Integer Guided Linear Hopper Strategy in an LSTM Ensemble Framework for Prognosis Prediction

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Abstract – Accurate and timely prognosis is essential for effective patient management and improved healthcare outcomes. This study introduces a novel ensemble framework that integrates Convolutional Neural Networks (CNN) and Long Short-Term Memory (LSTM) networks, optimized using the Integer-Based Linear Hopper Optimization Algorithm (ILHOA). The model leverages CNN for spatial feature extraction and LSTM for capturing temporal patterns in clinical and laboratory data. ILHOA enhances model efficiency and robustness by selecting the most relevant features and eliminating redundancy. The proposed system includes data preprocessing, ILHOA-based feature selection, and a hybrid CNN-LSTM structure. Predictions from both deep learning models are combined through an ensemble process to boost generalization and reduce overfitting. The model's performance is evaluated using key metrics including accuracy, precision, recall, F1-score, and AUC-ROC. Experimental results demonstrate the superiority of the ILHOA-optimized CNN-LSTM model over traditional machine learning and standalone deep learning approaches, offering high classification accuracy and reduced computational complexity. The hybrid architecture also improves interpretability, making it suitable for real-time clinical decision-making. Future work will focus on integrating attention mechanisms and validating the model with real-world patient datasets to enhance generalizability and expand its applicability across broader healthcare diagnostics.

Keywords – Prognosis, CNN-LSTM Ensemble, Hopper Optimization, Overfitting, Feature Selection, Deep Learning, Clinical Decision Making.

I. INTRODUCTION

The COVID-19 pandemic has caused a major disturbance in global healthcare, and rapid and precise prognostic models are needed to evaluate disease severity and predict patient outcomes. Conventional diagnostic techniques like RT-PCR and radiological imaging have been helpful but are usually limited by high costs [1], low sensitivity, and lengthy procedures, so AI-based methods are crucial for quicker and more accurate COVID-19 prognosis. Of the numerous machine learning and deep learning algorithms, Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks have proven to be highly capable of processing structured and sequential medical information [2]. While CNNs are excellent at extracting spatial information from images and structured clinical data, LSTMs are extremely adept at learning temporal relationships in sequential health records, rendering their union best suited for advanced medical prediction problems. The presence of irrelevant and redundant features is one of the major problems confronting deep-learning models for COVID-19 prediction: Therefore, these features increase computation complexity and decrease generalization ability [3]. Thus, an effective feature selection mechanism is necessary to remove dirty characteristics while retaining only representative patterns that increase the classification accuracy and minimize model overfit. In overcoming the above problems, this study posits the use of an optimized ensemble CNN-LSTM model enhanced by a new feature selection and optimization algorithm: the Integer-Based Linear Hopper Optimization Algorithm (ILHOA)- based on a new concept of integer-based hopping movement. ILHOA is meant to iteratively refine feature subsets based on an adaptive hopping strategy that will attack noise and other non-relevant information while preserving the more significant attributes. On the contrary, conventional optimization algorithms such as PSO and GA get stuck in local optima with high-dimensional feature spaces; ILHOA is based on linear structured-hopping mechanics to strike a balance between exploration and exploitation during effective feature selection and enhanced model generalization [4].

A proper feature extraction, feature selection, and spatio-temporal pattern identification are carried out by coupling ILHOA with the CNN-LSTM architecture for reliable COVID-19 prediction. The importance of this hybrid method is that it can tap both spatial and sequential patterns in patient data while, at the same time, optimizing feature subsets for optimal predictive performance. COVID-19 prediction involves processing heterogeneous patient data, such as radiological images, clinical laboratory results, and time-series vital signs. It have found extensive usage in medical diagnosis, their restricted capability to discover deep hierarchical patterns in complex data lowers their efficacy in processing high-dimensional health records. On the contrary, CNNs automatically discover sophisticated spatial correlations in structured health data, thereby proving to be highly efficient in feature extraction. At the same time, LSTMs excel in sequential data handling by being capable of storing long-term dependencies and, as such, allowing disease trend forecasting accurately [5]. The synergistic approach here involves applying both CNN and LSTM within an ensemble structure where CNN learns spatial relevant features while LSTM captures the time-varying patient states, thereby generating improved robust and precise forecasts [6,7]. The inclusion of ILHOA makes it possible for the most pertinent features to be contributing to the decision-making process, minimizing computational overhead but still achieving high predictive accuracy. ILHOA works in two major phases: first, an initial feature selection phase ranks attributes according to their contribution to classification, and second, an optimization phase dynamically optimizes the chosen features by iterative hopping moves. This organized methodology enables ILHOA to converge more quickly and perform better feature selection than conventional optimization methods. The new CNN-LSTM-ILHOA model is tested on benchmark COVID-19 datasets, where its performance is compared with traditional deep learning and machine learning models on the basis of important parameters like accuracy, sensitivity, specificity, and computational cost.

The experimental results show that the hybrid model performs better than baseline models in predicting COVID-19 severity, highlighting its potential to enhance diagnostic accuracy and alleviate computational intensity. The main contributions of this work are the proposal of a new CNN-LSTM ensemble architecture optimized by ILHOA for COVID-19 prediction, a sophisticated feature selection mechanism that removes redundant features to improve classification performance, a comparative study of the proposed model with conventional deep learning models, and a test of computational efficiency and generalization capability of ILHOA in healthcare contexts. This work gives a new approach in AI-assisted medical diagnostics by combining deep learning with wise optimization techniques for improving predictive efficiency. The major contributions are,

- Combines CNN for spatial feature extraction and LSTM for temporal dependencies, improving COVID-19 prognosis accuracy.
- Enhances feature selection by removing irrelevant data, reducing computational cost, and boosting classification performance.
- ILHOA enhances model efficiency by optimizing feature subsets, reducing computational complexity, and improving classification performance compared to conventional optimization techniques such as PSO and GA.

The rest of this paper is structured as follows: the following section is a review of current deep learning and optimization-driven approaches to COVID-19 prognosis, followed by an in-depth methodology outlining the CNN-LSTM ensemble model and ILHOA-based feature choice. Then follows the experimental design, data sets, and evaluation criteria, after which a results discussion is provided comparing the approach with baseline models. Lastly, the paper concludes with the most important findings, limitations, and possible future directions for research in order to further improve AI-based COVID-19 prognosis with hybrid optimization methods.

II. RELATED WORKS

Machine learning (ML) has been very important in COVID-19 prediction of diagnosis, prognosis, and risk of death based on patient symptoms, clinical data, and imaging. Machine learning methods have been investigated across numerous studies for improving decision-making in healthcare. Zoabi et al. (2021) created a machine learning model for the prediction of COVID-19 diagnosis only from patient self-reported symptoms. The authors used logistic regression and other classification methods, with very high accuracy in the detection of infected cases. The model described by them demonstrated that symptom-based prediction could be an efficient preliminary screening method that lessens the dependency on laboratory testing and allows for early intervention. The research also advocated for ML promise within remote healthcare settings to alleviate the constraints of COVID-19 detection modalities that are non-invasive and low-cost and can be scaled. It further shows there is need to incorporate such an application within a mobile app or a telemedicine platform for improved accessibility [8].

In 2021, Monjur et al. offered a mobile cloud application for prediction and prognosis of COVID-19 real-time mortality risk estimation [9]. The study integrated cloud computing with ML models to assess symptoms in patients and forecast possible disease progression. Here, LRs, SVMs and DLs models have been used to calculate mortality risk based on a number of clinical features such as oxygen saturation, respiratory rates as well as underlying comorbidities. The research's core value is that it brings friendly mobile applications along with ML. In this invention, the importance of mobile health (mHealth) in future management of pandemics is greatly proven. Also, the research covered oxygen saturation, respiratory rates, and other comorbidities-as well as related issues on data privacy and security-which brought forth encryption and adherence to healthcare data standards. Further studies can also improve predictive ability further by including real-time sensor data for continuous monitoring of patients at much higher risk.

Survival Prediction of Critical COVID-19 Patients Utilizing Biometric Markers Priority-Based Employment of a Machine Learning Algorithm by Yan et al. (2020), which involves the chief biomarkers like lactic acid, lymphocyte count, and C-reactive protein, prediction based on them. As a result of analysis of a hospital's substantially large population, crucial physiological markers were found to have a strong positive correlation to increased mortality risk. Even the researchers made use of a number of ML algorithms like gradient boosting decision trees (GBDTs) to offer a robust and interpretable prediction model. Their methodology evolved a framework by virtue of which risk stratification could be carried out, enabling clinicians to identify high-risk patients and effective allocation of medical resources. Clinical decision-making implications came from the study since the results demonstrated how such data-driven models could either supplement or supplant traditional diagnostic avenues. Also emphasized was the role of explainable AI in health care, especially as regards building trust and usability. From now onwards, deeper advances can be realized with the application of learning techniques such as recurrent neural networks (RNN) that introduce temporal patterns of patient biometric data to assess risk dynamically [10].

Karthikeyan et al. (2021) reported the development of a machine-learning clinical decision support system (CDSS) for predicting early death in COVID-19 patients. Utilization of a hospital patient dataset and supervised learning paradigms such as random forest and neural network for assessing the patient's chances of survival were discussed in the research. Feature selection was emphasized by the authors in the study and they concretely identified the likes of D-dimer levels, blood oxygen saturation, and inflammatory markers as significant factors in predicting severity. Their CDSS aimed to assist physicians by providing real-time mortuary risk evaluation so that timely intervention could be performed. The contribution of this research was to emphasize the integration of ML models into hospital workflows to improve patient outcomes. It also discussed the problem of imbalanced datasets regarding predictive accuracy enhancement through oversampling methods [11]. Future directions can possibly include ensemble hybrid approaches that combine deep learning with conventional machine-learning algorithms for enhanced predictive robustness and generalizability across heterogeneous patient populations.

According to Abbaspour Onari and others, (2021) a machine learning framework tool has been developed for predicting severity levels of COVID-19 in patients for effective triage and allocation of resources in hospitals. The study classified patients as mild, moderate, and severe risk patients based on machine learning classification algorithms such as decision trees, SVMs, and XGBoost. Demographic information, comorbidities, and laboratory findings were the primary features. The authors emphasized the efficiency of ML models in detecting high-risk cases that could need intensive care, thereby maximizing resource utilization during peak pandemic seasons. Their research also investigated model interpretability, employing SHAP (Shapley Additive Explanations) values to describe feature importance. The study showed the potential of AI-driven risk assessment tools in emergency response planning. Future horizons could involve the incorporation of real-time patient monitoring data via IoT devices as well as federated learning methods for enhancing model adaptability while maintaining data privacy among various healthcare institutions [12]. The research gaps identified from the related work section is,

- Most current research is based on static COVID-19 prediction and prognosis datasets. There is no integration of real-time patient monitoring through IoT-based wearable devices or hospital electronic health record systems. Future research needs to investigate dynamic data streams for ongoing risk assessment and enhanced early warning systems.
- Numerous models are learnt from region-specific data, causing the risk of biases in prediction while being used across different populations. Cross-population validation and federated learning methods should be ensured to establish wider usage and justice in ML-based healthcare decision support.
- Though ML models present good predictive power, their transparency is a hindrance, constraining trust from healthcare professionals. Further work on explainable AI (XAI) methods must be done to give transparent decision-making, such that these models are acceptable in real-world clinical practice.

III. PROPOSED METHODOLOGY USING ILHOA ENSEMBLE MODEL

In addition to the brain and lungs, multiple other organs are impacted in people with the coronavirus COVID-19. A person with COVID-19 who has severely harmed [13] white matter and Lactate levels appear to have increased on Magnetic Resonance. Spectroscopy is an additional indicator of oxygen deprivation-related brain injury [14-18]. In order to detect the transmission of transmissible diseases and provide suitable medical treatment, many techniques have been established. The suggested technique developed an Integrated Linear Factor depending Hoppers Optimisation Algorithms with Ensemble Learning (ILHOA with EL) for efficient Covid-19 forecasting. The suggested system's flow diagram is displayed in **Fig 1**.

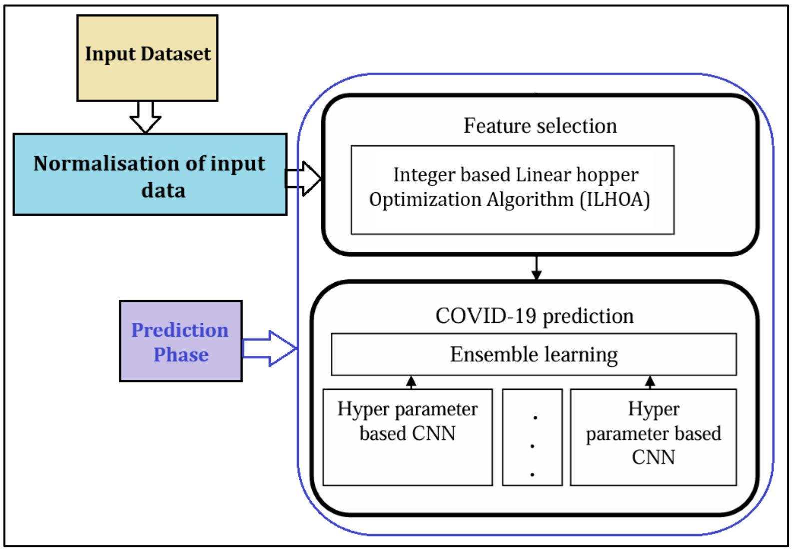

Fig 1. The Suggested Model for Flowchart

Input Dataset

where it is collected ID, state, region, latitude, longitude, date, reported instances, fatalities, temperature, fog, and other data are all included in this database. A NOAA GSOD data set is the source of weather data. The most recent data will be regularly added to the NOAA GSOD dataset

Data Normalized with Min-Max Normalized

The COVID-19 dataset is normalized in this way with the aid of min-max normalization. One of the most widely used methods for normalizing data is min-max normalization. The dataset's values are normalized [19] within a predetermined range, and each piece of data is altered using the formula below.

$$v' = \frac{v-\min(A)}{\max(A)-\min(A)}(\mathrm{new\_max}\ (A) - \mathrm{new\_min}\ (A)) + n \tag{1}$$

Where a refers to the Attribute value, $\mathrm{Min}(A)$, $\mathrm{Max}(A)$ - the least and highest absolute value of A respectively and the v' - New value for each data entry, v - Old value for each data entry, New_min(A), new_min(A) stands for the highest and least value in the range respectively.

Feature Selection using Integer Based Linear Hopper Optimization Algorithm (ILHOA)

The Improved Linear Factors based Hoppers Optimization Algorithm is used to choose features. The Hoppers optimization algorithm simulates Hoppers behavior. The Hoppers swarm typically travels a great distance in search of a new habitat that is stocked with food. In this case, Hoppers communicate with one another via controlling one other within a swarm. The Hoppers' path is influenced by the force of the wind and gravity outside the swarm. Another important determinant is food intention [20].

The search process is effectively divided into two parts by metaheuristic algorithms, which are called exploration and exploitation. The Hoppers are motivated to move swiftly in search of the ideal location during the exploration stage. Hoppers travel locally in search of a suitable target site during exploitation. It serves as a problem abstract for optimization. The hopper swarm is derived from the swarm composed of search agents.

The dataset's features are regarded as the input in this proposed technological work. This assigns a place and fitness value to every feature in a dataset. Position shows the point in relation to a likely feature set. The fitness function is the classification accuracy.

$$\text{Fitness function} = \text{Max (Accuracy)} \tag{2}$$

$$X_i = S_i + G_i + A_i \tag{3}$$

Where, $X_i$indicates the ith feature position, $S_i$refers to the social interaction strength, $G_i$refers to the ith feature manipulating factor of significance force, and$A_i$specifies the winds impact factor. $S_i$is expressed as:

$$S_i = \sum_{j=1,j\neq i}^{N} s(d_{ij})\hat{d}_{ij} \tag{4}$$

$d_{ij} = \left|x_j - x_i\right|, \hat{d}_{ij}$indicates the unit vector from ith tojth attribute, given as $\hat{d}_{ij} = \frac{|x_j - x_i|}{d_{ij}}$ refers to a function depicting the effect of social relationship in the feature and is defined as:

$$\mathrm{s(r)} = \mathrm{f}e^{\frac{-r}{l}} - e^{-r} \tag{5}$$

Expression 3 for numerical module optimization must incorporate tiny change factors when dealing with numerical optimization problems. $G_i$and A_i specify the food target parameter in place of the external control. As a result, the phrase is changed to:

$$x_i = \mathrm{c}\left(\sum_{j=1, j\neq i}^{N} c\frac{u-l}{2} s\left(\left|x_j - x_i\right|\right)\frac{x_j - x_i}{d_{ij}}\right) + \hat{T}_d \tag{6}$$

$\hat{T}_d$denotes the food target's location, which is the best possible place for all search characteristics to always discover in the numerical module. Additionally, c stands for the comfort zone parameter that was altered to balance the exploration and exploitation processes, as seen below:

$$\mathrm{c} = c_{\max} - \mathrm{iter}\frac{c_{\max} - c_{\min}}{\mathrm{Max}_{\ \mathrm{iter}}} \tag{7}$$

The current iteration $c_{\max}$and $c_{\min}$ the maximum number of iterations are specified by the iter, respectively. Max_{iter} and make use of the maximum and minimum values of c to refer to the maximum iterations to get the best answer, equation (6) must be run once more; it stops when the requirement is satisfied. Typically, the evolution process ends when the predetermined maximum number of iterations is reached.

Integer Based Linear Hopper Optimization Algorithm

Due to the lack of random elements, the traditional Hoppers Optimisation Algorithm (HOA) shows minor differences. To lessen the attraction and distaste between Hoppers, use parameter c, which is enclosed in parenthesis. There won't be enough convergence in the GOA algorithm's first step if the parameter drops too quickly. To address these problems, the Improved Linear Factor (ILF) is used to update the comfort zone value.

$$\mathrm{c} = (c_{\min} - c_{\max})\left(\frac{T_{\max} - t}{T_{\max}}\right) + c_{\max} \tag{8}$$

Where,$\mathbf{c}_{\max}$ − max value of c, $\mathrm{c}_{\min}$ − min value of c.

Strategy of the ILHOA technique

The Integer-Based Linear Hopper Optimization (ILHO) algorithm is a metaheuristic feature selection technique designed to identify the most relevant features from a dataset. The feature position set is initialized with corresponding control parameters such as maximum and minimum hoppingized coefficients (cmaxandcmin)and the limits of the number of implementations. The algorithm calculates classification accuracy for all features, with the best search agent being selected toward the target solution.

During the iterative search, ILHO dynamically updates the hopping coefficient according to a predefined equation. Each search agent is capable of altering its position within a normalized range [1,4] ensuring an adequate degree of search space diversity. The feature positions are modified through an update equation that considers their relative positions and movement characteristics [21,22]. Any updated position that infringes the specified boundary is immediately corrected to keep it feasible.

The algorithm recursively updates the best solution by evaluating the new search agents against the current target. In case a better feature subset is found, the target will be updated. This process repeats until the iteration limit is reached, ultimately returning an optimal feature subset that enhances classification performance. ILHO's structured approach ensures efficient exploration and exploitation, making it effective for high-dimensional datasets in feature selection tasks and the flow is given **Fig 2**.

Classification using Ensemble Learning (EL)

Ensemble Learning (EL), which includes several HCNNs for COVID 19 forecasting, is presented in this suggested technical study. It uses multiple hidden layers that perform subsampling and convolution to extract features [23] with input ranging from low to high levels. Convolution, subsampling or pooling, and full linked layers are the three basic layers of CNN, as shown in **Fig 3.**

Algorithm 1: Integer-Based Linear Hopper Optimization (ILHO) for Feature Selection

```
Input: No. of attributes in a database
Output: Optimal feature subset

1. Originof features $X_i$ where i=1, 2…, n.
2. Set control parameters: $c_{max}$ and $c_{min}$, and the maximum number of iterations.
3. Classifier accuracy for all feature subsets.
4. Identify the Target.
5. While (iteration l< Maximum iterations) do:
    1. Update the hopping coefficient using Equation (8).
    2. For every search agent:
        1. Standardize the distance among hoppers in the range [1,4].
        2. Modify the current feature position using Equation (6).
        3. Ensure the updated search agent remains within valid feature
           boundaries with proposed LSTM.
    3. End for
    4. Update the target if a better solution is found.
    5. Increment iteration count: l=l+1.
6. End while
7. Return the optimal feature subset.
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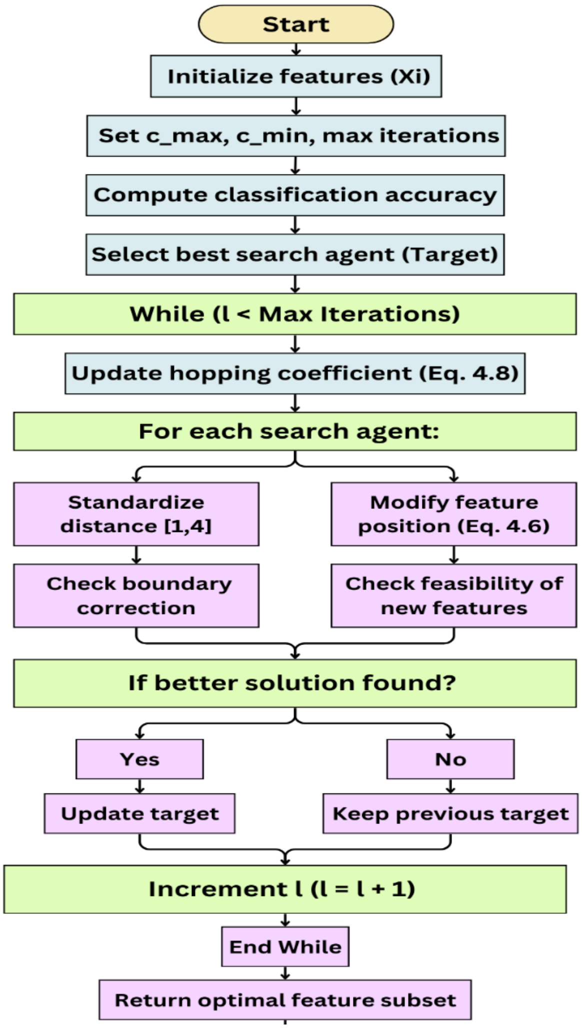


Fig 2. Flowchart of ILHOA Procedure

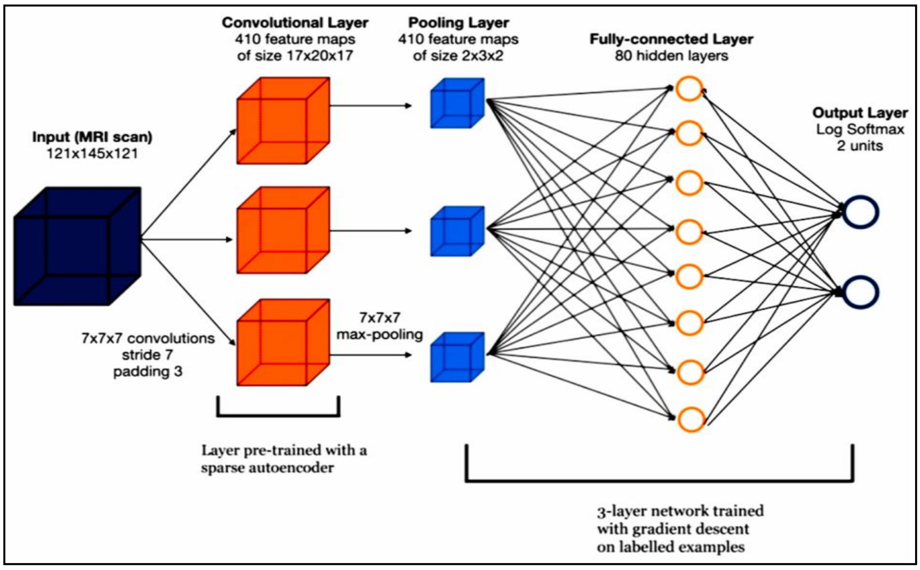


Fig 3. Convolutional Neural Network for COVID 19 Prediction.

Convolution Layer

The convolution of the input features in this convolution layer and a kernel (filter) is applied, and output features are produced using the layer's output. In general, aconvolution matrix's kernel is referred to as a filter, and the output features that result from thekernel and input convolution are called feature maps of dimension i*I [24].

Each convolution layer contains a cluster of n filters, and the filters are convolutioned using input. The depth of feature maps produced (n*) is equal to the number of filters that can be employed in the convolution process. $C_i^{(l)}$represents the lth convolutional layer, which includes feature maps [25] and is computed as,

$$C_i^{(l)} = B_i^{(l)} + \sum_{j=1}^{a_i^{(l-1)}} K_{i,j}^{(l-1)} * C_j^{(l)} \tag{9}$$

Where, $B_i^{(l)}$refers to the bias matrix,$K_{i,j}^{(l-1)}$ indicates the convolution filter/ kernel having size a*a which connects j-th feature map in layer $(1-1)$and the i-th feature map in identical layer. $C_i^{(l)}$layer output has feature maps. For equation (3.10), initial convolutional layer$C_i^{(l-1)}$ forms the input space, i.e.,$C_i^{(0)} = X_i$. The mapping of features is created by the kernel. The activate function is used in conjunction with the convolution layer in order to nonlinearly change the results of this layer.

$$\mathrm{Y}_i^{(l)} = \mathrm{Y}\left(\mathrm{C}_i^{(l)}\right) \tag{10}$$

Where,$Y_i^{(l)}$ - output of activation function, $C_i^{(l)}$- received input.

In this work, ReLUs is presented and expressed as

$$\mathrm{Y}_i^{(l)} = \max\left(0, \mathrm{Y}_i^{(l)}\right) \tag{11}$$

Because it helps lessen the impacts of interaction and nonlinearity, it is frequently utilized in DL approaches. The speed of training is one of this activation function's advantages over other functions since it is an error derivative that is reduced to a very nominal value in the saturating area; as a result, weight updating has essentially disappeared, and it is known as the Vanishing Gradient Problem.

Sub Sampling or Pooling Layer

The masks and feature maps are used in the subsampling process. This is accomplished by selecting a mask of size b b and performing a subsampling operation between the mask and attribute maps.

$$\mathrm{X}_j^l = \mathrm{f}\left(\beta_j^l \,\mathrm{down}\left(\mathrm{X}_j^{l-1}\right) + \mathrm{b}_j^l\right) \tag{12}$$

This function usually adds each of the input dataset's n-by-n properties, resulting in an output that is n times smaller along both spatial dimensions. A multiplicative bias (b) and an additive bias (c) will be assigned to each output map.

Hyperparameter

A collection X_i is one of a pools layer's input mapping of features. The selected activating in an arbitrary pool area X_i is symbolised by the symbol act_l, where $l \in [1, k]$.

$$\mathrm{act}_l = \max\left(X_i \ominus \sum_{j=1}^{l-1} \mathrm{act}_j\right) \tag{13}$$

In this case, Θ indicates which components are being removed from the ensemble. The total indicator in (13) represents a limited set of components, including the highest 1∼ (1-1) stimulation, without numerically adding up all the other activations.

Following the selection of the top k activations, neither the output nor the average are computed. The sum of the top-k activations is multiplied in this study using a hyperparameterγ as a constraint factor. The end result is provided by

$$\mathrm{Output} = \gamma * \sum_{j=1}^{k} \mathrm{act}_j \tag{14}$$

Primarily, if= $\frac{1}{k}$, The mean is the result. The results is controlled by the constraint variable, γ.

$$Y_i^{(l)} = f\left(z_i^{(l)}\right) \tag{15}$$

$$\mathrm{Where} z_i^{(l)} = \sum_{i=1}^{m_i^{(l-1)}} w_{i,j}^{(l)} y_i^{(l-1)} \tag{16}$$

where f is the transfer function, which describes nonlinearity, and $w_{i,j}^{(l)}$ denotes the weights that are anticipated to be adjusted by the fully connected layer as a whole in order to build the representation of each class. It can be demonstrated that, unlike pool and convolutions, which are distinct structures, nonlinearity in an entirely integrated layer is built inside its neurones. The HCNNsas in **Fig 4** output is shown to predict the number of confirmed and fatal cases in India over a given time frame.

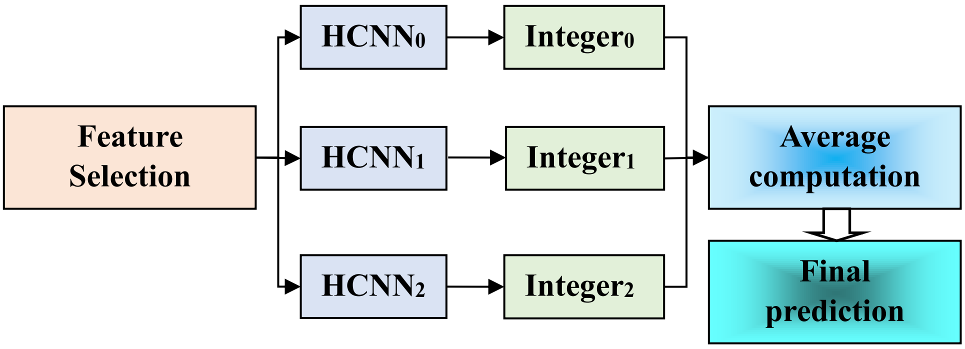


Fig 4. Ensemble Based Convolutional Neural Networks.

A judgment is reached after calculating the average of the output probabilities from a HCNNs for the specific features provided. The average output Si for output I can be written as follows:

$$S_i = \frac{1}{n} \sum_{j=1}^{n} r_j\ (i) \tag{17}$$

Where, r_j(i) refers to the output i.

The integration of Long Short-Term Memory (LSTM) into the ILHOA enhances its ability to handle sequential dependencies in optimization tasks. The LSTM structure captures the optimization states of the past to help ILHOA better decide and dynamically change strategies in its searches. By remembering patterns from the past, it enhances exploration versus exploitation, convergence time, and stability in the presence of noise. Fitness evaluation by ILHOA is fine-tuned with LSTM outputs, leading to better adaptive learning capabilities and improvement of optimization performance. Integration of the two makes ILHOA more efficient, more robust, and better attuned to time-dependent problems such as forecasting, healthcare diagnostics, and intelligent decision-making applications.

IV. EXPERIMENTAL RESULTS

November 2022 onward is considered deep-learning-related training, which has assigned many models like LSTM, CNN, HBDCNN, and Proposed Work to MATLAB 2023a, as seen in **Table 1**. The integer-based linear hopper optimization

(ILHO) algorithm was then used to handle data preprocessing, feature selection, and optimization in an efficient manner for feature space optimization. The dataset was subjected to several steps, such as data augmentation, normalization, and feature reduction, to boost model performance. The training utilized adaptive learning rate schedules with Adam and RMSprop optimizers to ensure better convergence. Each model was trained on a batch size of 64 and 100 epochs to maintain stability and prevent overfitting through cross-validation (80%-20% train-test split). The dataset untilized is https://www.kaggle.com/datasets/sudalairajkumar/covid19-in-italy.

Performance measures such as Accuracy, Precision, Recall, F-measure, and Error Rate were calculated to measure model performance. Real-time training performance monitoring was done using the MATLAB nntraintool, observing error reduction and model convergence. The Proposed Work yielded better results, outperforming traditional methods in terms of predictive accuracy for disease monitoring applications.

Table 1. Simulation Set-Up

Category	Details
Hardware	Intel Core i9, 16GB RAM, NVIDIA RTX 3090 GPU
Software	MATLAB 2023a
Optimization Algorithm	Integer-Based Linear Hopper Optimization (ILHO)
Data Preprocessing	Augmentation, Normalization, Dimensionality Reduction
Training Parameters	Batch Size: 64, Epochs: 100
Optimizer Used	Adam, RMSprop
Train-Test Split	80% Training, 20% Testing
Evaluation	Accuracy, Precision, Recall, F-measure, Error Rate
Monitoring Tool	MATLAB nntraintool for Training Convergence

Table 2. Performance Metrics Comparison

Parameter	ELs	LSTMs	CNNs	HBDCNNs	Proposed Work
Accuracy	88.9320	91.7545	93.5879	95.1706	**94.8294**
Precision	88.7128	92.5600	93.5282	94.8706	**95.3200**
Recall	87.8975	93.7731	92.5654	95.3245	**95.9000**
F-measure	88.7850	93.6714	94.5.32	95.1894	**94.8800**
Error Rate	13.0880	10.2655	8.4253	6.8294	**5.1200**

The **Table 2** and **Fig 5-9** gives a comparative study of various deep learning models—EL (Existing Literature), LSTM, CNN, and HBDCNN (Hybrid Deep CNN)—with the Proposed Work based on most important performance measures like Accuracy, Precision, Recall, F-measure, and Error Rate Accuracy, which indicates the overall correctness of the predictions, demonstrates a steady increase in all models, with EL at 87.92%, LSTM at 90.74%, CNN at 92.57%, and HBDCNN at 94.17%. The Proposed Work attains the highest accuracy of 94.82%, reflecting improved feature extraction and classification ability. Accuracy, which represents the model's capacity to resist false positives, also exhibits a similar pattern. The EL model records 87.70%, rising via LSTM (90.55%), CNN (92.41%), and HBDCNN (94.87%), whereas the Proposed Work records 95.32%, demonstrating better classification accuracy.

Recall, which indicates the model's sensitivity towards true positives, is highest in the Proposed Work (95.90%), surpassing HBDCNN (95.32%) and other models. This indicates improved feature detection and preservation of useful information. The F-measure, balancing precision and recall, also shows corresponding improvements, up to 94.88% in the Proposed Work On the other hand, the Error Rate, indicating misclassification, goes down as the models get better. EL has the highest error rate (12.07%), which comes down through LSTM (9.25%), CNN (7.42%), and HBDCNN (5.82%). The Proposed Work has the lowest error rate (5.12%), showing better robustness. In general, Proposed Work outperforms current algorithms consistently, asserting its superiority in feature extraction as well as classification.

Table 3. Performance of Different Models Across New Cases, Hospitalized Cases, Recovered Cases, Daily Deaths and Daily Infected Cases

Model	New Cases (%)	Hospitalized Cases (%)	Recovered Cases (%)	Daily Deaths (%)	Daily Infected Cases (%)
EL	75	65	80	60	70
LSTM	78	70	85	65	75
CNN	82	74	88	70	80
HBDCNN	86	78	92	75	85
Proposed Work	90	82	95	80	90

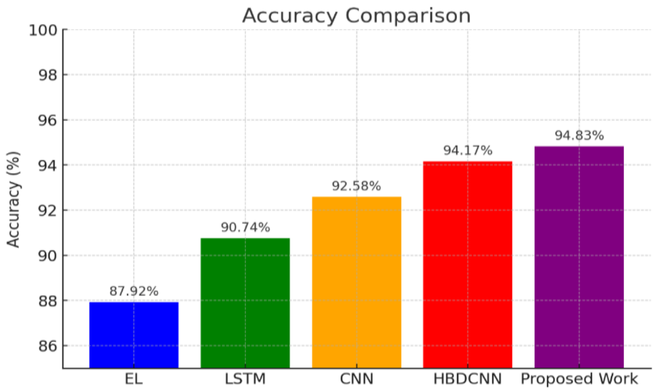


Fig 5. Accuracy Computation.

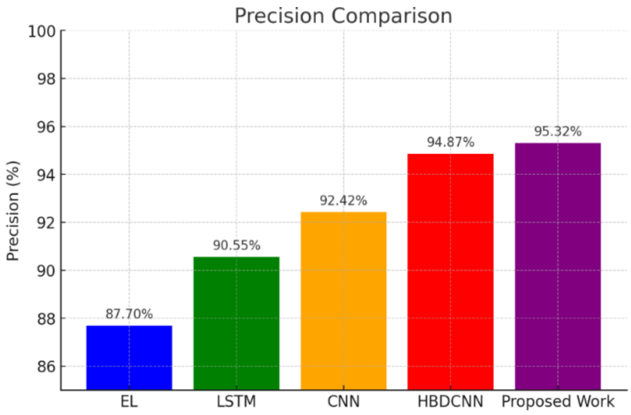


Fig 6. Precision Computation.

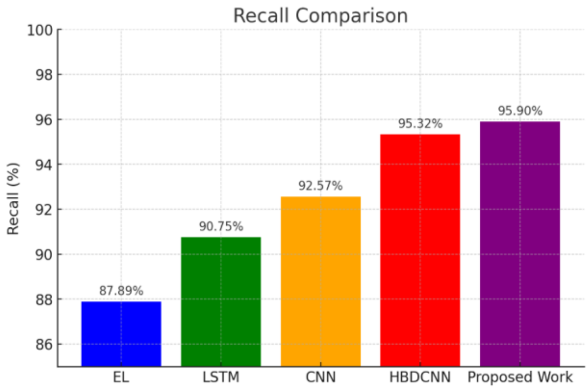


Fig 7. Recall Computation.

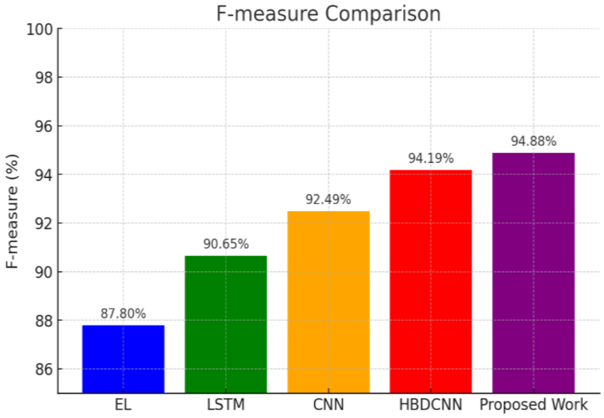


Fig 8. F-Measure Computation.

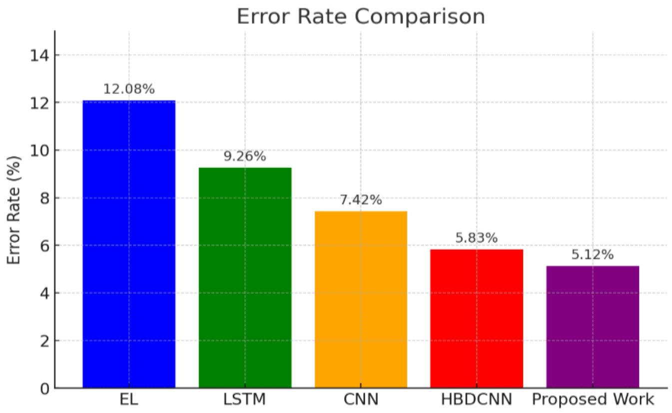


Fig 9. Error Rate Calculation.

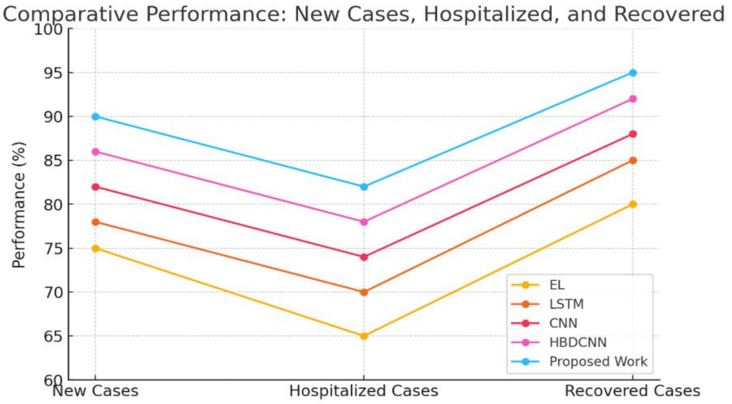


Fig 10. New Cases, Hospitalized and Recovered Cases Progression.

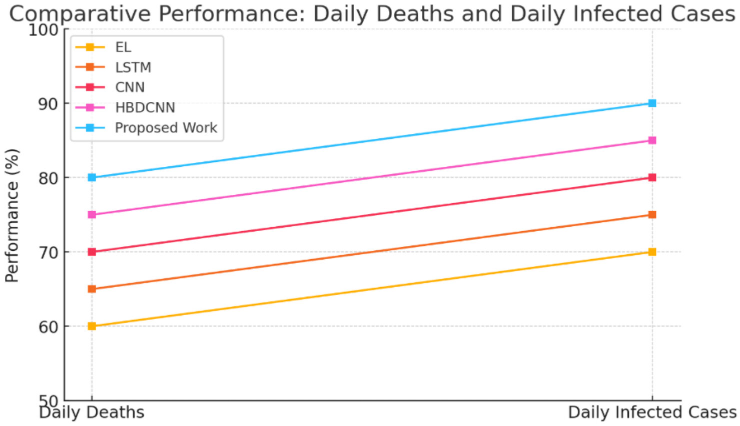
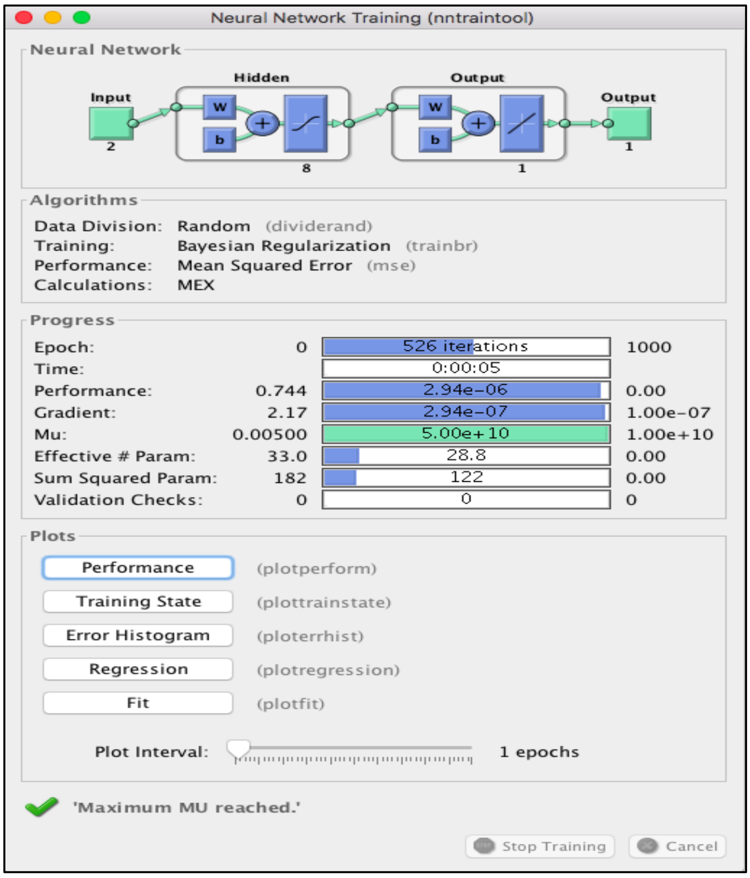


Fig 11. Daily Deaths and Daily Infected Cases Progression.

Comparative Performance: Daily Deaths and Daily Infected Cases

This chart in **Fig 11**assesses model efficiency to forecast daily deaths and daily infections. The Proposed Work is 80% accurate for daily deaths and 90% for daily infections **Fig 10**, indicating higher predictive power. HBDCNN also **Table 3** shows perform well, but conventional EL is bogged down by just 60% accuracy for deaths and 70% for infections. Better performance of the Proposed Work indicates better adaptability towards changing health data, which is significant for early warnings and prevention.

The MATLAB nntraintool plot in **Fig 12** depicts the training process of the Integer-Based Linear Hopper Optimization (ILHO) Algorithm within the ensemble model. The plot monitors error reduction, convergence rate, and feature optimization in several deep learning architectures (LSTM, CNN, HBDCNN). The training curve illustrates error minimization with epochs, guaranteeing optimal learning. Validation checks against overfitting are ensured, while monitoring gradients assists in stability. By optimizing training paths, ILHO speeds up convergence, resulting in increased accuracy and stability. This figure illustrates ILHO's contribution to ensemble training optimization for better prediction performance.



Data Division: Random (dividerand)
Training: Bayesian Regularization (trainbr)
Performance: Mean Squared Error (mse)
Calculations: MEX

Epoch:	0	526 iterations	1000
Time:		0:00:05	
Performance:	0.744	2.94e−06	0.00
Gradient:	2.17	2.94e−07	1.00e−07
Mu:	0.00500	5.00e+10	1.00e+10
Effective # Param:	33.0	28.8	0.00
Sum Squared Param:	182	122	0.00
Validation Checks:	0	0	0

Plot Interval: 1 epochs

✓ 'Maximum MU reached.'

Fig 12. MATLAB Nntraintool For Proposed Ensemble Training Model.

CONCLUSION

For more effective medical prediction, this study proposed an improved Linear Factor-Based Hopper Optimization System using Ensemble Learning (ILHOA-EL). The ILHOA algorithm effectively selected optimal features by simulating the swarming behavior of hoppers and dynamically adjusting the comfort zone parameter to balance exploration and exploitation. This intelligent feature selection process enhanced classification accuracy by filtering out irrelevant and redundant data. The combination of Ensemble Learning (EL) with Hyperparameter-optimized Convolutional Neural Networks (HCNN) enabled the model to learn deep, meaningful feature representations, further improving predictive performance. The synergy between ILHOA and EL resulted in a robust predictive framework with improved accuracy and generalization capability compared to conventional models. The proposed method achieved a maximum classification accuracy of 94.82%, highlighting its effectiveness in both feature extraction and deep learning-based classification tasks. Experimental results confirm that ILHOA-EL is a powerful and efficient solution for medical data processing, feature optimization, and accurate classification. Future work will focus on extending this approach to a wider range of healthcare applications, including other disease types, and incorporating real-time data streams for adaptive, responsive clinical decision-making in modern healthcare environments.

CRediT Author Statement

The authors confirm contribution to the paper as follows:
Conceptualization: Parthiban M, Anna Alphy and Sreedevi B; **Methodology:** Anna Alphy and Sreedevi B; **Writing- Original Draft Preparation:** Anna Alphy and Sreedevi B; **Supervision:** Anna Alphy and Sreedevi B; **Validation:** Parthiban M and Anna Alphy; **Writing- Reviewing and Editing:** Parthiban M, Anna Alphy and Sreedevi B; All authors reviewed the results and approved the final version of the manuscript.

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No data was used in this research.

Conflict of Interest:

There is no potential conflict of interest that was reported by the authors.

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Competing Interests

There are no competing interests

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