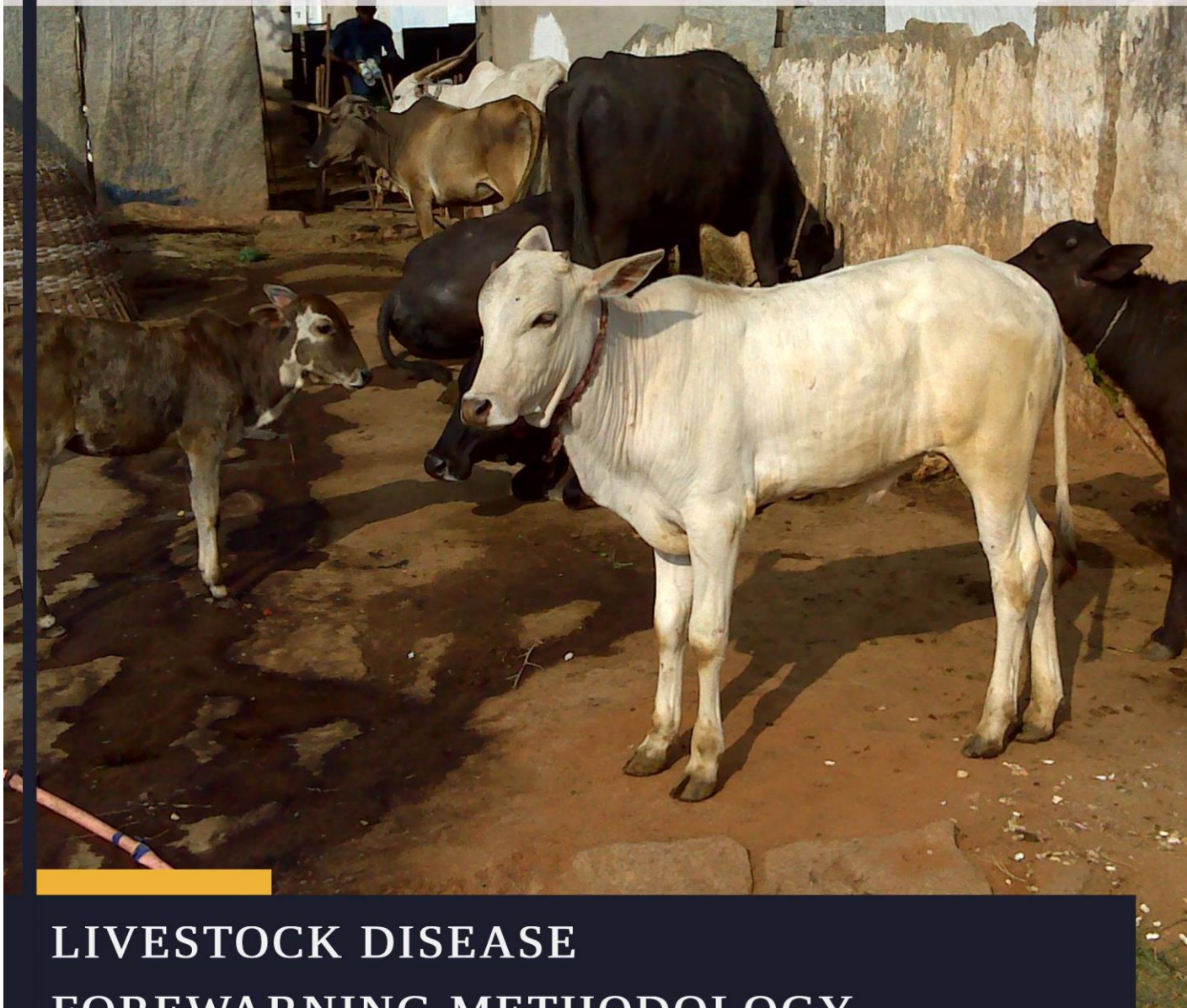


AUGUST 2023, Volume 11, Issue 8



LIVESTOCK DISEASE FOREWARNING METHODOLOGY

Powered by Artificial Intelligence

2023
OCTOBER



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FARMER REGISTRATION AND UNIFIED
BENEFICIARY INFORMATION SYSTEM(
(FRUITS)



ICAR - NATIONAL INSTITUTE OF
VETERINARY EPIDEMIOLOGY AND
DISEASE INFORMATICS

(ICAR - NIVEDI)



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Prepared By : Dr. K. P. Suresh
Dr. Rajeswari Shome
Dr. D. Hemadri
Dr. S. S. Patil
Dr. P. Krishnamoorthy
Dr. S. J. Siju
Dr. Gulati BR (Overall supervisor)

Front Page Design by: Ms. Apoorva Hemadri
Technical support: Dikshitha J, Chandrashekhar T M, Sushma R, Jayashree A, Ashwini M

Disclaimer

The forewarnings are based on the retrospective disease data available in the NADRES database. Hence, for those states wherein data is limited/less, the forewarning may not be realistic. Further the forewarning will not take into consideration the control measures that are *in situ*.

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Director
ICAR- NIVEDI

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1. ABOUT THE METHODOLOGY...

Livestock sector plays a crucial role in the rural economy of India as around 20.5 million people depend upon livestock for their livelihood. Even though the investment in the livestock sector is meagre, tremendous achievements have been observed in the sector during the last decade. As it is an important component in poverty alleviation programmes, continuous emphasis is being laid on this sector for enhancing the quality of the primary and secondary products in the international market, which in turn demands improved animal health. Therefore, livestock development programmes cannot succeed unless a well-organized animal health service is built up and in place for safeguarding the livestock against economically important diseases.

India has made a noteworthy success in the eradication of Rinderpest (RP), CBPP, AHS and Dourine. However, there are several other infectious and non-infectious diseases prevailing in the country causing huge annual economic loss. Prevention, control and eradication of the animal diseases need a thorough understanding of the epidemiology as well their economic impact.

National Institute of Veterinary Epidemiology and Disease Informatics (NIVEDI) has the mandate to carry out research activities in the area of veterinary epidemiology and disease informatics. With the eradication of RP successfully, India has not only proved its ability to face the challenges but also to succeed, despite various limitations. Similar efforts are needed to control and eradicate diseases like FMD, PPR, Brucellosis, CSF, HS etc., which cause huge economic loss annually to the livestock industry. To this end, ICAR-NIVEDI has identified 14 priority livestock diseases, based on the past incidence patterns and has built a strong database of these diseases. The database, which is the backbone of the National Animal Disease Referral Expert System (NADRESv2), is used for providing monthly livestock disease forewarning, which is compiled in this monthly bulletin to alert the animal husbandry departments, both at the National/state level, to take appropriate control measures. We hope users/stakeholders find this bulletin useful in their quest to control livestock diseases. This forewarning bulletin will assist the field Veterinarians in adopting appropriate preventive and control measures, thereby reducing the occurrence of livestock disease outbreaks.

2. SUMMARY OF THE FOREWARNING METHODOLOGY....

The association between infectious diseases and the climate was known from ancient times. Hippocrates observed in the 5th century that epidemics were associated with natural phenomena rather than divinities or demons. In modern times, our increasing capabilities to detect and predict climate variations joined with growing evidence for global climate change, have powered interest in understanding the impacts of climate on animal health, particularly the emergence and transmission of infectious disease agents. Simple reasoning suggests that climate can affect infectious disease patterns because the pathogens (viruses, bacteria, and parasites) and their vectors are sensitive to temperature, moisture, and other ambient environmental conditions.

India being an agriculture-based country, the livestock sector plays a vital role in contributing to the economy. A robust reporting and forewarning system enable the concerned authorities in disease preparedness and awareness of the risk associated with livestock diseases. Therefore, the economic loss due to morbidity and mortality of the animals is reduced thereby helps to increase the productivity in terms of egg, meat, and dairy products. National Animal Disease Referral Expert System database is a weather-based forewarning system enabled with an artificial intelligence system developed by ICAR-National Institute of Veterinary Epidemiology & Disease Informatics Bengaluru, Karnataka state, India that forecast potential threats from pathogens two months in advance to provide the stakeholders with sufficient timeline for awareness and preparedness to act. Artificial Intelligence (AI) and Machine Learning (ML) models use the programmed algorithms that receive and analyse input data to predict output (Infectious risk prediction) values within an acceptable range. As new data fed into these algorithms, they learn and optimize their operations to improve performance, developing intelligence over time.

The livestock disease forewarning for October 2023 revealed Jharkhand (145), Uttar Pradesh (117), Assam (51), Karnataka (49) and Kerala (48) as the leading states anticipated to experience significant outbreaks of livestock diseases.

In terms of projected disease occurrences, Jharkhand is poised to encounter a higher number of anticipated babesiosis outbreaks, while Uttar Pradesh is foreseen to experience a greater incidence of predicted trypanosomosis outbreaks. Moreover, the simultaneous presence of babesiosis and Theileriosis is likely to be observed in Uttarpradesh, Jharkhand, Kerala, Assam and West Bengal. Among the different diseases in livestock, the predicted outbreaks are expected to be high for Babesiosis (85), Theileriosis (82) and FMD (76).

The primary obstacles facing an efficient disease control program include inadequate comprehension of the intricate disease dynamics, the extensive host range of pathogens, and the broadening pathogen niches attributed to climate change. Moreover, India has observed the emergence and resurgence of numerous infectious agents over the past decade, with a majority of these ailments having zoonotic attributes. This underscores the pressing need to enhance the nation's monitoring and surveillance systems. To effectively tackle significant livestock diseases within the country, a strategic approach involves implementing existing control measures in high-risk regions, coupled with routine disease surveillance and monitoring. This combination can contribute to a well-structured control program capable of addressing major livestock diseases.

Table S1. Summary of Statewise Livestock Disease forewarning for October- 2023

Sl. No	State Name	Anthrax	Babesiosis	BQ	BT	CSF	ET	Fasciolosis	FMD	HS	LSD	PPR	S&G Pox	Theileriosis	Trypanosomosis	Total number of districts predicted for risk of disease
1	Andaman & Nicobar	0	0	0	0	0	0	3	0	0	0	0	0	0	0	3
2	Andhra Pradesh	4	0	1	0	0	1	0	0	2	0	1	2	0	0	11
3	Arunachal Pradesh	0	0	0	0	0	0	5	1	0	0	0	0	0	0	6
4	Assam	0	5	7	0	9	6	10	0	1	0	7	3	3	0	51
5	Bihar	0	2	0	0	1	0	0	1	1	0	1	0	3	2	11
6	Chhattisgarh	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2
7	Daman & Diu	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
8	Goa	0	1	0	0	1	0	0	1	0	0	0	0	1	0	4
9	Gujarat	0	0	0	0	0	0	0	2	2	0	3	1	0	1	9
10	Haryana	0	0	0	0	3	0	0	1	0	0	3	0	2	0	9
11	Himachal Pradesh	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
12	Jammu & Kashmir	0	0	0	0	0	0	0	3	0	0	1	6	0	0	10
13	Jharkhand	1	24	3	0	5	6	24	15	3	0	14	3	23	24	145
14	Karnataka	9	0	2	5	0	2	0	19	1	0	3	5	3	0	49
15	Kerala	1	10	0	0	4	1	0	10	4	0	5	0	13	0	48
16	Madhya Pradesh	1	1	1	0	0	0	0	1	4	0	1	0	0	0	9
17	Maharashtra	0	0	0	0	0	0	0	3	2	0	4	0	1	0	10
18	Manipur	0	0	1	0	3	0	3	1	2	0	0	1	0	0	11
19	Meghalaya	0	0	3	0	0	0	0	3	1	0	0	0	0	0	7
20	Nagaland	0	0	0	0	2	0	0	2	0	0	0	0	0	0	4
21	Odisha	1	0	1	0	0	2	0	3	1	0	1	1	0	0	10
22	Puducherry	0	1	0	0	0	0	1	0	0	0	0	1	0	0	3
23	Punjab	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
24	Rajasthan	0	0	0	0	0	1	0	0	0	0	3	1	0	0	5
25	Sikkim	0	1	0	0	2	0	0	0	0	0	0	0	1	0	4
26	Tamil Nadu	6	0	0	0	0	0	0	5	1	6	1	1	0	0	20
27	Tripura	1	4	1	0	4	0	5	3	0	0	3	5	0	0	26
28	Uttar Pradesh	0	34	0	0	0	0	5	0	0	0	9	1	25	43	117
29	West Bengal	3	2	1	0	0	0	1	1	1	0	2	1	7	0	19
Total number of districts likely for risk of disease		27	85	21	5	34	19	57	76	26	6	66	32	82	70	606

3. INTRODUCTION TO NADRES v2

The geographic and seasonal distribution of many infectious diseases are associated with climate and therefore the possibility of using seasonal climate forecasts as predictive indicators in disease early warning system (EWS) became imminent. In this context, ICAR-NIVEDI, in its quest for achieving better livestock health, had developed an interactive web portal named “National Animal Disease Referral Expert System (NADRES)” during early part of the first decade of the millennium. The web portal, which was developed from the financial support of National Agricultural Technology Project, was launched in the year 2005. The portal which is interactive, allows the user/stakeholder to access livestock disease forewarning (n=14) at the district level for entire country two months in advance. The portal which was initially built on oracle platform was later changed to MySQL platform to store the administrator provided disease information and other relevant meteorological and risk factor information. However, with the availability of remote sensed satellite images and the advancement in information technology and statistical algorithms, the upgradation of NADRES became inevitable. To this end, a newer version of NADRES (NADRES V2) has been developed.

How it is different from previous version?

In brief, it can be said that NADRES v₂ underwent a sea change not only in its internal structure but also in its physical design. As a result, now the central menu bar consists of Home, about us, Risk factors, Analysis, Livestock disease, post prediction validation and contact details. Risk factors menu comprises of details on resolution, time interval, units and source of 11 meteorological and 5 remote sensing parameters. Analytics menu has various analysis options. The newly created livestock disease menu has the details regarding species affected, clinical signs and preventive measures to be adopted for the 14 economically important diseases. Post prediction validation menu contains the outbreak reports vs prediction. The menu bar on the RHS tabs include online GIS, state wise Livestock disease forecast, district wise Livestock disease forecast, Epi-calculator, download links for mobile app, etc. The website now hosts disease maps in the form of choropleth maps for 14 diseases in two time periods (1990-2000 and 2000-2018). Similarly, disease trends plots exhibit periodic regression plots providing future trend for the disease. On the LHS, Login menu is provided for authorized persons to login and enter disease details and other related parameters. Disease maps provide choropleth maps for 14 diseases in two time periods (1990-2000 and 2000-2018) is presented. Disease trends- Periodic regression plots are exhibited for prediction of the diseases. Auto-messaging option has been created to send the reminders in the form of text messages to concerned PI's and Co-PI's of NADEN centers for submission of outbreak reports. This message is sent weekly to all the concerned officials. Additionally, a message is sent to the concerned veterinary officers in Karnataka for initiation of preventive measures for the forewarned diseases at the block level. Plans are in place to incorporate farmers' and local vets' mobile numbers in to the list so that they may be asked to initiate preventive measures for the forewarned diseases.

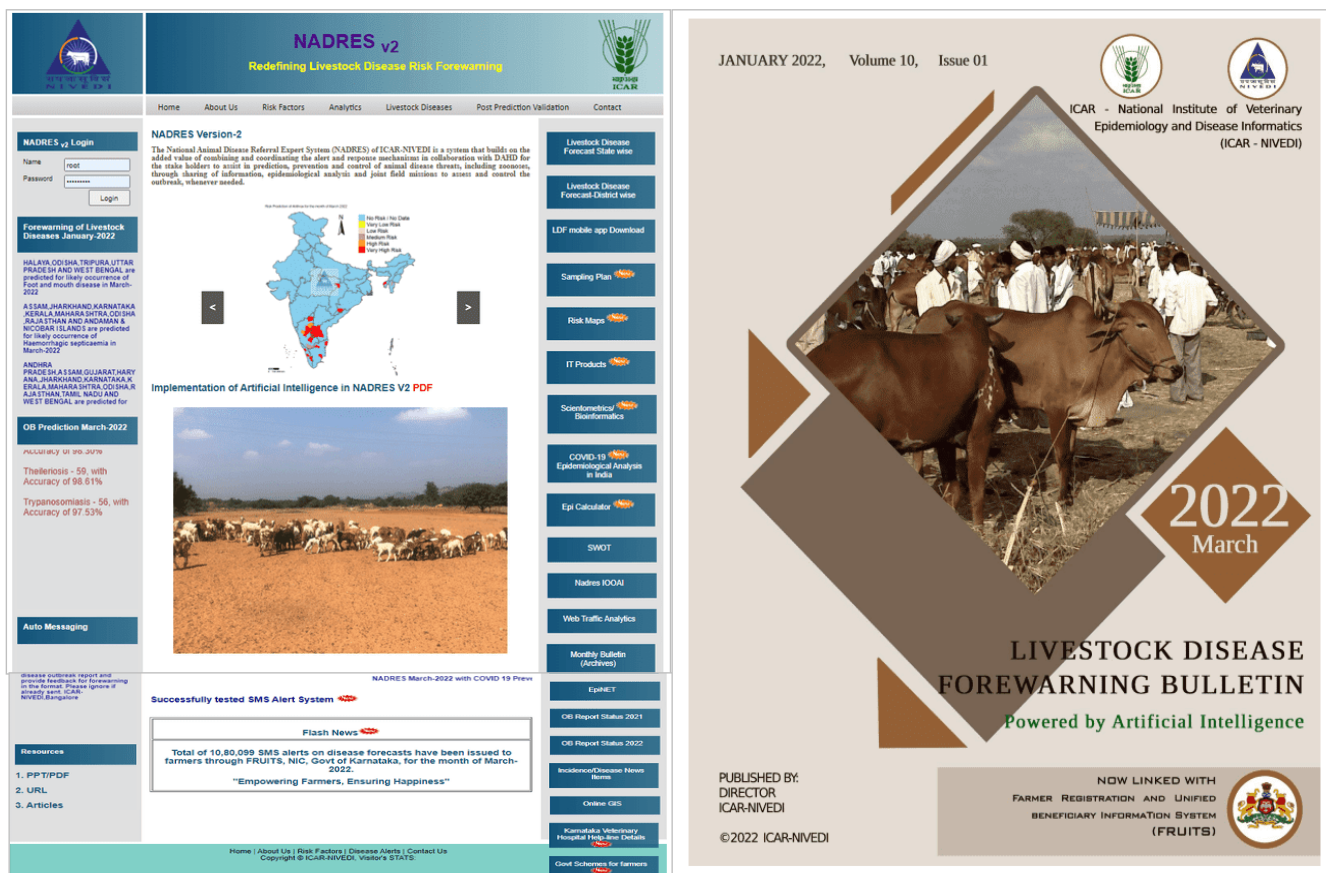


Fig 3.1.NADRES V₂ Home page

The forewarning methodology used is unique and has not been used earlier for livestock disease forewarning in India. Following few paragraphs describe about the forewarning methodology used. It is a well-known fact that weather plays an important role in the precipitation of many diseases and therefore, the climatic parameters such as land surface temperature (LST), precipitation, wind velocity, humidity etc are considered as risk parameters. These parameters along with other non-climatic parameters such as livestock population, density, Normalized Differential Vegetation Index (NDVI), soil moisture constitute the overall risk parameters. A total of 24 such parameters are collected/generated at village level and then aggregated to district level before these are used for analysis.

In addition to the output provided at interactive web portal, the NADRES output are also published in the form of monthly livestock disease forewarning bulletins. The prediction results come with a disclaimer that forewarnings do not take into account of the control measures that already in situ and also may not be realistic for those regions where the data is either unavailable or limited. This bulletin provides the likely occurrence of the 14 shortlisted diseases two months in advance at the district level, disease forewarning maps, prediction accuracy, details on diseases, species affected, clinical signs and its preventive measures.

In summary, it can be said that NADRES v₂ has underwent substantial changes not only in its internal structure but also in its physical design and can be a useful tool for visitors of the website, farmers, vets, policy makers etc.

4. Forewarning Methodology

Preamble

NADRES v2 is an early warning system powered by Artificial Intelligence with set of capacities needed to generate and disseminate timely and meaningful warning information that enables at-risk livestock population, farmers and organizations to prepare and act appropriately and in sufficient time to reduce the livestock disease incidence.

Objectives

- Development of forecasting model for the major livestock diseases and predicting the risk of livestock diseases in advance of two months.
- Development of state of art of communication models to communicate risk of livestock diseases to the stake holders.

I. Materials and data aquisition

Livestock disease data

Previous 10 years' livestock disease outbreak data retrieved from the NADRES database linked with Risk factors data.

Livestock population data

The population data at village level for five major livestock species viz., cattle, buffalo, sheep, goat and pigs were obtained from 20th Livestock census (2019) from Department of statistics, DAHD, GOI.

Species-wise & Category-wise Livestock Population (in thousands)					
Sl No	Species	Category	Population in 2012	Population in 2019	% Change
1	Cattle	Exotic	39732	51356	29.3
		Indigenous	151172	142106	-6
		Total	190904	193462	1.3
2	Buffalo	Total	108702	109852	1.1
3	Sheep	Exotic	3781	4088	8.1
		Indigenous	61288	70172	14.5
		Total	65069	74260	14.1
4	Goat	Total	135173	148885	10.1
5	Pig	Exotic	2456	1897	-22.8
		Indigenous	7837	7159	-8.7
		Total	10293	9056	-12
6	Yaks	Total	77	58	-24.7
7	Mithuns	Total	298	386	29.5
8	Horses & Ponies	Total	625	342	-45.3
9	Mules	Total	196	84	-57.1
10	Donkeys	Total	319	124	-61.1
11	Camels	Total	400	252	-37
Total Livestock			512056	536761	4.8

Meteorological and Remotely Sensed Data:

The parameters such as air temperature ($^{\circ}\text{C}$), perceptible water (mm), pressure (millibar), relative humidity (%) and sea level pressure (millibar) were extracted from National Centre for environmental prediction (NCEP). The parameters such as potential evapotranspiration (PET), Enhanced Vegetation Index (EVI), Leaf Area Index (LAI), Land Surface Temperature (LST), Normalised Difference Vegetation Index (NDVI) were extracted from remote sensed images from MODIS website (<https://modis.gsfc.nasa.gov/>). In brief, the MODIS products from NASA-TERRA satellite was downloaded for the Indian locations by specifying the tiles (H24V5, H25V6, H24V6, H24V7, H25V7, H25V8, H26V7, H26V6) from 2001 to till date.

The details are given below;

PRODUCT	Science Data Sets (HDF Layers)
MOD15A2H	Lai_500m (Leaf area index) 8 days average
MOD16A2	PET_500m (Total Potential Evapotranspiration) 8 days average
MOD11A2	LST_Day_1km (Daytime Land Surface Temperature) 8 days average
MOD13A1	i. 500m 16 days NDVI (Normalized Difference Vegetation Index) ii. Enhanced Vegetation Index (EVI) 16 days average

The downloaded HDF files (Datasets, which are multidimensional arrays (layers) of a homogeneous type) were converted to GeoTIFF files (single layer data) using R packages, which were later used to extract the parameters by linking it with the sinusoidal values of the Indian villages. The scale factors were multiplied for the extracted values as specified by the MODIS data products to get the values of the parameters. As shown above, the atmospherically corrected NDVI was collected on 16-day interval at 250-meter resolution using MODIS product MOD13A1 and LST was collected on 8-day interval using MOD11A2 at 1 KM resolution.

The parameters such as rainfall, soil moisture and wind speed were obtained from Global Land DataAssimilation System of NASA (<https://disc.gsfc.nasa.gov>). The remaining parameters were downloaded from climatic research unit (CRU) of University of East Anglia website. It is worth mentioning that the entire process of extraction, assimilation, processing and aligning have been done using R programming language and R environment. After aligning the climatic and non-climatic data with the disease and the livestock population data (aggregated at the district level), the statistical analysis was performed in the R environment.

Initially, two regression models and six machine learning models were applied to test their suitability to fit the data and in all, three models; one regression model (Generalized Linear Model (GLM) and two machine learning models, viz., Gradient Boosting Machine Learning Algorithm (GBM) and Random Forest (RF), which fitted to data well were incorporated for the purpose of disease prediction. The models were trained using the case and control data available at ICAR-NIVEDI. Validation of the models were done by dividing the total observations for a particular disease into marker samples and validation samples and accuracy was tested in terms of discrimination power, which was done using Receiving Operating Characteristics (ROC), Cohen Kappa (Heildke Skill Score) and True Skill statistics (TSS). Once the models produce the probability value, it was used for categorizing the risk. Briefly, when all the models produce the p value of more than 0.5, then the highest p value is used for determining the high-risk category. If all the models or any one model produces the p value of less than 0.5, then the lowest p value was used for categorizing lower risk. This was done to minimize the false alert. Thus, the risk predictions based on the probability values ranging from 0-1 are made as follows; Very High Risk ($p=0.81-1.0$), High Risk ($p=0.61-0.80$), Moderate Risk ($p=0.41-0.60$), Low Risk ($p=0.21-0.40$), Very Low Risk ($p=0.0-0.20$) and No Risk ($p=0.0$) for the occurrence of a said disease. It is believed that categorizing districts in to various risk categories will help the stake holders to effectively utilize the available resources (money and manpower).

II.NADRES v2 Data Flow and Data Processing Diagram

A) Data Flow Diagram:

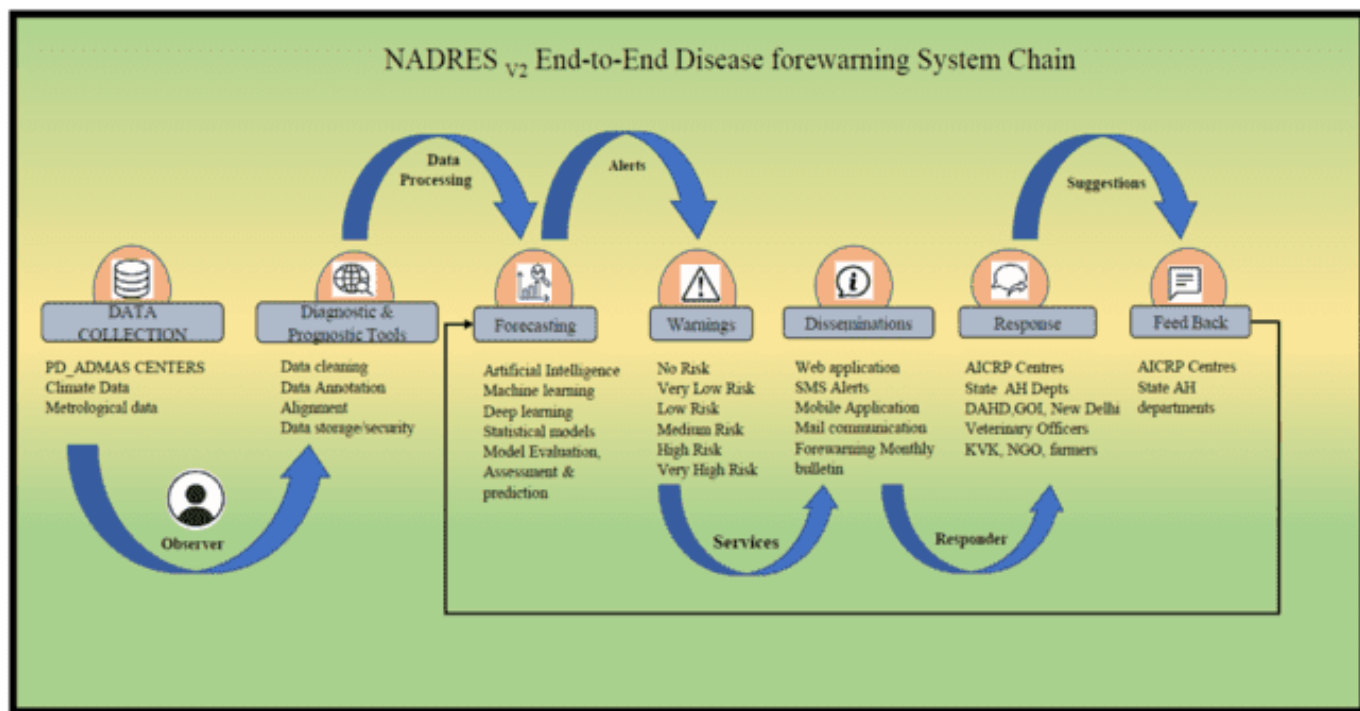


Fig 4.1. NADRES v2 Data Flow Diagram.

B) Artificial Intelligence enabled Data Capturing and Forewarning System:

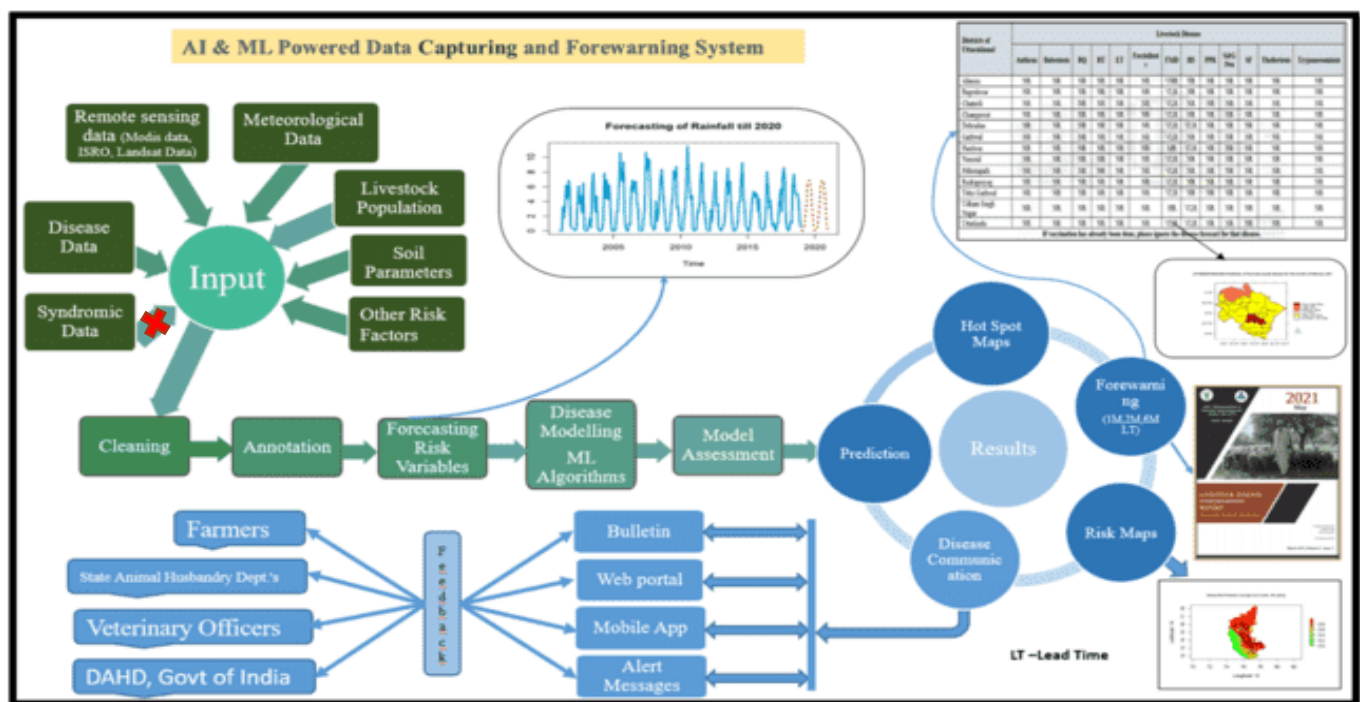


Fig 4.2. Data Capturing and Forewarning system

III. Weighted Outbreak Score

The outbreak data for the month of forecasting is extracted from NADRES database for the period of 10 years from current year. Outbreak data of 14 important livestock diseases are considered. The data is aggregated at district level and the weighted score is defined based on the number of outbreaks for each district in each month considering last 10 years. The weightage score was assigned as 0 for less than three number of outbreaks in the last 10 years for selected month, score 1 for 3–6 number of outbreaks and 2 for more than 6 outbreaks. This weightage score for each district is labelled as risk variable in building the models and risk maps.

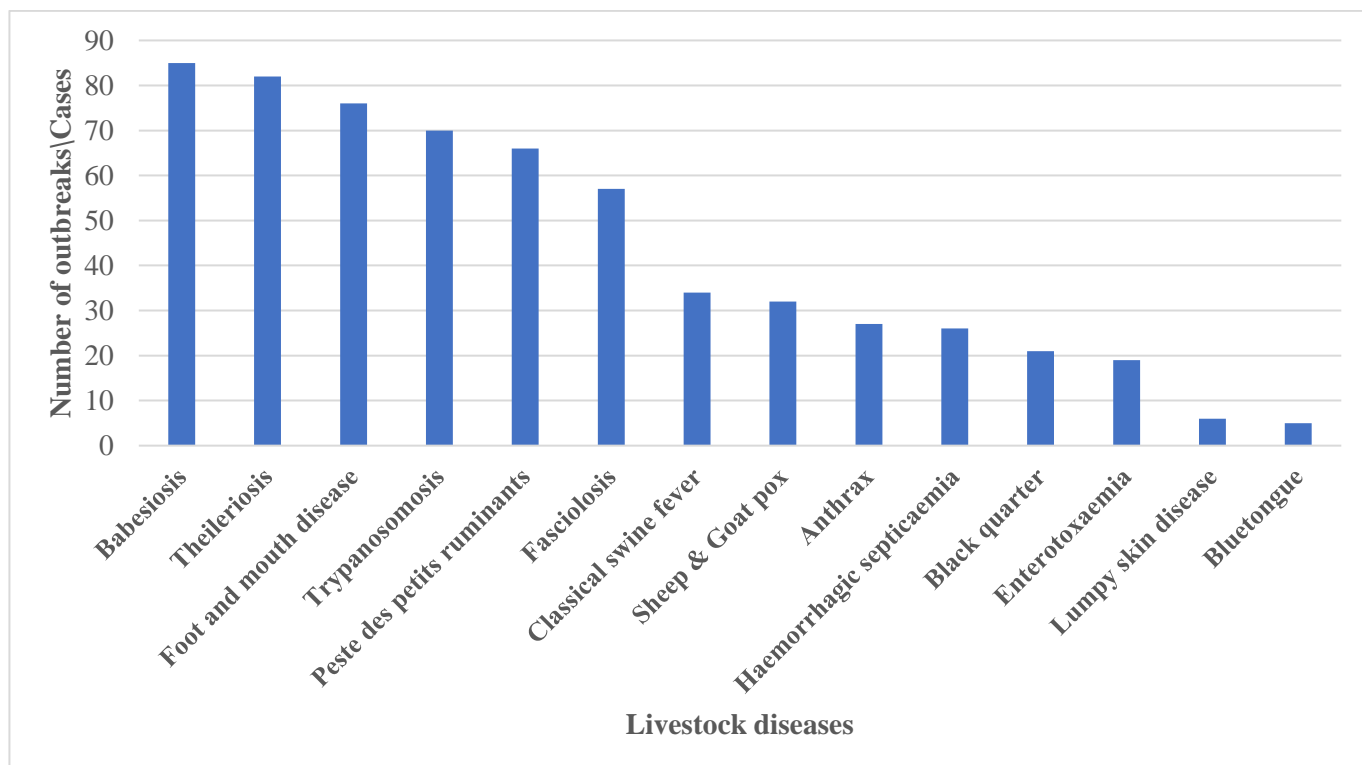


Fig 4.3. Top ten livestock diseases (2023)

IV. Feature extraction and Data engineering

Data collection from different sources could be internal and or external to satisfy the objectives of forewarning requirements, data can be of any format, CSV, XML, JSON etc. In this processing of data and feature engineering, we focus mainly on understanding the specified data set and cleaning the dataset, a better understanding of features and their relationships, extracting essential variables, handling missing values and human error, identifying outliers, transforming features if there are outliers so that either truncates a data above a threshold or transform the data using log or any other transformation, scaling the features extracted. This process would be maximising the insights into a dataset.

V. Forecasting of Weather Parameters

Weather forecasting has been one of the most challenging problems around the world because of both its practical value in meteorology and the popular sphere for scientific research. Weather forecast systems are among the most complex equation systems that computer has to solve. A great quantity of data, coming from satellites, ground stations and sensors located around our planet send daily information that must be used to foresee the weather situation in next hours and days all around. Weather forecasts provide critical information about future weather. There are various techniques involved in weather forecasting, from relatively simple observation of the sky to highly complex computerized mathematical models. Further, forecast products by Indian Metrological department were used for validation of our forecasts (https://mausam.imd.gov.in/imd_latest/contents/extendedrangeforecast.php).

Following are the basic steps of forecasting process:

1. Determine the forecast's purpose
2. Establish a time horizon
3. Select a forecasting technique
4. Gather and analyse data
5. Perform the forecast
6. Monitor the forecast and use it in prediction of disease

Statistical Models used for forecasting of weather and remotely sensed variables

ARIMA stands for Autoregressive Integrated Moving Average. ARIMA is also known as Box-Jenkins approach. Box and Jenkins claimed that non-stationary data can be made stationary by differencing the series, Y_t . The general model for Y_t is written as,

$$Y_t = \phi_1 Y_{t-1} + \phi_2 Y_{t-2} \dots \phi_p Y_{t-p} + \epsilon_t + \theta_1 \epsilon_{t-1} + \theta_2 \epsilon_{t-2} + \dots \theta_q \epsilon_{t-q}$$

Where, Y_t is the differenced time series value, ϕ and θ are unknown parameters and ϵ are independent identically distributed error terms with zero mean. Here, Y_t is expressed in terms of its past values and the current and past values of error terms.

The ARIMA Model combines three basic Methods:

- Auto Regression (AR) – In auto-regression the values of a given time series data are regressed on their own lagged values, which is indicated by the “p” value in the model.
- Differencing (I-for Integrated) – This involves differencing the time series data to remove the trend and convert a non-stationary time series to a stationary one. This is indicated by the “d” value in the model. If $d = 1$, it looks at the difference between two-time series entries, if $d = 2$ it looks at the differences of the differences obtained at $d = 1$, and so forth.
- Moving Average (MA) – The moving average nature of the model is represented by the “q” value which is the number of lagged values of the error term.

This model is called Autoregressive Integrated Moving Average or ARIMA (p, d, q) of Y_t . We will follow the steps enumerated below to build our model. ARIMA models were run in 18 combinations of p, d, q. Based on the minimum AIC value, the order of ARIMA model was selected. This order was used for the prediction of all the weather parameters used in developing disease forewarning models.

VI. Implementation of Principal Component Analysis

Large datasets are gradually common and are often difficult to interpret. Principal Component Analysis (PCA) is a technique for reducing the dimensionality of such datasets, increasing the interpretability but at the same time, minimizing the information loss. The PCA is employed in NADRES v2 by creating new uncorrelated variables that successively maximize the variance. This means that `preserving as much variability as possible` translates into finding new variables that are linear functions of those in the original dataset, that successively maximize variance and that are uncorrelated with each other. Determining such new variables, the principal components (PCs) reduce to solve an eigenvalue/eigenvector problem. PCA can be based on either covariance matrix or the correlation matrix and the main use of PCA are descriptive. In the present study, all the meteorological and remote sensing variables are considering for PCA, with correlation matrix, the final output of principal components which are independent of each were considered for further ML modelling and risk estimation.

VII. Machine Learning Models

Disease outbreak data were aligned with generated risk variables to the respective latitude and longitude, which were subjected to climate-disease modelling. A number of models were fit to aligned data and tested for accuracy in terms of discrimination power. Two regression models, Generalized Linear Models (GLM) and Generalized Additive Models (GAM) and six machine learning algorithms, i.e. Random Forest (RF), Boosted Regression Tree (BRT), Artificial Neural Network (ANN), Multiple Adaptive Regression Spline (MARS), Flexible Discriminant Analysis (FDA) and Classification Tree Analysis (CTA) were employed for disease modelling. Different modelling methods return different types of 'model object' and all these model objects could be used for the predict function to make predictions for any combinations of values of independent variables. Response plots were created to explore and understand model predictions.

The fitted models were assessed for their discriminating power using Receiving Operating Characteristic (ROC) curve, Cohen's Kappa (Heildke Skill Score) and True Skill Statistics (TSS). These measures were used to evaluate the quality of predictions based on presence-absence data. Raster Stack was used to combine the results of individual predictions by different model methods. All the models were assessed for overfitting.

The outcome of best fitted models was in probability of disease occurrence and was categorised into 6 risk levels as No risk (NR), Very low risk (VLR), Low risk (LR), Moderate risk (MR), High risk (HR) and Very high risk (VHR) for enabling the stakeholders to take appropriate control measures by suitably allocating available resources.

5. ACCURACY OF PREDICTION

Serial No.	Diseases	Accuracy (%)
1.	Anthrax	99.72
2.	Babesiosis	98.07
3.	Black quarter	98.49
4.	Bluetongue	99.31
5.	Classical swine fever	98.76
6.	Enterotoxaemia	99.17
7.	Fasciolosis	99.04
8.	Foot and mouth disease	96.56
9.	Haemorrhagic septicaemia	97.94
10.	Lumpy skin disease	100.00
11.	Peste des petits ruminants	96.97
12.	Sheep & Goat pox	99.72
13.	Theileriosis	98.07
14.	Trypanosomosis	98.07

Aggregation and prediction of livestock diseases at district level leading to higher accuracy.

- **Formula Used:** The **Accuracy** of disease prediction was calculated using the following formula.

$$\frac{TP + TN}{Total} * 100$$

TP-True Positive Observations, TN-True Negative Observations, Total- Total observations.

- Internal Accuracy was performed using 10 years of data. Accuracy obtained was >90% for all the diseases predicted.
- Despite the power of climate and disease risk models, considerable uncertainties remain, identifying these uncertainties, highlighting importance of improved data may improve the model accuracy, realism, confidence, together with translating uncertainties in model inputs into uncertainties in model outputs, are important benefits of modelling.

6. MORAN'S I FOR CLUSTERING OF LIVESTOCK DISEASES

Moran's I is a tool that measures spatial autocorrelation (feature similarity) based on both feature locations and feature values simultaneously. Given a set of features and an associated attribute, it evaluates whether the pattern expressed is clustered, dispersed, or random. The tool calculates the Moran's I Index value and both a Z score and p-value evaluating the significance of that index. In general, a Moran's Index value near +1.0 indicates clustering while an index value near -1.0 indicates dispersion.

Autocorrelation tool, the null hypothesis states that "there is no spatial clustering of the values associated with the geographic features in the study area". When the p-value is small and the absolute value of the Z score is large enough that it falls outside of the desired confidence level, the null hypothesis can be rejected. If the index value is greater than 0, the set of features exhibits a clustered pattern. If the value is less than 0, the set of features exhibits a dispersed pattern.

7. R SOFTWARE

R is a programming language and software environment for statistical analysis, graphics representation and reporting. R is a simple and effective programming language, which includes conditionals, loops, user defined recursive functions and input and output facilities. R statistical software version 3.1.3 (version 3.4.3, R Foundation for Statistical Computing, Vienna, Austria. <https://www.R-project.org/>) was used as an integrated suite for data mining, calculation and graphical display. Several R packages like *openxlsx*, *raster*, *RMySQL*, *rgdal*, *RColorBrewer*, *sqldf*, *sp*, *spdep*, *xlsx*, *plyr*, *randomFores*, *dismo*, *SDMTool*, *dplyr*, *tmap* and *data table* were used for data extraction, data alignment, annotation, analysis, modelling and risk mapping.

8. FOREWARNING OF LIVESTOCK DISEASE FOR THE MONTH OF AUGUST, 2023

I. Diseases, Species affected Clinical signs and its preventive measures.

Sl No.	Disease	Species Affected	Clinical Signs	Preventive Measures
1	Anthrax (AX)	Most of the mammals and ruminants are highly susceptible. Pigs and Horses are moderately susceptible. Carnivores are relatively resistant.	Convulsion and sudden death with oozing of blood from natural orifices such as rectum and nose prior to death. Occasionally oedema develops in the throat and shoulder over a period of one week before death.	Ring vaccination and reporting of the disease is advised. Vaccination to be done in consultation with the veterinarians and as decided by state animal husbandry authorities. Strict biosecurity measures may be followed. Carcass may be disposed by deep burying covered with lime powder. Contaminated area may be disinfected with 4% formalin or 10% caustic soda. Grazing area may be restricted.
2	Babesiosis (BA)	Cattle. Cross breeds are more susceptible.	High temperature, jaundice like symptoms, yellowish mucosal membrane of eye, rectum and coffee colour urine.	Periodical application of acaricides in and around the animal shed and on the animals. For therapeutic application, Diaminazine or Imidocarb can be useful.
3.	Black Quarter (BQ)	Common disease of cattle and sheep, but occasionally goats and pigs also suffer from the disease.	High fever and lameness followed by swelling in the neck, shoulder, lumbar, gluteal and sacral regions. Skin over the affected area become dark and crepitae on palpation. Loss of feed intake, colic, lateral recumbency, dyspnoea and death.	Affected animals may be treated with suitable antibiotics. Vaccination to be done in consultation with the veterinarians and as decided by state animal husbandry authorities. Strict biosecurity measures may be followed. Grazing area may be restricted. Carcass may be disposed hygienically.

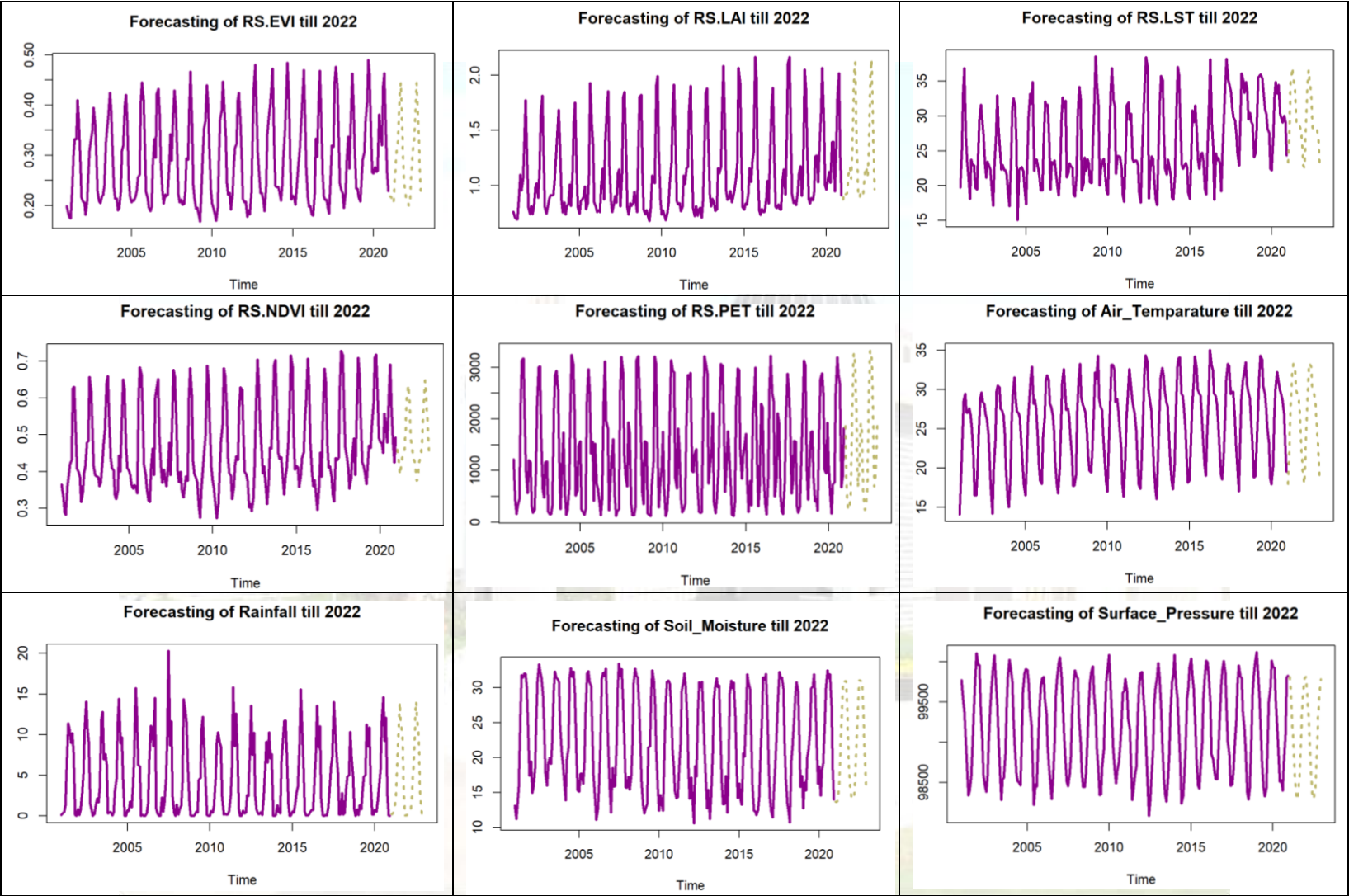
4.	Bluetongue (BT)	Sheep are more susceptible than goats.	Fever, swelling of face, neck, eyelids respiratory distress, nasal discharge, Salivation, necrotic ulcers on tongue, dental pad, gum, lips hyperaemia of muzzle and may bleed at mucocutaneous junction. Affected tongue may become swollen, cyanotic and purple blue in colour – 'bluetongue'.	Vector control using insecticides and good water management. Vaccination of susceptible animals preferably in the month of May. Do not shear sheep during winter months. Restriction in animal movement, segregation of affected animals and symptomatic treatment. Strict biosecurity measures.
5.	Enterotoxaemia (ET)	Common disease of sheep and goats especially among the young animals.	Dullness, opisthosomas, convulsions, coma and sudden death. Affected adult sheep, which survive for several days May show diarrhoea and staggering.	Affected animals may be treated with suitable antibiotics. Vaccination to be done in consultation with the veterinarians and as decided by State Animal Husbandry Authorities. Strict biosecurity measures may be followed. Carcass may be disposed hygienically. Grazing area to be restricted, stall fed, vitamins and probiotics may be provided.
6.	Fasciolosis (FA)	Cattle, buffalo, sheep and goats.	Progressive anaemia, pale mucous membrane, submandibular oedema (Bottle jaw), loss of appetite, weakness, isolated from flock while grazing, loss in production.	The animal should not be allowed to graze in water stagnant fields or submerged fodder should not be given directly to the animals. The submerged fodder can be processed through hay/silage preparation in order to destroy the metacercariae. The affected animals can be treated with Carbon tetrachloride/ Rafoxanide/Nitroxynil/ Niclofolan/Closantel/Oxyclozanide, under the strict supervision of veterinarian.

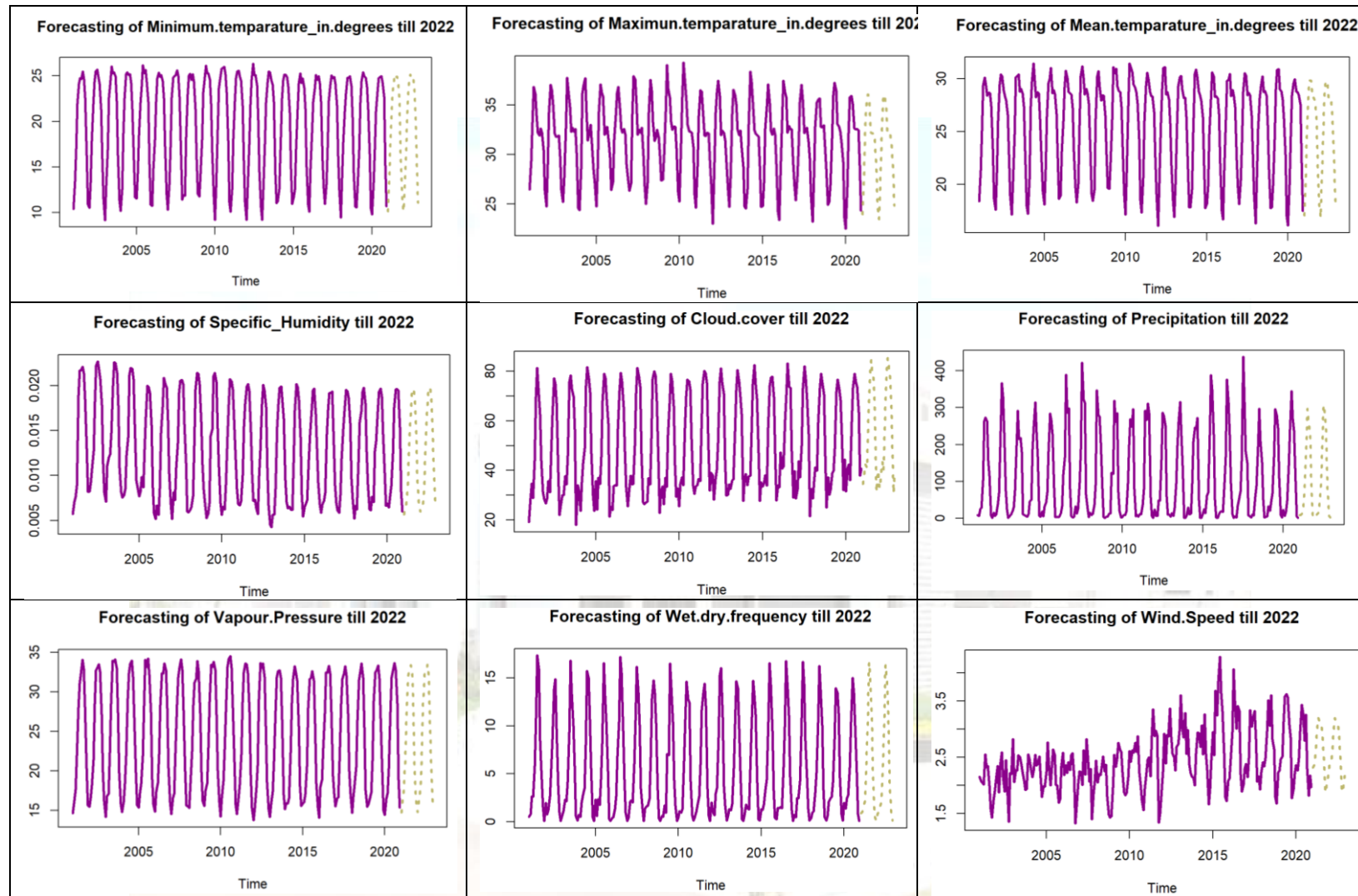
7.	Foot and Mouth Disease (FMD)	Cattle, buffalo, sheep, goats and pigs are often affected domesticated species, but the disease is more severe in cattle and pigs.	Fever, loss of feed intake, drop in milk production, drooling of saliva like ropey string, vesicles develop on the tongue, lips, gums, and palate and eventually rupture. Concurrent to oral lesions, vesicles also appear in inter digital skin and coronary band of the feet. The animal may open and close its mouth with a characteristic smacking sound. Sheep and goats may show lameness. In pigs, lesions may be seen on snout and also on the feet.	Regular vaccination and seromonitoring. Disinfection with sodium carbonate (4%) or 10% washing soda and strict biosecurity measures to be followed and animal movement may be controlled.
8.	Haemorrhagic septicaemia (HS)	Common disease for cattle and buffaloes, but can also occur among other species such as pigs, sheep, goats and many wild animals.	The disease starts with high fever, respiratory distress and haemorrhages maybe seen on the mucous membranes. There is lacrymation, nasal discharge, drop in milk production and anorexia. As the disease progress ear droops and the animals will be prostrated with cyanosis of mucous membranes. There may be oedema along the head, neck, thorax, vulva and anal areas. Sudden death occurs within few hours of clinical signs.	Affected animals may be treated with suitable antibiotics. Vaccination to be done in consultation with the veterinarians and as decided by state animal husbandry authorities. Strict biosecurity measures may be followed. Carcass may be disposed hygienically and stress factors may be reduced by following good animal husbandry practices.

9.	Lumpy skin disease (LSD)	Common disease for Cattle, Buffalo and other domestic animals	Fever, reduced milk production and skin nodules. Mastitis, swelling of peripheral lymph nodes, loss of appetite, increased nasal discharge and watery eyes are also common. Temporary or permanent infertility occur among infected cows and bulls	Vaccination of susceptible animals of above 3 months old age. Restriction on animal movement, strict biosecurity measures and proper disposal of carcass.
10.	Peste des Petits Ruminants (PPR)	Goats and sheep are most affected domestic animals.	Fever, nasal and ocular discharge, respiratory distress, necrotic lesions in buccal mucosa, gum, dental pad, palate, tongue and diarrhoea. Animals may die because of dehydration and pneumonia.	Vaccination of susceptible animals of above 3 months old age. Restriction on animal movement, strict biosecurity measures and proper disposal of carcass.
11.	Sheep and Goat pox (SGP)	Sheep and Goats	Respiratory distress and pock lesions over the non-hairy parts of body, more common in teat, udder, scrotum, head, neck, ear, perineum, inner aspect of thighs and under tail.	Vaccination of susceptible animals of above 3 months old age. Symptomatic treatment of affected animals. Restriction on animal movement, strict biosecurity measures and proper disposal of carcass.
12.	Swine Fever (SF)	Pigs	Fever, Conjunctivitis, purplish discolouration of snout, ears, abdomen, inner side of the legs and staggering gait.	Vaccination of susceptible animals. Restriction on animal movement, strict biosecurity measures and proper disposal of carcass.

13.	Theileriosis (TE)	Large Ruminants. Crossbreed cattle are more vulnerable.	High temperature, yellowish eye, sometime eyes may be heavily swollen, icteric mucosal membrane of rectum, dark yellowish urine, sometime may reach to coffee colour. Antibiotic is of no use to check the fever.	Periodical application of acaricides in and around the animal shed and on the animals. Therapeutic treatment with Buparvaquone can be useful in both early and advanced stages of the infection.
14.	Trypanosomosis (TR)	Domestic and wild carnivores and herbivores including cattle, buffalo, horse, donkey, camel, dog and cats. Buffaloes are known as carriers.	Fluctuating high fever which is not responded by antibiotics, swollen lymph gland, chronic emaciation and weakness, loss of appetite, gradual loss of production.	The affected animal should be treated with Diaminazine compounds or chloride and sulphate salts of Quinapyramine. Periodical spray of insecticide in and around animal shed to remove the flies.

II. Forecasting of remote sensing and meteorological parameters till, 2022(Ex. Jharkhand)





III. SIGNIFICANT WEATHER PARAMETERS TABLE USING DISCRIMINANT FUNCTION ANALYSIS

Disease Names	Significant Parameters
Anthrax	Precipitable Water, Surface Pressure
Babesiosis	Air Temperature, Precipitation, Surface Pressure, Minimum Temperature, Vapour Pressure, Dew Point Temperature, Wind Speed, NDVI and LST Night
Black quarter	Precipitable Water, Precipitation, Surface Pressure, Sea Level Pressure and Vapour Pressure
Bluetongue	Air Temperature, Cloud, Precipitable Water, Precipitation, Surface Pressure, Uwind, Vwind, Vapour Pressure, Elevation, NDVI and PET
Classical Swine Fever	Cloud, Precipitation, relative humidity Minimum Temperature, Vapour Pressure and Rainfall
Enterotoxaemia	Surface Pressure, NDVI and PET
Fasciolosis	Air Temperature, Precipitation, relative humidity, Temperature, Maximum Temperature, Vapour Pressure, Vwind, Rainfall, Soil Moisture, NDVI and EVI
Foot and Mouth Disease	Precipitable Water, Uwind, Vwind, wet dry frequency, LST Night and EVI
HaemorrhagicSepticaemia	Cloud, Precipitation and Vwind
Lumpy skin disease	Precipitation, minimum Temperature, relative humidity
Peste des Petits Ruminants	Cloud, Precipitable Water, Surface Pressure, Sea Level Pressure, Maximum Temperature, Vwind and NDVI
Sheep & Goat pox	Cloud, Surface Pressure, Maximum Temperature, Vwind, DTP, NDVI and PET
Theileriosis	Air Temperature, Precipitation, Vapour Pressure, NDVI and LST Night
Trypanosomosis	Air Temperature, Precipitation, Surface Pressure, Vapour Pressure, NDVI and LST Night

Table 7.1: Significant weather parameters govern the Livestock disease incidence (forecast).

9. POST PREDICTION VALIDATION

DIMAPUR | Publish Date: 4/14/2019 AH&VS TEAM VISITS AFFECTED AREAS UNDER MEDZIPHEMA,
Source: <http://www.nagalandpost.com>

Following reports of a good number of buffaloes dying in a recent outbreak of suspected Haemorrhagic septicaemia (HS), a team from Animal Husbandry and Veterinary Services (AH&VS) department visited the affected areas under Medziphema on April 12. (Haemorrhagic septicaemia is a contagious bacterial disease that affects cattle and water buffaloes with a high mortality rate in infected animals).

AH&VS, deputy director & principal investigator, AICRP-ADMAS, Dr S. Amenla Walling, in a press release reported that the team consisted of the department's director, Dr Temsummeren, along with additional director, Dr. Budhi Lama, and other officials from the department. The press release added that the area is prone to such kind of disease outbreaks and the department officials reminded villagers to cooperate with the department and vaccinate their animals against such outbreaks. The team told the villagers that even an outbreak can be contained more effectively if villagers report the matter on time to the nearest Veterinary Health Centre.

The villagers admitted in the meeting that they had not reported the recent outbreak to the department initially. The director appreciated the CVO Dimapur and his Rapid Response Team for their quick action after receiving information and for remaining stationed in the outbreak area to date. Free medicine was also distributed among the villagers. The department, through the press release also appealed to everyone to report such matters to the nearest Veterinary Health Centre (so that qualified staff may intervene quickly), instead of publicizing it in other ways. It stated that the department is prepared to extend services to any outbreak of diseases in animals to control such things.

The press release also pointed out that to control the recent outbreak, the department had to direct its officials to make their own transport arrangements to go to the affected areas because the State Election department did not consider an appeal to exempt the department's emergency duty vehicle from election duty.

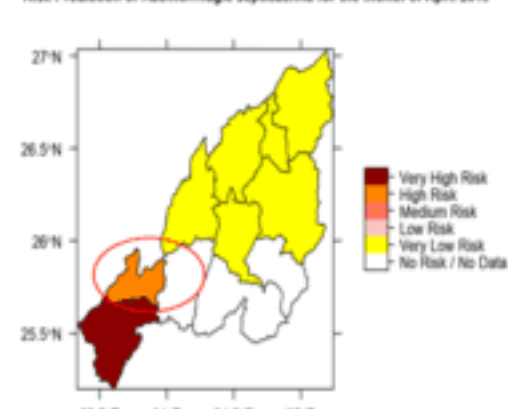
Meanwhile, when contacted, Dr S. Amenla Walling told Nagaland Post that it is difficult to say if the disease has been fully contained since its free grazing season for the animals, but the department is doing its best under the circumstances.

NIVEDI PREDICITONS

Districts of Nagaland	HS prediction for February 2019	HS prediction for March 2019	HS prediction for April 2019
Peren	VLR	VLR	VHR
Dimapur	VLR	NR	HR
Kohima	VLR	VLR	NR
Wokha	VLR	NR	VLR



Risk Prediction of Haemorrhagic septicaemia for the month of April 2019



Note: Spatial and temporal neighbours

NIVEDI Prediction

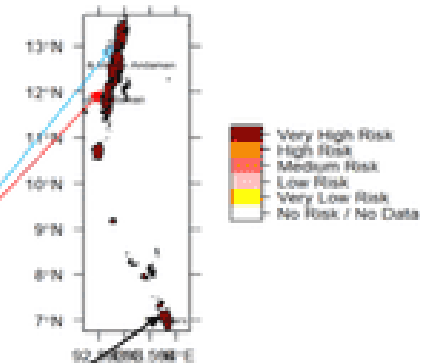
District wise Livestock Disease forwarning for June 2020: Andaman and Nicobar

Districts of Andaman and Nicobar	Livestock Diseases												
	anthrax	Buberculosis	BQ	BT	ET	Fasciolosis	FMH	HN	PPH	S&G Pex	SF	Theileriosis	Trypanosomiasis
Nicobar	NR	NR	NR	NR	NR	VLR	NR	NR	NR	NR	NR	NR	NR
North & Middle Andaman	NR	NR	NR	NR	NR	VLR	NR	NR	NR	NR	NR	NR	NR
South Andaman	NR	NR	NR	NR	NR	VLR	NR	NR	NR	NR	NR	NR	NR

If vaccination is already been done please ignore the disease forecast for that disease.

*No risk/No data available (NR), Very low risk (VLR), Low risk (LR), Moderate risk (MR), High risk (HR)/Very high risk (VHR)

NDAMAN & NICOBAR ISLANDS Risk Prediction of Fascioliasis for the month of June 2020



Andaman and Nicobar Report June-2020



Number of cases of of parasitic cases and other diseases reported from A. & N Islands during the month of June 2020

CASES	FASCIOLIASIS	ASCARIASIS	AMPHISTOM	STRONGYLID	COCCIDIOSIS	MASTITIS	TOTAL
South Andaman	24	48	192	34	2	7	307
N&M Andaman	78	43	14	5	3	10	333
Nicobar	79	31	0	0	0	0	110
TOTAL	361	122	206	39	5	17	750

Dr. Jai Sunder
FI, AICRP-ADMAS
Port Blair

NIVEDI Prediction

District wise Livestock Disease forecasting for July 2020: Himachal Pradesh

Districts of Himachal pradesh	Livestock Diseases												
	Anthrax	Babesiosis	BQ	BT	ET	Fasciolosis	FMD	HIS	PPV	S&G Flu	ST	Tuberculosis	Typhus/malaria
Bilaspur	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR
Chamba	NOR	NOR	NOR	NOR	NOR	NOR	LTB	NOR	NOR	NOR	NOR	NOR	NOR
Hamirpur	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR
Kangra	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR
Lahaul & Spiti	NOR	NOR	NOR	VLR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR
Rohru	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR
Shimla	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR
Sirmaor	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR
Solan	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR
Una	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR	NOR


If vaccination has already been done please ignore the disease forecast for that disease.

HIMACHAL PRADESH Risk Prediction of Sheep and Goat pox for the month of July 2020

Map showing risk levels across Himachal Pradesh districts. Legend:

- Very High Risk (Dark Red)
- High Risk (Red)
- Medium Risk (Orange)
- Low Risk (Yellow)
- Very Low Risk (Light Yellow)
- No Risk / No Data (White)

KERALA REPORT JUNE-2021



HOME ABOUT OUR TEAM IN THE NEWS FROM THE FIELD

SUBMIT INFO SEARCH POSTS

ProMED-mail Portuguese Español Pyrexia Mekong Basin Afrique Francophone

Anglophone Africa South Asia Middle East/North Africa Antimicrobial Resistance

Published Date: 2021-06-18 03:52:33 IST

Subject: PRO/AH/EDR> Foot & mouth disease - India (02): (KL) cattle, RFI

Archive Number: 20210617.8456180

FOOT & MOUTH DISEASE - INDIA (02): (KERALA) CATTLE, REQUEST FOR INFORMATION

A ProMED-mail post
<http://www.promedmail.org>
ProMED-mail is a program of the
International Society for Infectious Diseases
<http://www.isid.org>

Date: Wed 16 Jun 2021 12:34 IST
Source: The Hindu [edited]
<https://www.thehindu.com/news/national/kerala/steps-to-tackle-fmd-in-alappuzha/article34822360.ece>

The Animal Husbandry Department has ramped up measures to tackle the spread of foot-and-mouth disease (FMD) in Alappuzha.

Around 3000 head of cattle have been affected by the outbreak in the district in the last 1.5 months. At least 193 cattle died of the disease during the period. Around 550 head of cattle have contracted the disease, and 100 perished in the worst-affected Ambalapuzha South and Ambalapuzha North grama panchayats. [for Kerala's decentralised administrative structure terminology, see <https://kerala.gov.in/local-self-government-Mod.AS>]. The disease has also been reported from Thakazhi, Thalavady, Edathua, Chettikulangara, Aryad, Pandanad, and Chengannur.

Treatment and vaccination are being carried out to check the spread of the disease. The department has deployed 140 teams in the affected areas. Special teams with doctors have been deployed to the worst-affected Ambalapuzha South and Ambalapuzha North grama panchayats. Doctors have been appointed to Chengannur, Ambalapuzha, and Veliyanad blocks to deal with emergencies during night.

Minister of Animal Husbandry J. Chinchurani said the department had taken measures to bring the outbreak under control.

District Animal Husbandry Officer A.G. Geo said the department had started a vaccination drive on 22 Apr [2021] soon after the FMD cases started to [be reported] in the district. As many as 6140 cattle in 51 grama panchayats have so far been vaccinated against FMD.

The outbreak of the disease was attributed to missed rounds of vaccination due to the COVID-19 pandemic.

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Communicated by:
ProMED
<promed@promedmail.org>

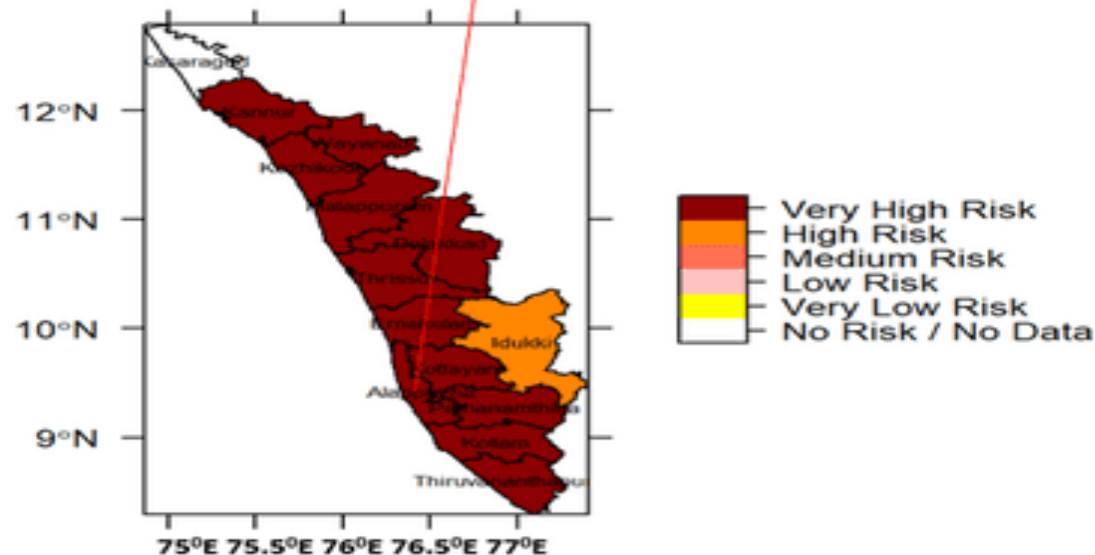
NIVEDI prediction in June 2021

District wise Livestock Disease Risk Forewarning for June 2021: Kerala

Districts of Kerala	Livestock Diseases													
	Anthrax	Babesiosis	BQ	BT	ET	Fascioliasis	FMD	HS	PPR	S&G Pox	SF	Theileriosis	Trypanosomiasis	
Alappuzha	NR	NR	NR	NR	NR	NR	VHR	MR	VLR	NR	NR	NR	NR	
Ernakulum	NR	NR	NR	NR	NR	NR	VHR	HR	HR	NR	VHR	NR	NR	
Idukki	VHR	VLR	VLR	VLR	NR	NR	HR	NR	VLR	NR	NR	NR	NR	
Kannur	NR	VLR	NR	NR	NR	NR	VHR	VHR	VLR	NR	NR	NR	NR	
Kasaragod	NR	NR	NR	NR	NR	NR	NR	NR	VLR	NR	NR	NR	NR	
Kollam	NR	VLR	VLR	NR	NR	NR	VHR	VHR	HR	NR	NR	NR	NR	
Kottayam	NR	NR	NR	NR	NR	NR	VHR	VHR	VLR	NR	NR	NR	NR	
Kozhikode	NR	NR	NR	NR	NR	NR	VHR	NR	VHR	NR	NR	NR	NR	
Malappuram	NR	VLR	NR	NR	NR	NR	VHR	VHR	VLR	NR	NR	NR	NR	
Palakkad	NR	VLR	NR	NR	NR	NR	VHR	HR	HR	NR	NR	VHR	NR	
Pathanamthitta	VHR	VLR	NR	NR	NR	NR	VHR	VLR	VLR	NR	NR	NR	NR	
Thiruvananthapuram	NR	NR	NR	NR	NR	NR	VHR	VHR	HR	NR	NR	NR	VHR	
Thrissur	NR	VLR	NR	NR	NR	NR	VHR	VHR	HR	NR	NR	NR	NR	
Wayanad	NR	VLR	NR	NR	NR	NR	VHR	NR	NR	NR	NR	VHR	NR	

If vaccination has already been done please ignore the disease forecast for that disease.

KERALA Risk Prediction of Foot and mouth disease for the month of June 2021



KARNATAKA REPORT SEPTEMBER-2021



Published Date: 2021-09-30 11:40:53

Subject: PRQ/ISDAS> Foot & mouth disease - India (10) (Karnataka) cattle

Archive Number: 20210930_8698795

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By Wanda G. Smith, M.D., M.P.H.

© 2004 Blackwell Publishing Ltd, *Journal of Internal Medicine* 255: 111–118

Finally, we note that the results of the present study are consistent with the findings of other studies that have shown that the use of a computer-based system can improve the accuracy of data collection and analysis.

Anderson, J. W. 1993. *Soil Microbiology*. New York: Macmillan.

1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 2679, 26

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District wise Livestock Disease Risk Forewarning for September 2021: Karnataka

Districts of Karnataka	Livestock Diseases												
	Axifex	Balvacin	BC	BT	ET	Favosulin	FMD	HV	PPS	M/G Fes.	IF	Dullness	Cryoprecipitate
Cochin	NB	NB	VLB	VLB	NB	NB	VLB	VLB	NB	HBH	NB	NB	NB
Dharwad	NB	NB	HBH	VLB	NB	NB	HBH	VLB	VLB	HBH	NB	NB	NB
Gowari	HBH	NB	VLB	NB	NB	NB	HB	HB	NB	HB	NB	NB	NB
Kodagu	NB	NB	HB	NB	NB	NB	HBH	VLB	NB	NB	NB	NB	NB
Kolar	NB	NB	NB	VLB	NB	NB	HB	VLB	NB	NB	NB	NB	NB
Koppal	HBH	NB	VLB	VLB	NB	NB	LH	NB	VLB	NB	NB	NB	NB
Mandya	NB	NB	NB	VLB	NB	NB	HBH	VLB	NB	NB	NB	NB	NB
Mysore	NB	NB	HBH	NB	NB	NB	HBH	VLB	VLB	NB	NB	NB	NB
Rachur	HBH	NB	VLB	NB	NB	NB	VLB	LH	VLB	NB	NB	NB	NB
Saranagudi	NB	NB	NB	VLB	NB	NB	HBH	NB	VLB	NB	NB	NB	NB
Sivmoga	NB	NB	HBH	NB	HBH	NB	HBH	NB	VLB	NB	NB	NB	NB
Tankar	HBH	NB	HB	VLB	NB	NB	HBH	HBH	VLB	NB	NB	NB	NB
Udupi	NB	NB	NB	NB	NB	NB	HB	NB	NB	NB	NB	NB	NB
Uttara Kannadi	NB	NB	NB	NB	NB	NB	HB	VLB	NB	NB	NB	NB	NB
Yadgi	NB	NB	VLB	VLB	NB	NB	VLB	VLB	VLB	NB	NB	NB	NB

The authors of 2002 and 2003 studies showed FMO₃ activity in humans has both genetic and environmental sources.

Cases have been reported from Adalgañ, Andalus, Chantagagatha, and Salsichan. While the sporting community, depending on cattle for regular income, are worried about their livelihood, the veterinarians are struggling hard to provide treatment, amidst a dearth of staff members.

The Department of Veterinary and Animal Husbandry has reported over 150 cases in the district so far. As of 24 Sep 2020, the animals in 16 villages of the district are being treated. So far the death of one animal had been reported. However, farmers claim more animals have died over the last month. The death of cattle has an impact on milk production, affecting milk production.

The vaccination for typhoid is done only in six months under the National Aerial Disease Control Programme. However, the vaccination drive was not done in the last year owing to the COVID-19 pandemic. "The outbreak of SFT and Hantaan disease is due to the failure of the government in conducting the vaccination. If the vaccination had been done as per the schedule, the virus would not have spread", H Naga Ramesh, president of Prastha Club in Arkabul, told media.

Following results of the discussion, interviewees have been broadly affected persons. "Against 24 new food products of voluntary doctors in Ankara (2018), we are only 300 people. Every doctor is in charge of 2 or more hospitals. We are struggling hard to treat people," said a subordinator.

Others for now are more than at the department cannot deliver services fully. There are a shortage of staff members of other cities as well be added.


Considering this issue, the department has launched a ring vaccination programme. Under this, the animals in a 5-kilometre (3.1-mile) radius of the village, where the disease outbreak was reported, should be vaccinated. "We have sufficient stock for the ring vaccination. We are planning a mass vaccination in December (2022), where we will cover 6.55 lakh (658 000) animals," said MR Bhambhani, Deputy Director of Veterinary and Animal Husbandry in Gujarat.

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ARUNACHAL PRADESH REPORT APRIL-2022



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Published Date: 2021-04-14 00:02:23 IST

Subject: PRO/AH/EDR> Foot & mouth disease - India: (AR)

mithun, RFI

Archive Number: 20210413.8305677

FOOT AND MOUTH DISEASE - INDIA: (ARUNACHAL PRADESH) MITHUN, REQUEST FOR INFORMATION

A ProMED-mail post
<http://www.promedmail.org>
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 International Society for Infectious Diseases
<http://www.isid.org>

Date: Tue 13 Apr 2021
 Source: Sentinel Assam [abridged, edited]
<http://www.sentinelassam.com/north-east-india-news/arunachal-news/many-mithuns-infected-with-fmd-foot-and-mouth-disease-533689>

A large number of mithuns have been affected by FMD (foot and mouth disease) in various parts of Arunachal Pradesh, and a few have died, said official sources on Monday (13 Apr 2021).

Animal Husbandry & Veterinary Department Deputy director Dr Taba Heli, a top mithun expert in North Eastern region, reported that the disease has taken a severe form in the entire Siang belt, particularly in East Siang, West Siang, and Upper Siang districts [map at <https://tinyurl.com/tft28s3c>].

Though the number of deaths is yet to be known, the disease has spread in

scattered areas of Papum Pare district also. The Department has allocated district funds for procurement of medicines to take all possible steps to contain the disease, he said. Mithun deaths have been reported also from Itanagar and Juliang area.

Pointing out that mithuns are the pride of indigenous people in the state, Nyishi Elite Society president Bengla Tolum has urged the department to take all possible steps to save them.

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Communicated by:
 ProMED from HealthMap Alerts
promed@promedmail.org

(Mithun, also known as "Cattle of Mountain," is a bovine species of the northeastern hill region of India. This massive bovine is reared under free-range conditions in the hill forests at an altitude of 1000 to 3000 meters above mean sea level.

It is important to obtain information on the serotype and genotype of the virus strain involved, as well as of the vaccination history of the affected animals.

FMD is a disease of cloven-hoofed animals, including cattle, buffalo, small ruminants, and swine. It is the most contagious disease of mammal animals, having a great potential for causing severe economic loss in susceptible animals. Mortality, generally, is up to 2-3% but may be significantly higher in young stock.

The disease is regarded as endemic in India; effective mass vaccination, applying potent vaccines -- which include matching vaccine strains -- is essential for its control. Continued circulation of the virus may affect India's exports, such as frozen buffalo meat, of which India is the largest producer and exporter, globally. An example of the said export issue is to be found at <https://agriculture.gov.in/Documents/Report/foot%20and%20mouth%20disease.pdf>. - Mod.A5

NIVEDI prediction in April 2021

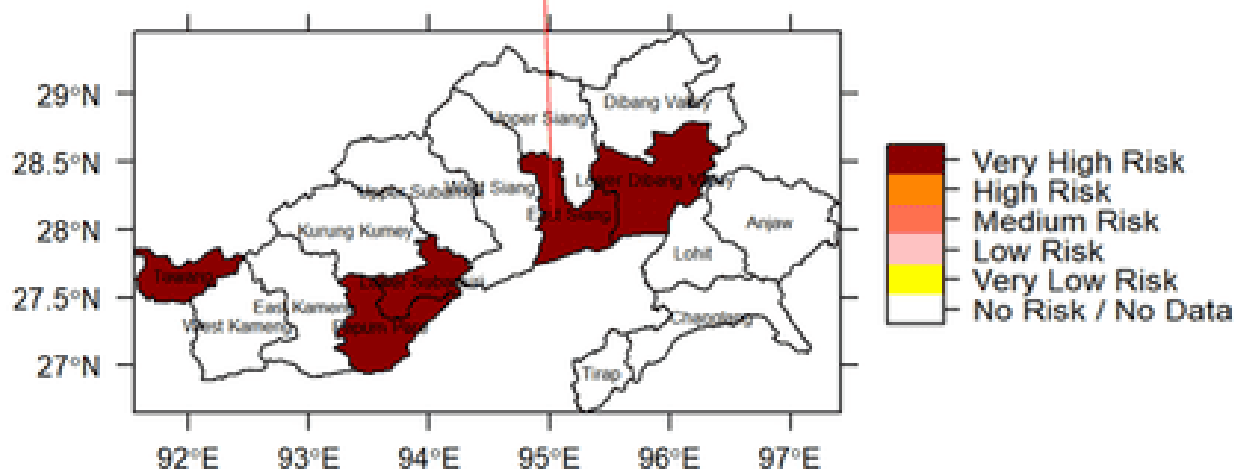
District wise Livestock Disease Risk Forewarning for April 2021: Arunachal Pradesh

Districts of Arunachal Pradesh	Livestock Diseases													
	Anthrax	Babesiosis	BQ	BT	ET	Fascioliasis	FMD	HS	PPR	S&G Pox	SF	Theileriosis	Trypanosomiasis	
Anjaw	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	
Changlang	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	
Dibang Valley	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	
East Kameng	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	
East Siang	NR	NR	NR	NR	NR	NR	VHR	NR	VLR	NR	VHR	NR	NR	
Kurung Kumey	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	
Lohit	NR	VLR	VLR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	
Lower Dibang Valley	NR	NR	VLR	NR	NR	NR	VLR	VLR	VLR	NR	VHR	NR	NR	
Lower Subansiri	NR	NR	NR	NR	NR	NR	VHR	NR	NR	NR	NR	VLR	NR	
Papum Pare	NR	NR	NR	NR	NR	NR	VHR	NR	VHR	NR	VHR	NR	NR	
Tawang	NR	NR	NR	NR	NR	NR	HR	NR	NR	NR	NR	NR	NR	
Tirap	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	
Upper Siang	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	
Upper Subansiri	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	
West Kameng	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	
West Siang	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	

If vaccination has already been done please ignore the disease forecast for that disease.

*No risk/No data available (NR), Very low risk (VLR), Low risk (LR), Moderate risk (MR), High risk (HR), Very high risk (VHR)

ARUNACHAL PRADESH Risk Prediction of Foot and mouth disease for the month of April 2021



9.1 Correlational Assessment

The number of outbreaks predicted and outbreaks actually reported were mentioned in table 9.1. It has been observed from the table that outbreaks predicted two months in advance and timely alerts were issued that helped the stakeholders to take appropriate preventive measures with in time and accordingly the reported outbreaks were very less. Though the use of artificial intelligence system is more beneficial for accurately predicting the livestock disease outbreaks, there are yet number of limitations, namely, there are expected to be under reporting and also non-reporting cases which created the uncertainties in the model predictions while translating model inputs in to model outputs. However, identifying these uncertainties in the prediction using statistical models and highlighting the importance of quality data may improve the model accuracy and confidence while building the model for livestock disease forecasting.

Table 9.1: Number of districts predicted for livestock diseases risk events and reported outbreaks



Sl No	Livestock diseases	April-2022		May-2022	
		No. of districts predicted for the disease risk events	No. of districts reported the disease outbreaks*	No. of districts predicted for the disease risk events	No. of districts reported the disease outbreaks*
1	Anthrax	27	2	16	1
2	Babesiosis	47	32	61	35
3	Black Quarter (BQ)	46	7	60	3
4	Bluetongue (BT)	0	0	0	2
5	Enterotoxaemia (ET)	22	7	9	15
6	Fasciolosis	46	15	44	10
7	Foot & Mouth Disease (FMD)	53	4	48	3
8	Haemorrhagic Septicaemia (HS)	46	3	42	5
9	Peste des Petits Ruminants (PPR)	76	11	55	17
10	Sheep & Goat Pox	50	9	38	12
11	Swine Fever	64	6	45	5
12	Theileriosis	62	18	62	29
13	Trypanosomosis	30	29	68	25

*Which takes in to account of action taken for prediction and non-reporting of cases

10. LAUNCH OF MOBILE ANDROID APP&LINK TO DOWNLOAD

Livestock forewarning application (LDF) can be downloaded following the link provided:http://www.nivedi.res.in/android_nadres/LDF.apk and google play store link also provided <https://play.google.com/store/apps/details?id=info.androidhive.ldf>

Further launch of LDF application was done, the news provided below.



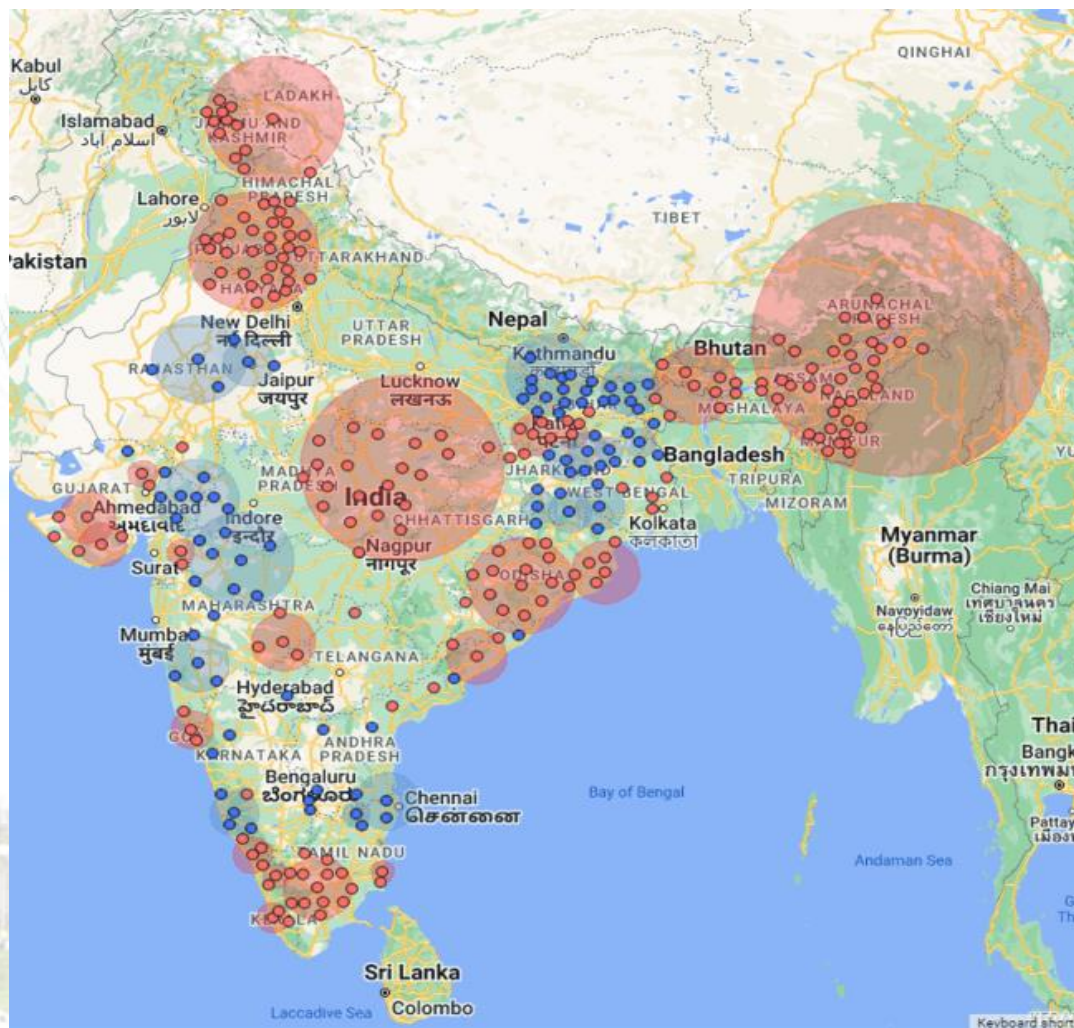
Livestock Disease Forewarning (LDF Mobile App)

The image displays three screenshots of the Livestock Disease Forewarning (LDF Mobile App) interface. The first screenshot shows the home screen with a language selector, logos of ICAR and NIVEDI, and an 'About App' section. The second screenshot shows the main form with dropdown menus for disease name (Anthrax), state name (KARNATAKA), district name (Bagalkot), and month name (December), along with SUBMIT and RESET buttons. The third screenshot shows a 'Result' pop-up window displaying the prediction: Disease name: Anthrax, State name: KARNATAKA, District name: Bagalkot, Month: December, Result: Very Low Risk.

To extend the reach of the NADRES forewarning bulletin among the various stakeholders, a Mobile Application named Livestock Disease forewarning app “LDF-Mobile App” was developed. The forewarning methodology adapted in the “mobile app” remains the same as monthly bulletin; it provides user interface to know the predicted forewarning results stored in NADRES MySQL database. A PHP web-based service is developed in Java to extract the results of forewarning two months in advance by keying state name, district name and disease name and display the same in the mobile app. In addition to forewarning, the LDF-Mobile App also provides the details of clinical samples to be collected in case of outbreaks of the listed diseases for laboratory confirmation and immediate preventive measures to be taken up in case of positive prediction/disease confirmation. The LDF mobile app is available at ICAR-NIVEDI website. It is available on Google play store.

11.1. MODEL BASED HOT-SPOT AREA MAPS OF LIVESTOCK INFECTIOUS DISEASES IN INDIA

a) FMD Hotspot by Poisson Model: FMD in India (1989-2022)



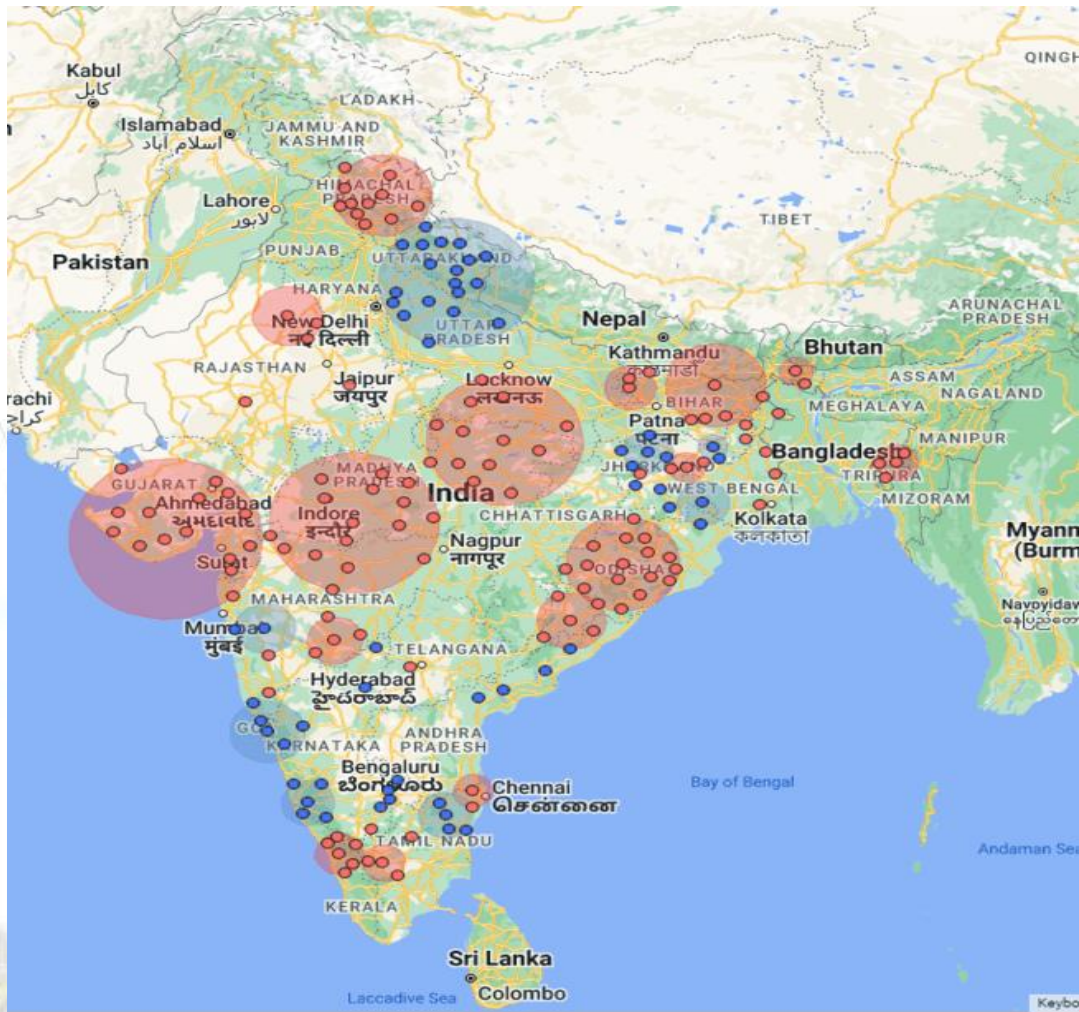
Model Specifications

- **Retrospective Analysis: Space-Time**
- **Probability Model: Space-Time Poisson Model**
 - With the Space-Time Poisson model, the number of cases in each location is Poisson-distributed.
 - The model requires case and population counts for a set of data locations and geographical coordinates for each of the locations.
 - SaTScan does a linear interpolation based on the population at the census times immediately preceding and following.
- **Advance Analysis Features:**
- **Circle radius:** 1 km.
- **Time Aggregation:** 1 year.
- **Output obtained with no geographical overlap-** Total hotspots–69 (High- 36, Low- 33).
- The output is generated using SaTScan v9. 6.

Note: Red Dot: High Disease Cluster

Blue Dot: Low Disease Cluster

b) PPR Hotspot by Poisson Model: PPR in India (1995-2022)



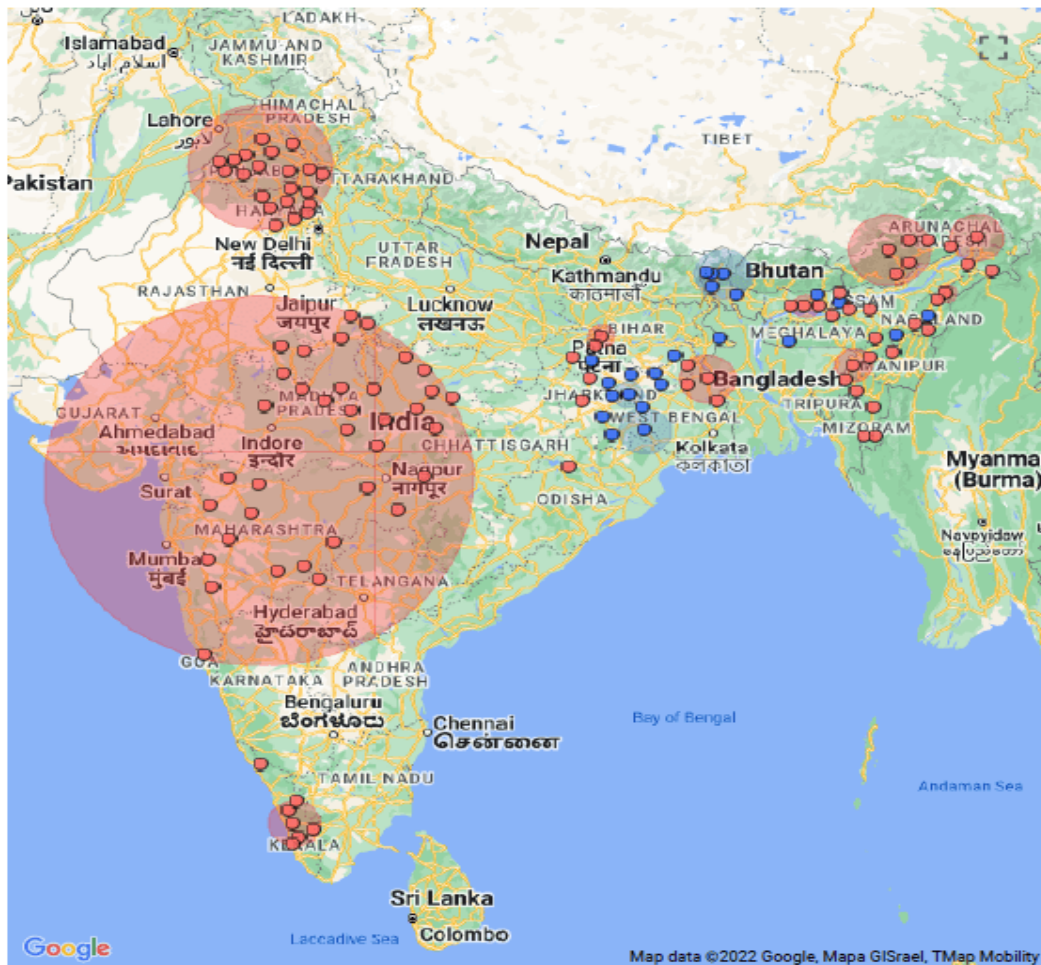
Model Specifications

- **Retrospective Analysis: Space-Time**
- **Probability Model: Space-Time Poisson Model**
 - With the Space-Time Poisson model, the number of cases in each location is Poisson-distributed.
 - The model requires case and population counts for a set of data locations and geographical coordinates for each of the locations.
 - SaTScan does a linear interpolation based on the population at the census times immediately preceding and following.
- **Advance Analysis Features:**
 - Circle radius:** 1 km.
 - Time Aggregation:** 1 year.
 - Output obtained with no geographical overlap-** Total hotspots– 51 (High- 30, Low- 21).
 - The output is generated using **SaTScan v9. 6.**

Note: Red Dot: High Disease Cluster

Blue Dot: Low Disease Cluster

c) CSF Hotspot by Poisson Model: CSF in India (1992-2022)



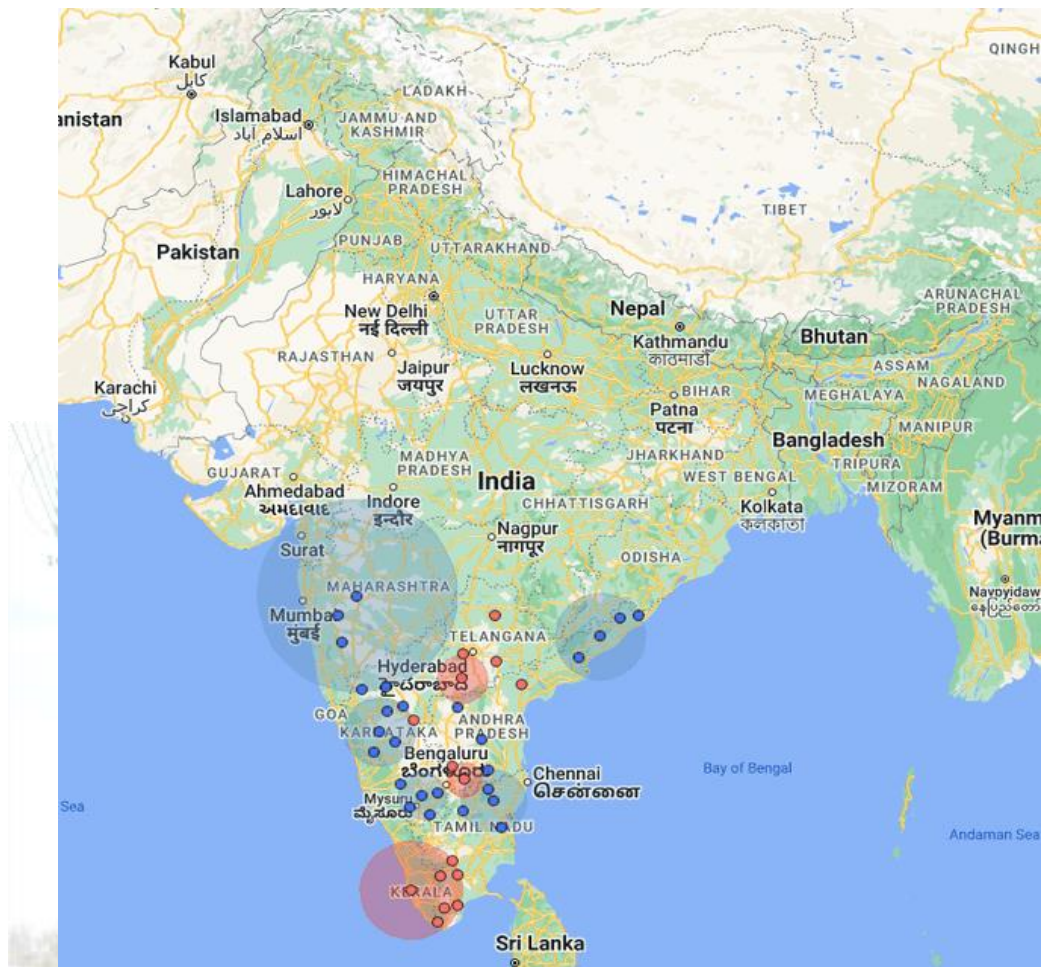
Model Specifications

- **Retrospective Analysis: Space-Time**
- **Probability Model: Space-Time Poisson Model**
 - With the Space-Time Poisson model, the number of cases in each location is Poisson-distributed.
 - The model requires case and population counts for a set of data locations and geographical coordinates for each of the locations.
 - SaTScan does a linear interpolation based on the population at the census times immediately preceding and following.
- **Advance Analysis Features:**
 - Circle radius:** 1 km.
 - Time Aggregation:** 1 year.
 - Output obtained with no geographical overlap-** Total hotspots– 46 (High- 29, Low- 17).
 - The output is generated using **SaTScan v9. 6**.

Note: Red Dot: High Disease Cluster

Blue Dot: Low Disease Cluster

d) Bluetongue Hotspot by Poisson Model: Bluetongue in India (2001-2022)



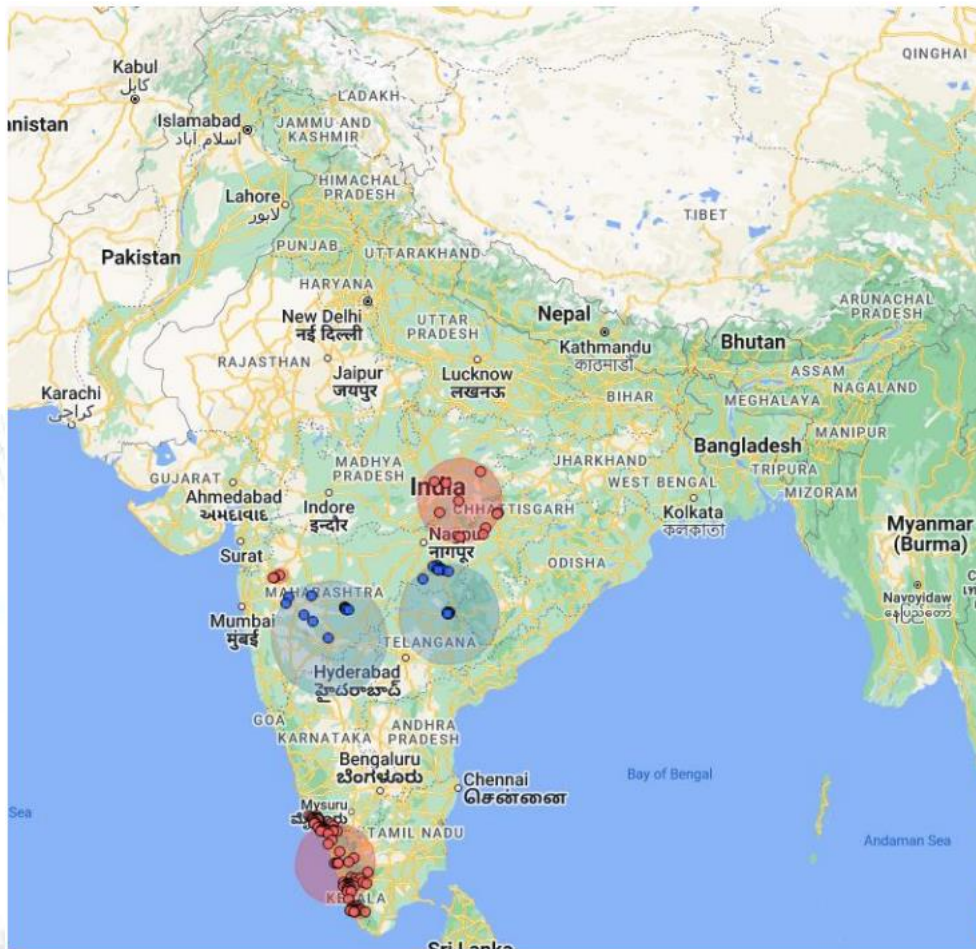
Model Specifications

- **Retrospective Analysis: Space-Time**
- **Probability Model: Space-Time Poisson Model**
 - With the Space-Time Poisson model, the number of cases in each location is Poisson-distributed.
 - The model requires case and population counts for a set of data locations and geographical coordinates for each of the locations.
 - SaTScan does a linear interpolation based on the population at the census times immediately preceding and following.
- **Advance Analysis Features:**
- **Circle radius: 1 km.**
- **Time Aggregation: 1 year.**
- **Output obtained with no geographical overlap- Total hotspots– 14 (High- 7, Low- 7).**
- The output is generated using **SaTScan v9. 6.**

Note: Red Dot: High Disease Cluster

Blue Dot: Low Disease Cluster

e) LSD Hotspot by Poisson Model: LSD in India (2019-2022)



Model Specifications

- **Retrospective Analysis: Space-Time**
- **Probability Model: Space-Time Poisson Model**
 - With the Space-Time Poisson model, the number of cases in each location is Poisson-distributed.
 - The model requires case and population counts for a set of data locations and geographical coordinates for each of the locations.
 - SaTScan does a linear interpolation based on the population at the census times immediately preceding and following.
- **Advance Analysis Features:**
- **Circle radius: 1 km.**
- **Time Aggregation: 1 year.**
- **Output obtained with no geographical overlap- Total hotspots– 7 (High- 5, Low- 2).**
- **The output is generated using SaTScan v9. 6.**

Note: Red Dot: High Disease Cluster

Blue Dot: Low Disease Cluster

f) Anthrax Hotspot by Poisson Model – Anthrax in India (1989-2022)



Model Specifications

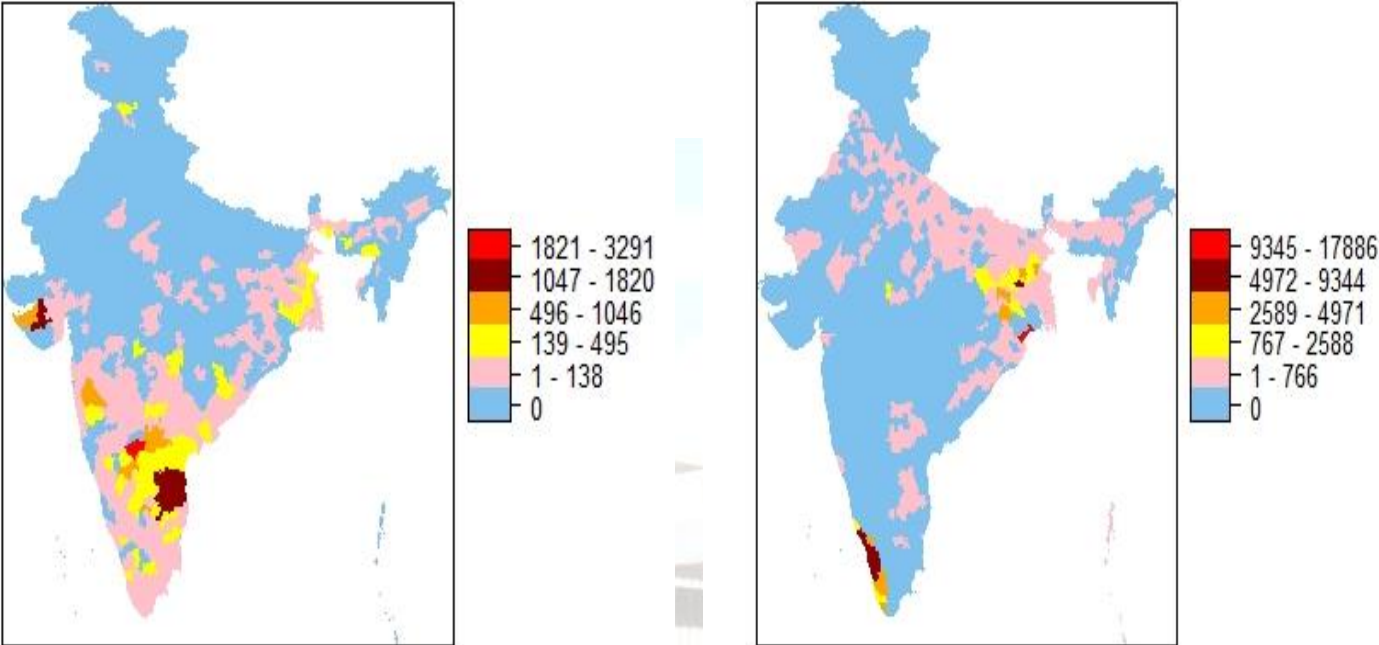
- **Retrospective Analysis: Space-Time**
- **Probability Model: Space-Time Poisson Model**
 - With the Space-Time Poisson model, the number of cases in each location is Poisson-distributed.
 - The model requires case and population counts for a set of data locations and geographical coordinates for each of the locations.
 - SaTScan does a linear interpolation based on the population at the census times immediately preceding and following.
- **Advance Analysis Features:**
 - Circle radius: 1 km.**
- **Time Aggregation: 1 year.**
- The output is generated using **SaTScan v9. 6.**

Note: Red Dot: High Disease Cluster

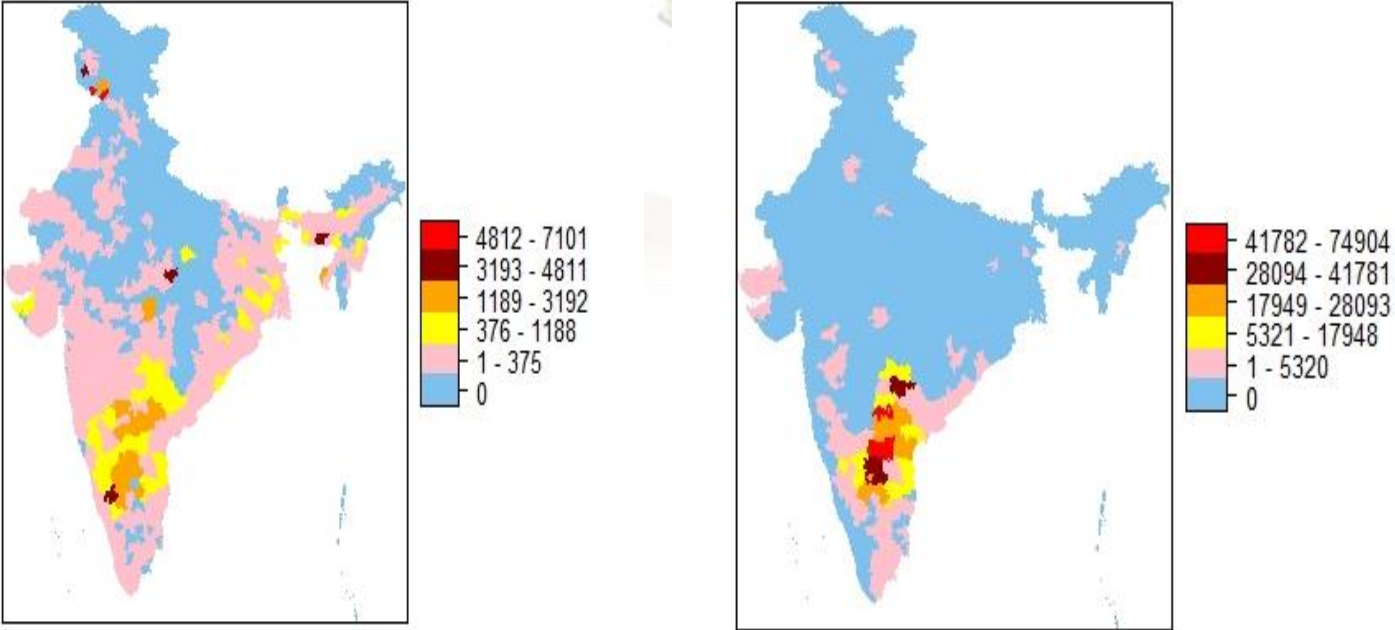
Blue Dot: Low Disease Cluster

11.2. MODEL BASED OUTBREAK/INCIDENCE MAPS OF LIVESTOCK DISEASE IN INDIA

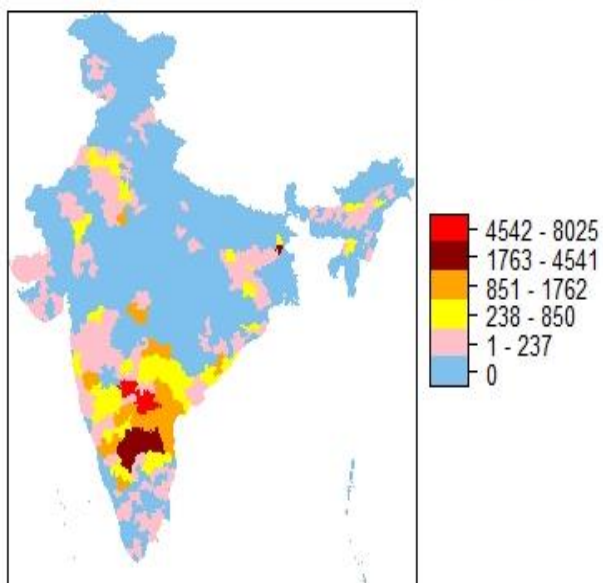
Outbreaks/Incidence- Anthrax(1990-2022) Outbreaks/Incidence- Babesiosis(1990-2022)



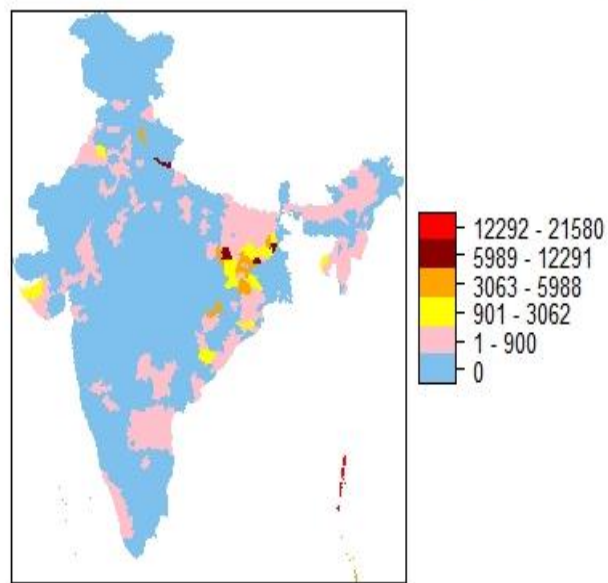
Outbreaks/Incidence- Blackquarter(1990-2022) Outbreaks/Incidence- Bluetongue(1990-2022)



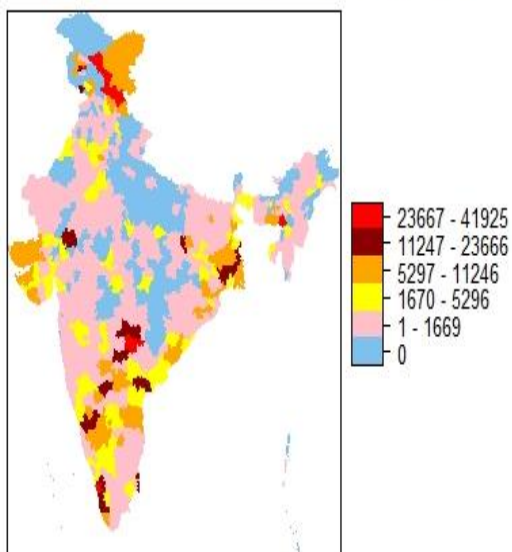
Outbreaks/Incidence- Enterotoxaemia(1990-2022)



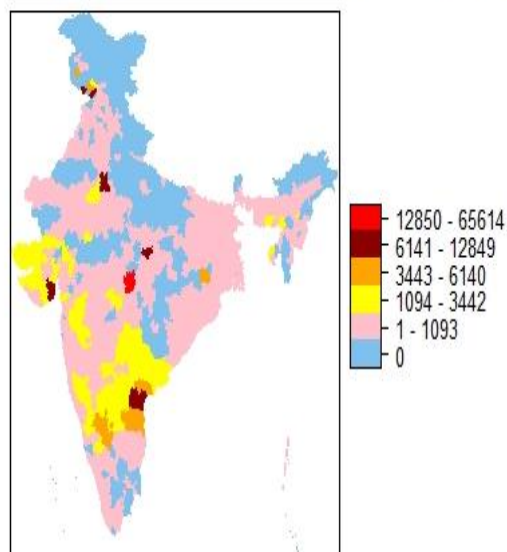
Outbreaks/Incidence- Fascioliasis(1990-2022)



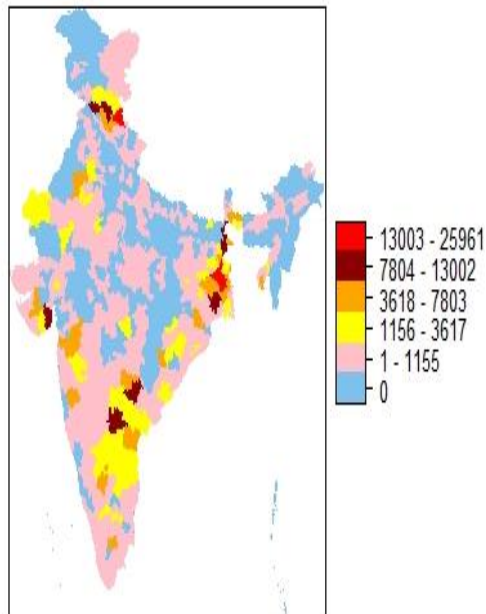
Outbreaks/Incidence-Foot and Mouth Disease(1990-2022)



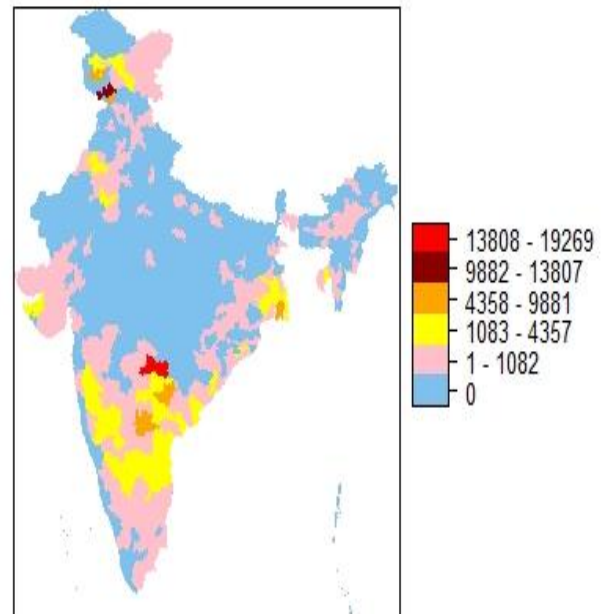
Outbreaks/Incidence-Haemorrhagic Septicaemia(1990-2022)



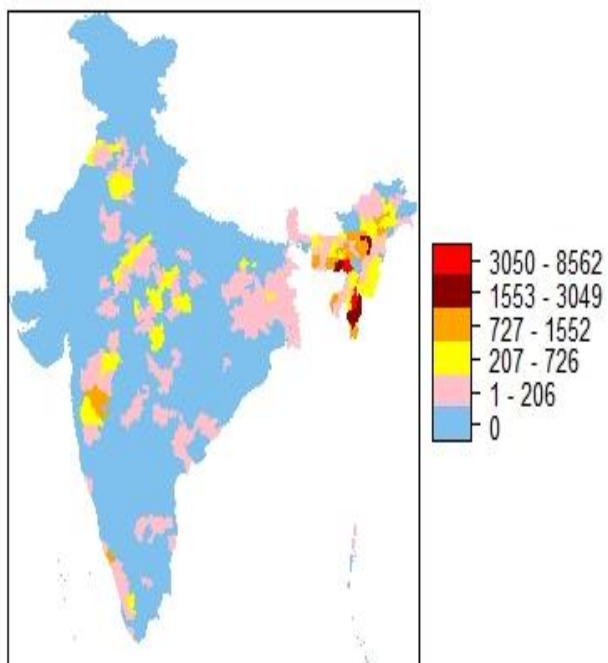
Outbreaks/Incidence-Peste des petits Ruminants(1990-2022)



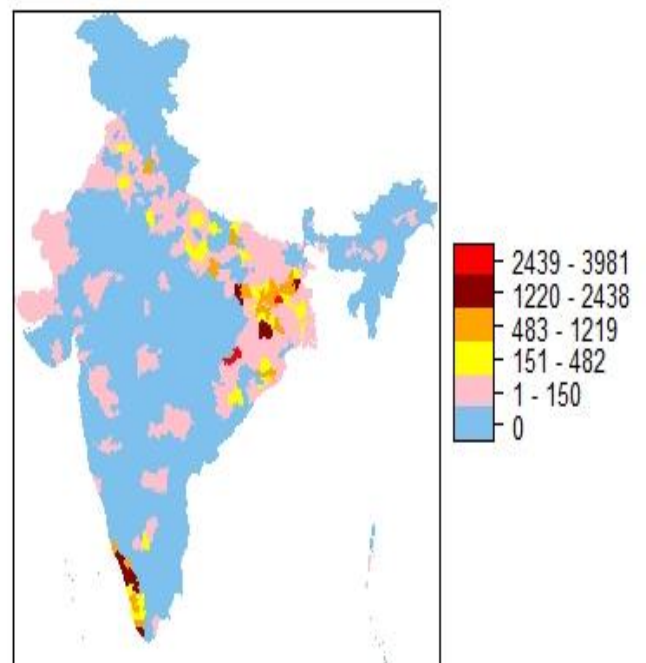
Outbreaks/Incidence-Sheep & Goat Pox(1990-2022)



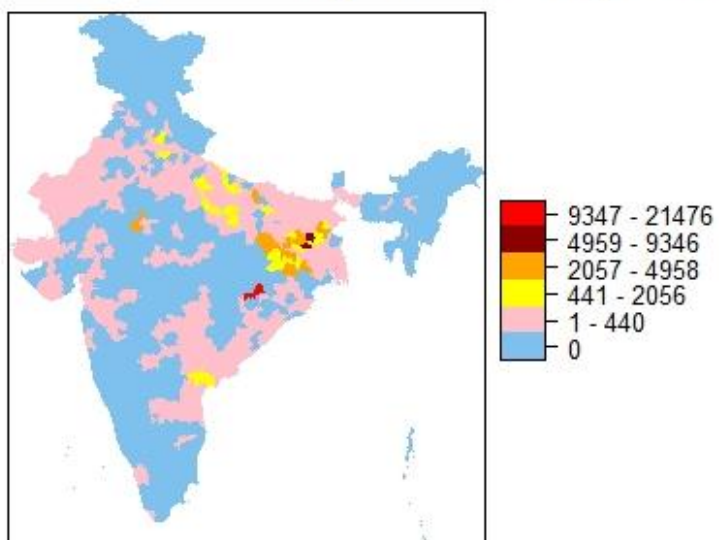
Outbreaks/Incidence-Swine Fever(1990-2022)



Outbreaks/Incidence-Theileriosis(1990-2022)

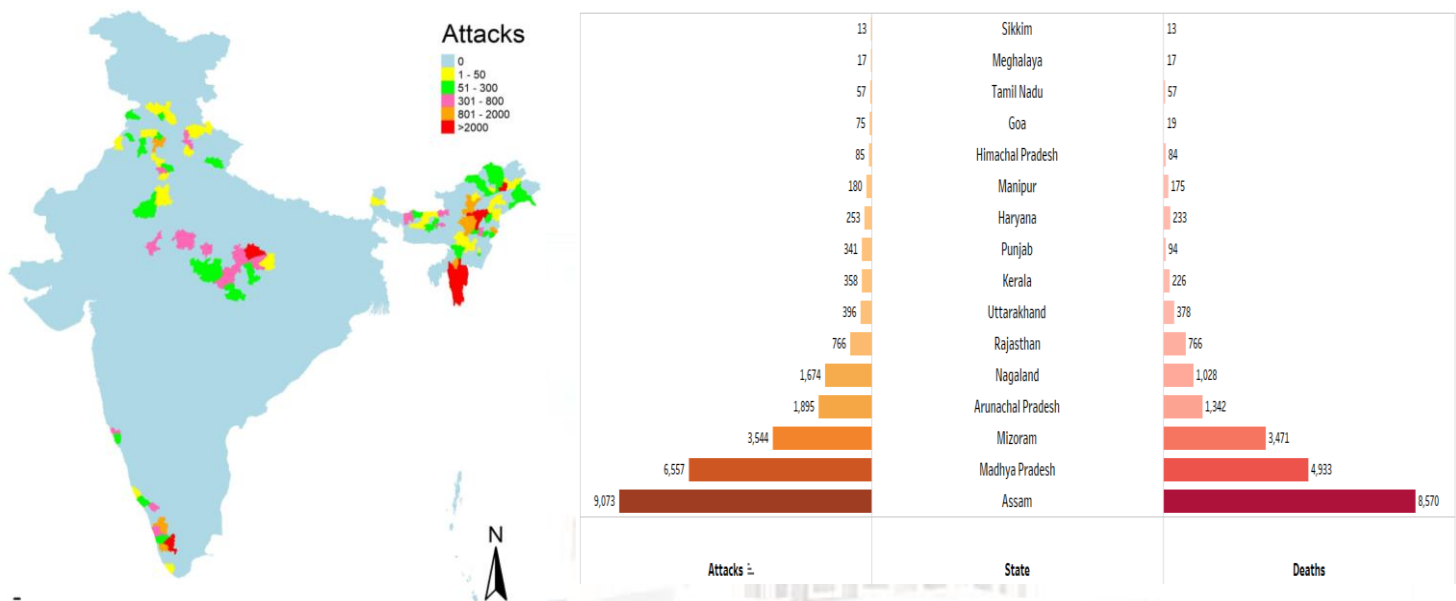


Outbreaks/Incidence-Trypanosomiasis(1990-2022)



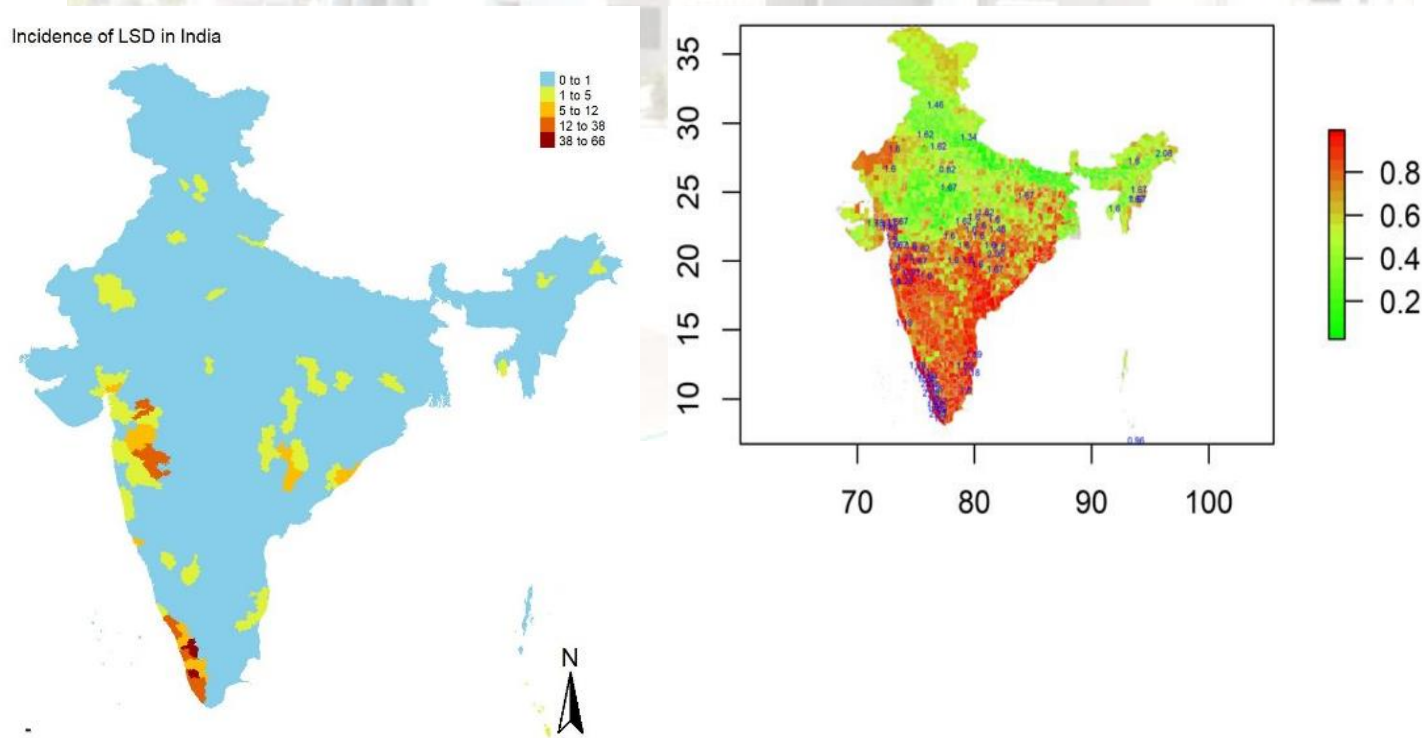
11.3. MODEL BASED RISK MAPS OF LIVESTOCK INFECTIOUS DISEASES IN INDIA

Disease map considering attacks of ASFV in India

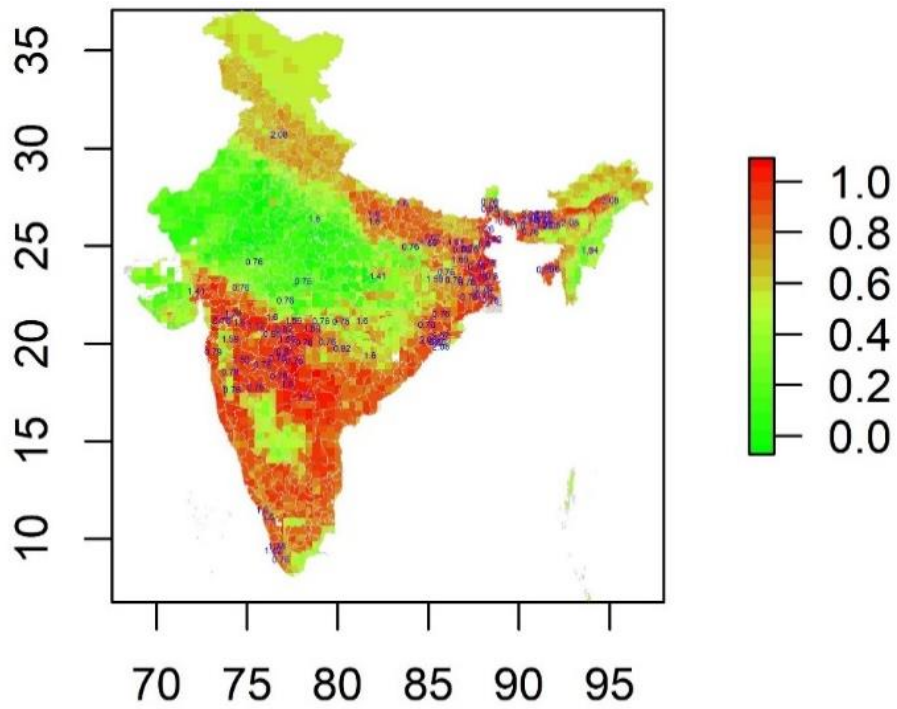


Incidence of LSD in India

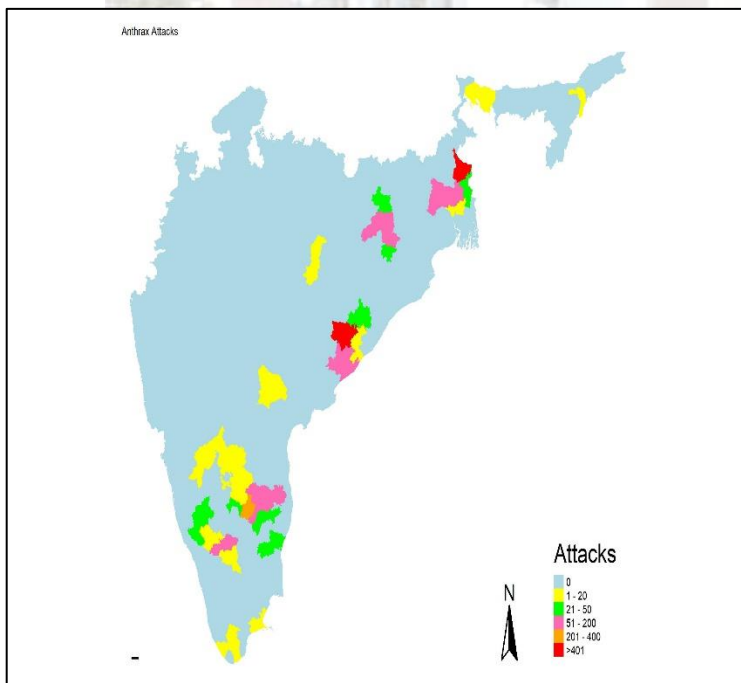
Risk map for LSD in India



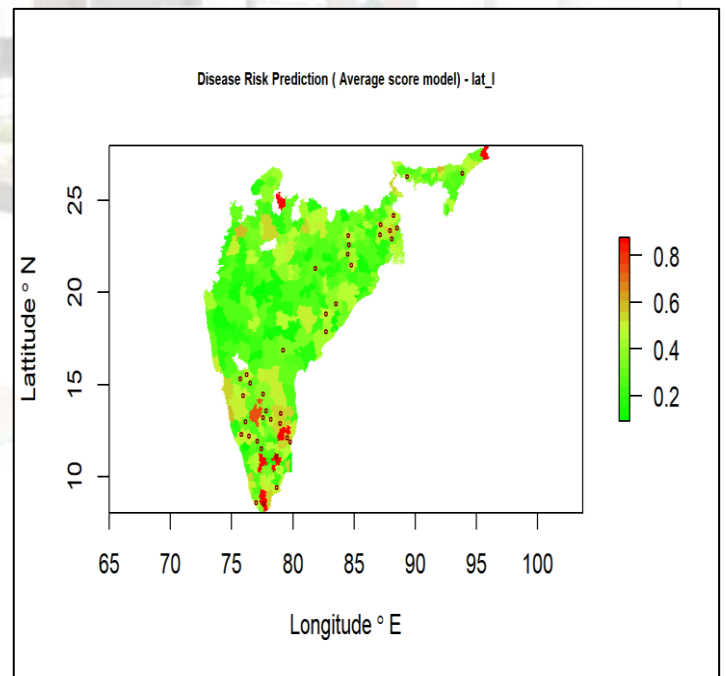
Risk map for Avian Influenza in India



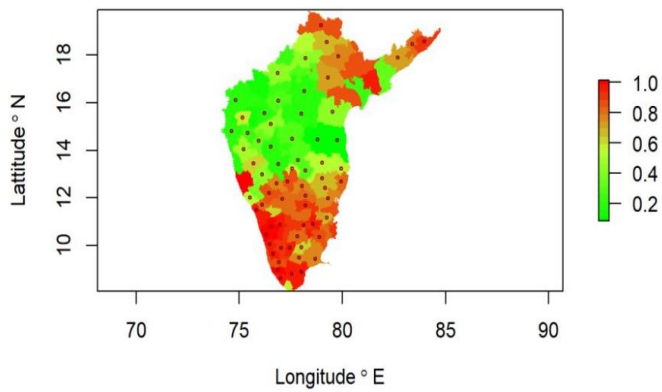
Disease Map for Anthrax on Attacks



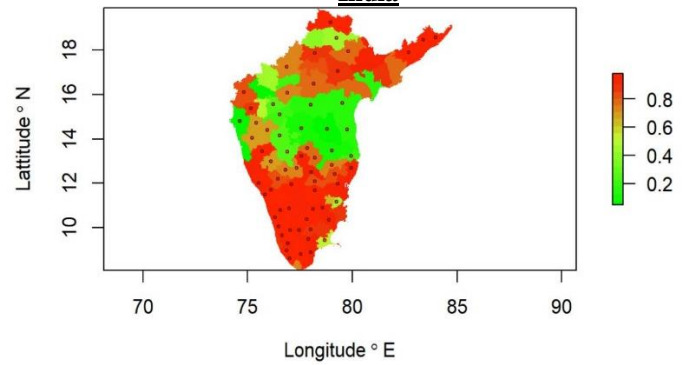
Risk map for Anthrax in India



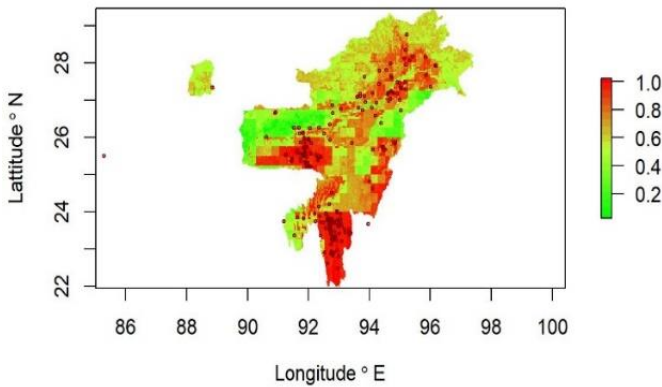
Risk prediction for Anthrax Disease for Southern India



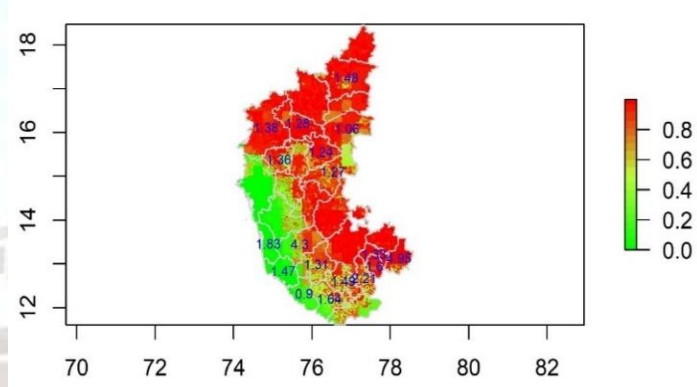
Risk prediction for Enterotoxaemia Disease for Southern India



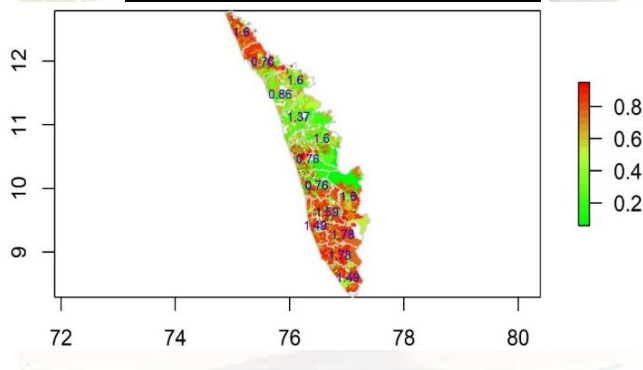
Risk prediction for ASF for North Eastern India



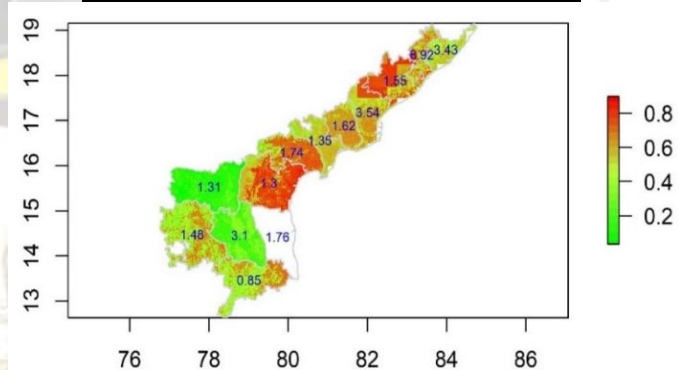
Karnataka Risk map Bluetongue



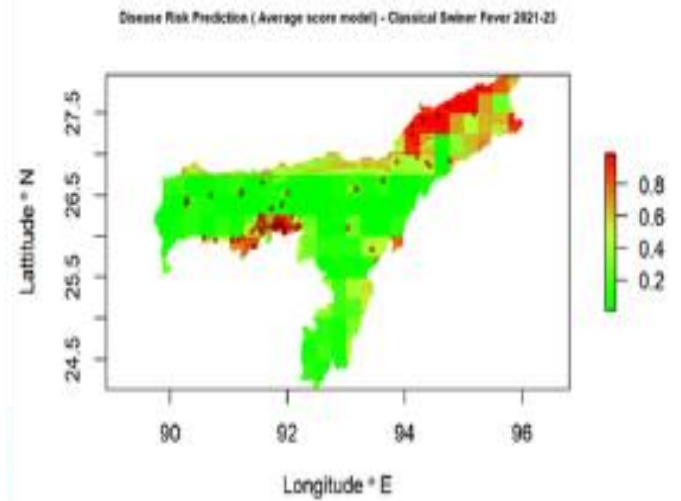
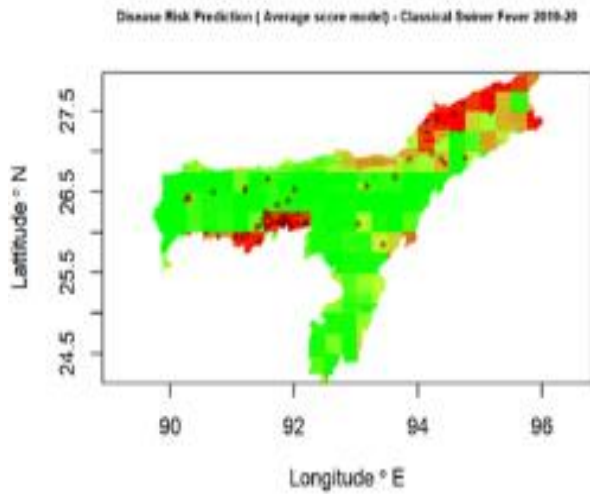
Risk map of Anaplasmosis in Kerala



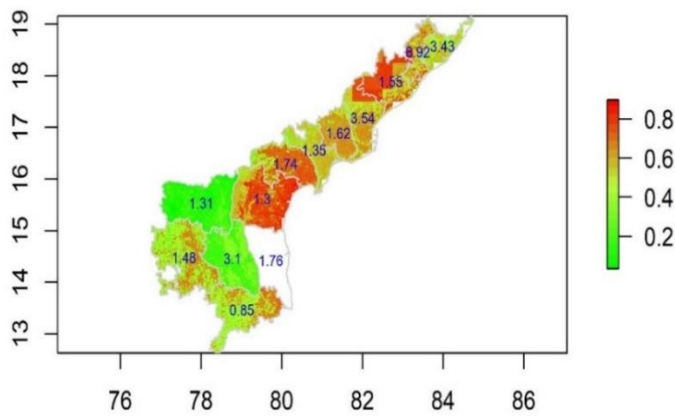
Risk map of Bluetongue in Andhra Pradesh



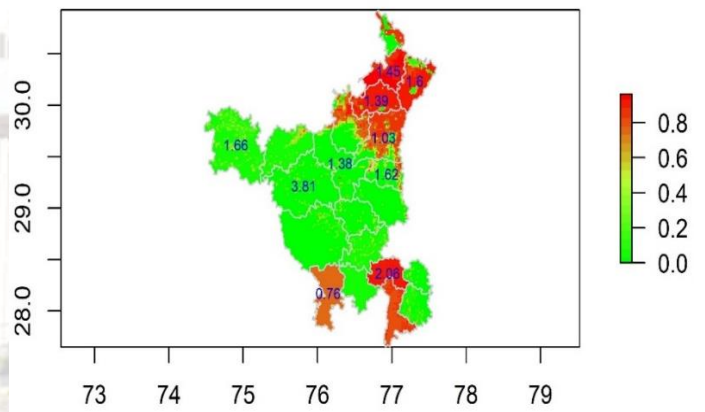
Forecasted risk maps for Classical Swine Fever disease in Assam



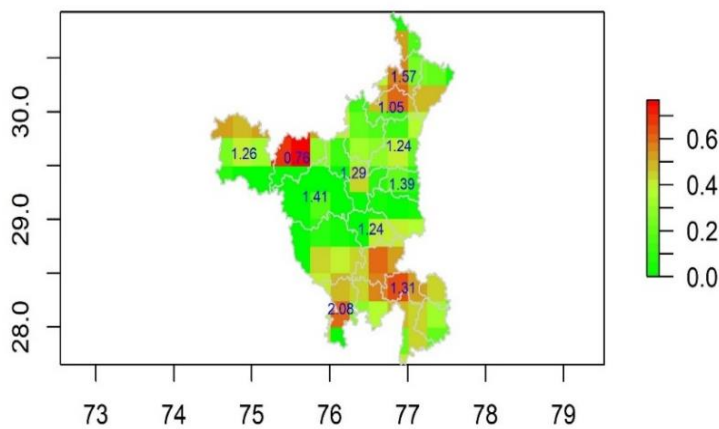
Risk map for Bluetongue in Andhra Pradesh



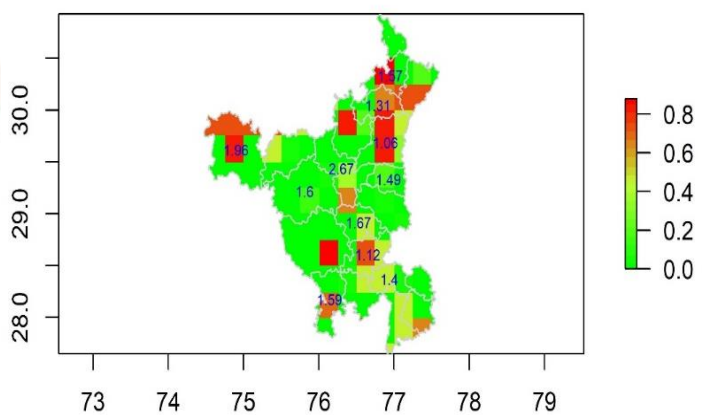
Risk map for Babesiosis in Haryana



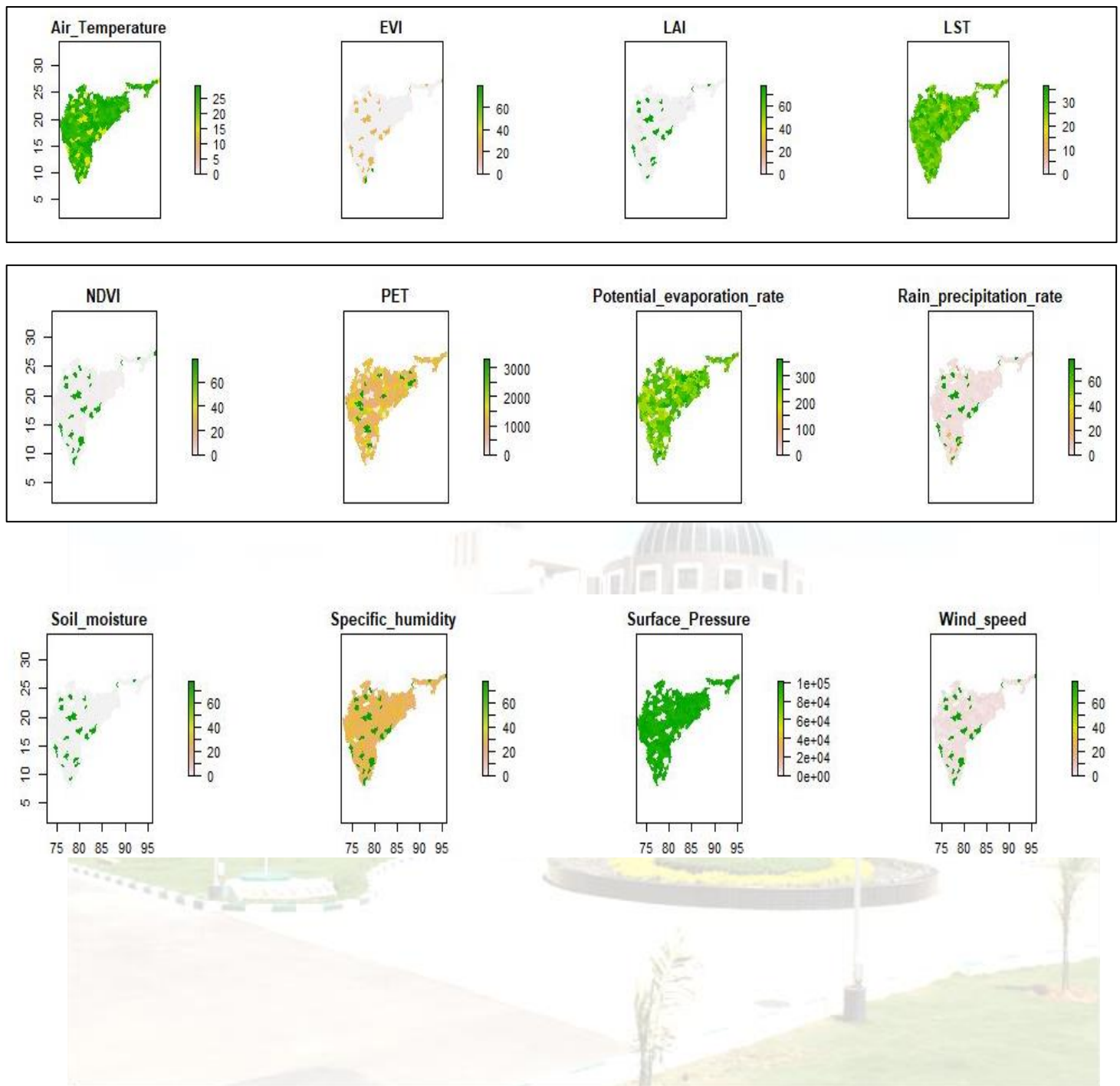
Risk map for Theileriosis in Haryana



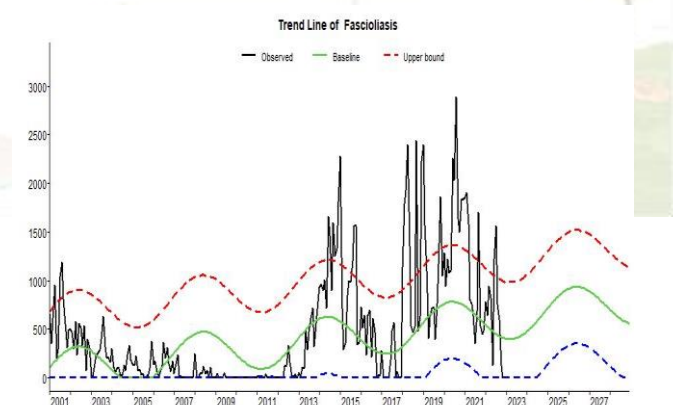
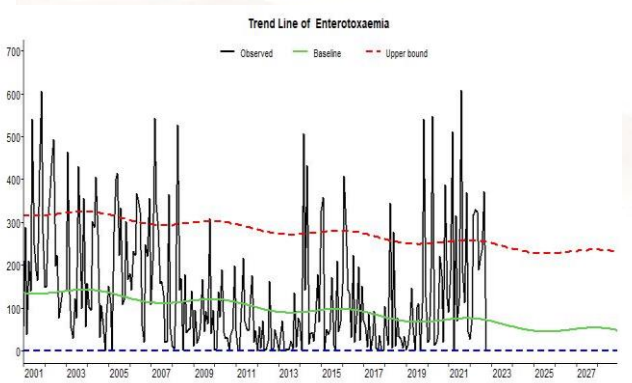
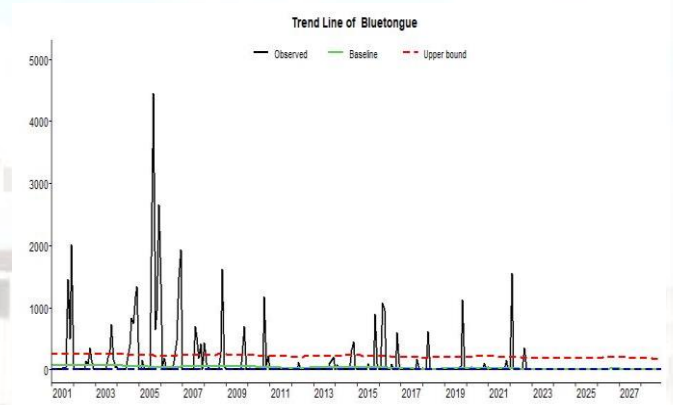
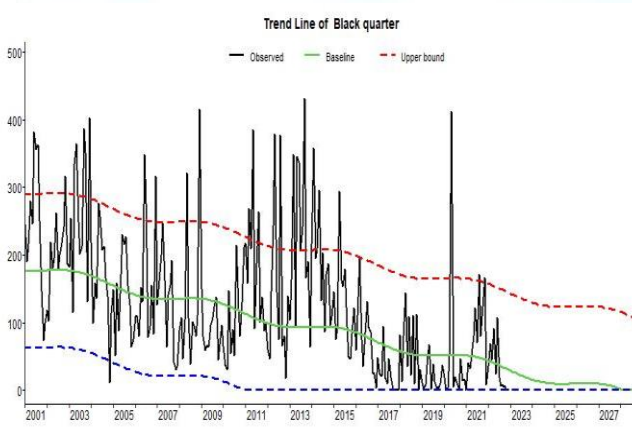
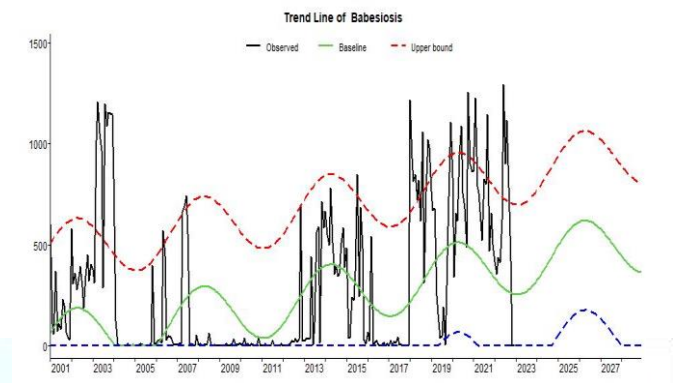
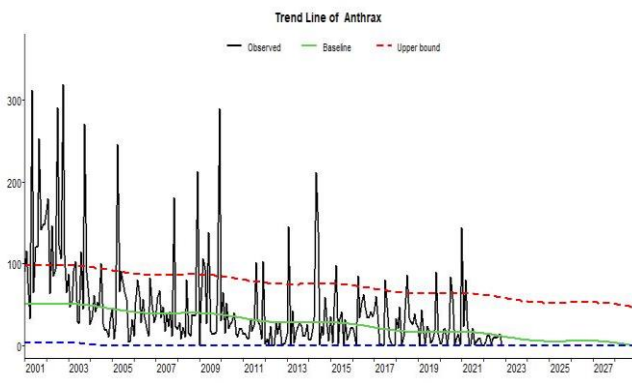
Risk map for Trypanosomiasis in Haryana

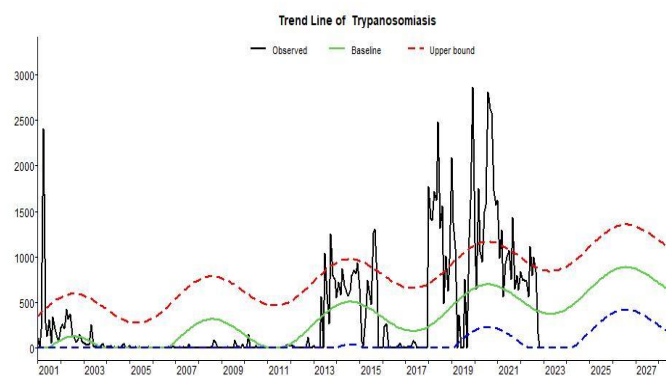
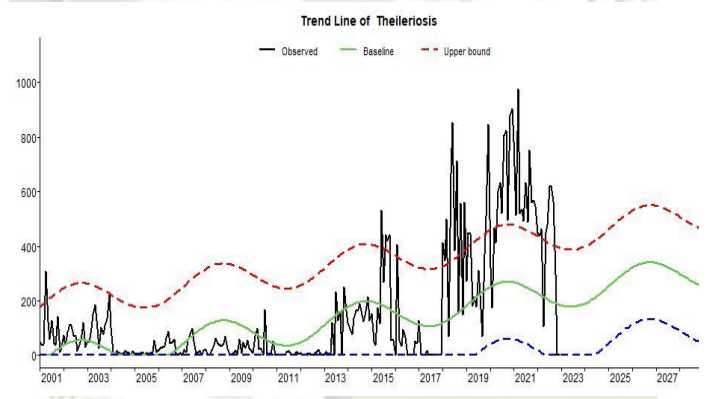
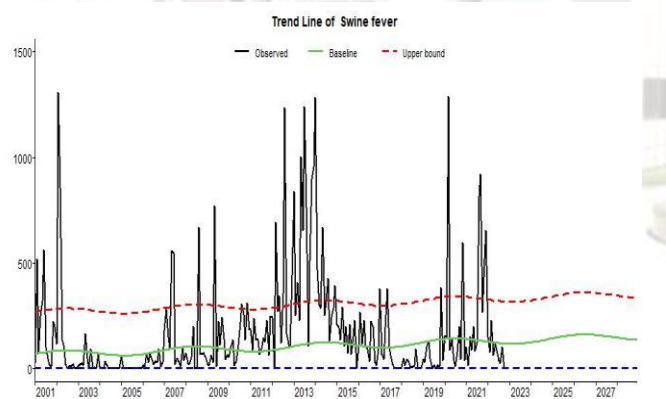
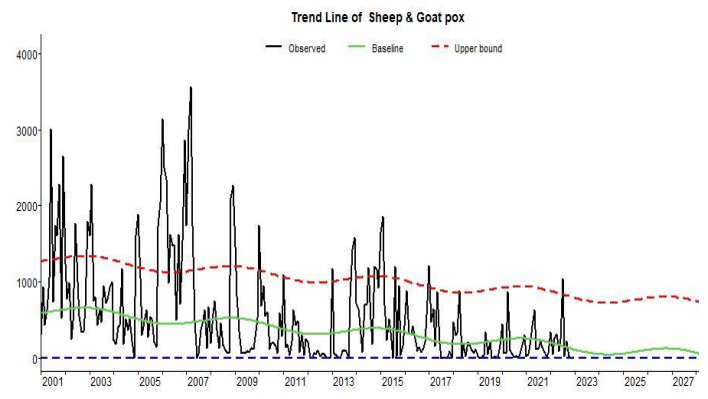
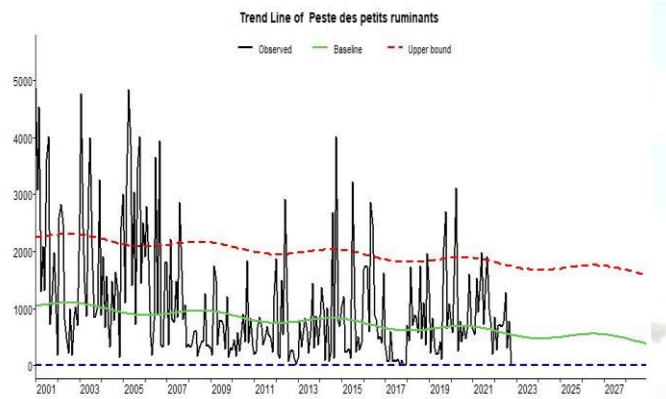
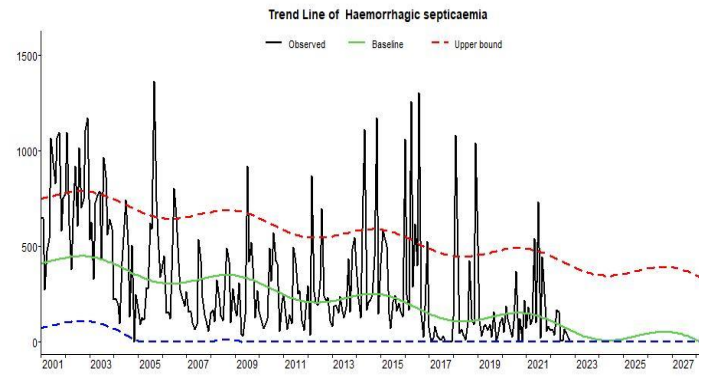
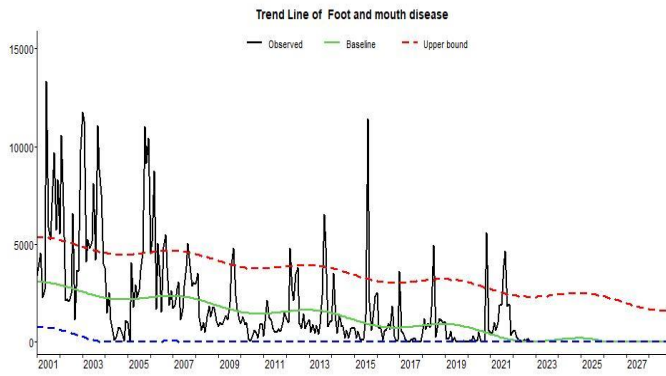


Effects of different parameters on Anthrax disease



11.4. Model based Periodic Regression Model 2023





12. APPLICATION OF META ANALYSIS FOR UNDERSTANDING THE DISEASE PREVALENCE

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RESEARCH ARTICLE

Open Access

Meta-analysis of classical swine fever prevalence in pigs in India: A 5-year study

S. S. Patil, K. P. Suresh, S. Saha, A. Prajapati, D. Hemadri and P. Roy

Indian Council of Agricultural Research - National Institute of Veterinary Epidemiology and Disease Informatics (ICAR-NIVEDI), PBNO-6450, Yelahanka, Bengaluru, Karnataka, India.

Corresponding author: S. S. Patil, e-mail: ss.patil@icar.gov.in

Co-authors: KPS: sureshkp97@gmail.com, SS: sneha.saha88@gmail.com, AP: avi75prajapati@gmail.com, DH: divakar.hemadri@gmail.com, PR: director.nivedi@icar.gov.in

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doi: 10.14202/vetworld.2018.297-303 **How to cite this article:** Patil SS, Suresh KP, Saha S, Prajapati A, Hemadri D, Roy P (2018) Meta-analysis of classical swine fever prevalence in pigs in India: A 5-year study, *Veterinary World*, 11(3): 297-303.

Abstract

Aim: The aim of the study was to determine the overall prevalence of classical swine fever (CSF) in pigs in India, through a systematic review and meta-analysis of published data.

Materials and Methods: Consortium for e-Resources in Agriculture, India, Google Scholar, PubMed, annual reports of All India Coordinated Research Project on Animal Disease Monitoring and Surveillance, and All India Animal Disease database of NIVEDI (NADRES) were used for searching and retrieval of CSF prevalence data (seroprevalence, virus antigen, and virus nucleic acid detection) in India using a search strategy combining keywords and related database-specific subject terms from January 2011 to December 2015 in English only.

Results: A total of 22 data reports containing 6,158 samples size from 18 states of India were used for the quantitative synthesis, and overall 37% (95% confidence interval [CI]=0.24, 0.51) CSF prevalence in India was estimated. The data were classified into 4 different geographical zones of the country: 20% (95% CI=0.05, 0.55), 31% (95% CI=0.18, 0.47), 55% (95% CI=0.32, 0.76), and 34% (95% CI=0.14, 0.62). CSF prevalence was estimated in northern, eastern, western, and southern regions, respectively.

Conclusion: This study indicates that overall prevalence of CSF in India is much lower than individual published reports.

Keywords: Classical swine fever, India, meta-analysis, pigs, prevalence.



Meta-analysis of the prevalence of livestock diseases in North Eastern Region of India

Nagendra Nath Barman¹, Sharanagouda S. Patil², Rashmi Kurli³, Pankaj Deka¹, Durlav Prasad Bora¹, Giti Deka¹,
Kempanahalli M. Ranjitha², Channappagowda Shivaranjini², Parimal Roy⁴ and Kuralayanapalya P. Suresh³

1. Department of Veterinary Microbiology, College of Veterinary Science, Assam Agriculture University, Guwahati, Assam, India; 2. Department of Virology, ICAR-National Institute of Veterinary Epidemiology and Disease Informatics, Bengaluru, Karnataka, India; 3. Department of Spatial Epidemiology, ICAR-National Institute of Veterinary Epidemiology and Disease Informatics, Bengaluru, Karnataka, India; 4. Director, ICAR-National Institute of Veterinary Epidemiology and Disease Informatics, Bengaluru, Karnataka, India.

Corresponding author: Kuralayanapalya P. Suresh, e-mail: sureshkp97@gmail.com

Co-authors: NNB: nnbarman@gmail.com, SSP: ss.patil@icar.gov.in, RK: rashmikurli@yahoo.in, PD: drpankajaau@gmail.com, DPB: drdpbora@gmail.com, GD: gitideka8906@gmail.com, KMR: ranjuckm10@gmail.com, CS: shivaranjinicveena@gmail.com, PR: director.nivedi@icar.gov.in

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Abstract

Aim: The study aimed to determine the overall prevalence of livestock diseases in North Eastern Region (NER) of India, through a systematic review and meta-analysis of published data.

Materials and Methods: The articles used for the study were retrieved from PubMed, J-Gate Plus, Indian Journals, and Google scholar, R open-source scripting software 3.4.3. Metafor, Meta. The Chi-square test was conducted to assess for the heterogeneity, forest plot (confidence interval [CI] plot) is a method utilized to present the results of meta-analysis, displaying effect estimate and their CIs for each study were used for searching and retrieval of livestock diseases prevalence data in India using a search strategy combining keywords and related database-specific subject terms from 2008 to 2017 in English only.

Results: The prevalence of various livestock diseases are foot-and-mouth disease (21%), bluetongue (28%), brucellosis in bovine (17%), brucellosis in caprine (2%), brucellosis in porcine (18%), brucellosis in sheep and goat (3%), babesiosis (6%), theileriosis (26%), porcine reproductive and respiratory syndrome (1%), porcine cysticercosis (6%), classical swine fever (31%), *Porcine circovirus* (43%), and Peste des petits ruminants (15%). This information helps policymakers to take appropriate measures to reduce the disease burden.

Conclusion: This study indicates that the overall prevalence of various livestock diseases in NER of India.

Keywords: babesiosis, brucellosis, classical swine fever, foot-and-mouth disease, forest plot, livestock, meta-analysis, North Eastern regions, Peste des petits ruminants, *Porcine circovirus*, porcine cysticercosis, porcine reproductive and respiratory syndrome, prevalence, seroprevalence, theileriosis.



Review Article

Peste Des Petits Ruminants in Atypical Hosts and Wildlife: Systematic Review and Meta-Analysis of the Prevalence between 2001 and 2021

Sowjanya Kumari, S^{1,2}, Bhavya, A. P¹, Akshata, N¹, Kumar, K, V¹, Bokade, P. P¹, Suresh, K. P¹, Shome, B. R¹, Balamurugan, V^{1*}

1. Indian Council of Agricultural Research, National Institute of Veterinary Epidemiology and Disease Informatics (ICAR-NIVEDI), Yelahanka, Bengaluru, Karnataka, India

2. Department of Microbiology, Jain University, Bengaluru, Karnataka, India

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Corresponding Author: balavirol@gmail.com

Abstract

Peste des petits ruminants (PPR) or goat plague is considered a leading, highly contagious, and most lethal infectious viral disease of small ruminants affecting the worldwide livestock economy and international animal trade. Although sheep and goats are the primarily affected, the PPR Virus (PPRV) host range has expanded to other livestock (large ruminants) and wildlife animals over the last few decades, resulting in serious concern to the ongoing PPR global eradication program, which is primarily optimized, designed, and targeted towards accessible sheep and goat population. A systematic review and meta-analysis study was conducted to estimate the prevalence and spill-over infection of PPRV in large ruminants (bovine and camel) and wildlife. Published articles from 2001 to October 2021 on the "PPR" were searched in four electronic databases of PubMed, Scopus, Science direct, and Google Scholars. The articles were then selected using inclusion criteria (detection/prevalence of PPRV in bovine, camel, and wildlife population), exclusion criteria (only sheep or goats, lack of prevalence data, experimental trial, test evaluation, and reviews written in other languages or published before 2001), and the prevalence was estimated by random effect meta-analysis model. In the current study, all published articles belonged to Africa and Asia. The overall pooled prevalence of PPR estimates was 24% (95% CI: 15-33), with 30% in Asia (95% CI: 14-49) and 20% in Africa (95% CI: 11-30). The overall estimated pooled prevalence at an Africa-Asia level in bovine and camel was 13% (95% CI: 8-19), and in wildlife, it was 52% (95% CI: 30-74) with significant heterogeneity ($I^2 = 97\%$) in most pooled estimates with a high prevalence in atypical hosts and wildlife across Asia and Africa. Over the last two decades, the host range has increased drastically in the wildlife population, even for prevalent PPR in the unnatural hosts only for a short time, contributing to virus persistence in multi-host systems with an impact on PPR control and eradication program. This observation on the epidemiology of the PPRV in unnatural hosts demands appropriate intervention strategies, particularly at the livestock-wildlife interface.

Keywords: PPR; Bovine; Camel; Wildlife; Systemic Review; Meta-analysis; Prevalence

Web Link https://nivedi.res.in/Nadres_v2/bioinfo.php

13. APPLICATION OF BIOINFORMATICS FOR UNDERSTANDING THE DYNAMICS OF LIVESTOCK INFECTIOUS DISEASES

- a) **An extensive analysis of Codon usage pattern, Evolutionary rate and Phylogeographic reconstruction in Foot and mouth disease (FMD) serotypes (A, Asia 1 and O) of six major climatic zones of India: A Comparative study**

Abstract

Foot and mouth disease (FMD) is a major economically important viral disease of cloven mhoofed livestock globally. The FMD virus (FMDV) spreads widely in confined, cool and humid climatic conditions. Being an RNA virus, FMDV is genetically unstable, and its genome evolution is highly influenced by the mutational pressure. The climatic and environmental conditions have a significant impact on mutational pressure. The present study is a primary effort to establish a comprehensive relationship between climatic factors and molecular evolutionary pattern of serotypes FMDV circulating in India. In this study, isolates of three serotypes (A, Asia 1 and O) were selected from six major climatic zones of India (Montane, Humid subtropical, Tropical wet and dry, Tropical wet, Semi-arid and Arid). Based on the full genome nucleotide sequence data, the codon usage bias, evolutionary and phylogeographic analysis were carried out. The study revealed that the codon use bias indicators in the FMDV serotypes differed significantly depending on the climatic zones. It implies that the selection and mutational pressure influence the codon usage pattern indices (eNC, CAI, RCDI, GRAVY, Aromo), with mutational pressure taking precedence in determining the codon usage bias of the FMDV genome. The tMRCA was estimated to be 1960, 1956 and 1961 for Indian FMD virus serotype-A, Asia 1 and O respectively, which is around 17, 29 and 36 years before its actual identification in the field. Virus transmission across the region was evident from phylogeographic analysis. The integrated analysis of codon usage bias, evolutionary rate and phylogeography analysis signifies the major role of mutational and selection pressure, implying that the in FMD virus co-evolution and adaptations are highly influenced by the climatic/environmental factors.

- b) **Relative Analysis of Codon Usage and Nucleotide Bias between Anthrax Toxin Genes Subsist**

Inpxo1 Plasmid of *Bacillus Anthracis*

Abstract

Anthrax is an ancient and acute illness that affects a large quantity of animal species and is caused by a bacterium *Bacillus anthracis*, which is a rod-shaped, gram-positive and spore forming bacterium. Virulent forms of *B. anthracis* has two large pathogenicity related plasmids pXO1 and pXO2. pXO1 has the different anthrax toxin genes *cya*, *lef*, and *pagA* where as pXO2 has the genes accountable for capsule synthesis and degradation, *capA*, *capB*, *capC*, and *capD*. *B. anthracis* express its pathogenic activity mostly over the capsule and the manufacture of a toxic compound involving three proteins known as edema factor (EF), lethal factor (LF) and protective antigen (PA). These two enormous plasmids of *B. anthracis* are crucial for full pathogenicity, exclusion of either of the plasmids extremely weakens the malignity of *B. anthracis*. In the current study we conducted the relative analysis of the codon usage and nucleotide bias of virulent genes subsist in pXO1 plasmid of *B. anthracis*. Codon usage bias not only plays a substantial role at the extent of gene expression, but also supports to improve the efficacy and accurateness of translation. Codon usage pattern analysis of *B. anthracis* genome is essential for understanding the evolutionary characteristics in the different species. To examine the codon usage arrangement of the *B. anthracis* genome, Nucleotide sequences

of the virulent genes viz *cya*, *lef* and *pag* were collected from National Center for Biotechnology Information (NCBI). The correlations between GC3s, whole GC content, Effective No. of Codons (ENC), Codon Adaptation Index (CAI), Codon Bias Index (CBI), Frequency of Optimal Codons (FOP), General average hydropathicity (Gravy) and Aromaticity (Aroma), of the selected genes were determined. The ENC-plot i.e., ENC values vs GC3s, Pr2 plot i.e., relationship between $A3 / (A3 + T3)$ and $G3 / (G3 + C3)$, Neutrality plot i.e., GC12 versus GC3s, and the RSCU of the genes, all shows codon usage bias existence in all the virulent genes subsists in pXO1 plasmid of *B. anthracis* genome. These results express the codon usage bias existing in the pXO1 plasmid's virulent genes of *B. anthracis* genome could be utilized for further exploration on their evolutionary analysis as in design of primers, design of transgenes, determine of origin of species as well as prediction of gene expression level and gene function.

c) **Reverse vaccinology based *in silico* analysis of Epitope prediction in *cya*, *lef* and *pagA* genes from *Bacillus anthracis* against Anthrax infected species: An Immunoinformatics approach**

Abstract

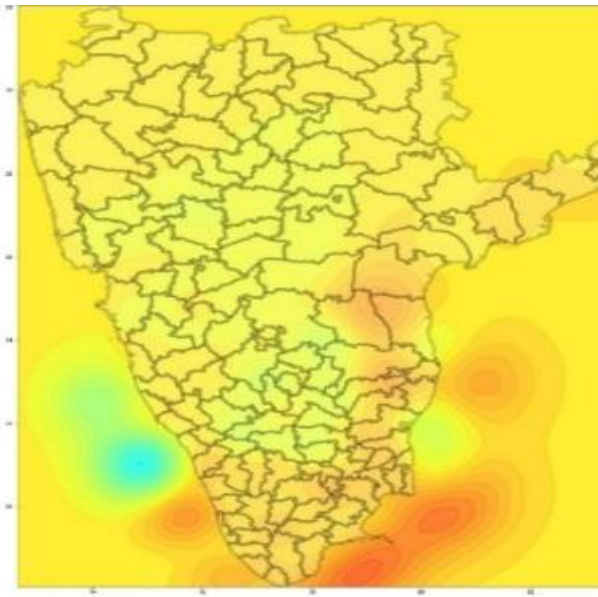
Bacillus anthracis is a Gram-positive spore-forming bacterium that causes the zoonotic disease: anthrax, an abrupt illness that disproportionately impacts grazing livestock and wild ruminants. Anthrax's geographical reach despite years of research on anthrax epizootic and epidemics behaviour, to date, remains to be elucidated. Existing therapeutics, however, are ineffective in combating this infectious disease, necessitating the development of a better vaccine to pause the pandemic using immunoinformatics approaches, this study intended to predict an efficient epitope for a vaccine against anthrax in animals and humans of the toxin genes such as *cya*, *lef* and *pagA* of *B. anthracis* against anthrax. The B-cell and T-cell epitopes were predicted utilizing various bioinformatics tools/software and docking analysis was performed. Consequently, it was found that the evaluated epitopes had no allergenicity, no toxicity and had high antigenicity that provides an effectual and most rapid technique to estimate peptide synthetic vaccines to impede anthrax.



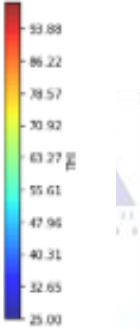
14. IMPACT OF CLIMATE CHANGE ON LIVESTOCK DISEASE INCIDENCE

14.1 Southern StatesTemperature Humidity Index (THI) 2001-2021

THI for 2001



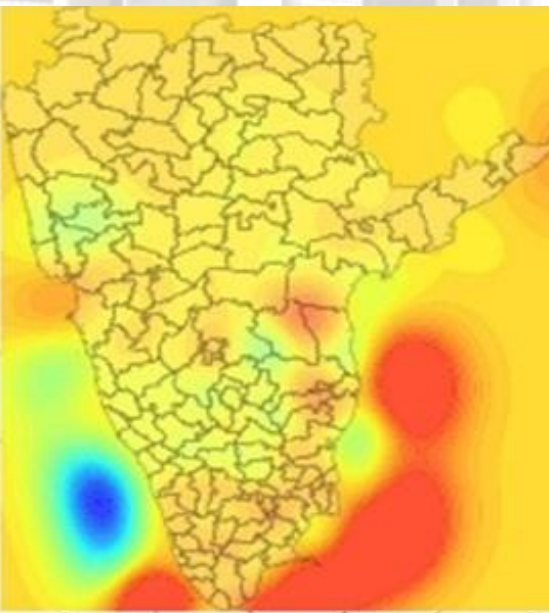
THI for 2011



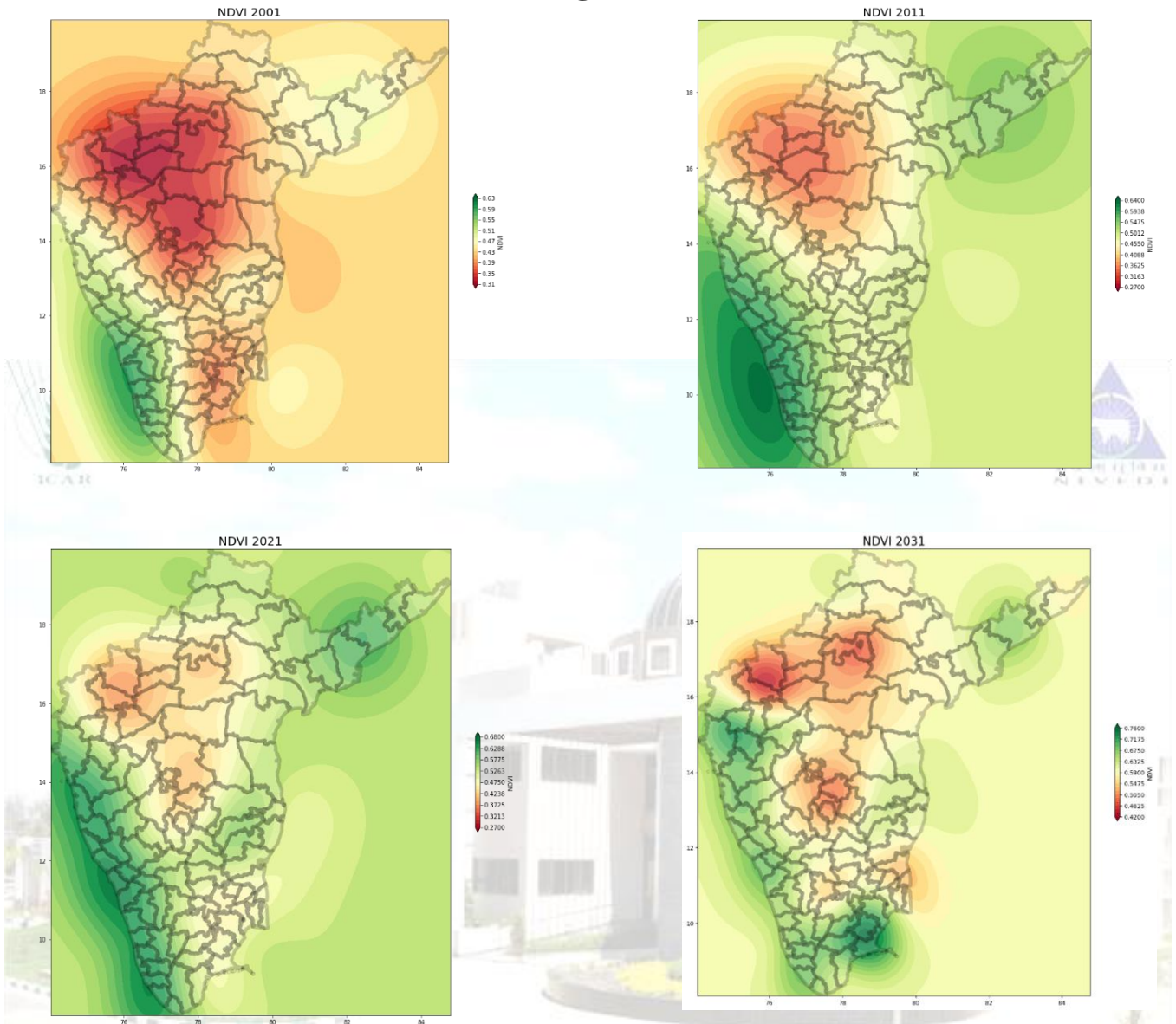
THI for 2021



THI for 2023 (Predicted)

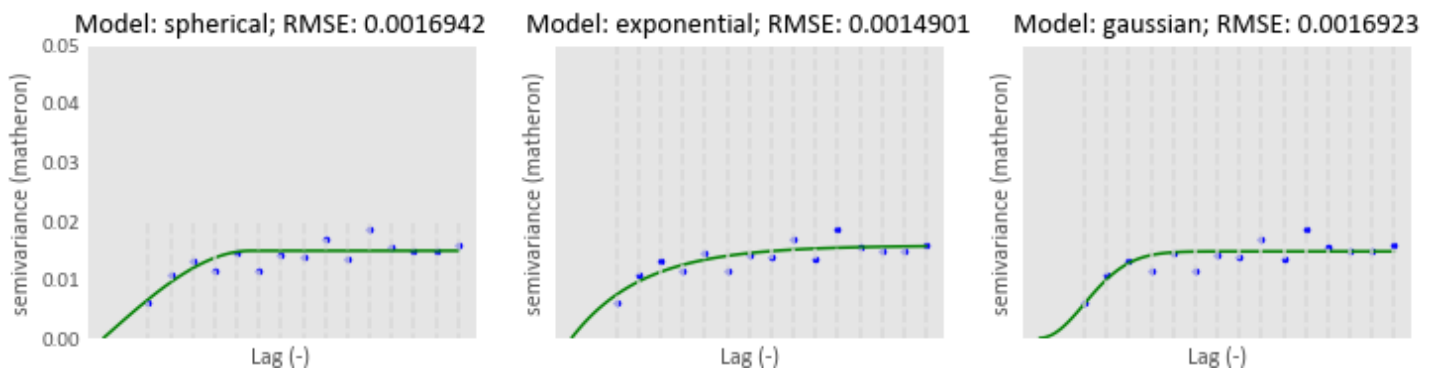


14.2. Southern States Normalized Difference Vegetation Index (NDVI)

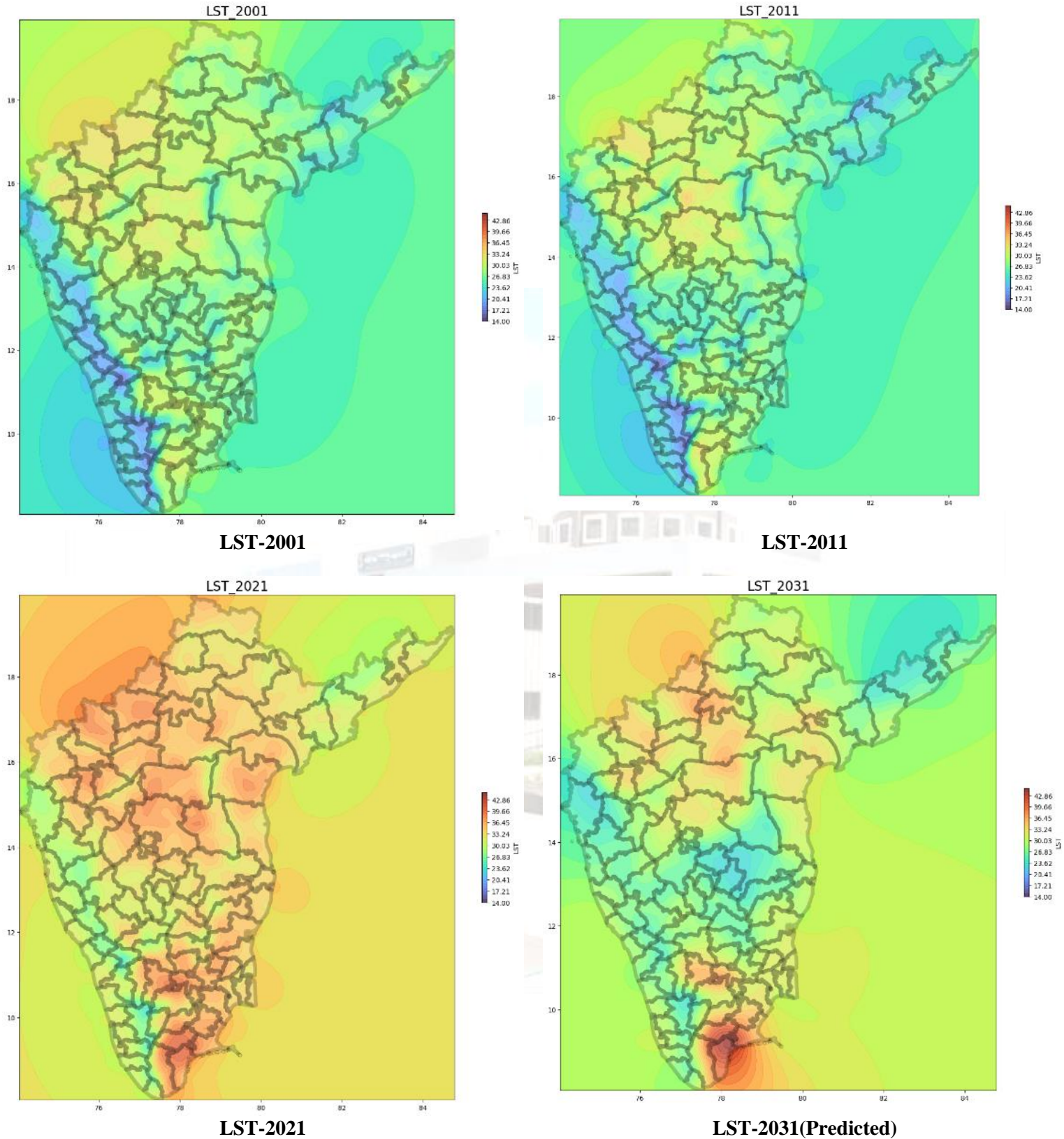


Best fit Variogram model for NDVI:

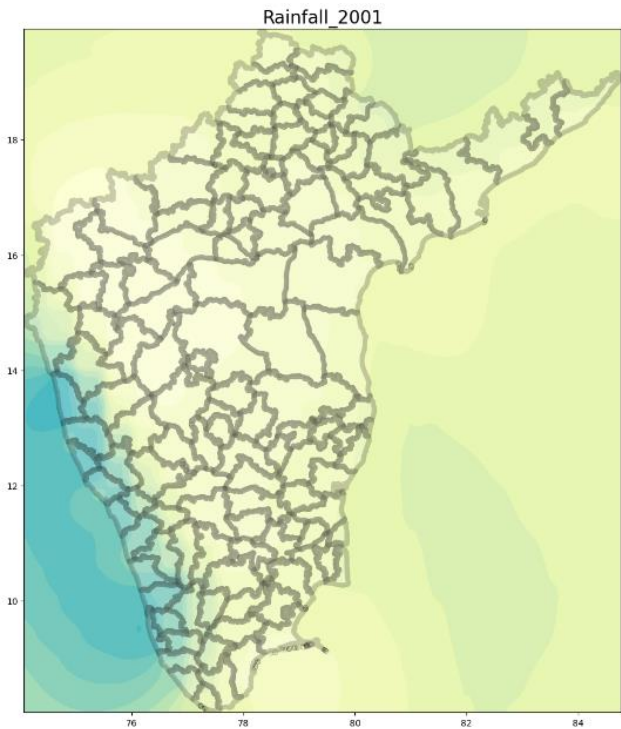
After comparing various variogram models, we could choose the one that would fit kriging the best based on the RMSE value. Based on the result with the lowest RMSE, we may say that the exponential model was best specified.



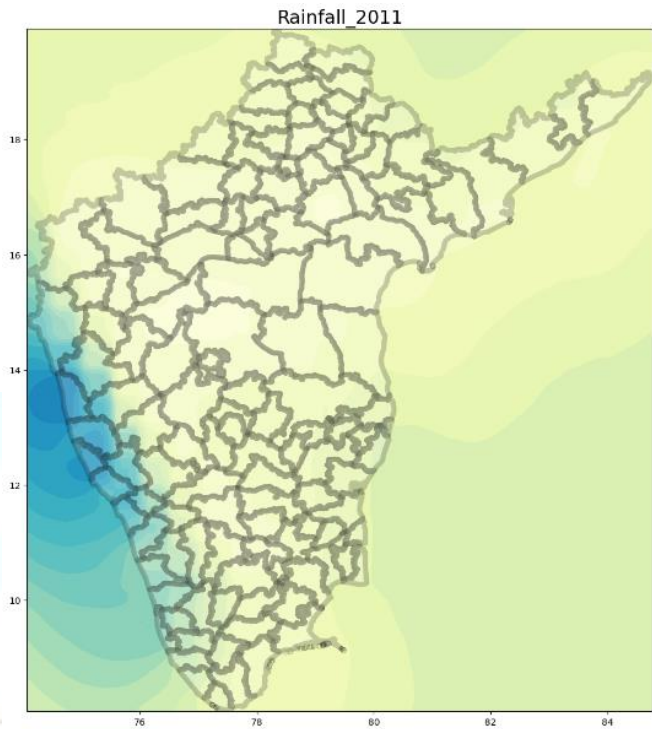
14.3 Land Surface Temperature (LST) - 2001-2031



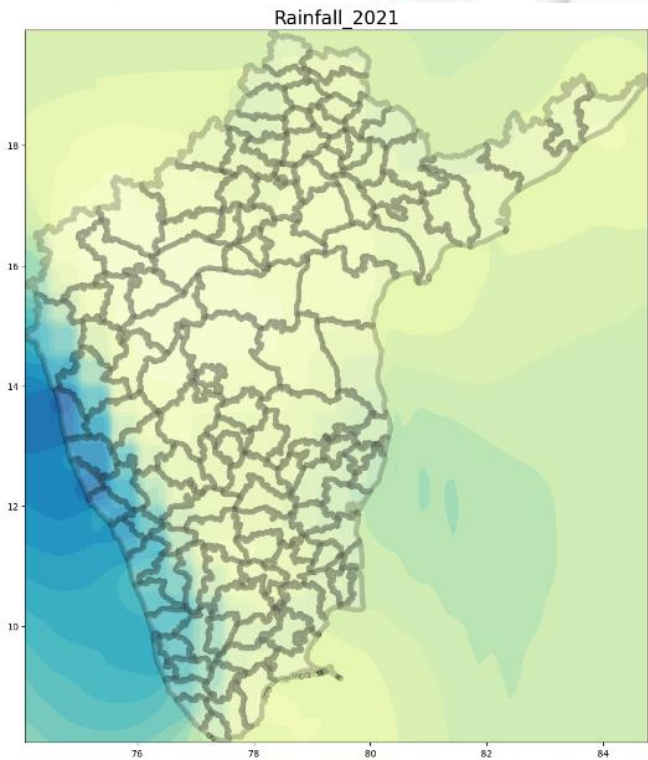
14.4 Rainfall - 2001-2031



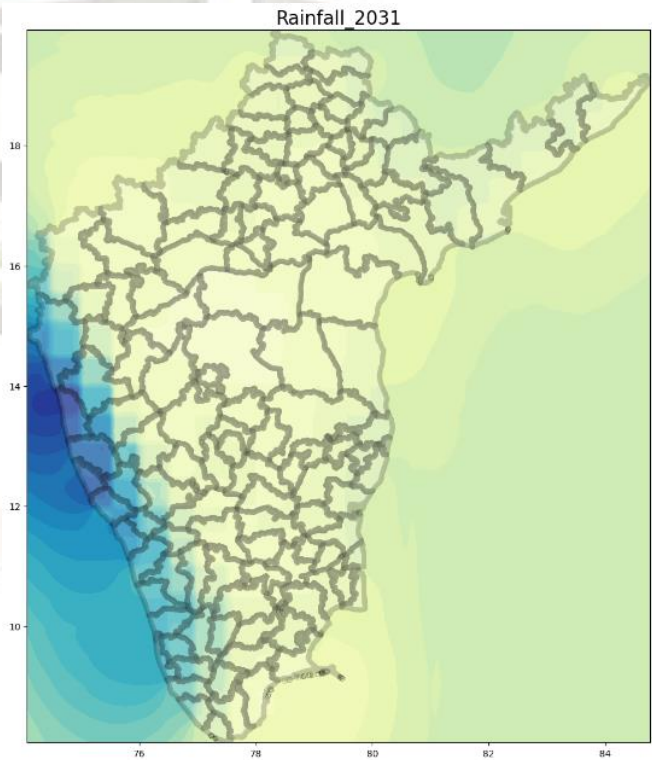
Rainfall 2001



Rainfall 2011

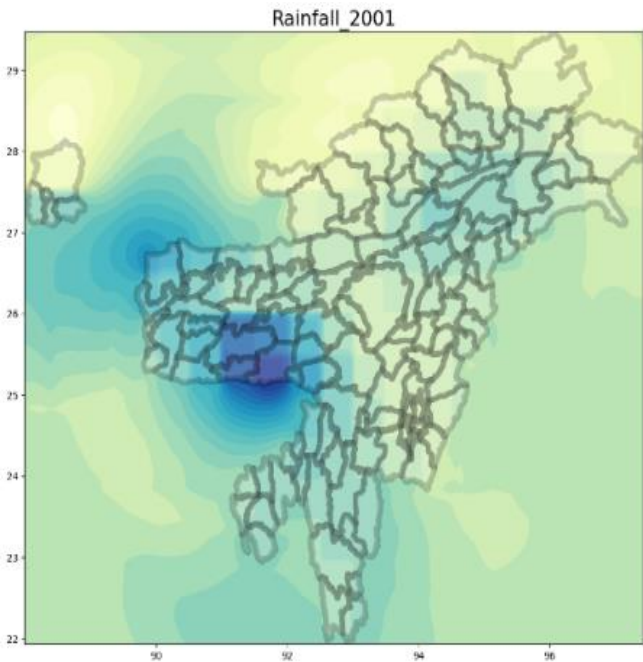


Rainfall 2021

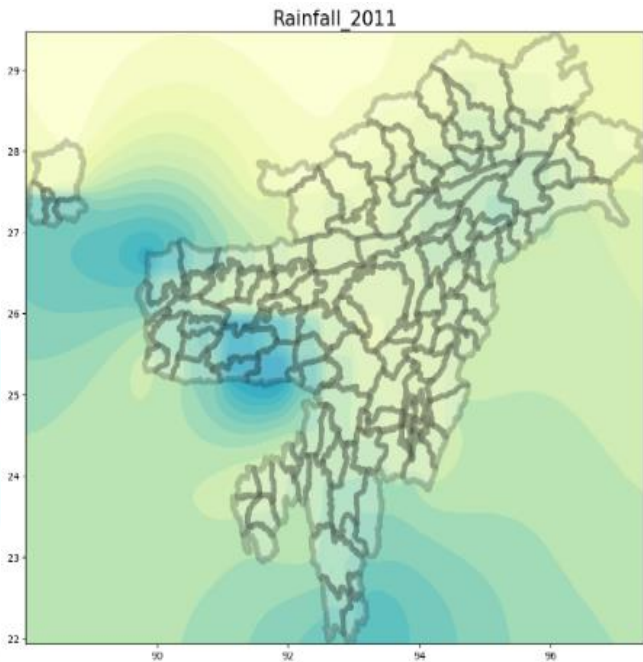


Rainfall 2031 (Predicted)

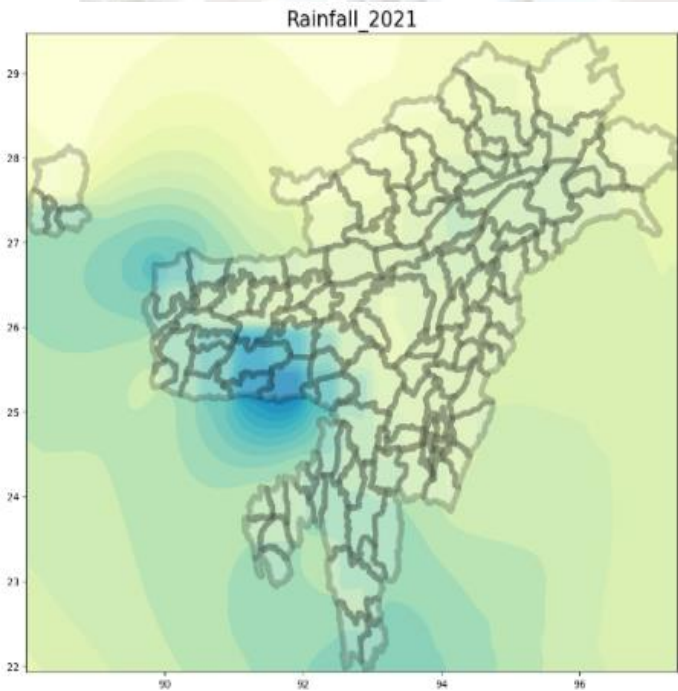
14.5 Rainfal NER 2001-2031



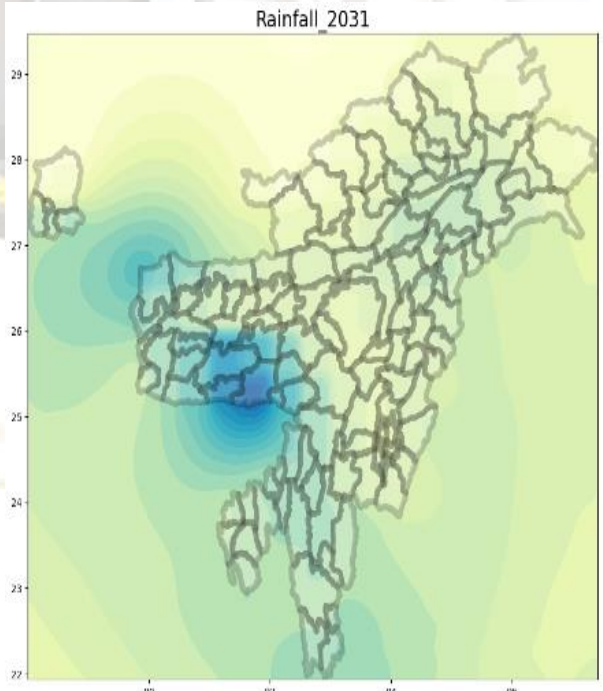
Rainfall 2001



Rainfall 2011

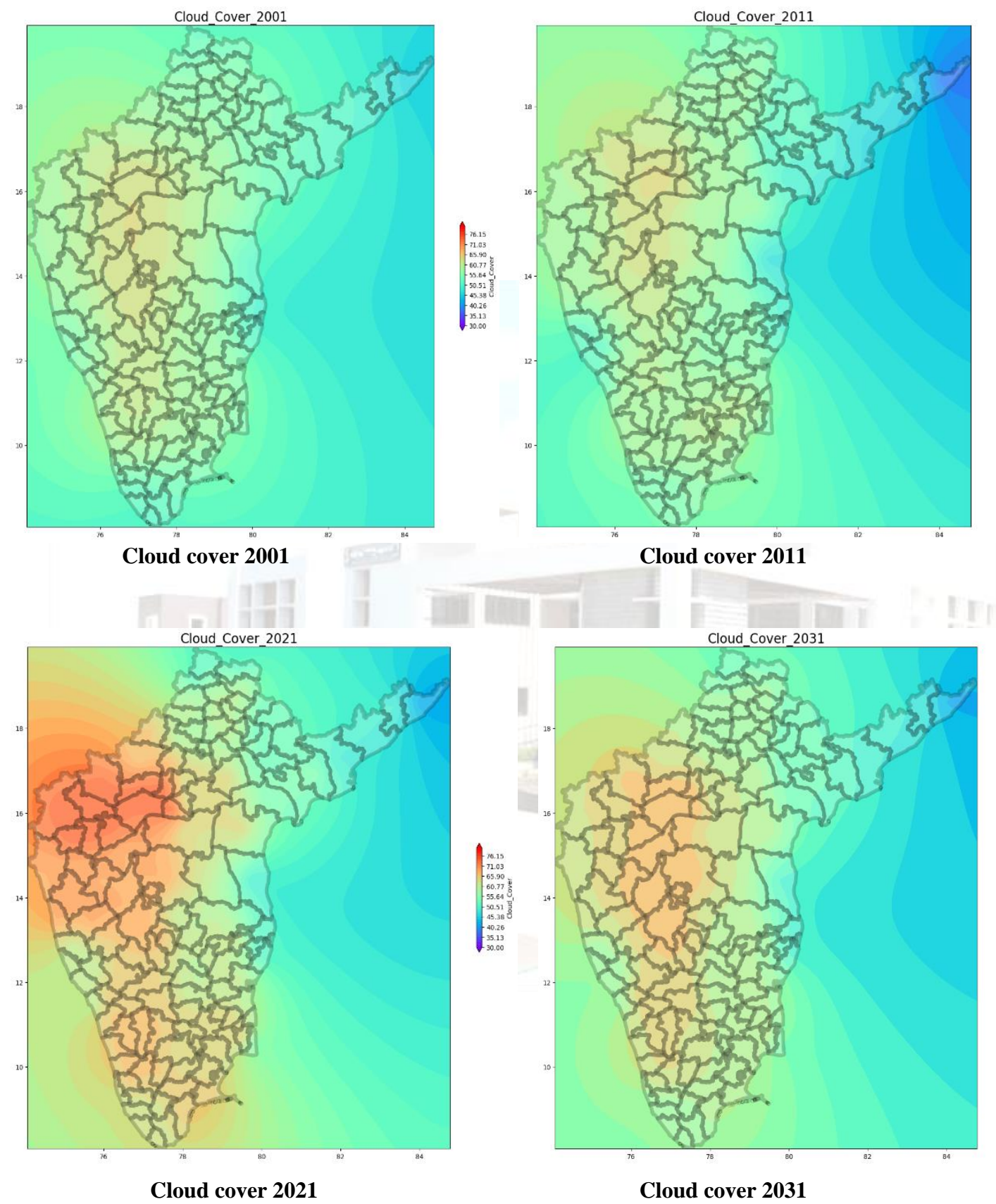


Rainfall 2021

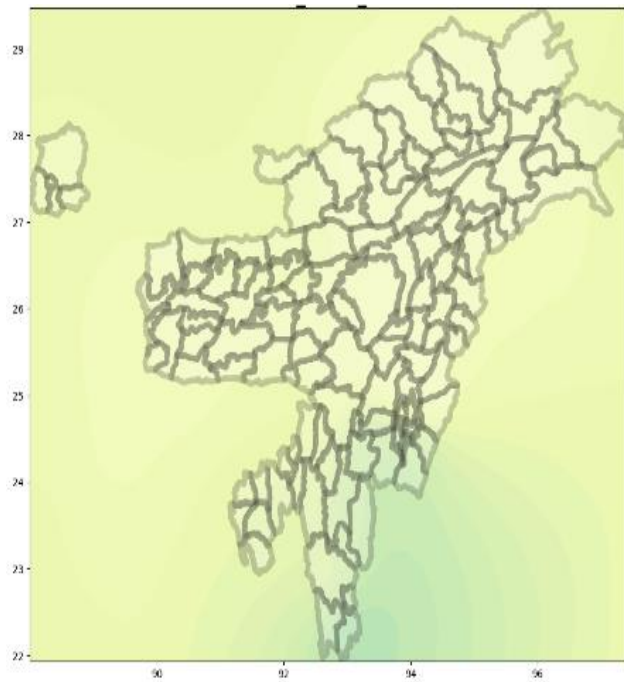


Rainfall 2031(Predicted)

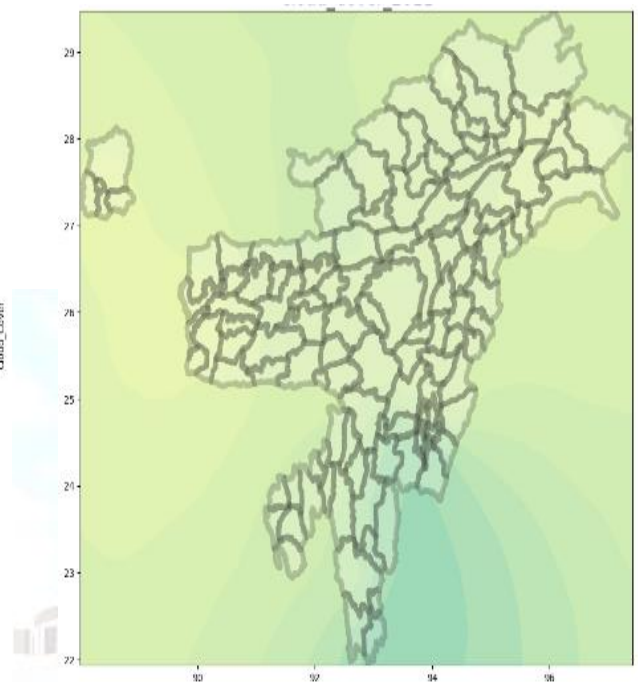
14.6 Cloud cover – 2001-2031



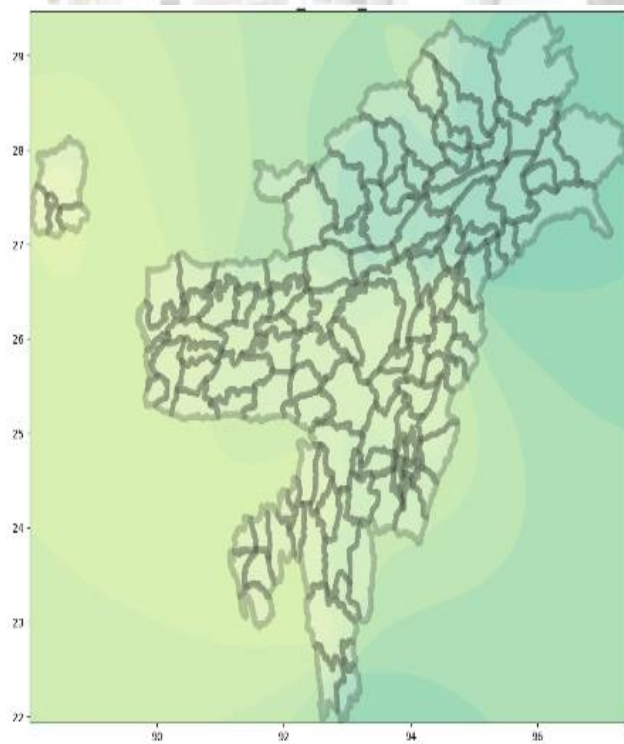
14.7 Cloud cover NER 2001-2031



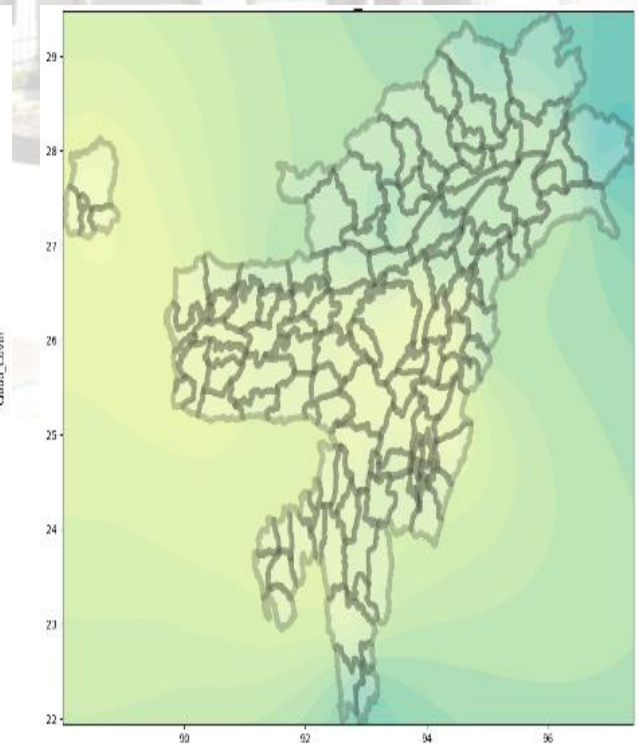
Cloudcover – 2001



Cloudcover - 2011



Cloudcover- 2021



Cloudcover- 2031

Kriging Results

Models:

- **Ordinary Kriging:** Ordinary Kriging is a spatial estimation method where the error variance is minimized
- **variogram_model:** Gaussian Model
 $p \cdot (1 - e^{-d^2/(47r)^2}) + n$

Variables are defined as:

dd = distance values at which to calculate the variogram

pp = partial sill (psill = sill - nugget)

rr = range

nn = nugget

ss = scaling factor or slope

ee = exponent for power model

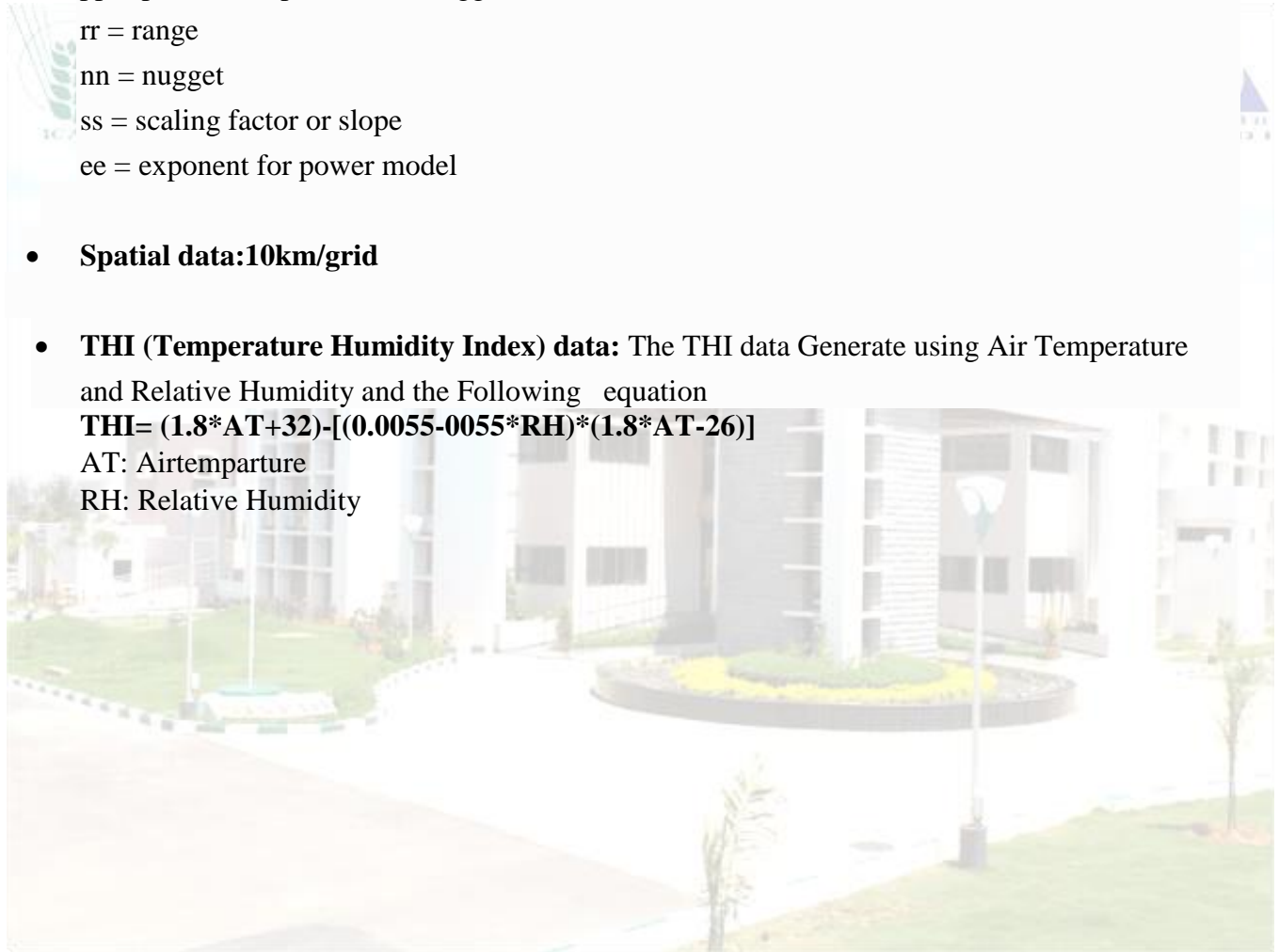
- **Spatial data:10km/grid**

- **THI (Temperature Humidity Index) data:** The THI data Generate using Air Temperature and Relative Humidity and the Following equation

$$\text{THI} = (1.8 \cdot \text{AT} + 32) - [(0.0055 - 0.0055 \cdot \text{RH}) \cdot (1.8 \cdot \text{AT} - 26)]$$

AT: Airtemparture

RH: Relative Humidity



APPENDIX

Abbreviations

NADRES : National Animal Disease Referral Expert System

R : R environment for statistical computing

BQ : Black Quarter

BT : Bluetongue

CSF : Classical Swine Fever

ET : Enterotoxaemia

FMD : Foot and Mouth disease

HS : Haemorrhagic Septicaemia

PPR : Peste des Petits Ruminants

SGP : Sheep and Goat pox

hPa : Hectopascals

NR : No risk/No data available

VLR : Very low risk

LR : Low risk

MR : Moderate risk

HR : High risk

VHR : Very high risk



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ICAR-National Institute of Veterinary Epidemiology and Disease Informatics (ICAR_NIVEDI),

P. B. No.6450, Yelahanka, Bengaluru-560064

Phone: +91-80-23093111, Fax: +91-80-23093222, E-mail: director.nivedi@icar.gov.in