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Advanced Multilayer Perceptron Networks method for Predict the Survival in Liver Transplantation

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Abstract: Recently, the computerized medical domain based technologies are improved; liver transplantation (LT) plays a significant handling approach among liver disease patients. However, in several cases patients may have poor survival rate of prediction when undergoes LT, this is the main concern faced in many scenario. Many scholars had performed various applications of prediction to overcome these challenges. Therefore, the current research is concentrated on designing accurate and effective prediction approach for using advance multilayer perceptron (MLP) technique. The proposed prediction technique is performed on some stages. In the initial stage, the medical data are collected from United Nations Organ Sharing (UNOS) database. From that UNOS, we taken only liver related information. The data are given to the principal component analysis (PCA), it will reduce the attributes dimension for minimizing the complexity. After that, the Advance MLP classifier will predict the attributes into two accurate classes such as, best survival and worst survival with the help of these prediction ranges the patients will definitely get the excellent survival after LT.

Keywords: Artificial Neural Networks, Liver Transplantation, Machine Learning, Multilayer Perceptron, Post-Liver Transplantation Survival Prediction.

I. INTRODUCTION

Liver transplantation (LT) is thought to be a definitive treatment for acute and chronic end-stage liver disease. Despite the fact that surgery is costly, many patients opt for it because of technological advancements that have resulted in a higher survival rate. The patient's survival is determined by the quality of the graft, the availability of a donor, and the severity of the disease afflicting him. LT has two main objectives. The first is long-term survival, and the second is life quality. We discovered that the model for end-stage liver disease (MELD) score is employed for optimal organ allocation in clinical research [1]. The MELD score is based on the sickest person first policy. The liver is given to the first patient on the waiting list, regardless of donor or recipient qualities. Medical experts render judgment on LT and predict the outcome of LT based on the MELD score. Creatinine, one of three MELD score components (bilirubin, Creatinine, and international normalized ratio (INR), can fluctuate depending on the body weight of the liver recipient [1]. Despite the fact that, in the absence

of advancements in other scoring systems, medical specialists rely on the MELD score to predict survival. Patients undergoing LT, however, may still have a dismal prognosis even after applying the MELD score. Because of the operations' low survivability and high recurrence rates, this is the case [2]. The low survival rate is primarily caused by poor parameter and model selection. Because the problem is life-related, the input parameters should be chosen with extreme caution. The LT attributes accounted for 256 of the 389 attributes we gathered from the UNOS database. Without using any data mining algorithms, we were able to manually delete 59 attributes from the 256 attributes. We used principal component analysis (PCA) and ranking on the remaining 197 attributes. We chose 27 high-ranking attributes based on the standard deviation, which were used as input to the model. Association rule mining algorithms like treap, apriori, and tertius are used to forecast long-term survival after LT. By constructing rules between the characteristics, association rule mining algorithms discover the co-occurrence of attributes [3]. When employing these algorithms to create rules using attributes, it was confirmed that attribute selection plays a vital effect in predicting survival after LT. The multilayer perceptron (MLP) artificial neural network (ANN) is an appropriate allocation and prediction model for allocating livers to suitable recipients who otherwise die would but have a high chance of surviving after LT. For the prediction of LT survival, many traditional statistical models are used in medicine. However, ANNs outperform traditional statistical approaches and logistic regression models by avoiding local optimum. In the case of donor–recipient characteristics and transplant organ, ANN models have been demonstrated to be more successful than traditional statistical techniques in resolving survival [4]. Continuous research of high-accuracy models for survival after LT resulted in the development of precise models, such as ANNs, rather than MELD scores. Researchers have looked at survival rates throughout time, but none of them have assessed the accuracy of models for long-term LT survival. Follow-up data following LT is required for accurate survival estimation. The six-month survival rate, combined with a 13-year survival rate, is a favorable predictive indicator for LT patients [5].

II. BACKGROUND OF EXISTING SOLUTIONS

Recently, many researchers had to enhanced multiple machine learning techniques for predicting best survival after LT. several articles related to various machine learning approaches is reviewed as follows.

Raji et al. [16] had presented various healthcare aspects of liver transplantations and its prediction of survival utilizing Multilayer Perceptron Artificial Neural Network model. This research considered various parameters about post-transplantation and pre-transplantation for predicting the survival of a LT patient. The developed analysis includes several scores, such as End Stage Liver Disease Model (MELD), Emory Score and Kid Score, were also investigated. The result of LT with MELD score are used to take decisions for specialist physicians. Also this analysis adds more information about health aspects of liver transplantation and here, multiple machine learning techniques used in this fields. Furthermore, child score as well as Emory score survival also predicted based on comparing different scores including in MELD score LT. The dataset are here considered into two stages and one for training set and another one is for testing. The suitable pairs of donor recipients were discovered and the best liver survival was achieved during the transplantation of the training process.

Vinod et al. [17] had introduced the predicting survival utilizing a nonlinear approach as artificial neural network approach for graft following liver transplantation. In order to address the problem of organ allocation and survival prediction, this research work developed an artificial neural network approach. This method gathers the appropriate characteristics and identifies the dataset for training and testing. Suitable donor and recipients were chosen based on health information and the training involving ten-fold cross validation. Comparing previous models utilizing different performance features ensures precision. By using a vast amount of data from the United Network for Organ Sharing Registry to train the algorithm. The analysis approach done a 12-year survival analysis that uses vast amount of data to predict survival probability and compare them with current methodologies.

III. PROPOSED METHODOLOGY

A liver transplant also termed as hepatic transplant, when liver is affected by some disease at that time liver transplant can helps to save the patient's life. Due to numerous advances in the field of medical technology, much number of patients is subjected to liver transplantation. However lot of difficulties arises in finding proper donor and recipient. Mostly final stage of liver infected patients are widely undergoes liver transplantation. Most of the researchers developed various prediction techniques for detecting rate of survival after liver transplantation. But, a promising model that can predict the survival outcome after liver transplantation is very challenging. Lot of researches uses machine learning technique to build predictive model. To achieve effective prediction, this research work focuses on designing a neural network based prediction model of survival after LT. Basic architecture of the proposed methodology is given below.

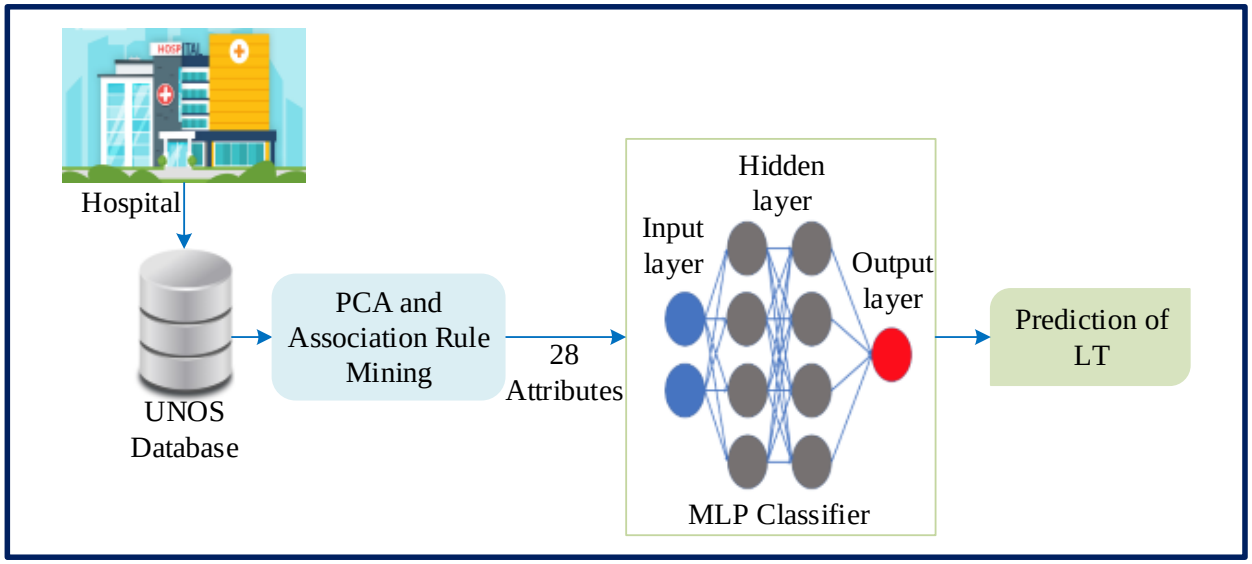

Figure 1: Proposed Architecture

Figure 1 illustrates the proposed architecture. In the initial stage the medical data was collected from hospitals, which is stored UNOS database. Pre-transplantation and post-transplantation of multiple organ data are stored in UNOS database. From there we collect the liver related datasets. The data from UNOS database are fed to PCA, the PCA separates the relevant and irrelevant data, at that same time PCA will reduce the high attribute dimensions to small dimension attributes. After that, 28

attributes which are related to liver is got by this PCA. The PCA output is given to the MLP classifier, A MLP is an artificial, deep neural network. MLPs are generally suitable for classification prediction issues where inputs are assigned a class or label. They are also suitable for regression prediction problems where a real-valued amount is predicted given a set of inputs. With the help of MLP classifier, the proposed method predicts the accurate survival rate of liver transplantation. The prediction is done based on End-stage Liver Disease (MELD) score, if the score is less than 40 the patient found to be best survival and if the core is greater than 40 the patient to be found poor survival. The stepwise procedure involved in this proposed design will be described briefly in the following section.

IV. TECHNIQUE INVOLVED IN PROPOSED METHODOLOGY

The proposed framework is mainly designed to accomplish an accurate prediction of survival after liver transplantations. There are various researchers involved to predict MELD score based LT, but the prediction rate of MELD score will not accurately predicted in many researches. Mostly 15 percent to 18 percent of the patients with chronic liver disease listed for liver transplantation. In this proposed design will predict the MELD score very accurately. The step by step process will be described in the following.

4.1. Dataset collection

The dataset was collected from various hospitals, which are stored in UNOS database. Generally the UNOS based database contain all types of medical data related with multiple organs such as, adults and pediatric liver patients of their clinical and non-clinical attributes are included in this UNOS database. Data from UNOS database, 389 attributes of patient's data are taken. Around 256 attributes were related with LT among these 398 attributes. After that, 59 irrelevant attributes will be removed manually in this stage. Remaining 197 attributes are then subjected to principal component analysis (PCA) to reduce it to 28 attributes. In the next stage is based on data preprocessing by using PCA, it will be described briefly in the following section.

4.2. Data Preprocessing

The raw data which is converted into understandable or efficient format in this data preprocessing technique. Here, PCA is utilized to reduce the attributes dimension. Furthermore attributes rule mining technique also used here for find out the co-occurrence of attributes by generating rules among the attributes. To implement the attribute selection by using PCA technique with data preprocessing. The elaborate description of PCA and attributes rule mining technique is given following.

4.2.1. PCA

The aim of PCA are to reduce the most essential data from the database and in addition, the size of the dataset to be compressed by keeping only this important information, data set description to be simplified and the structure of the variation and observation are also analyzed. All these goals are achieved by finding the PCA, which represents the direction of the maximum variance of the given data. The covariance matrix which is used to estimate the principal components (PCs). Using PCA the redundancy of the data get extracted in order to achieve dimension reduction. The steps involved

in PCA for dimension reduction is explained as follows and in addition the step by step procedure involved in the PCA is illustrate in figure 2 [21].

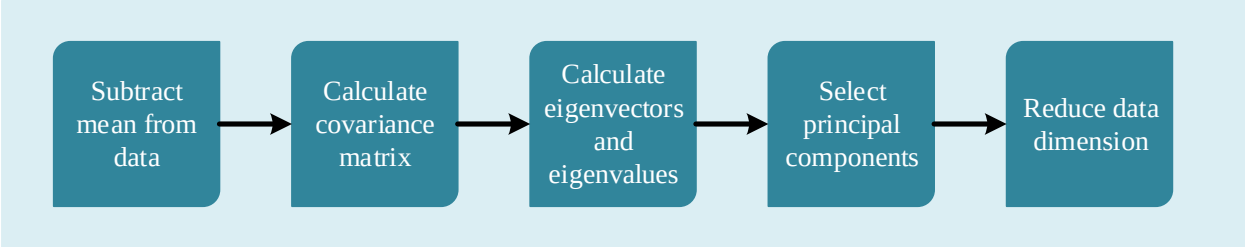

Figure 2: Procedure for PCA

Step 1: Consider the dataset which is named as A $A = [A_1, A_2 \ldots . A_N]$ and the dimension of the dataset is x here the mean related to this dataset is calculated. The mean calculation is expressed in equation 1.

$$\sigma = \frac{1}{x}\sum_{k=1}^{x} x_i \qquad (1)$$

In the above expression, the value for k ranges from 1 to x, x denote the total number of sample considered for analysis and σ terms the mean calculation.

Step 2: The covariance matrix related to the sample dataset is calculated with the help of the attained mean value. The realization of covariance matrix is expressed as follows.

$$\rho = \frac{1}{x}\sum_{k=1}^{x}(a_1 - \sigma)(a_i - \sigma)^T \qquad (2)$$

In equation (2) σ represents the calculated mean value and ρ represents the covariance matrix related to sample set.

Step 3: In this step using the framed covariance matrix the feature values and feature vectors were calculated. The calculation of feature values and feature vectors is represented as following.

$$\rho = \mathcal{H}.\mathcal{S}\,\mathcal{H} \qquad (3)$$

$$\mathcal{S} = \mathrm{diag}(\omega_1, \omega_2 \ldots . \omega_m) \qquad (4)$$

$$\mathcal{H} = (h_1, h_2 \ldots . h_n) \qquad (5)$$

In equation (5) $\mathcal{S}$ signifies the diagonal created using the covariance matrix with k feature values. And this diagonal matrix is arranged in descending order. Where ω_m illustrates the feature values in the covariance matrix. $\mathcal{H}$ Represents the feature matrix that comprises the correlated feature vectorh_n.

Step 4: The calculated feature value and feature vector are used to estimate the cumulative variance contribution rate related to beginning v-row element is expressed as follows.

$$\delta = \sum_{i=1}^{v} \omega_i / \sum_{j=1}^{v} \omega_j \qquad (6)$$

In equation (6) the calculated value δ must be higher or equal to 0.9. δ Represents the rate of contribution with cumulative variance for first v-row elements. According to select the identified issue the calculated value δ is used. The considered sample dataset can be found by the selection of δ value the v-row element.

Step 5: At the final step, using the v-row feature vector to reduce the dimension in the given sample dataset.

$$\mathcal{B} = \mathcal{H}_{\mathrm{v}} \quad (7)$$

$$\mathcal{N} = \mathcal{B}.\mathrm{A} \quad (8)$$

In equation (8) $\mathcal{B}$ illustrates the feature matrix. Feature vectors related to beginning v-row elements involved in this feature matrix. The dataset A is converted into$\mathcal{B}$ and x-dimension is reduced into v-dimension. $\mathcal{N}$ Denotes the dimension reduced dataset. The original dataset is reduced by using PCA, which achieve effective dimension reduction. The classification accuracy can be enhanced by means of dimensionality reduction. PCA perform ranking the by using Weka ranker.

Weka ranker:

The Ranker detects strong attributes from PCA filtered attributes and ranks them according to strength and standard deviation. The obtained 70 relevant attributes according to the standard deviation ranking, here 28 attributes are only used for predicting survival after LT. The proposed method utilized Weka-knowledge flow analysis to predict the strong attributes from PCA filtered attributes. The PCA filters the essential information related to LT, which contains the attributes such as, transplantation attributes, recipient and donor attributes. For survival prediction after liver transplantation, when ranking 28 attributes will clear that all attributes such as, transplant, recipient and donor have equal importance.

4.2.2. Associating Rule Mining

The new frequency patterns are discovered by using Association rule mining in the database. Association rule mining goals to reduce the correlation between datasets, interesting associations and frequency patterns in the data sources. Support and confidence (c) are the two general basic significant association rules. Normally users mostly concern about only frequently brought items due to the large size of the database. The proper declaration of association rules mining are described as follows.

Let $\mathrm{K} = \mathrm{K}, \mathrm{K}_2, \ldots, \mathrm{K}_{\mathrm{m}}$ be a dataset of m difference attributes, Txn be the transaction that includes a set of data such that $\mathrm{Txn} \sqsubseteq \mathrm{K}$, DB denoted as a database with $\mathrm{Txn}_{\mathrm{s}}$ difference transactions. $\mathrm{M} \Rightarrow \mathrm{Y}$ is an insinuation format of association rule, where $\mathrm{M}, \mathrm{N} \sqsubset \mathrm{K}$ are sets of items defined ad datasets and $\mathrm{M} \cap \mathrm{N} = \emptyset$. Antecedent is termed ad X and Y is known as consequent. The rule means M impliesN. The two association rules of thresholds of confidence (c) and support (s) are pre-defined by the users to drop the rules and that kinds of rules are not useful.

Support (s) is termed as proportion of records in the database, which contain whole records of $\mathrm{M} \cup \mathrm{N}$ in the database. For each attributes in the dataset are improved by one attribute. During the course

of the scanning is occur then the dataset crossed over in different transaction in any database. The support is expressed as follows.

$$\text{Support (MN)} = \frac{\text{Support sum of MN}}{\text{Whole records in the database DB}} \qquad (9)$$

Confidence(c) is termed as proportion of the number of transaction, it contain the whole records of $M \cup N$ which have M, an association rule $M \Rightarrow N$ to be generated by the threshold of confidence ratio will be outperforms. Confidence is a degree of strength of the association rules. The confidence is expressed as follows.

$$\text{Confidence (M/N)} = \frac{\text{Support(MN)}}{\text{Support(M)}} \qquad (10)$$

By using this support and confidence in an association rule mining based rules set we can easily match the donor and recipient LT [22]. After performed association rule mining the output attributes which are fed into the MLP classification to find the accurate prediction of LT. The MLP classification will be describe in the following section.

4.3. MLP Classification

To perform survival prediction after liver transplantation utilizing Advance MLP classifier. The input attributes are trained in MLP model with Block propagation algorithm. Using PCA, the attributes are reduced to 28 attributes, this is the input of this MLP model. The outputs from preprocessor which is fed into the input of MLP classifier. The input data consist of transplant, donor and recipient attributes related with several attributes such as, Aspartate Aminotransferase, sgpt, sgot, alkphos, Alkaline_Phosphotase, Alamine_Aminotransferase, Total_Protiens, Albumin, ag_ratio, Meld_Score, Albumin_and_Globulin_Ratio, Dataset, Gender, Age_recipient, Total_Bilirubin, Direct_Bilirubin and Age_doner. The clinical data are trained using sigmoid functions in the hidden layers. The best survival of LT patients have a proper matching of donor and recipient, this can be done by using hidden layers during training.

4.3.1. Multilayer Perceptron

In Multilayer Perceptron the neurons are structured in layers, it contain one or many hidden layers among its input layer and output layer. The neurons in the same layers are always not interconnected and the layers always connected directly from lower layers to upper layers [23]. The architecture design of MLP is shown in figure 3.

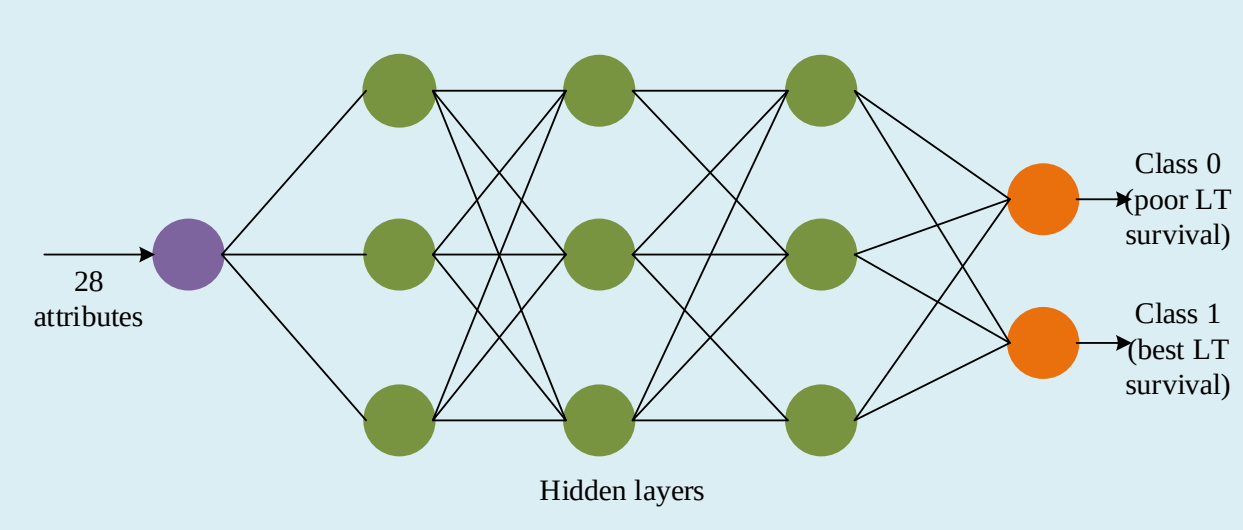

Figure 3: Architecture Design of MLP

Figure 3 illustrates the general MLP architecture used in this proposed methodology. The amount of measurement for the pattern issue which is equal to amount of neurons in the input layer. The amount of neurons in the output layers equal to the amount of class. For the multiple layer selection and the connections and neurons in each layers are define the architecture issue. The goals of MLP is to generalize good classification by optimize the suitable network with sufficient parameters.

4.3.2. Back-propagation and Learning for de MLP

MLP is the process of attaining a minimal difference among the preferred output and the network output by adapt the connections weights for this purpose the algorithms are mostly known as Back-propagation with based on descent gradient technique. Assume that, the input layer have u_0 neurons which is expressed as $S = (s_0, s_1, \ldots., s_u)$, and a sigmoid activation function is denoted as,

$$f(s) = \frac{1}{1+e^{-s}} \qquad (11)$$

To determine the output of each unit in each layer then only we attain the network output. Now consider a set of hidden layers as $(q_1, q_2, \ldots., q_N)$. Consider that u_i ate the neurons amount by each hidden layer q_i.

For the output first hidden layer

$$q_i^j = f\left(\sum_{k=1}^{u_{i-1}} G_{k,j}^0 s_k\right) j = 1, \ldots. u_i \qquad (12)$$

The outputs q_i^j of neurons in the hidden layers are computing as follows.

$$q_i^j = f\left(\sum_{k=1}^{u_{i-1}} G_{k,j}^{i-1} h_{i-1}^k\right) i = 2, \ldots N \text{ and } j = 1, \ldots, u_i \qquad (13)$$

Where $G_{k,j}^i$, is the weight among the neuron k in the hidden layer i and the neuron j in the hidden layer $+1$, u_i is the number of the neurons in the ith hidden layer. The output of the ith can be formulated as follows.

$$q_i = (q_i^1, q_i^2, \dots, q_i^{u_i})^t \quad (14)$$

The network output are calculated as follows.

$$y_i = f(\sum_{k=1}^{u_N} G_{k,j}^N \, q_N^k) \quad (15)$$

$$Z = (z_1, \dots, z_j, \dots, z_{N+1}) = F(G, S) \quad (16)$$

Where $u_N$is the number of the neurons in the Nth hidden layers, $G_{k,j}^N$ is the weight among the neuron k in the Nth hidden layer and the neuron j in the output layer, F is the transfer function, Z is the vector of output layer, and G is the matrix of weights, its defined as follows.

$$G = [G^0, \dots, G^j, \dots., G^N] \quad (17)$$

$$G^i = (G_{k,j}^N)_{\substack{0 \le i \le N \\ 1 \le j \le u_{i+1} \\ 1 \le k \le u_1}} \text{ Where } G_{k,j}^N \in \mathbb{R} \quad (18)$$

Where S is the input of neural network and f is the activation function, to simplify we can take $u = u_i \forall\, i = 1, \dots, N$ for all hidden layers and G^i is the matrix of weights among the i^{th} hidden layer and the $(i+1)^{th}$ hidden layer for $i = 1, .., N-1$, $G^0$is the matrix of weights among the input layer and the first hidden layer and $W^N$is the matrix of weights among the N^{th} hidden layer and output layer [24]. By using MLP the prediction rate is very accurate and more effective. In the following section will be described based on prediction of LT using MLP outcome.

4.4. Prediction of LT

The prediction system makes the decision of LT survival which is entirely based on MELD score. The MELD score is estimated by using the following expression.

$$M = 9.6 \times \log_e(P) + 3.8 \times \log_e(Q) + 11.2 \times \log_e(INR) + 6.4 \times L \quad (19)$$

Where P and Q are the amounts (mg/dl) of Creatinine and bilirubin, respectively and L is expressed as

$$L = \begin{cases} 0 & \text{if cholestatic liver disease} \\ 1 & \text{otherwise} \end{cases} \quad (20)$$

Using MELD score the MLP will predict survival rate of LT patients. The MLP outputs are considered as class 1 and class 0. If MELD < 50 the survival of the liver patient is good survival after LT and if MELD>50 then the survival of the liver patient is very poor survival after LT.

Table 1: Assessment of MLP classes

Score	Class	Prediction
MELD<50	Class 0	Best Survival
MELD>50	Class 1	Poor Survival

Table 1 illustrates the assessment of MLP classes. This system is to predict the best survival rate outcome and it is more effective for patients after LT. In addition, accuracy parameter used to evaluate the effectiveness of the model and proved that the highest accuracy has been obtained in the model with the data set.

V. CONCLUSION

This research work concentrate on developing the excellent prediction technique for Liver Transplantation Using Advanced Multilayer Perceptron Network. The technology improvement attains a best survival rate, so various liver disease patients undergoes LT treatment. Lot of advancements had been developed in the policies of surgical procedures pre- and post-transplant care of the patient and organ allocation. In order to overcome the issues in the existing approaches in healthcare domain this research focus to solve these challenges. In this, way the most relevant attributes based on liver are successfully extracted from the dataset using PCA mining algorithm and association rules mining algorithm

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