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Review Paper

A State to Art on Utilizing Immunopathogenesis for Nipah Virus Prediction Through Machine Learning Approaches

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Abstract

Immunopathogenesis can come into direct contact with viral illness. The Nipah virus is one of the human-transmitted viruses related to the Hendra virus (HeV), which can spread by contact with pets or the crash of Pteropus bats or flying foxes. It can cause encephalitis and other serious illnesses. The NiV was first discovered in Malaysia in 1998. Lung illness was then just found in the district of Kerala. The season of sap harvest, which is from winter to spring, corresponds with the onset of zoonotic diseases, which is one of the major stimuli and causes of numerous epidemics, according to WHO statistics. The new Paramyxovirus pathogen, which causes the devastating Nipah sickness, is a member of the large Henipavirus family. The goal of this work is to forecast and detect viruses by determining the maximum amount of machine learning efficacy before it dies. In modern medicine, PCR or serology are useful tools for diagnosing virulent infections, where the virus infects the body with blood immune cells and causes subclinical symptoms. This study attempts to map out the machine learning (ML) technique, which is one of the primary fields in data analysis, even though it is more important in many real-time applications; the health-care industry evaluates various machine learning algorithms for disease prediction and/or solution analysis. Clarifying the test results may take some time due to small issues in the healthcare sector. From a medical perspective, neither syringes nor approved medications are available to combat the Nipah virus. The outcome has so far resulted in a high death rate. Here, the synopsis of Nipah reports prepares researchers to closely monitor the illness during its initial stages and also monitors the medications connected to Nipah. In modern medicine, machine learning algorithms play a critical role in identifying the viruses causing suspicious and urgent cases by utilizing machine learning predictions.

KEYWORDS: Nipah Virus, Immunopathogenesis, Hendra virus, Henipaviruses.

1. INTRODUCTION

A wide term used to describe an organization that produces medical services to address the population's medical requirements is a healthcare center. In the healthcare industry, maintaining and retrieving medical records requires the cooperation of patients, doctors, suppliers, healthcare organizations, and IT companies. One of the world's industries

with the quickest growth rates over the past ten years has been healthcare in India. According to recent studies, healthcare analytics can predict a variety of ailments, including cancer, diabetes, stroke, and infectious diseases like COVID, Nipah, and Dengue, among others, by utilizing machine learning It is crucial to comprehend clinical data and then provide accurate and effective findings in the current era of artificial intelligence and data science. Furthermore, before developing intelligent prognostic models, handling medical data in machine learning is the essential step. Digital documentation of a patient's clinical history is called electronic health records, or EHR. It covers all of a patient's administrative clinical information inside a healthcare organization, including, among other things, his/her demographics, diagnosis, prescriptions, laboratory data, and associated costs. The extensive longitudinal patient data available in an EHR can be exploited to develop patient-centered, cost-inclusive healthcare solutions. A variety of medical data (such as sensitive clinical information, or EHR), might be difficult for people to infer from and use to guide their decisions. To better analyze data and make useful decisions, machine learning has been suggested for use in the healthcare industry. Therefore, this chapter addresses the crucial part that machine learning plays in the healthcare diagnosis phase while also introducing readers to traditional and contemporary medicine, zoonotic diseases, and machine learning.
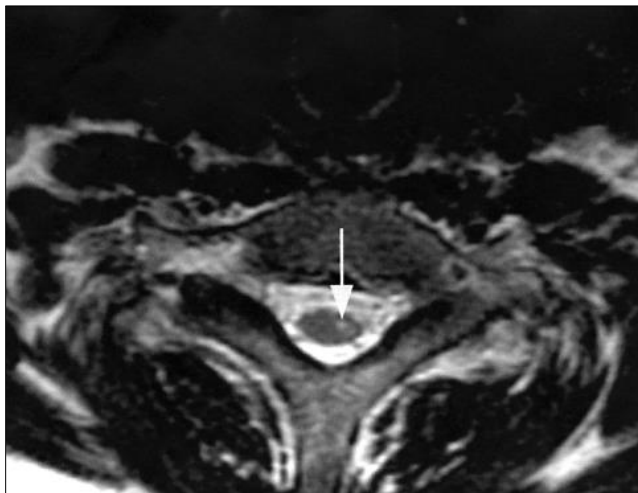

Fig 1: Nipa Virus Infected with MRI

Greek words zoon ("animal") and noses ("disease") are the roots of the word zoonosis, which is a combination of both. According to the World Health Organization (WHO), zoonoses are diseases and infections that are naturally spread from humans to other vertebrates [1]. Zoonoses are made easier since zoonoses depend on human-animal contact which cannot be eradicated in the future. Cohabitation between humans and animals is common in developing nations, particularly among rural communities. Pathogens circulating in wildlife travel closer to per-inland areas and aid in infecting animals and people in these environments as land-use changes, illegal wildlife trade, and other economic activities enhance proximity to wildlife. Such interaction

between animals and people has the potential to spread new infectious epidemics.

Table 1: NiVD Case Report (1998 to 2018)

Year	Country	Total Cases	Total Deaths
1998-99	Malaysia	265	105
1999	Singapore	11	1
2001	Bangladesh	13	9
2001	India (Siliguri)	66	45
2003	Bangladesh	12	8
2004		67	50
2005		12	11
2007		18	9
2007	India (Nadia)	5	5
2008	Bangladesh	11	9
2009		4	1
2010		16	14
2011		44	40
2012		12	10
2013		24	21
2014		18	9
2014	Philippines	17	9
2015	Bangladesh	9	6
2018	India (Kozhikode)	19	17

Hendra virus (HeV) and Nipah virus (NiV) are categorized as Biosafety Level-4 (BSL-4) agents due to the severe pathogenicity of Henipaviruses. It can be argued that it is difficult to collect and handle samples of a non-destructive sickness carefully. Therefore, by World Health Organization (WHO) recommendations [2], stringent operating procedures are being allowed for physical infrastructure, personal protection equipment, and clinical research operations. In many local areas, BSL-4 amenities could be scarce. In such circumstances, virus inactivation after sample collection may reduce human-to-human transmission when agents with BSL-3 and BSL-2 equipment are involved.

Fig 2: Map of NiVD Outbreak

NiV Encephalitis Detection using MRI

The Japanese encephalitis virus, which is believed to be the disease's cause, appeared in Malaysia and many other countries of Asia as a result of an epidemic of deadly infectious encephalitis among pig farmworkers [3]. A previously unidentified virus, however, was shown to be the primary cause of encephalitis eruption in March 1999, according to virus isolated and serum samples. Not known as the Nipah virus and categorized as a member of the Paramyxoviridae family, this unique virus is taxonomically separate from the Japanese encephalitis [4] virus (Figure 1.4).
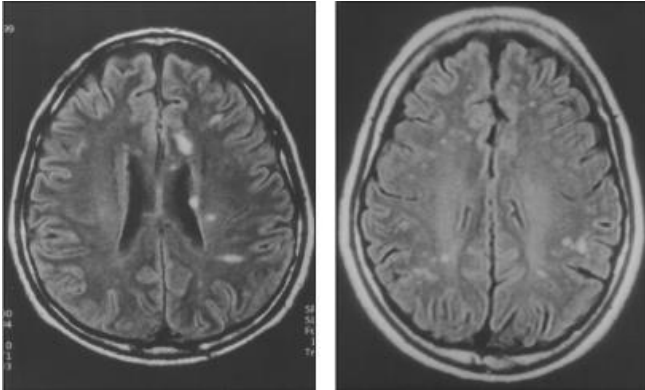

Fig 3: NiV Encephalitis findings in Humans during MRI Examination

2. RESEARCH OBJECTIVES AND SCOPE OF THE STUDY

Based on the pathological phenomena defined and the proposed solutions with the help of a machine and deep learning, it can be seen that no computerAided Diagnosis (CAD) model for humans has yet been proposed for animal-to-human transmission of Nipah. Therefore, the following is the primary goal of this research:

a) RO1: Investigate how Nipah disease is transmitted from animals to humans
b) RO2: Determine the actuality of the infection with information collected during the incubation phase.
c) RO3: Use the Restricted Boltzmann Machine (RBM) algorithm to select significant or beneficial parameters for early disease detection.
d) RO4: Integrate efficient machine learning algorithms to develop a new computer-aided prediction model (ensemble) for Nipah disease in humans.
e) RO5: Diagnose the infection of the Nipah disease by injecting the newly developed model with the clinical parameters obtained by RBM
f) RO6: Use the SHAP method to determine the extent to which the value of the clinical parameters studied and obtained may be indicative of Nipah disease.

RESEARCH CONTRIBUTION

The health sector has a challenging job limiting the spread of such a lethal disease because of some medical blunders and/or constraints. However, there are only a few licensed laboratories with the ability to diagnose such lethal diseases globally, including BSL-4 and BSL-3 [5], and NiV, which is also anticipated to cause another epidemic in the future [6]. Given the limitations of the medical field as described above, it is imperative to create a prediction model that can effectively treat human populations while also allowing quick pathogen detection. Therefore, a prognostic model must be put out to identify serious illnesses and forecast patient outcomes. There are numerous methods for doing this in the area of Artificial Intelligence. In today's clinical practice [7], machine learning predictive modeling can accurately diagnose patient health. Therefore, the machine learning techniques employed in NiVD diagnosis have been the focus of this research.

RESEARCH'S SIGNIFICANT CONTRIBUTIONS:

➤ For an optimal feature selection, a restricted Boltzmann machine is applied.
➤ Employing the most contemporary ML technology, an effective prediction model is developed.
➤ A hybrid ensemble algorithm (SEMC+RBM) has been proposed as a solution against NiVD prediction.

RESEARCH LIMITATIONS

➤ This study describes certain research limitations below based on previous research investigations.
➤ 1. Nipah does not yet have any recognized medical therapies or vaccinations due to its ferocity and lethal infectious nature.
➤ 2. No AI-based prediction model for human NiV illness has yet to be proposed.
➤ 3. The World Health Organization (WHO) has outlined the COVID-19 infection's precursor symptoms. But as of yet, there are no definite presymptoms for Nipah.

3. RELATED WORKS

Since Nipah disease is extremely severe, the paper only identified case-based study articles on "Diagnosis and Epidemiology", "Vaccination Development", "A rare and incurable disease", "Nipahvirus Analysis", and "Prioritization of surveillance of Nipah virus in India". As a reason, this chapter takes into account data from a variety of medical journals mentioned from Google Scholar, IEEE, Springer, Elsevier, MDPI, Hindawi, and PubMed, as well as recent case reports gathered from the websites of the WHO and NCDC. Nipah virus infection has been the subject of a thorough review by Aditi and M. Shariff [8]. The report includes biological data on Nipah agents and immunopathogenesis diagnostics that will be used in the hospital sector. Information was acquired by using several study publications. Additionally, methods for antibody detection are examined. An anti-Nipah web server was designed by Akanksha Rajput, Archit Kumar, and Manoj Kumar [9] using information gathered from several academic publications (PubMed) and patents. All resources are viral information and NiV inhibitors are available on the online source, and all information is merged with the QSAR model with the use of ML. it is a brand-new effort-calculating tool, however, no technique

is offered for this computation task. Sayantan Banerjee, *et al.,* [10] explained an incurable illness. Nipah epidemics on a broad scale were documented. It describes certain scientific tests as well as how and where Nipah affects the human body. They also offer some fundamental illness preventive measures

G Sharma, P. *et al.,* [11] employed a hybrid ML technique to forecast the T-Cell Lymphotropic pathogen, one of the series of retroviruses identified in 1980. This virus has been predicted using ML algorithms such the K-Means, RF, and various feature selection techniques. Some heuristic strategies, such as the AUROC method and K-fold cross-validation procedures, have been utilized to analyze and measure the performance of the proposed hybrid model. These techniques have allowed researchers to further study and understand the projected outcomes. Furthermore, hybrid models are trained and evaluated through the utilization of optimum features. To assess the reliability of the prediction model for HBsAg seroclearance, the authors [12] provide a framework of several ML models that includes four ML algorithms: XGBoost, RF, DT, and LOR (Logistic Regression). Authors [13] conducted research with the primary goal of predicting Kyphosis disease using the three classifiers most commonly used in the healthcare sector: RF, ANN, and SVM. During the model cross-validation process, the proposed models performed well, obtaining more than 80 percent accuracy. Davi C, *et al.,* [15] proposed an ML algorithm to diagnose dengue infection from the human genome. The purpose of the ML algorithm is to improve the patient report's accuracy. A manual sample collection of dengue-infected populations yielded 102 samples (Brazil). Here, the ANN is utilized to classify the patient's disease scenario, determining whether the case is severe or mild. The SVM is used to observe the ideal subset loci [14].
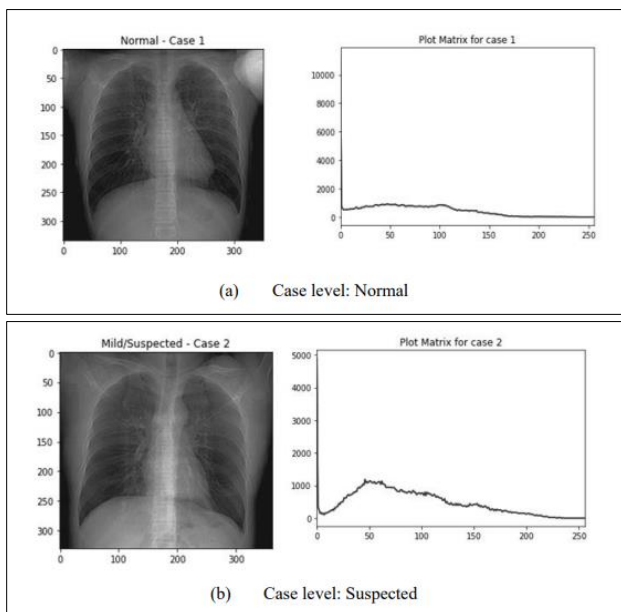

Fig 4: a) case level is normal **b)** suspected level

The action of the human genome serves as the foundation for this prognostic model. For the diagnosis of hepatitis disease [15], The stochastic methods of SVM and the simulated annealing (SA) algorithm are used. An estimated 1.5 million people die each year from hepatitis. Typically, it disrupts liver activity and causes inflammation. Weka, which is primarily used for predicting or forecasting tasks in the data mining field, was used to obtain the model result. When compared to other classification algorithms such as simple SVM, KNN, Naïve Bayes, K-Means, C4.5, RBF, and SMO, 31 the proposed SVM-Simulated Annealing algorithm achieved an accuracy of 88.08%, 0.814 Recall, and an F-measure of 0.844.

Table 2: explores a classification performance for tourist sentiment analysis the proposed method produces better performance results

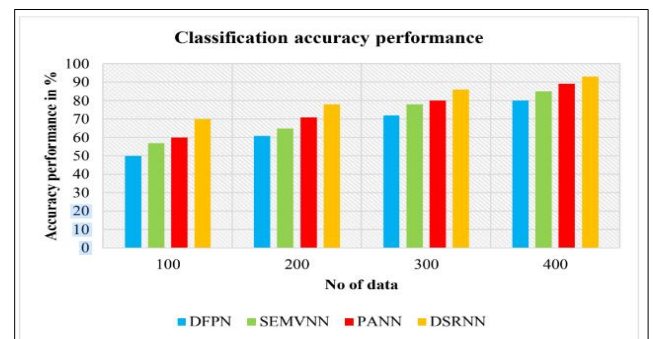| No of data	DFPN in %	SEMVNN in %	PANN in %	DSRNN in %
100	50	57	60	70
200	61	65	71	78
300	72	78	80	86
400	80	85	89	93

Fig 5: Comparison of Accuracy performance

Exploration of classification performance the proposed performance provides better result shown in figure 6. The proposed DSRNN gives at 93% for 400 data likewise the previous method result is DFPN is 80%SEMVNN result is 85%, PANN result is 89% and DFPN algorithm result is 80%.

RESEARCH GAP

All the research works are carried out concentrates on the CT scan images. In CT scan machine a facility is available to detect the blocks in the angiograms automatically. The cost of CT scan machine is very high compared to x-ray and also it may not be available in the remote areas. In x-ray angiograms no automated method available to detect the blocks in the coronary vessels of angiograms. The stenosis(block) detection is done by the doctors manually. The accuracy of manual detection depends upon the expertise of doctor. The existing methods provide an accuracy of maximum 89% in stenosis detection. The proposed research model automatically detects the blockages in the coronary vessels of x-ray angiograms.
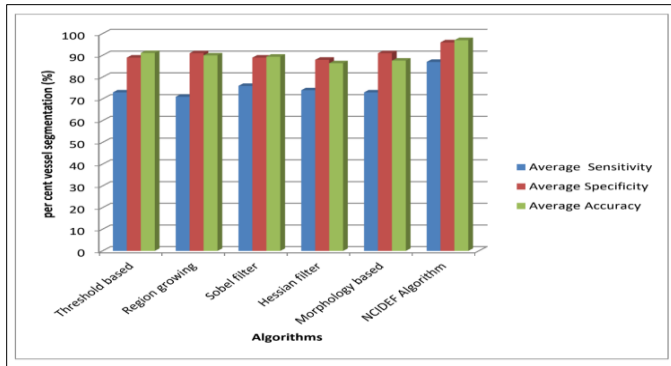
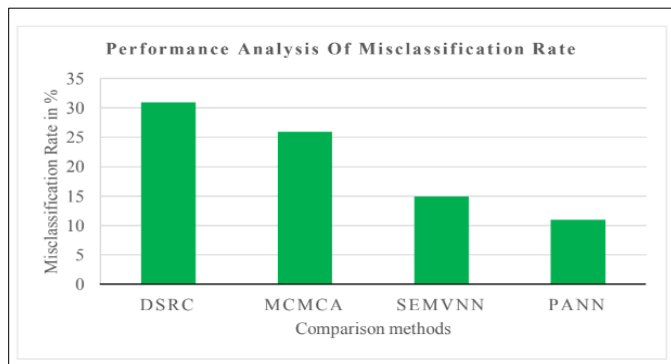**Fig 6:** Comparison of Features sensitivity, specificity, Accuracy

Fig 7: Performance analysis of misclassification rate

The above figure 7 shows the analysis of misclassification rate. The existing DSRC provides 31%, MVMCA provides 26%, SEMVNN provides 15% and the proposed PANN produces only 11%.

4. CONCLUSION

In-depth knowledge about Nipah disease and how NiVD is spread through animals is also discussed in this paper, along with the fundamentals of AI, machine learning, and its techniques, as well as the importance of machine learning throughout healthcare applications. The major goals of the research work are summarized in this chapter, which also highlights the clinical difficulties of the problem under consideration. The implications of various research strategies for symptoms-based or continuous blood test-based predictive models for various clinical or health issues were discussed in this section. This chapter demonstrates the widespread usage of supervised learning and ensemble learning algorithms in healthcare applications, particularly SVM, RF, DT learning, KNN, and Artificial Neural Networks. Additionally, integrating many healthrelated factors can result in the construction of a very accurate prediction model. The information regarding the precautions made against the forecast for the Nipah outbreak has also been reviewed in detail in this chapter. Clinical studies show that the illness of NiVD can induce inflammation in the human brain even in the absence of any preceding symptoms and that diffusion-weighted MR imaging techniques can detect the abnormalities in the human brain only after exposure to the virus, not at its early stages.

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