In [1]:
```
# Module: Data Science in Finance, Machine Learning in 30 minutes!
# Version 1.0
# Topic : Clustering and building models
# Example source: https://www.kaggle.com/wendykan/lending-club-loan-data
#########################################################################
# For support or questions, contact Sri Krishnamurthy at
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#########################################################################
```

Clustering and building models

This notebook deals with understanding the lending data obtained from https://www.kaggle.com/wendykan/lending-club-loan-data (https://www.kaggle.com/wendykan/lending-club-loan-data). We will cluster the data using K-Means clustering to see patterns in the dataset.

Imports

In [2]:
```
# for numerical analysis and data processing
import numpy as np
import pandas as pd
import itertools

from IPython.display import Image

# for Machine learning algorithms
from sklearn import preprocessing
from sklearn.cluster import KMeans
from sklearn.manifold import TSNE
from sklearn.linear_model import LinearRegression
from sklearn.ensemble import RandomForestRegressor
from sklearn.neural_network import MLPRegressor
from sklearn.metrics import mean_squared_error, mean_absolute_error
from scipy.spatial.distance import cdist

# for vizualizations
%matplotlib inline
import matplotlib.pyplot as plt
from matplotlib import cm as cm
from mpl_toolkits.mplot3d import Axes3D
import seaborn as sns
```

Dataset

The data set is the lending data for lendingclub from August 2011 to December 2011 for some borrowers. The feature descriptions for the data are also provided. Not all the features are required

for making predictions, some features are redundant in the original data file. The provided data file is already cleaned and only relevant features are provided. There are two types of features, numerical and categorical.

Reading the input data from csv file.

In [3]:
```
df = pd.read_csv("../data/LendingClubLoan.csv", low_memory=False)
del df['issue_d'] # removing issue date as it wont affect the prediction (redundan
df_description = pd.read_excel('../data/LCDataDictionary.xlsx').dropna()
```

Preparing categorical features

Categorical data is best processed by algorithms when converted to numerical format.The most common way is by mapping each category to an integers. Ex. [A, B, C] can be mapped to [0, 1, 2]. Another way is one-hot encoding which we will look into while building the models.

In [4]:
```
numeric_columns = df.select_dtypes(include=['float64','int64']).columns
categorical_columns = df.select_dtypes(include=['object']).columns
```

In [5]:
```
for col in categorical_columns:
    df[col] = df[col].astype('category')
```

In [6]:
```
p_categories = df['purpose'].cat.categories.tolist()
s_categories = df['addr_state'].cat.categories.tolist()
df[categorical_columns] = df[categorical_columns].apply(lambda x: x.cat.codes)
```

Storing interest rate statistics

In [7]:
```
min_rate= df['int_rate'].min()
max_rate= df['int_rate'].max()
print(min_rate, max_rate, max_rate- min_rate)
```

```
5.42 24.11 18.689999999999998
```

Clustering - k-Means Clustering

The k-means algorithm searches for a pre-determined number of clusters within an unlabeled multidimensional dataset. According to this algorithm, a simple cluster:

1. has a "cluster center" which is the arithmetic mean of all the points belonging to the cluster
2. has each point closer to its own cluster center than to other cluster centers

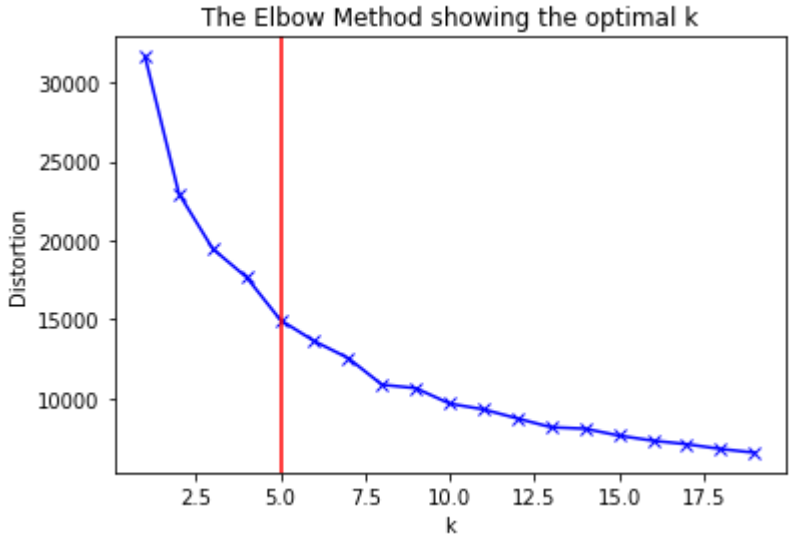
One of the most important parameters that has to be decided by the user is the value of k, the number of cluster. K random centroids are selected and the centroids are moved with each iteration

of the algorithm until all points are assigned a cluster.

To select the value of K, one of the widely used method is called the Elbow Curve method. Logically, K-Means attempts to minimize distortion defined by the the sum of the squared distances between each observation and its closest centroid. This is called the cost function or distortion. We plot the values of dstortion against K and select where the plot forms an 'elbow joint' i.e. the point after which there is a gradual decrease in the distortion.

In [8]:
```
# this cell takes a few minutes to execute
distortions = []
K = range(1,20)
for k in K:
    kmeanModel = KMeans(n_clusters=k).fit(df[0:9999])
    kmeanModel.fit(df[0:9999])
    distortions.append(sum(np.min(cdist(df[0:9999], kmeanModel.cluster_centers_, '
```

In [9]:
```
plt.plot(K, distortions, 'bx-')
plt.axvline(5, color='r')
plt.xlabel('k')
plt.ylabel('Distortion')
plt.title('The Elbow Method showing the optimal k')
plt.show()
```



The distortion values will eventually reach 0 when the value of K is equal to the number of samples in the dataset, which is same as having one cluster for each point and is undesireable. In this experiment, the distortion changes by 15000 in the first 5 K values and then by 5000 in the next 15 K values. So we select K = 5 as the elbow point.

In [10]:
```
num_clusters = 5
num_samples = 9999
```

In [11]:
```
kmeans = KMeans(n_clusters=num_clusters, algorithm='elkan')
kmeans.fit(df[0:num_samples])

unique, counts = np.unique(kmeans.labels_, return_counts=True)
cluster_indices = np.asarray((unique, counts)).T[:,1].argsort()[-3:][::-1] # chang

print('Samples per cluster:')
print (np.asarray((unique, counts)).T)
```

```
Samples per cluster:
[[   0 5210]
 [   1 1054]
 [   2  108]
 [   3    1]
 [   4 3626]]
```

Add the cluster label to the dataframe.

In [12]:
```
df_cluster = df.join(pd.DataFrame({'cluster': kmeans.labels_}), lsuffix='_caller',
```

In [13]:
```
clusters = []
for i in cluster_indices:
    clusters.append(df_cluster[df_cluster['cluster']==i].loc[:, df.columns != 'clu
```

t-SNE

It is easy to vizualize data that has 2 or even 3 dimensions. It gets tricker to do so once we move over 3 dimensions. t-SNE (t-Distributed Stochastic Neighbor Embedding) (https://lvdmaaten.github.io/tsne/) is a technique for dimensionality reduction that is particularly well suited for the visualization of high-dimensional datasets. Here, we will try to represent our 16 dimensional data (16 feature) in 3 dimensions.

For a t-SNE plot, the relative distances between clusters or the relative distances within points of a single cluster do not signify anthing. It is just a way of visually representing the separation of clusters.

In [14]:
```
dimensions = 3
# t-SNE parmeters
iterations = 5000
perplexity = 40
# vizualisation is computationally intensive, so we'll stick to 500 samples
num_samples = 500
```

In [15]:
```
# this cell takes a few minutes to execute
tsne = TSNE(n_components=dimensions, random_state=0, perplexity=perplexity, n_iter
embeddings = tsne.fit(df[0:num_samples])
# X_2d.embedding_
```

The new 3 dimensions as assigned by t-SNE

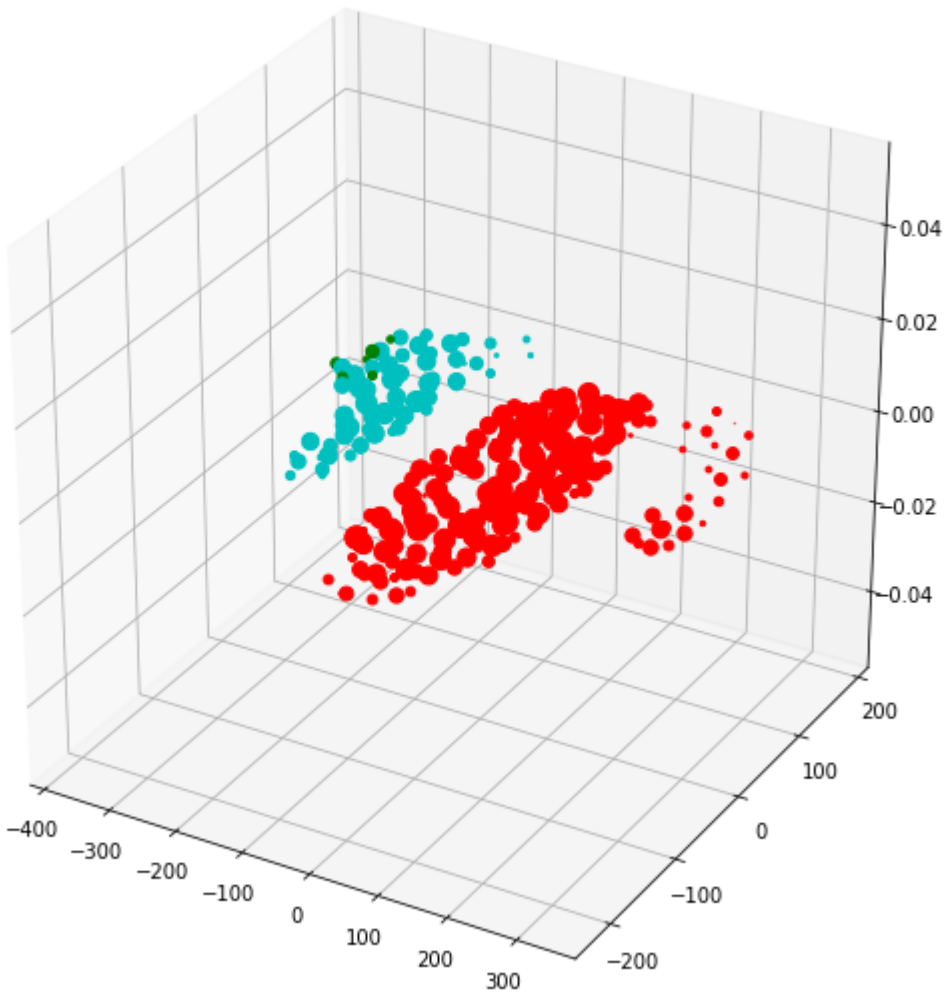
In [16]:
```
embeddings.embedding_[0:5]
```

Out[16]:
```
array([[ 288.7012   ,   -7.7664275,   -8.215757 ],
       [ 246.7552   ,  -62.43229  ,  -71.17717  ],
       [ 257.74905  ,  -40.62806  ,   52.882473 ],
       [  20.292011 , -112.72798  ,  120.49461  ],
       [-193.28879  ,  -90.44925  ,   19.583723 ]], dtype=float32)
```

Plotting in 3d

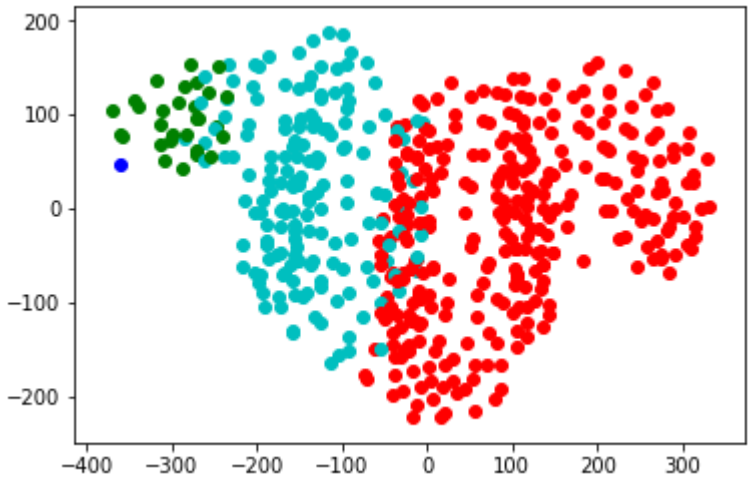
In [17]:
```
fig = plt.figure(figsize=(10,10))
ax = fig.add_subplot(111, projection='3d')
colors = ['r', 'g', 'b','black', 'c','k']
for i, val in zip(range(len(embeddings.embedding_)),kmeans.labels_):
    plt.scatter(embeddings.embedding_[i,0], embeddings.embedding_[i,1], embeddings
plt.show()
```

```
c:\users\atharva jakkanwar\anaconda3\envs\tensorflow\lib\site-packages\matplot
lib\collections.py:902: RuntimeWarning: invalid value encountered in sqrt
  scale = np.sqrt(self._sizes) * dpi / 72.0 * self._factor
```



2d top view of the same 3d plot

In [18]:
```
for i, val in zip(range(len(embeddings.embedding_)),kmeans.labels_):
    plt.scatter(embeddings.embedding_[i,0], embeddings.embedding_[i,1],c=colors[va
```



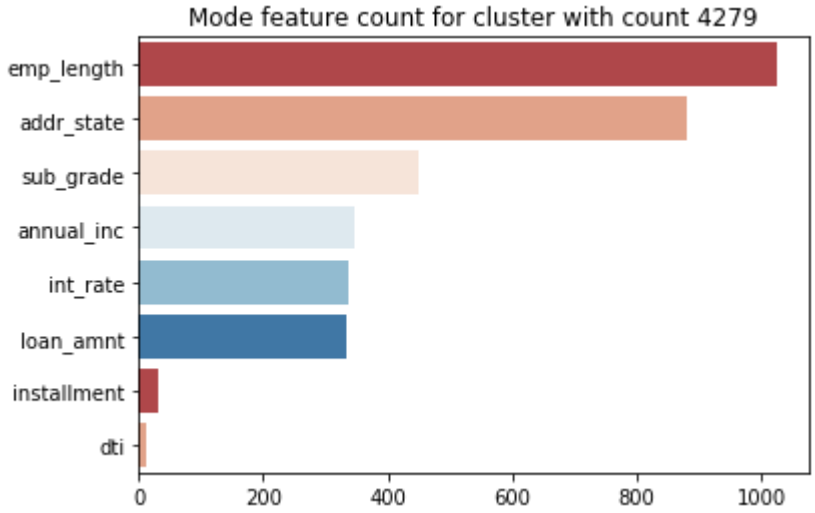
In [19]:
```
from scipy.stats import mode

def print_mode(cluster, display = True):
    df_mode = mode(cluster)
    if display == True:
        print("%20s | %8s | %9s | %s" % ('Column', 'Mode', 'Mode Count', 'Mean'))
#         print(type(cluster.mean()))
        print("-----------------------------------------------------------------------"
        for c1, c2, c3, c4 in zip(df_cluster.dtypes.index, df_mode.mode[0], df_mod
            print ("%20s | %8s | %9s | %s" % (c1, c2, c3, c4))
        print()
    return df_cluster.dtypes.index, df_mode.mode[0], df_mode.count[0]

def display_cluster_mode_feature(cluster):
    # showing from 8 onwards as previous all features have similar distribution ac
    sns.barplot(y = cluster[0][cluster[2].argsort()[::-1]][8:], x = np.sort(cluste
    plt.title('Mode feature count for cluster with count %s'  % (cluster[2][-1]))
    plt.show()
```

We can see that the clusters are somewhat based on *annual income* and its relate features. The two clusters with the highest count have somewhat similar mean and mode annual income but vary mostly based on the installments. The cluster with lower count has drastically higher mean and mode income.

These factors along with other statistics can be taken into consideration while selection of models.

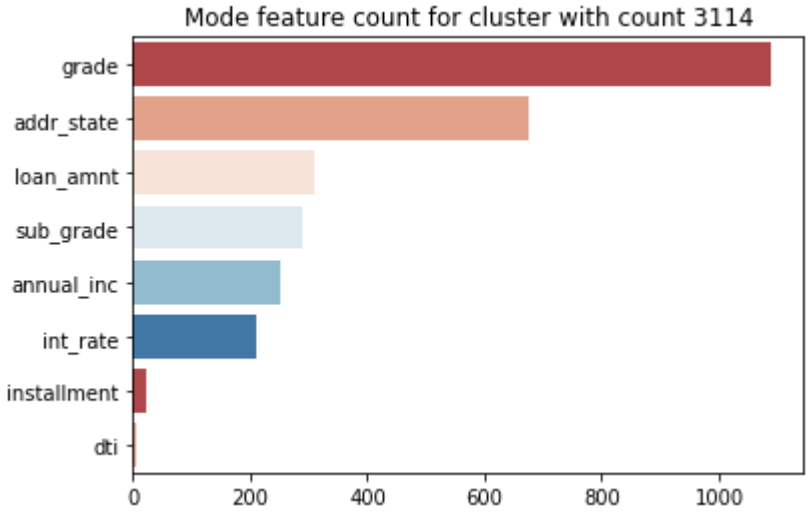
In [20]:
```
for cluster in clusters:
    cluster = print_mode(cluster)
    display_cluster_mode_feature(cluster)
```

Column	Mode	Mode Count	Mean
loan_amnt	12000.0	333	9629.96641074856
term	0.0	3803	0.27005758157389637
int_rate	11.71	336	12.05252783109376
installment	330.76	30	278.38429174664077
grade	1.0	1698	1.3775431861804224
sub_grade	7.0	451	8.80134357005758
emp_length	1.0	1025	3.77658349328215
home_ownership	2.0	2951	1.2301343570057581
annual_inc	60000.0	348	42513.3904069098
verification_status	0.0	1952	0.9197696737044145
purpose	2.0	2651	3.3245681381957772
addr_state	4.0	881	19.03877159309021
dti	21.6	12	14.816911708253409
delinq_2yrs	0.0	4731	0.12437619961612284
inq_last_6mths	0.0	2550	0.817658349328215
loan_status_Binary	0.0	4279	0.17869481765834933

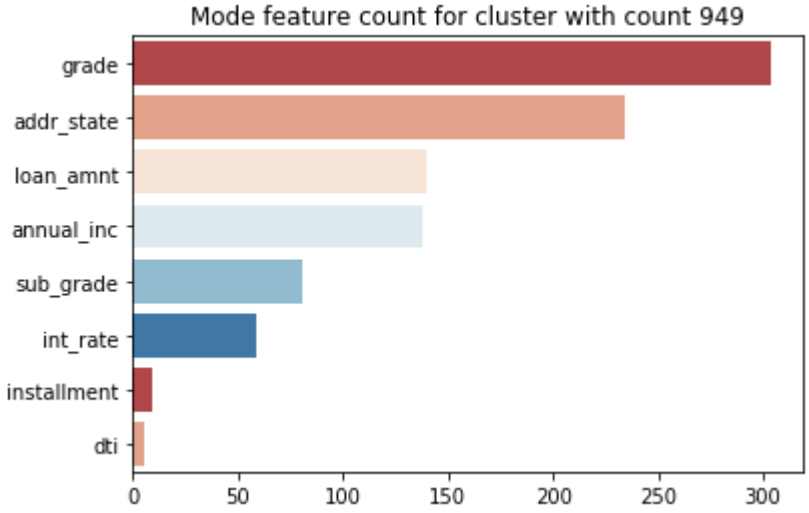


Column	Mode	Mode Count	Mean
loan_amnt	12000.0	310	15348.297021511307
term	0.0	2154	0.4059569773855488
int_rate	11.71	212	12.73715940430188
installment	307.04	22	426.41574738003175
grade	1.0	1090	1.6249310535024821
sub_grade	7.0	288	10.065912851627138
emp_length	1.0	1141	3.636238279095422
home_ownership	0.0	2035	0.8243243243243243
annual_inc	65000.0	251	80659.7797931605
verification_status	2.0	1690	1.1971869829012687
purpose	2.0	1958	3.203530060672918
addr_state	4.0	674	19.052399338113624
dti	10.45	7	13.74099282956427
delinq_2yrs	0.0	3257	0.13623827909542197

inq_last_6mths	0.0	1757	0.8736900165471594
loan_status_Binary	0.0	3114	0.14120242691671264



Column	Mode	Mode Count	Mean
loan_amnt	35000.0	140	19115.251423149904
term	0.0	631	0.40132827324478176
int_rate	7.9	59	13.043510436432598
installment	1111.37	9	537.4373529411761
grade	1.0	304	1.7552182163187855
sub_grade	3.0	81	10.734345351043643
emp_length	1.0	347	3.6394686907020875
home_ownership	0.0	740	0.5559772296015181
annual_inc	120000.0	138	144498.7320398482
verification_status	2.0	592	1.4478178368121442
purpose	2.0	503	3.462998102466793
addr_state	4.0	234	18.61764705882353
dti	9.94	5	11.40123339658444
delinq_2yrs	0.0	925	0.150853889943074
inq_last_6mths	0.0	511	0.9060721062618596
loan_status_Binary	0.0	949	0.09962049335863378



Preparing the dataset

Normalize the data set for ease of calculations so that all features have values between 0 and 1.

In [21]:
```
df=(df-df.min())/(df.max()-df.min())
```

Randomize the dataset so that any ordered patterns dont influence the prediction. (We have already skipped date as an influencing factor)

In [22]:
```
df = df.iloc[np.random.permutation(len(df))]
```

The data is split into training and testing data. x represents the input features whereas y represents the output i.e. the interest rate.As a rule of thumb, we split the data into 80% training data and 20% testing or validation data.

In [23]:
```
y = df.iloc[:,df.columns.isin(["int_rate"])]
x = df.loc[:, ~df.columns.isin(["int_rate"])]

total_samples=len(df)
split = 0.8

x_train = x[0:int(total_samples*split)]
x_test = x[int(total_samples*split):total_samples]
y_train = y[0:int(total_samples*split)]
y_test = y[int(total_samples*split):total_samples]
```

In [24]:
```
def mean_absolute_percentage_error(y_true, y_pred):
    '''
    Calculates mean absolute error of the true and predicted values.
    '''
    y_true, y_pred = np.array(y_true), np.array(y_pred)
    count = 0
    sum = 0
    for a, p in zip(y_true, y_pred):
        if(a!=0):
            sum+=(abs(a-p)/a)
            count+=1
    return (sum/count) * 100
```

In [25]:
```
def view_metrics(y_test, predictions, algorithm, samples, total_samples):
    '''
    Plots the true and predicted values and prints RMS, MAE and MAPE metrics.
    '''
    fig = plt.figure(figsize=(18,5))
    plt.scatter(x=[i for i in range(samples)], y=[x for x in predictions[0:samples
    plt.scatter(x=[i for i in range(samples)], y=[x[0] for x in y_test.values[0:sa
    plt.title('True and Predicted values for test dataset - %s' % algorithm)
    plt.legend()
    plt.show()

    fig = plt.figure(figsize=(18,5))
    plt.scatter(x=[i for i in range(total_samples)], y=[x for x in predictions], l
    plt.scatter(x=[i for i in range(total_samples)], y=[x[0] for x in y_test.value
    plt.title('True and Predicted values for test dataset - %s' % algorithm)
    plt.legend()
    plt.show()

    RMS =  np.sqrt(mean_squared_error(y_test, predictions, multioutput='raw_values
    MAE = mean_absolute_error(y_test, predictions, multioutput='raw_values')
    MAPE = mean_absolute_percentage_error(y_test, predictions)
    print("Root Mean Squared Error:", RMS)
    print("Mean Absolute Error", MAE)
    print("Mean Absolute Percentage Error", MAPE)
    return RMS, MAE, MAPE
```

Metrics for regression models

Root Mean Squared Error

It represents the sample standard deviation of the differences between predicted values and observed values.

$$\mathrm{RMSE} = \sqrt{\frac{1}{n}\sum_{j=1}^{n}(y_j - \hat{y}_j)^2}$$

Mean Absolute Error

MAE is the average of the absolute difference between the predicted values and observed value. The MAE is a linear score which means that all the individual differences are weighted equally in the average.

$$\mathrm{MAE} = \frac{1}{n}\sum_{j=1}^{n} |y_j - \hat{y}_j|$$

Mean Absolute Percent Error

MAPE measures the size of the error in percentage terms. It is calculated as the average of the unsigned percentage error.

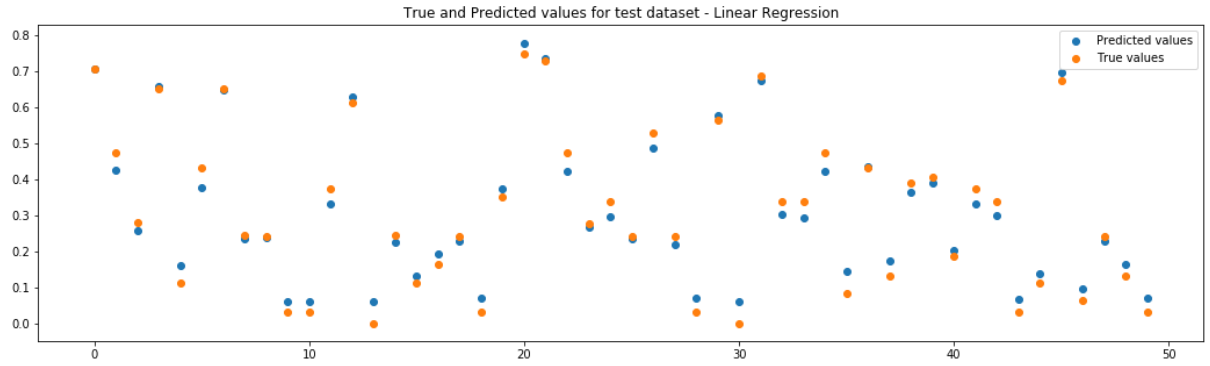
$$\mathrm{MAPE} = \frac{1}{n}\sum_{i=1}^{n} \frac{|Y_i - \widehat{Y}_i|}{Y_i}$$

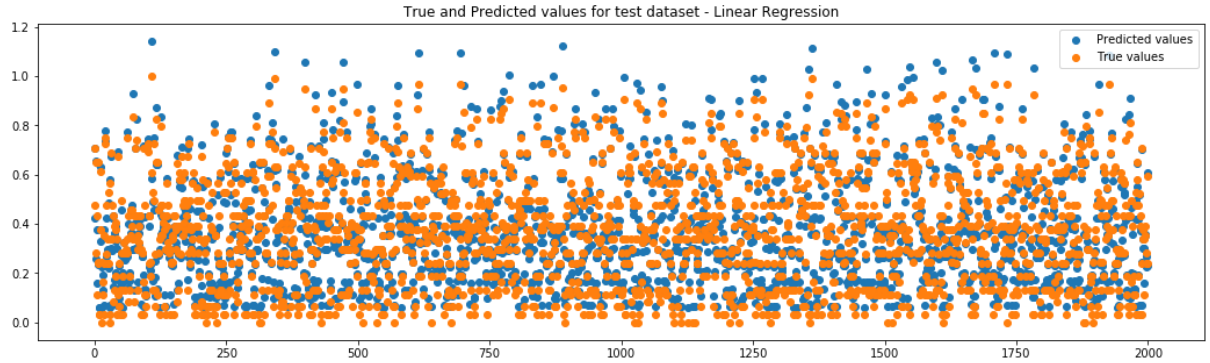
Linear Regression Model

In [26]:
```
lin_reg_model = LinearRegression() # build model
lin_reg_model= lin_reg_model.fit(x_train, y_train) # train model
R2 = lin_reg_model.score(x_train, y_train) # coefficient of determination
```

In [27]:
```
lin_reg_model_predictions = lin_reg_model.predict(x_test) # make predictions
```

In [28]:
```
lin_reg_model_metrics = view_metrics(y_test, lin_reg_model_predictions,'Linear Reg
## If predicted value is same as true value, the points will be overlapping. Close
```



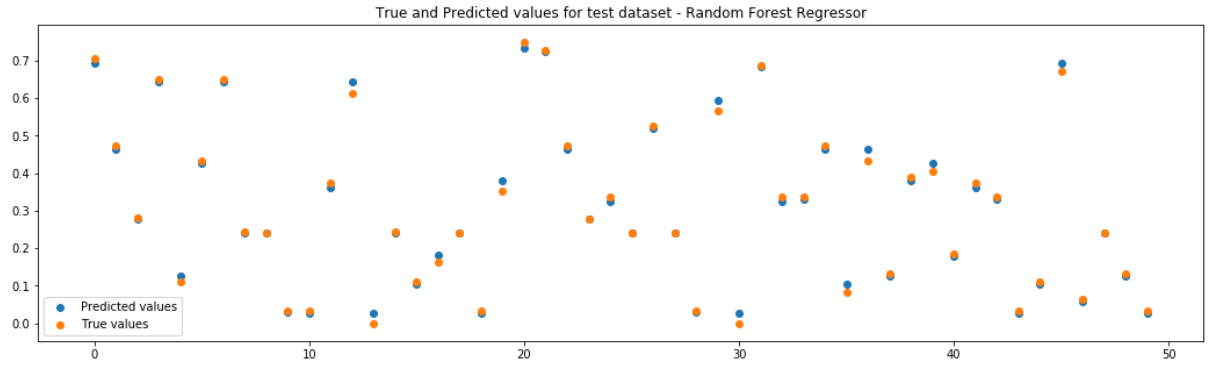


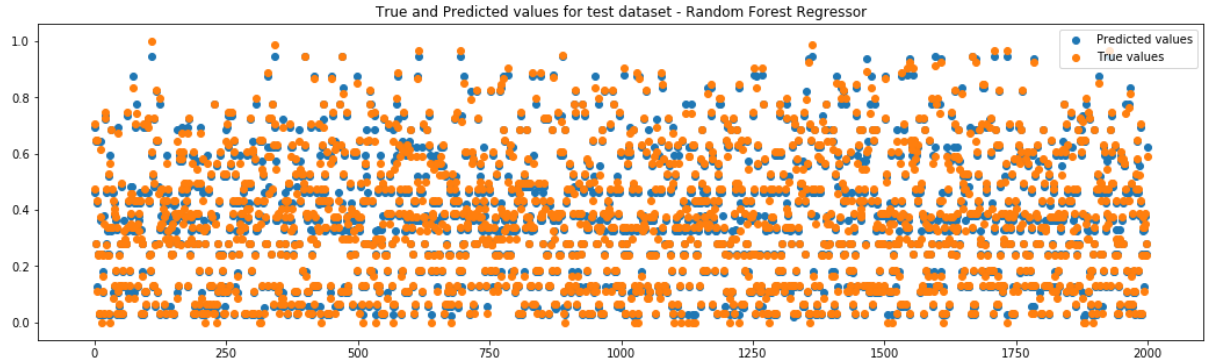

```
Root Mean Squared Error: [0.03795809]
Mean Absolute Error [0.03115924]
Mean Absolute Percentage Error [19.33082824]
```

Random Forest Regressor Model

In [29]:
```
rand_forest_model = RandomForestRegressor(max_depth=5, random_state=0) # build mod
rand_forest_model = rand_forest_model.fit(x_train, y_train.values.ravel()) # train
RandomForestRegressor(bootstrap=True, criterion='mse', max_depth=5,
           max_features='auto', max_leaf_nodes=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=1,
           oob_score=False, random_state=0, verbose=0, warm_start=False)
feature_importance = rand_forest_model.feature_importances_
R2 = rand_forest_model.score(x_train, y_train) # coefficient of determination
rand_forest_model_predictions = rand_forest_model.predict(x_test) # make predictio
```

In [30]:
```
rand_forest_model_metrics = view_metrics(y_test, rand_forest_model_predictions,'Ra
```






```
Root Mean Squared Error: [0.01694133]
Mean Absolute Error [0.01180371]
Mean Absolute Percentage Error [6.07508803]
```

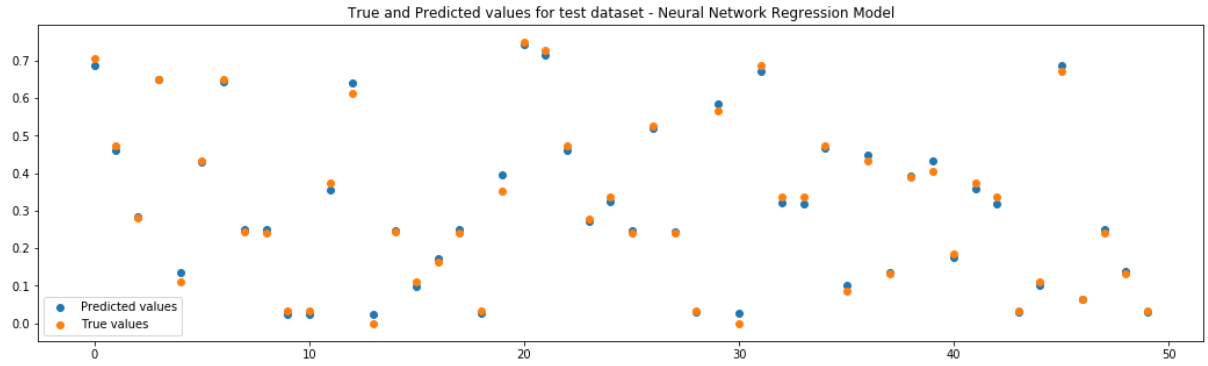
Neural Network Regression Model

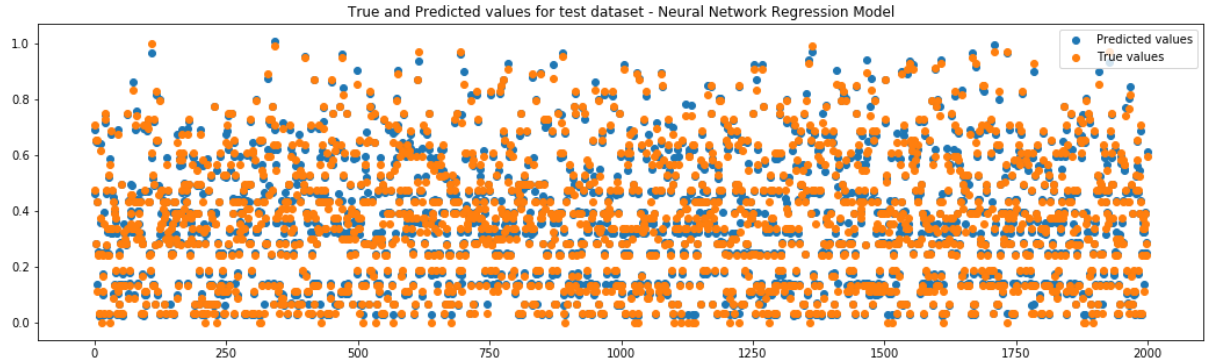
In [31]:
```
nn_model = MLPRegressor(hidden_layer_sizes=(10,4),
                                    activation='relu', # activation function in th
                                    solver='adam', # optimizer algorithm
                                    learning_rate='constant',
                                    learning_rate_init=0.001, # initial learning r
                                    max_iter=300, # max iterations to train for
                                    tol = -1, # tolerance for when to stop trainin
                                    shuffle=True,
                                    verbose=True) # show details at each iteration
nn_model = nn_model.fit(x_train, y_train.values.ravel())
```

```
Iteration 1, loss = 0.13710534
Iteration 2, loss = 0.04697399
Iteration 3, loss = 0.02773502
Iteration 4, loss = 0.01892204
Iteration 5, loss = 0.01342491
Iteration 6, loss = 0.00908341
Iteration 7, loss = 0.00565302
Iteration 8, loss = 0.00327734
Iteration 9, loss = 0.00194878
Iteration 10, loss = 0.00143035
Iteration 11, loss = 0.00120003
Iteration 12, loss = 0.00105150
Iteration 13, loss = 0.00094479
Iteration 14, loss = 0.00085955
Iteration 15, loss = 0.00078672
Iteration 16, loss = 0.00072359
Iteration 17, loss = 0.00066763
Iteration 18, loss = 0.00061663
Iteration 19, loss = 0.00057085
```

In [32]:
```
nn_model_predictions = nn_model.predict(x_test)
```

In [33]:
```
nn_model_metrics = view_metrics(y_test, nn_model_predictions,'Neural Network Regre
```






```
Root Mean Squared Error: [0.01827546]
Mean Absolute Error [0.01309697]
Mean Absolute Percentage Error [6.56480156]
```

Comparing model performances

In [34]:
```
print("%10s | %7s | %7s | %7s" % ('MODEL', 'RMSE', 'MAE', 'MAPE'))
print('_____________________________________________')
for name,metrics in zip(['LIN_REG','RAND_FRST','NN'],[lin_reg_model_metrics, rand_
    print ("%10s | %.5f | %.5f | %.5f %%" % (name, metrics[0][0], metrics[1][0], m
print()
print('Note: Lower values are better')
```

```
     MODEL |    RMSE |     MAE |    MAPE
_____________________________________________
   LIN_REG | 0.03796 | 0.03116 | 19.33083 %
 RAND_FRST | 0.01694 | 0.01180 | 6.07509 %
        NN | 0.01828 | 0.01310 | 6.56480 %

Note: Lower values are better
```

Predicting interest rates

In [35]:
```
def get_interest_rate(model, features):
    return (model.predict(features))*(max_rate-min_rate) + min_rate
```

In [36]:
```
sample = x_test[2:3] # substitute with the input you want to predict the rate for
interest_rate = get_interest_rate(rand_forest_model, sample)
print('Predicted interest rate is:', interest_rate)
print('for the following user profile:')
sample
```

```
Predicted interest rate is: [10.63925742]
for the following user profile:
```

Out[36]:

	loan_amnt	term	installment	grade	sub_grade	emp_length	home_ownership	annual_inc
5126	0.470588	1.0	0.272092	0.166667	0.176471	0.909091	0.0	0.043289

Saving the models

In [37]:
```
# this cell may take a few seconds to execute depending on model size

# for saving models
import pickle
# import _pickle as cPickle # try this if previous import fails

model_name = 'best_model.model'
pickle.dump(rand_forest_model, open(model_name, 'wb'))
```