A Survey on Prediction and Detection of Epidemic Diseases Outbreaks

Ravi Kumar Suggala

Research Scholar,

Department of Computer Science and Engineering,

Centurion University of Technology and Management, Paralakhemundi, Odisha

Dr.Anurag

Pro Vice Chancellor,

Department of Computer Science and Engineering,

Centurion University of Technology and Management, Paralakhemundi, , Odisha

Abstract- These days, the web can be utilized for diseases surveillance. In daily lives, early seasonal epidemics prediction like malaria, influenza may diminish their effect. In world the subtropical and tropical regions, the dengue outbreaks are endemic mainly in sub-urban and urban areas. One of the fundamental ten infections affecting the most deaths worldwide is the outbreak. The fundamental aim of this paper is to show a strategy to research and forecast the epidemic diseases spreading practices before they happen. In densely populated area, the various instances of epidemics widespread outbreaks are reported. These methodologies can limit outbreak to a little restricted region. Therefore, to decrease losses in human death form this would guarantee a superior way of dealing with stress is provided study the diseases spread and sufficient control mechanisms. Through this paper, we develop a prediction model that can expect the individual likeliness is influenced by a specific epidemic through surveying of early manifestations.

Keywords-Bio-surveillance, disease forecast, epidemic diseases, pathogen detection, tropical region, subtropical region.

I. INTRODUCTION

In world, the epidemics cause significant economic, health and the social impacts [1, 2]. The contagious diseases are the epidemic a disease [2, 3], when measurement of contagion entered to the level of outbreak, then to the whole nation it is possible to distribute [4]. To the entire population the epidemics diseases can manage to wipe out [5]. Some of the famous epidemic outbreaks are cholera, influenza, yellow fever, dengue, bird flu, and diphtheria, in the entire world these were manifested [6]. One of the aspects caused 43% in life lost globally is contagious disease and it cause critical world health issues. In current and past era India has noticed re-emerging disease outbreaks and emerging disease in diverse sectors of country. So, the data from various sectors needs to be analyzed to implement these measures. For instance, climatic, demographic, hospital records, queries of web search, social media content, etc, are used for getting the present medical scenario (disease information) along with past medical data for investigation. Figure 1 exhibits the analysis of traditional and modern data sources. Diphtheria may cause [8]. Usually, via contaminated air and direct contact the transmission were happened. However, by the irregular of vaccination, these diseases were caused. Towards prediction, detection, controlling, and identification via

classification of features, these factors may contribute. Also, between the features due to the integration involvement, the features' clustering technique was presented and causes the adjustment of weight to the input. The result of features' clustering method is approximate detection, prediction and less accurate on epidemic diseases.
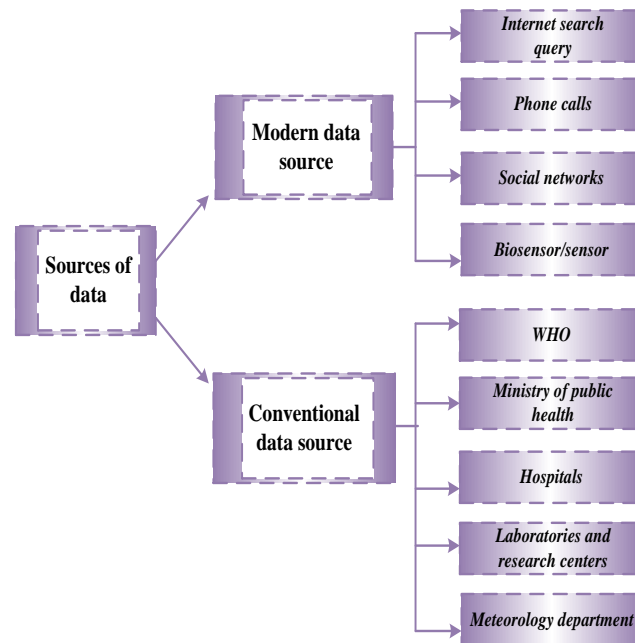

Figure 1: Modern and Traditional data sources for prediction of epidemics outbreaks

To alleviate the negative impacts of pandemics, the infectious diseases granular and reliable forecasting facilitates targeted resource distribution and intervention planning. To forecast seasonal as well as emerging disease outbreaks there have been multiple efforts. The recent efforts relied on mathematical compartment models such as SIR [9] and SEIR. By considering the individual-level interactions across the social networks some studies improved model fidelity [10]. Rising the unknown parameters number, through data assimilation that should be adjusted however, on computational resources these individual-based models impose an additional burden. Furthermore, the accuracy performance of the epidemic model can drastically affected by the choice of calibration scheme. Thus in epidemic forecasting contexts a diversity of filtering approaches have been utilized [11, 12].

Most of the research works utilize the social communication sites like Twitter and Face Book. Because of few reasons it is a proficient asset to track patterns. High recurrence of presented messages at first, aides to perform investigation in minute-by-minute. For public the Twitter posts are accessible and more descriptive while contrasting with search engine logs. Additionally, more analysis is performed for client's profiles dissecting like demographic data [13]. The focus of this research is to survey the current procedures, methodologies, tools and frameworks of predicting the epidemic illnesses in machine learning strategies, data mining, time serious analysis, hybrid models and the social media data. Studied techniques assess various posts related to epidemic diseases for faster detection in an effort to maintain and accomplish healthier networks. Rest of the paper is sorted as follows: Section 1 includes the introduction part. Section 2 discusses the various predictions of epidemic outbreaks techniques. Finally, section 3 concludes the paper.

II. EPIDEMIC OUTBREAKS PREDICTION METHODS

There are numerous approaches to discover learning and predict epidemic disease. This section glances at different existing techniques. The surveys were selected to incorporate the current procedures and methods applied to different information for prior disease outbreak prediction. Examined techniques and methods are within the past recent years that fall in categories of data mining, time analysis, hybrid models, social media data and machine learning techniques. Figure 2 shows the various epidemic outbreaks prediction methods.
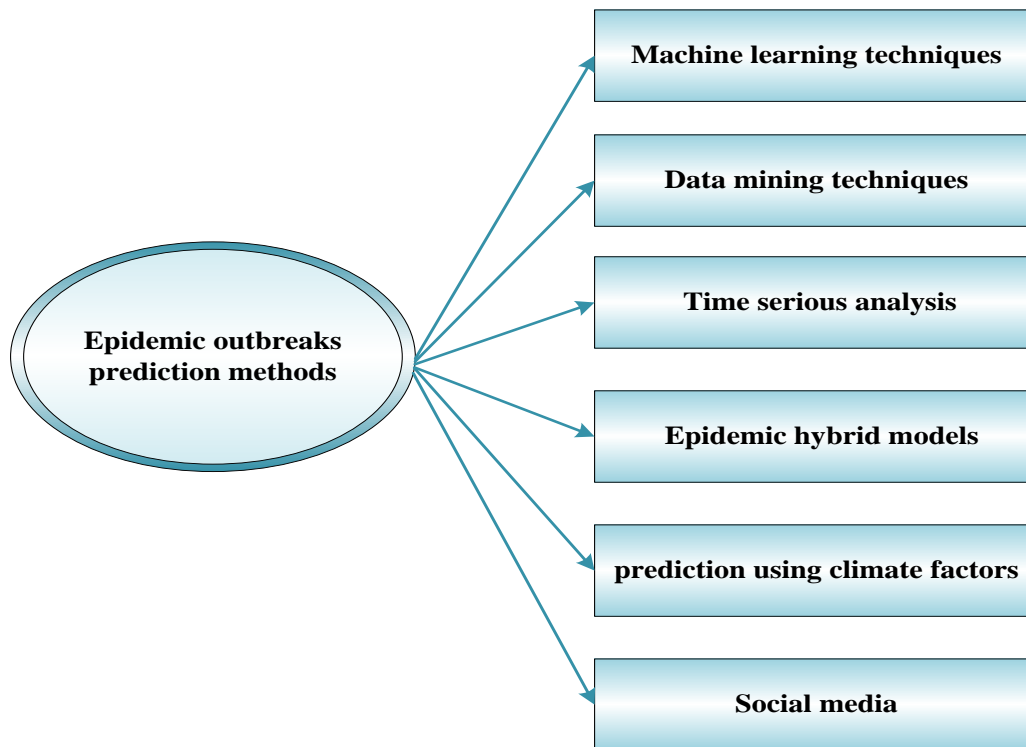

Figure 2: Epidemic outbreaks prediction methods

2.1. Prediction of Epidemic Outbreaks Using Machine Learning Techniques

In machine learning, several techniques like native Bayes, SVM, Neural network, random forest are used for prediction of epidemic diseases. Method for supervised learning is SVM (Support Vector Machine). The objective of flu related posts classifications the SVM is most commonly used [14-16].

Nadejda Lupolova et al. [14] have applied the SVM machine learning procedure to anticipate the bacterial (bovine E. coli O157) zoonotic potential. For human health more probable recognizing cow's strains is danger. In addition, it was conceivable to produce a probability of host affiliation that show that only a minor (0.9) by utilizing an SVM classifier. At the point when tested across datasets the predictive limit was held. Public health management of illness the authors finding have profound implications because of dairy cattle mediations, for example, vaccination. Further, pathogen biology understanding the learning methods should be used broadly.

Using twitter posts, to distinguish influenza like disease in Portugal Santos et al. [15] applied SVM-based classifier. A dataset with 2704 posts was physically explained with 650 printed highlights to test and preparing. To prepare the classifier a set of clarified dataset was used. Utilizing feature choice process and Bag-of-Words feature

representation, the classifier was actualized. In light of Mutual Information (MI) esteem it is utilized to elect the top highlights set.

In Beijing, from the networking sites (Chinese) to foresee influenza patterns Yang et al. [16] have applied a SVM-based strategy. From the sites of Chinese social networking the authors privilege that it is the main investigation to anticipate flu trend. For classification purposes the word weighting types such as Term Frequency (TF) weighting, TFIDF (Term Frequency-Inverted Document Frequency), Boolean and Inverted Document Frequency (IDF) weighting were considered by the TFIDF strategy.

Gregory F. Cooper et al. [17] have portrays a Bayesian framework, in a population that joins clinical diagnosis of individuals, in populace the epidemiological demonstrating of disease outbreaks. To build up a framework the authors applied this structure distinguishes the outbreaks of influenza detection from ED (Emergency Department) reports. Utilizing both the genuine information from outbreak and simulated data the authors assessed their strategy. In view of artificial Beijing the EVD process of propagation and its intrusion were simulated by Peng Zhang et al. [18].

To demonstrate the interaction between the occurrence probability of 4 various infections and bio-security rehearses on Canadian Swine Farms Ruth Cox et al. [19] have made a apparatus based on BBN (Bayesian Belief Network). The authors utilized two datasets to construct the BBN. First datasets clarifies the bio security practices utilized in swine farms and the second datasets explains the disease occurrence and the animal health status. Also, to appraise the risks of disease outbreak at various spatial scales Yilan Liao et al. [20] have presented a BBN technique, in view of virus detection rates. Simulation result shows the presented technique is specific than other conventional techniques. If some data were inaccessible the displayed method makes vulnerability estimates.

2.2. Prediction of Epidemic Outbreaks Using Data Mining

For the dengue outbreak prediction Anna L Buczak et al. [21] have introduced a novel prediction strategy using FARM (Fuzzy Association Rule Mining). The acquainted prediction method was utilized to concentrate between climatic information, meteorological information, socio-political information, and clinical data from Peru and these connections were in the rules form. The authors automatically chose the best set of rules and then form the classifier. Future the incidence of dengue was predicted as no outbreak (LOW) or outbreak (HIGH) the classifier was utilized.

In the Philippines, for predicting the incidence of dengue the author's et al. [22] have presented FARM methods to excerpt affiliation rules from historical environmental, climate data and socio-economic data, and epidemiological indicating the patterns of future weather. The presented model predict low/high dengue incidence, proceed in four weeks in Philippines. To historical data incidence the threshold between low/high were resolved.

Linking the Bio-PEPA modeling with data mining techniques tested to mumps was exhibited by Dalila Hamami et al. [23], in both model parameter optimization and structure identification. In the information suggesting areas the authors recognize the tough features by preceding association rule learning with the clustering. The introduced model suggested the vaccination, seasonality and age with correlated features were included in this method.

For the HPAI (Highly Pathogenic Avian Influenza) analysis utilizing livestock disease information gathered over an extended period, Zhenshun Xu et al. [24] have introduced a data mining techniques with a model of data cube. Based on data cube model construction, to assess the spatial and temporal perspectives of the disease spread

utilizing OLAP (Online Analytical Processing) actions with varying abstraction levels a multidimensional analysis of HPAI was performed. By applying sequential pattern mining and association rule mining the presented method provides useful data that achives routes for potential sequential dissemination and site connectedness of HPAI outbreaks.

2.3. Prediction of Epidemic Outbreaks Using Time Serious Analysis

The data gathered over particular time with internal structures like seasonal variety and auto correlation that is dissected to recognize the different patterns is called time series analysis. At different granularities levels the clinical information is regularly the time series gathered information. Further predictions are made based on these data parameters.

From *C difficile* infections to investigate ecological elements of clinical burdens Lawes et al. [25] presented a quasi-experimental study and non-linear time-series analysis. In all populaces a blended the intervention of persuasive-restrictive 4C antibiotic stewardship was initiated. A prediction model for DHF (Dengue Hemorrhage Fever) and the dengue fever using Seasonal Auto Regression Integrated Moving Average (SARIMA) scheme was developed by Gupta et al. [26], for year 2011 to predict monthly DF/DHF occurrence. The developed model was an extension of ARIMA series in which over a time the pattern repeats seasonally. Their model was given as SARIM (P, D, and Q). With estimating criteria like MAPE (Mean Absolute Percentage Error), stationery R-squared and BIC (Bayesian Information Criteria) the authors used SARIMA(0,0,1)(0,1,1) technique in Rajasthan for predicting dengue fever.

By accumulating month occurrence data as revealed by nation -level surveillance system the authors [27] have presented the database for global first bacterial meningitis. Computing the gravity centre distribution of cases the authors supposed the activity of mean timing of disease. For bacterial meningitis most cases the authors introduced the synchrony exists in between pathogens. Their discoveries provide key insight to bacterial meningitis seasonal dynamics and include knowledge about host and meningitis global epidemiology and the earth.

In Nanjing, China to build up a climate -based model of forecasting for HFMD (Hand, Foot, and Mouth Disease) utilizing the HFMD surveillance information and climatic variables Sijun Liu et al. [28] have developed an Multivariate SARIMA (Seasonal Autoregressive Integrated Moving Average) technique. To approve the execution of prediction the authors used weekly data prediction model. Their results show 80% of sensitivity and 96.63% of specificity with high agreement rate between the observed values and the predicted values.

2.4. Prediction of Epidemic Outbreaks Using Hybrid Models

Sudheer *et al.* [29] have presented a novel technique dependent on coupling the SVM and Firefly algorithm (FFA) to estimate the malaria occurrences. SVM models execution relies upon the appropriate SVM parameters choice. In their work for decide the SVM parameters, the FFA have been utilized. The malarial incidences in Jodhpur and Bikaner area were anticipated by embracing the SVM-FFA model. The input variables are monthly averages of malarial incidences, temperature, rainfall and relative humidity. From primary health centers, monthly notifications of malaria cases time series have been obtained. Further, fro contrasted with other traditional techniques the outcome demonstrates that the SVM-FFA model provides more precise estimates.

Massimo Buscema et al. [30] have developed a TWC method (Topological Weighted Centroid) for distinguishing the sources of epidemic with German Escherichia coli outbreak application. To a real world example these novel mathematical tools was tested to point out the real source of outbreak. As indicated by four independent indexes such as sensitivity, searching area, specificity and peak distance the result of TWC algorithm were predominant in comparison with different techniques like LVM, NES, Mexican Prob, and Rossmo Algorithm.

In the regards of stochastic nonlinear filtering, Alex Skvortsov and Branko Ristic [31] have displayed a scheme for epidemic outbreak syndromic surveillance. With inhomogeneous mixing utilizing the model of epidemiological stochastic compartmental, the epidemic dynamics was modeled. In order to avert the shortages of asthma health care resource in progress Li Luo et al. [32] have introduced a search index, that was linked with weather, historical admissions and pollution data using the techniques of machine learning. Simulation result shows best area under curve in test set of 0.832 was accomplished by utilizing their technique.

2.5 Prediction of Epidemic Outbreaks Using Climate Factors

In French Guiana Antoine Adde et al. [33] have assessed the potential of utilizing atmospheric and oceanic conditions to predict the outbreaks of dengue fever. To recognize the climatic conditions the composite studies and diminished correlations were performed. At that point to build a forecast model a logistic regression was performed. Based on the temperatures of surface of Pacific Ocean Sea the author's exhibit the model and it predict 80% of outbreaks in Azores High sea-level pressure. m meteorological records relative humidity, rainfall and temperature have been obtained. At that point when At regional scales and within the districts to investigate correlation maps, Andres Baeza et al. [34] have introduced a remote sensing data for the NDVI (Normalized Difference Vegetation Index). The introduced NDVI methods were used as a rainfall integrated measures. Analysis addresses the pairing between the climate variability and malaria incidence whether the irrigation has diminished. Also the introduced method reflects NDVI breakdown as useful risk indicator and increase in malaria transmission control.

2.6 Prediction of Epidemic Outbreaks Using Social Media

These days, from a huge range of web and social media sources the large amounts of health and emergency data are increasingly coming. Over the recent years, this data is useful for earlier detection of outbreak and disease surveillance, and few public web surveillance projects in this field have developed.

For monitoring and model the influenza activity in China, Q. Yuan et al. [35] have presented a technique in Baidu that utilized an data from internet search query. Main objective of their research was to present the comprehensive technique for keyword filtering and selection, influenza activity modeling and detection in China and composition of index. With Chinese influenza data case the sequential time series for elected composite index was correlated significantly. To determine the twitter usage as actual time method, Michelle Odlum et al. [36] have used Twitter of Ebola outbreak detection. To detect the similarities content analysis was conducted and develops clusters. On the tweet corpus trend analysis was performed. To build the clusters the presented method utilized the k-means algorithm.

In Google search volume epidemic-associated to predict the disease trends, X. Zhou et al. [37] have introduced a syndromic surveillance framework. To lessen the noise level with multiple alert levels the authors initially indicated the epidemic trend. Thus to monitor both regional and national levels of epidemic alert (U.S) the respective models

were built. For crime prediction Matthew S. Gerber [38] have presented the research by the spatiotemporally tagged tweets usage. To naturally recognize analysis fields across a major city in US the authors use statistical topic modeling and Twitter-specific linguistic analysis. The summary of the reviewed methods and techniques is shown in table 1.

Table 1**:** Summary of the Reviewed Methods and Techniques

Method category	Author	Technique name	Performance
Machine learning	Nadejda Lupolova et al. [14]	SVM	Predict bacterial (bovine E. coli O157) zoonotic potential
	Carlos Santos et al. [15]	SVM based classifier	Detect flu-like illness in Portugal using twitter posts
	Yang et al. [16]	SVM	Flu trend were predicted from Chinese social networking sites
	Gregory F. Cooper et al. [17]	Bayesian framework	Detects the outbreaks of influenza from Emergency Department reports
	Peng Zhang et al. [18]	Geodemographics and large scale machine learning	Analyze the propagation mechanism of Ebola virus disease
	Ruth Cox et al. [19]	Bayesian Belief Network	Model the occurrence of four different diseases and bio-security practices on Canadian swine farms
	Yilan Liao et al. [20]	BBN with virus detection rates	Assess disease outbreak risks at different spatial scales
Data mining	Anna L Buczak et al. [21]	Fuzzy Association Rule Mining	Predict future dengue incidence either as outbreak or no outbreak
	Buczak et al. [22]	FARM methods with rules extraction	Predict low/high dengue incidence within 4- weeks in Philippines
	Dalila Hamami et al. [23]	Bio-PEPA modeling with data mining	Applied in both model parameter optimization and structure identification
	Zhenshun Xu et al. [24]	data mining techniques with data cube scheme	Provides useful information for HPAI outbreaks
Time serious analysis	Lawes et al. [25]	Quasi and non-linear time serious analysis	Initiated Mixed Persuasive-Restrictive 4C antibiotic

			stewardship intervention
	Gupta et al. [26]	SARIMA	Measure MAPE, BIC and stationery R-squared technique for dengue fever prediction in Rajasthan
	Paireau [27]	SARIMA technique	Developed the first bacterial meningitis global database
	Sijun Liu et al. [28]	SARIMA	For HFMD Develop a forecasting model based on weather with 80% of sensitivity and 96.63% of specificity
Hybrid models	Sudheer *et al.* [29]	SVM-FFA	Malarial incidences in Jodhpur and Bikaner area were predicted.
	Massimo Buscema et al. [30]	Topological Weighted Centroid algorithm	Identify epidemic sources with German Escherichia coli outbreak application and measured sensitivity, searching area, specificity and peak distance.
	Skvortsov and Branko Ristic [31]	Syndromic-like observations algorithm	For estimation and early outbreak prediction of epidemic
	Li Luo et al. [32]	Search index combined with environmental data and machine learning	In advance avoid asthma resource shortages and result show best area under curve in test set of 0.832 was achieved
Climate factors	Adde et al. [33]	Atmospheric and oceanic conditions	composite analyses and lagged correlations were achieved to recognize the atmospheric conditions with epidemic disease prediction
	Andres Baeza et al. [34]	remote sensing data for NDVI methods	Increase in malaria transmission control
Social media	Q. Yuan et al. [35]	Internet search query data	Detect and model the influenza activity in China
	Michelle Odlum et al. [36]	Twitter posts	Build clusters with k-means algorithm for Ebola outbreak detection
	Xichuan Zhou et al. [37]	disease-related Google search volume	Design syndromic surveillance system to predict the epidemic

		trends and reduce the noise level.
Matthew S. Gerber [38]	spatiotemporally tagged tweets	Automatically identify disease Using statistical topic modeling and Twitter-specific linguistic analysis.

3. CONCLUSION

This paper analyses the various approaches and schemes that is utilized in epidemic outbreak prediction model. It can be concluded that, these models are based only on the clinical disease data. By taking social, political, geological and climatic data the presented models can be improved and yield more accurate forecasts. The information exchange became much fast and efficient while communicating through social channel increases. Through various mining techniques these channels can be tapped and obtained the real time feedback along with more accurate outbreak detection. So, an enhancement to the prediction model along with machine learning technique can be proposed as a future work.

REFERENCES

[1]N. Molinari, I. Ortega-Sanchez, M. Messonnier, W. Thompson, P. Wortley, E. Weintraub and C. Bridges, "The annual impact of seasonal influenza in the US: Measuring disease burden and costs", Vaccine, vol. 25, no. 27, pp. 5086-5096, 2007.

[2]C. Gilbert, "Retinopathy of prematurity: A global perspective of the epidemics, population of babies at risk and implications for control", Early Human Development, vol. 84, no. 2, pp. 77-82, 2008.

[3]S. Alasaad, "War diseases revealed by the social media: massive leishmaniasis outbreak in the Syrian Spring", Parasites & Vectors, vol. 6, no. 1, p. 94, 2013.

[4]H. Barkema, M. Green, A. Bradley and R. Zadoks, "Invited review: The role of contagious disease in udder health", Journal of Dairy Science, vol. 92, no. 10, pp. 4717-4729, 2009.

[5]J. Bradford, C. Kunz, R. Kohavi, C. Brunk and C. Brodley, "Pruning decision trees with misclassification costs", Machine Learning: ECML-98, pp. 131-136, 1998.

[6]L. Madoff and J. Woodall, "The Internet and the Global Monitoring of Emerging Diseases: Lessons from the First 10 Years of ProMED-mail", Archives of Medical Research, vol. 36, no. 6, pp. 724-730, 2005.

[7]M. Mustafa, V. Rasotgi, S. Jain and V. Gupta, "Discovery of fifth serotype of dengue virus (DENV-5): A new public health dilemma in dengue control", Medical Journal Armed Forces India, vol. 71, no. 1, pp. 67-70, 2015.

[8]J. Brillman, T. Burr, D. Forslund, E. Joyce, R. Picard and E. Umland, "Modeling emergency department visit patterns for infectious disease complaints: results and application to disease surveillance", BMC Medical Informatics and Decision Making, vol. 5, no. 1, 2005.

[9]H. Hethcote, "The Mathematics of Infectious Diseases", SIAM Review, vol. 42, no. 4, pp. 599-653, 2000.

[10]L. Meyers, "Contact network epidemiology: Bond percolation applied to infectiousdisease prediction and control", Bulletin of the American Mathematical Society, vol. 44, no. 01, pp. 63-87, 2006.

[11]W. Yang, A. Karspeck and J. Shaman, "Comparison of Filtering Methods for the Modeling and Retrospective Forecasting of Influenza Epidemics", PLoS Computational Biology, vol. 10, no. 4, p. e1003583, 2014.

[12]Hyo Jin Do, Chae-Gyun Lim, You Jin Kim and Ho-Jin Choi, "Analyzing emotions in twitter during a crisis: A case study of the 2015 Middle East Respiratory Syndrome outbreak in Korea", 2016 International Conference on Big Data and Smart Computing (BigComp), 2016.

[13]T. Correa, A. Hinsley and H. de Zúñiga, "Who interacts on the Web?: The intersection of users' personality and social media use", Computers in Human Behavior, vol. 26, no. 2, pp. 247-253, 2010.

[14]N. Lupolova, T. Dallman, L. Matthews, J. Bono and D. Gally, "Support vector machine applied to predict the zoonotic potential ofE. coliO157 cattle isolates", Proceedings of the National Academy of Sciences, vol. 113, no. 40, pp. 11312-11317, 2016.

[15]J. Santos and S. Matos, "Analysing Twitter and web queries for flu trend prediction", Theoretical Biology and Medical Modelling, vol. 11, no. 1, p. S6, 2014.

[16]X. Cui, N. Yang, Z. Wang, C. Hu, W. Zhu, H. Li, Y. Ji and C. Liu, "Chinese social media analysis for disease surveillance", Personal and Ubiquitous Computing, vol. 19, no. 7, pp. 1125-1132, 2015.

[17]G. Cooper, R. Villamarin, F. (Rich) Tsui, N. Millett, J. Espino and M. Wagner, "A method for detecting and characterizing outbreaks of infectious disease from clinical reports", Journal of Biomedical Informatics, vol. 53, pp. 15-26, 2015.

[18]P. Zhang, B. Chen, L. Ma, Z. Li, Z. Song, W. Duan and X. Qiu, "The Large Scale Machine Learning in an Artificial Society: Prediction of the Ebola Outbreak in Beijing", 2018. [19]R. Cox, C. Revie, D. Hurnik and J. Sanchez, "Use of Bayesian Belief Network techniques to explore the interaction of biosecurity practices on the probability of porcine disease occurrence in Canada", Preventive Veterinary Medicine, vol. 131, pp. 20-30, 2016.

[20]Y. Liao, B. Xu, J. Wang and X. Liu, "A new method for assessing the risk of infectious disease outbreak", Scientific Reports, vol. 7, no. 1, 2017.

[21]A. Buczak, P. Koshute, S. Babin, B. Feighner and S. Lewis, "A data-driven epidemiological prediction method for dengue outbreaks using local and remote sensing data", BMC Medical Informatics and Decision Making, vol. 12, no. 1, 2012.

[22]A. Buczak, B. Baugher, S. Babin, L. Ramac-Thomas, E. Guven, Y. Elbert, P. Koshute, J. Velasco, V. Roque, E. Tayag, I. Yoon and S. Lewis, "Prediction of High Incidence of Dengue in the Philippines", PLoS Neglected Tropical Diseases, vol. 8, no. 4, p. e2771, 2014.

[23]D. Hamami, B. Atmani, R. Cameron, K. Pollock and C. Shankland, "Improving process algebra model structure and parameters in infectious disease epidemiology through data mining", Journal of Intelligent Information Systems, 2017.

[24]Z. Xu, J. Lee, D. Park and Y. Chung, "Multidimensional analysis model for highly pathogenic avian influenza using data cube and data mining techniques", Biosystems Engineering, vol. 157, pp. 109-121, 2017.

[25]T. Lawes, J. Lopez-Lozano, C. Nebot, G. Macartney, R. Subbarao-Sharma, K. Wares, C. Sinclair and I. Gould, "Effect of a national 4C antibiotic stewardship intervention on the clinical and molecular epidemiology of Clostridium difficile infections in a region of Scotland: a non-linear time-series analysis", The Lancet Infectious Diseases, vol. 17, no. 2, pp. 194-206, 2017.

[26]V. Lal, S. Gupta, O. Gupta and S. Bhatnagar, "Forecasting incidence of dengue in Rajasthan, using time series analyses", Indian Journal of Public Health, vol. 56, no. 4, p. 281, 2012.

[27]J. Paireau, A. Chen, H. Broutin, B. Grenfell and N. Basta, "Seasonal dynamics of bacterial meningitis: a time-series analysis", The Lancet Global Health, vol. 4, no. 6, pp. e370-e377, 2016.

[28]S. Liu, J. Chen, J. Wang, Z. Wu, W. Wu, Z. Xu, W. Hu, F. Xu, S. Tong and H. Shen, "Predicting the outbreak of hand, foot, and mouth disease in Nanjing, China: a time-series model based on weather variability", International Journal of Biometeorology, vol. 62, no. 4, pp. 565-574, 2017.

[29]S. Ch, S. Sohani, D. Kumar, A. Malik, B. Chahar, A. Nema, B. Panigrahi and R. Dhiman, "A Support Vector Machine-Firefly Algorithm based forecasting model to determine malaria transmission", Neurocomputing, vol. 129, pp. 279-288, 2014.

[30]M. Buscema, E. Grossi, A. Bronstein, W. Lodwick, M. Asadi-Zeydabadi, R. Benzi and F. Newman, "A New Algorithm for Identifying Possible Epidemic Sources with Application to the German Escherichia coli Outbreak", ISPRS International Journal of Geo-Information, vol. 2, no. 1, pp. 155-200, 2013.

[31]A. Skvortsov and B. Ristic, "Monitoring and prediction of an epidemic outbreak using syndromic observations", Mathematical Biosciences, vol. 240, no. 1, pp. 12-19, 2012.

[32]L. Luo, C. Liao, F. Zhang, W. Zhang, C. Li, Z. Qiu and D. Huang, "Applicability of internet search index for asthma admission forecast using machine learning", The International Journal of Health Planning and Management, vol. 33, no. 3, pp. 723-732, 2018.

[33]A. Adde, P. Roucou, M. Mangeas, V. Ardillon, J. Desenclos, D. Rousset, R. Girod, S. Briolant, P. Quenel and C. Flamand, "Predicting Dengue Fever Outbreaks in French Guiana Using Climate Indicators", PLOS Neglected Tropical Diseases, vol. 10, no. 4, p. e0004681, 2016.

[34]A. Baeza, M. Bouma, A. Dobson, R. Dhiman, H. Srivastava and M. Pascual, "Climate forcing and desert malaria: the effect of irrigation", Malaria Journal, vol. 10, no. 1, p. 190, 2011.

[35]Q. Yuan, E. Nsoesie, B. Lv, G. Peng, R. Chunara and J. Brownstein, "Monitoring Influenza Epidemics in China with Search Query from Baidu", PLoS ONE, vol. 8, no. 5, p. e64323, 2013.

[36] M. Odlum and S. Yoon, "What can we learn about the Ebola outbreak from tweets?", American Journal of Infection Control, vol. 43, no. 6, pp. 563-571, 2015.

[37] X. Zhou, Q. Li, Z. Zhu, H. Zhao, H. Tang and Y. Feng, "Monitoring Epidemic Alert Levels by Analyzing Internet Search Volume", IEEE Transactions on Biomedical Engineering, vol. 60, no. 2, pp. 446-452, 2013.

[38] M. Gerber, "Predicting crime using Twitter and kernel density estimation", Decision Support Systems, vol. 61, pp. 115-125, 2014.