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Enhanced Healthcare Intelligence for Vaccination Prediction and Recommendation Using Deep Swarm Feature Engineering with Hyper Capsule Generated Adversarial Neural Network

S. Saranya[1], Dr. Agusthiyar R[2]

[1]Research Scholar – Part time (External), Department of Computer Applications, SRMIST, Ramapuram, Chennai.
E-mail: saranyasivapragasam88@gmail.com
[2]Professor, Department of Computer Applications, SRMIST, Ramapuram, Chennai. E-mail: agusthir@srmist.edu.in.

ABSTRACT
In recent years we have witnessed significant growth of healthcare protocols through vaccines to safeguard individuals from diseases without side effects. Especially various diseases that affect people's lead series effects caused by COVID-19, H1N1, Flu type of viruses. Vaccination protects us before it affects us to defend ourselves. Identifying all over-vaccination apart from other immunity-less people's prediction is challenging for early identification and recommendation. Most traditional methods failed to analyze active threshold margins' feature dimension and mutual dependencies, leading to a higher false negative and degrading prediction accuracy. The active false rate reduces the precision and recall accuracy and increases the false rate. To resolve this problem, we propose an enhanced deep feature engineering based on swarm intelligence whale optimization algorithm (SIWOA) with Hyper Capsule Generated Adversarial Neural Network (HCGANN) for vaccination prediction and recommendation. Initially, the Min-max normalizer is applied to preprocess the patient data, including patient information and vaccination details. The vaccination impact rate (VIR) is estimated using the scalar decision algorithm to calculate the absolute feature limits. Then, the Swarm Intelligence Whale Optimization Algorithm (SIWOA) is applied to select the essential features to reduce the non-mutual feature weights. The Generated adversarial neural network takes ideal feature limits of mutual dependencies of correlation vector to predict the vaccination recommendation people depend on a class by category. The proposed system improves the active false optimistic rate prediction by effectively evaluating the vaccination impact on people to improve prediction accuracies. The increased precision, recall rate, and f1 measure project higher evaluation results than the other systems.

Keywords: healthcare sectors, people, COVID-19, vaccination, min-max normalizer, VIR, scalar decision, SIWOA, HCGANN

Introduction

Healthcare intelligence enabled by Artificial Intelligence (AI) and Deep Learning (DL) delivers advanced outcomes in medical choices, disease diagnoses, and epidemic control management. Medical facilities deploy DL systems to handle worldwide health crises such as COVID-19 and generate better predictions and health system outcomes, as well as enhanced resource organization [1]. AI system analytics develop healthcare intelligence to forecast vaccinations while generating recommendations for optimal vaccine delivery approaches. The public practice of vaccination blocks infectious diseases and prevents fatalities, which protects both community wellness systems. Screening smallpox from extinction continues as healthcare employees incorporate AI to track population-level distributions of measles and polio. The extensive benefits of vaccines have been well-proven yet the general public shows significant hesitation toward their use. Public health remains at serious risk because people avoid vaccination participation because of misinformation together with distrust thus resulting in weaker global vaccine distribution systems [2].

The proliferation of false information on social media has worsened vaccine reluctance thus requiring artificial intelligence solutions which aim to fight incorrect vaccine content while spreading fact-based facts. Research shows that false information on Twitter and Reddit is widespread because misleading statements about vaccine facts compromise public understanding [3, 4]. To ensure effective vaccine misinformation control and evidence-based recommendations health organizations need identification methods that are efficient at detecting vaccine misinformation. The traditional vaccination recommendation approach depends on set guidelines by experts while showing limitations when evaluating epidemiological statistics and unique medical elements in vaccine administration choices. The conventional system models demonstrate restricted versatility because they do not respond well to newly evolving health threats together with personalized risk assessment requirements. Current AI systems that predict vaccines show numerous drawbacks due to their vulnerability against adversarial attacks, data biases and uninterpretable behaviors that prevent their use in practical

settings.

An Enhanced Healthcare Intelligence system using Hyper Capsule Generated Adversarial Neural Network (HCGANN) operates to resolve these problems while performing prediction and recommendation tasks for vaccinations. The HCGANN model allows medical professionals to obtain improved vaccination recommendations based on internal health profiles, external epidemiological statistics, and vaccine misinformation detection functions. The system uses adversarial learning to find deceptive vaccine-related information, which allows it to provide scientifically proven recommendations. Hyper capsules offer the model enhanced capability to detect healthcare data relationships of different levels, leading to better predictions and improved performance when dealing with changing public health needs. The innovative method strengthens vaccine prediction reliability while raising public vaccination program trust because it deals with misinformation in its original form [5]. With the deployment of HCGANN, healthcare institutions can use modern AI methodologies to increase vaccination strategies, minimize vaccine hesitancy and achieve global health protection.

2. Literature Survey

Multiple studies investigated machine learning applications because scientists use it extensively for vaccine development and recommendation systems and optimization processes. The Machine Learning Algorithm (MLA) presented by [6] aims to forecast lipid nanoparticles for mRNA vaccine applications as part of developing powerful vaccine formulations. The performance of this study is limited by an incomplete dataset base that may affect its universal application. The researchers in [7] investigated low influenza vaccination adherence among cardiovascular disease patients through Machine Learning Models (MLM). The research method shows key information about vaccine practices yet fails to adjust instantly to evolving vaccination uptake patterns in real time.

The Personal and Social Pattern-based Model (PSPM) implemented in [8] determined which social and personal elements influence vaccination choices. The predictions become less accurate because they exclusively depend on self-reported information that creates specific distortions. The authors in [9] extended vaccine recommendation through prediction of antigenicity by applying Convolutional Neural Networks (CNN) to select vaccines for human influenza virus A (H3N2). The success of this method relies on having accessible high-quality information about antigens.

A different approach presented in [10] developed Enhanced Vaccine Recommender System (EVRS) which merges clustering and classification techniques to achieve maximal COVID-19 vaccination results. Practical use of the method remains restricted because fundamental real-world implementation and validation tests still need to be conducted. Reinforcement Learning-enhanced Vaccine Allocation model (RLVA) introduced in [11] employed multi-factor contact networks to handle large-scale COVID-19 vaccine distribution. Reliable predictions can result from using this model yet its quantity of required computational power represents a barrier toward real-time implementation.

The researchers applied an Ensemble-Boosted ML method (EBML) to forecast COVID-19 infection patterns and suggest vaccinations in [12] but more evaluation studies are needed to determine if it surpasses alternative models. The researchers developed IVaccine-Deep (IVD) through deep learning to predict the shelf-life degradation of COVID-19 mRNA vaccines according to [13]. The model shows limitation regarding its capacity to work with different vaccine formulations.

The model lacks complete capability to handle external interruptions including supply chain problems that would impact its real-world operational effectiveness. The Vaccine Dissemination optimizer (VDO) presented by [14] uses ML technology in daily COVID-19 vaccine distribution to maximize vaccine administration efficiency. The research of [15] applied a Vaccine Hesitancy predictor (MLVH) based on ML to explore trends regarding hesitancy rates in high-income countries. The research investigation does not extend its data beyond high-income locations because economic variables have a substantial impact on vaccine reluctance.

Ensemble Learning (EL) served to enhance vaccine recommendation procedures through forecasting vaccine types and mortality risk evaluation for COVID-19 immunization regimens [16]. The speed at which the virus changes reduces the dependability of these models in the long run. Researchers utilized ML techniques known as MLUR to classify public responses regarding COVID-19 vaccines which resulted in identifying vaccine perception patterns [17]. The recognition of delicate or ironic remarks within sentimental analysis frameworks negatively impacts overall accuracy rates in classification processes.

HML-PV from [18] introduces a Hybrid ML approach that helps healthcare professionals estimate vaccine-derived poliovirus outbreak risks. Simply implementing this approach needs further confirmation through extensive epidemiological evidence testing. The authors developed an ML-based prediction model (ML-H1N1) according to [19] to monitor seasonal flu and H1N1 vaccination patterns. The model serves as a useful predictor for vaccine acceptance although it does not take into account alterations in virus genetic makeup and changes in vaccine protection strength.

The research by [20] used MLVC to investigate COVID-19 mortality trends related to vaccination through an ML model evaluation. The study faces limitations from using static data because these datasets may not represent current pandemic evolution properly. The research uses ML methods to explore multiple vaccine-

related applications which range from public opinion tracking and vaccine hesitancy evaluation to vaccine preparation and deployment and advice generation.

Table 1. Survey of the Various ML&DL methods to Predict Vaccination

Author/Year	Proposed Method	Evaluation Metrices	Limitations
Muhammad, L et al., (2021)	Naïve Bayes (NB)	Accuracy: 94.30%, Precision: 92.3%,	It might not accurately reflect larger populations, which would restrict its relevance in various demographic or geographical contexts.
Ong, E et al., (2021)	Vaxign-ML	Accuracy: 87.2%, Recall: 84.3%,	However, the accuracy and dependability of the model may be impacted by biases and false information in the suggested approach.
Sharma, A et al., (2021)	AI-data driven	Accuracy: 92.7%	It might have trouble adapting in real time because of changing virus mutations and shifting public health circumstances.
Rasool et al., (2023)	AI-driven methods	Accuracy: 84.3%	The concept raises issues related to permission, patient data privacy, and the abuse of medical forecasts produced by AI.
Lv, H., Shi et al., (2021)	AI/ML	Accuracy: 91.2%, F1-score: 89.7%	Due to the high processing power requirements, the AI/ML are difficult to implement in environments with low resources.
Bushaj, S et al., (2023)	Simulation-Deep Reinforcement Learning (SiRL)	Accuracy: 75%	SiRL's accuracy in forecasting may gradually decline as it may not always accurately represent present or future circumstances.
Fares, S et al., (2021)	Bidirectional Encoder Representations from Transformers (BERT)	Accuracy: 88.4%, AUC-ROC: 0.91	The suggested approach lacks comprehensive clinical validation, which makes practical application difficult.
Tavoschi, L et al., (2020)	Lexicon-based approaches	Accuracy: 83.5%	The suggested model reduces model robustness and produces biassed predictions.
To, Q et al., (2020)	BERT	Accuracy: 85.7%, Precision: 83.1%,	Due to overfitting, BERT struggles with unobserved real-world data yet performs well on training data.
İ. Aygün et al., (2022)	mBERT-base, BioBERT, ClinicalBERT and BERTurk	Accuracy: 90.2%, AUC-ROC: 0.94	The high processing needs and data requirements of the suggested solutions make them difficult to scale effectively.

A Stacking Ensemble-based Intelligent ML methodology (SEIML) was deployed to predict post-COVID-19 complications [31]. The predictive model employs various base learners in combination to increase its accuracy. Its practical deployment is restricted because the system lacks real-time responsiveness while neglecting the inclusion of dynamic patient healthcare information. The research team employed ML Analysis to analyze COVID-19 vaccination-related tweets and their sentiments in the Australian population [32]. The algorithms used sentiment classification to analyze public opinions. The analysis of information extracted from Twitter encounters limitations because it produces results that fail to adapt across the complete populace.
A DenseNet-201 (DN201) investigation presented a model to differentiate between COVID-19 and pneumonia cases [33]. Worldwide COVID-19 vaccination progress analysis utilized Machine Learning Classification Algorithms (MLCA) as the study method [34]. Researchers used classification methods for vaccination trend analysis in their study. The model did not include population data and geographical differences to determine vaccination results. The ML-based classification methodology developed a system that analyzed antibody activity information to determine BNT162b2 vaccine longevity [35]. However, the proposed method is not effectively separated vaccination durations that occurred after testing.

3. Implementation of Proposed Method

In this phase, we briefly illustrated the deployed methodology stages to accurately predict and recommend the specific vaccinations. This deployed methodology has three stages: preprocessing, finding the impact rate, feature selection and classification. The Min-max normalizer method is used for preprocessing the patient data, the to find the impact rate of vaccination through scalar decision algorithm, the SIWOA method is used for select the appropriate vaccination features, then we use HCGANN method to predict and recommend the vaccination.

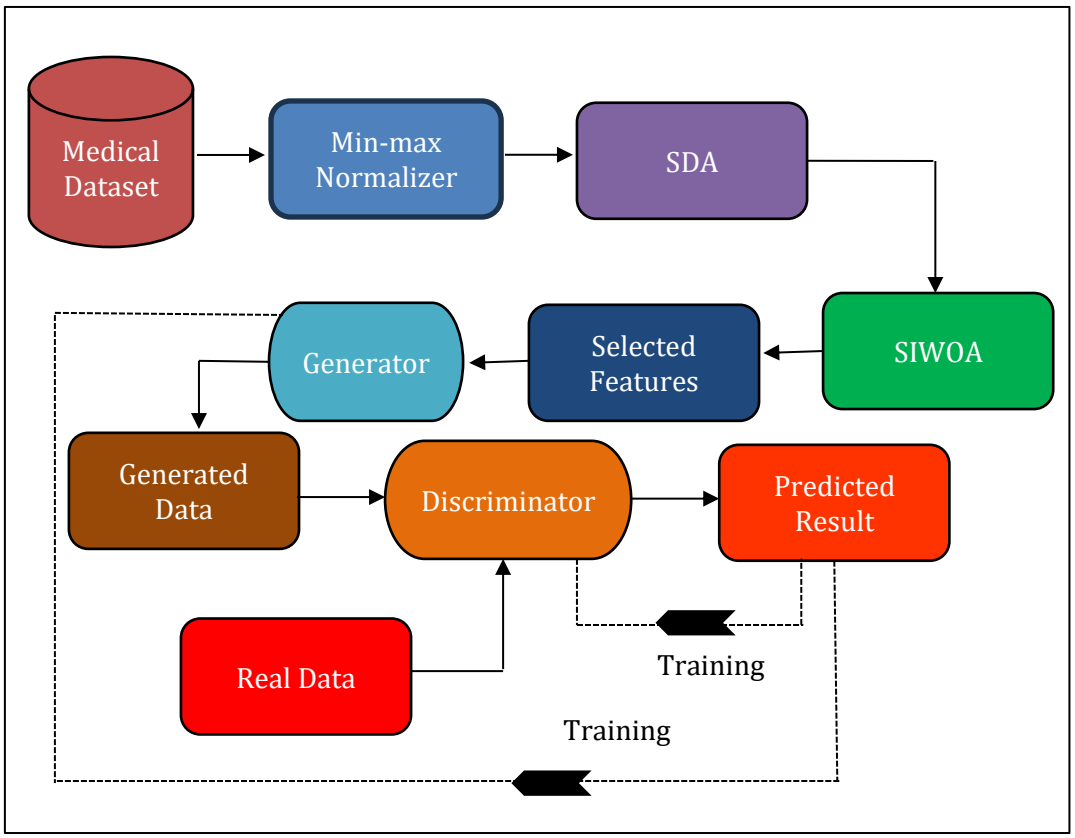
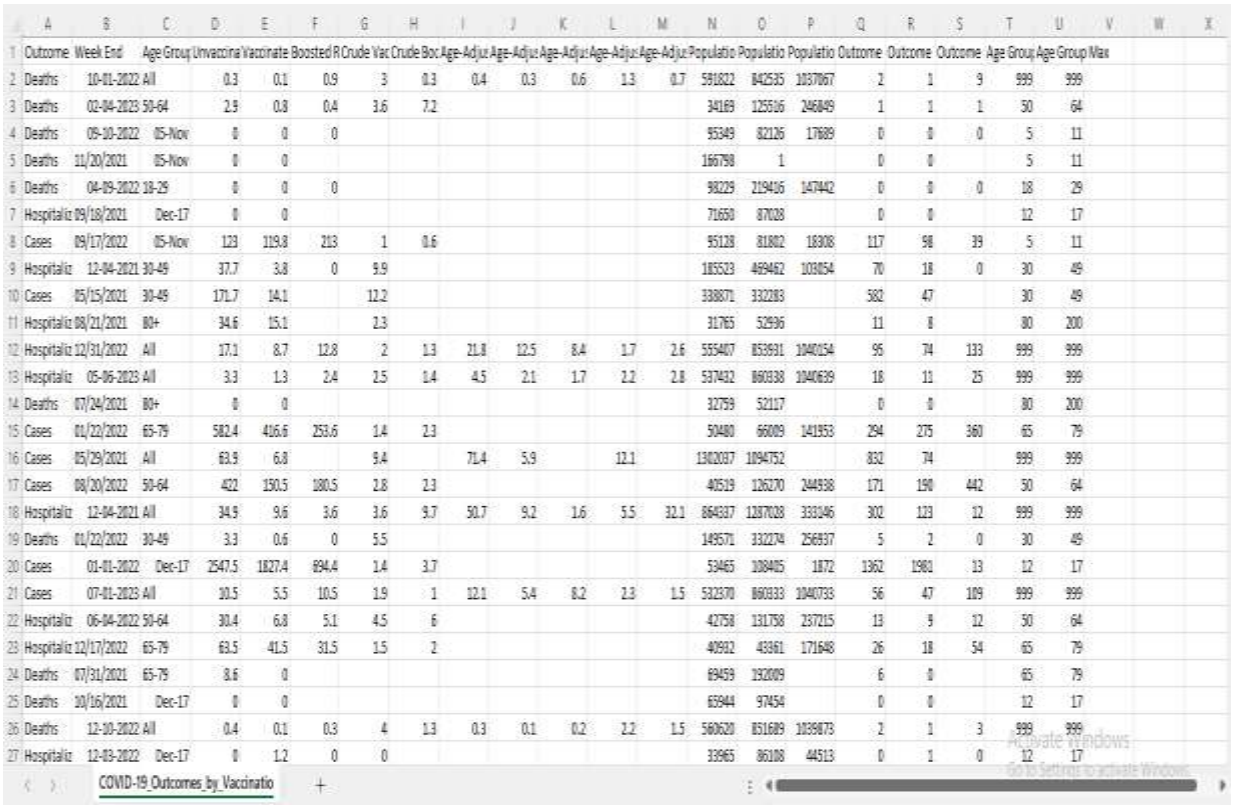


Figure 1. Architecture diagram of the proposed method

The figure 1 illustrate how DL methodologies develop predictive recommendations for vaccinations. First Medical data that contains patient records and vaccination information passes through the Min-max Normalizer to normalize all features into determined ranges. The SDA resorts to feature limit calculation to determine the VIR. The SIWOA selects the most critical features as well as eliminating those with non-mutual feature weights to optimise efficiency of the model operational. The HCGANN will be used as the primary instrument to train the model and predict vaccination under this purpose. The Generator generates artificial data, using the features extracted, whereas the Discriminator only tries to distinguish real and artificial data to refine the model. The Production which is the Red Predicted Result is continuously improved throughout advisarial training to give the correct vaccination prediction.

3.1 Dataset Description

The COVID-19 Outcomes by Vaccination Status - Historical dataset provides data surrounding the health outcomes derived by vaccinated and non-vaccinated people. The results obtained in this data collection are as follows: the total number of deaths along with the number of hospital admissions and the incidence of cases in unvaccinated patients and vaccinated patients (who got the booster). The data processed by age groups and presented weekly in the dataset will allow the researcher to examine the effect of vaccination on the incidence of severe COVID-19 cases. The database has a number of key characteristics, including raw and adjusted rates per each segment and population statistics depending on vaccination status and relative risk indicators.



Outcome	Week End	Age Group	Unvaccina	Vaccinate	Boosted R	Crude Vac	Crude Boc	Age-Adjus	Age-Adjus	Age-Adjus	Age-Adjus	Age-Adjus	Populatio	Populatio	Populatio	Outcome	Outcome	Outcome	Age Group	Age Group Max
Deaths	10-01-2022	All	0.3	0.1	0.9	3	0.3	0.4	0.3	0.6	1.3	0.7	591822	842535	1037867	2	1	9	999	999
Deaths	02-04-2023	50-64	2.9	0.8	0.4	3.6	7.2						34169	125516	246849	1	1	1	50	64
Deaths	09-10-2022	05-Nov	0	0	0								95349	82126	17689	0	0	0	5	11
Deaths	11/20/2021	05-Nov	0	0									166798	1		0	0		5	11
Deaths	04-09-2022	18-29	0	0	0								98229	219416	147442	0	0	0	18	29
Hospitaliz	09/18/2021	Dec-17	0	0									71650	87028		0	0		12	17
Cases	09/17/2022	05-Nov	123	119.8	213	1	0.6						95128	81882	18308	117	98	39	5	11
Hospitaliz	12-04-2021	30-49	37.7	3.8	0	9.9							185523	469462	103054	70	18	0	30	49
Cases	05/15/2021	30-49	171.7	14.1		12.2							338871	332283		582	47		30	49
Hospitaliz	08/21/2021	80+	34.6	15.1		2.3							31765	52936		11	8		80	200
Hospitaliz	12/31/2022	All	17.1	8.7	12.8	2	1.3	21.8	12.5	8.4	1.7	2.6	555407	853931	1040154	95	74	133	999	999
Hospitaliz	05-06-2023	All	3.3	1.3	2.4	2.5	1.4	4.5	2.1	1.7	2.2	2.8	537432	860338	1040639	18	11	25	999	999
Deaths	07/24/2021	80+	0	0									32759	52117		0	0		80	200
Cases	01/22/2022	65-79	582.4	416.6	253.6	1.4	2.3						50480	66009	141353	294	275	360	65	79
Cases	05/29/2021	All	63.9	6.8		9.4		71.4	5.9		12.1		1302037	1094752		832	74		999	999
Cases	08/20/2022	50-64	422	150.5	180.5	2.8	2.3						40519	126270	244938	171	190	442	50	64
Hospitaliz	12-04-2021	All	34.9	9.6	3.6	3.6	9.7	50.7	9.2	1.6	5.5	32.1	864837	1287028	333046	302	123	12	999	999
Deaths	01/22/2022	30-49	3.3	0.6	0	5.5							149571	332274	256937	5	2	0	30	49
Cases	01-01-2022	Dec-17	2547.5	1827.4	894.4	1.4	3.7						53465	108405	1872	1362	1981	13	12	17
Cases	07-01-2023	All	10.5	5.5	10.5	1.9	1	12.1	5.4	8.2	2.3	1.5	532370	860333	1040733	56	47	109	999	999
Hospitaliz	06-04-2022	50-64	30.4	6.8	5.1	4.5	6						42758	131758	237215	13	9	12	50	64
Hospitaliz	12/17/2022	65-79	63.5	41.5	31.5	1.5	2						40912	43361	171648	26	18	54	65	79
Deaths	07/31/2021	65-79	8.6	0									69459	192009		6	0		65	79
Deaths	10/16/2021	Dec-17	0	0									65944	97454		0	0		12	17
Deaths	12-10-2022	All	0.4	0.1	0.3	4	1.3	0.3	0.1	0.2	2.2	1.5	560620	851689	1039873	2	1	3	999	999
Hospitaliz	12-03-2022	Dec-17	0	1.2	0	0							33965	86108	44513	0	1	0	12	17

COVID-19_Outcomes_by_Vaccinatio

Figure 2. Sample Image of the COVID-19 Outcomes by Vaccination Status - Historical dataset

The dataset occurs 21 attributes which provide key data about COVID-19 results. The outcome attribute categorizes events according to death totals, hospitalization figures, and recorded cases. Instead, it is in the Week End field but the information is classified by Age Group parameter. The results are measured by the number of outcomes per 100,000 individuals in each cohort where that is captured by the Unvaccinated Rate, Vaccinated Rate, and Boosted Rate. Two measures, the Crude Vaccinated Ratio and the Crude Boosted Ratio are the proportion rates of the outcomes. The data regarding the population groups, namely, that was not vaccinated and that was vaccinated as well as population boosted will assist in the evaluation of outcome information. The data set also has age-adjusted rates that corrects the statistical assessment across various age groups. Direct cases, hospitalizations, or deaths of the vaccinated and unvaccinated populations and even those who have taken boosters are mentioned in the Outcome Unvaccinated, Outcome Vaccinated, and Outcome Boosted attributes. The characteristics referred to as the Age Group Min and Age Group Max determine the precise limits of each segment of the population identified by age-defined levels.

3.2 Min-max normalizer

Min-Max Normalizer standardizes the numerical by modifying the values to fall between 0 and 1 or -1 to 1. The method carries out the transformation of the patient data through transformation of date variables to numbers and by performing proportional scaling on all the age and quantity of doses variables. It is possible to say that the original distribution of the dataset would not change when Min-Max normalization is utilized, though the scales of attributes would become normalized and this would help to improve the performance and to compare the variable types with one another. The standardization method will prove effective in healthcare systems in that it enhances the quality of analysis insights and predictive accuracy given that all the features are measured on the same scale.

Algorithm 1: Min-Max Normalizer for patient data

Start

Input the Healthcare Dataset

Identification of the dataset containing a numeric nature with the characteristics of vaccination dates along with dose volume and also ages of the patients.

Extract the needed numerical columns needed for normalization from the dataset.

Identify the Range for Normalization

Select the normalization goal range, which is often [0,1] or [-1,1], depending on the system.

Find the min and max values for each attribute i

For each numerical attribute in the X in the I:

Evaluate minimum X of i

Evaluate maximum X of i

end for
Deploy the Min-Max Normalization equation
For each X in the numerical i:
calculate the normalized value X′ utilizing the equation below,

$$X' = \frac{X - X_{min}}{X_{max} - X_{min}} \times (z_{max} - z_{min}) + z_{min}$$

while X, as X′, and as desired range $(z_{max} - z_{min})$ (default is 0 and 1 for [0,1] scaling).
end for
Replace the X with X′
Replace the X with the X′ or save them in a new column in
Verify the X′
Check if:
all X are within the $(z_{max} - z_{min})$
else
no data distortion occurred during normalization.
Use the X′ for Further Processing
The preprocessed data is now ready for use in analyses impact rate, feature selection, and classification.
Stop
Algorithm 1 enables different numerical attributes to obtain comparable formats without displacing their original data distribution. Patient records treated through Min-Max normalization become standardized, which means that significant value differences affect statistical analysis performance less. Healthcare data receives significant advantages through this method because standardized representations lead to better accuracy in predictions together with improved trend assessment and superior patient treatment selection as well as vaccine monitoring.

3.3 Scalar Decision Algorithm (SDA)

The Scalar Decision Algorithm (SDA) estimates the Vaccination Impact Rate (VIR) by establishing absolute feature limits through the processed dataset. The decision algorithm analyses essential patient criteria, from age to prior immunity experiences and dosage records, to measure vaccination success among distinct population groups. The method utilizes absolute feature limits in analysis to prevent skewed results from uncritical or inconsistent values, thereby maintaining accurate VIR calculation. Public health decision-making improves through the vital application of this approach for measuring vaccine effectiveness and finding high-risk populations alongside optimal vaccination practices.

$$FL_i = \alpha_i . \max(X_i') + \beta_i \quad (1)$$

in this equation the FL_i is the absolute feature limit for attribute i, X_i' normalized value of i, α_i as scaling factor which is used to adjust attribute importance, and β_i as bias term, fine-tuning impact rate. The equation 1 equation determines the feature limit (FL) for each patient attribute X_i, ensuring extreme values do not distort VIR calculations. The scalar decision factors α_i and β_i control feature weight and bias. By equation 2 we compute the VIR (R),

$$R = \frac{\sum_{i=1}^{n}(X_i' . W_i)}{\sum_{i=1}^{n} W_i} \quad (2)$$

the R is the effectiveness of vaccine based on patient data, X_i' is the normalized patient attribute (age, prior immunity, dosage history), W_i is used to assigned the weight to each i for determining its impact, and n is considered as the total number of attributes. This equation estimates the (R) by computing a weighted sum of normalized patient attributes. The weights W_i determine the influence of each feature on the final (R) value.

$$R_d = \begin{cases} HI & \text{if } R \geq T_H \\ MI & \text{if } T_L R < T_H \\ LI & \text{if } R < T_L \end{cases} \quad (3)$$

In this equation the R_d is known for final classification of vaccine effectiveness, T_H is the high vaccination impact (Upper threshold), T_L is the moderate vaccination impact rate (Lower threshold), HI as high impact, MI as moderate impact, and LI as low impact. The decision ensures a clear categorization of vaccination effects for different patients. The equation 3 classifies the vaccination impact rate into HI, MI, or LI based on predefined thresholds T_H (high threshold) and T_L (low threshold). The methodology enables the healthcare decisions to be made by using risk groups and optimized stratification of the strategy along with offering a tangible method to accurately estimate the effectiveness outcomes of vaccination. It assists medical professionals to correctly interpret patient information thus giving improved healthcare policies and more specific vaccination programs.

3.4 Swarm Intelligence Whale Optimization Algorithm (SIWOA)

Swarm Intelligence Whale Optimization Algorithm (SIWOA) is a bio-inspired optimization approach that incorporates whale social hunting behavior patterns that manifests in solving complex systems problems. IWOA can be used to predict vaccination and make recommendations based on their application to the process of feature selection literitely selecting relevant attributes and lessening weights of attributes that do not depict

any relationships to one another. This kind of approach enhances the predictive models by enhancing its accuracy and efficiency of the model in terms of reduced dimension and assuring better results of classification. exploration and exploitation are maintained by using swarm intelligence with SIWOA, which generates optimal precise sets of recommended vaccines based on key features identified.

$$X(t+1) = X^*(t) - A.D \quad (4)$$

were,

$$D = |C.X^*(t) - X(t)| \quad (5)$$

and

$$A = 2a.r - a, \ C = 2r \quad (6)$$

The equations determine how candidate feature subsets relocate through space to discover their best possible selection. At iteration t, the feature set position is represented by X(t), but the best solution found so far is expressed as $X^*(t)$. The value labeled A maintains the proportion between two phases: intense search for new features and the refinement of chosen features. The coefficient C accumulates random fluctuations to avoid premature convergence thus enabling the algorithm to search and discover important vaccine predictor attributes.

$$X(t+1) = X^*(t) - A.|D| \quad (7)$$

were,

$$D = |C.X^*(t) - X(t)| \quad (8)$$

Whales' actions to circle their prey are described through Equations 7 and 8, where feature subset refinement occurs through solution updates compared to the best-known feature subset. During its operation, the algorithm selects features that achieve maximum prediction accuracy for vaccination statuses while eliminating unneeded features from the selection. The distance function D enables respective whale (solution) entities to modify their behavior based on the best feature set development.

$$X(t+1) = D'.e^{bl}.\cos(2\pi l) + X^*(t) \quad (9)$$

were,

$$D' = |X^*(t) - X(t)| \quad (10)$$

The whale hunting simulation through Equations 9 and 10 enables solutions to track different feature combinations using helical movements. A non-linear search behavior emerges from the exponential term e^{bl}, improving optimization by preventing suboptimal solution trapping. Additional movement variation comes from the $\cos(2\pi l)$ term, which maintains only important vaccinations-related features. The feature selection mechanism is essential to optimize prediction accuracy levels.

$$a = 2 - \frac{2t}{T} \quad (11)$$

here the T is the maximum number of iterations. The parameter a adjusts the exploration-exploitation balance, which steadily decreases during optimization. The exploration phase starts with a high value of a which enables scanning broad ranges of features in the initial stages. The rising value of t causes, a decline in a which leads the algorithm to concentrate on exploiting chosen features for refinement. The gradual change mechanism culminates in a last feature selection that combines efficiency with relevance to vaccine forecasting outcomes.

$$F(X) = \alpha \times A(X) - \beta \times \frac{|X|}{|X_{total}|} \quad (12)$$

The equation 12 contains two weight factors (α and β) with classification accuracy A as one variable and the number of selected features |X| responding to the total amount of available features $|X_{total}|$. Equation 12 provides evaluations about the selected feature subset quality. Using the selected features maintains high classification accuracy because of the first position's $\alpha \times A(X)$ term. The second term, $\beta \times \frac{|X|}{|X_{total}|}$, applies a penalty to feature selection that goes beyond necessity to achieve an optimal minimum subset. The vaccination prediction model maintains high predictive performance levels through SIWOA, while this function ensures the efficient operation of the model. The algorithm selects dominant features by consuming multiple strategies that perform feature subset updates through encircling movements, exploration steps, and spiral movements. An improved framework for vaccine forecasting accuracy results when model efficiency is improved through the combination of convergence control and fitness evaluation.

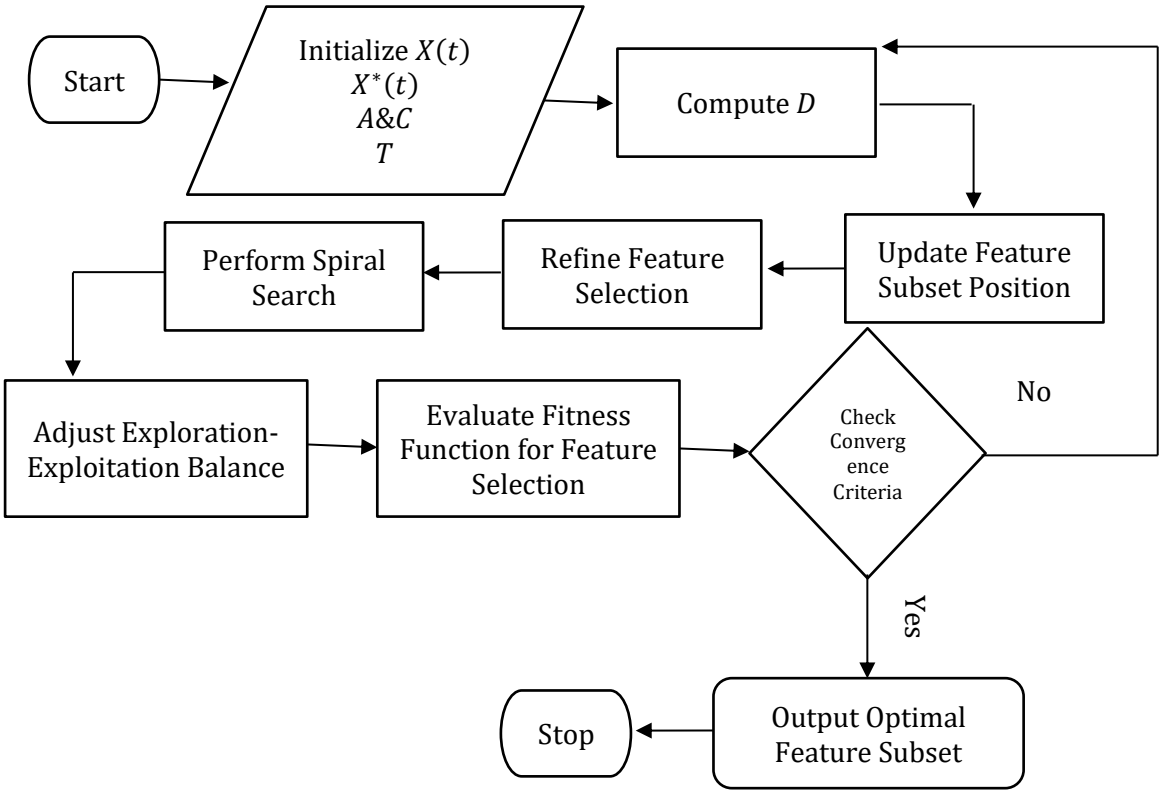


Figure 3. Flowchart of the SIWOA

Figure 3 shows SIWOA using a defined process for selecting features that predict vaccinations. The algorithm sets parameters and runs the distance function to change feature subset locations. The SIWOA conducts further refinements of feature selection through combinations of encircling methods and spiral search procedures, as well as adaptive control of exploration and exploitation dynamics. A fitness function determines the accuracy and efficiency of features that undergo evaluation. The SIWOA proceeds by running multiple cycles that end when it finds the best feature subset, providing enhanced vaccine prediction accuracy with reduced essential features.

3.5 Hyper Capsule Generated Adversarial Neural Network (HCGANN)

The Hyper Capsule Generated Adversarial Neural Network (HCGANN) represents an advanced DL framework dedicated to vaccine prediction and making recommendations. HCGANN utilizes hyper capsules to work with complex feature dependencies through an adversarial learning system which improves its robustness performance. HCGANN discovers the optimal feature relationships between dependent attributes through analysis of the correlation vector before recommending vaccines. The model segments its predictive outcomes through the class-by-category organization to distribute patients into appropriate vaccination categories based on demographics, medical background, and risk evaluation.

$$H_c = \sum_{i=1}^{n} w_i \, . \, X_i \quad (13)$$

The network uses H_c as the hyper capsule representation to process X_i through learned transformation weights w_i. The system converts input elements X_i into H_c capsule representations using weighting techniques for summation. With the help of Equation 13, the model undertakes numerous vaccination-related characteristics to unmask that which makes the body-core aspects of the recommendation of vaccination.

$$C_v = \frac{1}{n}\sum_{i=1}^{n}(X_i - \overline{X})(Y_i - \overline{Y}) \quad (14)$$

This equation describes the relative associations among correlation vector $C_v$and involving two sets of feature $X_i$and $X_i$as well as their averages $\overline{X}$, $\overline{Y}$. Equation 14 gives the definitions of the relationship between the sets of different features through correlation analysis. This procedure identifies the severity of correlations among many variables, such as age and health history, to identify the best options of recommendations

$$P(V|C) = \frac{e^{W_c . H_c + b_c}}{\sum_j e^{W_j . H_j + b_j}} \quad (15)$$

The probability P(V|C) for vaccination recommendation depends on category C with weight W_c and bias b_c, requiring normalization before computation. Through the softmax-based equation, the model determines vaccination recommendation probabilities across different categories ranging from age groups to risk levels. The system bases its recommendation decisions on capsule embeddings H_c and learned weights W_c.

$$L_{adv} = E_x[\log D(X)] + E_{\overline{X}}\left[\log\left(1 - D(G(Z))\right)\right] \quad (16)$$

The schema of where L adv is a representation of adversarial loss associated to the discriminator function D

(X) and that of the generator function G(Z) with X treating X treated as an adversarial output. The model can train a generator (G(Z)) in order to produce synthetic data that can be used to generalize better, using Equation 16. D(X) functions discriminate among the genuine examples and those the generator created, which enhances the data fault resistance of the model.

$$L_{total} = L_{pred} + \lambda L_{adv} \quad (17)$$

The overall loss function L_{total} consists of the vaccination prediction classification loss combined with the balance weight denoted as λ. Equation 17 unifies the prediction accuracy objectives L_{pred} with the adversarial loss L_{adv} to achieve accurate classification in addition to being robust. The λ controls the weight of adversarial training in the optimization process. HCGANN performs vaccination prediction recommendations through hyper capsules and adversarial learning methods.

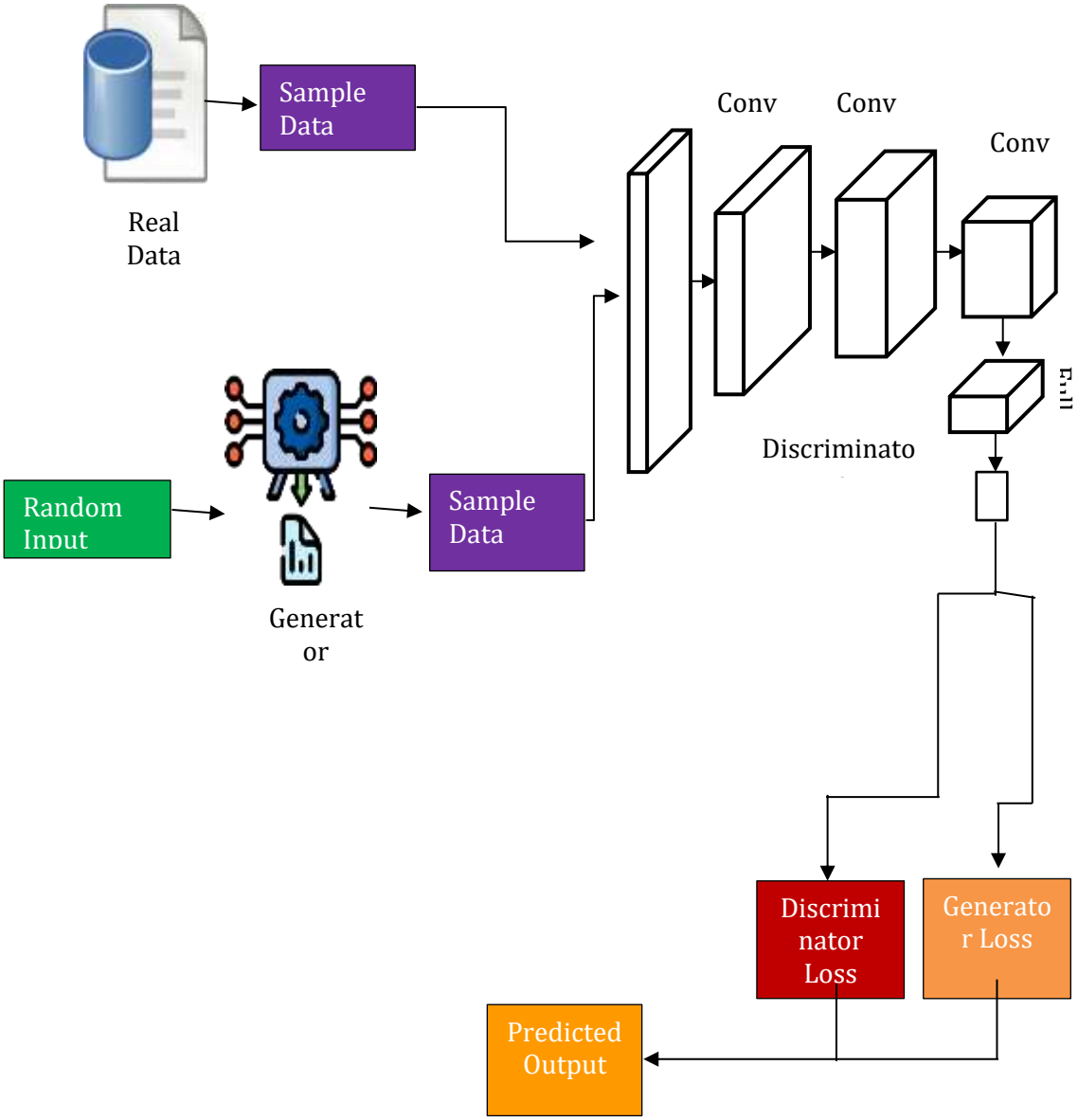


Figure 4 HCGANN method block diagram for vaccination prediction

Figure 4 shows the execution of the HCGANN method for vaccine prediction. The architecture is based on a GAN framework that consists of a Generator and Discriminator, whose designs include convolutional blocks to achieve optimum levels of predictions. The Generator serves as an input receiver which generates artificial vaccination data that look similar to those specified in real laboratories. The Discriminator checks on data authenticity generated by the system through the Conv 5x5 layer network system and compares the same with real data. The training occurs in iterations where the model optimizes the Generator and Discriminator networks based on the loss functions and Generator Loss and Discriminator Loss, which will increase reliability levels of the system. The ultimate Predicted Output produces the forecasts of vaccination so you could develop the immunization strategy.

4. Result and Discussion

The section outlines the step-by-step procedure of creating a new DL approach that would predict and advise injections. DL methods differ from CNN EVRS and EMBL algorithms because they ignore variations in virus genetic information and vaccine resistance against HCGANN. The proposed method concentrates exclusively on improving vaccination prediction accuracy through recommendation. The methodology classification depends on performance metrics which include accuracy, precision, recall, F1 measure and time complexity. The HCGANN gain prediction accuracy on the basis these metrics. The Simulation Parameter receives presentation through Table 1.

Table 2. Simulation Parameter

Simulation	Parameter
Name of the Dataset	COVID-19 Outcomes by Vaccination Status - Historical
No of Attributes	21
No of Values	3754
Used Tool	Jupyter
Used Language	Python

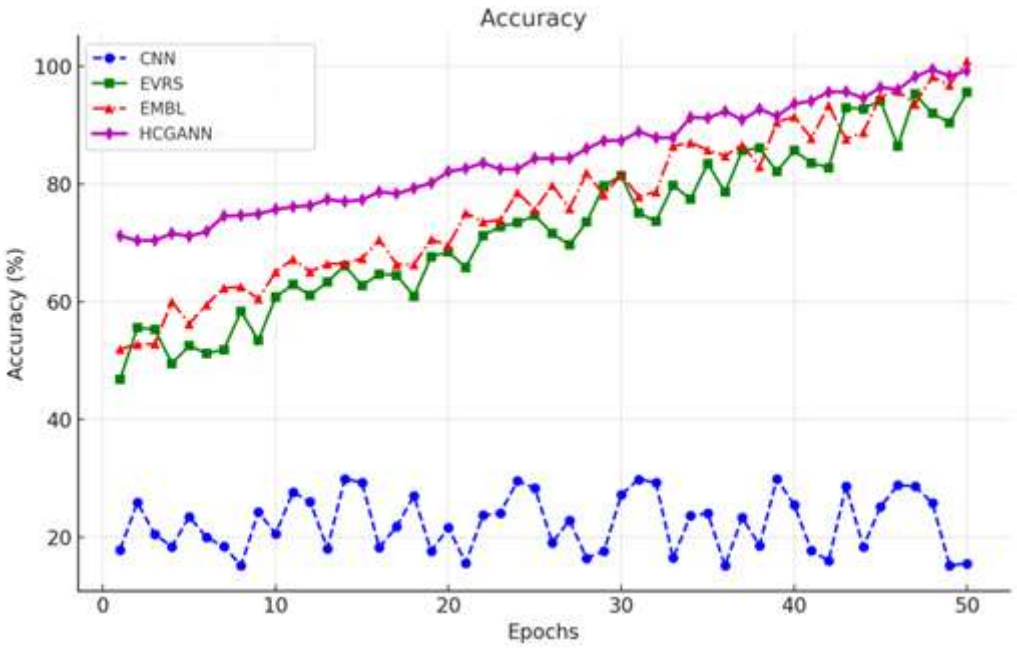


Figure 5. Performance Analysis of Accuracy in %

Figure 5 demonstrates the accuracy results of CNN, EVRS, EMBL, and HCGANN methodologies when processing the COVID-19 Outcomes by Vaccination Status—Historical dataset. The HCGANN method achieves better results than previous methods by maintaining elevated and consistent accuracy trends. CNN's accuracy rate decreases the most, but EVRS and EMBL gradually improve their performance throughout epochs. The results show that HCGANN reaches the maximum accuracy, confirming its classification duties' excellence.

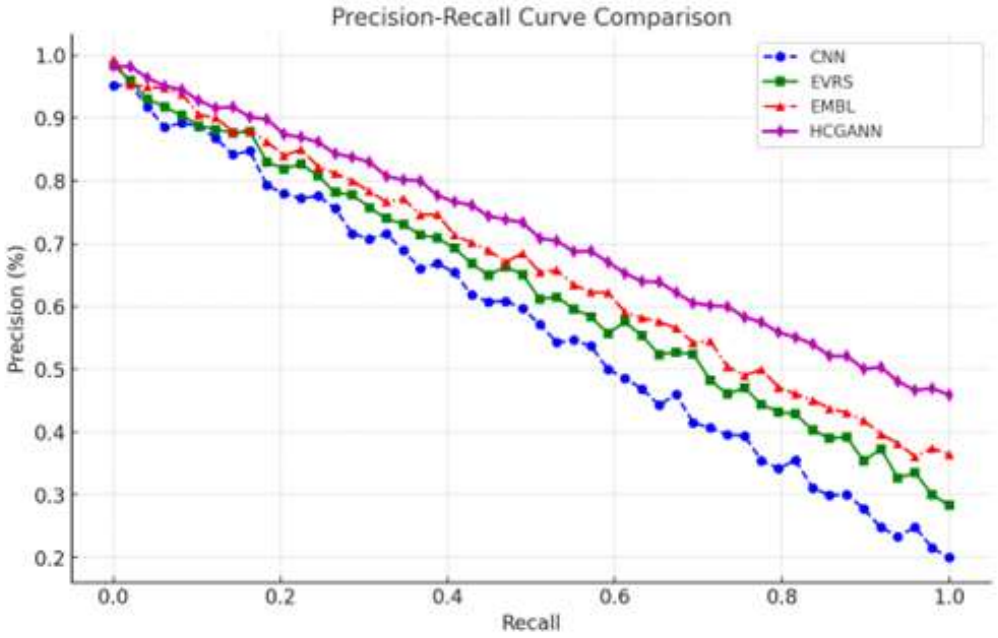


Figure 6. Curve Comparison based on Precision-Recall

The precision outcomes of the CNN, EVRS, EMBL and HCGANN are depicted in Figure 6 since they differ by respect to particular recall levels. The CNN model follows the most distinctive level of precision, steeply declining as the memory goes up. The EVRS and EMBL models will have better precision rates, but when the recall values increase strongly their performance levels drop down. HCGANN shows superior results through all recall levels compared to the previously used approaches by maintaining superior precision levels. The advanced nature of HCGANN succeeds in detecting positive outcomes without producing excessive false positives, making it an optimal predictive model for COVID-19 diagnosis.

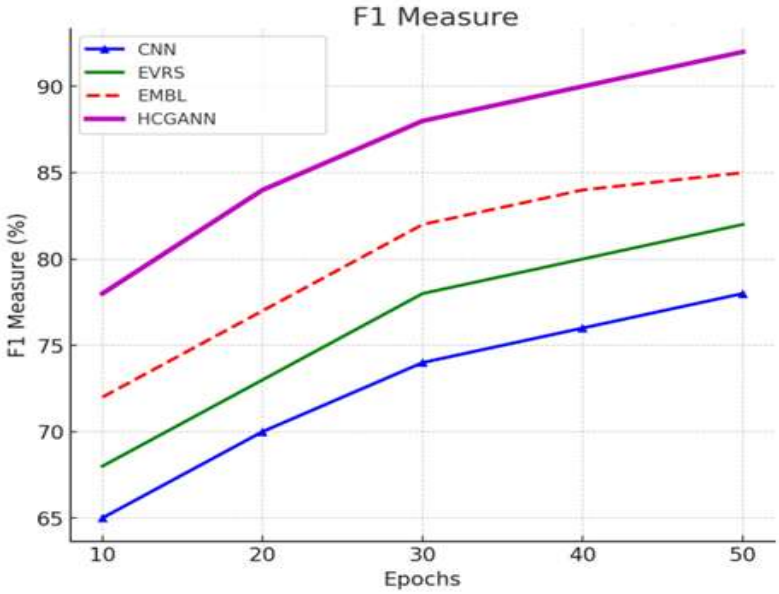


Figure 7. Analysis of F1 measure in %

Figure 7 shows the performance evaluation of CNN, EVRS, EMBL, and HCGANN using the F1 measure (%) between different training epochs. HCGANN achieves the best F1 measure among all the previous methods while consistently delivering performance enhancements. The implemented HCGANN demonstrates superior efficiency in the learning process by boosting F1 scores through each epoch, establishing its position as an advanced classifier for the specific dataset.

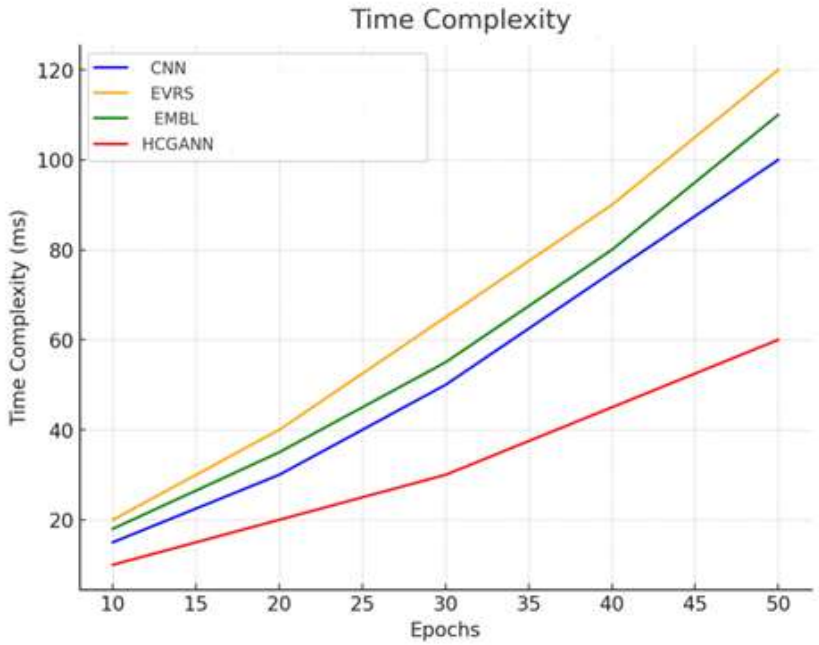


Figure 8. Analysis of Time Complexity in ms

Figure 8 displays the time analysis in ms for CNN, EVRS, EMBL, and HCGANN during rising epoch numbers. The time complexity of CNN, EVRS, and EMBL rises progressively as the number of epochs increases, resulting in EVRS's most rapid complexity expansion. The analysis shows that HCGANN computes with dramatically reduced complexity than other methods, indicating an efficient operation process. The experimental data demonstrates that HCGANN delivers superior computational capabilities, making it a better selection for large dataset analysis within COVID-19 outcome prediction.

5. Conclusion

The proposed system uses a systematic method to boost prediction accuracy for vaccination impact by joining advanced modelling approaches. The Min-Max normalizer processes initial patient data by scaling all data attributes to maintain uniformity of range values. The preservation of data consistency at this stage eliminates potential sources of wrong data that could affect later calculations. The SCA works within the system by finding absolute feature limits that reveal the main factors which affect vaccination results. Feature selection receives enhancement through the SIWOA that triggers a reduction in non-mutual feature weights to maintain essential analytical attributes for analysis isolation. Removing redundant attributes accelerates system computing operations while leading to more precise forecast outcomes. An HCGANN uses the processed dataset to perform an evaluation utilizing the ideal feature limits and correlation vectors to detect interdependent features. The solution enables the system to produce exact vaccine recommendations by organizing individuals according to risk factors and vaccination requirements through appropriate classification methods.

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