Data Glacier

Your Deep Learning Partner

Healthcare – Drug Persistency

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Exploratory Data Analysis

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Introduction

Machine learning methods would be the best approach to analyze the efficiency of drugs due to the high number of factors and their complex relationship that affect on the results of drug therapy.

Machine learning methods have higher accuracy in the prediction of drug administration results such as the drug persistency of patients that is the aim of this research.

Before starting to use methods, we will have a look at the data we are going to use in this model and the problem we want to solve.

Data understanding

There are 3424 rows (patients) and 69 columns (features). The target variable is the Persistency_Flag variable that includes 1289 drug persistent patients and 2135 non persistent patients.

In previous research, I have discussed three ways to handle missing values. So, in this research we focus on development the predicting model, testing and evaluating its accuracy.

Problem Statement

After reading the data, the data set is separated into a y vector that is the Persistency_Flag variable and an X matrix of explanatory variables including other variables. The problem is predicting y given a set of variables of the X matrix.

In this research different predicting models have been developed to see which one has higher accuracy.

Random Forests

The first method we used is random forest. Random forest is a Supervised Machine Learning Algorithm that is used widely in Classification and Regression problems. It builds decision trees on different samples and takes their majority vote for classification and average in case of regression.

```
1  import sklearn as sk
2  from sklearn.ensemble import RandomForestClassifier
3
4  y = data_without_null_1.iloc[:,1]
5  X = data_without_null_1.iloc[:,1:]
6
7  RF = RandomForestClassifier(n_estimators=100, max_depth=2, random_state=0)
8
```

Random Forests

We can again fit them using sklearn, and use them to predict outcomes, as well as get mean prediction accuracy. The accuracy of this method on our data is 0.89.

```
RF.fit(X, y)

# define the model evaluation procedure
cv = KFold(n_splits=3, shuffle=True, random_state=1)
# evaluate the model
result = cross_val_score(RF, X, y, cv=cv, scoring='accuracy')
# report the mean performance
print('Accuracy of the model is: %.3f' % result.mean())
```

```
Accuracy of the model is: 0.897
```

k-Fold Cross-Validation

In the above code k-Fold Cross-Validation is used to determine the accuracy of the model (0.89). It is common to evaluate machine learning models on a dataset using k-fold cross-validation.

The k-fold cross-validation procedure divides a limited dataset into k non-overlapping folds. Each of the k folds is given an opportunity to be used as a held-back test set, whilst all other folds collectively are used as a training dataset. A total of k models are fit and evaluated on the k hold-out test sets and the mean performance is reported.

Prediction

Now, we can use the developed model to predict the drug persistency of a patient. For example, assume we want to use it for a patient with information mentioned in the row 3000:

```
yhat = RF.predict([list(data_without_null_1.iloc[3000,1:])])
if yhat == 1:
    print('The patient is predicted to be persistent' )
else:
    print('The patient is predicted to be non-persistent')
```

```
The patient is predicted to be persistent
```

ROC Curves

In this part, we discover Receiver Operating Characteristic curve, or ROC Curves that is used to interpret the prediction of probabilities for binary classification problems.

When making a prediction for a binary or two-class classification problem, there are two types of errors that we could make.

False Positive. Predict an event when there was no event.

False Negative. Predict no event when in fact there was an event.

ROC Curves

ROC is a plot of the false positive rate (x-axis) versus the true positive rate (y-axis) for a number of different candidate threshold values between 0.0 and 1.0. Put another way, it plots the false alarm rate versus the hit rate.

The true positive rate is calculated as the number of true positives divided by the sum of the number of true positives and the number of false negatives. It describes how good the model is at predicting the positive class when the actual outcome is positive.

ROC Curves summarize the trade-off between the true positive rate and false positive rate for a predictive model using different probability thresholds.

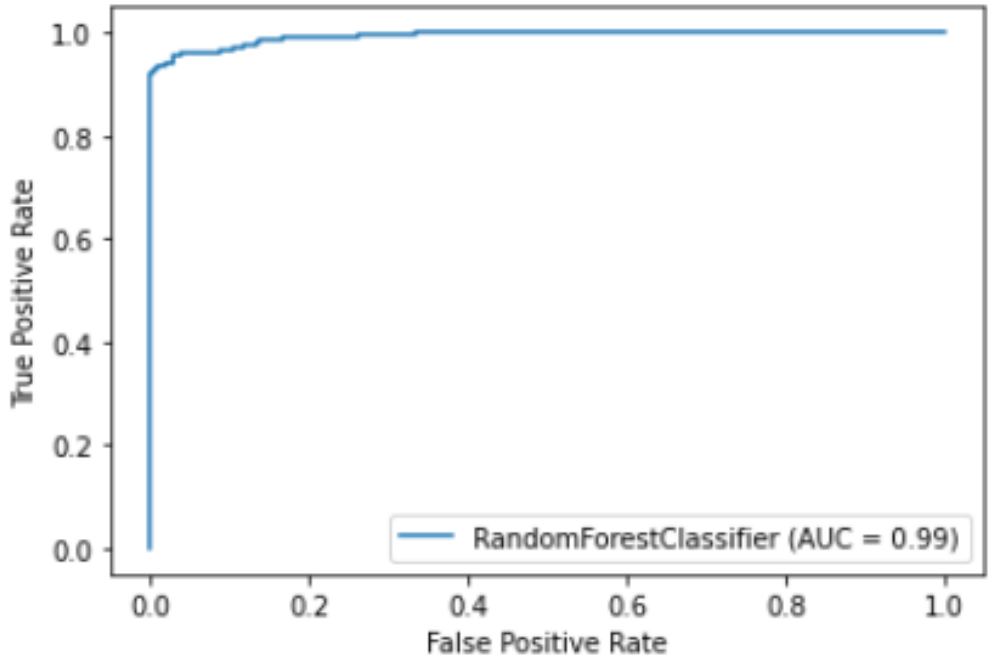
ROC Curves

The area under the curve (AUC) can be used as a summary of the model skill. A skilful model will assign a higher probability to a randomly chosen real positive occurrence than a negative occurrence on average. This is what we mean when we say that the model has skill. Generally, skilful models are represented by curves that bow up to the top left of the plot.

A no-skill classifier is one that cannot discriminate between the classes and would predict a random class or a constant class in all cases.

ROC Curves

As it is shown the are under curve for the random forest we developed is big enough to trust to the predictions of the model.



Effect of gender

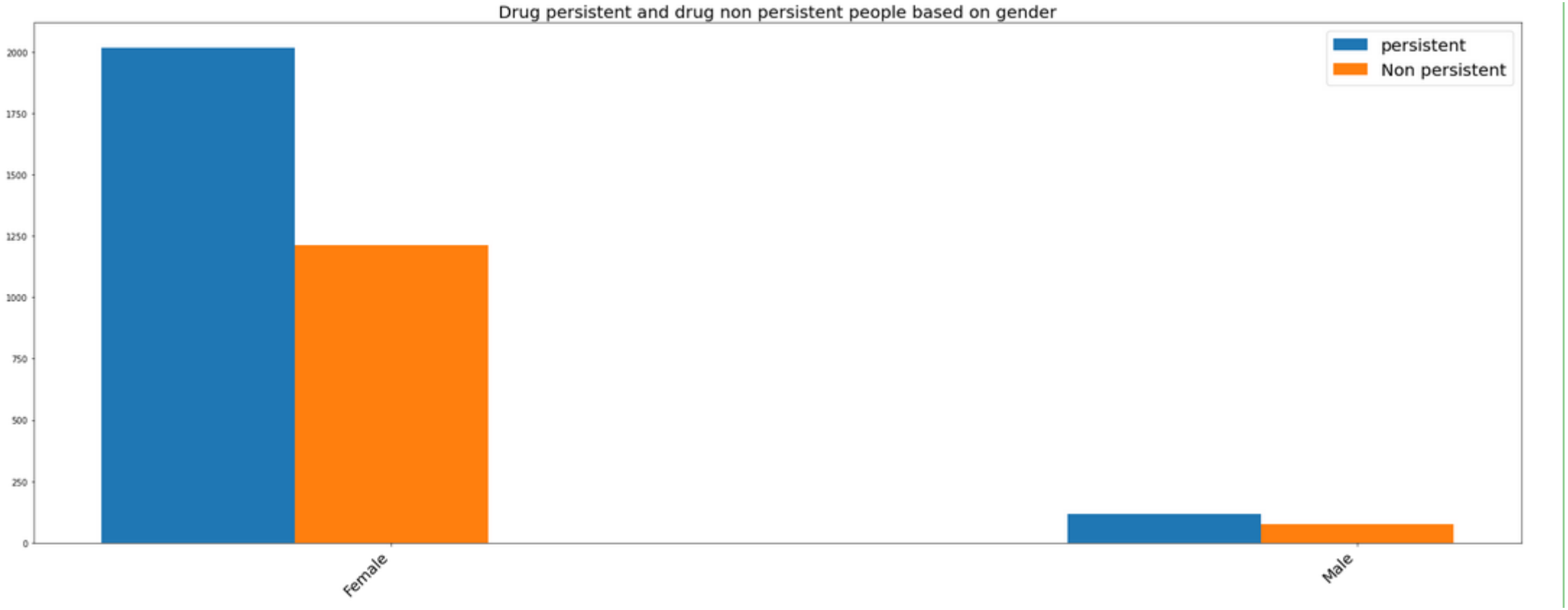
Drug persistent and drug non persistent people based on gender

```
1
2 target['persistent'] = target1['Persistency_Flag']
3 target['Non persistent'] = target['Persistency_Flag']
4 target.drop('Persistency_Flag', axis=1, inplace=True)
5 target
6
```

	Gender	persistent	Non persistent
0	Female	2018	1212
1	Male	117	77

Effect of gender

Most of the data is related to female and in both genders most of people das drug persistence behavior.



Effect of gender

Since most of the data are females and there is big difference between persitence and non persistence people, one may want to create the prediction model just using female data set.

Therfore, we droped all rows having gender of male and applied the remain data to build the random forest prediction model to predict drug persistency of females. Similarly, the model can be created using just data of male to predict drug persistency of males.

Effect of gender

Making prediction model based on just data of female has not significant increase in accuracy.

Making prediction model based on just data of female has not significant increase in accuracy

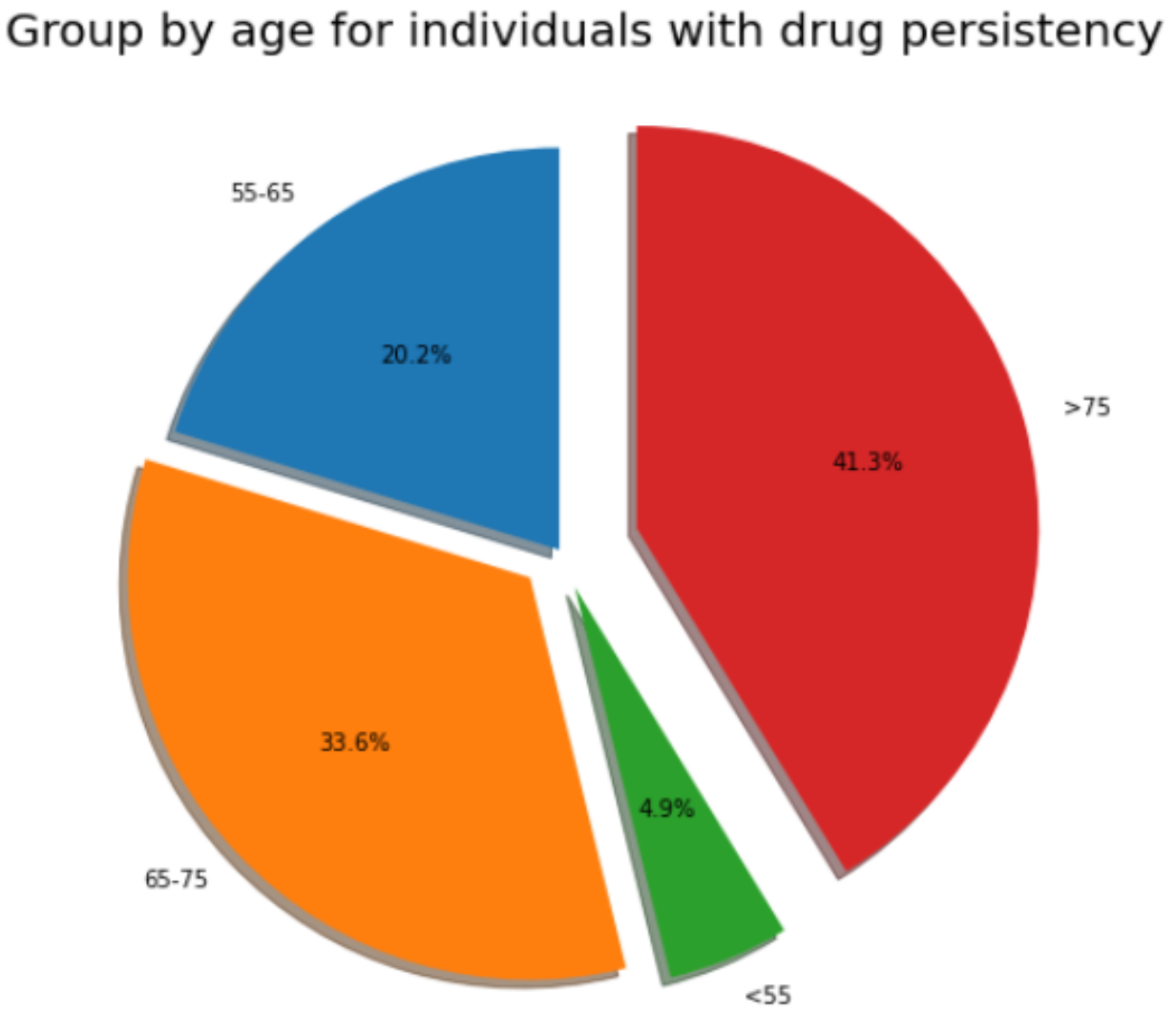
```
df_male = data_without_null_1[data_without_null_1['Gender']== 1]
df_Female = data_without_null_1[data_without_null_1['Gender']== 2]
```

```
import sklearn as sk
from sklearn.ensemble import RandomForestClassifier

y = df_Female.iloc[:,1]
X = df_Female.iloc[:,1:]

RF = RandomForestClassifier(n_estimators=100, max_depth=2, random_state=0)

RF.fit(X, y)

# define the model evaluation procedure
cv = KFold(n_splits=3, shuffle=True, random_state=1)
# evaluate the model
result = cross_val_score(RF, X, y, cv=cv, scoring='accuracy')
# report the mean performance
print('Accuracy of the model is: %.3f' % result.mean())
```

```
Accuracy of the model is: 0.902
```

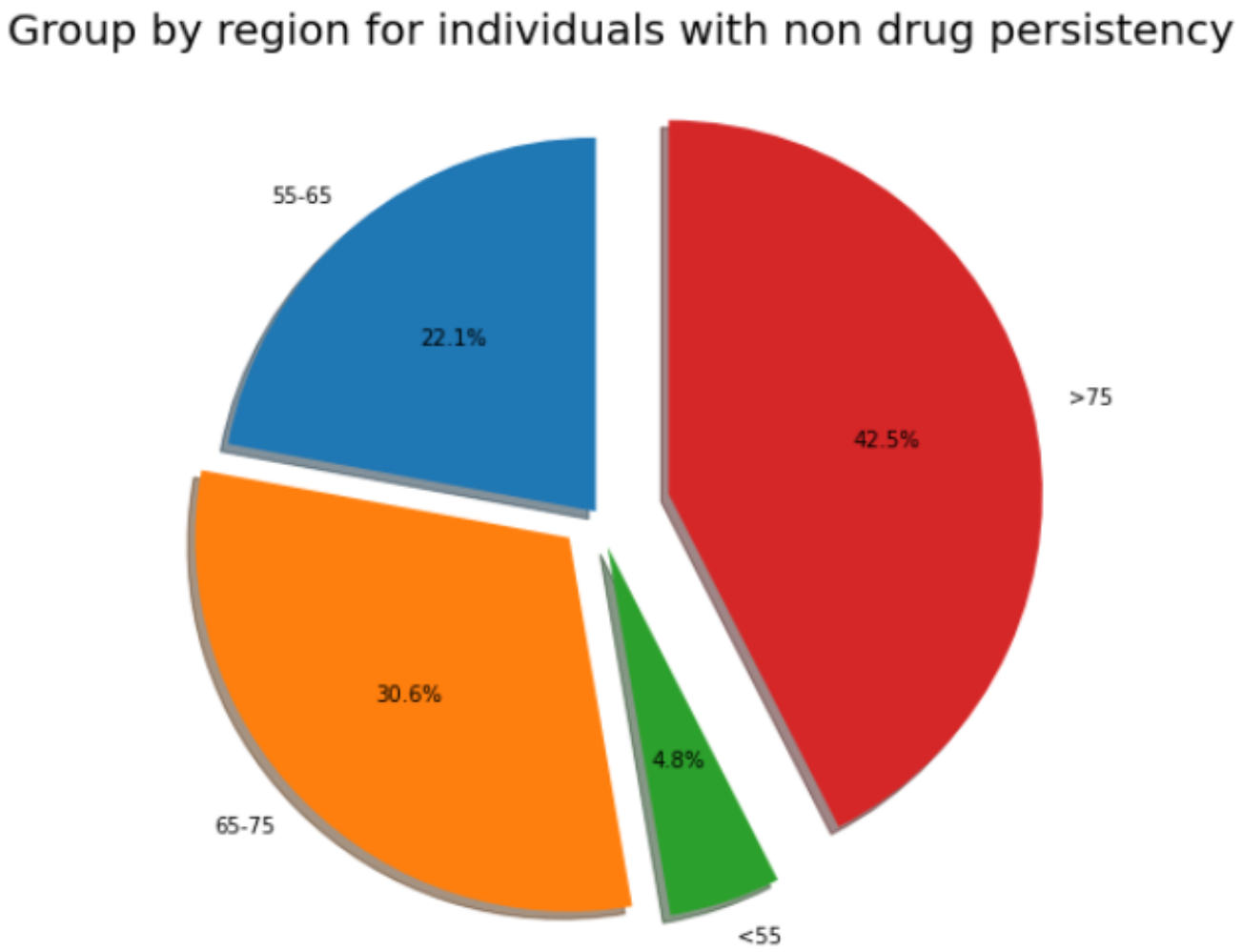
Effect of age

We can separate drug persistent people from non drug persistent and consider the effect of different variables such as age.



Effect of age

Both drug persistent and not persistent have similar percentages of different groupe ages.



Effect of age

Similarly, making prediction model based on just data of people with age more than 75 has not significant increase in accuracy for prediction of drug persistency of individuals in this age range.

```
import sklearn as sk
from sklearn.ensemble import RandomForestClassifier

y = df_75.iloc[:,1]
X = df_75.iloc[:,1:]

RF = RandomForestClassifier(n_estimators=100, max_depth=2, random_state=0)

RF.fit(X, y)

# define the model evaluation procedure
cv = KFold(n_splits=3, shuffle=True, random_state=1)
# evaluate the model
result = cross_val_score(RF, X, y, cv=cv, scoring='accuracy')
# report the mean performance
print('Accuracy of the model is: %.3f' % result.mean())
```

```
Accuracy of the model is: 0.901
```

Final Recommendation

All machine learning models are some kind of mathematical model that need numbers to work with. The target variable in this research was a categorical type that is a type of data that is used to group information with similar characteristics, while numerical data is a type of data that expresses information in the form of numbers.

Therefore we encoded the categorical variable into numbers to be able to use in different machine learning methods.

Final Recommendation

If we had just few explanatory variables, we could use frequency tables, pie charts, or bar charts to analyse their relationship on the target variable. But due to the high number of variables we used random forests machine learning methods to predict the drug persistency of patients. It has more than 0.8% accuracy in prediction. In next practices we will work on other methods such as logistic regression in order to compare efficiency of different methods on predicting the drug persistency of patients.

Data and code link

Data and code are uploaded at:

https://github.com/Alireza-Ehiaei/Data_Sciences/tree/main/Drug_Persistency1/EDA

Thank You