

Donor-Recipient Matching in Bipartite Graph Using Enhanced DRMLT Algorithm for Liver Transplantation

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Datasets , Bipartite Graph, MELD Score, DRMLT algorithm.

Abstract

The matching preference for the liver transplanatation is taken from MELD Score which is more important between D-R(Donor to Recipient) using bipartite graph .In order to support the medical system or to help for the chronic failure. The characteristics of both donor to recipient features or parameters plays an important role.The final stage of the liver patient is chronic failure then necessity of the liver transplantation.The prediction of donor-recipient matching and the method is correlation to identifies exact donor- recipient matching. The correlation techniques shows the complete analysis of D-R matching for liver transplantation. To predict the long term survival of liver patients after liver transplanatation based on the Donor-Recipient matching using the Bipartite graph method. To propose an efficient algorithm to collect the number of matching with minimum computation using DRMLT algorithm.

1. Introduction

In terms of graph theory, Hall's Marriage Rules is both necessary and sufficient for the complete matching in a bipartite graph. The people who are paired are not happy with the partners that they are assigned. This situation leads to a remarkable model, named as as Gale-Shapley Stable Marriage Model. Stable Marriage problem(SM), Three Dimensional Stable Matching problem (TDSM) and Popular matching are consolidated for matching problems with preferences. The problem has engendered

interest from a number of communities, most notably from game theorists, economists and algorithmists. There is lot of matching problem and relevant algorithms are specified to overcome the matching problem. In the case of stable marriage problem, the preferences for the man and women are taken as complicated, for that STMP algorithm, BOSMA algorithm which gives better improvement for the stable marriage problem. Similarilly, SMAR algorithm gives solution to Satisfactory Roommates Problem with Incomplete List. This concept has been

applied for matching in the liver transplanatation with the help of MELD score for the survival of life.

2. Related works

D. Gale and L.S. Shapley(1962) described the problem of involving guesswork and also difficult which is required to admit first. It describes the difficulties of the applicant whether they have applied for some other colleges. This provides the uncertainty and chose according to the desired quota which gives the optimum in quality.

Robert W. Irving (1985) introduced the stable marriage problem which shows that of matching of number of men and number of women and also ranked the members of the opposite sex according to the order of preference, then there is no unmatched couple and both of them prefer each other to their partners under the matching. There is at least one stable matching occurs for every stable marriage instance and algorithms have to be efficient for finding a matching. The stable roommates problem which involves a set of even cardinality n and each of them which ranks all the others members according to the order of preference.

D. Gusfield (1988) described the stable roommates problem for the problem of matching $2n$ people into disjoint pairs to shows a stability. The problem strictly indicates the improvementof the stable marriage problem. The stable assignment properties for the efficiency of this method. At last gives a characterization of the set of all stable pairs and those pairs of people who is connected to that roommates in at least one stable assignment.

Ramachandran, K. Velusamy and T. Selvakumar (2011) described the Satisfactory Roommates problem and it is a version of Stable Roommates problemwhich consist of just one set. An algorithm of SMAR is described the preference value for the Roommates instance and satisfactory value matrix of preference list. In

this algorithm matching attains maximum satisfactory level of pair.

Ismel Brito and Pedro Meseguer(2005) described about the stable marriage problem is a problem of combinatorial which is solved with algorithm of polynomial time. In this require to have public lists of preferences and agents act like to keep private. In this provide the distributed version of problem and also constraint-based method to keep privacy. R.W. Irving (2004) described a classical stable marriage problem. In this not require to prefer two men and each of whom prefers the other's partner in the matching. This problem is encourages the practical medical matching for the use stable matching. This produces the same result for the hospitals and also residents problem.

R. Ramachandran, K. Velusamy and T. Selvakumar (2011) Gale and Shapely proposed a GS algorithm which used to solve stable marriage problem. This algorithm produces the results a man optimal and woman optimal matching. This provide a best optimal stable matching preference value by using Best Optimal Stable Matching Algorithm which ic named as BOSMA in order to find stable matching.

The following websites <https://towards data science.com/matching-of-bipartite-graphs-using-networkx-6d355b164567>, Matching in Bipartite Graphs, Matching (Graph Theory) described about the Graph matching problem which consist of making connections within graphs and do not share common vertices. The pairing of students according to the qualification in a class by using bipartite matching. The graph theory describes graphs and the mathematical structures used to model the lnk as pairwise between objects.

3. Research Methodology

3.1 Collection of data

The data collection from UCI datasets which is a multi organ datasets since from 1987

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and data is extracted only liver patient record which involves female and male liver patient records.

3.2 Preprocessing data

The data which is preprocess from the available datasets. In this, which is used to read, check, extract and fill the null value from the datasets. This provides the filtering of the relevant data from the dataset.

4. Dimesionality Reduction Method

4.1 Data Selection

To finding the most meaning inputs such as Age, Gender, Direct Bilirubin, Aspartate_Aminotransferase, Albumin and Globulin Ratio, Total_Protiens, Albumin, Alamine Aminotransferase, Alkaline Phosphotase, Blood Glucose Random, Total Bilirubin, Blood Urea, Serum Creatinine, Hemoglobin, Blood Pressure.

4.2 Data Analysis

Correlation map shows a direct relationship between the filtering data such as Albumin and Globulin_Ratio, Total Protiens, Albumin, Direct Bilirubin, Total Bilirubin, Aspartate Aminotransferase, Blood Urea and Serum Creatinine. These data gives similar performance and that alone taken for matching process using bipartite graph for D-R matching.

5. Donor to Recipient Bipartite Graph Matching

Donor- Recipient Matching for Liver Transplantation(DRMLT)

It is used to find the maximum cardinality matching. Each and every node is associated with edges and it is not share the common endpoint. The proposed algorithm (DRMLT) is taken the idea of the algorithms such as SMAR, STMP, BOSMA and these algorithms only based on preference value and satisfactory value which is not sufficient for matching. In the proposed algorithm Donor-Recipient Matching for Liver Transplantation

(DRMLT) gives maximum number of matching between D-R matching using the bipartite graph method with MELD score. The survival rate can be found by fixing the MELD score range to give the maximum number of preference like Poor survival rate, Low survival rate, Good survival rate and Higher preference rate. In the proposed algorithm DRMLT which list out the higher preference values alone considered as important.

MELD Score

The MELD score is replace of Child-Pugh score and this is proposed by Mayo clinic on February 27, 2002. The MELD score involves three variables including Creatinine, Bilirubin and International Normalized Ratio named as INR. The Prothrombin Time which is term as PT is replaced by International Normalized Ratio in the Model for End Stage Liver disease score. The International Normalized Ratio is the Prothrombin

Time ratio calculated in terms of the appropriate ISI of the local Prothrombin Time test system. International Normalized Ratio can be calculated using the formula,

$$INR = \frac{Patient'sPT}{MNPT}$$

The geometric mean of prothrombin time (MNPT). The MELD score is calculated by the formula,

$$MELD = 9.6 \times \log_e(X) + 3.8 \times \log_e(Y) + 11.2 \times \log_e(INR) + 6.4 \times C$$

Here, X and Y are the amounts specified as mg/dl of Creatinine and Bilirubin and C is given as

$$C = \begin{cases} 0 & \text{if alcoholic or cholestatic liver disease} \\ 1 & \text{otherwise} \end{cases}$$

Doctors prefer more with patients are having MELD<15 to get best survival rate. At the same time the doctors are not preferring the patients with MELD>40 because of poor survival rate. MELD score is the reliable measure.

MELD score	Range	Survival rate
MELD	> 40	Poor
MELD	>25	Low
MELD	15-25	Good
MELD	<15	Higher preference

Table 1. Meld Score

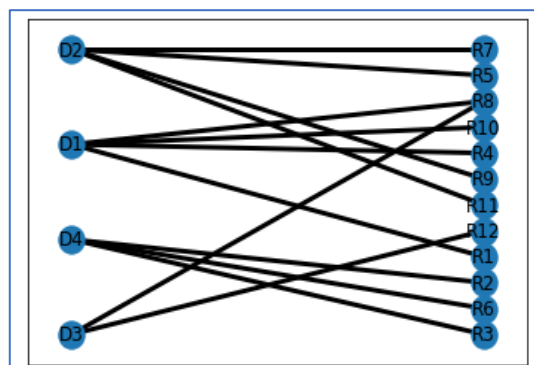


Fig 1. Number of D-R Matching

The table 1 shows the MELD score range. In the case of bipartite graph method, multiple D-R matching nodes is associated with each other. The figure 1 which shows the matching of Donor to Recipient nodes.

matching.

4. After bipartition of donor to recipient matching.
5. Gives the maximum number of donor to recipient matching.

PROPOSED ALGORITHM: DRMLT ALGORITHM

Pseudo Code:

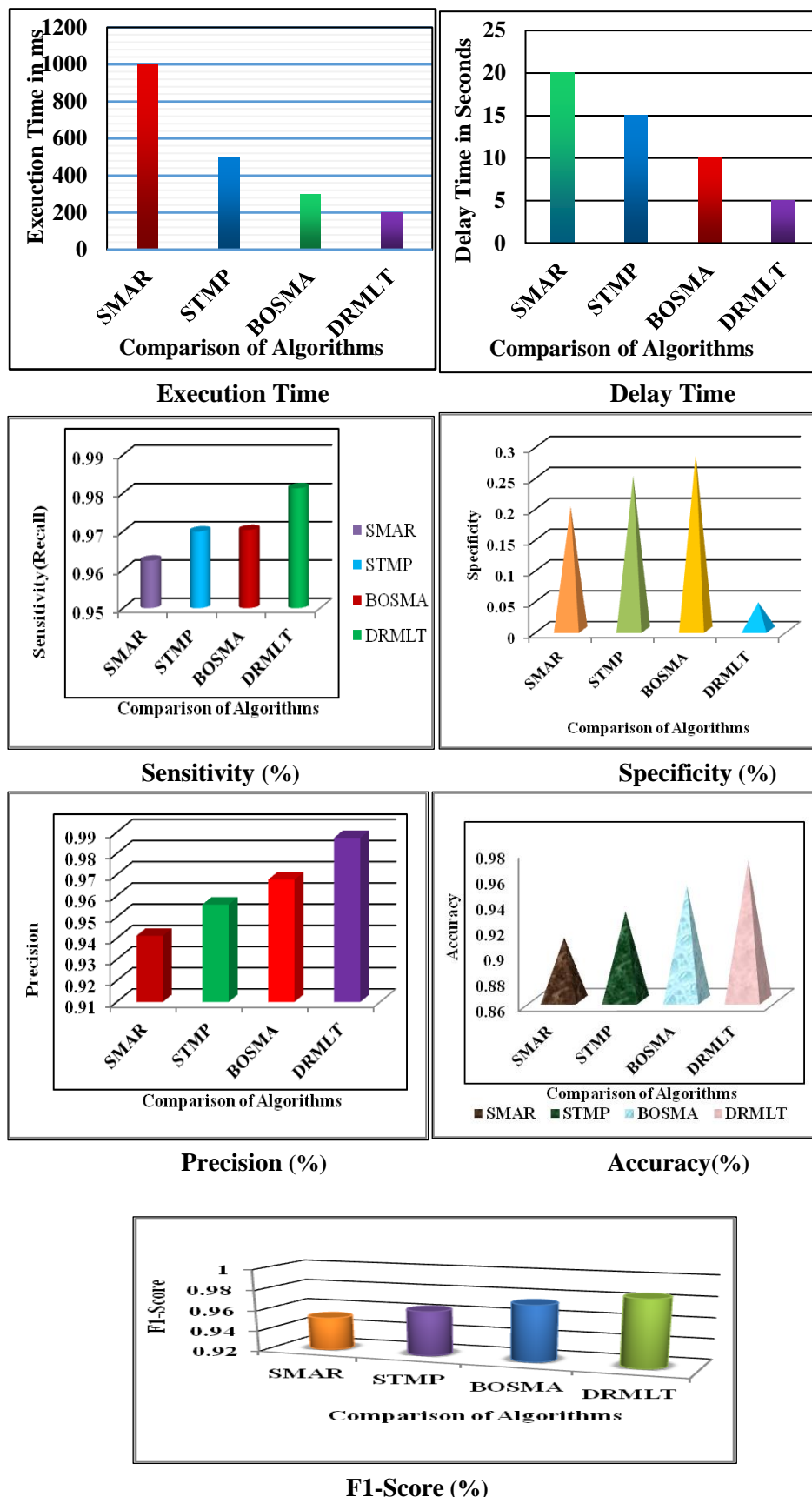
1. Get the preprocessing attributes from the dataset.
2. Fit the selected attributes in the bipartite graph method for donor to recipient matching using the MELD score(Model for End Stage Liver Disease).
3. Take the MELD score with less than 15 gives the high preferences for D-R

6. Results & Discussions

In the table which shows the performance of the metrics and ranges. The proposed algorithm DRMLT is compared with SMAR, STMP, BOSMA algorithms. DRMLT algorithm compare with performance metrics such as Sensitivity, Specificity, Precision, Accuracy and F1-Score.

Measure	SMAR	STMP	BOSMA	DRMLT
Sensitivity	0.9624	0.9701	0.9804	0.9813
Specificity	0.2	0.25	0.2857	0.0143
Precision	0.9412	0.9559	0.9677	0.9874
Accuracy	0.9091	0.9296	0.95	0.9701
F1 Score	0.9517	0.963	0.974	0.9843

Table 2. Range of all the performance Metrics



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7. Conclusion

The proposed algorithm (DRMLT) is compared with other algorithms such as SMAR, STMP, BOSMA and found that these algorithms only based on preference value and satisfactory value which is not sufficient for matching. The algorithm Donor- Recipient Matching for Liver Transplantation(DRMLT) gives maximum number of matching between D-R matching using the bipartite graph method with MELD score .

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