Model for predicting of swine Flu disease using Artificial Neural Network

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Abstract:
Machine learning technology adds a new potential to medical diagnosis systems. This paper presents an Artificial Neural Network (ANN) based swine flu diagnosis model. The proposed model selects significant features for swine flu diagnosis by a feature selection algorithm using random forest classifier reduces the size of data to be used for training the ANN model with an objective of making the training more efficient and accurate. A threshold value is determined by ANN to identify positive and negative cases and the model classifies the test cases either positive or negative based on the threshold value. Those results get from the proposed model demonstrate the ability of the model to provide high level of accuracy for swine flu diagnosis. The assessment (classification) ability of the proposed ANN based model is compared with that of Case Based Reasoning (CBR) approaches and this is compared with the proposed model is gives good result with to others models.
Keywords- Swine Flu, Disease detection, swine flu diagnosis, Machine Learning, Neural Network, Naïve Bayes classifier etc.

I. Introduction:

Swine flu is respiratory disease which found the one the most infectious diseases which contain different variants of virus which may cause the death of people.Hence the data mining techniques are used to predict the disease like Naïve Bayes classifier which may help to reduce the laboratory time and cost. The purpose of the paper is to help the medical practitioner to take intelligent clinical decision based on the symptoms and machine learning techniques. The prediction system for Swine flu prediction is able to give prediction about the individual is infected with the swine flu or not. The binary classification is able to classify the decision in either yes or No. Even decision tree is also able to use to predict the system.

At initially level of research the influenzas virus causes the swine flu as respiratory disease which comes from the pig. It may result the nasal secretion, restless, savior cough, decrease in appetite such symptoms are found in human when this virus causes human[4].

Swine influenza, is also called pig influenza or swine flu, hog flu and pig flu, is an infection caused by any one of several types of swine influenza viruses. Swine influenza virus (SIV) or swine-origin influenza virus (S-OIV) is any strain of the influenza family of viruses that is endemic in pigs. In 2009, the known influenza include in strain and there are some subtypes of influenza A known as H1N1, H1N2, H2N1, H3N1, H3N2, and H2N3. Swine influenza virus is common throughout comes from pig populations worldwide[7].Some common symptoms of Swine flu are runny Nose, temperature, cough, sore throat, headache, chill and fatigueless, nausea etc. As per the author has Currently, the swine flu virus kill more than 1500 people in India and it will rapidly spreading all over the world so recently there are not notice large numbers of people infected with H3N2v.Unfortunately, another virus termed H3N2 (note no "v" in its name) has been found and caused flu, but this strain is different from H3N2v. In general, all of the influenza A viruses have a structure similar to the H1N1 virus; each type has a somewhat different H and/or N structure .

II. Literature review:

For the study of swine flu prediction system the different study of some previous research has done which is mention below.

Virendra Singh et al, mentioned thatthe pandemic of swine flu (H1N1) influenza spread to involve the whole world rapidly. Many patients manifested a mild clinical illness but some developed pneumonia and respiratory failure. High mortality was observed in patients with severe disease. Among survivors, studies are limited. Ground-glass opacities on a high-resolution computerized tomography scan and reduced diffusion capacity were noted after 3 months in a study. But long-term complications in patients with swine flu

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pneumonia have not been studied well. They presented an unusual case of swine flu pneumonia who developed interstitial lung disease after recovery [1].

Saroj Kr. Biswas et al, studied Machine learning technology adds a new potential to medical diagnosis systems. That paper presents an Artificial Neural Network (ANN) based swine flu diagnosis model. That model selects significant features for swine flu diagnosis by a feature selection algorithm using KNN means K-Nearest Neighbour classifier, which reduces the size of the data to be used for training the ANN model with an objective of making the training more efficient and accurate. A threshold value is determined by ANN to identify positive and negative cases and the model classifies the test cases either positive or negative based on the threshold value. The results obtained with the existing model demonstrate the ability of the model to provide high level of accuracy for swine flu diagnosis. The assessment (classification) ability of the proposed ANN based model is compared with that of Case Based Reasoning (CBR) approaches and is observed that model is superior [2].

Priyanka Lokwani et al, has mentioned in their research is that the Swine influenza is a respiratory disease caused by the viruses like influenza viruses which belonging to Orthomyxoviridae family. Such virus infects the respiratory tract of pigs and result in nasal secretions, a barking-like cough, decreased appetite, and listless behaviour. Oseltamivir (Tamiflu) and zanamivir (Relenza) is the recommended drug both for prophylaxis and treatment. The best treatment for influenza infections in humans is prevention by vaccination [3].

Megha Kadam et al, mentioned that the swine flu refers to swine influenza or the viral infection caused by any of the several types of swine influenza virus. Only people who used to have direct contact with pigs were observed to get swine flu in the past H1N1 is Influenza a virus.

Meghna R. et al, describes that Swine origin influenza was first recognized in the border area of Mexico and United States in April 2009 and during a short span of two months became the first pandemic. The currently circulating strain of swine origin influenza virus of the H1N1 strain has undergone triple reassortment and contains genes from the avian, swine and human viruses. It is transmitted by droplets or fomites. Incubation period is 2 to 7 days. Common clinical symptoms are indistinguishable by any viral respiratory illness, and include fever, cough, sore throat and myalgia. A feature seen more frequently with swine origin influenza is GI upset. Less than 10% of patients require hospitalization. Patients at risk of developing severe disease are – younger than five years, elderly, pregnant women, with chronic systemic illnesses, adolescents on aspirin[9].

Saganiragasa et al, describes that Swine flu is a highly contagious respiratory viral disease which is caused by influenza a virus. The disease can be found everywhere in the world especially in those peoples rearing pigs. The virus can circulate between human, avian, and swine. It spread through aerosol transmission, via contact with affected pigs and contaminated objects with the virus. Different factors including immune suppression predispose individuals to the disease. Swine influenza manifested by coughing, anorexia and lethargy in pigs while sudden fever and cough in human. The disease can be diagnosed either by laboratory or by observing signs and symptoms[10].

III. Existing system:

The existing system uses the algorithm which uses feed forward neural network. In this technique the algorithm backpropagation algorithm is used for learning procedure and for training the multilayer feed-forward network with backpropagation.

Mostly such algorithms are used in the medical diagnosis, Image processing chatcaterregonnition and pattern recognition. Traditionally, this algorithm is based on the hidden layer. Number of hidden layer is causes the complex algorithm is needed to determine the number of units in the hidden layer before training is started in the neural network. The different algorithm have been propsed to overcome the difficulty to construct a network dynamically. Such as the well-known constructive algorithms are dynamic node creation (DNC), feed-forward neural network construction (FNNC) algorithm, and the cascade correlation (CC) algorithm. As shown in the given figure Fig.1 which indicates thealgorithm feed forwards neural network algorithm.
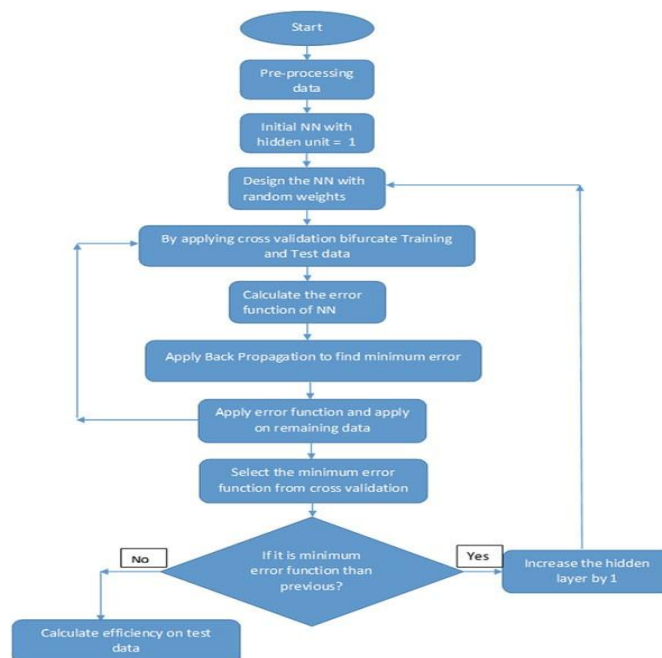
As per mentioned in the figure Fig 1, the first step is the creation and the initialization of neural network with one hidden layer and the different attributes of dataset along with the random weights is given to featuresin the hidden layer.Also the LDA algorithm is applied to reduce the dimensionality of the swine flu data. For design and developing the neural network,a hidden layer which have number of nodes equivalent to number of important properties of the data. We forwarded preprocessed data into neural network and train the network. To produce the best result, we used cross-validation techniques, where data are split in 80–20% ratio. After the completion of the first cycle of neural network, we used the backpropagation algorithm to modify the best weights of neural network. The error function is used as given below. Once after minimizing the error function on 80% data, apply the same on in remaining 20% data to predict the either patient has swine flu or not. We continue the same process for all the remaining iterations and select best weights to classify patterns. We have done the same thing by increasing the one more hidden layer and finding the accuracy of algorithm; if calculated efficiency is lesser then the previous one, we stop the execution, else we will add one more hidden layer and randomize the weights again and initialize it until we get a better result.

IV. Implementation:

Naive Bayes Classifier:
Naive Bayes or Bayesian Rule is a very efficient data mining technique which calculates the variousprobabilities "on the fly" and gives a result on the basis of these probabilities.

4.1 Classifier Module

Th powerful tool for solving the classification problem one of the technique is Naïve Bayes Classifier which is applied in different domains. Naïve Bayse classifier is based on posterior probability decision. It is a model which is based on joint probability distribution on the set of values that are stochastic variables. It is consist of the single class variable the modelling the outcome that are possible outcomes or class for the said problem. A set of features, modeling features that provide for distinguishing between the different classes the feature variable are assumed to be mutually independent given the class variable. In the classification problem under the study which are being used to classifiers as the combination of different features values and classifies and then it returns the posteriors distribution over the class variables which is the probabilistic summary for each of the class of the model. In medical domain the Naive Bayesian classifiers have been successfully applied where they are used for solving diagnostic problems. Naive Bayesian classifiers are typically learned from data. Learning such a classifier amounts to establishing the prior probabilities of the different classes and estimating the conditional probabilities of the various features given each of the classes.

Naive Bayes or Bayes' Rule is a very efficient data mining technique which calculates the various probabilities "on the fly" and gives a result on the basis of these probabilities.Swine flu symptoms are are collected for the required number of cases for training and testing the model. By contacting with the medical practitioner from the hospital vision the symptoms are categorized in the rages according to the which we generated a few cases and authenticated the same with the practitioners. Nearly 100 records are collected which having

the different factors i.e. 17 medical attributes validated int the hospital database. Following are the swine flu symptoms predictable Attribute:The swine flu can be diagnosed only with medical tests wherein the swabs from nasal or pharyngeal passage are taken and the virus is detected, only then can the type of the flu be detected. The different input attributes were considered like body temperature, body ache, blood pressure cough, chill, age etc.

Input Attributes:

1. Fever- (Value 0:98-99.9f, Value 1:100-102 f, Value2:100-102 f)
2. Body ache-(Value 0: No, Value 1: Yes, Value 2:Severe)
3. Blood Pressure-(Value 0:120/80, Value 1: Abnormal
4. Color of Nails-(Value 0: Pink, Value 1: Blue)
5. Breathlessness-(Value 0: No, Value 1: Moderate, Value2:Severe)
6. Diarrhea-(Value 0: No, Value 1: Sometimes)
7. Vomiting-(Value 0: No, Value 1: Occasionally)
8. Cough-(Value 0: No, Value 1: Yes, Value 2: Severe
9. Skin Color-(Value 0: Not Applicable, Value 1: Blue)
10. Sore Throat-(Value 0: No, Value 1: Occasionally,Value 2: Severe)
11. Chills-(Value 0: No, Value 1: Occasionally, Value 2:Severe)
12. Age-(Value 0:0-18 years, Value 1:18-30 years, Value2:31-45 years, Value 3: Above 45)
13. Gender-(Value 0: Male, Value 1: Female)
14. Lung Disease-(Value 0: No, Value 1:Yes)
15. Chest Pain-(Value 0: No, Value 1: Yes)
16. Pandemic Area-(Value 0: No, Value 1: Yes)
17. Service in the health industry-(Value 0: No, Value 1:Yes)

Based on the input attributes the database is splitted for training and testing purpose. 70% of data was considered for training and 30% for the training dataset. Cross validation is applied also. All these records are randomly selected to form the dataset for training and testing purpose. Categorical attributes were used for training the model. Those data were non categorical were transferred into categorical data. All the non-categorical medical attributes were transformed to categorical data. Those data were missing and inconsistent are preprocessed and data cleaning is done to remove the duplicate data.

V. Result Analysis

We have done the experiments of both data synthetic and real. Real data was provided from major hospital after hiding the patient details.Although the real data are really less, based on the same, we generate our own synthetic data to do more experiments. After data processing, the dataset is divided into two sets for training and testing purpose and to investigate the accuracy of the solution. In Fig. 2, we have plot the
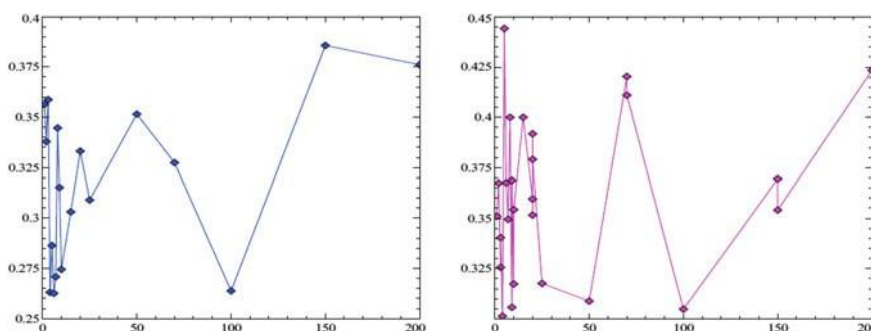

Fig. 2 Accuracy of the NN with number of hidden nodes

have found that after a couple of iteration, we are able to find minimum error function, although it is not the optimum one but acceptable as it is near to local minima. We note down that one algorithm is producing good accuracy in small iteration, so we can avoid the further iteration, so computation time can be reduce.

Related Medical Diagnosis

Many research projects have been done in the field of biomedicine and Naïve Bayes technique has proved to be a powerful tool. The following data illustrates the importance of Naïve Bayes.

1. In Heart disease prediction, Naïve bayes technique gives the best result of 95% accuracy compared toneural network (93.54%) and decision tree(94%).

2. Naïve Bayes technique gives 49% accuracy in case of primary tumor,78% in case of breast cancer,70% in case of thyroid and 67% in case of rheumatology predictions as compared to 54%,64%,64%and 56% in case of physician's predictions respectively. Naïve Bayes technique has proven to be superior amongst the other data mining techniques in the biomedical field.

Conclusion

In proposed Disease prediction system can predict particular disease using training dataset. In this proposal, we propose disease prediction system as web/mobile based online application for patient's healthcare. Naive Bayse and ANN based binary pattern classification algorithm has been proposed and implemented for swine flu pattern classification problem. Firstly, important and meaningful Features of swine flu are determined using random forest classifier and cross-validation technique. Then the structure of a pattern is represented by these important features along with a class label. Then a multilayer feed-forward neural network is trained and tested to resolve swine flu classification problem. The proposed algorithm manifests a better approach of pattern classification. After result predict the disease, and then recommendation system will work on their predicted disease. If positive results show to user, then recommended doctor will display on same page. If negative result, then precautions for same disease will display.

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