FML Assignment Report

Predicting the price of a football

A Course Work Report Submitted

In Partial Fulfillment of the Requirements

For the Degree of

B.Tech

In

CSC Department

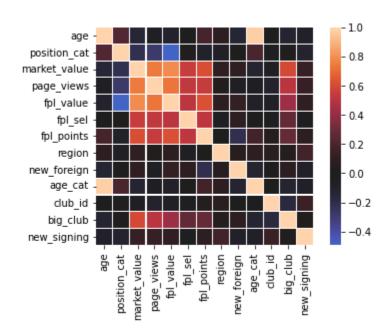
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School of Engineering and Technology BML Munjal University Gurgaon December, 2021

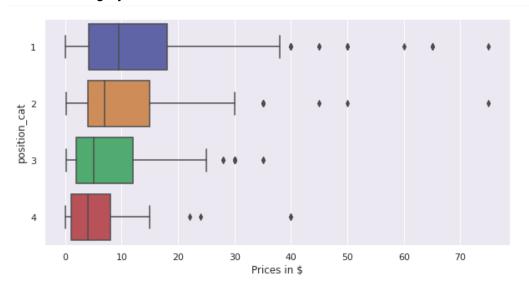
Part- 1
Heat Map for correlation of different features:



In the above heatmap, the lighter the color, the more the correlation between the features. Notice that for higher market value, page_views, fpl_value and fpl_ points matters the most because they have very bright colors.

Box Plots:

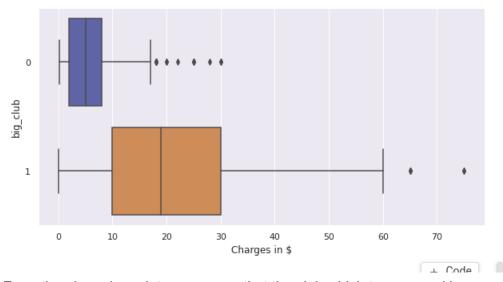
Position Category vs Prices



From the above box plot we can see that the players with higher salary are less in numbers and

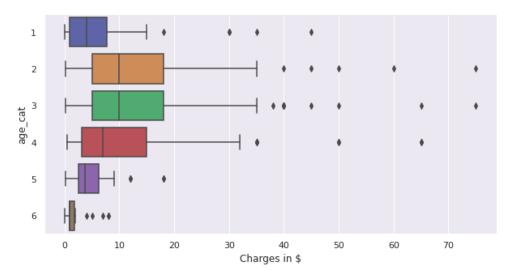
are considered as outliers. And they should be exempted while doing the predictions. If we will including these values our prediction will go wrong drastically. We can also observe that the attackers have the most number of higher charges.

2. Big club vs charges



From the above box plot we can see that the club which tops on ranking earns the most, i.e they have the highest amount of charges.

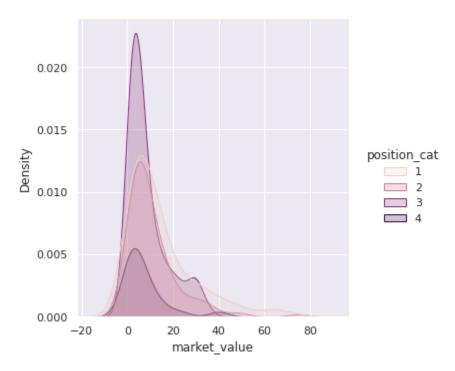
3.age_Cat vs charges



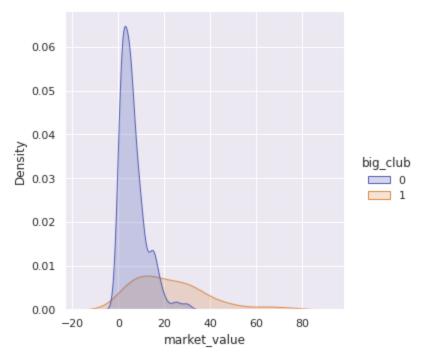
From the above box plot we can see that the charges for most of the players lies from 5-20 for players whose age lies between 22 to 30. The higher the age, the less the charges for that player.

Player who's age is between 22 to 28 has the most higher charges i.e more no. of outliers lie in this age group.

Various other plots for visualization

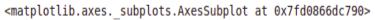


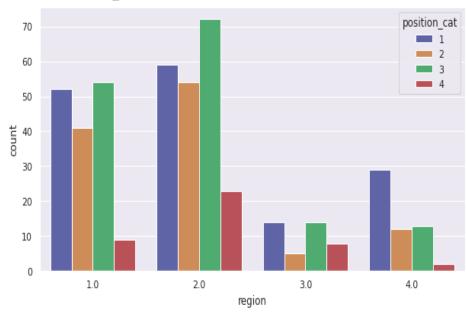
From the above displot we can see that the highest number of position_cats market value lies in 0 to 20 and secondly the defenders have the highest den



From the above displot we can see that the clubs which are not in top 6 rank have lower market_value than the clubs which are in top 6 and are concentrated in the market_value range of 0 to 20.

Some more plots for better visualization of data





[Text(0, 0.5, 'Market Val'), Text(0.5, 0, 'Age')]

70

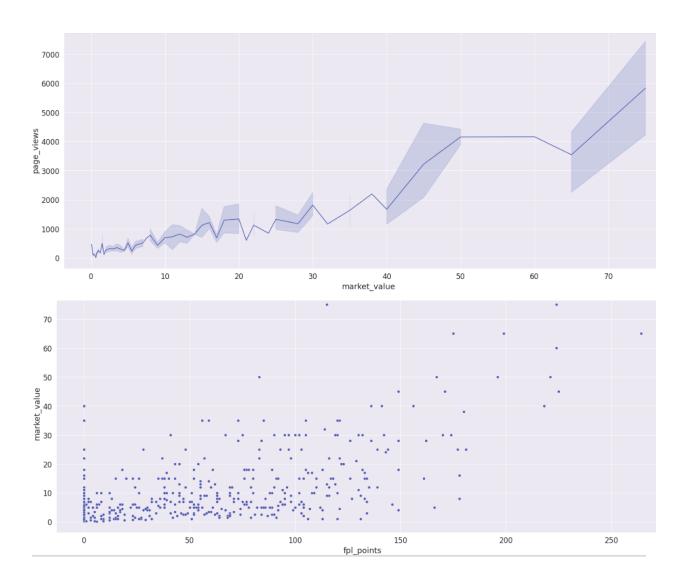
60

30

20

17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38

Age



Models mentioned in the questions are built using sklearn. Their execution and results are as follows:

Part- 2&3

```
Linear Regression
[62] 1 linear_reg = LinearRegression()
       2 run_CrossValidation(linear_reg,X,Y)
      Mean: 0.6753747991296591, Std: 0.155843202298518, Min: 0.37360151208566117, Max: 0.8148228077247442
Lasso Regressor
Lasso Regressor
[63] 1 lasso_params = {'alpha':[0.02, 0.03, 0.01, 0.1, 0.05, 0.5, 0.2, 0.3, 0.25], 'max_iter': [100,1000, 500, 5000, 200]}
      2 lasso reg = Lasso()
      3 lasso_reg = hyperParameter(lasso_reg, lasso_params, X, Y)
    Best Score: 0.6812413321438472
    Best Params: {'alpha': 0.2, 'max iter': 100}
    Cross validation on model with best params
    Mean: 0.6812413321438472, Std: 0.13200194572154217, Min: 0.4340098482152186, Max: 0.8171582084239042
Ridge Regressor
[63] 1 ridge_params = {'alpha':[0.01, 0.1, 0.5, 1, 5, 10, 20, 25, 30, 100]}
       2 ridge_reg = Ridge()
       3 ridge_reg = hyperParameter(ridge_reg, ridge_params, X, Y)
 Best Score: 0.6827599266185473
     Best Params: {'alpha': 20}
     Cross validation on model with best params
     Mean: 0.6827599266185473, Std: 0.12985710734018865, Min: 0.437735853307734, Max: 0.8137127804933832
KNeighborsRegressor
🔝 l n_params = {'n_neighbors': [1,2,3,4,5,6,7,8,9,10], 'weights': ['uniform', 'distance'], 'algorithm': ['auto', 'ball_tree', 'kd_tree', 'brute'], 'n_jobs': [-1]}
     2 neigh = KNeighborsRegressor()
     3 neigh = hyperParameter(neigh, n params, X, Y)
 Best Score: 0.47067905679853184
    Best Params: {'algorithm': 'auto', 'n_jobs': -1, 'n_neighbors': 8, 'weights': 'uniform'}
    Cross validation on model with best params
    Mean: 0.47067905679853184, Std: 0.19743170854894004, Min: 0.08856843158218541, Max: 0.6584860384646545
Support Vector Regressor
[66] 1 param = {'kernel' : ('linear', 'poly', 'rbf', 'sigmoid'),'C' : [1,5,10],'degree' : [3,8],'coef0' : [0.01,10,0.5],'gamma' : ('auto','scale'), 'max iter': [100, 100
     2 \text{ syr} = \text{SVR}()
     3 svr = hyperParameter(svr, param, X_mms, Y.values.ravel())
```

Best Score: 0.7192476506560381

Best Params: {'C': 5, 'coef0': 10, 'degree': 3, 'gamma': 'auto', 'kernel': 'poly', 'max_iter': 2000}

Cross validation on model with best params

Mean: 0.7192476506560381, Std: 0.11864754406551849, Min: 0.4956130483257061, Max: 0.822573717695521

Random Forest Regressor

```
[68] 1 param = {
    2 'max_depth': [10, 50, 90, 100],
    3 'max_features': ['auto', 'sqrt'],
    4 'n_estimators': [100,1000,2000]}
    5 rfr = RandomForestRegressor()
    6 rfr = hyperParameter(rfr, param, X_ss, Y.values.ravel())
```

```
Best Score: 0.7393239407974654
Best Params: {'max_depth': 50, 'max_features': 'sqrt', 'n_estimators': 100}
Cross validation on model with best params
Mean: 0.7203383567504688, Std: 0.08593885301881521, Min: 0.578383343330517, Max: 0.8357472041181881
```

Gradient Boosting Regressor

```
[69] 1 param = {
    2 'n_estimators': [500, 900, 1000],
    3 'max_depth': [2,3, 5, 10, 15],
    4 'max_features': ['auto', 'sqrt', 'log2']}
    5 gbr = GradientBoostingRegressor()
    6 gbr = hyperParameter(gbr, param, X_mms, Y.values.ravel())

Best Score: 0.7383142821634368
```

Best Params: {'max_depth': 2, 'max_features': 'log2', 'n_estimators': 500} Cross validation on model with best params Mean: 0.7400364925053476, Std: 0.03989609746657331, Min: 0.6846820427087643, Max: 0.7796071177751461

Part - 4

Our best model after hyper parameter tuning is Random Forest Regressor with a score of 0.7393

```
Best Paramteres : {'max_depth': 50, 'max_features': 'sqrt',
'n_estimators': 100}
```

Part 5 :

Implement a Genetic Algorithm for learning attribute weights for the Nearest Neighbour

Algorithm. Implement at least one mechanism for maintaining Diversity within the

```
Population
Code :
import csv
import random as rand
import math
import operator
def manhattan(a, b,length):
   return sum(abs(val1-val2) for val1, val2 in zip(a,b))
def getNeighbors(trainingSet, testInstance, k):
   distances = []
   length = len(testInstance) - 1
   for x in range(len(trainingSet)):
       dist = manhattan(testInstance, trainingSet[x], length)
       distances.append((trainingSet[x], dist))
   distances.sort(key=operator.itemgetter(1))
   neighbors = []
   for x in range(min(k, len(distances))):
       neighbors.append(distances[x][0])
   return neighbors
def getResponse(neighbors):
  classVotes = {}
   for x in range(len(neighbors)):
       response = neighbors[x][-1]
       if response in classVotes:
           classVotes[response] += 1
       else:
           classVotes[response] = 1
   sortedVotes = sorted(classVotes.items(), key=operator.itemgetter(1),
reverse=True)
   return sortedVotes[0][0]
def getAccuracy(testSet, predictions):
```

```
correct = 0
   for x in range(len(testSet)):
       if testSet[x][-1] == predictions[x]:
           correct = correct+1
   return (correct / float(len(testSet))) * 100.0
def generateChromosome(chromosome):
   return [rand.randint(1, 100) for x in range(chromosome)]
def desimal(biner):
  return int (biner, 2)
def kNN(k, testSet, trainingSet):
  predictions = []
   for x in range(len(testSet)):
       neighbors = getNeighbors(trainingSet, testSet[x], k)
       result = getResponse(neighbors)
       predictions.append(result)
   accuracy = getAccuracy(testSet, predictions)
   return accuracy
def crossover(one, two):
  parent = [one, two]
   zero = '0'
  male = "{0:b}".format(parent[0])
   female = "{0:b}".format(parent[1])
  length = max(len(male), len(female))
  if length % 2 == 1:
       length = length + 1
   while len(male) < length:</pre>
       male = zero + male
   while len(female) < length:</pre>
       female = zero + female
```

```
child = []
   half = int(length / 2)
   male1 = male[:half]
  male2 = male[half:]
   female1 = female[:half]
   female2 = female[half:]
   child.append(desimal(male1 + female2))
   child.append(desimal(female1 + male2))
   return child
# prepare data
trainingSet = x train
testSet = x test
split = 0.50
print('Train set: ' + repr(len(trainingSet)))
print('Test set: ' + repr(len(testSet)))
accResult = [[]]
chromosome = 10
population = generateChromosome(chromosome)
for x in range(len(population)):
accResult.append([population[x], kNN(population[x], testSet,
trainingSet)])
del accResult[0]
for x in range (200):
       status one = True
       status zero = True
       accResult = sorted(accResult, key=lambda 1: 1[1], reverse=True)
       newChromosome = crossover(accResult[0][0], accResult[1][0])
       for i in accResult:
           if newChromosome[0] == i[0]:
               status_zero = False;
```

```
if newChromosome[1] == i[0]:
               status one = False
       if status zero:
           accResult.append([newChromosome[0], kNN(newChromosome[0],
testSet, trainingSet)])
       if status one:
           accResult.append([newChromosome[1], kNN(newChromosome[1],
testSet, trainingSet)])
accResult = sorted(accResult, key=lambda 1: 1[1],reverse=True)
print("accuracy of Genetic Algorithm:")
print(accResult[0][1])
Result of Genetic Algorithm:
Train set: 322
Test set: 139
accuracy of Genetic Algorithm:
99.28057553956835
```

Part 6: Deploy your model as a RESTful Web Service

The best model that we found was RandomForestRegressor with the following parameters and R2 score.

```
Best Score: 0.7393239407974654
Best Params: {'max_depth': 50, 'max_features': 'sqrt', 'n_estimators': 100}
Cross validation on model with best params
Mean: 0.7203383567504688, Std: 0.08593885301881521, Min: 0.578383343330517, Max: 0.8357472041181881
```

