Comparative Analysis of Optimization Algorithms for Enhancing Artificial Neural Network Accuracy in Predicting Global Monkeypox Cases Trends

Selmi Dina Aulia[1] **Alam Rahmatulloh**[1]* **Siti Yuliyanti**[1]

[1]*Siliwangi University, Indonesia*
* Corresponding author's Email: alam@unsil.ac.id
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Abstract

Monkeypox (MPXV) was declared a Public Health Emergency of International Concern (PHEIC) by the World Health Organization due to its rapid global spread and public health impact. This study proposes a trend-aware prediction model using an Artificial Neural Network (ANN) evaluated under four schemes: baseline ANN and ANN optimized using Particle Swarm Optimization (PSO), Harris Hawks Optimization (HHO), and Genetic Algorithm (GA). A global cumulative MPXV dataset obtained from Our World in Data, covering the period from June 2022 to June 2024, was utilized. Model performance was evaluated using Root Mean Squared Error (RMSE) and R-squared (R^2). Experimental results indicate that the ANN-GA model achieved the best performance, reducing RMSE by 29.59% from 0.196 to 0.138 and improving R^2 from 0.9936 to 0.9968. These findings demonstrate that metaheuristic optimization, particularly GA, can effectively enhance ANN performance for trend-based prediction of global monkeypox cases and provide a reliable framework to support public health decision-making.

Keywords: Artificial neural network, Epidemiology prediction, Genetic Aagorithm, Hyperparameter optimization, Monkeypox.

1. Introduction

Monkeypox (MPXV) is a zoonotic infectious disease that has become a global concern. First identified in monkeys in 1958, MPXV spreads through direct contact or respiratory droplets and causes symptoms such as fever, rash, and lymphadenopathy [1-4]. Although its transmission rate is lower than COVID-19, global cases have risen sharply, reaching more than 5,000 by 2020 and spreading beyond Africa since 2022 [5]. The absence of specific treatment underscores the need for accurate predictive tools to support global mitigation efforts [6].

Artificial intelligence, especially Artificial Neural Networks (ANN), has shown strong performance in epidemiological modeling, including COVID-19 forecasting [7-11] and MPXV classification and prediction [8-14]. A key study [15] reported that ANN outperformed LSTM and GRU in forecasting MPXV cases using data from June 2022 to February 2023 [16], but the dataset was limited in duration and coverage.

To address this gap, the present study uses a longer and globally comprehensive MPXV dataset (up to mid-2024) and evaluates ANN performance enhanced with three metaheuristic optimizers—Harris Hawks Optimization (HHO), Particle Swarm Optimization (PSO), and Genetic Algorithm (GA). These algorithms have previously improved prediction tasks such as groundwater modeling, air quality forecasting, and disease classification [17-20].

This research compares the optimization performance of HHO, PSO, and GA on ANN for global MPXV prediction by tuning key hyperparameters and evaluating models using RMSE and R^2. The novelty lies in combining a longer global dataset with a comparative analysis of three optimization algorithms, which has rarely been applied simultaneously in MPXV forecasting.

2. Related work

Various studies have shown that Artificial Neural Networks (ANN) play an important role in predicting infectious diseases, including MPXV. ANN has been widely applied in forecasting cardiovascular diseases, air quality, agricultural output, electricity load, and infectious diseases such as tuberculosis and monkeypox. These studies highlight the need for more accurate ANN-based models to support epidemic mitigation, especially when combined with optimization algorithms such as Genetic Algorithm

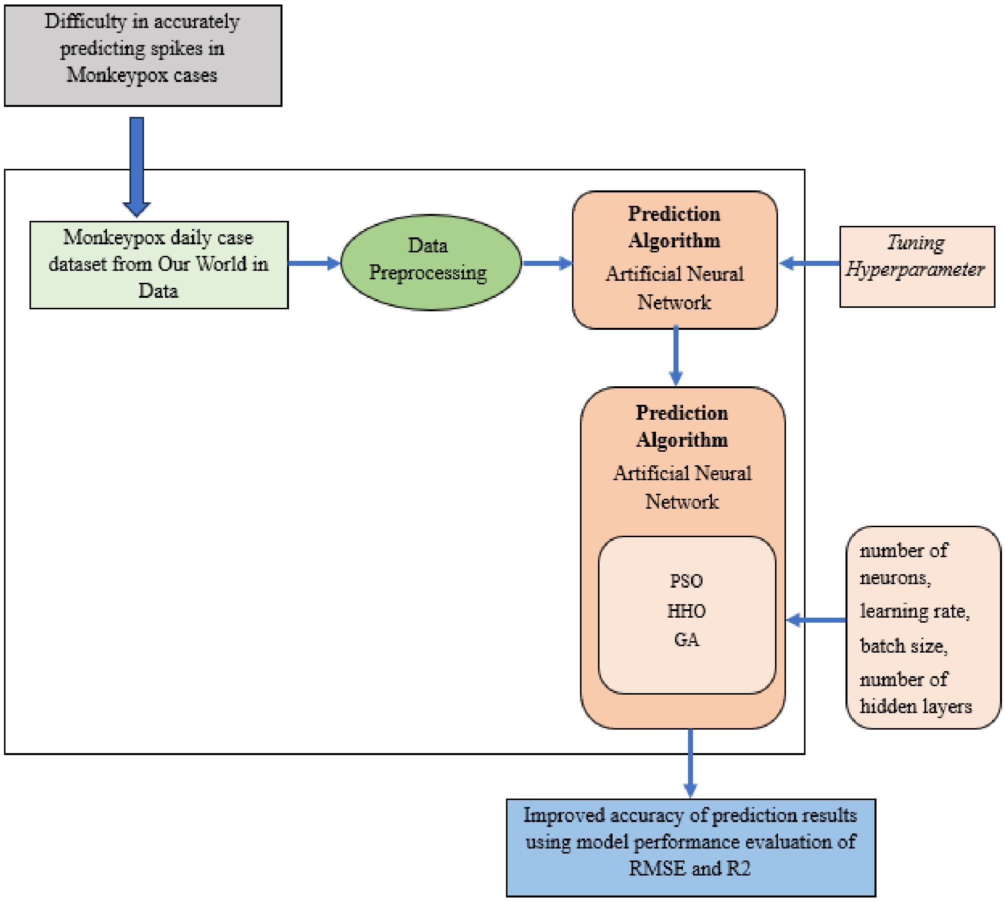

Figure. 1 Research Framework

(GA), Particle Swarm Optimization (PSO), and Harris Hawks Optimization (HHO), which have been shown to significantly enhance model performance.

AI-based epidemiological modeling has grown rapidly, with ANN demonstrating high accuracy in predicting COVID-19 cases and mortality in Egypt, Saudi Arabia, and Pakistan [9-11]. Deep learning models like VGG16 have also been used to classify MPXV infections [8], while NAR-ANN has supported various forecasting tasks. For MPXV specifically, ANN models using ECDC datasets have been used to project case growth in several countries [12], complemented by machine learning–filtering hybrids [13] and stochastic or time-series approaches [14].

Key literature also shows that ANN outperformed LSTM and GRU when predicting MPXV cases using OWID data from June 2022 to February 2023 [15, 16]. However, these studies were limited by short timeframes and restricted geographic coverage, indicating the need for broader global datasets.[15], [16].

Research on optimization algorithms further supports their effectiveness: GA improved cardiovascular disease prediction by 5.08% [19], PSO increased air quality prediction accuracy to 99.03% [18], and HHO produced strong results in groundwater and erosion prediction [17]. ANN combined with PSO or GA has also yielded improvements in forecasting tuberculosis [20], gold prices [21], tidal patterns [22], and industrial production [23]. Additional studies reinforce ANN's strong performance across domains such as electricity load forecasting [24-26], inflation prediction [27], and water production forecasting.

Thus, based on the literature evidence, the integration of ANN with HHO, PSO, and GA has significant potential to improve epidemiological prediction performance, particularly in MPXV cases. This study evaluates the optimal hyperparameter combinations in the ANN model to achieve more accurate and reliable predictions.

3. Material and method

This research method is designed to build and evaluate ANN models in predicting MPXV cases with global data coverage and a longer period. In addition, this research compares several optimization algorithms to improve the prediction accuracy of the model. Fig. 1 illustrates the main stages in the research process.

	date	Andorra	Angola	Argentina	Aruba	...	total_cases
0	2022-06-03	0	0	2	0	...	1372
1	2022-06-04	0	0	2	0	...	1392
2	2022-06-05	0	0	2	0	...	1410
3	2022-06-06	0	0	2	0	...	1504
4	2022-06-07	0	0	3	0	...	1919

Figure. 2 Monkeypox cases

	date	total_cases
0	2022-06-03	1372
1	2022-06-04	1392
2	2022-06-05	1410
3	2022-06-06	1504
4	2022-06-07	1919

Figure. 3 Data used

3.1 Data acquisition

This study uses time series data obtained from the official Our World In Data site, which provides open data on the cumulative number of monkeypox (Monkeypox Virus – MPXV) cases globally. This dataset is published openly to support transparency and collaboration in research related to infectious diseases. The data is sourced from reports submitted by each member country and is regularly compiled for epidemiological analysis and case trend prediction purposes. Fig. 2 shows the raw monkeypox case data from around the world before any preprocessing.

The dataset used in this study has a univariate time series format, where only one main variable is observed over time: the total cumulative number of cases. The observation period for this dataset spans from June 3, 2022, to June 3, 2024, with a total of 732 observations. The attributes used in this study consist of two main columns:

a. date: reporting date.
b. total_cases: cumulative number of confirmed monkeypox cases up to that date.

Fig. 3 shows the first five entries in the dataset used.

To gain an initial understanding of the trend in case development, a time series graph was visualized showing the number of cases against the reporting date. Fig. 4 shows the growth trend in the cumulative number of global monkeypox cases during the observation period. A sharp exponential growth phase was observed between June and October 2022,

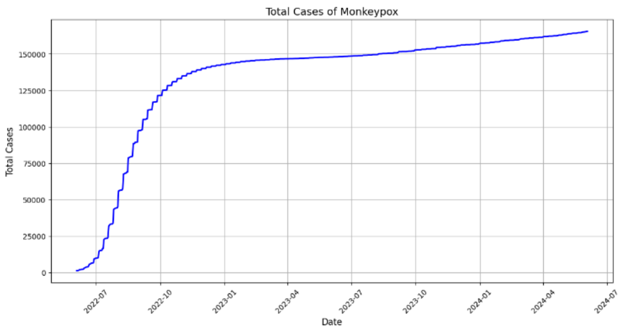

Figure. 4 Growth trend of the cumulative case number

indicating a highly active spread phase. By the end of 2022 to 2023, the growth rate showed a flattening trend, although the number of cases continued to increase. Throughout 2023 to mid-2024, case growth remained stable and linear, reflecting that disease transmission was still occurring but at a lower intensity compared to the early stages of the pandemic.

3.2 Data preprocessing

The global Monkeypox dataset obtained from Our World in Data contains 732 daily observations of cumulative MPXV cases spanning from June 3, 2022, to June 3, 2024. The dataset contains no missing values, duplicate entries, or gaps in the date sequence, allowing it to be used directly without imputation. The date column was converted into a datetime format, and calendar-based features (day of year, month, and week of year) were extracted to support temporal learning

The target variable (total_cases) was separated from the input features, and Min–Max normalization was applied to scale all variables into the range [0,1] to improve training stability. To preserve the temporal structure of the time series, the dataset was split chronologically, with the earliest 80% of observations used for training and the most recent 20 % used for testing, and data shuffling disabled. The Min–Max scaler was fitted only on the training data and subsequently applied to the validation and test sets to avoid information leakage. Model stability was further evaluated using Time Series Cross Validation (TimeSeriesSplit) with five folds, which maintains temporal order by progressively expanding the training set and validating on subsequent data segments. All reported evaluation metrics were computed after inverse transformation to the original data scale.

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3.3 Data preprocessing

3.3.1. Particle swarm optimization

Particle Swarm Optimization (PSO) is a population-based optimization algorithm that mimics the social behavior of swarms in searching for optimal solutions. This algorithm was first introduced by Kennedy and Eberhart in 1995 and further developed in 1997. PSO operates by modeling each individual in the population as a particle, which updates its position and velocity based on its personal best (pbest) and the global best (gbest) of the entire population. This algorithm mimics the mechanisms of a colony in finding the fastest path to a food source, making it applicable to various computational problems to find efficient solutions [28]. The movement of each particle is updated based on its previous velocity and two main components: individual exploration and global exploration.

Eq. (1) represents the update of the particle's velocity in dimension d, Eq. (2) represents the update of the particle's position in dimension d, and in this process, fitness is calculated by performing forward propagation of the ANN model with a combination of tested hyperparameters. The particle's position here represents the new hyperparameter values that will be used to train the ANN model in the next iteration. This process is used to evaluate the quality of the model based on its predictive ability

$$v_{i,d}^{t+1} = w\, v_{i,d}^{t} + c_1 r_1 \left(pbest_{i,d} - x_{i,d}^{t}\right) + c_2 r_2 \left(gbest_d - x_{i,d}^{t}\right) \quad (1)$$

$$x_{i,d}^{t+1} = x_{i,d}^{t} + v_{i,d}^{t+1} \quad (2)$$

$$w = W_{max} - \frac{(W_{max} - W_{min}) \text{ x } iter}{iter_{max}} \quad (3)$$

Where :

$v_{i,d}^{t+1}$	: velocity of particle i in dimension d at iteration t
$x_{i,d}^{t+1}$	: position of particle i in dimension d
$pbest_{i,d}$	: best individual position
$gbest_d$	: best global position
$c_1 c_2$	: learning factors
$r_1 r_2$	: random numbers in the range [0,1]
w	: inertia weight

3.3.2. Harris hawks optimization

The Harris Hawks Optimization (HHO) algorithm is a population-based optimization algorithm inspired by the hunting behavior of Harris hawks (Parabuteo unicinctus), which includes prey search, sudden attack, and siege. This algorithm consists of two main phases: exploration and exploitation. Harris hawks act as candidate solutions, and the best solution is considered the prey. The optimization process is carried out through the updating of the hawks' positions, which are adjusted based on the hunting strategy used, mathematically optimized to maximize the search for the best solution.

In the exploration phase, the hawk searches for solutions using two strategies based on a random value q. If q ≥ 0.5, the hawk perches near other individuals to expand the search. If q < 0.5, the eagle selects a random location to explore further. This exploration phase aims to expand the search for solutions, while the exploitation phase is used when energy |E| < 1, where the eagle will focus on the best solution found. This strategy is modeled in Eq. (4) and (5), and Fig. 5 shows the phases of the HHO optimization algorithm.

$$X(t+1) = \begin{cases} X_{rand}(t) - r_1 \left|X_{rand}(t) - 2r_2 X(t)\right|, & q \geq 0.5 \\ \left(X_{rabbit}(t) - X_m(t)\right) - r_3\left(LB + r_4(UB - LB)\right), & q < 0.5 \end{cases} \quad (4)$$

Where :

X_{rand}	: Random position in the search space
$X_{rabbbit}$	: Best position found (prey)
X_m	: Average position of the eagle population
LB, UB	: Lower and upper search limits
r_1, r_2, r_3, r_4, q	: Random parameters in the interval [0,1]

The average position of the eagle is calculated in the interval [0,1]

$$X_m(t) = \frac{1}{N}\sum_{i=1}^{N} x_i(t) \quad (5)$$

where N is the total population of eagles.

Next, the exploitation phase is performed when the energy E satisfies |E| < 1. The energy value is calculated as follows: using Eq. (6).

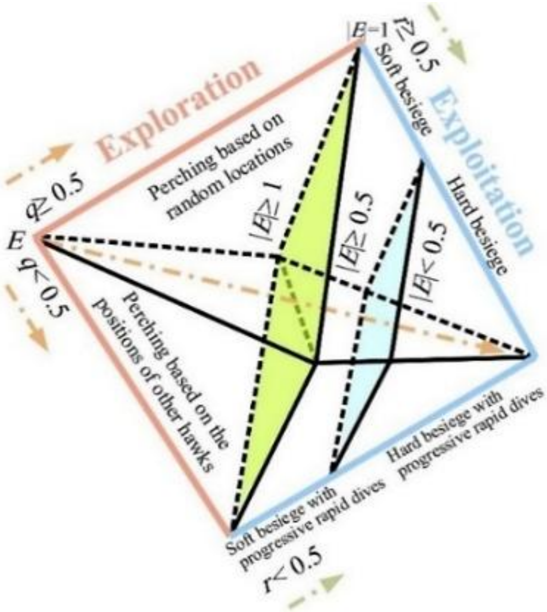

Figure. 5 Phase of the HHO algorithm [29]

$$E = 2E_0\left(1 - \frac{t}{T}\right) \tag{6}$$

t is the current iteration, and T is the maximum number of iterations. T and E_0 take values between -1 and 1, indicating that the prey's energy decreases as it escapes. If $|E| \geq 1$, the eagles search for a new area (exploration), while if $|E| < 1$, they exploit the existing solution environment. When $|E| \geq 0.5$, the prey can still escape, so a soft besiege is applied. If $|E| < 0.5$, the prey is too exhausted to escape, so the Harris hawk applies a strict, hard besiege before launching the final attack. Iterations continue until the termination condition is met, such as the maximum number of iterations or convergence of the best solution. The final result is the best location found by the hawk and the associated fitness value [29].

3.3.3. Genetic algorithm

Genetic Algorithm (GA) is an evolutionary optimization algorithm inspired by Darwin's theory of natural selection, which emphasizes natural selection [31]. GA is used to explore the solution space of a problem through evolutionary stages such as selection, crossover, and mutation to obtain the best solution.

The GA process begins with the formation of chromosomes and populations. Chromosomes represent potential solutions in the form of genes, which can be binary numbers, real numbers, or permutations. A set of chromosomes forms a population, and the population size is determined by initial parameters. Each chromosome is then evaluated using a fitness function to assess how well the solution addresses the problem the higher the fitness value, the better the solution.

Next, the two best chromosomes are selected through the parent selection process for reproduction. This reproduction process includes crossover, which involves combining two parents to produce new offspring, and mutation, which randomly alters gene values to maintain solution diversity. The next stage is survivor selection, which involves selecting the best individuals from the previous population and offspring to form a new generation. This process is repeated until an optimal solution is achieved, fitness converges, or the iteration reaches its maximum limit [30].

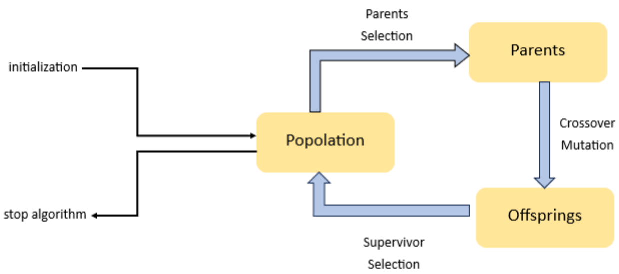

Figure. 6 Genetic algorithm process [30]

3.4 Modelling

Fig. 7 illustrates the Artificial Neural Network (ANN) architecture used in this study. The model adopts a simple feedforward structure with one hidden layer containing 64 neurons using a ReLU activation function, and a single output neuron for predicting the next value of MPXV cases. The baseline model is trained using Mean Squared Error (MSE) as the loss function..

To enhance predictive accuracy, the ANN is further optimized using three metaheuristic algorithms—Particle Swarm Optimization (PSO), Harris Hawks Optimization (HHO), and Genetic

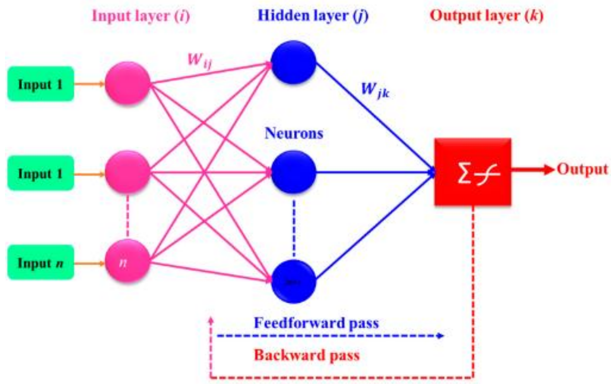

Figure. 7 ANN structure [32]

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Table 1. Scheme model

Scheme	Algorithm	Parameters	Optimized Hyperparameters
1	ANN Baseline	- 1 hidden layer, 64 neurons (ReLU) - Output layer: 1 neuron (linear) - Optimizer: Adam (default) - Loss: MSE - Epoch: 100 - Batch Size: 32 - Learning Rate: 0.001 - Callback: - EarlyStopping (patience=10)	Custom parameter baseline
2	ANN-PSO	- Particles: 10 - Iterations: 10 - Inertia weight: 0.5 - Learning factor: c1 = 1.5, c2 = 1.5 - Fitness: RMSE	- Number of neurons: 8 – 128 - Learning rate: 0.0001 - 0.01 - Batch size: 16 – 64 - Number of layers: 1 - 3
3	ANN-HHO	- Hawks: 10 - Iterations: 10 - Strategy: Soft/Hard besiege + Rapid dives - Initial energy $E_0 \in [-1, 1]$ - Fitness: RMSE	- Number of neurons: 8 – 128 - Learning rate: 0.0001 - 0.01 - Batch size: 16 – 64 - Number of layers: 1 - 3
4	ANN-GA	- Population: 10 - Generation: 10 - Parent selection: 4 best - Crossover: 1 random point - Mutation rate: 0.1 - Fitness: RMSE	- Number of neurons: 8 – 128 - Learning rate: 0.0001 - 0.01 - Batch size: 16 – 64 - Number of layers: 1 - 3

Algorithm (GA). These optimizers search for the best hyperparameters, including the number of neurons, learning rate, and batch size. Four model schemes, including the baseline and the three optimized versions, are compared as summarized in Table 1.

3.5 Evaluation

The evaluation assesses how accurately the model predicts MPXV cases compared to actual data. Two metrics are used: Root Mean Squared Error (RMSE) and R-Squared (R^2). RMSE measures the average difference between predicted and actual values, where smaller values indicate higher accuracy. R^2 represents the proportion of variance in the actual data explained by the model, with values closer to 1 indicating excellent predictive performance. The mathematical formulas for these two metrics are listed in Eqs. (7) and (8). All RMSE and R^2 values reported in this study were calculated on denormalized (original-scale) data after inverse transformation to ensure meaningful interpretation of prediction errors.

$$\text{RMSE} = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(y_i - y^{\wedge})^2} \tag{7}$$

$$\text{R2} = 1 - \frac{\sum\left(y^i - y^{\wedge}\right)^2}{\sum(y_i - y^{-})^2} \tag{8}$$

Where :

y_i : actual value
$y^{\wedge}$: predicted value
y^{-} : average value of actual values
n : number of data points

4. Result and discussion

This study formulates the prediction task as a trend-aware estimation of cumulative MPXV cases rather than short-horizon autoregressive forecasting. Calendar-based temporal features are employed to capture long-term epidemic dynamics, while lag-based inputs are intentionally excluded to ensure a consistent and fair comparison of metaheuristic optimization algorithms within the same ANN framework.

After baseline model training is complete, ANN model optimization is carried out using three metaheuristic algorithms, namely GA, PSO, and HHO. This optimization focuses on finding the best hyperparameter values to improve model performance. The best hyperparameter combination obtained from each algorithm can be seen in Table 2.

Table 2. Best hyperparameter

Scheme	Number of Neurons	Learning Rate	Batch Size	Number of Hidden Layers
1	64	0.001	32	1
2	128	0.000717	27	1
3	116	0.000100	44	1
4	86	0.001176	42	1

Table 3. Evaluation of each model

Scheme	RMSE	R^2
1	0.196	0.9936
2	0.265	0.9883
3	0.271	0.9877
4	0.138	0.9968

The hyperparameter is obtained based on the evaluation of the lowest fitness value (RMSE) during the training and validation process. This configuration is then used to rebuild the ANN model with the best performance from each optimization algorithm. After optimization is completed, each optimized model is then evaluated using three main metrics, namely RMSE and R^2. The evaluation results of each tested model are presented in Table 3.

After the baseline model training is completed, ANN optimization is performed using three metaheuristic algorithms: GA, PSO, and HHO. The optimization process aims to identify the optimal hyperparameter configurations that minimize RMSE during training and validation, as summarized in Table 2. The resulting configurations are then used to reconstruct each optimized ANN model for final evaluation.

The evaluation results, presented in Table 3, indicate that the baseline ANN model achieves an RMSE of 0.196 with an R^2 of 0.9936, demonstrating a strong ability to capture the overall trend of MPXV case progression. However, the relatively higher RMSE suggests limited precision in quantitative estimation.

Among the optimized models, ANN-PSO and ANN-HHO yield RMSE values of 0.265 and 0.271, respectively, with R^2 values above 0.98. Although these models maintain strong trend representation, their higher RMSE values compared to the baseline indicate reduced accuracy in estimating extreme values, likely due to extensive exploration during optimization. In contrast, the ANN-GA model achieves the best performance, with an RMSE of 0.138 and an R^2 of 0.9968, indicating superior accuracy and robustness in reproducing the actual data pattern.

Figure. 8 Training & loss validation ANN-GA

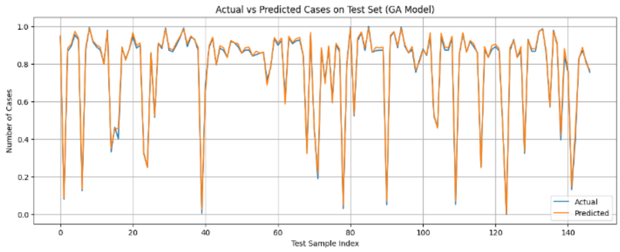

Figure. 9 Actual and predicted comparison on ANN-GA

Fig. 8 illustrates the training and validation loss curves of the ANN-GA model, showing stable convergence without overfitting. Fig. 9 compares the actual and predicted values on the test set, where the predictions closely follow the observed trend, confirming excellent generalization performance.

Furthermore, the results will be compared with several previous studies that also discuss the prediction of monkeypox cases, to see how competitive the performance of the proposed model is compared to other approaches, both in terms of methods, data coverage, and evaluation metrics used. Table 4 below presents a comparison of the prediction performance of this research with previous relevant studies.

As shown in Table 4, the RMSE values obtained in this study are consistently lower than those reported in previous works. This improvement can be attributed to the longer observation period used (June 2022–June 2024), which enables the model to learn more complete epidemic trends compared to earlier studies limited to data up to February 2023. Consequently, the lower RMSE values reflect enhanced trend learning rather than anomalous performance.

5. Conclusions

This study presents a comparative analysis of metaheuristic optimization algorithms for enhancing ANN performance in predicting global cumulative

Table. 4 Comparison of research results

Research	Title	Dataset	Model	Optimization	RMSE	R2
[33]	Machine Learning In Epidemiology: Neural Networks Forecasting Of Monkeypox Cases	Our World in Data (June – Feb 2023)	**ANN**	Levenberg Marquardt (LM)	**1.053**	**0.9999**
			GRU		1.249	0.9980
			LSTM		1.204	0.9988
[15]	A Comprehensive Analysis Of The Artificial Neural Networks Model For Predicting Monkeypox Outbreaks	Our World in Data (June – Feb 2023)	**ANN**	Levenberg Marquardt (LM)	**1.74**	**0.9999**
			LSTM		1.75	0.9976
			GRU		1.76	0.9980
This research	Comparative Analysis of Optimization Algorithms for Enhancing Artificial Neural Network Accuracy in Predicting Global Monkeypox Cases	Our World in Data (June 2022- June 2024)	ANN	-	0.196	0.9936
				HHO	0.271	0.9877
				PSO	0.265	0.9883
				GA	**0.138**	**0.9968**

MPXV cases using a long-term dataset spanning June 2022 to June 2024. Experimental results demonstrate that Genetic Algorithm (GA) provides the most effective optimization, achieving the lowest RMSE (0.138) and the highest R^2 (0.9968), outperforming both the baseline ANN and models optimized using PSO and HHO. The findings confirm that metaheuristic optimization does not uniformly improve performance across all metrics, and that GA is particularly effective in refining ANN hyperparameters for trend-aware epidemic prediction. Although lag-based inputs were not incorporated in this study, the proposed framework provides a fair and consistent basis for evaluating optimization strategies, and can be extended in future work to support short-term forecasting tasks.

Conflicts of interest

The authors declare no conflict of interest.

Author contributions

Conceptualization, Selmi Dina Aulia and Alam Rahmatulloh; methodology, Selmi Dina Aulia; software, Selmi Dina Aulia; validation, Selmi Dina Aulia; formal analysis, Selmi Dina Aulia; investigation, Selmi Dina Aulia; resources, Alam Rahmatulloh and Siti Yuliyanti; data curation, Selmi Dina Aulia; writing—original draft preparation, Selmi Dina Aulia; writing—review and editing, Alam Rahmatulloh and Siti Yuliyanti; visualization, Selmi Dina Aulia; supervision, Alam Rahmatulloh and Siti Yuliyanti; project administration, Alam Rahmatulloh.

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