K-means Algorithm on Heart Failure Survival from Serum Creatinine and Ejection Fraction Dataset

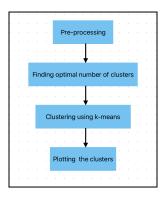
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Background

The original dataset comprises the heart failure records from 299 patients collected in 2015 emphasized by 12 attributes and 1 target column respectively, namely: 'age', 'anaemia', 'creatinine phosphokinase', 'diabetes', 'ejection fraction', 'high blood pressure', 'platelets', 'sex', 'serum creatinine', 'serum sodium', 'smoking', 'time', and (target) 'death_event'. The dataset was collected from UCI Irvine Machine Learning Repository and the data mostly represents a set of multivariate data of either integer or float data type. This rich set of bioinformatics data entails essential and interesting insights about the impact on the survival of heart failure patients from serum creatinine and ejection fraction, as well as crucial information that can be used to rank attributes that impact the survival of heart failure patients.[1][2]

Methods

All the technical analysis and implementation of the algorithm was performed in Python along with its various machine learning modules like sklearn and data processing libraries. Firstly the entire dataset heart failure clinical records dataset.csv file was loaded into a data frame using pandas and preprocessed to replace any missing value with the median value of the respective column. Methods like head() and dtypes were used to get more insight into the dataset's structure to plan the next few steps to construct the algorithm. It was preferred not to replace it with the mean value to avoid relying on the assumption that the data represents a normal distribution. The data frame was then scaled and normalized employing the StandardScaler() and fit transform() methods in the preprocessing library in the sklearn module (a machine learning module in Python). A new data frame was created to extract the serum creatinine and ejection fraction using the values method for the original data frame. Next, the silhouette score method from the metrics library was used to determine the k-value with the given number of clusters to determine the optimal number of clusters. Furthermore, KMeans was used and fit predict was used on the data frame to create k-means clustering as well as cluster centers to create centroids for the clusters. In addition to that, PCA was used to structure the data into two dimensions for ease in visualization purposes followed by fit transform and transform to scale and transform the dataset and centroids respectively. Finally, pyplot was used to plot and visualize the resulting clusters and corresponding centroids as plots (Figure 2). [3][4][5][6]



<u>Figure 1</u>: Simplified structure of the algorithm as a flowchart.

Results

After running the *silhouette_score* method, the corresponding Silhouette scores were noted and k=3 was picked for its highest score.

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k	Silhouette Score
2	0.46090358321807523
3 (Optimal k)	0.5024395254100789
4	0.44656679677254907
5	0.47980073144546537
6	0.45967156981022
7	0.4787069816264261
8	0.47972617342611823
9	0.48012323326380535
10	0.4669169898416124

Table 1: Results of respective k-values and Silhouette Score.

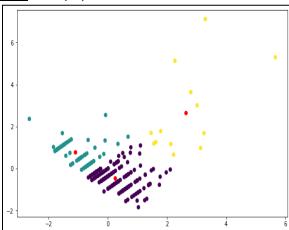


Figure 2: Cluster plotting from the results of the k-means algorithm for optimal k, red points are centroids, and the other colors represent distinguished cluster points.

Conclusions

From Figure 2, it can be observed that data points have been grouped as distinguished cluster points around their respective centroids (red points). Due to the optimal k value being 3, three distinct clusters have been plotted based on attributes 'serum_creatinine' and 'ejection_fraction'. Some outliers can also be observed especially in the case of the yellow cluster points which are further separated from their respective centroid. However, the clusters are fairly well-separated from each other with most of the points strongly near the centroids.

References

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