)
lr_pred=lr_model.predict(X_test)
print(lr_pred)

```

```
[0 0 0 ... 0 0 0]
```

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 leads to overfitting and poor performance on test data.

Undersample 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 million of rows.
- Drawback is that we are removing information that may be valuable. This may leads to underfitting and poor performance on test data.

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

Synthetic Minority Oversampling Technique(SMOTE)

SMOTE uses a nearest neighbors algorithm to generate new and synthetic data to used for training the model.

In [34]:
```
from imblearn.over_sampling import SMOTE
#Synthetic Minority Oversampling Technique
sm = SMOTE(random_state=42)
#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)

```

Let us see how baseline logistic regression model performs on synthetic data points.

In [35]:
```
#Logistic regression model for SMOTE
smote=LogisticRegression(random_state=42)
#fitting the smote model
smote.fit(X_smote,y_smote)

```

Accuracy of model

In [36]:
```
smote_score=smote.score(X_smote,y_smote)
print('Accuracy of the smote_model :',smote_score)

```

```
Accuracy of the smote_model : 0.7885208654687956
```

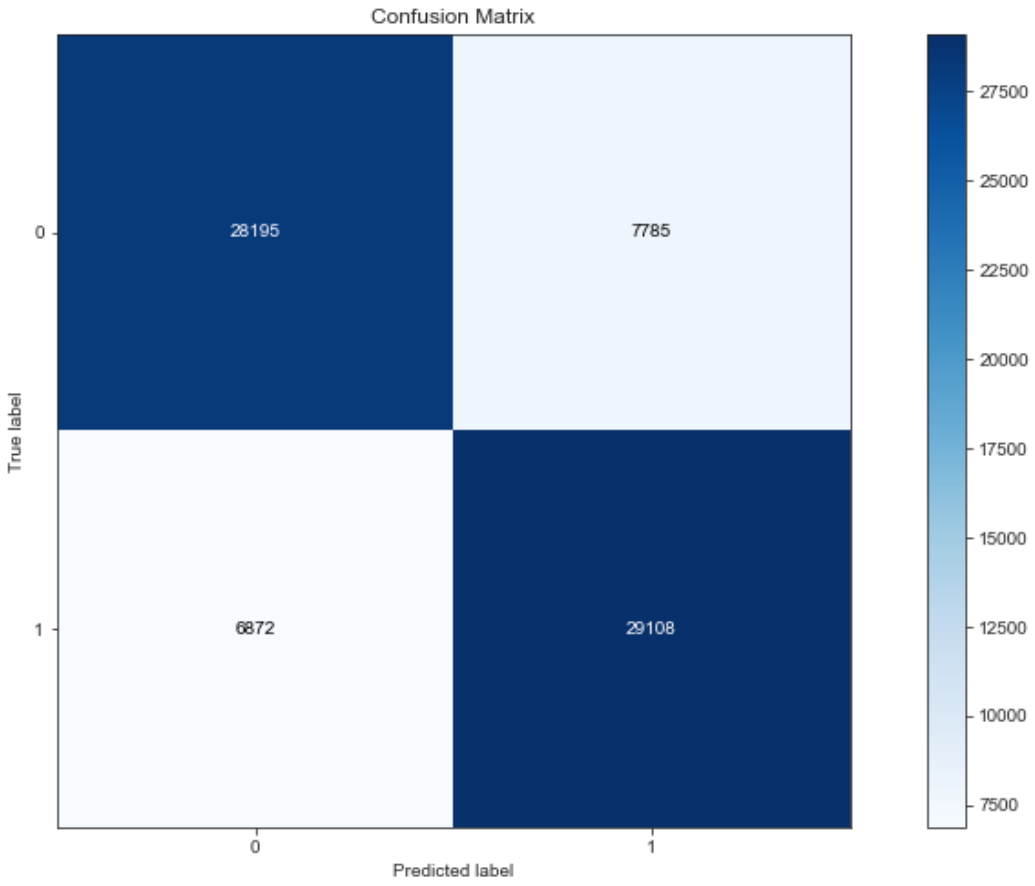
Cross validation prediction of smote model

In [37]:
```
#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))

```

```
cross_val_score : 0.7963173985547526
```

Confusion matrix

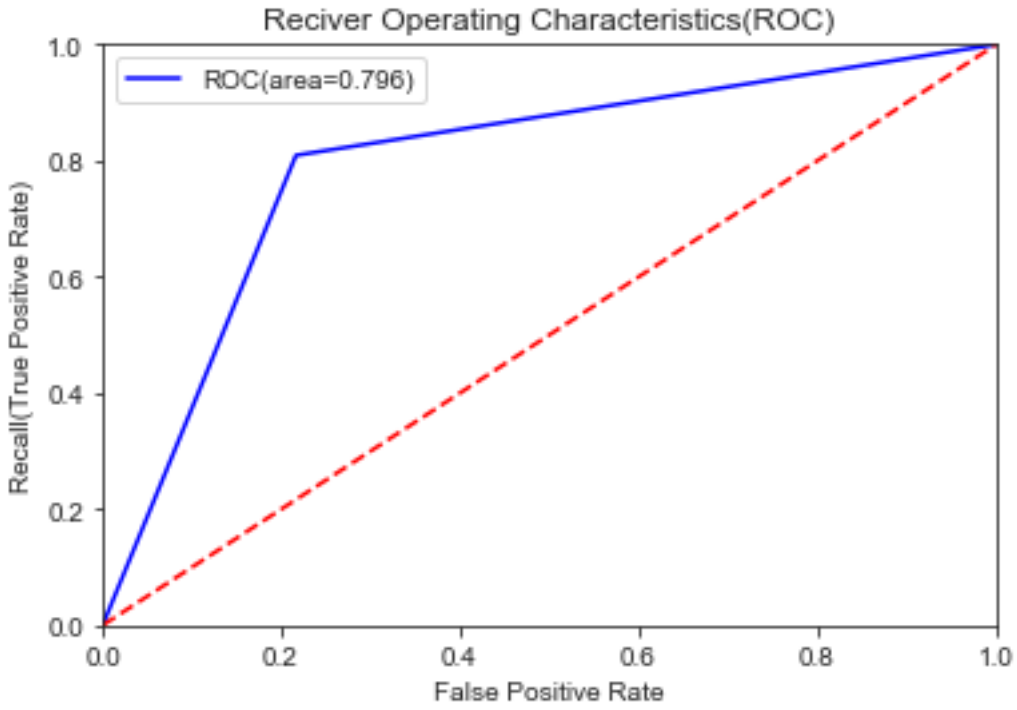
In [38]:
```
#Confusion matrix
cm=confusion_matrix(y_smote_v,cv_pred)
#Plot the confusion matrix
plot_confusion_matrix(y_smote_v,cv_pred,normalize=False,figsize=(15,8))

```



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

In [39]:
```
#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)

```

```
ROC score : 0.7963173985547527
```




```
AUC: 0.7963173985547527
```

Classification report

In [40]:
```
#Classification report
scores=classification_report(y_smote_v,cv_pred)
print(scores)

```

```
              precision    recall  f1-score   support

           0       0.80      0.78      0.79     35980
           1       0.79      0.81      0.80     35980

    accuracy                           0.80     71960
   macro avg       0.80      0.80      0.80     71960
weighted avg       0.80      0.80      0.80     71960
```

Model performance on test data

In [41]:
```
#Predicting the model
X_test=test_df.drop(['ID_code'],axis=1)
smote_pred=smote.predict(X_test)
print(smote_pred)

```

```
[1 1 0 ... 0 0 1]
```

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

LightGBM

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

Let us build LightGBM model

In [42]:
```
#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)

```

Choosing of hyperparameters

In [43]:
```
#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': 20,
          'metric':'auc',
          'num_leaves': 50,
          'learning_rate': 0.01,
          'max_bin': 100,      #default 255
          'subsample_for_bin': 100,
          'subsample': 1,
          'subsample_freq': 1,
          'colsample_bytree': 0.8,
          'bagging_fraction':0.5,
          'bagging_freq':5,
          'feature_fraction':0.08,
          'min_split_gain': 0.45, #>0
          'min_child_weight': 1,
          'min_child_samples': 5,
          'is_unbalance':True,
          }

```

Training the lgbm model

In [44]:
```
num_rounds=10000
lgbm= lgb.train(params,lgb_train,num_rounds,valid_sets=[lgb_train,lgb_valid],verbose_eval=1000,early_stopping_round
lgbm

```

```
Training until validation scores don't improve for 5000 rounds
[1000]  training's auc: 0.938309        valid_1's auc: 0.887942
[2000]  training's auc: 0.957945        valid_1's auc: 0.892205
[3000]  training's auc: 0.971593        valid_1's auc: 0.893526
[4000]  training's auc: 0.981333        valid_1's auc: 0.894011
[5000]  training's auc: 0.988169        valid_1's auc: 0.893938
[6000]  training's auc: 0.992771        valid_1's auc: 0.893874
[7000]  training's auc: 0.995759        valid_1's auc: 0.893498
[8000]  training's auc: 0.997638        valid_1's auc: 0.893374
Early stopping, best iteration is:
[3804]  training's auc: 0.979706        valid_1's auc: 0.89418
```

lgbm model performance on test data

In [45]:
```
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)

```

```
[0.43204216 0.6001353  0.47570884 ... 0.03934805 0.25337599 0.30022367]
[0 1 0 ... 0 0 0]
```

Let us plot the important features

In [46]:
```
#plot the important features
lgb.plot_importance(lgbm,max_num_features=50,importance_type="split",figsize=(20,50))

```


Feature importance
var_34 1338
var_53 1308
var_94 1296
var_9 1269
var_99 1263
var_13 1257
var_78 1225
var_184 1223
var_1 1222
var_154 1214
var_188 1213
var_2 1193
var_148 1190
var_21 1190
var_71 1188
var_174 1178
var_122 1175
var_107 1164
var_146 1161
var_40 1159
var_179 1157
var_108 1154
var_92 1154
var_128 1149
var_177 1142
var_22 1142
var_5 1139
var_190 1131
var_133 1131
var_80 1128
var_173 1127
var_137 1126
var_164 1124
var_18 1121
var_6 1120
var_150 1119
var_127 1117
var_165 1115
var_33 1112
var_169 1109
var_31 1104
var_12 1100
var_166 1092
var_110 1092
var_167 1089
var_109 1085
var_67 1082
var_43 1082
var_147 1080
var_121 1080
Features
0
200
400
600
800
1000
1200
1400
Feature importance

Conclusion :

We tried model with logistic regression, smote and lightgbm. But lightgbm model is performing well on imbalanced data compared to other models based on scores of roc_auc_score.

Final Submission

In [47]:
```
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
sub_df.to_csv('submission.csv',index=False)
sub_df.head()

```

	ID_code	lgbm_predict_prob	lgbm_predict
0	test_0	0.432042	0
1	test_1	0.600135	1
2	test_2	0.475709	0
3	test_3	0.437665	0
4	test_4	0.228739	0

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(x=target,y=1:nrow(train_df)))+theme_bw()+geom_violin(f
ill='lightblue')+facet_grid(train_df$target)+geom_jitter(width=0.02)+labs(
y='Index') grid.arrange(plot1,plot2, ncol=2)
```

Distribution of train attributes

```
#Distribution of train attributes from 3 to 102 for (var in
names(train_df)[c(3:102)]){

target<-train_df$target
plot<-ggplot(train_df, aes(x=train_df[[var]],fill=target)) +
geom_density(kernel='gaussian') + ggtitle(var)+theme_classic() print(plot)

}
#Distribution of train attributes from 103 to 202 for (var in
names(train_df)[c(103:202)]){

target<-train_df$target
plot<-ggplot(train_df, aes(x=train_df[[var]], fill=target)) +
geom_density(kernel='gaussian') + ggtitle(var)+theme_classic() print(plot)
```

```
}
```

Distribution of test 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 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 per row
in train and test dataset")
```

Distribution of standard deviation in train and test dataset

```
#Applying the function to find standard deviation values per row in train
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='b lue')+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 kurtosis values
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<-cor(test_df[,c(2:201)])
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" partialPlot(rf,valid_data[,-
c(1,2)],valid_data$var_81,xlab='var_81

#We will plot "var_12" partialPlot(rf,valid_data[,-
c(1,2)],valid_data$var_12,xlab='var_12')
```

Handling of imbalanced data

```
#Split the data using CreateDataPartition
set.seed(689) train.index<-
createDataPartition(train_df$target,p=0.8,list=FALSE) train.data<-
train_df[train.index,] valid.data<-train_df[-train.index,]

dim(train.data)

dim(valid.data)

#training dataset

set.seed(682)
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
```

```
#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)
```

```
#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) head(sub_df)
```

References

https://www.kaggle.com
http://rprogramming.net/
https://medium.com/
https://stackoverflow.com/
https://www.rdocumentation.org
https://www.analyticsvidhya.com/blog
R for Data Science by *Garrett Grolemund*, *Hadley Wickham*
Practical Machine learning with Python book by by Dipanjan Sarkar, Raghav Bali and Tushar Sharma Python Data Science Handbook by *Jake VanderPlas*