Engineering and Scientific International Journal (ESIJ)
Volume 10, Issue 2, April – June 2023
ISSN 2394-7187(Online)
ISSN 2394 - 7179 (Print)

Donor-Recipient Matching using Enhanced Maximum Matching Bipartite Graph for Liver Transplantation

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Abstract— A matching of set of pairs or parameters between donor to recipient is considered as important for liver transplantation. By using the maximum and minimum matching able to find out the exact or relevant parameters between the donors to recipient matching. Divide the set of parameters as donor sets and recipient sets using bipartite graph. Donor to Recipient Hopcroft Karp matching used for the final relevant pair of matching between the donors to recipient. Each set of parameters is assign as nodes for the donor to recipient set of pairs. Bipartite graph visualization shows the important donor to recipient matching.

Keywords — *Bipartite Graph; Maximum Cardinality Matching; Maximum and Minimum; Donor-Recipient Matching.*

1. Introduction

A matching gives an assignment of people to tasks and get many tasks done as possible. In a bipartite graph, two sets of vertices U and V recognized as bipartitions and each edge is incident on one vertex in U and one vertex in V. There will not be any edges connecting two vertices in U or two vertices in V. A basic introduction to bipartite graphs and graph matching using the python library network X.

Matching of Bipartite Graphs: An edge set associate graph may be a set of edges while not common vertices. An identical may be a graph wherever every vertex has either zero or one edge incident in the bipartite graph, the matching can contains edges connecting one vertex in U and one vertex in V and every vertex (in U and V) has either zero or one edge incident. A vertex is taken into account as matched if it connects to at least one of the sides within the matching. Otherwise, the vertex is taken into account unmatched. The matching condition can be defined as follows:

> If a bipartite graph G={U, V} has a matching of U, then $|N(S)|\geq|S|$ for all $S\subseteq U$.

Maximum Bipartite Matching: A maximum matching is one bipartite graph and produces a maximum cardinality matching as output. Since a bipartite that contains as many edges as possible. Given a bipartite graph G = (A ∪ B, E), find an S ⊆ A × B that is a matching is as large possible. Given A and B. S is a perfect matching if all vertex is matched. A matching is considered as a maximal matching if no other edges can be added to the matching because every vertex is matched to another vertex. i.e., we cannot add more edges without increase of one of the vertices to two.

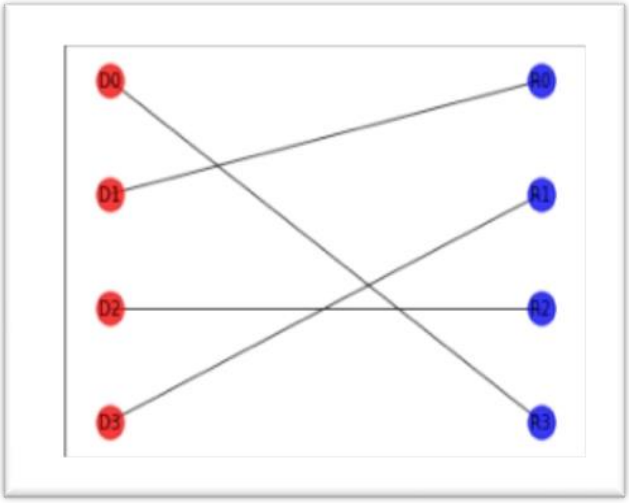

Fig.1: Sample bipartite matching

Maximum Cardinality Matching: In a maximum cardinality matching if it contains the largest possible number of edges and each edge will cover two vertices exactly, it is equivalent to finding a matching that must covers as many vertices as possible and this problem can be used to solve by Hopcroft-Karp algorithm. A matching in a bipartite graph is a set of the edges that chosen in such a way that no two edges share an endpoint. A maximum matching is a matching of maximum size that is maximum number of edges. In a maximum matching, if any edge is added to it and it is cannot be a matching. In this, more than one maximum matching for a given bipartite graph. A library based on Hopcroft Karp's Algorithm and it takes as input a graph might have more than one maximum matching, it is worth noting that the algorithm may output any one of all possible maximum matchings.

DOI: **10.30726/esij/v10.i2.2023.102002**

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Maximum Weight Matching: In a weighted bipartite graph, a matching is considered with maximum weight matching if the sum of weights of the matching is maximised. This can be used Hungarian algorithm to solve this problem. The Hungarian Algorithm which is used to find the minimum cost in assignment problems that involve assigning people to activities. A Python 3 graph implementation of the Hungarian Algorithm (Kuhn-Munkres algorithm), an O(n^3) solution for the assignment problem or maximum / minimum-weighted bipartite matching problem.

Minimum Weight Matching: In minimum weight matching with a weighted bipartite graph, a matching is considered as if the sum of weights of the matching is minimised. The Karp algorithm which can be used to solve this problem. Rabin-Karp algorithm can used for matching patterns in the text using a hash function.

Bipartite graph applications: Bipartite graph matching which can be found in different fields and include data science and computational biology. Many systems which can be modelled as bipartite graphs. A matching can be obtained to identify the most similar pairings and used in scheduling problems when we want to assign jobs to machines within different time slots provided that some constraints (*e.g.*, scheduling advertisements, scheduling trains on tracks, etc.).

2. Related Works

In paper [1], graph theory and basic formula for the bipartite graph which is used to analysis the basic information of the bipartite graph. In paper [2], brief introduction about the bipartite graph and maximum, minimum matching, cardinality matching. In paper [3], given the basic concept of digraph, directed graph (paths and walks), colouring and connectivity. In paper [4], describes about the matching and theorem condition and also mathematical concept for bipartite graph. In paper [5], matching algorithm which is used to solve the graph matching problem in graph theory. In paper [6], NetworkX is to use a node attribute named bipartite with values 0 or 1 to identify the sets and also identify which belongs to each node. In paper [7], Stanford Network Analysis Platform is a general purpose network analysis and graph mining library which is used for data collection. In paper [8], describes about the community detection, path finding, and centrality in graph algorithm.

In paper [9], identify proteins that interact with a known protein by the use of a simple galactose selection. In paper [10], bipartite graphs can solve the challenging of biological problems. In paper [11], gender difference in donor quality is considered as important factor in liver transplantation. In paper [12], identify the most important factors for the survival of liver patient after transplantation. In paper [13], by using the Evolutionary Multi Objective Artificial Neural Networks which predict the survival of the liver patient. In paper [14], artificial Neural Networks which is used to prolong the survival rate of the liver patients. In paper [15], to introduce a high-accuracy model for predicting the best outcome of patients following liver transplantation.

3. Research Methodology

3.1 Data Collection

The UCI dataset has been used which is a Medical, Scientific and Educational Organization. Dataset accessed from UCI ML Repository. The UCI dataset is a multi-organ dataset since 1987 from which extracted the liver patient records. The dataset which consists of male and female liver patient records. Data gathering about patient records, Information about data fields. Statistical information about numerical columns is also available in the dataset.

3.2 Preprocessing Data

Load the Features which is available in the dataset. Read the dataset. Checking Null value or Missing value. Extracting the missing value. Filling the null value with the mean value of that particular feature. Checking whether null value is changed or not.

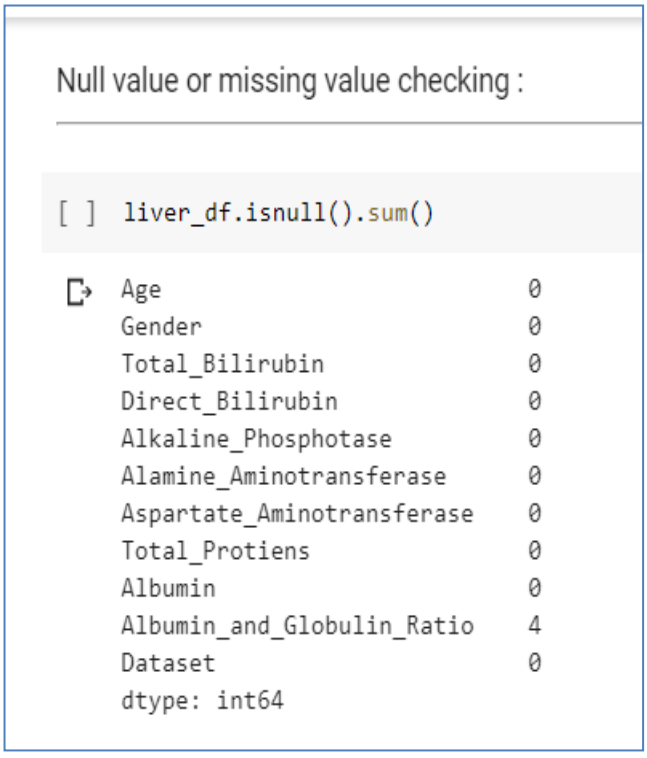

Fig.2: Finding missing value

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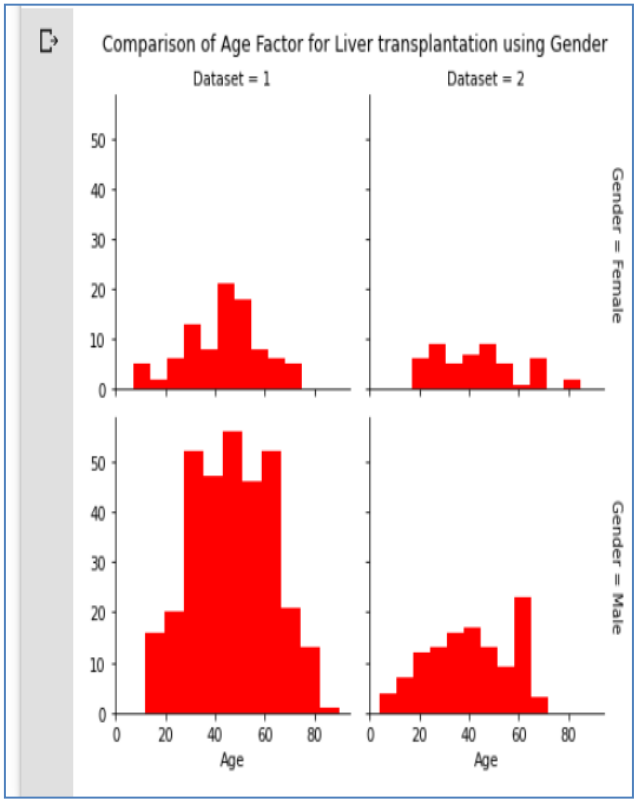

Fig.3: Comparison of Age factor using Gender

4. Dimensionality Reduction Techniques

In this, reduce the random variables and used the Data Extraction and Data Analysis are followed with Correlation method.

4.1 Feature Extraction

Refer to the process of extracting useful information or features or data from existing data. The number of recipient patients with liver disease. The number of donors ready for liver transplantation.

4.2 Feature Analysis

From the above Correlation map, we find that, there is a direct relationship between the following features are Direct_Bilirubin ,Total_Bilirubin,Aspartate_Aminotransferase,Alamine_Aminotransferase,Total_Protiens,Albumin,Albumin and Globulin_Ratio, Albumin. Hence, both the features are similar, it will give similar performance. The following data or features alone for futher matching process using bipartite graph which is used to divide the pair D-R matching. All the donors are connected to the respective recipient by bipartite matching. Further, these are taken for the D-R Hopcroft Karp matching in order to give each pair individual matching.

Fig.4: Analysis of D-R Match with Total bilirubin and Direct bilirubin

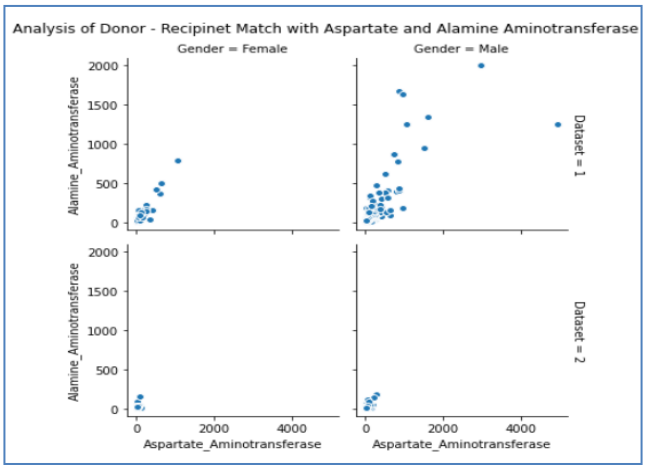

Fig.5: Analysis of D-R Match with Aspartate and Alamine Aminotransferase

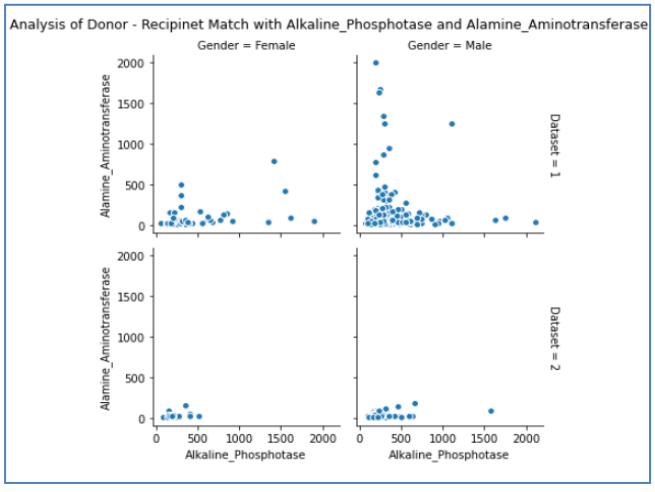

Fig.6: Analysis of D-R Match with Alkaline_Phosphate and Alamine Aminotransferase

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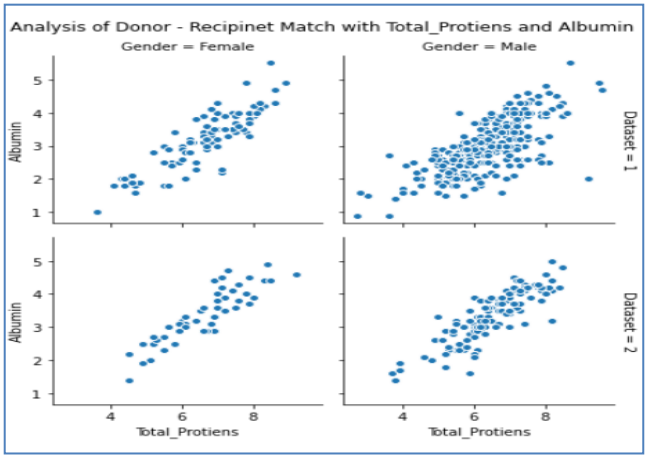

Fig.7: Analysis of D-R Match with Total proteins and Albumin

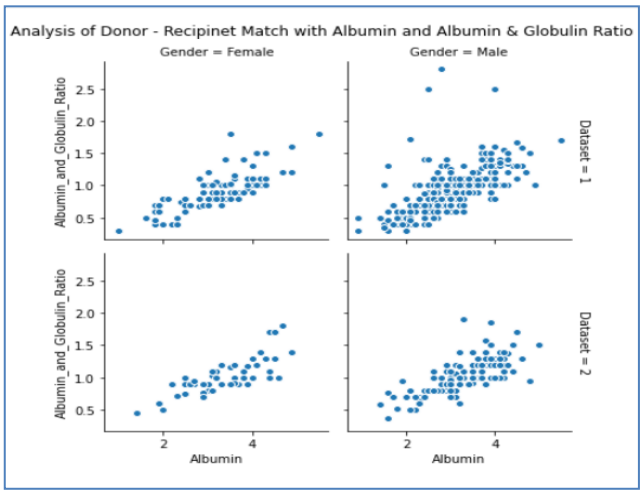

Fig.8: Analysis of D-R Match with Albumin and Albumin and Globulin Ratio

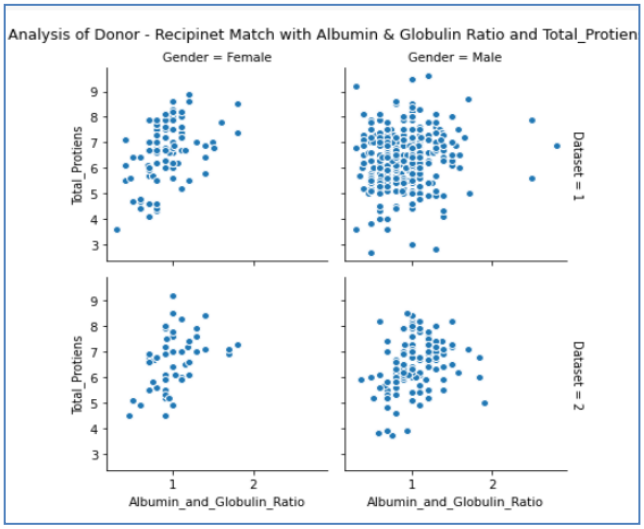

Fig.9: Analysis of D-R Match with Albumin and Albumin and Globulin Ratio and Total proteins

5. Experimental Results

For matching these features that is D-R matching such as Total _ Bilirubin, Alamine _ Aminotransferase, Total _ Protiens, Albumin _ and _ Globulin _ Ratio, Albumin considered as an important parameters and each parameters are assigned as nodes and connected with edges using networkX library. D-R Hopcroft Karp matching are used to predict the exact Donor availability of the parameters for recipient.

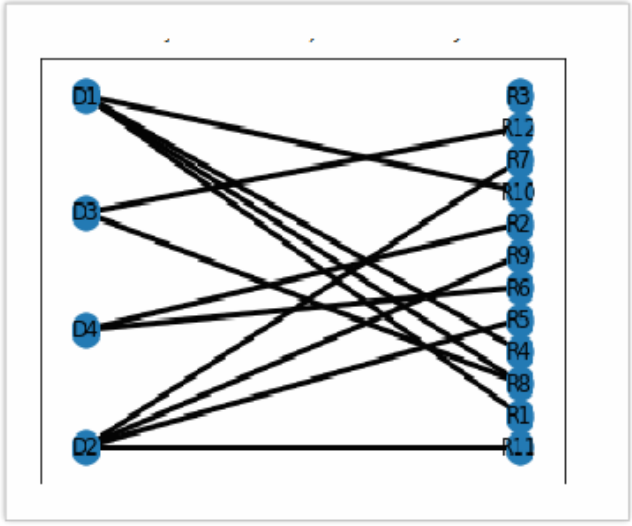

Fig.10: Donor to Recipient Bipartite Matching

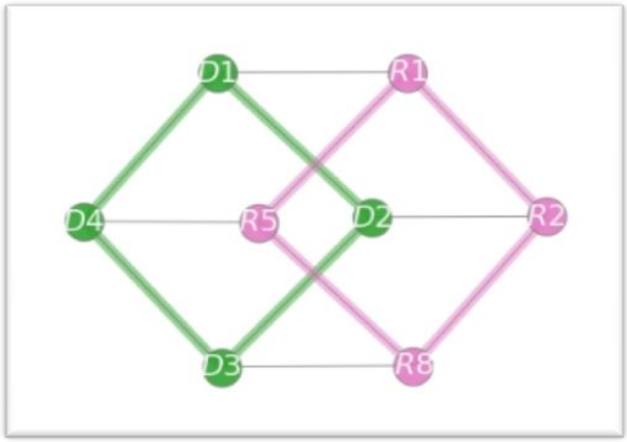

Fig.11: Donor to Recipient Hopcroft Karp Matching

6. Conclusion

To predict for donor to recipient using bipartite graph which is used to divide the set of pair of D-R matching. The concept of the bipartite graph used for separate the each set of nodes (each node contains set of parameters). Hopcroft–Karp algorithm which is used to takes input in a bipartite graph and produces as output a maximum

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cardinality matching. Hopcroft karp algorithm can predict the individual pair matching for the long term survival of the liver patients. It is also compare the following donor-recipient matching parameters with the correlation method which is used to find the donor to recipient matching to reduce the number of parameters. These are the features or data used for matching in the bipartite graph with hopcroft karp matching algorithm for the donor to recipient matching which includes Total _ Bilirubin, Alamine _ Aminotransferase, Total _ Protiens, Albumin _ and _ Globulin _ Ratio, Albumin and improves the long term survival of the liver transplantation.

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