Hybridization of Deep Learning Model with Optimization Algorithm for DNA Based Genetic Disorders Detection and Classification

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Abstract

Genetic diseases are diseases produced by anomalies in the DNA of the person. These abnormalities may be larger-scale chromosomal mutations or irregularities in the particular gene. These diseases significantly influence some body functions and systems and are hereditary or develop automatically. Traditional models such as genetic testing and karyotyping might fail to identify complex or rare modifications, requesting more detailed techniques namely whole-genome sequencing (WGS). In recent decades, regardless of important technological evolution, uncommon genetic diseases continue to cause problems, with a significant portion of patients (50–66%) remaining unidentified according to clinical condition alone. An accurate analysis is important to provide equal support to patients and their relations, despite particular therapeutic intrusions. Presently, machine learning (ML), and in detail the DL subspecialties, have been utilized to determine clinically relevant prediction devices in other medical areas. For mental disorders, ML methods have presented major promise in forecasting either diagnosis or prediction in mental disorders. In this manuscript, we design and develop a Hybrid Deep Learning and Metaheuristic Optimization Algorithm for Detecting Genetic Disorders (HDLMOA-DGD) model. The proposed HDLMOA-DGD algorithm's main goal is to detect and classify genetic disorders using an advanced deep-learning model. At first, the Z-score normalization is employed in the data pre-processing phase for converting an input data into a uniform format. Moreover, the proposed HDLMOA-DGD model implements a hybrid deep learning model of the temporal convolutional network, bi-directional long- and short-term memory network, and Self-Attention mechanism (TCN-BiLSTM-SA) technique for the classification process. At last, the modified gannet optimization algorithm (MGOA)-based hyperparameter selection process is performed to optimize the detection and classification results of the TCN-BiLSTM-SA system. The experimental validation of the HDLMOA-DGD model is verified on a benchmark dataset and the results are determined regarding several measures. The experimental outcome underlined the development of the HDLMOA-DGD model in the genetic disorder detection process.

Keywords: Hybrid Deep Learning; Metaheuristic Optimization Algorithm; Genetic Disorder Detection; Data Pre-processing; DNA

1. Introduction

The genetic disorder is caused by changes in the structure of a gene or genome. As the genome holds the data, the changes in the genome may lead to a change in the function or structure of an organism [1]. The genes are made by deoxyribonucleic acid (DNA), and any changes in the order of DNA lead to genetic illnesses. The genome data comprises significant data and medical care measures that can be employed to investigate the genetic disorders that cause illness. A dedicated part of genomics, bio-informatics intends to the analysis of genomes, abnormalities, their structure, and more [2]. There are some genetic illnesses: mitochondrial genetic inheritance disorders or

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chromosomal disorders, single gene inheritance disorders, and multi-factorial genetic inheritance or complex disorders and they are inspected depending on the structure of DNA [3]. The single-gene type of disorder is induced by changes in a single gene in the DNA. The chromosomal type of disorder is affected while a chromosome or a part of chromosomes is replaced or deleted in the structure of DNA. Intricate disorders are induced by variations in more than one gene existing in the DNA [4].

DNA is a molecule that originated from human cells and around living beings. Almost every cell in the human body comprises the similar DNA [5]. It contains data employed in our day-to-day physiological activities and metabolism that affect the features. The particular DNA code offers the guidelines for every protein to function in a certain way [6]. Every gene in the DNA encrypts a particular protein that can include diverse functions and can perform a vital role in the cell like pathogenesis and cell signalling process of human illnesses. DNA is a perfect substance for nanofabrication of rigid compositions because its application is moderately simple and controlled by base pairing and minimal cost [7]. The identification of DNA sequences performs a significant role in inspecting specific illnesses. The molecular diagnostics-based analysis of genomic sequences provides quantitative and highly sensitive approaches for the recognition of infectious illnesses, genetic variations, and pathogens [8]. Currently, Machine Learning (ML) and Deep Learning (DL) methodologies have been executed effectually in a range of biological conditions in recent years. ML and DL-based models are sufficient to address huge databases with higher levels of noise, imperfection, and/or complexity creating some guesses likelihood distribution and data formation models [9]. Prediction is the primary goal of ML and DL approaches against the inferential method of conventional statistical models [10].

In this manuscript, we design and develop a Hybrid Deep Learning and Metaheuristic Optimization Algorithm for Detecting Genetic Disorders (HDLMOA-DGD) model. The proposed HDLMOA-DGD algorithm's main goal is to detect and classify genetic disorders using an advanced deep-learning model. At first, the Z-score normalization is employed in the data pre-processing phase for converting an input data into a uniform format. Besides, the proposed HDLMOA-DGD model implements a hybrid deep learning model of the temporal convolutional network, bi-directional long- and short-term memory network, and Self-Attention mechanism (TCN-BiLSTM-SA) technique for the classification process. At last, the modified gannet optimization algorithm (MGOA)-based hyperparameter selection process is performed to optimize the detection and classification results of the TCN-BiLSTM-SA system. The experimental validation of the HDLMOA-DGD model is verified on a benchmark dataset and the results are determined regarding several measures.

2. Related Works

In [11], a method for identifying many childhood illnesses utilizing a variety of sophisticated Convolutional Neural Network methodology, and the hybrid structure InceptionResNet-V2 is projected. These methods are skilled in MRI imaging of brain syndromes for attaining higher prediction accuracy. This model employs data visualization methodologies like segmentation and contour-based extraction of feature for eliminating ROI. These methods are enhanced utilizing either RMSprop or ADAM optimizers. In [12], a new facial image-based genetic disease recognition method intended to categorize genetic syndromes is projected. This method also presents an innovative and robust method that improves weight optimizer, data pre-processing, and feature attention inside the structure of DL. In addition, to enhance disorder classification, an end-to-end structure combining TL with a specialized attention mechanism and DCNN is projected.

Li et al. [13] project an explainable DL-based timely Parkinson's illness analytical method, Parkinson's Integrative Diagnostic Gated Network (PIDGN) by combining brain sMRI data and Single Nucleotide Polymorphism (SNP). Primarily, unimodal internal data is removed by utilizing the EmsembleTree dimensionality reduction model, 3D ResNet, and Transformer encoder. Then, the fusion model of gated attention has been employed to discover inter-modal communications. The Grad-CAM and SHAP values are employed to assist the significance of brain regions and SNPs for PD. Saeed et al. [14] develop the Predictive Analytics of Complex Healthcare Systems Utilizing the DL-based Disease Diagnosis Method (PACHS-DLBDDM) methodology. In the initial phase, the projected model employs GF to pre-process the input image. Then, the presented model utilizes the Faster SqueezeNet for making vector features. Additionally, the CNN-LSTM method was leveraged to categorize LCC. To enhance the hyper-parameter values of the Chaotic Tunicate Swarm Algorithm (CTSA) and CNN-LSTM methodologies were applied.

Lakshmanaprakash et al. [15] projected an innovative DL-based model named the Convoluted Recurrent Attention Networks (CRANs) that can classify and identify several illnesses connected to genetic disorders, heart-related or chronic disorders, to maintain lower time complexity with higher efficacy. The hyperparameters of CRAN methods are fine-tuned utilizing the Cray Fish Optimizer model, letting optimum classification learning. Arsalan et al. [16] project dual CNN-based segmentation which integrates multi-scale aspects by spatial data fusion: triplet spatial fusion networks (TSF-Nets) and single spatial fusion network (SSF-Net). TSF-Net leverages triplet spatial data fusion for safeguarding the segmentation of retinal pigment signs without pre-processing. The authors [17]

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inspected DL-based models for automated multi-class classification of brain tumors, and a novel model associating quantum genetic algorithms (QGA) and DL is projected. The dominant feature extraction capability of the pre-trained EfficientNet-B0 was employed and integrated with this QGA, a novel method was introduced. It is focused on advancing the feature selection model.

3. Proposed Methodologies

In this manuscript, we designs and develops an HDLMOA-DGD system. The proposed HDLMOA-DGD algorithm's main goal is to detect and classify genetic disorders using an advanced deep-learning model. To attain that, the proposed HDLMOA-DGD technique contains various stages such as data pre-processing, classification method, and hyperparameter tuning model. Fig. 1 depicts the overall working process of the HDLMOA-DGD method.

A. Stage 1: Data pre-processing

At first, the Z-score normalization is employed in the data pre-processing phase for converting input data into an even format. It also called standardization, which is a statistical model applied for measuring data depending on the standard deviation and mean [18]. In genetic disorder studies, it aids in evaluating levels of gene expression, biomarker variations, or mutation frequencies, across dissimilar samples. By converting values into standard deviations from the mean, this normalization allows researchers to classify outliers and important deviations related to genetic irregularities. This technique is mainly convenient in genome-wide association studies (GWAS) and clustering examines, certifying that data from varied resources remain analogous. It improves pattern detection, which aids in early diagnosis and precision medicine methods.

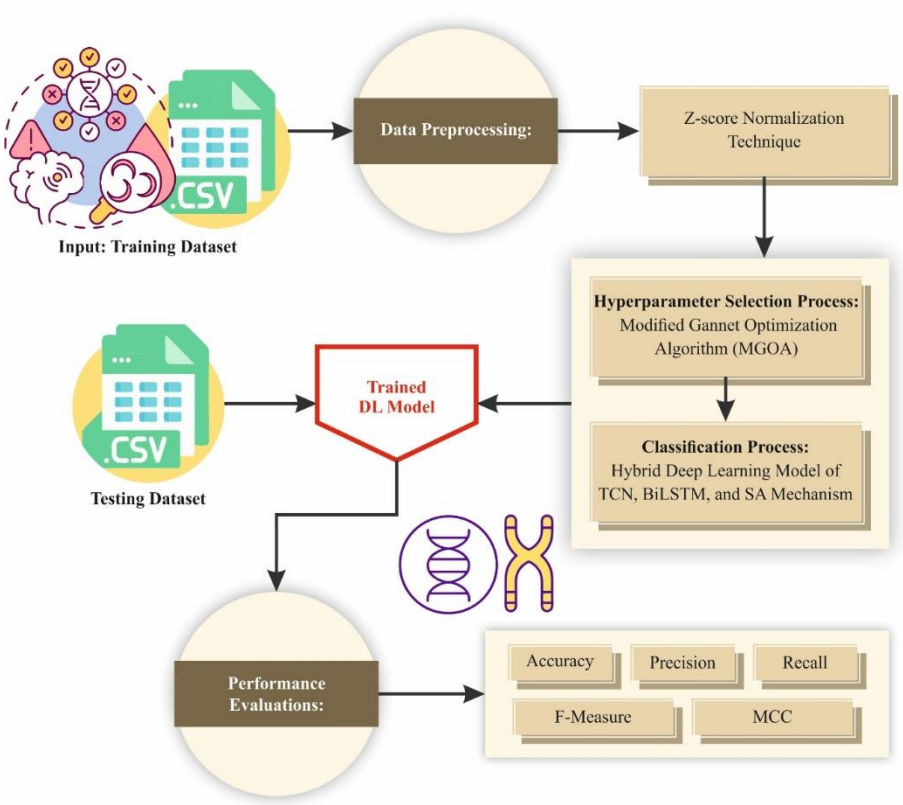

Figure 1. Overall Workflow of HDLMOA-DGD algorithm

B. Stage 2: Classification Model

Besides, the proposed HDLMOA-DGD model implements a hybrid deep learning model of the TCN-BiLSTM-SA technique for the classification process [19]. TCN is a NN method to process text data and time series. In comparison with the conventional recurrent neural network (RNN), it utilizes convolutional layers to take the

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temporal features and making it more beneficial in the classification procedure. Here, x_t refers to time-series data, y_t denote prediction, d signifies the rate of dilation of all convolution layers. It contains dual significant processes.

Causal convolution

It designates the fact that a component in the sequence of output is only associated with the component which leads it. Specifically, based on the input sequence $x_1, x_2, \dots x_{t-1}$ and the present moment input x_t. The computation equation was shown in Eq. (1):

$$P(x) = \prod_{t=1}^{T} p\,(x_t | x_1, x_2, \dots x_{t-1}) \quad (1)$$

Dilation convolution

It is also known as atrous convolution. Expanding the receptive area by an addition of inserted voids to the convolutional kernel is equal to improve the convolutional kernel dimensions. Learn text features for as promising is completed by improving the network layer's depth. Nevertheless, as the layer counts improve, the gradient vanishing problem could rise, thus residual links are presented in the networking architecture to resolve it.

The LSTM method is a different version of RNNs with a basic of gating structures and memory cell components capable of gaining long-range dependences in sequences. Memory cells are generally applied for transmitting and storing data and gating structures controls the forgetting or addition of data. The LSTM technique is enhanced according to Adam's algorithm. The inputs of each 3 gating contain the present input x_t by the hidden layer (HL) h_{t-1} from the preceding stage and the output utilizing the function of sigmoid activation.

Assume i_t, o_t, and f_t characterize the values of an input, output, and forgetting gates, correspondingly, x_t specifies an input value at tth moment, h_{t-1} signifies the last output at the preceding time-step $t-1$, W and b represent the weighted bias and matrix, correspondingly, σ and $tanh$ denote the function of sigmoid and hyperbolic tangent activation. The LSTM networking method can be calculated as shown.

(1) Compute the forgetting gating that controlling the data be neglected, using the subsequent Eq. (2):

$$f_c = \sigma\left(W_{xf} x_c + W_{hf} h_{c-1} + W_{cf} C_{c-1} + b_f\right) \quad (2)$$

(2) Compute the input gating for controlling the sum of data together with memory cells using the succeeding Eq. (3):

$$i_t = \sigma(W_{xi} x_c + W_{hi} h_{c-1} + W_{ci} C_{c-1} + b_i) \quad (3)$$

(3) Compute the output gating by the next Eq. (4):

$$o_t = \sigma(W_{XO} x_t + W_{ho} h_{t-1} + W_{co} C_{t-1} + b_o) \quad (4)$$

(4) Controlling the data that wants to memorized. The mathematical formualtion of candidate memory cell C_t was shown below:

$$C_t' = tanh(W_{xc} x_t + W_{hc} h_{t-1} + b_c) \quad (5)$$

The equation for the state of the cell C_t is as shown:

$$C_t = f_t C_{t-1} + i_t C_t' \quad (6)$$

(5) ht refers to the last output of the method at instant t. The equation is presented in Eq. (7):

$$y_t = o_t tanh(C_t) \quad (7)$$

Temporal data is transferred unidirectional from the front and the back in unidirectional LSTM systems that decline to reflect the contextual temporal data in detail. BiLSTM method can train dual LSTMs in opposing directions simultaneously, for example: they can get the data front, back a word together, and utilize them for prediction, thus normally speaking, bi-directional LSTMs are additionally efficient than unidirectional LSTMs. The Bi-LSTM last output method is a calculation of an outputs of dual unidirectional LSTM systems. The forward and reverse outputs are denoted as $\underline{h_t}$ and $\underline{h_t}$ correspondingly. An output equation of Bi-LSTM method is:

$$h_t = \overrightarrow{h_t} \oplus \overleftarrow{h_t} \quad (8)$$

Either the forward or backward systems of Bi-LSTM utilize a similar amount of neural components in hidden layer (HL).$\{h_0 \to h_1 \to h_2 \to \cdots \to h_n\}$ denote sequences of HLs produced for a forward LSTM, $\{h_n \to \cdots h_2 \to h_1 \to h_0\}$ specify a sequence of HLs made for a reverse LSTM.

The Self-attention mechanism is highly experienced differentiating the significance of sentiment characteristics. Here, the representation vector of all words (tokens) of an input X is worked with the consistent weighting matrix

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to get 3 vectors such aas value (V), the query (Q), and the key (K). To calculate an output to every input, the mathematical steps are demonstrated below.

(1) The K and Q vectors experience dot product computation, for example: multiplying the Q vector of the present token and the K vector of another token through the dot-product significancex amount s of all tokens should be calculated, and the solving expression is shown below:

$$s = QK^T \tag{9}$$

(2) Smoothening by SoftMax and multiplying it by the vector V to obtain an output vector Z, whereas d_k refers to the penalty feature. The output vector was calculated below:

$$Z = softmax\left(\frac{s}{\sqrt{d_k}}V\right) \tag{10}$$

Implementing a similar activity on every token should finally make a novel representation vector for all tokens that has its contextual information. Here, according to the Bi-LSTM module, the feature vector is enhanced by utilizing the self-attention mechanism such that the method gives further attention to particular data and improves the module's capability for removing the significant features. Fig. 2 represents the structure of TCN-BiLSTM-SA model.

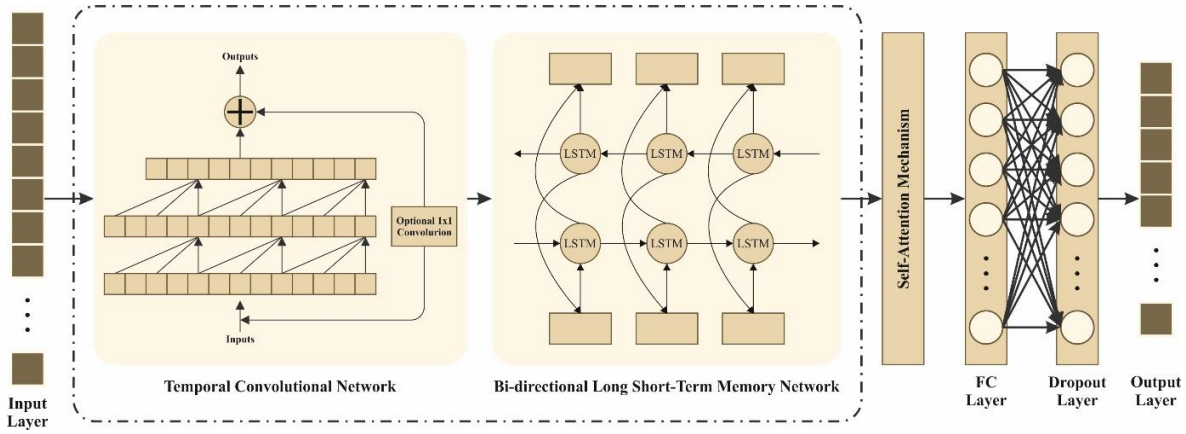

Figure 2. Structure of TCN-BiLSTM-SA technique

C. Stage 3: Hyperparameter Tuning Model

At last, the MGOA-based hyperparameter selection process is performed to optimize the detection and classification results of the TCN-BiLSTM-SA system. GOA is a group-based metaheuristic model that is stimulated by the outstanding predatory ballet of Gannet [20]. The hunting tactic is explained in dual different phases for example: Exploitation and Exploration. During this Exploration stage, the gannet undertakes a search for an appropriate hunting area after a promising place is discovered they consider strategic dives such as V- and U-shaped. As with all optimizer methods, GOA additionally begins with a primary stage, in which a solution matrix of dimensions $[NP, D]$ is arbitrarily made inside the pre-defined searching region utilizing the relation:

$$X = X_{\min} + (X_{max} - X_{\min}) \times rand[NP, D] \tag{11}$$

Exploration Stage: Gannets control their diving patterns according to the location of prey. In general, they follow dual kinds of diving patterns such as (1) a U-shaped dive that is longer and deeper, or (ii) V-shaped dive that is shorter and superficial. These dual diving patterns are modeled numerically as below:

$$a = 2\cos(2\pi r_1) \times t$$

$$b = 2 \times V(2\pi r_2) \times t$$

Whereas, r_1 and r_2 denote randomly generated numbers in the interval $[0,1]$ and $t = 1 - \frac{iter}{itermax}$, $iter$ refers to the present iteration number, $itermax$ stands for maximal iteration counts, and $V(x)$ is specified as:

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$$V(x) = \begin{cases} \frac{-1}{\pi}x + 1 when x \in [0, \pi] \\ \frac{1}{\pi}x - 1 when x \in [\pi, 2\pi] \end{cases} \quad (12)$$

Gannets select the U-shaped or V-shaped dive approach by the similar possibility to capture their target. Thus, the next equation was applied to upgrade the first location of the gannets for example: the first population.

$$X_1 = \begin{cases} X + u_1 + u_2 \; if p \geq 0.5 \\ X + v_1 + v_2 \; if p < 0.5 \end{cases} \quad (13)$$

Whereas, $u1$ (U-dives) and $v1$ (V-dives) denote arbitrary numbers within the range $[-a, +a]$ and $[-b, +b]$ correspondingly, and u_2 and v_2 are computed utilizing the relations:

$$u_2 = A \times (X - X_r)$$

$$v_2 = B \times (X - X_m)$$

Whereas,

$$A = 2 \times (r_3 - 1) \times a$$

$$B = 2 \times (r_4 - 1) \times b$$

X_r denote possible solutions selected at random and X_m refers to the mean location of the complete population and is provided as:

$$X_m = \frac{1}{NP} \sum_{i=1}^{NP} X$$

Exploitation Stage: During this stage, gannets use a number of energy to catch the prey. Now the capturability for example capture ability is computed utilizing the relations:

$$Capturability = \frac{1}{R \times T_2}$$

where, $T_2 = 1 + \frac{iter}{Itermax}$

$$R = \frac{M \times v}{L}$$

$$L = 0.2 + (2 - 0.2) \times r_5$$

Here, M denote the weight of the gannet that can be regarded as 2.5 kg, v stands for the velocity of the gannet which is categorized as 1.5 m/s and r_5 represents randomly generated numbers captured in the interval [0-1]. When the capturability of gannet is lower than the capture ability, then it upgrades its location by capturing a levy fight.

$$X_2 = \begin{cases} iter \times delta \times (X_1 - X_{best}) + X_1, \; if \; Capturability \geq C \\ X_{best1} - (X_1 - X_{best1}) \times P \times iter \; \text{ if } Capturability < C \end{cases} \quad (14)$$

Whereas,

$$delta = Capturability \times |X_1 - X_{best1} \quad |$$

$$P = Levy = 0.01 \times \frac{\mu \times \sigma}{|v|^{\frac{1}{\beta}}}$$

$$\sigma = \left(\frac{\Gamma(1+\beta) \times \sin\left(\frac{\pi\beta}{2}\right)}{\Gamma\left(\frac{1+\beta}{2}\right) \times \beta \times 2^{\left(\frac{\beta-1}{2}\right)}} \right)^{\frac{1}{\beta}}$$

C is considered as 0.2, μ and σ means randomly generated numbers in the interval [0,1] and β is viewed as 1.5. X_{best1} denote top-performing solutions in X_1.

In traditional mass of the velocity (V) and gannet (M) are considered as 2.5 kg and 1.5 m/s correspondingly. These dual parameters plays a significant part in the GOA's exploration stage. Therefore, in this study, these dual features are optimally calculated utilizing the general particle swarm optimizer (PSO) model. The mass range of

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gannets and their speed are considered as [14] kg and [0.5−3] m/s individually. PSO is generally a great model, which contains of dual stages.

Initialization Stage: Here, a primary population for the velocity (V) and mass (M) of gannets are arbitrarily initialized in the interval [14] and [0.53] correspondingly. Older velocity matrix for velocity (M_V^{0ld}) and Mass (V_M^{0ld}) of gannets are generated at random. Capturability of all gannets (for example: every population of X_1 matrix gained in Eq. (13) was computed and the gannets locations are upgraded utilizing the relation specified in Eq. (14).

b. Updation Stage: Here, the velocity and mass of gannets are upgraded with the succeeding relation:

$$M_V^{new} = w \times M_V^{old} + C_1 \times rand_1 \times (P_{bM} - M) + C_2 \times rand_2 \times \left(P_{gM} - M\right)$$

$$y_V^{new} = w \times y_V^{old} + C_1 \times rand_1 \times (P_{bV} - V) + C_2 \times rand_2 \times \left(P_{gV} - V\right)$$

$$M^{new} = M + M_V^{new} \quad (15)$$

$$V^{new} = V + V_V^{new} \quad (16)$$

Here, w reduces linearly from 0.9 to 0.4 with iteration amount, C_1&C_2 are considered as 2.05; $rand_1$ and $rand_2$ denote randomly generated numbers in the interval [0,1], P_b&P_g are called global and local best.

Afterward the update of the gannet's velocity and mass, newly the capture ability is measured and the gannet's locations are upgraded utilizing Eq. (14).

The fitness selection is the substantial feature prompting the MBES model performance. The process of hyperparameter selection includes the solution encrypting technique to assess the efficiency of candidate solutions. Here, the MBES method reflects accuracy as the basic requirement to propose the fitness function. The mathematical model is shown below:

$$Fitness = \max(P) \quad (17)$$

$$P = \frac{TP}{TP + FP} \quad (18)$$

Whereas, FP and TP denote the positive values of false and true.

4. Experimental Analysis

The simulation validation of the HDLMOA-DGD technique is examined under the genetic disorders dataset of genomes [21]. This dataset contains 18962 instances under 3 class labels as displayed in Table 1.

Table 1: Details of dataset

Class Labels	Description	No. of Instances
MIGID	Mitochondrial genetic inheritance disorders	9686
SGID	Single-gene inheritance diseases	7291
MUGID	Multifactorial genetic inheritance disorders	1985
Total Number of Instances		18962

Fig. 3 shows the classifier analysis of the HDLMOA-DGD technique. Figs. 3a-3b display the confusion matrix through precise classification and identification of all different classes under 70%TRAPHA and 30%TESPHA. Fig. 3c exemplifies the PR study, notifying increased outcome through all classes. At last, Fig. 3d signifies the ROC examination, representing proficient outcome through high ROC values for distinct classes.

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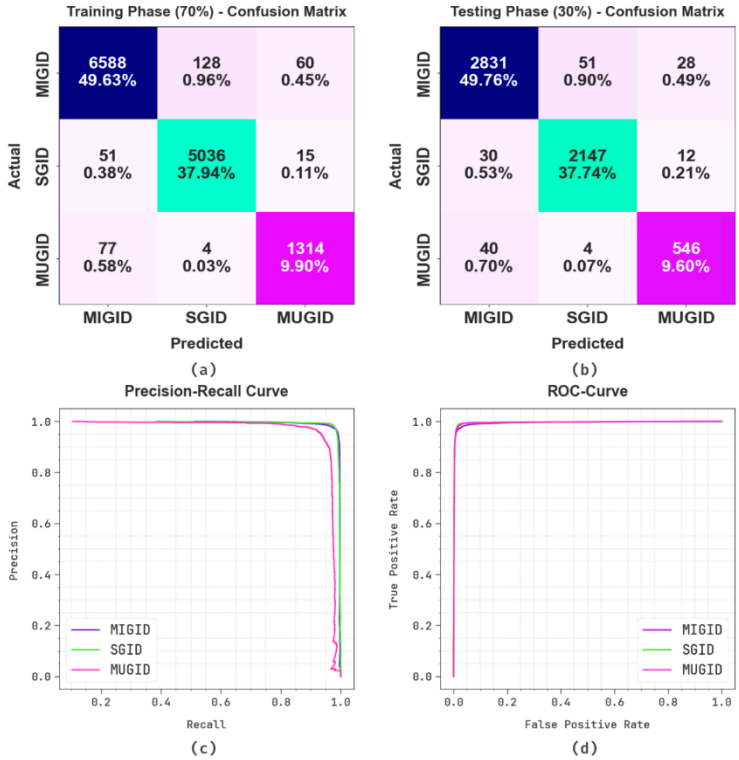

Figure 3. Classifier outcome of (a-b) 70% and 30% confusion matrices and (c-d) curves of PR and ROC

Table 2 and Fig. 4 examines the genetic disorders detection of HDLMOA-DGD technique under 70%TRAPHA and 30%TESPHA. The performances implied that the HDLMOA-DGD approach suitably categorized all the samples. Based on 70%TRAPHA, the HDLMOA-DGD algorithm provides typical $accu_y$ of 98.32%, $prec_n$ of 96.71%, $reca_l$ of 96.71%, $F_{Measure}$of 96.71%, and MCC of 95.28%. In addition, based on 30%TESPHA, the HDLMOA-DGD model delivers typical $accu_y$ of 98.07%, $prec_n$ of 96.09%, $reca_l$ of 95.97%, $F_{Measure}$of 96.03%, and MCC of 94.40%.

Table 2: Genetic disorders detection of HDLMOA-DGD method below 70%TRAPHA and 30%TESPHA

Class Labels	$Accu_y$	$Prec_n$	$Reca_l$	$F_{measure}$	MCC
Training Phase (70%)					
MIGID	97.62	98.09	97.23	97.66	95.24
SGID	98.51	97.45	98.71	98.07	96.86
MUGID	98.82	94.60	94.19	94.40	93.74
Average	98.32	96.71	96.71	96.71	95.28
Testing Phase (30%)					
MIGID	97.38	97.59	97.29	97.44	94.76
SGID	98.29	97.50	98.08	97.79	96.40
MUGID	98.52	93.17	92.54	92.86	92.03
Average	98.07	96.09	95.97	96.03	94.40

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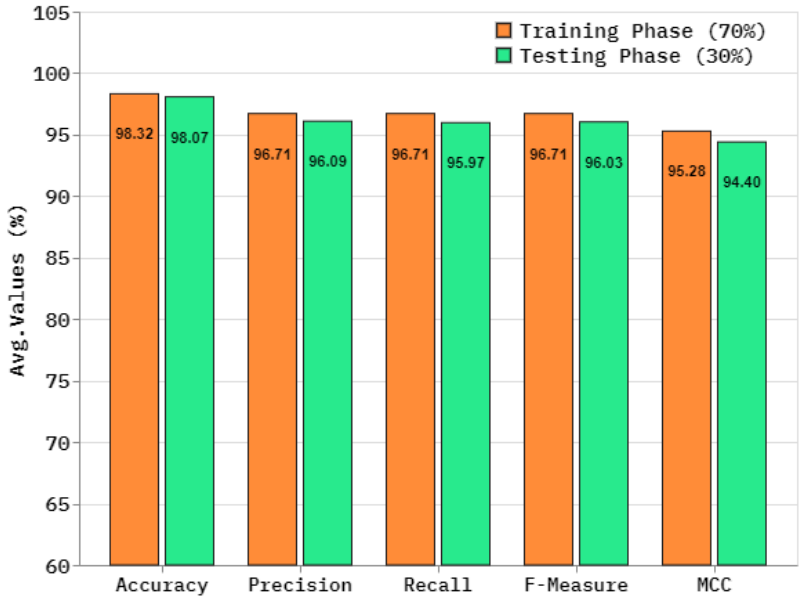

Figure 4. Average of HDLMOA-DGD technique below 70%TRAPHA and 30%TESPHA

In Fig. 5, the training (TRAN) $accu_y$ and validation (VALN) $accu_y$ performances of the HDLMOA-DGD method is showcased. The values of $accu_y$ are computed through a time of 0-50 epochs. The figure underscored that the values of TRAN and VALN $accu_y$ illustrates an increasing propensity notifying the capacity of the HDLMOA-DGD system through maximum outcome through multiple repetitions. In addition, the TRAN and VALN $accu_y$ ruins closer through the epochs, notifying decreased overfitting and expresses higher outcome of the HDLMOA-DGD algorithm, assuring steady calculation on hidden samples.

Figure 5. $Accu_y$ Curve of HDLMOA-DGD method

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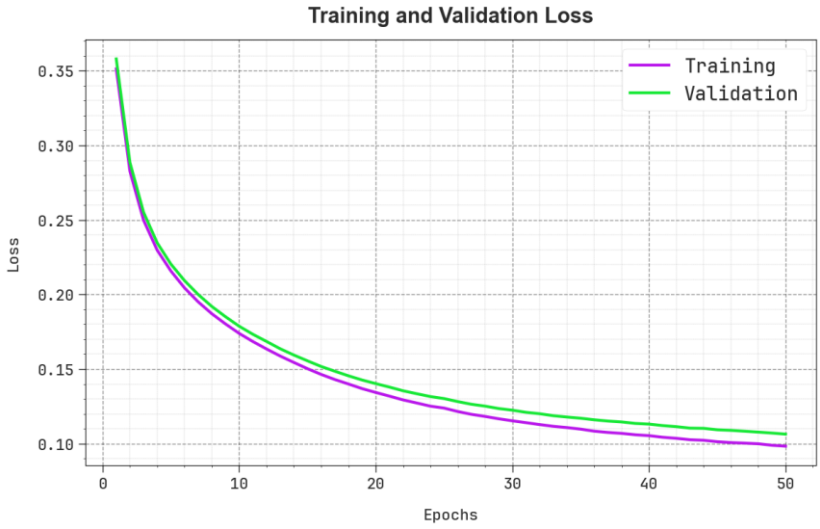

Figure 6. Loss curve of HDLMOA-DGD model

In Fig. 6, the TRAN loss (TRANLOS) and VALN loss (VALNLOS) graph of the HDLMOA-DGD methodology is revealed. The values of loss are computed through a time of 0-50 epochs. It is depicted that the TRANLOS and VALNLOS values represent a diminishing propensity, indicating the competency of the HDLMOA-DGD approach in equalizing an equilibrium between generalization and data fitting. The consecutive dilution in values of loss as well securities the superior outcome of the HDLMOA-DGD system and tune the calculation performances gradually.

The comparative study of HDLMOA-DGD approach through existing techniques are shown in Table 3 and Fig. 7 [22 and 23]. The model outcome reported that the HDLMOA-DGD model outperformed greater solutions. According to $accu_y$, the HDLMOA-DGD system has increased $accu_y$ of 98.32% whereas the CNN-MGP, SVM, RNN, LSTM-RNN, CNN-GRU, DT, and KNN methodologies have minimal $accu_y$ of 91.07 %, 93.06%, 88.07%, 95.17%, 97.29%, 93.07%, and 93.45%, correspondingly. Additionally, according to $prec_n$, the HDLMOA-DGD technique has maximum $prec_n$ of 96.71% whereas the CNN-MGP, SVM, RNN, LSTM-RNN, CNN-GRU, DT, and KNN models have diminish $prec_n$ of 85.07%, 90.07%, 89.06%, 88.05%, 96.15%, 92.25%, and 92.55%, correspondingly. Also, according to $F_{Measure}$, the HDLMOA-DGD technique has superior $F_{Measure}$ of 96.71% whereas the CNN-MGP, SVM, RNN, LSTM-RNN, CNN-GRU, DT, and KNN algorithms have lower $F_{Measure}$ of 87.06%, 92.06%, 68.08%, 87.07%, 95.04%, 89.85%, and 89.07%, respectively.

Table 3: Comparative outcome of HDLMOA-DGD model with existing techniques

Methods	$Accu_y$	$Prec_n$	$Reca_l$	$F_{measure}$
CNN-MGP	91.07	85.07	89.07	87.06
SVM Classifier	93.06	90.07	91.37	92.06
RNN Method	88.07	89.06	81.07	68.08
LSTM-RNN	95.17	88.05	85.56	87.07
CNN-GRU	97.29	96.15	95.51	95.04
Decision Tree	93.07	92.25	93.6	89.85
KNN Algorithm	93.45	92.55	90.69	89.07
HDLMOA-DGD	98.32	96.71	96.71	96.71

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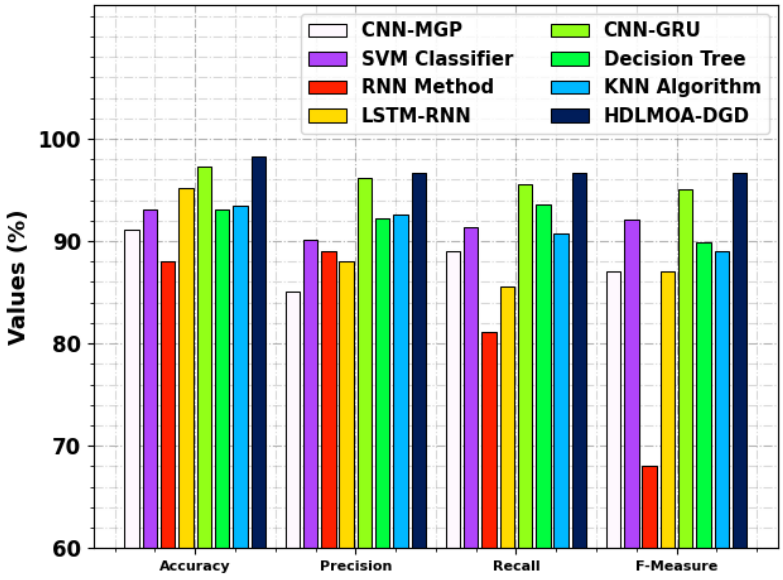

Figure 7. Comparative outcome of HDLMOA-DGD method with existing algorithms

In Table 4 and Fig. 8, the computational outcome (CT) solution of HDLMOA-DGD technique with existing methodologies. On CT, the HDLMOA-DGD system offers minimal CT of 6.35sec while CNN-MGP, SVM, RNN, LSTM-RNN, CNN-GRU, DT, and KNN models gain better CT values of 14.07sec, 8.44sec, 24.01sec, 11.87sec, 11.93sec, 14.41sec, and 19.23sec, correspondingly.

Table 4: CT outcome of HDLMOA-DGD method with existing techniques

Methods	Computational Time (sec)
CNN-MGP	14.07
SVM Classifier	8.44
RNN Method	24.01
LSTM-RNN	11.87
CNN-GRU	11.93
Decision Tree	14.41
KNN Algorithm	19.23
HDLMOA-DGD	6.35

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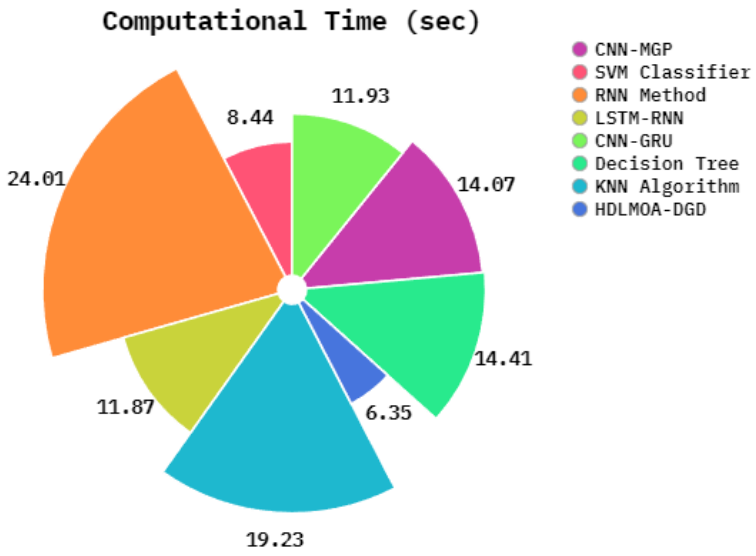

Figure 8. CT outcome of HDLMOA-DGD approach with existing models

5. Conclusion

In this manuscript, we designs and develops an HDLMOA-DGD system. The developed HDLMOA-DGD algorithm's main goal is to detect and classify genetic disorders using an advanced deep-learning model. At first, the Z-score normalization is employed in the data pre-processing phase to renovate input data into an even format. Moreover, the proposed HDLMOA-DGD model implements a hybrid deep learning model of he TCN-BiLSTM-SA technique for the classification process. At last, the MGOA-based hyperparameter selection process is performed to optimize the detection and classification results of the TCN-BiLSTM-SA system. The experimental validation of the HDLMOA-DGD model is verified on a benchmark dataset and the results are determined regarding several measures. The experimental outcome underlined the development of the HDLMOA-DGD model in the genetic disorder detection process.

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References

[1] J. Logeshwaran, N. Adhikari, S. S. Joshi, P. Saxena, and A. Sharma, "The deep DNA machine learning model to classify the tumor genome of patients with tumor sequencing," *Int. J. Health Sci.*, vol. 6, no. S5, pp. 9364-9375, 2022.

[2] N. Wan, D. Weinberg, T. Y. Liu, K. Niehaus, E. A. Ariazi, D. Delubac, A. Kannan, B. White, M. Bailey, M. Bertin, and N. Boley, "Machine learning enables detection of early-stage colorectal cancer by whole-genome sequencing of plasma cell-free DNA," *BMC Cancer*, vol. 19, pp. 1-10, 2019.

[3] L. Koumakis, "Deep learning models in genomics; are we there yet?," *Comput. Struct. Biotechnol. J.*, vol. 18, pp. 1466-1473, 2020.

[4] C. Park, J. Ha, and S. Park, "Prediction of Alzheimer's disease based on deep neural network by integrating gene expression and DNA methylation dataset," *Expert Syst. Appl.*, vol. 140, p. 112873, 2020.

[5] P. Luo, Y. Li, L. P. Tian, and F. X. Wu, "Enhancing the prediction of disease–gene associations with multimodal deep learning," *Bioinformatics*, vol. 35, no. 19, pp. 3735-3742, 2019.

[6] N. Liang, B. Li, Z. Jia, C. Wang, P. Wu, T. Zheng, Y. Wang, F. Qiu, Y. Wu, J. Su, and J. Xu, "Ultrasensitive detection of circulating tumour DNA via deep methylation sequencing aided by machine learning," *Nat. Biomed. Eng.*, vol. 5, no. 6, pp. 586-599, 2021.

DOI: https://doi.org/10.54216/FPA.200107
Received: December 19, 2024 Revised: March 05, 2025 Accepted: April 03, 2025

[7] Z. Liu, L. Zhu, R. Roberts, and W. Tong, "Toward clinical implementation of next-generation sequencing-based genetic testing in rare diseases: where are we?," *Trends Genet.*, vol. 35, no. 11, pp. 852-867, 2019.

[8] X. Guo, M. A. Khalid, I. Domingos, A. L. Michala, M. Adriko, C. Rowel, D. Ajambo, A. Garrett, S. Kar, X. Yan, and J. Reboud, "Smartphone-based DNA diagnostics for malaria detection using deep learning for local decision support and blockchain technology for security," *Nat. Electron.*, vol. 4, no. 8, pp. 615-624, 2021.

[9] N. Mahendran and D. R. V. PM, "A deep learning framework with an embedded-based feature selection approach for the early detection of the Alzheimer's disease," *Comput. Biol. Med.*, vol. 141, p. 105056, 2022.

[10] M. Alosta and A. Souri, "Design of effective lossless data compression technique for multiple genomic DNA sequences," *Fusion Pract. Appl.*, vol. 6, pp. 17-25, 2021.

[11] Y. Kumar, P. Bhardwaj, S. Shrivastav, and K. Mehta, "Predicting Paediatric Brain Disorders from MRI Images Using Advanced Deep Learning Techniques," *Neuroinformatics*, vol. 23, no. 2, p. 9, 2025.

[12] T. U. Islam and T. A. Shaikh, "A lightweight attention-based deep learning facial recognition system for multiple genetic syndromes," *Int. J. Data Sci. Anal.*, pp. 1-19, 2024.

[13] W. Li, Q. Rao, S. Dong, M. Zhu, Z. Yang, X. Huang, and G. Liu, "PIDGN: An explainable multimodal deep learning framework for early prediction of Parkinson's disease," *J. Neurosci. Methods*, p. 110363, 2025.

[14] M. K. Saeed, A. Al Mazroa, B. M. Alghamdi, F. S. Alallah, A. Alshareef, and A. Mahmud, "Predictive analytics of complex healthcare systems using deep learning based disease diagnosis model," *Sci. Rep.*, vol. 14, no. 1, p. 27497, 2024.

[15] S. Lakshmanaprakash, A. Abirami, R. Madanachitran, R. Mekala, and V. H. Vaishali, "DON: Deep Optimized Network model based on Coot and Convoluted Recurrent learning algorithms for healthcare monitoring in IoMT systems," *Measurement*, vol. 242, p. 116226, 2025.

[16] M. Arsalan, A. Haider, C. Park, J. S. Hong, and K. R. Park, "Multiscale triplet spatial information fusion-based deep learning method to detect retinal pigment signs with fundus images," *Eng. Appl. Artif. Intell.*, vol. 133, p. 108353, 2024.

[17] K. Gencer and G. Gencer, "Hybrid deep learning approach for brain tumor classification using EfficientNetB0 and novel quantum genetic algorithm," *PeerJ Comput. Sci.*, vol. 11, p. e2556, 2025.

[18] M. R. Lincoln, N. Connally, P. P. Axisa, C. Gasperi, M. Mitrovic, D. van Heel, C. Wijmenga, S. Withoff, I. H. Jonkers, and L. Padyukov, "Genetic mapping across autoimmune diseases reveals shared associations and mechanisms," *Nat. Genet.*, vol. 56, no. 5, pp. 838-845, 2024.

[19] D. Chi, T. Huang, Z. Jia, and S. Zhang, "Research on Sentiment Analysis of Hotel Review Text Based on BERT-TCN-BiLSTM-Attention Model," *Array*, p. 100378, 2025.

[20] B. Begum, N. K. Jena, B. K. Sahu, M. Bajaj, V. Blazek, and L. Prokop, "Frequency stability improvement in EV-integrated power systems using optimized fuzzy-sliding mode control and real-time validation," *Sci. Rep.*, vol. 15, no. 1, p. 5782, 2025.

[21] Kaggle, "Predict the genetic disorders dataset of genomes," [Online]. Available: https://www.kaggle.com/datasets/aibuzz/predict-the-genetic-disorders-datasetof-genomes.

[22] T. Alshammari, "Applying machine learning algorithms for the classification of sleep disorders," *IEEE Access*, 2024.

[23] O. R. Shahin, F. M. Alanazi, M. K. ElDeeb, F. A. Kuriri, F. A. Kwa, F. O. Alenazy, and T. M. Kamal, "Construction of Saudi computational gene models: Applications in healthcare of prevalent genetic disorders," *Alexandria Eng. J.*, vol. 117, pp. 13-26, 2025.

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