International Journal of Scientific Research in Engineering and Management (IJSREM)
Volume: 07 Issue: 09 | September - 2023 SJIF Rating: 8.176 ISSN: 2582-3930

Machine Learning Methods in Skin Disease Recognition

Prof. Sneha S.Chahande Nagpur,440034,
Nagpur,sneha78chahande@gmail.com
Prof. Priyanka S.Dewalkar,Nagpur,440026,
priyadevalkar93@gmail.com

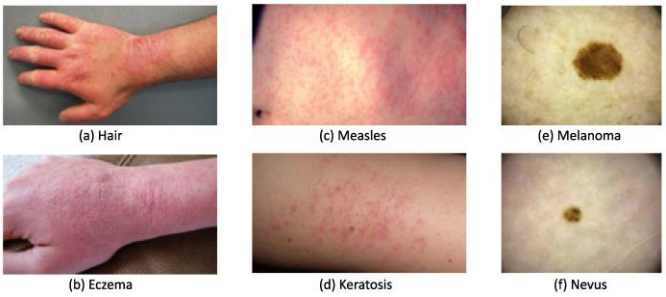
Abstract **- Skin diseases affect millions of people worldwide. They can be easily recognized as they often have a different texture and color but are difficult to diagnose because of the similar symptoms of some types of disease. The motivation for this study is to collect and analyze machine learning (ML) data in skin research, with the aim of supporting the development of technology for the diagnosis of skin diseases. To help dermatologists in their diagnosis, many skin photos are created and published online. These efforts have encouraged researchers and medical professionals to develop automated skin diagnosis techniques using image segmentation and classification techniques.**

Index Terms - SARIMA Model, . PDLM Model, Multiple linear regressions, Sensitivity Test and Model Validation, Poisson Distribution Analysis

I. INTRODUCTION

Skin protects the human body from harmful external factors and is the largest organ in the human body. Skin diseases can be caused by many factors, such as fungi, bacterial infections, allergies or infections [1]. Skin diseases, as one of the most common diseases, affect many people around the world.

Skin diseases are easily recognized by their appearance and/or coloration, but can be difficult to accurately diagnose due to similar symptoms in different types of disease. Figure 1a,b, show that both contact dermatitis and eczema present similarly with redness, swelling, and chapping on a hand. Similarly, as seen in Figure 1c,d, measles and keratosis show red dots that are sporadically distributed on the skin. These similarities lower diagnosis accuracy, particularly for dermatologists with less than two years of clinical experience. To administer appropriate treatment, it is essential to identify skin lesions correctly and as early as possible. Early diagnosis usually leads to a better prognosis and increases the chance of full recovery in most instances. The training of a dermatologist requires several years of clinical experience as well as high education costs.



Artificial intelligence (AI) has made great strides in image analysis over the past decade using techniques such as machine learning (ML) and deep learning (DL). Simulation models can be developed using ML and DL models. ML The ML method is more flexible compared to the DL method, which uses knowledge and selects features as input [4]. The DL method can easily identify the underlying reasons and identify explanations and key features of image analysis and processing. These advances have greatly encouraged medical professionals to explore the potential of applying artificial intelligence methods to disease diagnosis, especially in the diagnosis of skin diseases. Moreover, DL has already demonstrated its ability in this field by achieving diagnostic accuracy similar to that of dermatologists with 5 years of clinical experience [5]. Therefore, DL is considered a potential tool for cost-effective diagnosis of skin health.

The success of AI applications relies heavily on the support of big data to ensure reliable performance and generalization capabilities. In order to accelerate the progress of the application of artificial intelligence in the diagnosis of skin diseases, it is necessary to establish reliable databases. Researchers from multiple institutions collaborated to create the International Skin Imaging Collaboration (ISIC) database for dermatology research and organizational challenges from 2016 to 2020 .

2. LITERATURE SURVEY

Literature Survey Several researchers have proposed various machine learning based to detect the type of skin diseases. Here we briefly review some of the techniques as reported in the literature. Usually, other studies first they will apply feature selection than rating. The execution time of the model recorded high. Ahn and Hur [1] proposed genetic algorithm first classify and select the feature set. He proposed a filter base selection in the local region. The proposed model search for local neighbors sample and correlated with each other [12, 14, 24]. Antimicrobial resistance is a critical problem globally. The proposed method uses a time series technique explicitly to forecast the outbreak of diseases. They use the wrapper method for feature selection technique. The author proposed

the Artificial Neural Network based feature selection technique to reduce and remove irrelative characteristics. In the unstructured text, clinical data increase in all health departments, and availability of such data is free. The author applied the dictionary-based technique. It is the hybrid approach which handles missing value and other data issue. The author proposed a two-step approach (I) to compress high dimension data and (ii) to different categorical and numeric value data with the missing value. The multi-label selection is always a complex problem because labeling is done one by one. The author proposed discriminative and relevant feature selection. The author suggested the X variance feature section approach in gene selection [12, 18, 19, 23].

A. Data Collection

1) In this study, data of the quarterly and monthly number of reported skin cancer cases in Hyderabad city from January month 2000 to December month 2018 was collected from the disease control department of Hyderabad medical center (HMC).HMC is the chief agency in charge of analysis and obtaining reported data for prevention of contagious in the city. Daily weather data from 18 Jan 2000 to 24 December 2018 was collected from IMD Indian Metrological Department Pune India. The data was collected through satellite sensors at Hyderabad city including daily Maximum, Average and Minimum Temperature, daily rainfall, humidity. The obtain complete data has to be converted to average, mean temperature and maximum and increasing rainfall and monthly humidity for investigation.

2) Data Analysis

In the initial stage, the relation among metrological attributes was inspect by utilize different machine learning regression methods Standard Multiple Regression, Poisson distributed lag model and Seasonal autoregressive integrated moving average .Above 3 models are most commonly applied in a literature that to assesses the association between climatic changes and skin diseases, in the next step, the algorithms were validated to examine the machine learning models for prediction of skin cancer incidence and skin diseases outbreak.

3) Standard Multiple Regression: The initial phase of the investigation applied cross correlation technique to analysis the relationship among the skin diseases outbreak and various lags of the exploratory attributes like rainfall, humidity, temperate to regulate the best time interval for the initial model. which is expressed in Eq. 1.

$$In(S) = Y0 + Y1Tmin + Ymax + Y3Hmin + Y4Hmax + Y5R \quad \ldots Eq\ (1)$$

Where S is the monthly count of skin diseases, Tmin and T max are monthly minimum and maximum of temperature; H min and H max as monthly min and max humidity and rainfall is denoted as R.

4) SARIMA Model: The SARIMA algorithm is first proposed by author Jenkins and we have try to hybrid the model and expanded using skin disease occurrence data from 2000 to 2018.Than the train algorithm was used to forecast skin disease occurrence in 2018.

ARIMA algorithm with S as seasonal SARIMA try to examination seasonal period, which is express by SARIMA[x, y, z] [X, Y, Y] s,is given through model Eq-(2)

Pt = +x...Eq (2)

Where Θx(Bs) is the seasonal auto regression(AR) Θx(B) is the AR operator, Θy(B) moving average(MA) Θy is seasonal and ordinary different components, X external variable Pt is dependent variable and at is white-nose.

The SARIMA model includes several steps during the research. Initially, the variance value of the number of skin diseases was extracted using the natural lag variation of the data set. Tested with a fuller index tail. Using time series data, the mean is the stabilization of the selection of the series of different characteristics [D and d] found on the time series diagram, and the time series with a more stabilizing mean should be taken into account when compared to their standard deviation. The next step was to examine the sequence of non-seasonal and seasonal characteristics [AR(X,x),MA(Y,y)] using ACF and PACF. Using several possible methods, we tested the goodness of fit between different methods using AIC. Depending on the algorithm, the low AIC score is chosen for prediction. At least the best model was developed for the period from 2000 to 2018, a fine-tuning of the climatic feature that is significantly associated with the occurrence of skin diseases. In this way, we can predict the occurrence of skin diseases in 2019.

5. *PDLM Model:*

By combining the distributed lag [DLM] algorithm and the passion time series model, it was used to predict the effect of climate feature on skin diseases and build a prediction model. There are many interpretable participants in building the model. Initially, in order to control the seasonality and the long-term trend of the collected data, we create a pair of base variables that is part of the main time variables, we use 3 degrees of freedom per year, to create the trough base, we use 4 knots per year, multiplying 8 years At 4 and minus 1 gives to create a mathematical spline function. Even if there is no agreement on the choice of degrees of freedom. Based on previous studies, we took 3 years and thought they were a balance between properly managed trends and the seasonality of the monthly data, which provides more accurate information for assessing exposure effects..

Everything they have is incorporated into the PDLM model for both multivariate regression and bivariate analysis. Next-stage skin disease auto regression suggested a very strong autocorrelation between present and past cases; in PACF [2B. Fig.] Cutting off the 1-month delay time. Few studies have looked at the link between climate and infectious diseases, showing a strong relationship between the two. Therefore, in this study, we study the lag time every 2-3 months and select the optimal lag time for the predictive model. In the third

phase, due to the delay, it affects the independent variable of skin diseases, which was determined on the basis of a systematic literature review and cross-correlation function. Therefore, we formulate a combined Poisson model to identify the autocorrelation sequence.A backward phase-wise analysis was considered for selecting the final model in the level which is approximant vale 0.04.with the help of AIC value as lowest help to build the best predicting model for skin diseases in upcoming years.

$In(\mu t) = \beta 0 + \sum 2x=1\ \beta t\text{-}x\ AR + \sum pL=1\ \beta tl(Templ,p) + \sum pL=1\ \beta hl(Humidl,p) + \sum pL=1\ \beta rl(Rainl,p) + S(t) + \varepsilon t + In(POP)$.

Where In(μt) is average predict skin diseases at model; βr is constant number of skin diseases cases; ARt-x is skin diseases cases at lag period k, Templ,p, Humidl,p, Rainl,p are matrix for DLM to rainfall, humidity, temp respective; βt-x is parameter of auto regression at lagperiod k; L is lag month; βtl, βhl, βrl are coefficient for Rainl,p, Humidl,p, Templ,p in lag period; p consider to be maximum lag; S(t) is the Spline function. Which help to control seasonally trends.

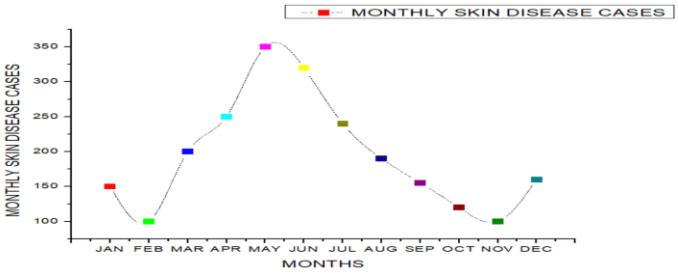


FIG.1 MONTHLY COUNTS OF SKIN DISEASE CASES (2000-2018) IN HYDERABAD CITY.

6. Sensitivity Test and Model Validation.

The accuracy of the prediction of each model they developed was abscess, comparing a precise outbreak with actual diagnosed cases of skin disease. Some indicators, such as the mean absolute percentage error [MAPE], were used to verify and validate the forecasting model for different time periods 3 lags 6 lags, 9 lags and 12 lags and models with a lower value MAPC consider the model best suited for further analysis .

$MAPE = \sum nt=1\ |\ xt - x^{\wedge} / xt\ |$

Where n is a number of the month, xt and $x^{\wedge}$ are observed cases and predicted cases no. of skin diseases in a month.

Our study shows that we have examined skin diseases that have increased 80% of skin diseases between the years 2000 and 2018. Moreover, the best algorithm used as ROC should calculate and analyze the sensitivity of the train model in the diagnosis of their skin diseases. be used further, the ROC metric is used to identify the true positive (TP) or sensitivity of the bacteria. train a model to estimate the probability versus the false positive rate (FP) [1-specificity]. The ROC curve shows accurate and unbiased analysis on a case-by-case basis.

II. RESULT

A. *Descriptive analysis*

There were 6000 skin disease cases in the city of Hyderabad during study. On the mean monthly in decent number of skin diseases, instances were 65 with occurrence rate as 5.4per 99999 person in a month. The occurrence estimate the rising from summer period [Feb – June] to wets period [July – Dec]the excessive monthly occurrence rate 80 per 100000 person month was in April, and lowest occurrence rate is 2.5 per 99999 people was in the of January. This is show in [Fig 1].

Table 1
Summary of skin diseases and climate attributes from 2000 to 2018 in Hyderabad

Variables	Minimum	Maximum	Average	Median	Std.Deviation
Skin diseases cases	10	629	127	105	96
Min Temp	23.2	27.4	25	25.1	0.93
Max Temp	29.3	36	32	32.3	1.3
Min humidity	50.9	71	62	62	2.7
Max humidity	90.5	100	95.5	95	2.6
Rainfall	0	445	127	121	109

In regards of climate variable data the range of rainfall varies from 5MM in the month January to 160 MM in the month of May the mean peak temp varies from 37 0C in the month of Feb& March to 43 0Cin the month of April & May andthe average min Temp varies from 20C to 26C in November, Avg min & max humidity varies from 88% march to 92% may and from 49% in Nov & Dec to 60% in January. Respectively in table1 show different between dependent &independent variable using statically method.

B. *Multiple linear regressions*

Number The outcome of autocorrelation occurrence shows that the heights correlation among skin diseases rate and min temp were initiate at lag1, lag2(r,0.3), maximum temp at lag3,lag4,and lag5(r,0.34 and 0.31), min humidity at lag12 and lag1 (r,0.53,0.51), max humidity at lag3,lag4 (r,0.35,0.37) and relative rainfall at lag2,lag3 (0.53,0.45).based on this a new independent variable build added;Tmax3,4,Tmin1,2,Hmax12,1 and R2,3.In table 2 mention the effects of climate attributes (Tmax3,4,Tmin1,2,Hmax12,1 and R2,3) on skin disease and shows that gradually decreases in skin diseases instance value β= -0.1 and p value = 0.04 for correlated with 1C0 rise in Maximum temp, because 1C0 increase maximum humidity value β = 0.04,1MM of relative rainfall(40.002) monthly skin diseases significantly increase with a level significant value of 0.06.

Table 2 : SMR coefficient of the skin disease vs. Min and Max temperature, rainfall, and humidity for 2002 -2011 for Hyderabad city.

Variable	Root MSE	R-Squared	p-value	95% CI	Coefficients
Model 1					
$T_{min2,3}$ [a]	0.59	0.39	0.07	-0.5-0.009	-0.3
$T_{max4,5}$ [b]			0.7	-0.2-0.18	0.04
$H_{min0,1}$ [c]			0.09	-0.0008-0.0097	0.06
$H_{max0,1}$ [d]			0.9	-0.060-0.0078	0.010
$R_{1,2}$ [e]			0.0002	0.002-0.007	0.004
Constant			0.3	-2.9-11.9	4.45
Model 2					
$T_{min2,3}$	0.57	0.43	0.06	-0.39-0.03	-0.19
$H_{min0,1}$			0.06	-0.005-0.94	0.06
$R_{1,2}$			<0.02	0.003-0.007	0.005
Constant			<0.02	2.0-9.9	5.89

The model exhibit that min humidity and min temperature were no statistically significantly related to change in no. of skin diseases. After removing insignificant variables, the remaining independent variable are Hmax2,1, Tmax3,4, and R1,2 were significantly related to skin disease with much greater prediction strength R value = 0.38 compared with previous value = 0.35; RMSE0.49 compare with 0.51 ad second model used to predict skin diseases cases from Jan to Dec 2018.

C. SARIMA Analysis

Define In time series analysis, the lag of skin diseases cases confers the normal distribution i.e. ShapiroWalk Test with P-value 0.51 comparing with original skin diseases case with P-value <0.01 which has the lowest distribution. The plot between ACF and PACF using collected data sets from 2000-2018 mention in figure.2 [A and B]. The ACF metrics exhibits the very strong seasonal hidden information of skin diseases that has confirmed to add S with seasonal to build SARIMA model (X,Y,Z) with periodic length S is 12 and other is non seasonal (x,y,z).We anticipating or imagine as skin diseases occurrence has a different seasonal period.

PACF metics recommended that the value of X between 1 and 2 with the period interval of 12 month lags, as PAC was almost Zero at all lags excluding lag3 and lag5. The ACF recommends a moving average value Y from 3 to 5; mention that autocorrelation is all zero expect 4 with the period time of 12 months (Fig 2). Next differencing value d = 1 on plot ACF shoes a significant cut off 1 month lag among 12 months. (Fig.2 C), a basic test indicates that there is significant stability in data using Dickey- fuller Test, P<0.0.1 which is compared with original data i.e. P>0.4.Nevertheless, from the ACF still shows the seasonal patterns at

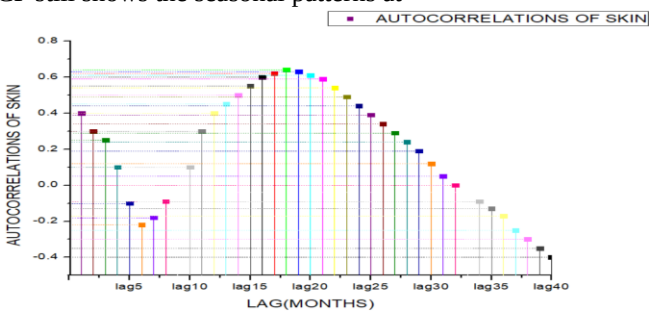


Fig.2. Autocorrelation functions calculate using log transformed skin disease cases from 2000 to 2018 in Hyderabad.

In Fig.2 with 12 lags, clearly shows better to add seasonal difference D = 1 month. Throughout 12 months autocorrelation shows positive significance, were SAR considers the value of x = 1.Table 3 exhibits the value of VIC and AIC for the SARIMA model. Selecting different x and y the model which has lowest BIC, AIC consider being best model as SARIMA (1, 1, and 1) (1, 1 and 0)12 alter as average temp, rainfall and humidity (BIC 38,AIC 29) respectively.The investigation of residuals does not have any significant in ACF, shown in Fig.3A. The inverse graph shows a reasonable probability of residual in Fig.3B by L jung- Box test establish residual value statistically not depended on P value greater than 0.04(Fig 3C).On the hand The SARIMA establishes the strong statistically significant result on monthly temperature as $\beta = 0.19$ and $p = 0.01$, humidity value $\beta = 0.09$ and p is <0.01, but rainfall is not significant with value as $\beta = -0.007$ and $p = 0.2$.Then SARIMA model is train to predict skin disease cases at Hyderabad.

D. Poisson Distribution Analysis

Number The correlation between skin disease cases and climate factors confer a uniform sine wave oscillation at 6 months for one rotation. 2-5 months are significant for min temp, humidity 2-3 months, 3-6 months interval for a max temp, 0-3 month for max rainfall and humidity. by removing the no significant attribute from the tested model, the final model shows all variable was; 2 auto regression value of skin 2-4 min humidity, lag 2-3of rainfall by adjusting Spline function of the population and time(table4).

Table 3
Ridings of BIC metrics and AIC metrics by different SARIMA model combination value (x, 1 and y) (1, 1 and 0)12.

Time series Model	BIC	AIC
Simple SARIMA		
(1,1 and 1)(1,1 and 0)$_{12}$	150	138
(1,1 and 2)(1,1 and 0)$_{12}$	153	139
(1,1 and 3)(1,1 and 0)$_{12}$	154	137
Complex SARIMA		
(1,1 and 1)(1,1 and 0)$_{12}$	44	33
(1,1 and 2)(1,1 and 0)$_{12}$	49	36
(1,1 and 3)(1,1 and 0)$_{12}$	54	39

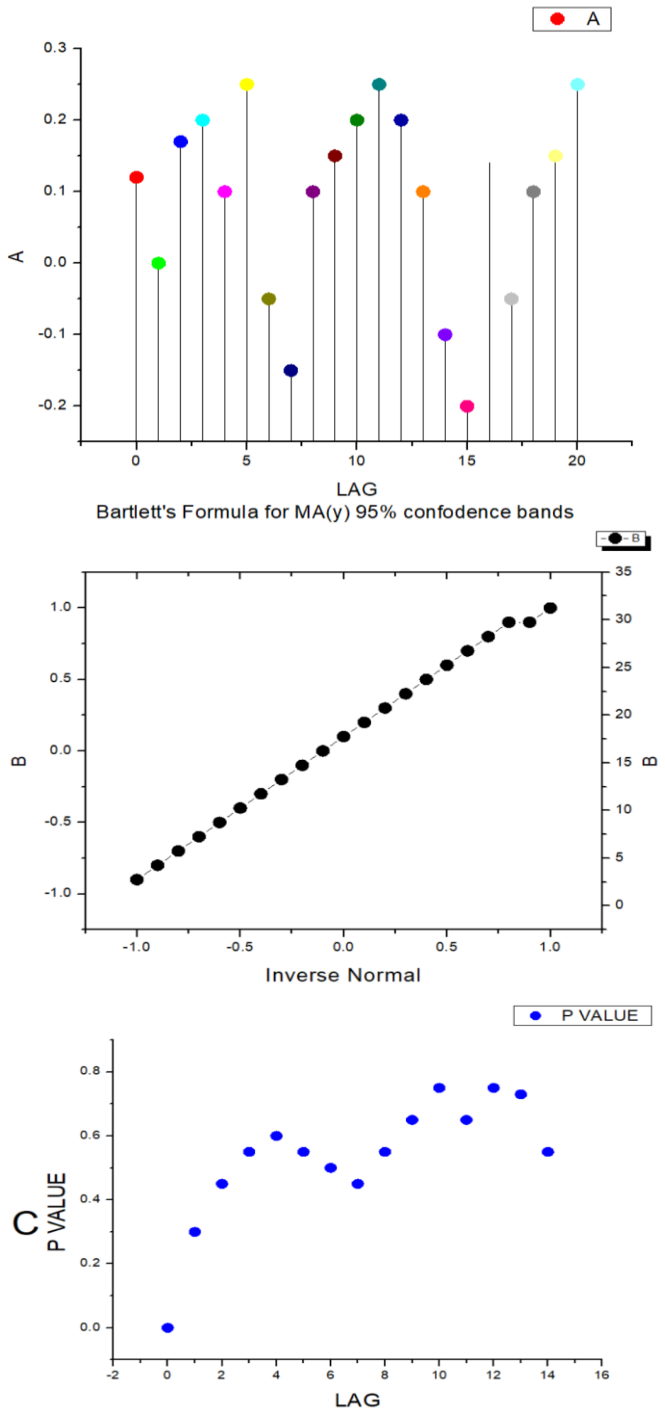


Fig.3.Graphical representation of SARIMA model: [A] and [B] plot of standardized residuals of Bartlett's formula and inverse, and [C] p value.

Table 4
Poisson distributed lag model regression coefficients of skin diseases vs. maximum and minimum temperature, rainfall, and humidity.

Variable	P-value	Coefficients	95% CI
Lag 1 Skin cases	<0.0.2	-0.001	-0.00027-(-0.0015)
Lag 2 Skin cases	<0.0.2	-0.002	-0.0036-(-0.0027)
Lag 1 Max Temp	<0.0.2	0.273	0.209-0.318
Lag 2 Max Temp	<0.0.2	0.220	0.168-0.29
Lag 1 Max Humidity	<0.0.2	0.046	0.034-0.058
Lag 2 Max Humidity	<0.0.2	0.061	0.047-0.074
Lag 3 Max Humidity	<0.0.2	0.025	0.009-0.0019
Lag 1 Rainfall	<0.0.2	0.002	0.00090-0.0019
Lag 2 Rainfall	<0.0.2	0.002	0.00097-0.0018
Lag 3 Rainfall	<0.0.2	0.008	0.0004-0.0013
Constant	<0.0.2	15.1	10.3-9.9

In type ML, maximum humidity and temperature are important .So that variable was removed from the building a final model. The R2 (0.74) of out Ml model intimated in the previous skin disease cases; min humidity, min temp, rainfall trends and seasonality explained 74 of the variances of the monthly skin disease distribution.

III. Conclusion

The evidence from this study can make public health programs aware of the high level of vulnerability of skin diseases to different types of weather, such as humidity, rain, heat. Our study further suggests that climate characteristics are significantly related to public health in Hyderabad city. Validation of algorithms used to suggest that PDLM or SARIMA are suitable for predicting skin diseases in Hyderabad, SARIMA model shows better prediction rate for 3 months onset and other PDLM models give better prediction and The next period is 6 to 12 months. High definition in knowing the skin disease level of Lag Distributed Type will be effective for prevention or control of skin disease in Hyderabad city. We recommend further research to validate the model and explore the possibility of early warning interventions for skin diseases for skin disease surveillance systems. This will promote early warning methods for the prevention of skin diseases in the city of Hyderabad and other economic opportunities in the future.

References

[1] [1] An Effective Machine Learning Approach for Clustering Categorical Data with High Dimensions, Syed Umar, Tadele Debisa Deressa, Tariku Birhanu Yadesa, Gemechu Boche Beshan, Endal Kachew Mosisa, Nilesh T Gole. International Conference on Artificial Intelligence and …, 2021Springer International Publishing

[2] [2] K. L. Ebi and J. Nealon, "Dengue in a changing climate," Environ. Res., vol. 151, pp. 115–123, 2016.

[3] [3] T. Chakraborty, S. Chattopadhyay, and I. Ghosh, "Forecasting dengue epidemics using a hybrid methodology," Physica A, vol. 527, p. 121266, 2019.

[4] [4] R. Conde and G. Sa, "Prediction of dengue outbreaks in Mexico based on entomological , meteorological and demographic data," pp. 1–14, 2018.

[5] [5] V. J. Jayaraj, R. Avoi, N. Gopalakrishnan, and D. B. Raja, "Acta Tropica Developing a dengue prediction model based on climate in Tawau , Malaysia," Acta Trop., vol. 197, no. February, p. 105055, 2019.

[6] [6] Y. Chen, C. Wenhan, M. I. C. Chen, and A. R. Cook, "The utility of LASSO-based models for real time forecasts of endemic infectious

diseases : A cross country comparison," J. Biomed. Inform., vol. 81, no. September 2017, pp. 16–30, 2018.
[7] [7] M. Cabrera and G. Taylor, "Spatial and Spatio-temporal Epidemiology Modelling spatio-temporal data of dengue fever using generalized additive mixed models," Spat. Spatiotemporal. Epidemiol., vol. 28, no. 2019, pp. 1–13, 2020.
[8] [8] R. Lowe et al., "Articles Climate services for health : predicting the evolution of the 2016 dengue season in Machala , Ecuador," Lancet Planet. Heal., vol. 1, no. 4, pp. e142–e151, 2016.
[9] [9] Y. Peng, Z. Wu, and J. Jiang, "A novel feature selection approach for biomedical data classification," J. Biomed. Inform., vol. 43, no. 1, pp. 15–23, 2010.
[10][10] H. Kaur and V. Kumari, "Applied Computing and Informatics Predictive modelling and analytics for diabetes using a machine learning approach," Appl. Comput. Informatics, no. xxxx, pp. 0–5, 2018.
[11][11] J. N. Taroni et al., "MultiPLIER : A Transfer Learning Framework for Transcriptomics Reveals Systemic Features of Rare Article MultiPLIER : A Transfer Learning Framework for Transcriptomics Reveals Systemic Features of Rare Disease," Cell Syst., vol. 8, no. 5, p. 380–394.e4, 2019.
[12][12] C. Zhu, C. Uwa, and W. Feng, "Informatics in Medicine Unlocked Improved logistic regression model for diabetes prediction by integrating PCA and K-means techniques," Informatics Med. Unlocked, no. January, p. 100179, 2019.
[13][13] M. Chen, P. Zhou, D. Wu, L. Hu, M. Mehedi, and A. Alamri, "AI-Skin : Skin disease recognition based on self-learning and wide data collection through a closed-loop framework," vol. 54, no. May 2019, pp. 1–9, 2020.
[14][14] O. Titus, P. Stephenson, M. Zahirul, and A. W. Taylor-robinson, "Long-term predictors of dengue outbreaks in Bangladesh : A data mining approach," Infect. Dis. Model., vol. 3, pp. 322–330, 2018.
[15][15] S. Wongkoon, M. Jaroensutasinee, and K. Jaroensutasinee, "Development of temporal modeling for prediction of dengue infection in Northeastern Thailand," Asian Pac. J. Trop. Med., vol. 5, no. 3, pp. 249–252, 2012.
[16][16] H. M. Aburas, B. G. Cetiner, and M. Sari, "Expert Systems with Applications Dengue confirmed-cases prediction : A neural network model," Expert Syst. Appl., vol. 37, no. 6, pp. 4256–4260, 2010.
[17][17] R. A. Vinarti and L. M. Hederman, "A personalized infectious disease risk prediction system," Expert Syst. Appl., vol. 131, pp. 266–274, 2019.
[18][18] D. Jain and V. Singh, "Feature selection and classification systems for chronic disease prediction : A review," Egypt. Informatics J., vol. 19, no. 3, pp. 179–189, 2018.
[19][19] S. Khan, R. Ullah, S. Shahzad, N. Anbreen, M. Bilal, and A. Khan, "Analysis of Tuberculosis Disease through Raman Spectroscopy and Machine Learning," Photodiagnosis Photodyn. Ther., 2018.
[20][20] P. Mohapatra, S. Chakravarty, and P. K. Dash, "An improved cuckoo search based extreme learning machine for medical data classi fi cation," Swarm Evol. Comput., pp. 1–25, 2015.
[21][21] V. K. Shrivastava, N. D. Londhe, R. S. Sonawane, and J. S. Suri, "Biomedical Signal Processing and Control A novel approach to multiclass psoriasis disease risk stratification : Machine learning paradigm," Biomed. Signal Process. Control, vol. 28, pp. 27–40, 2016.
[22][22] S. U. P, H. Hebbar, and A. Govindakarnavar, "Informatics in Medicine Unlocked A technology framework for remote patient care in dermatology for early diagnosis," vol. 15, no. March, 2019.
[23][23] T. Bikku, S. Rao, and A. Rao, "A contemporary feature selection and classification framework for imbalanced biomedical datasets," Egypt. Informatics J., vol. 19, no. 3, pp. 191–198, 2018.
[24][24] P. Guo et al., "Science of the Total Environment An ensemble forecast model of dengue in Guangzhou , China using climate and social media surveillance data," Sci. Total Environ., vol. 647, pp. 752–762, 2019.
[25][26] S. Rao, R. Mopuri, and S. Naish, "Spatial distribution and cluster analysis of dengue using self organizing maps in Andhra Pradesh , India , 2011 – 2013," Parasite Epidemiol. Control, vol. 3, no. 1, pp. 52–61, 2018.
[26][27] S. Atique, S. S. Abdul, C. Hsu, and T. Chuang, "Asian Paci fi c Journal of Tropical Medicine Meteorological influences on dengue transmission in Pakistan," Asian Pac. J. Trop. Med., vol. 9, no. 10, pp. 954–961, 2016.
[27][28] A. Awad, M. Bader-el-den, J. Mcnicholas, and J. Briggs, "International Journal of Medical Informatics Early hospital mortality prediction of intensive care unit patients using an ensemble learning approach," Int. J. Med. Inform., vol. 108, no. September, pp. 185–195, 2017