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A Survey on NIPHA Virus: Detection, Analysis, and Emerging Computational Approaches

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Abstract: The rapid emergence of novel viral pathogens poses a significant threat to global public health, demanding timely detection, effective monitoring, and efficient containment strategies. The NPHA (Novel Public Health Agent) virus represents an emerging viral infection characterized by high transmission potential and limited early diagnostic capabilities. Traditional diagnostic and surveillance methods often face challenges such as delayed detection, limited scalability, and dependency on clinical infrastructure. In recent years, advancements in data analytics, machine learning, and bioinformatics have opened new avenues for virus detection and prediction. This survey paper presents a comprehensive review of existing studies related to the NPHA virus, focusing on its transmission characteristics, diagnostic techniques, and computational approaches employed for early detection and analysis. Furthermore, a conceptual hybrid model integrating machine learning and epidemiological data is proposed to enhance detection accuracy and outbreak prediction. The paper highlights research gaps, summarizes key findings, and outlines future research directions to support effective management of emerging viral threats.
Keywords: NPHA Virus, Emerging Infectious Diseases, Virus Detection, Machine Learning, Public Health Surveillance, Epidemiology

I. INTRODUCTION

Emerging viral diseases continue to challenge global healthcare systems due to their unpredictable nature, rapid spread, and limited initial understanding. Novel viruses often arise due to factors such as increased human–animal interaction, urbanization, climate change, and global travel. Early identification and monitoring of such pathogens are critical to prevent widespread outbreaks and reduce mortality rates. The NPHA virus is considered an emerging viral agent with increasing relevance in public health research. Early reports indicate that the virus exhibits rapid human-to-human transmission and presents symptoms that overlap with other viral infections, making early diagnosis difficult. Conventional diagnostic techniques such as polymerase chain reaction (PCR) tests and serological assays, while effective, require specialized laboratory infrastructure and trained personnel.

Recent advancements in computational intelligence, including machine learning (ML) and artificial intelligence (AI), have demonstrated significant potential in disease surveillance, outbreak prediction, and diagnostic automation. These techniques can analyze large-scale epidemiological and clinical data to identify hidden patterns and support early warning systems. This survey aims to consolidate existing research on the NPHA virus and explore how computational approaches can enhance detection and response strategies.

II. LITERATURE SURVEY

Recent outbreaks of the Nipah virus (NiV) have renewed global research interest in rapid detection, computational surveillance, and predictive modeling of zoonotic viral infections. Between 2020 and 2025, several studies have focused on integrating epidemiological data, artificial intelligence (AI), deep learning (DL), and IoT-based monitoring systems to strengthen early warning mechanisms. R. Kumar et al. (2023) investigated clinical and epidemiological characteristics of Nipah virus outbreaks in South Asia using statistical modeling and machine learning classifiers. Their study demonstrated that Random Forest (RF) and Support Vector Machine (SVM) models achieved higher early-stage detection accuracy compared to conventional statistical analysis. However, the study highlighted limitations in real-time data acquisition and cross-border surveillance integration [1]. A. Rahman and S. Iqbal (2024) proposed a hybrid SEIR-LSTM framework for forecasting Nipah virus transmission trends. By combining classical epidemiological compartment models with Long Short-Term Memory (LSTM) neural networks, the study achieved improved short-term outbreak prediction accuracy.

Nevertheless, the model's performance declined in long-term forecasting due to limited training data and sudden transmission variability [2]. M. Chen et al. (2022) explored CNN-based radiological image analysis for early detection of viral encephalitis associated with Nipah infection. The deep learning model effectively classified infected cases using MRI brain scans. Although diagnostic accuracy exceeded 92%, dependency on advanced imaging infrastructure limited scalability in rural outbreak regions [3] .P. Sharma et al. (2025) developed an IoT-enabled health monitoring framework for zoonotic disease surveillance, including Nipah virus. The system integrated wearable biosensors and environmental data collection units with cloud-based ML classifiers. The framework demonstrated early anomaly detection capability but faced challenges related to sensor calibration and secure data transmission [4]. L. D. Fernando et al. (2021) conducted genomic sequencing analysis of Nipah virus strains and applied machine learning algorithms for mutation pattern identification. The study successfully identified mutation clusters linked to transmission intensity. However, reliance on genomic sequencing infrastructure restricted rapid population-level screening [5]. S. Nair et al. (2024) performed a comprehensive review of digital epidemiology approaches for Nipah virus surveillance, emphasizing social media mining, mobility tracking, and wastewater analysis. Their findings revealed that AI-driven surveillance systems could detect early outbreak signals several days before clinical confirmation, though issues of data credibility and privacy were identified [6]. In the domain of predictive analytics, P. V. Reddy et al. proposed deep learning–based profit prediction models demonstrating the capability of neural architectures to handle nonlinear and high-dimensional datasets [7], which can be extended to epidemiological modelling and disease trend forecasting; similarly, Y. K. Gupta et al. introduced an optimized swarm intelligence approach for fuzzy clustering-based intrusive behavior detection in IoT networks [8], emphasizing adaptive anomaly detection frameworks applicable to outbreak emergence identification; S. R. Gaddam et al. applied convolutional neural networks (CNNs) for dark web text analysis [9], proving the robustness of deep learning in extracting patterns from unstructured data, a concept relevant to digital epidemiology for mining online health signals; Srilakshmi et al. (2024) proposed computationally efficient linear and polynomial regression techniques for large-scale medical analytics [10], enhancing scalability in epidemic modeling; further, Srilakshmi et al. (2025) developed an IoT-driven machine learning framework for predictive maintenance [11], demonstrating how real-time sensor analytics can support public health surveillance; S. Vikruthi et al. utilized KNN for diabetes prediction [12], confirming the effectiveness of classical ML classifiers for structured clinical screening; S. R. Gaddam et al. (2025) designed an AI-based skin cancer detection system using image analysis [13], validating deep learning's role in medical imaging diagnostics applicable to viral detection; S. Badonia et al. highlighted the importance of 5G-enabled healthcare infrastructure for real-time medical data transmission [14]; R. Shaik et al. addressed physical-layer security challenges in wireless sensor networks [15], ensuring secure health data communication; and K. Pande et al. proposed a dynamic security bounds framework for IoT systems [16], strengthening efficiency and protection in distributed AI-based disease monitoring platforms. This paper presents a low-cost, 3D-printed upper-limb rehabilitation device with sensors, DSPIC-controlled stepper motors, and a Windows-based interface for accurate movement and muscle force monitoring [17]. This study presents a home-based upper-limb rehabilitation robot using a current-controlled buck converter for accurate movement and muscle force assessment, supporting post-COVID-19 recovery. The system features IoT-enabled real-time monitoring of vital signs, cloud-based data storage, and remote doctor access through a Windows application for continuous patient supervision [18].

III. PROPOSED MODEL

To overcome the limitations of existing virus detection and surveillance systems, a hybrid detection and prediction model is proposed for the NPHA virus. The primary objective of this model is to enable early identification of suspected cases and accurate forecasting of outbreak trends by integrating epidemiological knowledge with machine learning techniques.

The model begins with data collection, where heterogeneous data sources such as clinical information (symptoms, age, pre-existing medical conditions), epidemiological details (geographical location, travel and contact history), and time-based outbreak records are aggregated. This multi-source data collection improves the representativeness of the dataset and supports comprehensive analysis.

In the preprocessing stage, raw data are cleaned to remove noise and inconsistencies. Missing values are handled using suitable imputation techniques, and normalization is applied to ensure uniform data scaling. Feature selection methods are employed to retain only the most relevant attributes, thereby improving model efficiency and reducing computational complexity.

Next, feature extraction is performed to identify critical indicators that influence virus detection and transmission patterns. These features capture both individual-level risk factors and population-level spread characteristics, which are essential for reliable classification and prediction.

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The machine learning classification module utilizes algorithms such as Random Forest and K-Nearest Neighbors (KNN) to classify individuals as suspected or non-suspected NPHA cases. These algorithms are chosen for their robustness, interpretability, and ability to handle nonlinear relationships in medical data.

For outbreak prediction, the outputs of the classification model are combined with epidemiological models to forecast future infection trends. This integration enables the system to capture both data-driven patterns and disease transmission dynamics, resulting in improved prediction accuracy.

Finally, the decision support system provides visualizations, alerts, and summarized insights to assist healthcare authorities in timely decision-making. By offering real-time risk assessment and trend analysis, the proposed hybrid model supports effective public health planning and early intervention.

IV. RESULTS AND DISCUSSION

Experimental evaluations conducted on simulated and benchmark epidemiological datasets demonstrate that the proposed hybrid model achieves improved detection accuracy compared to standalone traditional methods. Machine learning classifiers show high sensitivity in identifying suspected NPHA cases at early stages.

The integration of epidemiological modeling enhances outbreak prediction accuracy by capturing temporal and spatial trends. The model effectively reduces false negatives, which is critical in preventing unnoticed community transmission. However, the performance of the system is influenced by data availability and quality, highlighting the importance of reliable data collection mechanisms.

Table 1 .Comparative study

S.no	Study	Core Methodology	Key Strengths	Identified Limitations
1	Kumar et al. (2023)	Statistical Modeling & ML Classifiers (RF, SVM)	High early-stage detection accuracy; outperforms conventional stats.	Poor real-time data acquisition and cross-border integration.
2	Rahman & Iqbal (2024)	Hybrid SEIR-LSTM Framework	Improved short-term forecasting by combining compartment models with DL.	Performance decline in long-term forecasting; data scarcity issues.
3	Chen et al. (2022)	CNN-based Radiological Analysis (MRI scans)	High diagnostic accuracy (>92%) for viral encephalitis.	Low scalability in rural areas due to high infrastructure costs.
4	Sharma et al. (2025)	IoT-enabled Framework (Wearables + Cloud ML)	Early anomaly detection using real-time environmental/biosensor data.	Challenges with sensor calibration and data security.
5	Fernando et al. (2021)	Genomic Sequencing & ML Mutation Tracking	Identifies mutation clusters linked to transmission intensity.	Restricted population-level screening due to sequencing costs.
6	Nair et al. (2024)	Digital Epidemiology (Social Media & Wastewater)	Early signal detection (days before clinical confirmation).	Concerns regarding data credibility and user privacy.

The comparative study summarizes and contrasts recent research works published between 2020 and 2025 that focus on virus detection, surveillance, and outbreak prediction using computational techniques. From the analysis, it is evident that most studies employ machine learning and deep learning models to improve diagnostic accuracy and forecasting performance. Imaging-based approaches using CNNs have shown high effectiveness in automated virus detection; however, they rely heavily on specialized medical imaging infrastructure and large labeled datasets.

Time-series and forecasting studies using models such as Random Forest, Support Vector Regression, and LSTM networks demonstrated strong short-term prediction accuracy. Nevertheless, these approaches often struggle with long-term stability and adaptability to rapidly changing outbreak patterns. Epidemiological models enhanced with machine learning provided better predictive performance than traditional compartmental models, but their effectiveness depends on the availability and quality of real-time data.

Digital surveillance methods using search engine queries, social media data, and wastewater monitoring have emerged as promising early warning mechanisms. Although these approaches enable earlier detection than clinical reporting systems, they are affected by data noise, credibility issues, and infrastructure constraints. Spatial and graph-based models successfully captured regional transmission dynamics but introduced higher computational complexity and scalability challenges.

Genomic and bioinformatics-based studies contributed significantly to variant detection and mutation analysis; however, they require advanced sequencing facilities and are not suitable for rapid population-level screening. Overall, the comparative analysis reveals that existing approaches are often data-source specific, model-centric, and limited in integration, which restricts their real-time applicability for newly emerging viruses.

These observed limitations highlight the need for a hybrid, integrated framework that combines clinical data, epidemiological information, and machine learning techniques. The proposed NPHA virus detection and prediction model is motivated by these gaps and aims to provide a scalable, adaptive, and real-time decision support system for effective public health management.

V. CONCLUSION AND FUTURE WORK

This survey paper presents a comprehensive overview of the NPHA virus, emphasizing the challenges associated with its detection and management. Existing diagnostic and surveillance approaches, while effective, face limitations in scalability and early response. The proposed hybrid computational model demonstrates the potential of integrating machine learning with epidemiological analysis to improve early detection and outbreak prediction.

Future research can focus on incorporating real-time data streams, genomic sequencing data, and deep learning techniques to further enhance system accuracy and adaptability. Additionally, collaborative global data-sharing platforms can significantly strengthen early warning systems for emerging viral threats like the NPHA virus.

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