

Pos And Neg Classified Using Chikungunya Symptoms Through Big Data Analytics

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Abstract: Instinctive disease of mosquito-borne transmitted to the human beings and it spread hastily into various countries, and people affected by Chikungunya virus (CHIKV). Chikungunya fever is onset of rapid, typically a febrile disease, characterize by headache, intense asthenia, rash and arthralgia. While the onset of illness test make to diagnose the infection of serum are collected approximately within the Six days. If the symptoms are obtainable more than a week, the antibody Chikungunya test is conducted using two serum types first develop the Immunoglobulin M (IgM) and it is followed by Immunoglobulin G (IgG). In the proposed system, the big data analytics used for categorizing the level of positive and negative using the t-Distributed Stochastic Neighbor Embedding (t-SNE) algorithm for prediction. t-SNE is applied to genetic data computing, human, even though it is usually used in the other data intensive of biological fields. Classified the predicted level of chekungunya using t-SNE by symptoms types of method our model predictions were finally predicting the accurate infection level often the output results in severe fever, debilitating polyarthralgia and rashes.

Index Terms: Big Data Analytics, Chikungunya prediction, t-SNE, Negative and positive result.

1 INTRODUCTION

ig Data challenge in real-time process of data in throughput and scalability of the techniques. A big data was proposed to gathering the optimal algorithm for energy efficiency and scalability for accurate analysis. Chikungunya is caused due to mosquitoes bite CHIKV considered as severe disease. There are several characteristic symptoms of Chikungunya shows by CHICKV disease infected person are joint pain, high fever, rash, nausea, joint swelling, headache and fatigue. In India the main reason for affecting the diseases due to the density of high population, lack of awareness and condition of socio-economic CHIKV virus spread easily to the wide areas. Due to late detection of health related problem there are many people are affected more frequently.

2 RELATED WORK

Bui D et.al, [2] a research carried out a particular location was considered as Malaysia. In this case study the disease mindset and location are considered. In practice, usually the disease affected persons are targeted in the study of strategy for implementing disease. Obviously the economic crisis is showed to find to show the rate of diseases increased. Rajinder Sandhu et.al, [4] the any government of nations and department of healthcare are major concerns for transmitting diseases. The most possible way to control many infections spread with the usage of increasing information technologies. Using cloud and the Social Network Analysis (SNA) are proposed this method used to predict the airborne H1N1 flu and also can prevent it. The key points of the research utilized SNA graph method for representing the H1N1 flu on global dependencies. Shobhit Verma, et.al, [9] chickengunya was considered has one of the diseases caused by bite of mosquitoes. But till now all about the globe scientists are lacking in finding the exact cure of this diseases.

Using the machine learning techniques the authors predict the chikungunya and adopted the accuracy factors. The result analysis the neural network models to produce the least mean error and hence it reveals the optimal forecast models in the term of accuracy

3 PROPOSED METHODOLOGY

A t-SNE ALGORITHM

Chikungunya infection caused by the viruses and here share some of the common symptoms/sign but forecast the determined symptoms differ and patient care. For differentiating the virus infected patients are essential for accurate diagnostic techniques. Under the different settings the t-SNE performance are highly robust through the perplexity. The t-SNE mostly depends on the value of appropriate density level of the data reduction techniques. The data-collection component is responsible for compiling the raw information from users using the t-SNE method. Large numbers of humans are affected due to microorganisms this can be broadcasted easily using various technologies. For monitoring the health, enhanced technology are widely used. However, technologies are help to predict the disease at the initial stages and hence it help to forecast diseases.

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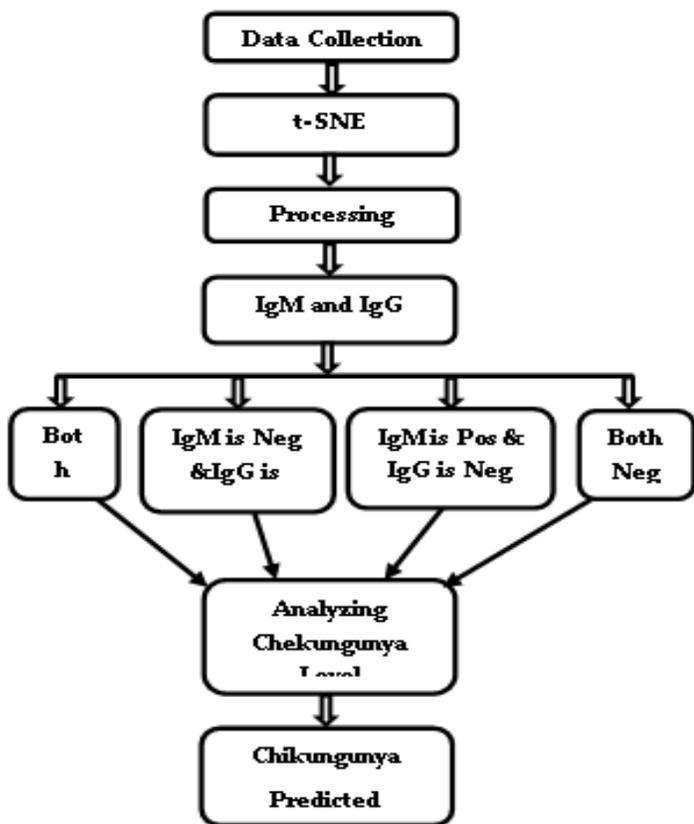


Figure: 1.1 t-SNE based Chikungunya Prediction process

B IgM AND IgG ANTIBIOTIC SERUM

In specifically there are two antibiotic IgG and IgM serum were screened for anti-virus for Chikungunya. CHIKV antigen is performed under the t-SNE techniques and the avidity of an anti-CHICKV of IgG was tested by t-SNE in the absent or present of the test. And the IgM was tested and it is followed by IgG testing through same techniques.

i) Mutually IgM and IgG are Pos:

This method exposed to suggest the patients are infected in very recently or past and they have to be treated for their constrained symptoms. If the symptoms of the results mutually positive then they are not affected by any of the disease but they should take

treatment for the symptoms.

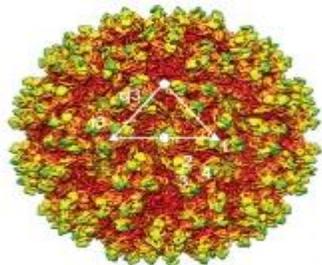


Figure: 1.2 Equally IgM & IgG are Pos.

However, the sensitive diseases are followed by the IgM & IgG serologies are positive. Using t-SNE techniques the both serums are applied for analyzing accurate results.

$$P_{x|y} = \frac{\exp(1 + \|T_{1x} - T_{1y}\| / \sigma^2)}{\sum_{k \neq i} \exp(-\|T_{1y} - T_{1k}\|)}^2$$

Where, T1 are defined as t-SNE testing and the 'σ' defined as testing of both serum are followed throughout of the exponential.

ii) Equally IgM and IgG are Neg:

Both the serum is negative then it indicates the infected patients has not exposed to the CHICKV virus. However, the sample test must be re-conducted after a week to finalize the result of the chikungunya.

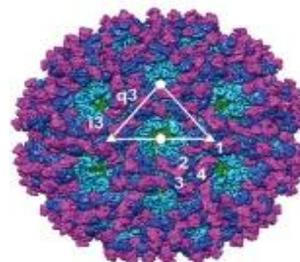


Figure: 1.3 Both IgM & IgG is Neg

The negative results of serum are assay for the chikungunya RNA and it was not surprising due to the late enquiry of the patients and the results are done after the two weeks of the onset symptoms. Between the discriminating chikungunya the person who are exaggerated by chikungunya and the lapse of time among the range of the onset chikungunya.

$$P_{y|x} = \frac{\exp(1 - \|T_x - T_y\|^2 / \sigma^2)}{\sum_{k \neq i} \exp(-\|T_x - T_k\|)}$$

Where, T is defined as t-SNE testing Px|y, and the 'σ' is distinct as testing of both the IgM and IgG are followed by the exponential.

iii) IgM is positive while IgG is negative:

If the serum level of this results is suggested has recently infected of the CHIKV diseases. These patients should test yet again between the 5 to 10 days to confirm their chikungunya diagnosis. When the disease level is increased that person will monitor the current situation of diseases and will take a necessary action.

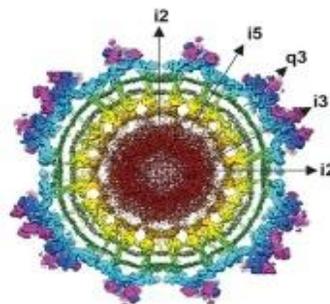


Figure: 1.4 IgM is Pos while IgG is Neg

Single test is not enough to finalize the result of disease affected persons they should recheck the issues for confirmation.

$$Q_{ij} = \frac{(1 + \|S_x - S_y\|^2 / \sigma^2)}{\sum_{k \neq i} \exp(1 - \|S_x - S_k\|^2)^{-1}}$$

Wherever, S is defined as t-SNE testing Qij, the exponential followed the 'σ' and it defined as testing of x and y of both IgM and IgG.

iv) Neg of IgM and Pos of IgG:

Therefore past infection are confirmed and suggested the CHICKV virus are existed in the antibodies of immune diseases. The prediction model of our research is initially quite inexact results using the prediction process the symptoms are finally rashes, severe fevers and joint pain. Finally using the t-SNE techniques the accurate results are seen in the forecasting methods of the immunology process.

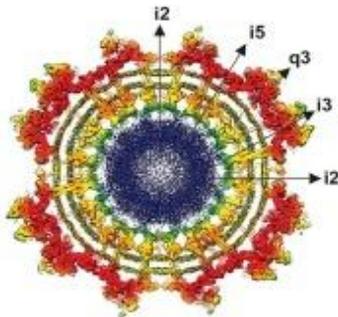


Figure: 1.5 IgM is Neg while IgG is Pos

Due to the overdue analyzing of the symptoms for the most part of the people are severely precious by diseases. Using the probability of symptoms the disease are categorized and the result of Pos and Neg will finalize the report.

$$Q_{ji} = \frac{(1 + \|S_y - S_z\|^2 / \sigma^2)}{\sum_{k \neq j} \exp(1 + \|S_z - S_y\|^2)^{-1}}$$

wherever, S defined as t-SNE model of sample testing Qji, constant 'k' are followed to exponent the 'σ' for y and z mean square of function. This all serum test are under taken for analyzing the accurate result of the diseases. The results proved if people are affected by CHICKV or not using the two level of ranges.

ALGORITHM FOR THE T-SNE ALGORITHM

STEP: 1

Data:

Data sets X={x1,x2,...,xn} and Y={y1,y2,...,yn},

Parameters of cost functions:

Perplexity defined as Perp,

Parameters optimization:

Number of iterations T, momentum α(t).

Result:

Low-dimensional data representation

Y(T) = {y1,y2,y3,...,yn}.

STEP: 2

Begin

compute pairwise affinities k ≠ j with Perp

Initial solution

Y(S)={z1,z2,z3,...,zn}

for t=1 to TT do

computer low-dimensional affinities qijqij

set

Y(S)=Y(t-1)*(Y(t-1)-Y(t-2))

End

End

4 RESULT AND DISCUSSION

Chikungunya disease is analyzed through the usage of t-SNE algorithm by using the serum test of IgM & IgG of sample test. This technique easy to detect the disease in early stages and it contribute the major concerns. The tests finally show the accurate level of the disease herewith discussed the best detection algorithms.

Table 1.1: CHICKV virus symptoms with their stages

STAGES OF CHIKUNGUNYA VIRUS			
Primary Symptoms	Secondary Symptoms	Tertiary Symptoms	High risk Level Condition Symptoms
<ul style="list-style-type: none"> ■ Joint Pain – Yes/No ■ Joint Pain – Mild/High/No ■ Body Rashes – Yes/No 	<ul style="list-style-type: none"> ■ Headache – Yes/No ■ Nausea- Yes/No ■ Muscular Pain – Yes/No ■ Fatigue – Yes/No 	<ul style="list-style-type: none"> ■ Vomiting – Yes/No ■ Rashes – Yes/No 	<ul style="list-style-type: none"> ■ Kidney Disease – Yes/No ■ Chronic Disease – Yes/No ■ Heart Disease – Yes/No ■ Liver Disease – Yes/No ■ Cancer – Yes/No

Accuracy Detection of Chikungunya The accuracy of CHICKV diseases is depending on the IgG and IgM detected diagnosis. The performance stage of proposed method in CHICKV is analyzed through the level of accuracy.

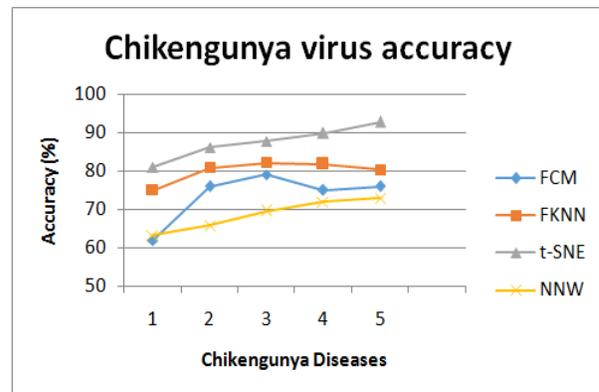


Figure: 1.6 CHICKV Accuracy analyzing using t-SNE

The accuracy level in proposed using t-SNE and existing methods are illustrated in figure 1.6. From the above comparison visual aid the t-SNE method having the high level of accurateness when it compared with the existing methods of FCM, FKNN and NNW.

5 CONCLUSION

The research concluded with neurologically analysis of viral antigen for CHICKV patients are detected by t-SNE method it gave more reliable diagnosis than the antibodies it can be used to highly develop the immunodiagnostic asserts with specificity. The sensitivity diagnostic of antigen detection of chekungunya using the t-SNE algorithm based system with the higher conventional of the serum tests and it is helpful to detect the antigen infection even in the previous stages. The t-SNE processing are used to analyze CHICKV with the limited

resource of sample test and also study is rapid, cost effective, specificity, sensitivity and accuracy.

REFERENCES

- [1] M. S. Hossain, & G. Muhammed, "Cloud-assisted industrial internet of things (iiot)-enabled framework for health monitoring". *Computer Networks*, vol. 101, pp. 192-202, 2016.
- [2] Bui D, Hussain S, Huh E, Lee S. "Adaptive Replication Management in HDFS based on Supervised Learning". 2016;4347(c):1-14.
- [3] R.Y. Chen, "An Intelligent Value Stream-Based Approach to Collaboration of Food Traceability Cyber Physical System by Fog Computing." *Food Control*, vol. 71, pp. 124-136, doi:10.1016/j.foodcont.2016.06.042, 2017.
- [4] Rajinder Sandhu, Sandeep and K.Sood "smart monitoring and controlling pandemic influenza A(H1N1)using social networking and cloud computing", pp. 1728-1739. doi:10.1109/JSAC.2016.2545559 2016.
- [5] M. Ahmad, M. B. Amin, S. Hussain, B. H. Kang, T. Cheong, and S. Lee. 2016. "Health Fog: A Novel Framework for Health and Wellness Applications.", doi:10.1007/s11227-016-1634-x.
- [6] Y.L.Zheng, X.R. Ding, C. C. Y. Poon, B. P. L. Lo, H. Zhang, X.L. Zhou, G.-Z. Yang, N. Zhao, and Y.-T. Zhang, "Unobtrusive Sensing and Wearable Devices for Health Informatics." *IEEE "Biomedical Engineering"*, vol. 61 (5), pp. 1538-1554. doi:10.1109/TBME.2014.2309951, 2014.
- [7] C.D. Maio, G. Fenza, V. Loia, and F. Orciuoli, "Unfolding Social Content Evolution along Time and Semantics.", vol. 66, pp. 146-159. doi:10.1016/j.future.2016.05.039, 2017.
- [8] S. Rani, S.H.Ahmed, R.Talwar, & J.Malhotra, "Can Sensors Collect Big Data? An Energy Efficient Big Data Gathering Algorithm for WSN". *IEEE Transactions on Industrial Informatics*, vol 13(4), pp. 1961-1968, 2017.
- [9] Shobhit Verma and Dr. Nonita Sharma "Statistical Models for Predicting Chikungunya Incidences in India", DOI: 10.1109/ICSCCC.2018.8703218.
- [10] A. Lounis, A. Hadjadj, and A. Boubdallah, "Healing on the Cloud: Secure Cloud Architecture for Medical Wireless Sensor Networks." vol. 55, pp. 266-277. doi:10.1016/j.future.2015.01.009, 2016.