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Chaotic Quantum Beetle Swarm Optimization Based Empowered Model of Bidirectional Long Short-Term Memory for Prediction of Survival of Paediatric Undergoing Hematopoietic Stem Cell Transplantation

Abstract: - For certain patients with hematologic diseases, hematopoietic stem-cell transplantation (HSCT) is a therapeutically restorative surgery. Although the danger of transplantation has decreased recently, morbidity and death are still high, thus choosing who, what, and when to do a transplant is crucial. Machine learning models play a crucial role in forecasting the mortality rate of paediatric patients following a transplant, the problem of voluminous dataset and class imbalance affect the detection accuracy of the prediction model greatly. Hence, in this paper we developed a two stage algorithms for potential feature selection and optimizing the functionality of the deep learning classifier. To reduce the irrelevancy and improve the accuracy rate of the survival prediction of HSCT children, a novel stochastic differential evaluation method is developed in this work to determine the most informative features that contribute more information about the survivability of the paediatric patients. The problem of overfitting due to the class imbalance and the inappropriate assignment of hyperparameters in long short-term memory is handled by devising an empowered model of Bidirectional Long Short-Term Memory (BLSTM) which conducts the learning process twice, to understand the input patterns in depth. Still, the problem of weight decaying is a major problem in BLSTM due to lack of knowledge in assigning values to the hyperparameters this proposed work utilize the Beetle Swarm Optimization food searching behaviour by achieving global optimization search space with chaos mapping improves the performance of the BLSTM effectively. The experimental results provide the evidential proof of the proposed chaotic Beetle Swarm Algorithm empowered Bidirectional Long Short Term Memory (CBS-BLSTM) produced highest accuracy rate of 98% compared with other deep learning models.

Keywords: Hematopoietic Stem Cells Transplant, inconsistency, class imbalance, overfitting, hyperparameter optimization, Beetle Swarm Optimization, Stochastic searching, differential evaluation, Bi-Directional Long Short-Term Memory, paediatric patient

1. INTRODUCTION

Haematological cancers, including leukaemia, lymphoma, and multiple myeloma, are treated with transplantation of hematopoietic stem cells (HSCT), a powerful immunotherapy technique [1]. Even with the latest developments, hematopoietic stem cell transplantation (HSCT) is still a challenging process that involves high-dose chemotherapy before autologous stem cells or those from an associated or unrelated donor that match the patient's HLA (allogeneic) [2]. Receivers of hematopoietic stem cell transplants confront a variety of post-transplant problems, which can result in morbidity and mortality. These consequences include graft-versus-host disease, recurrence or recurrence of disease, and potentially fatal infections [3].

The latest developments into the clinical process are starting to emerge from the contemporary usage of automated learning algorithms, which carry out statistical computations without requiring the assumptions necessary by traditional methods. These earlier machine learning algorithm-based research, however, were unable to address the arbitrary nature of changeable settings or to include comprehensive, unprocessed medical information [4].

Deep neural networks (DNN) are among the most promising machine learning algorithms. They are particularly good at extracting features, which makes them ideal for overcoming the drawbacks of the current approach [5]. The processing of natural languages, which is capable of converting complicated data in a central repository into a machine-readable representation, is a technique that the DNN-based approach is well-suited [6]. Due to the fact that, from a data processing perspective, the human leukocyte antigen information is similar to natural

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language, this property is beneficial for modelling HSCT. DNN can also show learning processes, which aid in clinical decision-making. However, the applicability of DNN-based prediction of prognosis in dialysis treatment has not yet been assessed.

In this work the long short-term memory is used for predicting the survival predictability of the children who underwent HSCT. The problem of weight decay is the major issue in LSTM, hence the Bidirectional LSTM (BiLSTM) is deployed in this work, the parameters fine tuning due to class imbalance is considered as the primary problem while performing prediction of survivability after HSCT. Instead of using gradient descent method, this work fuses the knowledge of beetle swarm algorithm to assign the fittest value inorder to improve the learning rate of the BiLSTM.

The clustered dataset of the HSCT is used for discovering the most relevant features which highly influence in classification of survivability of the children is accomplished by the stochastic searching algorithm. With the reduced features this proposed work performs classification of HSTC children using BiLSTM with beetle swarm optimization intelligence to handle overfitting due to class imbalance problem in bone marrow transplant dataset.

The detailed working principle of the proposed method chaotic quantum beetle swarm optimization boosted Bidirectional Long Short-Term Memory for survival prediction of children after HSTC is explained in the following sections.

Background study

Beetle Swarm Optimization (BSO)

The fluctuating chemical sensory system of insects, such as beetles, allows them to perceive and respond to a variety of environmental cues. Insect antennae are crucial chemical receptors. They mostly produce tactile and olfactory effects, while some can also hear. They assist insects in finding food, locating the other sex, communicating, and selecting breeding sites [7]. In order to attract or deter insects that are damaging to plants, people frequently employ this characteristic of insects by dispersing compounds with particular volatile scents. Beetles' long antennas serve two main purposes. The first is to investigate their surroundings. The second is using the body's antenna to detect the scent of food or locate possible partners.The beetle rotates in precisely the same path as the direction of a larger concentration of scent sensed on a particular side of the antenna; otherwise, it rotates to the opposite side.

This basic idea explains how beetles locate food efficiently. Jiang et al. [8] suggested a meta-heuristic optimisation method relying on the long-horned beetle's search habit. The Beetle Antennae Search (BAS) Algorithm, able to automatically carry out the optimisation method despite requiring knowledge of the gradient information and the function's precise shape. The main benefit of the BAS is that, because it just has one individual number, it can solve the optimisation problem faster and with less complexity in its design.

2. RELATED WORK

Styczyński et al [9] reported that about enhancement of prognosis following hematopoietic stem cell transplantation, information on incidence and variables linked to death is necessary. Factors relating to patients, diseases, types of donors, sources of stem cells, centres, and countries were linked to infectious fatalities. Throughout the post-transplant phases, their effects changed. Transplant centres have identified risk variables and successfully reduced death following haemodialysis (HSCT) in the initial and intermediary post-transplant stages. Attention to at-risk populations and increased detection of infections with unreported aetiology could lead to better late-peripheral care.

Choi Et al [10] developed a learning based gradient boosting algorithm to predict post transplantation survival of HSCT patients. They derived a risk score and with that computed score illustrated the potential for survival prediction based on many transplantation-related variables, together with a visualisation of each variable's significance.

RatulEt al [11] focused on predicting the survival of children undergoing bone marrow transplant by applying chi square as feature selection and grid search cross validation of optimization parameters of classification algorithms. They used 11 dataset features for efficient classification using conventional machine learning algorithms.

A robust risk detect model was developed by Yiwang Zhouet al [12] to discover the risk factor of dysfunction of lethal organ. They used baseline biological variables changes in clinical status of patients who underwent HSCT. For prediction Naïve Bayes classifies is used with longitudinal data for risk assessment of HSCT patients.

Hamed Shourabizadehetal [13] explored the use of several machine learning approaches on single-center allogeneic high-dose chemotherapy databases; this approach merits more research and could be a helpful tool for identifying characteristics with prognostic potential. The authors concluded from their findings that the highest accuracy rates are attained via logistic regression and random forest.

An XGBoost algorithm was developed by Erik et al. [14] to forecast survival following haemodialysis. To depict the impact of the primary factors, they employed an explanatory model. The authors claimed that the mortality risk following HSCT could be accurately predicted using an explainable machine learning model.

A novel feature selection approach called the mud ring algorithm was suggested by Bakrawy et al[15] to identify potential features in the BMT dataset in order to forecast the death of children following HSCT. Using test cases and a smaller feature set, many contemporary classification methods were employed to more accurately forecast the death rate of children.

3. METHODOLOGY

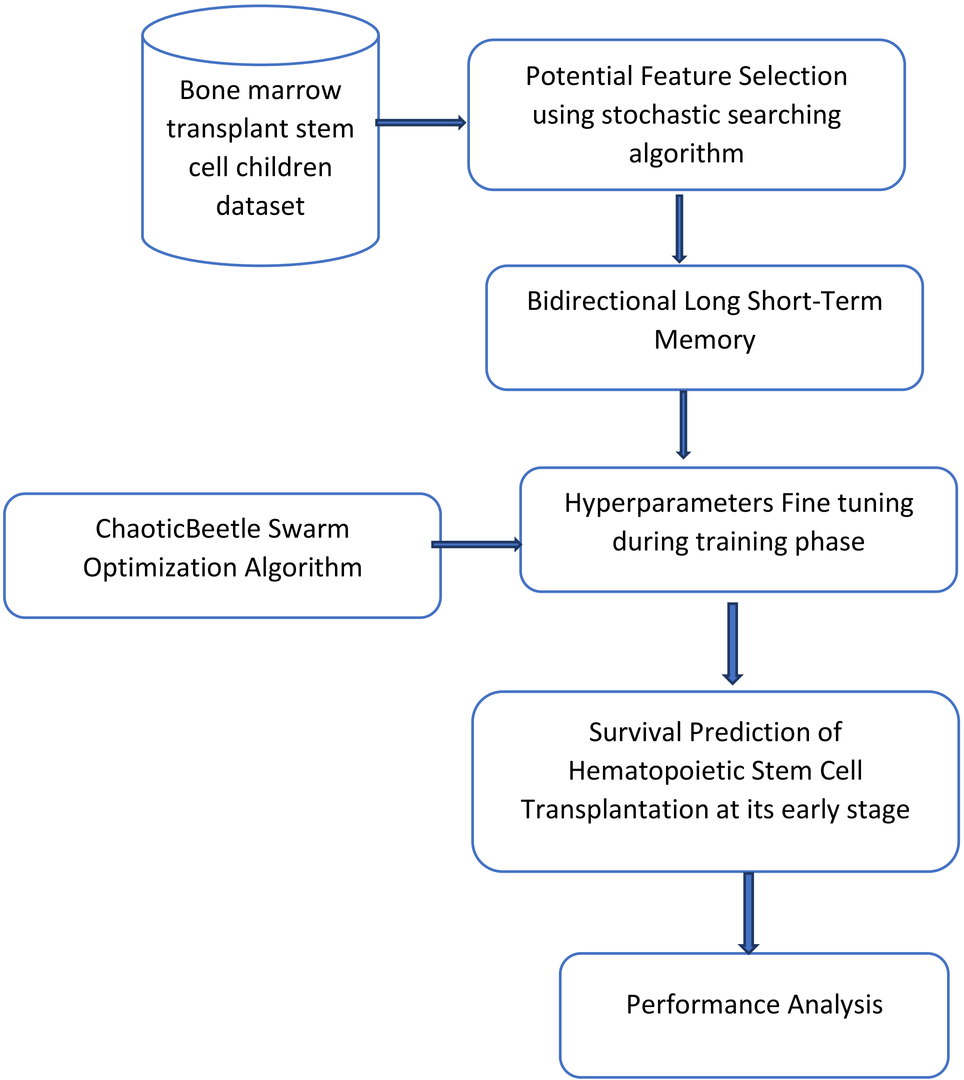

Figure 1: Overall Architecture of Chaotic Beetle Swarm Optimization empowered Bidirectional Long Short - Term memory for mortality prediction of paediatric patients

In this phase,the prediction of children's survival following hematopoietic stem cell transplantation is accomplished through the development and implementation of a Chaotic Beetle swarm optimized Bidirectional Long-short term memory classifier as depicted in figure 1. With the results obtained from pre-processing and clustering of the bone marrow transplant dataset, the potential features which highly contributes to determine the survival of HSCT children is discovered by a metaheuristic algorithm known as Differential Evaluation model a kind of stochastic searching method. With the reduced feature subset, the dataset is passed to the Bidirectional Long short memory, in which the learning rate and weight hyperparameters are fine-tuned by using chaotic quantum Beetle swarm optimization for paediatric survival prediction based on the type of disease as malignant or non-malignant.

Discovering Potential Features using Stochastic Algorithm in HSCT Dataset

In this proposed work Discrete Evolutionary based stochastic search algorithm is utilised for discovering the most relevant attributes that provides more information to the classifier for discriminating survivability prediction among children.

Discrete Evolutionary [17]precludes the usage of derivative information and has a tendency towards self-organization. It is a population-based, derivative-free approach as a result. Furthermore, since DE employs real integers as solution strings, no encoding or decoding is required. Assume that Y_i where i=1,2,...,n are the instances with D-dimensional optimisation problem with D features. Initially, a population of n vectors of solution is formed. This algorithmutilises the standard notation for every solution xi at every generation t.

$$\boldsymbol{x}_i^t = (x_{1,i}^t, x_{2,i}^t, \ldots, x_{D,i}^t),$$

--------------- (1)

It is composed of D elements in the D-dimensional domain. The genomes or chromosomes can be compared to this vector.Three primary processes comprise differential evolution: mutation, crossover, and selection. The mutation scheme is used to carry out the mutation. First randomly select three different vectors at t (xp, xq, and xr) for each vector xi at any given time or generation, and then we use the mutation technique to create a referred to as donor vector.

$$\boldsymbol{v}_i^{t+1} = \boldsymbol{x}_p^t + F(\boldsymbol{x}_q^t - \boldsymbol{x}_r^t),$$

-------------------- (2)

When the parameter F, often known as the differential weight, is defined as follows: F∈[0,2]. n≥4 is the smallest population size required. While F[0,2] in theory, a scheme using F[0,1] in fact is more stable and efficient. Actually, F∈(0,1) is used in nearly all of the research published in the literature.

The crossover parameter Cr∈[0,1] governs crossover, regulating the likelihood or pace of crossover. There are two methods to actually do the crossover: binomial and exponential. Crossover is performed on each of the D components, variables, or parameters by the binomial scheme. The jth element in vi is changed as follows: a random number with a uniform distribution ri∈[0,1] is generated.

$$\boldsymbol{u}_{j,i}^{t+1} = \begin{cases} \boldsymbol{v}_{j,i} & \text{if } r_i \le C_r, \\ \boldsymbol{x}_{j,i}^t & \text{otherwise,} \end{cases} \qquad j = 1, 2, \ldots, D.$$

-------------------------------- (3)

Therefore, it is possible for each component to choose at random which vector to swap with the donor vector's counterpart. A portion of the donor vector is chosen for the exponential scheme, and this segment begins with a random length L and random integer k, which may have several components. Mathematically, if we randomly select k∈[0,D−1] and L∈[1,D], thus we obtain

$$\boldsymbol{u}_{j,i}^{t+1} = \begin{cases} \boldsymbol{v}_{j,i}^t & \text{for } j = k, \ldots, k - L + 1 \in [1, D], \\ \boldsymbol{x}_{j,i}^t & \text{otherwise.} \end{cases}$$

----------------------- (4)

The process of selection is basically identical as that of genetic algorithms. It involves choosing the least feasible value for a minimising problem—the fittest. Consequently, we have

$$\boldsymbol{x}_i^{t+1} = \begin{cases} \boldsymbol{u}_i^{t+1} \text{ if } f(\boldsymbol{u}_i^{t+1}) \le f(\boldsymbol{x}_i^t), \\ \boldsymbol{x}_i^t \quad \text{otherwise.} \end{cases}$$

---------------------------- (5)

It is noteworthy to mention in this context that the utilization of v_it+1≠x_it could potentially enhance the evolutionary or exploratory effectiveness. The overall efficiency of the search process is determined by a pair of factors, namely the differential weight F and the crossover probability Cr.

Beetle Swarm Optimization Boosted Quantum Bidirectional LSTM (MFO-BLSTM) for survival Prediction of HSCT children

The primary goal of this suggested study is to enhance the efficiency of the Bidirectional LSTM in predicting survival outcomes among paediatric patients after hematopoietic stem cell transplantation.The bone marrow transplant dataset is clustered based on the similarity exhibited by each instance and it also handles optimized selection of cluster centroids to reduce the false clustering rate by devising Chaotic Harris Hawk Optimized Deep Clustering. The resultant clustered dataset is used in this phase, to discover most relevant features and improve the classification of survival rate of children underwent HSCT.

After performing significant feature selection using differential evaluation method, the reduced features are further used as input to the BiLSTM for mortality prediction of Children after HSCT.

This suggested work employs the Bidirectional LSTM (BLSTM), a standard LSTM extension that can improve the model's performance of predicting mortality for post transplant children [17].The regular LSTM model undergoes training on the input data only once, in contrast, the BLSTM model undergoes training twice. Initially, the model is trained using the original input data, followed by a second training phase utilizing the reversed duplicate of the input sequence. Consequently, this approach provides contextual information to the system, leading to quicker and improved results through comprehensive analysis of the problem. As the BLSTM[18, 19] is enhanced with knowledge induced by the Chaotic Beetle Swarm optimization technique, which aids in selecting parameter values via probable search of best values. Despite the utilization of random values in traditional LSTM models, the accuracy rate in news classification prediction is notably lower. As a result of this suggested model CBSO-BLSTM, the food searching behaviour of beetlesbased on their smelling skill discovers the best set of parameter values to achieves higher rate of accuracy. The figure 2 illustrates Workflow of the proposed Chaotic Quantum Beetle Swarm Optimization fused BiLSTM (CQBSO-BLSTM)

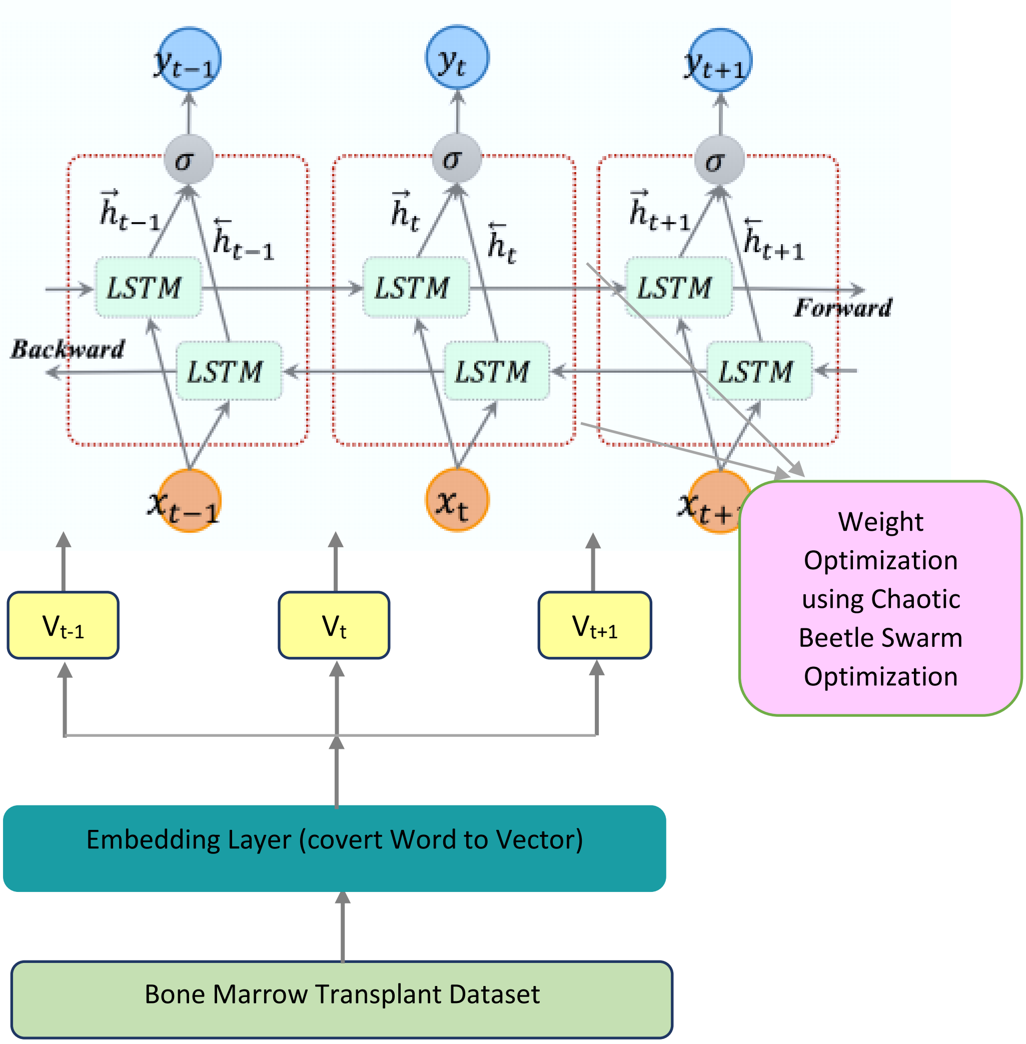

Figure 2: Working principle of proposed CBSO-BLSTM

In this work dataset used for mortality prediction of posttransplant of Bone marrow Transplant dataset to children was obtained from UCI Machine learning repository.The data set includes information on paediatric patients with a variety of hematologic illnesses, including both malignant and non-malignant conditions.The goal of this research was to determine the key variables that determine whether a transplant surgery is successful or not.

When using Beetle Swarm algorithmto optimize nonlinear systems, a simple two-step building procedure is employed as follows:(a) model the searching behaviour;(b) formulate the behaviour of detecting.

In this algorithm, each beetle represents a potential solution to the optimization problem, and each beetle corresponds to a fitness value determined by the fitness function. Similar to the particle swarm algorithm, the beetles also share information, but the distance and direction of the beetles are determined by their speed and theintensity of the information to be detected by their long antennae. The particle swarm optimization is the inspiration to develop the beetle swarm optimization in the mathematical derivative.

In mathematical form, beetle swarm optimization is developed by the inspiration of particle swarm algorithm. Assume there are m number of beetle populations in a r dimensional space denoted as

b = $(b_1, b_2, \ldots, b_m)$ ------------------ (6)

each beetle is represented with the r dimensional vector and optimal solution as

$B_i = (b_{i1}, b_{i2}, \ldots, b_{iR})^T$ ------------- (7)

The velocity of the ith beetle is mathematically formulated as

$S_i = (S_{i1}, S_{i2}, \ldots, S_{iR})^T$ --------------- (8)

Each beetle extremity is signified as

$U_i = (U_{i1}, U_{i2}, \ldots, U_{iR})^T$ ---------------- (9)

The swarm extreme value of the population of beetle is

$U_g = (U_{g1}, U_{g2}, \ldots, U_{gR})^T$ ----------------- (10)

The beetle swarm behaviour is formulated as

$B_{iR}^{j+1} = B_{iR}^{j} + \lambda S_{iR}^{j} + (1 - \lambda)\varphi_{iR}^{j}$ ------------- (11)

where $R = 1,2, \ldots, R; i = 1,2, \ldots, n; J$ is the current iterationS_{iR} is articulated as the speed ofbeetles,and φ_{iR}denotesthe upsurge in beetle place movement. λ is a confident and persistent. Formula of the speed is derived as

$S_{iR}^{J+1} = \beta S_{ir}^{J} + cn_1 rd_1 \left(U_{ir}^{J} - X_{ir}^{J}\right) + cn_2 rd_2 (U_{gr}^{J} - X_{gr}^{J})$ ---------- (12)

The two constant wit positive values are $cn_1$and cn_2, two random values rd_1 and rd_2their values range between 0 and 1. β is the decreasing inertia weight and it is computed as

$\beta = \beta_{max} - \frac{\beta_{max} - \beta_{min}}{J} * j$ --------------- (13)

Whereβ_{min}andβ_{max} respectively represent the minimum and maximum value ofβ. j and J are the current number of iterations and the maximum number of iterations. Asωgradually decreases, the beetle's speed decreases and then enters local search. The γ function, which defines the incremental function, is calculated as follows:

$\gamma_{ir}^{j+1} = \vartheta^{j} * S_{ir}^{j} * sign\left(fit\left(B_{mr}^{j}\right) - fit\left(B_{ir}^{j}\right)\right)$ ----------- (14)

ϑ indicates step size. B_{ir}^{j}andB_{mr}^{j} indicates present and mean position of beetles. The search behaviours of the right antenna and the left antenna are respectively expressed as:

$B_{mr}^{j+1} = B_{mr}^{j} + S_{ir}^{j} * d/2$ ------------------- (15)
$B_{ir}^{k+1} = B_{ir}^{k} + S_{ir}^{k} * d/2$ --------------------(16)
$d = \vartheta / cn_2$ --------------------(17)

Position of beetle is denoted by B_{mr}^{j} , distance between two beetlesare represented by ‘d’.

But this often leads to early convergence to overcome this global optima is achieved by fusing chaotic mapping theory while updating the position of the beetle’s using equation

$B_i^{j+1} = B_i^{j} \times (1 + \theta_{i,j} \times Rnd(0, \sigma^2))$---------------------(18)

Chaotic Beetle Swarm Optimization empowered Bi Directional LSTM for Mortality prediction of HSCT children

Input: NL, NHL, OL, DS = Bone marrow transplant Dataset

Output: Mortality prediction (Malignant / non-Malignant)

```
    Ino = Number of input layers
    Hn = Number of hidden layers
    Ono = Number of output layers
    DS = Number of data set instances
```

```
    For i=1 to Hn
    For j=1 to S
            Manipulate the forward pass for the forward hidden layer's activation function $\boldsymbol{h_t^f}$ using equations below
$i_t = \sigma(\hat{W}t_{inp}*[h_{t-1},x_t] + b_{inp})$
$C_t = tanh(\hat{W}t_c*[h_{t-1},x_t] + b_c)$
$frg_t = \sigma(\hat{W}t_{frg}*[h_{t-1},x_t] + b_{frg})$
$out_t = \sigma(\hat{W}t_{out}*[h_{t-1}, x_t] + b_{out})$
$\boldsymbol{h_t^f} = out_t * af\text{-}tanh(C_t)$
    end for
    for j=sq to 1
        Calculating the backward pass for the backward hidden layer's activation function $\boldsymbol{h_t^b}$ using equations
        Cell Outputs
                    $\forall_{co} \in CO, \in_{co} = \sum_{k \in N} wt_{kco} \delta_k (\beta + 1)$
        Output gate:
                    $\delta_k = f'(x_{wt}) \sum_{co \in CO} \in_{co} sq$
        Forget gate:
$frg_t = \sigma(\hat{W}t_{frg}*[h_{t-1},x_t] + b_{frg})$
        Input gate:
$i_t = \sigma(\hat{W}_{inp}*[h_{t-1},x_t] + b_{inp})$
$C_t = tanh(\hat{W}t_c*[h_{t-1},x_t] + b_c)$
        end for
    Update Weights
                Best- Weight (wt) = Call_Beetle-Swarm(Wt-list)
    end for
End
Procedure Beetle-swarm (wt-list)
Initilaize the population of beetle m
Initialize beetle positionpt$_i$arbitrarily
Initialize population velocity S
For  j=  1 to m
        Compute the fitness function fit$_i$
End for
While (itr<itr_max) do
Calculate the weight using equation
                    $\beta = \beta_{max} - \frac{\beta_{max} - \beta_{min}}{J} * j$
Update the distance of beetle and the antenna using equation
                    $d = \vartheta / cn_2$
For each individual beetle obtain left and right antenna position using equation
                    $B_{mr}^{j+1} = B_{mr}^{j} + S_{ir}^{j} * d/2$
                    $B_{ir}^{k+1} = B_{ir}^{k} + S_{ir}^{k} * d/2$
        Compute the increment movement of beetle
                    $\gamma_{ir}^{j+1} = \vartheta^j * S_{ir}^{j} * sign(fit(B_{mr}^{j}) - fit(B_{ir}^{j}))$
        Update the velocity of the beetle using equation
                    $S_{iR}^{J+1} = \beta S_{ir}^{J} + cn_1 rd_1 (U_{ir}^{J} - X_{ir}^{J}) + cn_2 rd_2 (U_{gr}^{J} - X_{gr}^{J})$
        Use beetle position using equation
                    $B_{iR}^{j+1} = B_{iR}^{j} + \lambda S_{iR}^{j} + (1 - \lambda) \varphi_{iR}^{j}$
        End For
        Calculate the fitness function fit$_i$
        Use Chaotic mapping to update the position of beetle
                    $B_i^{j+1} = B_i^{j} \times (1 + \theta_{i,j} \times Rnd(0, \sigma^2))$
        Store the present fitness value of beetle
        itr = itr + 1
End While
```

Output: Select the best values for weight matrix

4. RESULTS AND DISCUSSIONS

This section discusses in detail about the performance of the proposed feature selection based on stochastic method known as Differential Evaluation model and Chaotic beetle Swarm optimization empowered Bi Directional Long Short-TermMemory for the mortality prediction of post transplant HSCT among children. The dataset is collected from UCI machine learning repository which comprised of details about the bone marrow transplant to predict the mortality of paediatric patients and the model is implemented using python software. The effectiveness of the proposed model is compared with the other existing models namely MLP [20], DNN [21] and LSTM [22].

The bone marrow transplant dataset initially comprised of 187 records with 37 attributes of the paediatric patients' details. After performing the clustering of the dataset, the significant attributes which are influential in classification of the survivability of the patients after HSCT is discovered by the proposed stochastic based differential evaluation method and the feature subset is reduced to 11 attributes are listed in table 1.

Table 1: Potential Features Subset Selected by Differential Equation Method

Attribute Name	Description
Survival_time	Time of observation (if alive) or time to event (if dead) in days
Relapse	Relapse of the disease (yes, no)
Extensive_chronic_GvHD	Development of extensive chronic graft versus host disease (yes, no)
Risk_group	Risk group (high, low)
PLT_recovery	Platelet recovery defined as platelet count >50000/mm3 (yes, no)
tx_post_relapse	The second bone marrow transplantation after relapse (yes ,no)
recipient_CMV	Presence of cytomegalovirus infection in the donor of hematopoietic stem cells prior to transplantation (present, absent)
donor_age_below_35	Is donor age less than 35 (yes, no)
ANC_recovery	Neutrophils recovery defined as neutrophils count >0.5 x 10^9/L (yes, no)
stem_cell_source	Source of hematopoietic stem cells (Peripheral blood - 1, Bone marrow - 0)

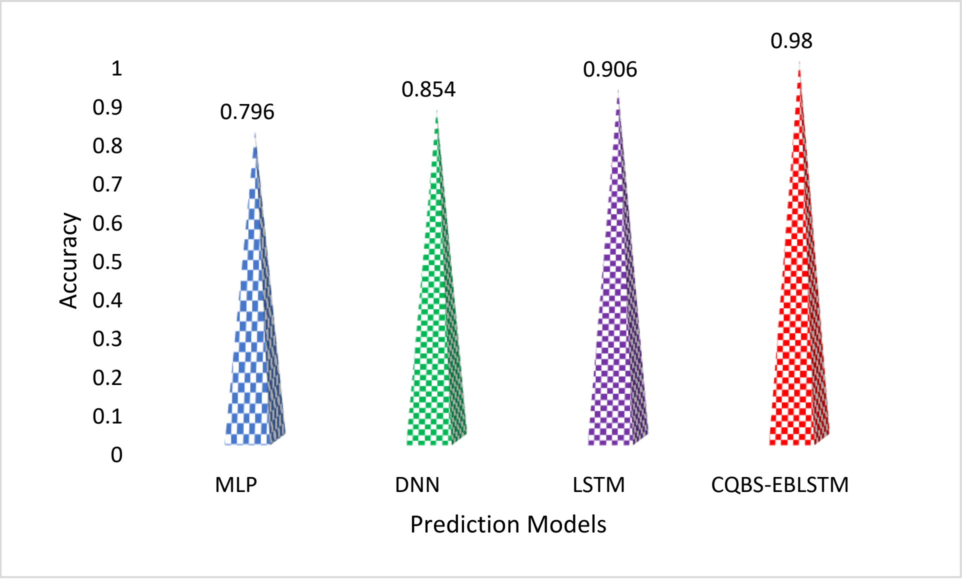

Figure 3: Results based on Accuracy

The figure 3 explores accuracy rate of four different deep learning models to predict the survival of children's after blood transplant. The proposed model produced highest accuracy rate because bidirectional LSTM hyper parameters are finetuned using chaotic Beetle search algorithm. With the sensing power of antenna, the beetle determines the optimal values that has to be assigned to the hyperparameters of BLSTM. The other algorithms due to class imbalance and random assignment of hyper parameter values the accuracy rates are very less.

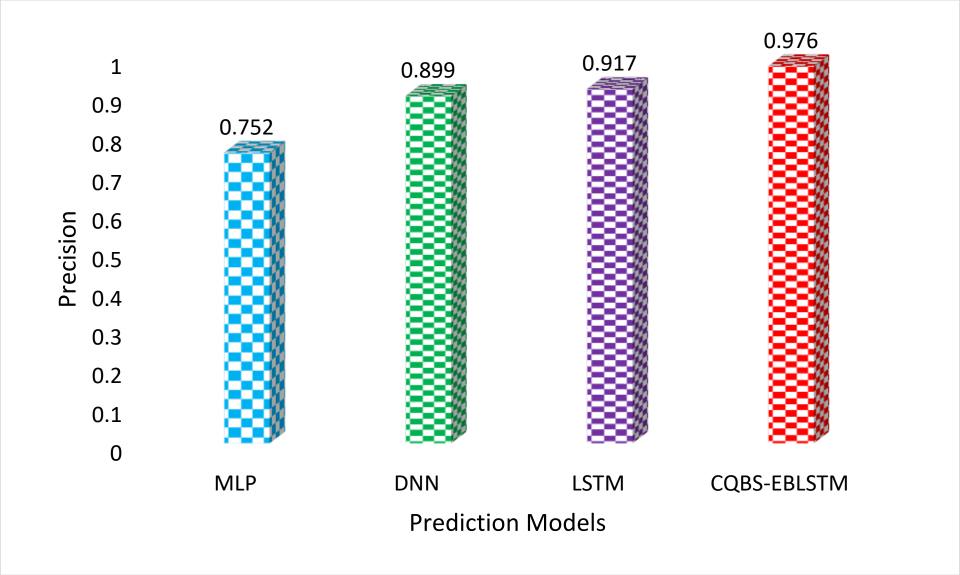

Figure 4: Result based on Precision

The proposed model CBS-EBLSTM optimize the process of classifying survival of children affected with Hematopoietic stem Cell Transplantation by empowering the process of bidirectional long short memory as illustrated in figure 4. The weight DK issue in conventional BLSTM is handled by introducing food searching behaviour of Beetle swam intelligence. While searching for best values to be assigned for hyper parameters in BLSTM, Beetle swam algorithm balances both global and local search by adopting chaos theory. Thus, the precision rate of CBS-EBLSTM is relatively higher while compared with other three classification model

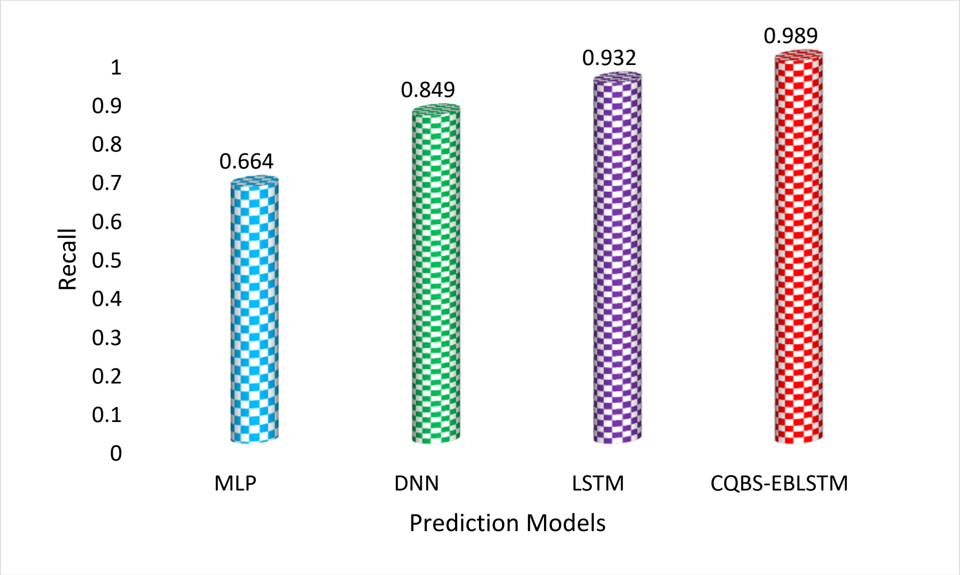

Figure 5: Results based on Recall

The over fitting problem in bone marrow transplantation dataset affects the training accuracy of the conventional deep learning models as explored in figure 5. They use gradient descent method to assign the values to learning rate, bias and weight during the process of training. This leads to decrease detection of survival after Hematopoietic stem Cell Transplantation. Hence, the proposed model CBS-EBLSTM utilizes Beetle search algorithm and understand pattern of dataset by traversing twice to improve the recall rate.

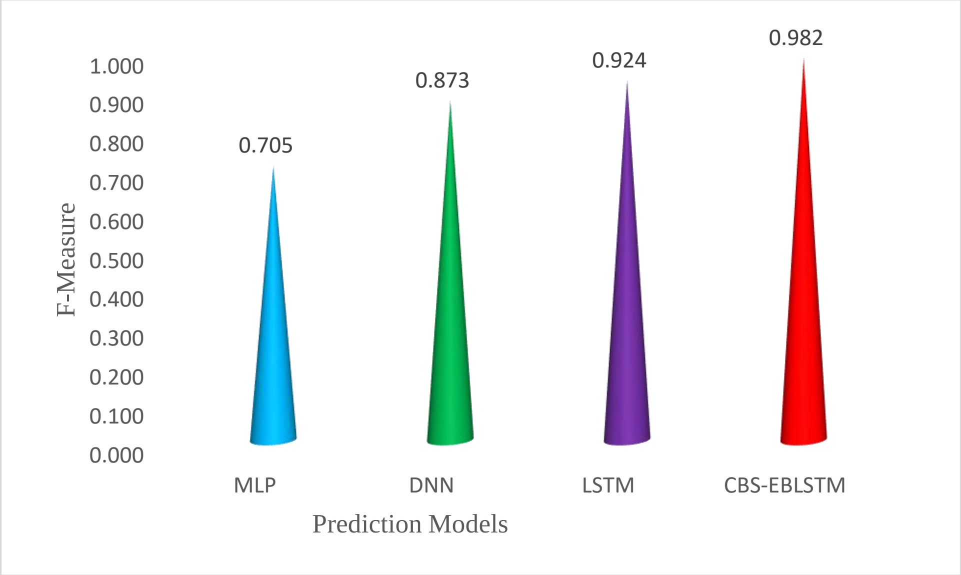

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Figure 6: Results based on F-Measure

The F-Measure explores the impact of precision and recall which evaluates the prominence of four different classification algorithms. The main problem while using deep learning algorithms are limited availability of labelled dataset to understand survival prediction. Thus, the proposed model CQBS-EBLSTM handles Hematopoietic stem Cell Transplantation with metaheuristic searching model and achieve highest F-Measure rate.

5. CONCLUSION

This paper focuses on two major issues that affects the accuracy rate of the mortality prediction of paediatric patients at its early stage due to the inconsistency due to the high irrelevancy and redundancy in bone marrow transplant dataset and indeterminacy due to the class imbalance during training phase. The voluminous feature set is managed through the implementation of a stochastic feature selection technique that identifies the features possessing high relevance and forming a subset with low redundancy for the purpose of classifying the dataset on mortality rate. The Bidirectional LSTM is optimized by fine tuning the hyperparameters such as learning rate, weight and bias value during the training phase, instead of using gradient descent method. The Chaotic Beetle Swarm Optimization algorithm, a metaheuristic model, is applied to enhance the efficacy of BiLSTM. It employs fitness value assessment incorporating hyper parameter value allocation to enhance the precision of predicting survival rates after Hematopoietic Stem Cell Transplantation in paediatric patients.

From the obtained results it is proved that the proposed method CBS-BiLSTM achieves highest accuracy rate compared with other existing deep learning model in prediction of mortality after posttransplant of HSCT paediatric patients.

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