ESTABLISHMENT OF MACHINE LEARNING BASED MATHEMATICAL MODELING FOR PREDICTION OF MALARIA AND PNEUMONIA DISEASE

Annu, Ph.D. Scholar[1], Dr. Prof. R. S. Parihar[2]

[1,2]Department of Mathematics, Sunrise University, Alwar.

Abstract:

Infectious disease treatment is an internal medicine sub-specialty that specializes on the prevention and control of infections. In addition to catching the more common illnesses, internists often manage infections that are impossible to heal. Infectious disease drugs include understanding of the history of infectious, fungus, fungal and parasitic infections in humans, as well as knowledge of antibiotics, vaccine, and other diseases. Immunomodulating doctors are ideally equipped to deal with natural, occupational and host factors, causing vulnerability to infection, as well as basic principles in epidemiology and diffusing. For disease preventive practices, there are several separate models. Infectious disease physicians work in specialized clinic or perform a specialization such as internal medicine under general anesthesia. Most physicians of infectious diseases act as advisors to other specialists, see patients at their offices or hospitals in consultation, and even follow patients when giving care for their illnesses Many experts in the infectious diseases conduct their specialty with appropriate medical facilities. Some practitioners serve as an infectious disease doctors as well as a medical epidemiologists or infection prevention specialists. In academia, infectious disease doctors give continuing surgical and patient care consulting programmers, conduct science and clinical analysis, and educate medical students and tenants. Data collection is getting ever more sophisticated and diverse, because researchers need to connect with the public in order to make judgments regarding public health protection. There were many issues in our review: the ability to understand and utilize visualizations; the role of customer trust and organizational support in the application of these methods. Interoperability has now been a big concern.

Keywords - Infectious disease**,** Decision Tree Algorithm, Fuzzy Predictable Model, Parasitic Infections

I.   Introduction:

The theory that rules are observed by the transmission and dissemination of contagious diseases may be conceived in ancient mathematical language. A paper explaining the effects of the breach of smallpox (Introduction to Pollination) on life expectancy using Statistical Life Research (Dietz and Heesterbeek 2000) was written by Daniel Bernoulli in 1766. It was not until the twentieth century, though, that the nonlinear mechanisms of the spread of infectious diseases were fully recognized. There was considerable controversy at the turn of the century on whether the outbreak had stopped until theories of changing the virulence of the pathogen after a pandemic struck all those exposed. One of the first to understand that a dwindling density of susceptible individuals alone could avoid a pandemic was Hammer (1906). Sir Ronald Ross, a 1902 Nobel Prize laureate, used statistical modelling for his illustration of the life cycle of the malaria parasite to examine the efficacy of multiple prevention methods to fight malaria.

A series of papers were published by Kermack and McKendrick in 1927 in which they defined the dynamics of disease transmission in terms of a differential equation method. The notion of the sum of a threshold dividing numerous dynamic systems was developed by them. The infectious disease will replicate in a susceptible community only if the so-called simple replication number is over the threshold amount. This refers to the idea of herd immunity in the form of vaccines, suggesting that there is no requirement to vaccinate the whole community in order to prevent an infectious disease. During the eradication of smallpox in the 1970s, this hypothesis showed its merit. In order to eliminate this epidemic, worldwide vaccine coverage of about 80 percent with annular vaccine was appropriate.

1.1 The Beginning of Mathematical Modeling in Epidemiology:

The first paper concerned with statistical disease prediction dates back to 1766. In order to examine the mortality rate from smallpox in England, which at the time was 1 in 14 of all fatalities, Daniel Bernoulli established a statistical model. His model was used by Bernoulli to prove that vaccination against the virus will improve life expectancy by around three years at birth. In Sally Blower (2004), an English translation and analysis of this work can be included, while in Dietz and Heesterbeek (2002), an analysis of the key observations and an exposition of D'Alembert's critique occurs. In 1772, Lambert continued Bernoulli's work by expanding the model by adding criteria based on age. Laplace focused on the same idea as well; this line of study, though, was not consistently established until the historical work of Ross in 1911. In this thesis, Ross uses a priori mechanical simulation method to estimate discrete time dynamics for malaria using a series of equations. Kermack and McKendrick published three background papers following Ross' work, which developed the deterministic model of a partial outbreak. They discussed the super event in the propagation period of the disease in these posts, suggesting that the possibility of a vulnerable person (disease virgin) infecting the number of encounters with infected persons. Therefore, k-SI offers the rate of infection of susceptible and infected subjects, where S and I reflect the population density of susceptible and infected individuals, respectively. The rate at which damaged individuals heal is given by I in this sense, while the rate at which healed individuals become vulnerable is given by μR; the calculation constants are K and μ. This automatic deterministic representation is closely related to the collective action rule adopted by Guldberg and Waage in 1864 and is referred to as the SIR paradigm, which involves a homogeneous mixture of contacts and total mass (population) retention, and therefore comparatively low interaction rates. Forty years after the Ross paper, MacDonald extended the model of Ross to describe the malaria transmission mechanism in detail and propose methods of eradicating the disease at an organizational stage. Mathematical models for the dynamics and regulation of mosquito-borne diseases are classified as Ross MacDonald models, considering the relevance of McDonald's contribution to this area by leveraging the usage of computers.

At this point, the work of Enko, who published a marvelous probabilistic model in 1889 to explain the measles outbreak at a different period, will be irresponsible for us not to note. Using the model, Enko measured the number of interactions in the community between infection and susceptibility. The Enko model is a precursor to the popular Reed-Frost binomial model applied by W.H. Frost at the Biostatistics Conferences of Johns Hopkins University in 1928 (not yet reported in a journal, but reported in 1979). This model suggests that, by Markov chain events at a discrete time, contamination spreads from an infected person to a susceptible individual. The roots for the new randomized disease paradigm were laid by this representation.

1.2 Implications for Epidemiologic Methods:

In offering a detailed viewpoint on evolving population trends, epidemiological transformation theory has been beneficial. Various critiques of the hypothesis suggest that the association between illness, death rates, and societies is more important as a means of thinking and learning than as a conclusive explanation or forecast.

One of the main critiques of the hypothesis is that essential parts of complicated processes are overlooked by an undue emphasis on death rather than cause and morbidity. It should not pay enough consideration to injury and quality of life to concentrate on death and life expectancy. In comparison, in the almost four decades after Imran's original paper appeared, our interpretation and approach to causal inference has evolved. Our thought and approaches have been informed by the relevance of the environmental hypothesis and so-called environmental epidemiology, and our perception of the differential dynamics of morbidity and mortality within and between communities and various segments of the population has increased.

Although it is clear that the burden of infectious diseases has been surpassed by the burden of chronic diseases and psychiatric illnesses in many nations that is the case in many nations and in many communities within countries where infectious diseases and health conditions have caused morbidity and mortality. Alimentation. Perinatal conditions predominate, with the most noticeable prominent feature being poverty. The proof of epidemiological change should not be taken to imply that our energy and money should be redirected away from the determinants of death and disease that continue to affect the health and well-being of a significant portion of the people of the planet. Yet this must still recognize that these same demographics are going to be casualties of the epidemics of obesity, lung disease, asthma, and diabetes that currently characterize the United States. Even as novel approaches to reducing the risks associated with sedentary lifestyles and over nutrition in developing countries continue to be developing, tested and introduced, we must still be mindful of the constant threat of infectious diseases, especially resistant strains or newly discovered agents. There is no longer a foregone conclusion on the relative security we receive from certain infectious diseases. Around the same period, several fronts in developed countries need to be addressed: historical risks from infectious agents, malnutrition and perinatal complications, as well as emerging threats of the same kind that we already see from infectious agent tolerant strains and new agent touch, and imminent chronic disease development. And degeneration, which is expected to accompany effective school improvement and poverty mitigation initiatives. One of the lessons learnt from the epidemiological transformation is that approaches must be adapted to the community and health risks they are already subject to, while we foresee the improvements that are expected to bring about progress in an environment and the potential new problems. Beyond the epidemiological transformation hypothesis, this would take different forms of thought.

1.3 Use of Modeling for Public Health Policy:

Mathematical models have been used widely to measure the efficacy of vaccine campaigns, to evaluate the best age and focus populations for vaccine, and to quantify the commitment needed by the community to prevent infection. More recently, statistical modelling has assisted disaster preparation to prepare for a future smallpox virus invasion (Ferguson et al. 2003) and to coordinate a public health response to an epidemic of an influenza pandemic strain. A (2006 by Ferguson et al). Other forms of intervention interventions, such as checking for asymptomatic contamination with Chlamydia trachomatis (Kretzschmar et al. 2001), touch tracking (Eames and Keeling 2003), and HIV antiviral treatment, have also been tested. A model was used to evaluate hospital-specific measures, such as grouping health care staff, increasing sanitation, and isolating colonized patients, in the area of hospital infection and spread of antibiotic resistant pathogens. Dynamic transmission models have been recognized as a critical prerequisite for successful cost-effectiveness analysis for the management of infectious diseases in health economic assessments (Jennifer & Torremorell; 2014).

From the creation of a mathematical theory of the dynamics of infectious diseases to its implementation in a specific public health scenario, this is an essential move. To order to determine how to develop a fitting model, the latter needs an intensive emphasis on the related data sources, clinical and microbiological expertise. Convenient here implies that the model incorporates existing information, is able to address policy makers' concerns, and is easy enough to grasp and view the complexities. In the future, to further enhance the efficiency of modelling as a public health tool, it will be necessary to reinforce the connation between advanced statistical methods and mathematical modelling.

1.4 Principles of Mathematical Modeling:
Mathematical modelling is a preliminary practice that has values and strategies that can be successfully implemented. Principles are basic principles or meta-principles conceived as concerns regarding mathematical simulation aims and purposes. In essence, these meta-principles are almost metaphysical. We will explain the concepts below, and we will discuss some of the methods briefly in the next portion. In Figure **1,** a graphic overview of the simple conceptual method is seen. The following list of questions and answers also integrates certain concepts of systemic modelling:

- Why? What are you in need of? Determine the model's necessity.
- Find it? What would you like to know? List the data for which we are scanning.
- Dice? How are we supposed to know? Identify the available relevant details.
- I suppose? What are we supposed to assume? Determine what words relate.
- How do I manage it? What can this model be looked at? Determine the physical concepts driving them.
- Forecast? What's our model going to predict? Define the equations to be used, the calculations to be done, and the answers that will be produced.
- Applicable? Are the projections correct? In order to verify the model, decide what experiments can be done, that is, does it agree with its values and assumptions?
- Is it verified? Are they decent prospects? Determine what experiments should be carried out to check the sequence, i.e. are they beneficial in terms of the initial cause?
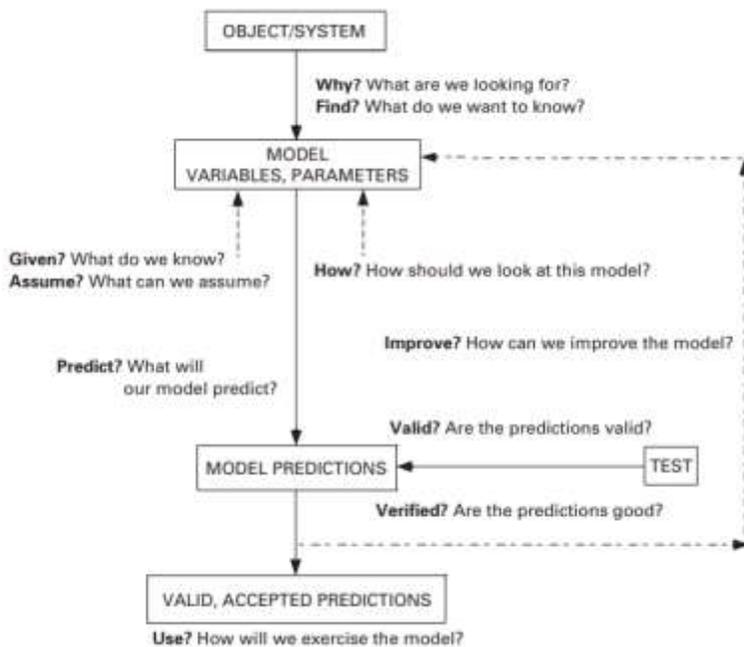

Fig.1: A first-class view of mathematical modelling illustrates how the problems raised in an initial model-building methodology apply to this model's growth (inspired by Carson and Copelli, 2001).

This set of questions and directions is not an equation for a successful mathematical model to be built. Specific concepts, though, are important to mathematical modelling, since they are key to the issue in general being conceived. Therefore, during the modelling phase, we should anticipate individual problems to be replicated regularly, and we should treat this list as a reasonably general guide to the ways of thought in mathematical modelling.

II.   Modeling of epidemics:

During epidemics, to educate both the health care sector and public health measures, there is a crucial need to consider both the possible amount and sequential path of diseases. Simulations of disease propagation and recovery dynamics 1, 2 or experimental alteration of data patterns may differ in approaches to forecasting the path of an epidemic. The use of incomplete models of the outbreak is a popular strategy. As a model of a susceptible infection (SIR).

SIR Model Used:

The aim of the SIR model is to predict how many people are susceptible to infection, are actively infected, or have recovered from the infection at any time. The model was introduced in 1927, less than a decade after the 1918 flu pandemic, and its popularity may be partly due to its simplicity, allowing designers to approximate disease behavior by estimating a small number of parameters.

Description of the SIR Model:

In segmented models, according to their disease status, persons within a closed population are divided into mutual classes or compartments. At every point, everybody is assumed to be in one space, but may switch from room to room according to the requirements of the model. The SIR model has been called one of the most fundamental segmented models for its three parts (injured, injured, and restored). In this model, by interaction with another infected person, the assumed progression is to infect a vulnerable individual. The individual transitions to a non-contagious condition, called recovery, after a time as an infectious entity, during which it is presumed that this person is contagious, although this stage can include death or active isolation.

The whole community starts in the vulnerable space (figure) in most model epidemics, containing individuals that will become sick if exposed to pathogens. This suggests that, at the onset of an epidemic, no one is resistant to the illness. The individual who has the ability to infect people in a susceptible cabin is known as an infected cabin. As such, transmitters for asymptomatic diseases as well as sick patients that need intensive treatment are included in this cabin. A simplification of the SIR paradigm is that the delay time after exposure is not taken into consideration, but rather implies that freshly contaminated persons are contagious instantly.

In any of the susceptible regions, the rate of infection of susceptible individuals depends on the number of individuals. In the onset of an epidemic, the illness progresses steadily because just a limited number of individuals are affected. It leads to the dissemination of infection and a spike in the prevalence of infection as more individuals get contaminated. The efficient touch rate (β) is an additional consideration for measuring the diffusion rate. The transmissibility of the disease is described by this parameter, as well as the average number of contacts per person. This importance is minimized by public prevention measures, such as quarantining infectious persons, social distancing, and school closures, thereby slowing the transmission. Although these interventions may shift the movement of people from the exposed chamber to the infected chamber, the transfer from the infected chamber to the restored chamber depends only on the amount of time the person is contagious, which is expressed in the rate of recovery (γ).

III.   Establishment of Mathematical Model &Algorithms:

Supervised Learning:

Machine learning uses programmed algorithms in the simplest context, which learn and optimize their operations by analyzing input data to render predictions within a reasonable range. These algorithms aim to make more detailed forecasts when fresh data is supplied. While there are several variations about how machine learning algorithms are classified, according to their intent and simple machine teaching process, they can be categorized into three general groups. These three groups are: moderated, unmonitored, and semi-monitored. To train the basic algorithm, the called training dataset is first used in supervised machine learning algorithms. The

unlabeled test dataset is then fed by this learned algorithm to divide it into related classes. Figure 1 illustrates an example of how supervised machine learning algorithms operate on both diabetic and non-diabetic populations, utilizing an abstract data collection of three diabetic patients. Two kinds of problems fit supervised learning algorithms: classification questions. And concerns regarding regression. The primary performance component in classification problems is discrete. This variable is labelled as "color" or "black" or may be "diabetic" or "non-diabetic" in various classes or divisions. A true value in regression issues, such as the coronary disease risk of a person, is the corresponding output variable. We briefly define the widely used supervised machine learning algorithms to forecast diseases in the following subsections.How it works: This algorithm consists of a vector of objective / outcome (or contingent variable) expected by a particular collection of predictors (independent variables). We generate a function with this collection of variables that maps the input to the desired output. If the model meets the necessary degree of precision in the training results, the training phase begins. Supervised learning examples: regression, decision tree, random forest, KNN, regression logistics, etc.

IV.   Proposed Machine Learning Algorithms for Infectious Disease (Malaria and Pneumonia)

Here is a collection of machines learning algorithms that are widely used. It is possible to extend these algorithms to virtually every data problem:

- ✓ Logistic Regression
- ✓ Decision Tree
- ✓ SVM
- ✓ K-NN
- ✓ Random Forest
- ✓ Gradient Boosting algorithms

Logistic Regression:
For supervised classification, Logistic Regression (LR) is a robust and well-established method [22]. It may be viewed as a standard regression extension and can only model a dichotomous attribute that typically describes an event's incidence or non-occurrence. LR aims to locate the possibility of a new instance belonging to a specific class. The outcome is between 0 and 1, since it is a chance. Therefore, to use LR as a binary classifier, to distinguish the two classes, it is important to set a cap. For instance, this would label a likelihood value greater than 0.50 for an input instance as 'Class A'; otherwise, 'Class B.' to model a categorical attribute of more than two values, the LR model may be extended. This extended variant of LR is regarded as logistic regression of polynomials.

Decision Tree:
One of the first algorithms for machine learning is the Decision Tree (DT). In order to categories data components into a tree-like framework, decision tree models are decision logical, i.e., they evaluate and match outcomes. In a DT tree, nodes typically include many tiers, where the root node is considered the first or top node. All internal nodes (i.e., nodes which contain at least one child) are input variables or characteristic checks. The classification algorithm branches through the required sub node, based on the test outcome, where the checking and branching phase iterates before it hits the terminal node [24]. The outcomes of the judgment are matched by the terminal paper or nodes. TDs have been shown to be simple to easily understand and read, and are a common component of several protocols for medical diagnosis [25]. The outcomes of all tests at each node along the road, while passing the tree to identify the sample, will provide enough details to guess about its cultivar. An example of DT with its components and bases is seen in Figure 2.
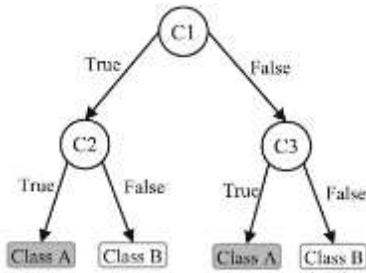
Fig. 2: Decision Tree

Figure above presented a Decision Tree Illustration. Every vector (C1, C2, and C3) is represented by a circle and rectangles show the decision results (Class A and Class B). To properly classify a sample into a subclass, based on the test result meaning of its predecessor node, each strand is called 'real' or 'fake'.
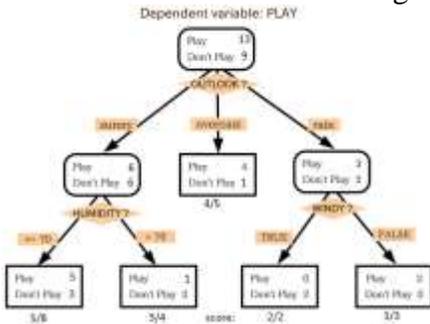

Fig. 3: Illustration of Decision Tree

SVM (Support Vector Machine)

It is necessary to define the Support Vector Machine (SVM) algorithm asLinear as well as non-linear data. The first map of any of thein the dimensional feature space n, the data part whereN reflects the number of workers. Then pick the hyper levelThis splits the components of knowledge into two groups.Maximize all marginal distancesCategories and the elimination of mistakes in classification [23].The marginal separation gap is the distance betweenthe elevated resolution standard and its nearest examplethe one that is a part of the class. MOREFormally, point of data is first plotted as a point atN dimensional space (where the number of characteristics is n)Being the worth of each land valueA specific format. To execute the classification,then we need to discover the super level that differentiatesThere is a maximum margin between the two grades. provides a simplified illustration of an SVM classifier.
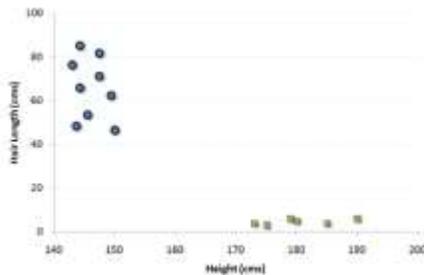

Fig. 4: Support Vectors

Now, we're going to see a line separating the details from two separate data sets classified differently. This would be the line in each of the outermost sets of lengths from the closest location.
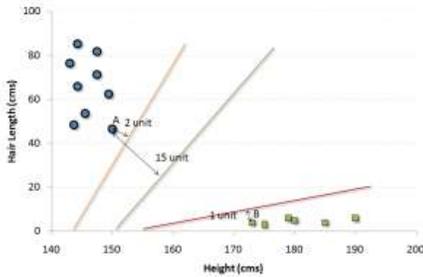
Fig. 5: Support Vector Machine - The line that divides the data into two distinctly graded classes is the black line

The line that divides the data into two distinctly graded classes is the black line in the above illustration, since the two closest points are the farthest from the line. Our classifier is this line. Then, this is the category in which we will assign the latest data based on whether the test data lies on each side of the graph.

KNN (k- Nearest Neighbors)
It can be used for both issues of grouping and regression. It is, however, commonly used in the sector for classification concerns. Nearest Neighbors K is a basic algorithm that stores all cases available and categorizes new cases for their neighbor's k by majority vote. Among its nearest neighbors, the case allocated to the class is more frequent than K calculated by the distance function.These distance functions may be the distance from Euclidean, Manhattan, Minkowski and Hamming. For the continuous function, the first three functions are used, and for categorical factors, the fourth (Hamming). If K = 1, then the state is clearly allocated to its nearest neighbor's class. When doing k-NN modelling, often the option of K is a problem.
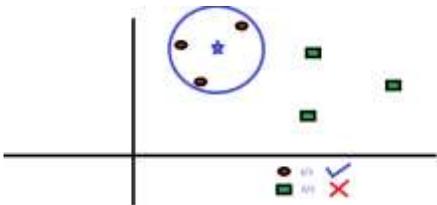

Fig. 6. KNN

KNN will conveniently be adapted to our daily lives. This will want to know their near associates, the circles in which they travel, and access their details if you want information regarding a person about which you do not have information.

Random Forest:
A proprietary word for a group of decision trees is Random Woodland. We have a collection of decision trees (also known as 'the jungle') in the random woodland. Each tree uses a classification to identify a new object based on the attributes, and we claim the tree "votes" for that type. With the most votes (of all trees in the forest), the forest selects the ranking.

Gradient Boosting Algorithms:
GBM is a momentum algorithm used to render a forecast of strong predictive power while working with a tone of details. In reality, Momentum is a group of learning algorithms that combine prediction on a single estimator with many simple capabilities to boost durability. To create a powerful predictor, combine several poor or

medium forecasters. In data science competitions such as Kaggle, AV Hackathon, and CrowdAnalytix, these reinforcement algorithms still perform well.

V.   Research Methodology:

This Thesis investigate the Pneumonia (Infectious Disease) Disease. The data sets taken from the Kaggle library. The prediction model has been established over the given data sets on the Python Tools. The prediction has based on the given data which after in form of images. The data has been bifurcated in two as one as the training and other as the test. The result has been explored in terms of detection accuracy and the Machine learning technique has been used to perform the task of detection.

Research Strategy:

A systematic review methodology will be used in the present research. A systematic review is a well-planned review to answer specific research questions using a systematic and explicit methodology to identify, select, and critically evaluate results of the studies done previously on the topic. Systematic l\e review articles are considered original work because they are conducted using rigorous methodological approaches.

Data Collection:

Data collection will be conducted using only secondary resources. It will describe each study's methodological approach (variables, sample, measures, and data analysis) and findings, which allow comparison between and/or among the selected studies. Using several sources to locate and retrieve scientific studies. These sources will include all relevant scientific databases as well as conference proceedings and relevant grey based on mathematical modeling for studying epidemics.

Data Analysis:

Studies will be grouped together according to their methodological similarities. This approach will be addressed in the project. Numerical and graphical presentation of the results will also be addressed in the project to facilitate reader understanding of the findings.

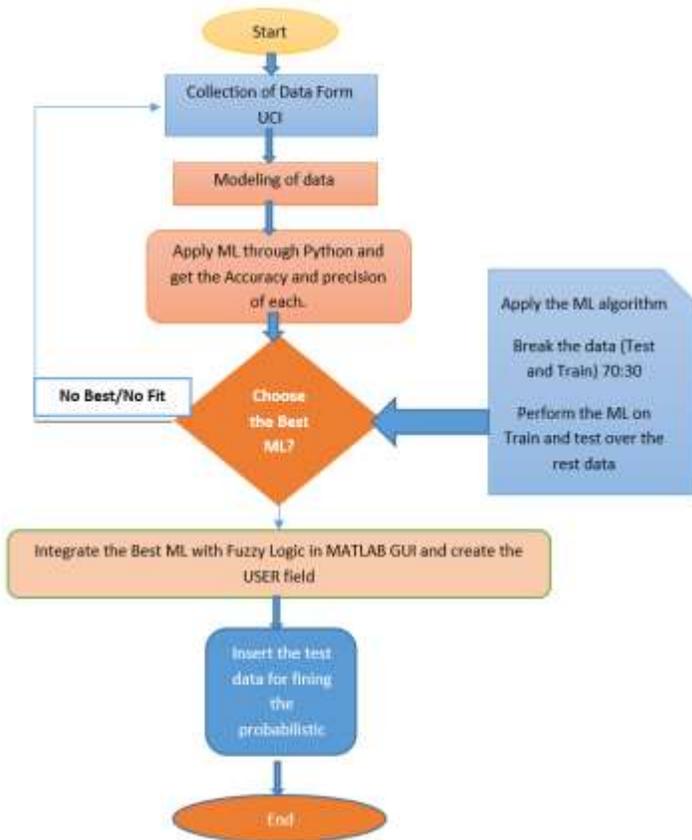## VI.   Flow Chart of the proposed work:

Fig. 7: Flow Chart of the proposed work

VII. Proposed Steps for Data Modeling:

Phase 1: first, ensure that the data sets are really relevant. The attribute with the smallest and largest values in our dataset is chosen for statistical research.

Phase 2: Tests the normality of the data through mathematical patterns of data.

Phase 3: For the missed values space, equate the "Evaluate column mean"

Phase 4: It is advised to fill in the missing values with the median and mean of the data sets.

Phase 5: Split the data in 70:30 ratio for train the data through ML algorithms and further test results.

Phase 6: Carry out the Machine learning algorithm on the train data sets.

Phase 7: Check the consistency of the test results with the test data sets.

Procedure:

Stage 1: Pre - processing of the data.
{
A figure displaying the data
Identify outliers and remove them.
With the missing details, classify and handle.
Applying suitable apply statistical to the results.
Replace missing space with data of the mean and median values.
}

Stage 2: Selection of the model.
{

Engendering data for the reason (classes)

Application for ML Algorithms and apply over the Python.

}

Stage 3: To find the best model the for classify the data.

{

Impress all of the information waiting onto the simulation using Python.

}

Stage 4: The performance is evaluated using level of accuracy

{

Calculate accuracy using the "Performance" operator. Then calculate the accuracy using the "accuracy measure".

}

VIII. Result Extracted:

Case 1: Pneumonia

Pneumonia Detection - 95 % Accuracy

Case 2: Malaria Prediction and Simulative Outcome as Accuracy

Methods	Accuracy on training set	Accuracy on test set
K-Nearest Neighbors	0.69	0.65
Logistic Regression	0.68	0.67
Decision Tree	**0.68**	0.67
Random Forest	0.70	0.67
Gradient Boosting	0.68	0.67
Support Vector Machine	0.90	0.58

IX. Conclusion and Future Scope:

Infectious disease treatment takes the early identification of a patient's viruses and steps, such as vaccines to deter and/or heal them. In addition to detecting the more serious diseases that internists are capable of healing, internists are capable of catching the pathogens that are difficult to treat. Studying infectious disease, such as fungal, bacterial and viral infections, is useful because it instructs in the understanding of the background of microbial, fungal, and parasitic complications in humans as well as in the awareness of antibiotics and vaccination, there are other pathogens. As there are doctors that practice in this field, they are easily able to cope with the environmental, occupational, and host factors that trigger vulnerability, as well as simple epidemiological principles. There is a number of various quality controls within the medical profession. Infectious disease clinicians (Disease's physicians) may conduct these critical activities with a specialized qualification or in a single clinic with extreme precision. Most doctors in infectious diseases serve as consultants to other professionals, see patients at their offices or hospitals in consultation, and also accompany patients while providing treatment for their illnesses Several experts in the infectious diseases perform their specialty with suitable medical facilities. Doctors that practice in infectious diseases can have general health services while they deal on people recovering from an array of diseases. In this research, infectious disease doctors offer continuing surgical and patient care consulting programmers, perform scientific and clinical review, and teach medical students and tenants.This studies also gathered more evidence, with a larger variety

of data sources, in the name of public health security. This research discovered that one of the difficulties in our analysis was the need to grasp and implement visualizations. This research also discovered that consumer trust and organization assistance played a major part in the assimilation of these approaches. We have now been quite serious with interoperability. When discussing a new product, one may solve difficulties with the usage of other tools, for example, by describing items that might be overlooked or that may communicate confusing knowledge.

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