

January 2024, Volume 12, Issue 01



## LIVESTOCK DISEASE FOREWARNING METHODOLOGY

Powered by Artificial Intelligence & Machine Learning

ICAR – NATIONAL INSTITUTE OF  
VETERINARY EPIDEMIOLOGY AND  
DISEASE INFORMATICS  
(ICAR – NIVEDI)



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**MARCH**  
**2024**

**NOW LINKED WITH FARMER REGISTRATION  
AND UNIFIED BENEFICIARY INFORMATION  
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# 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  
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# TABLE OF CONTENT

SI No	Content	Page Number
1	About the Methodology	1
2	Summary of the Forewarning Methodology	2-3
3	Introduction to NADRES v <sub>2</sub>	4-5
4	Forewarning Methodology	6
	I. Material	6
	II. NADRES v <sub>2</sub> Data flow and AI Based Data capturing diagram	9
	III. Weighted outbreak score	10
	IV. Features extraction and Data engineering	10
	V. Forecasting of weather parameters	10
	VI. Implementation of Principal Component Analysis	11
	VII. Machine Learning Models	11
5	Accuracy of Prediction	13
6	Moran's I for clustering of Livestock diseases	14
7	R Software	14
8	Forewarning of livestock disease for the month of January, 2024	15
	I. Diseases, Species affected, clinical signs and its preventive measures	15-19
	II. Forecasting of Remote Sensing and Metrological Parameters, till 2025 (Ex, Karnataka)	20-21
	III. Significant Weather Parameters Table	22
9	Post prediction Validation	23-30
	I. Correlational Assessment	31
10	A.Launch of Mobile Android app. & link to download	32-33
	B. The ADMAC_PDDES (Pig Disease Diagnosis Expert System) mobile app.	34
11	I. Model based hot spot area maps of Livestock infectious disease in India	35-40
	II. Model based FMD district wise Risk map(2000-2023)	41-46
	III.Model based Foot rot district wise Risk map (2001-2019)	46
	IV. Model based outbreak/incidence maps of Livestock disease in india	47-50
	V. Model based risk maps of Livestock infectious disease in India	51-57
	VI. Model based Periodic Regression Model 2023	58-59
12	Application of Meta-Analysis for understanding the disease burden	60-62
13	Application of Bioinformatics for understanding the dynamics of Livestock Infectious Disease	63-64
14	Impact of climate change on livestock disease incidence	65-76
	I. Southern States Temperature Humidity Index (THI) 2001-2021	65
	II. Southern States Normalized Difference Vegetation Index (NDVI)	66
	III. Land Surface Temperature (LST) - 2001-2031	67
	IV. Rainfall - 2001-2031	68
	V. Rainfall NER 2001-2031	69
	VI. Cloud cover 2001-2031	70
	VII. Cloud cover NER 2001-2031	71
	VIII. THI for Aravalli Central Plateau & Hills 2001-2033 (Predicted)	72
15	Appendix	78
	a) Abbreviation	78
16	References	79
17	List of NADEN Centres and Investigators	80-82

## **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 15 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 5<sup>th</sup> 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 March 2024 revealed Jharkhand (199), Uttar Pradesh (89), and Karnataka (70) 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 FMD and PPR outbreaks whereas a higher number of LSD outbreaks are anticipated in Karnataka, and ASF outbreaks are predicted to be more in Mizoram. Moreover, the simultaneous presence of FMD and HS is likely to be observed in Assam, Gujarat, Haryana, Jharkhand, Karnataka, Kerala, Madhya Pradesh, Maharashtra, Odisha, Rajasthan, Tamil Nadu, Tripura, Uttar Pradesh, Uttarakhand and West Bengal. Among the different diseases in livestock, the predicted outbreaks are expected to be high for Babesiosis (87) and PPR (86).

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 March- 2024**

Sl. No	State Name	ASF	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	0	3	0	0	0	0	1	0	0	4
2	Andhra Pradesh	0	3	0	1	1	2	0	0	0	3	0	2	1	0	0	13
3	Arunachal Pradesh	1	0	0	0	0	2	0	4	1	0	0	0	1	0	0	9
4	Assam	2	0	7	12	0	4	5	5	1	8	3	6	1	1	0	55
5	Bihar	0	0	3	1	0	1	0	0	0	0	1	0	0	0	2	8
6	Chandigarh	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
7	Chhattisgarh	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	2
8	Delhi	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
9	Goa	0	0	2	0	0	0	0	0	0	1	0	0	1	1	0	5
10	Gujarat	0	0	0	0	0	0	0	1	3	1	0	1	2	0	1	9
11	Haryana	0	0	0	0	0	2	2	0	1	2	0	4	0	4	2	17
12	Himachal Pradesh	0	0	0	0	0	0	0	0	3	0	0	2	3	0	0	8
13	Jammu & Kashmir	0	0	0	0	0	0	0	0	0	0	0	0	10	0	0	10
14	Jharkhand	0	1	25	10	0	9	12	24	23	15	1	20	9	25	25	199
15	Karnataka	0	7	0	6	0	0	2	0	17	7	0	13	18	0	0	70
16	Kerala	3	1	11	0	0	2	0	0	4	5	7	5	0	13	0	51
17	Lakshadweep	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	2
18	Madhya Pradesh	0	0	0	0	0	1	0	0	2	3	0	1	0	0	0	7
19	Maharashtra	0	0	0	2	0	0	1	0	2	3	0	7	3	3	0	21
20	Manipur	0	0	0	3	0	2	1	4	0	0	0	0	2	0	0	12
21	Meghalaya	0	0	0	1	0	2	0	0	3	3	0	0	0	0	0	9
22	Mizoram	5	1	0	0	0	4	0	1	0	0	0	0	0	0	0	11
23	Nagaland	3	0	0	0	0	1	0	0	2	0	0	0	0	0	0	6
24	Odisha	0	1	1	2	0	0	0	1	3	3	0	4	0	1	2	18
25	Puducherry	0	0	1	0	0	0	0	1	0	1	0	0	1	0	0	4
26	Punjab	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
27	Rajasthan	2	0	0	0	0	1	3	1	4	5	0	5	0	0	0	21
28	Sikkim	3	0	2	0	0	3	0	0	0	0	0	0	0	1	0	9
29	Tamil Nadu	2	3	0	2	0	1	0	0	1	4	1	2	7	0	0	23
30	Telangana	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
31	Tripura	0	1	3	2	0	2	0	5	3	5	0	1	5	0	0	27
32	Uttar Pradesh	0	0	29	0	0	0	0	3	2	1	0	1	0	20	33	89
33	Uttarakhand	0	0	0	1	0	0	0	0	1	2	0	1	0	0	0	5
34	West Bengal	0	0	3	6	0	0	0	2	3	3	0	10	1	8	2	38
<b>Total number of districts likely for risk of disease</b>		<b>21</b>	<b>19</b>	<b>87</b>	<b>49</b>	<b>1</b>	<b>40</b>	<b>26</b>	<b>55</b>	<b>81</b>	<b>77</b>	<b>13</b>	<b>86</b>	<b>67</b>	<b>77</b>	<b>67</b>	<b>766</b>



### 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=13) 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 18 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 15 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 15 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 15 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.

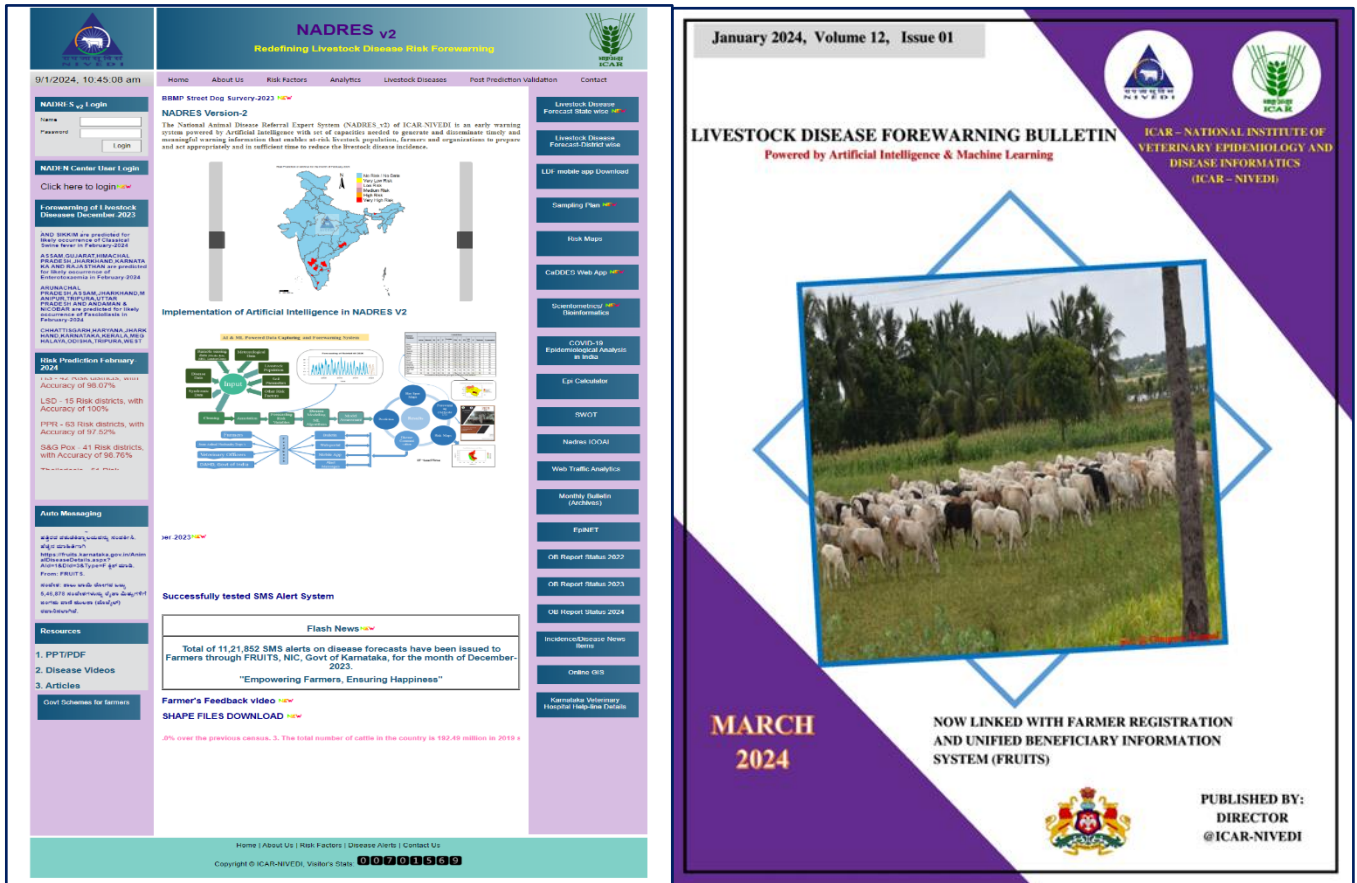


Fig 3.1.NADRES V<sub>2</sub> Home page

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 23 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 15 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 v<sub>2</sub> 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 20<sup>th</sup> 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
<b>Total Livestock</b>			<b>512056</b>	<b>536761</b>	<b>4.8</b>

### **Meteorological and Remotely Sensed Data:**

The parameters such as air temperature ( $^{\circ}\text{C}$ ), perceptible water (mm), Precipitation rate (mm), pressure (millibar), relative humidity (%), Vwind (m/s), Uwind (m/s), Soil temperature ( $^{\circ}\text{C}$ ), Vapour pressure(hPa), Wet day frequency, 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;

<b>PRODUCT</b>	<b>Science Data Sets (HDF Layers)</b>
<b>MOD15A2H</b>	Lai_500m (Leaf area index) 8 days average
<b>MOD16A2</b>	PET_500m (Total Potential Evapotranspiration) 8 days average
<b>MOD11A2</b>	LST_Day_1km (Daytime Land Surface Temperature) 8 days average
<b>MOD13A1</b>	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 (m/s) 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.

### **Delta-Weather parameter**

In the context of the National Animal Disease Referral and Export System (NADRES), made significant strides by enhancing database capabilities. original "Static Set" covered a 10-year average of 23 weather parameters from 2011 to 2022. Now, took a bold step forward, introducing a more intricate analysis. The upgraded "Static Set" remains the foundation but with a notable addition. Alongside the initial 23 parameters, we have included another set of 23 parameters known as "Delta" variables. These represent the differences between corresponding weather parameters from 2001 to 2021. This detailed differencing process offers valuable insights into long-term trends in meteorological conditions, especially relevant to understanding animal disease dynamics. In addition, we have introduced the "Dynamic Set" bringing another layer of sophistication. This set focuses on a more recent timeframe, using 2-year averaged parameter values for 2023 and 2024. Derived from data spanning from 2018 to 2023, the Dynamic Set also includes 23 "Delta" parameters, reflecting ongoing changes in climatic trends.

This dynamic approach ensures that NADRES stays updated with the latest meteorological patterns, crucial for timely responses in the early detection of animal diseases. With a total of 46 parameters now, this upgraded database is a cornerstone for NADRES. The integration of static and dynamic perspectives solidifies our position in meteorological analysis. NADRES is a reliable tool for animal disease management and a vital resource for informed decision-making in the intricate landscape of animal disease referral and export processes.

Initially, two regression models and Seventeen machine learning models were applied to test their suitability to fit the data and in all, Fourteen models; two regression model (Generalized Linear Model (GLM), Generalized Additive Model (GAM), and twelve machine learning models, *viz.*, Gradient Boosting Machine Learning Algorithm (GBM), Random Forest (RF), Multivariate Adaptive Regression Splines (MARS), Extreme Gradient Boosting Machine (XGM), Support Vector Machine (SVM), Decision Trees (Tree\_prob), Least Absolute Shrinkage and Selection Operator (Lasso), Functional Data Analysis (FDA), Gaussian Process (GP), Neural Network (NN), Multinomial Logistic Regression (Multinom\_probs), and Kernel Support Vector Machine (KSVM) 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) Accuracy, Error Rate, Precision, Sensitivity, Specificity, F1 score, Log Loss, and Gini-Coefficient. 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:

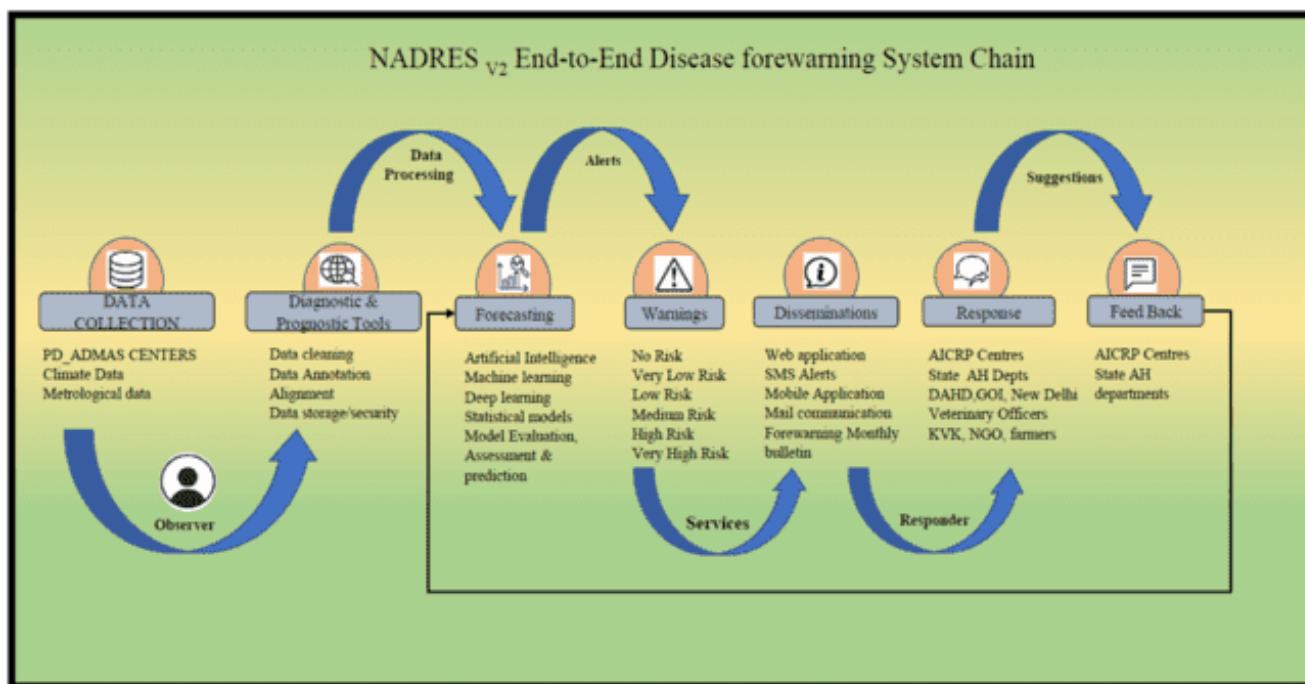


Fig 4.1. NADRES v2 Data Flow Diagram.

### B) Artificial Intelligence enabled Data Capturing and Forewarning System:

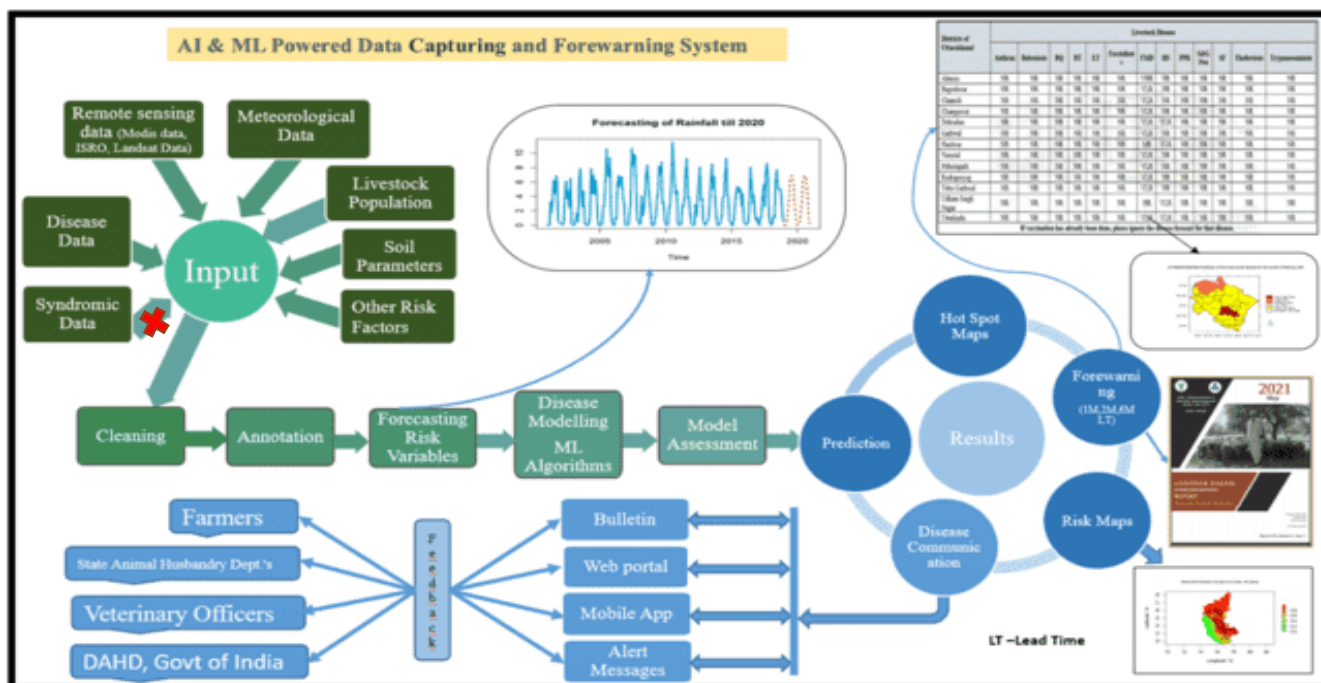


Fig 4.2. Data Capturing and Forewarning system

### 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 15 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.

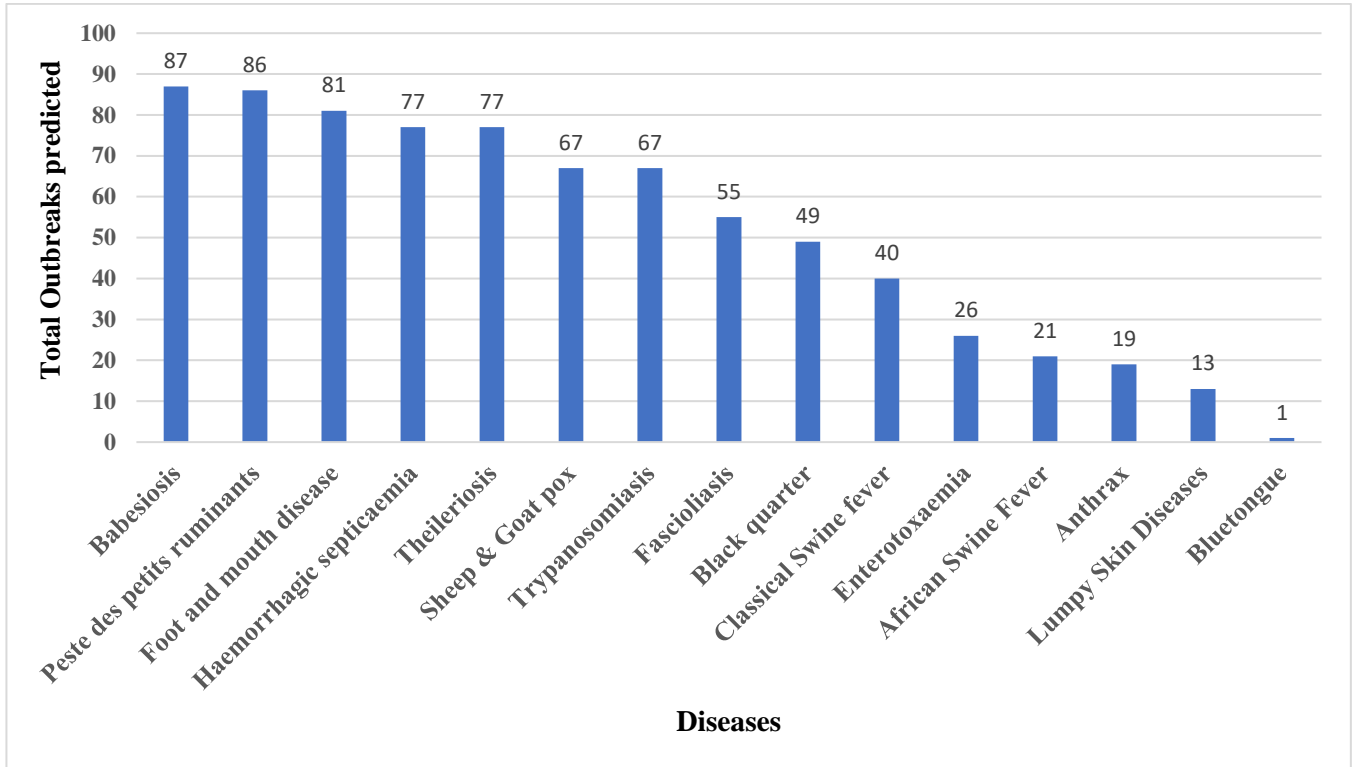


Fig 4.3. Top Fifteen livestock diseases (2024)

### 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](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,  $\phi$  and  $\theta$  are unknown parameters and  $\epsilon$  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 Seventeen 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), Classification Tree Analysis (CTA), Extreme Gradient Boosting Machine (XGM), Support Vector Machine (SVM), Decision Trees (Tree\_prob), Least Absolute Shrinkage and Selection Operator (Lasso), Functional Data Analysis (FDA), Gaussian Process (GP), Neural Network (NN), Multinomial Logistic Regression (Multinom\_probs), Kernel Support Vector Machine (KSVM), Ridge Regression, Naive Bayes 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), True Skill Statistics (TSS) Accuracy, Error\_rate, Precision, Sensitivity, Specificity, F1 score, Loglass, Gini-Coefficient. 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.	<b>Anthrax</b>	<b>100</b>
2.	<b>Babesiosis</b>	<b>99.45</b>
3.	<b>Black quarter</b>	<b>98.49</b>
4.	<b>Bluetongue</b>	<b>98.21</b>
5.	<b>Classical swine fever</b>	<b>99.59</b>
6.	<b>Enterotoxaemia</b>	<b>98.90</b>
7.	<b>Fasciolosis</b>	<b>99.73</b>
8.	<b>Foot and mouth disease</b>	<b>99.18</b>
9.	<b>Haemorrhagic septicaemia</b>	<b>96.15</b>
10.	<b>Lumpy skin disease</b>	<b>94.09</b>
11.	<b>Peste des petits ruminants</b>	<b>99.86</b>
12.	<b>Sheep &amp; Goat pox</b>	<b>97.25</b>
13.	<b>Theileriosis</b>	<b>97.39</b>
14.	<b>Trypanosomosis</b>	<b>98.76</b>

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 3.6.2 (version 3.6.2, R Foundation for Statistical Computing, Dark and Stormy Night. <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 JANUARY, 2024

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

Sl No.	Disease	Species Affected	Clinical Signs	Preventive Measures
1.	African Swine Fever (ASF)	Primarily affects domestic and wild pigs	High Fever, Lethargy and Weakness, Red or Blue Skin Discoloration, Pig display respiratory signs such as coughing, difficulty breathing, and nasal discharge, causes digestive symptoms, including diarrhea and vomiting.	involves strict measures like isolating new pigs, regularly disinfecting facilities, and controlling the movement of pigs and pig-related items. Early detection through surveillance, educating farm personnel, and managing wild boar populations are crucial, while proper disposal of infected material and quick reporting of suspected cases contribute to effective prevention and control. Collaboration among authorities, farmers, and the public, along with clear communication about ASF and its preventive measures, plays a key role in safeguarding pig populations and the swine industry.
2.	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.
3.	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.
4.	Black Quarter (BQ)	Common disease of cattle and sheep, but occasionally goats and pigs	High fever and lameness followed by swelling in the neck, shoulder, lumbar, gluteal and	Affected animals may be treated with suitable antibiotics. Vaccination to be done in consultation with the veterinarians and as decided by state animal

		also suffer from the disease.	sacral regions. Skin over the affected area become dark and crepitate on palpation. Loss of feed intake, colic, lateral recumbency, dyspnoea and death.	husbandry authorities. Strict biosecurity measures may be followed. Grazing area may be restricted. Carcass may be disposed hygienically.
5.	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.
6.	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.
7.	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.

8.	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.
9.	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.

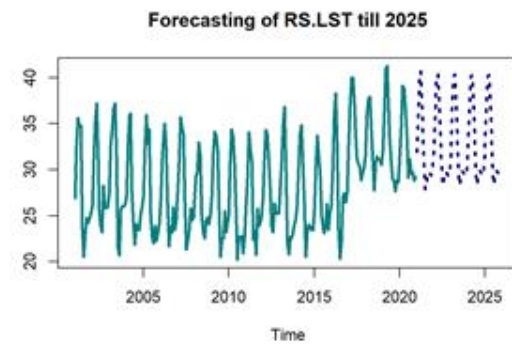
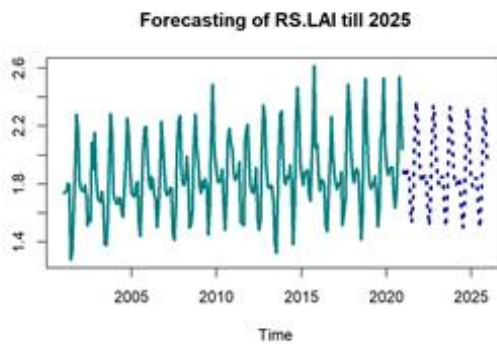
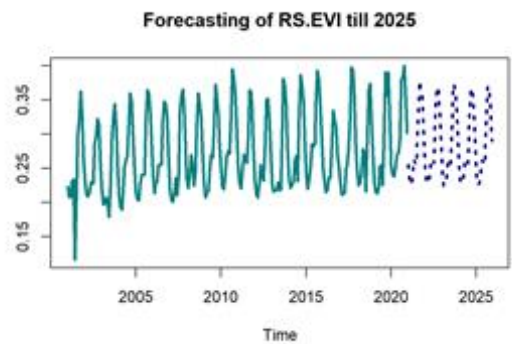
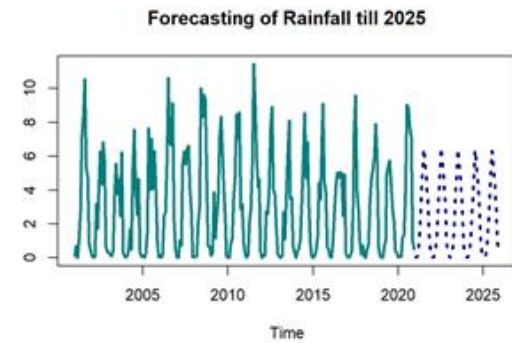
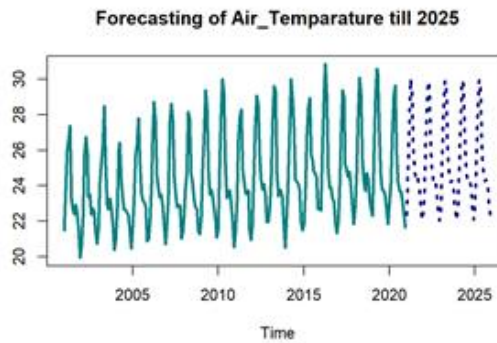
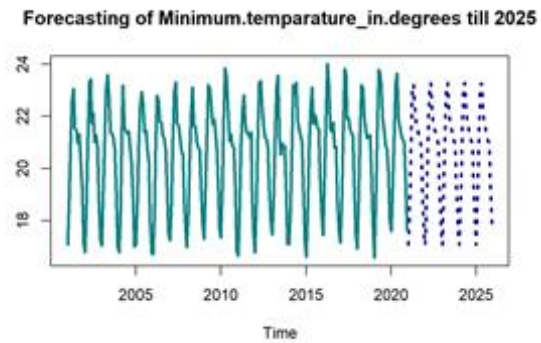
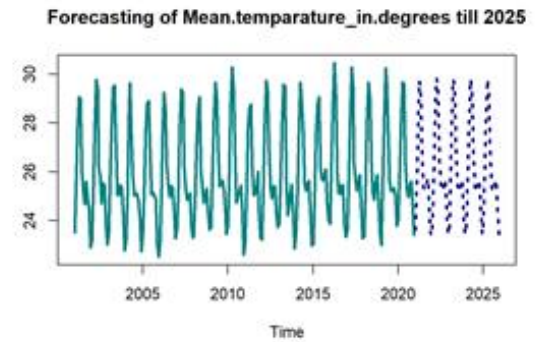
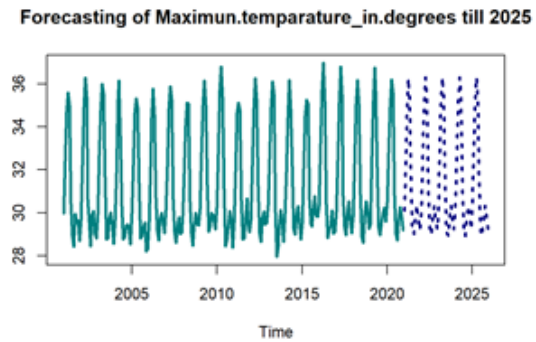
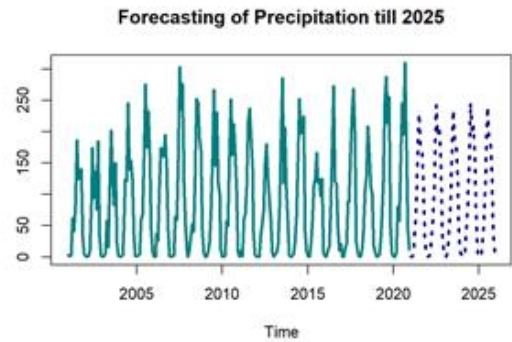
10.	Lumpy skin disease (LSD)	Common disease for Cattle, Buffalo and other domestic animals	Fever, reduced milk production and skin nodules. Mastitis, swelling of peripheral lymph nodes, loss of appetite, increased nasal discharge and watery eyes are also common. Temporary or permanent infertility occur 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.
11.	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.
12.	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.
13.	Classical Swine Fever (CSF)	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.

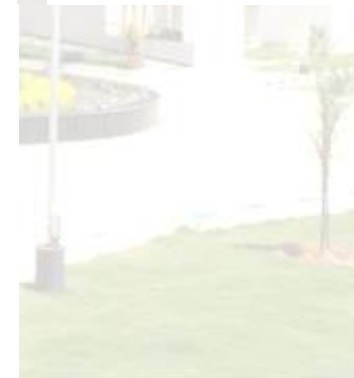
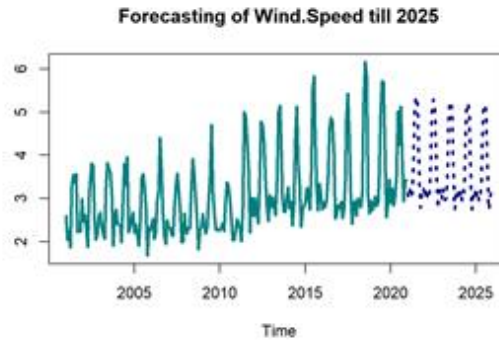
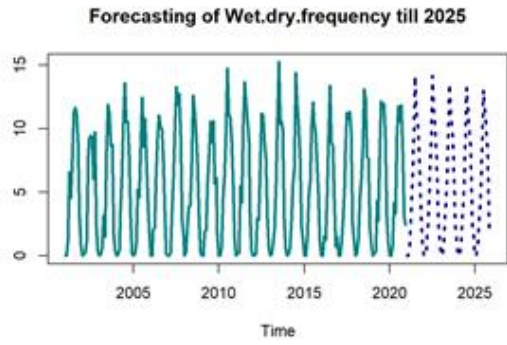
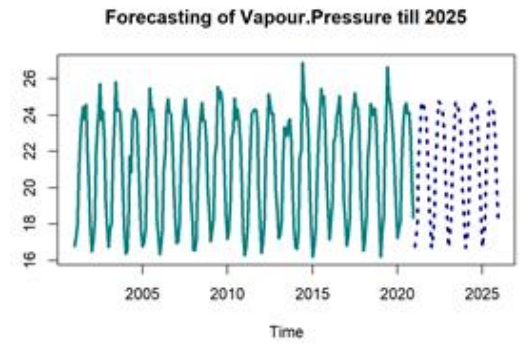
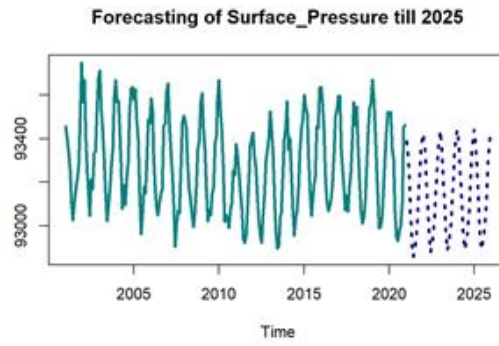
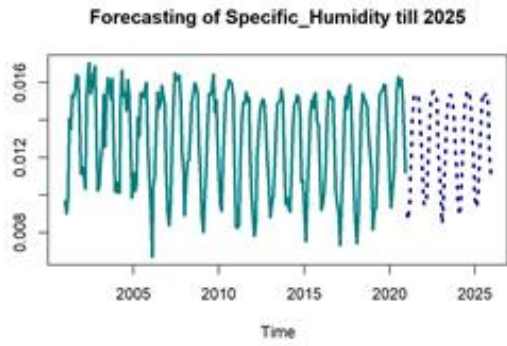
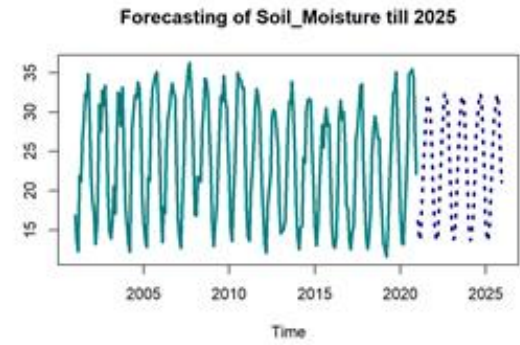
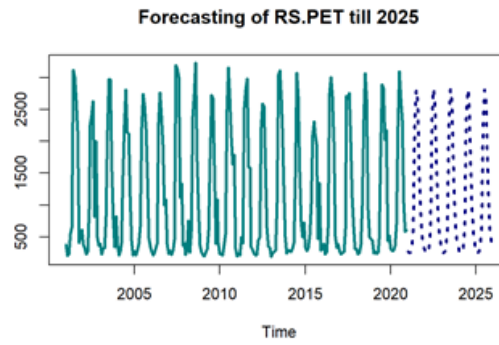
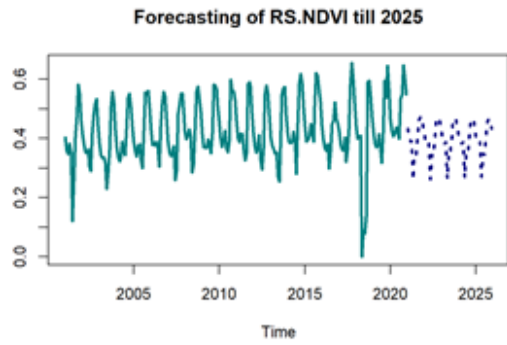
14.	Theileriosis (TE)	Large Ruminants. Crossbreed cattle are more vulnerable.	High temperature, yellowish eye, sometime eyes may be heavily swollen, icteric mucosal membrane of rectum, dark yellowish urine, sometime may reach to coffee colour. Antibiotic is of no use to check the fever.	Periodical application 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.
15.	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, 2025(Ex. Karnataka)





### III.SIGNIFICANT WEATHER PARAMETERS TABLE USING DISCRIMINANT FUNCTION ANALYSIS

<b>SI. No</b>	<b>Disease Names</b>	<b>ML Derived Significant Parameters</b>
1	<b>African Swine Fever</b>	Air Temperature, Delta-Precipitation, Delta-Leaf Area Index
2	<b>Anthrax</b>	WET, Maximum Temperature, Wind Velocity, Soil Temperature
3	<b>Babesiosis</b>	Delta-Relative Humidity, Precipitable-water, Delta-Minimum Temperature
4	<b>Black quarter</b>	Wind Velocity, Potential Evapotranspiration, Air Temperature
5	<b>Bluetongue</b>	Wind Velocity, Soil Temperature
6	<b>Classical Swine fever</b>	Air Temperature, Enhanced Vegetation Index, Relative Humidity
7	<b>Enterotoxaemia</b>	Soil Temperature, Precipitable water, Delta-Precipitable water
8	<b>Fascioliasis</b>	Precipitable Water, Air Temperature, Precipitation-rate
9	<b>Foot and mouth disease</b>	Delta-Temperature Minimum, Precipitation-rate, Precipitable water, Soil Temperature
10	<b>Hemorrhagic septicemia</b>	Precipitable Water, Delta-Pressure
11	<b>Lumpy Skin Diseases</b>	Delta-Vapour Pressure, Minimum Temperature, WET, Delta- Enhanced Vegetation Index, Pressure
12	<b>Peste des petits ruminants</b>	Delta-Minimum Temperature, Precipitable water, Delta-Relative Humidity
13	<b>Sheep &amp; Goat pox</b>	WET, Enhanced Vegetation Index, Relative Humidity
14	<b>Theileriosis</b>	Precipitable Water, Delta- Minimum Temperature, Precipitation-rate
15	<b>Trypanosomiasis</b>	WET, Precipitable-water, Delta-soil moisture

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 Temsumeren, 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.

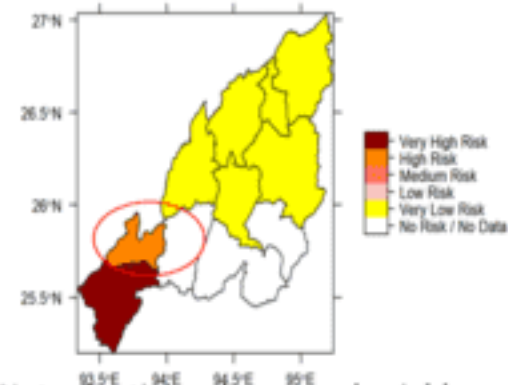
Meanwhile, when contacted, Dr S. Amenla Walling told Nagaland Post that it is difficult to say if the disease has been fully contained since its free grazing season for the animals, but the department is doing its best under the circumstances.

### 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

Andaman and Nicobar Report June-2020

## NIVEDI Prediction

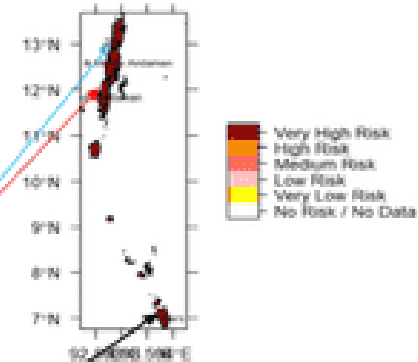
District wise Livestock Disease forwarning for June 2020: Andaman and Nicobar

Districts of Andaman and Nicobar	Livestock Diseases												
	Anthrax	Buberculosis	BQ	BT	ET	Fasciolosis	FMD	HN	PPV	SG Pez	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

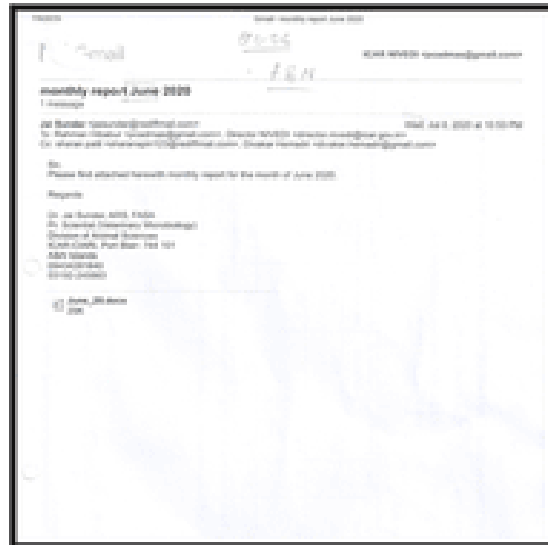
If vaccination is already been done please ignore the disease forecast for that disease.

\*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	FASCIOILLIASI	ASCARIANSI	AMPHISTOM	STRONGYLARD	COCCHIROMSI	MASTITI	TOTAL
South Andaman	24	48	192	34	2	7	307
N&M Andaman	78	43	14	5	3	10	353
Nicobar	79	31	0	0	0	0	110
<b>TOTAL</b>	<b>364</b>	<b>122</b>	<b>206</b>	<b>39</b>	<b>5</b>	<b>17</b>	<b>750</b>

Dr. Jai Sander  
 PL, ACRP-ADMAS  
 Port Blair

# HIMACHAL PRADESH REPORT AUGUST-2020

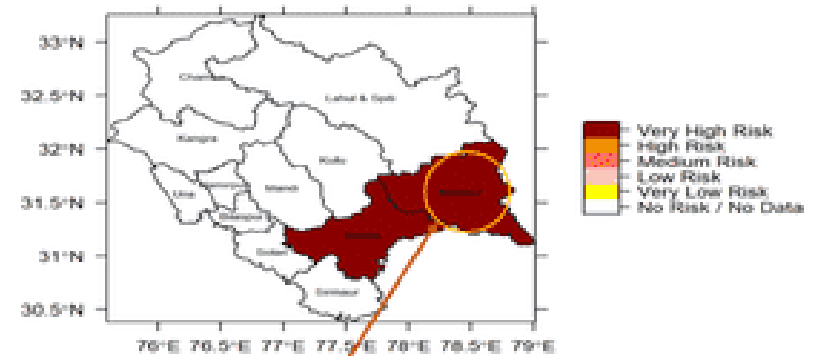
## NIVEDI Prediction

District wise Livestock Disease forecasting for July 2020 Himachal Pradesh

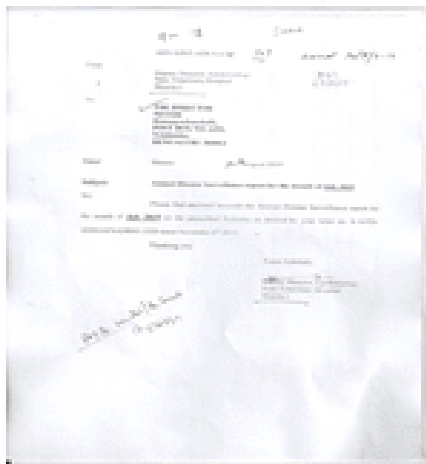
Districts of Himachal Pradesh	Livestock Diseases												
	Anthrax	Baharish	BQ	BT	ET	Fasciolosis	FMD	HS	PPV	MG/Pan	ST	Theileriosis	Trypanosomiasis
Bilaspur	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR
Chamba	NR	NR	NR	NR	NR	NR	17.8	NR	NR	NR	NR	NR	NR
Hamirpur	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR
Kangra	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR
Kasauli	NR	NR	NR	VLB	NR	NR	NR	NR	NR	17.8	NR	NR	NR
Kullu	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR
Lahul & Spiti	NR	NR	NR	17.8	NR	NR	NR	NR	NR	NR	NR	NR	NR
Shimla	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR
Shimla	NR	NR	NR	NR	NR	NR	NR	NR	NR	17.8	NR	NR	NR
Sirmaur	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR
Solan	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR	NR
Una	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.

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



## HIMACHAL PRADESH Report July-2020



FORMAT FOR SUBMITTING LIVESTOCK DISEASE OUTBREAK DATA TO REVEAL (REVISED REPORT-11/04/2016)

NAME OF THE COLLABORATING UNIT: \_\_\_\_\_

ADDRESS OF THE COLLABORATING UNIT: \_\_\_\_\_

REPORT FOR THE MONTH OF: July 2020

DATE OF REPORT: 01/08/2020

Name of the village*	Latitude and Longitude of the village	Postal pin code of the village	Name of the district	Name of the animal	Species of the animal	Year	Month	Number of outbreaks	Number susceptible	Number affected	Number of deaths	Number of recoveries
Arwa	30°55'N 76°55'E	171001	Kangra	Sheep Pox	Sheep	2020	July	1	100	41	0	000
Arwa	30°55'N 76°55'E	171001	Kangra	Sheep Pox	Sheep	2020	July	1	100	40	0	000

\* If you have the exact pin code of the village, please specify the exact pin code, latitude, longitude and postal services and working by writing separately for goats and sheep.

## KERALA REPORT JUNE-2021



HOME ABOUT OUR TEAM IN THE NEWS FROM THE FIELD

SUBMIT INFO SEARCH POSTS

ProMED-mail Portuguese Español Pyocast 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.

--  
Communicated by:  
ProMED  
<[promed@promedmail.org](mailto:promed@promedmail.org)>

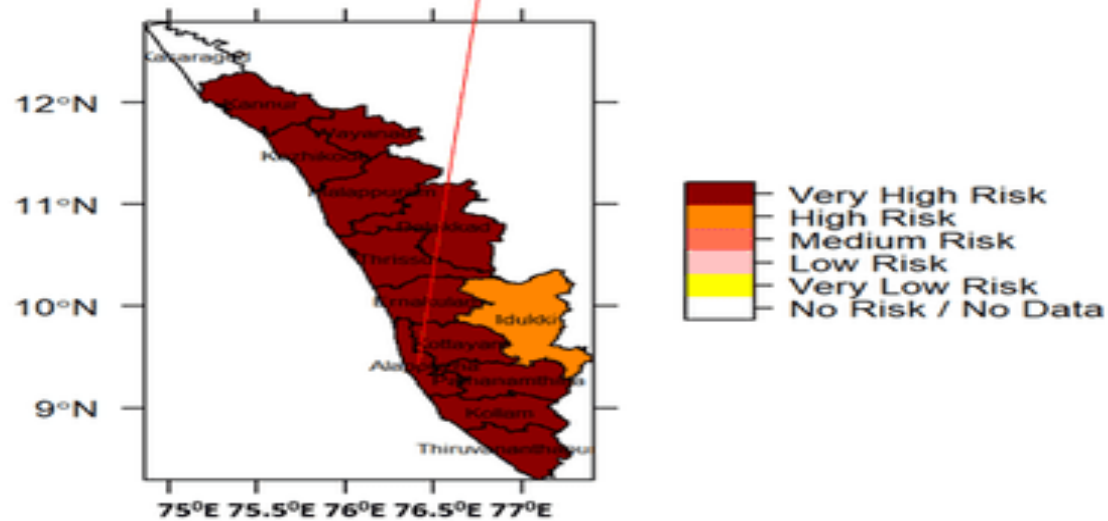
# NIVEDI prediction in June 2021

District wise Livestock Disease Risk Forewarning for June 2021: Kerala

Districts of Kerala	Livestock Diseases												
	Anthrax	Babesiosis	BQ	BT	ET	Fascioliasis	FMD	IHS	PPR	S&G Pox	SF	Theileriosis	Trypanosomiasis
Alappuzha	NR	NR	NR	NR	NR	NR	VHR	MR	VLR	NR	NR	NR	NR
Ernakulam	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	VLR	HR	NR	NR	NR	VHR
Thirissur	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: PRO/SOAS> Foot & mouth disease - India (10): (Karnataka) cattle  
 Archive Number: 20210930.8698795

FOOT & MOUTH DISEASE - INDIA (10): KARNATAKA CATTLE

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

Date: Fri 24 Sep 2021 08:33:57  
 Source: The Hindu (India)

<https://www.thehindu.com/news/national/karnataka/foot-and-mouth-disease-reported-in-karnataka/article2727271.ece>

District wise Livestock Disease Risk Forewarning for September 2021: Karnataka

District of Karnataka	Livestock Diseases												
	Acidosis	Breastitis	BC	BT	ET	Fasciolosis	FMD	IT	PPK	MG	PP	Duodenitis	Trypanosomiasis
Chikmagalur	50	50	50	50	50	50	50	50	50	50	50	50	50
Dakshina Kannada	50	50	100	50	50	50	100	50	50	100	50	50	50
Dodda Ballari	100	50	50	50	50	50	50	50	50	50	50	50	50
Kodagu	50	50	50	50	50	50	100	50	50	50	50	50	50
Kolar	50	50	50	50	50	50	50	50	50	50	50	50	50
Koppal	100	50	50	50	50	50	50	50	50	50	50	50	50
Mandya	50	50	50	50	50	50	100	50	50	50	50	50	50
Mysuru	50	50	100	50	50	50	100	50	50	50	50	50	50
Raichur	100	50	50	50	50	50	50	50	50	50	50	50	50
Ramanagara	50	50	50	50	50	50	100	50	50	50	50	50	50
Shimoga	50	50	100	50	100	50	100	50	50	50	50	50	50
Tandur	100	50	50	50	50	50	100	100	50	50	50	50	50
Udupi	50	50	50	50	50	50	50	50	50	50	50	50	50
Uttara Kannada	50	50	50	50	50	50	50	50	50	50	50	50	50
Yadri	50	50	50	50	50	50	50	50	50	50	50	50	50

The outbreak of foot-and-mouth disease (FMD) among cattle in Hassan has left both farmers and veterinarians worried.

Cases have been reported from Kolar, Channarayana, Channarayana, and Sakleshpur taluks. Within the farming community, depending on cattle for regular income, and 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 (31.29.2021), 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 producers.

The vaccination for cattle is done once in six months under the National Animal Disease Control Programme. However, the vaccination drive was not done in the last year, owing to the COVID-19 pandemic. "The outbreak of foot and mouth disease is due to the failure of the government in conducting the vaccination. If the vaccination had been done as per the schedule, farmers would not have suffered", H. Suresh Kumar, president of Proton Club in Kolar, told media.

Following reports of the disease, veterinarians have been treating affected animals. "Against 24 sanctioned posts of veterinary doctors in Kolar taluk, we are only five people. Every doctor is in charge of 2 or more hospitals. We are struggling hard to treat animals", said a veterinarian.

Owing to vacancies were filled up the department cannot deliver services fully. There was a shortage of staff members of other taluks as well, he added.

Considering the cases, the department has launched a ring vaccination programme. Under this, the animals in a 5-km radius (2.5 km radius of the village, where the disease outbreak was reported) would be vaccinated. "We have sufficient stock for the ring vaccination. We are planning a mass vaccination in October (2021), where we will cover 6.58 lakh (6,58,000) animals," said M. Ramani, Deputy Director of Veterinary and Animal Husbandry in Hassan.

Communicated by:  
 ProMED-SoAs from HealthMap (India)  
[reporter@so.asia.promedmail.org](mailto:reporter@so.asia.promedmail.org)

## ARUNACHAL PRADESH REPORT APRIL-2022



HOME ABOUT OUR TEAM IN THE NEWS FROM THE FIELD

SUBMIT INFO

SEARCH POSTS



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>  
ProMED-mail is a program of the  
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 Hell, 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 Jullang 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.

..  
Communicated by:  
ProMED from HealthMap Alerts  
<[promed@promedmail.org](mailto: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-footed 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

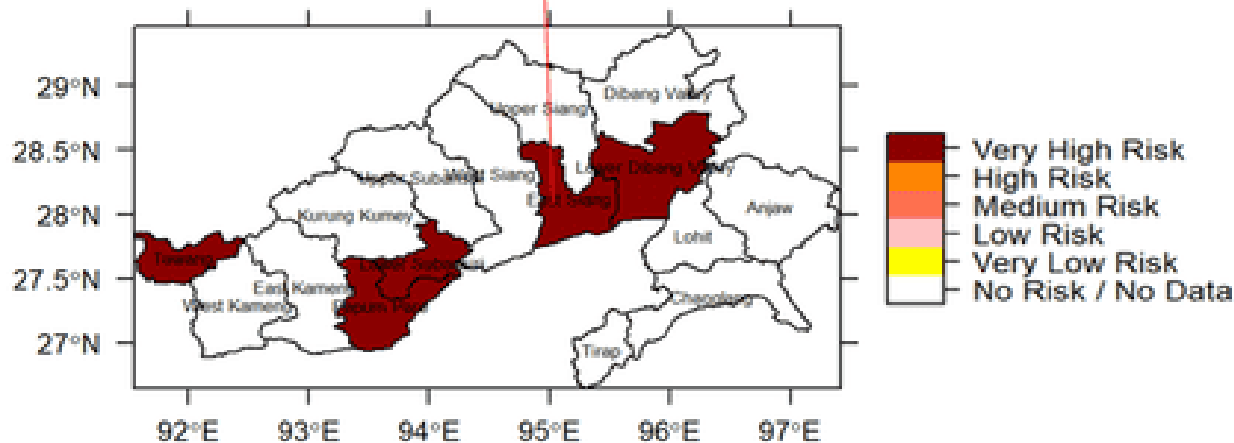
## District wise Livestock Disease Risk Forewarning for April 2021: Arunachal Pradesh

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
<b>East Siang</b>	NR	NR	NR	NR	NR	NR	<b>HR</b>	NR	VLR	NR	<b>HR</b>	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	<b>HR</b>	NR	NR
Lower Subansiri	NR	NR	NR	NR	NR	NR	<b>HR</b>	NR	NR	NR	NR	VLR	NR
Papam Pare	NR	NR	NR	NR	NR	NR	<b>HR</b>	NR	<b>HR</b>	NR	<b>HR</b>	NR	NR
Tawang	NR	NR	NR	NR	NR	NR	<b>HR</b>	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	MAY-2023		JUN-2023	
		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	<b>Anthrax</b>	15	0	27	1
2	<b>Babesiosis</b>	80	43	74	22
3	<b>Black Quarter (BQ)</b>	40	11	40	3
4	<b>Bluetongue (BT)</b>	0	0	0	0
5	<b>Enterotoxaemia (ET)</b>	32	4	19	3
6	<b>Fasciolosis</b>	45	19	47	3
7	<b>Foot &amp; Mouth Disease (FMD)</b>	36	4	59	2
8	<b>Haemorrhagic Septicaemia (HS)</b>	35	2	32	2
9	<b>Peste des Petits Ruminants (PPR)</b>	62	15	61	9
10	<b>Sheep &amp; Goat Pox</b>	47	9	29	12
11	<b>Swine Fever</b>	39	3	31	0
12	<b>Theileriosis</b>	73	59	67	54
13	<b>Trypanosomosis</b>	67	54	64	13

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

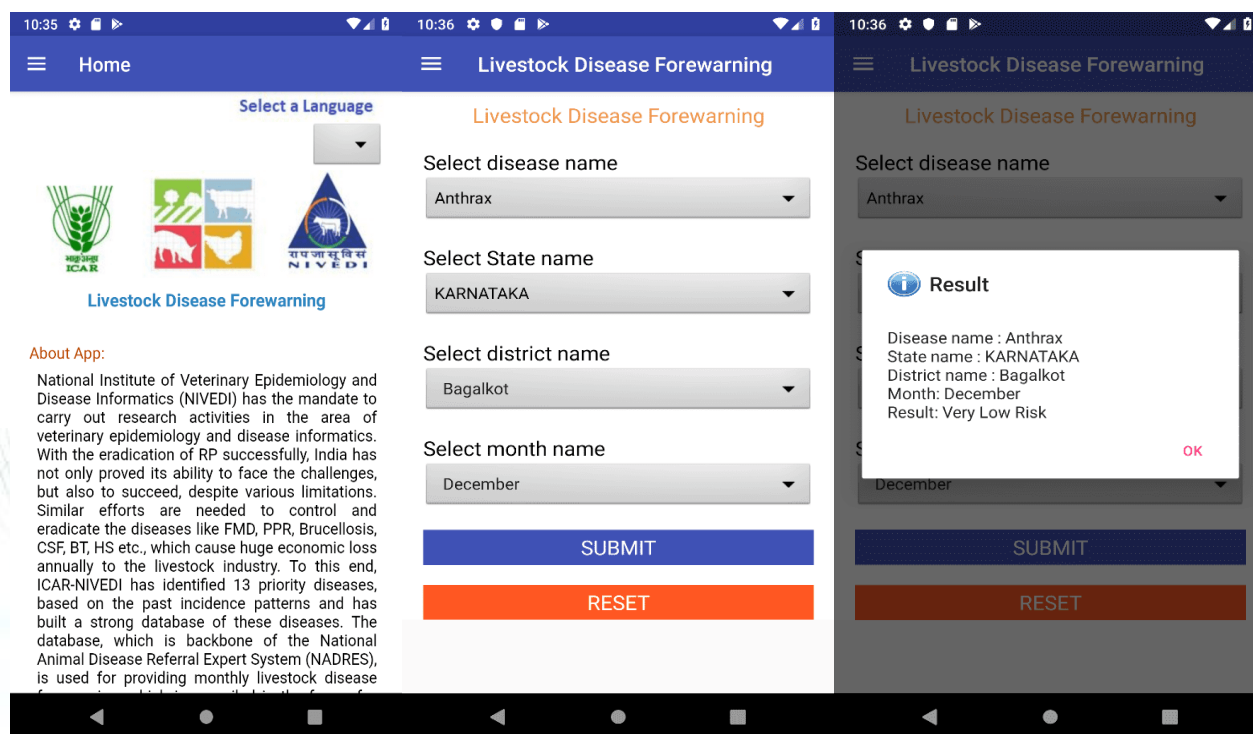
# 10 A. LAUNCH OF MOBILE ANDROID APP & LINK TO DOWNLOAD

Livestock forewarning application (LDF) can be downloaded following the link provided: [http://www.nivedi.res.in/android\\_nadres/LDF.apk](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)



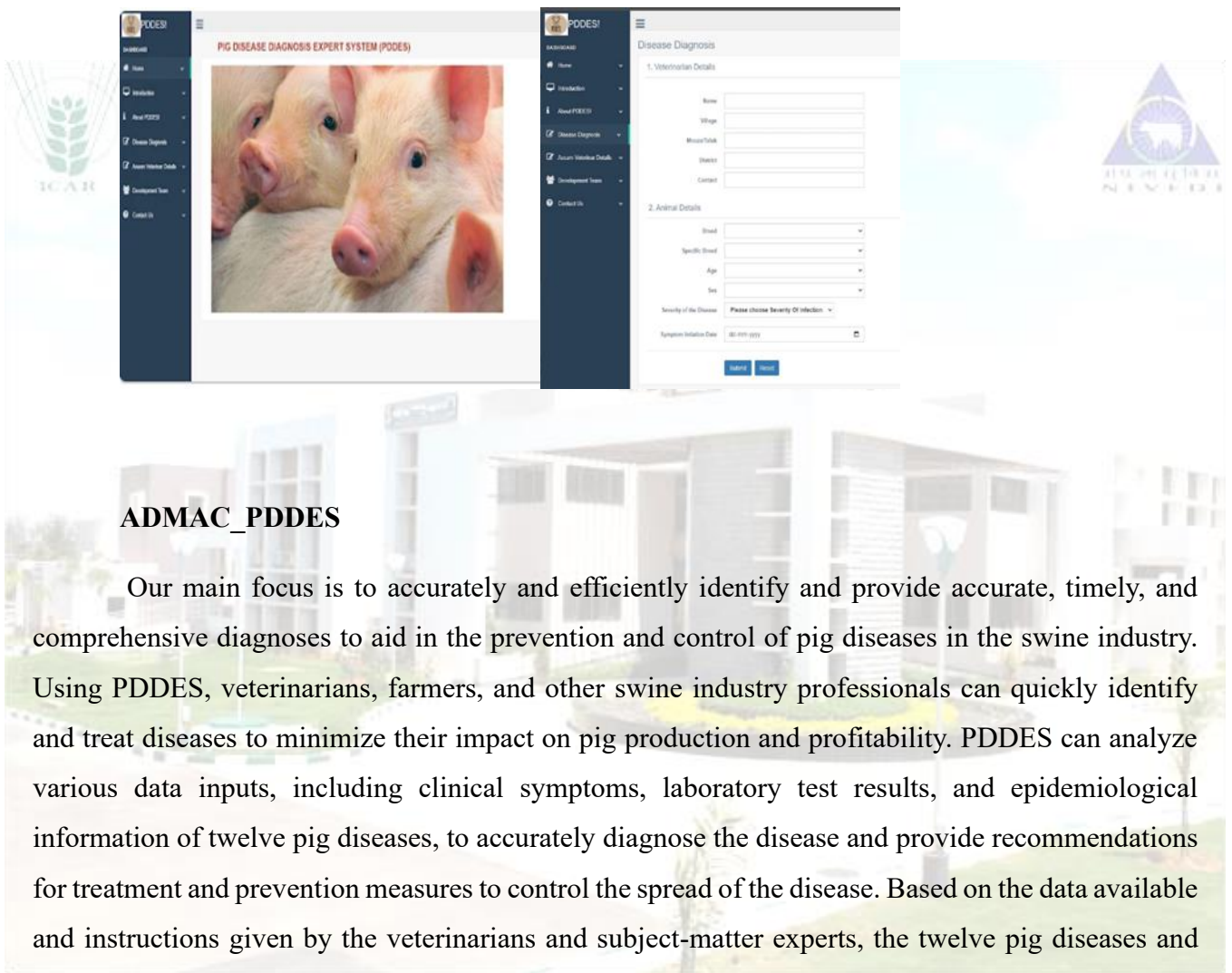
To extend the reach of the NADRES forewarning bulletin among the various stakeholders, a Mobile Application named Livestock Disease forewarning app “LDF-Mobile App” was developed. The forewarning methodology adapted in the “mobile app” remains the same as monthly bulletin; it provides user interface 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.

## 10 B. The ADMAC\_PDDES (PIG DISEASE DIAGNOSIS EXPERT SYSTEM) mobile app.

The ADMAC\_PDDES mobile app is available on Google play store which takes upto 3.8 MB space.

<https://play.google.com/store/apps/details?id=com.nivedi.myapplication>

Web application : <https://nivedi.res.in/PDDES/>

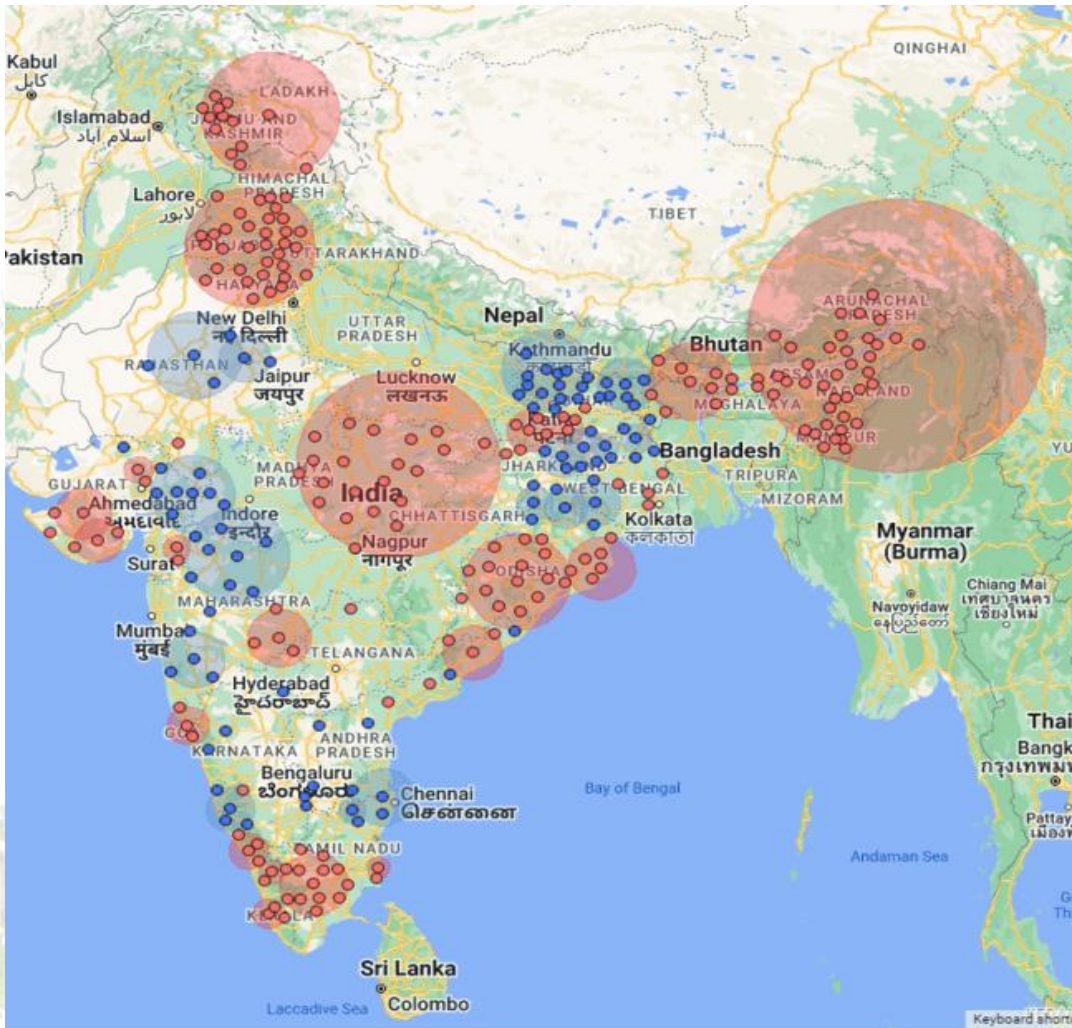


### ADMAC\_PDDES

Our main focus is to accurately and efficiently identify and provide accurate, timely, and comprehensive diagnoses to aid in the prevention and control of pig diseases in the swine industry. Using PDDES, veterinarians, farmers, and other swine industry professionals can quickly identify and treat diseases to minimize their impact on pig production and profitability. PDDES can analyze various data inputs, including clinical symptoms, laboratory test results, and epidemiological information of twelve pig diseases, to accurately diagnose the disease and provide recommendations for treatment and prevention measures to control the spread of the disease. Based on the data available and instructions given by the veterinarians and subject-matter experts, the twelve pig diseases and their clinical indications or symptoms were determined and Aiken's value index was calculated. The weighted matrix was created for a number of different clinical indicators or symptoms related to swine illnesses. Based on this, an expert system was developed as a mobile application.

# 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

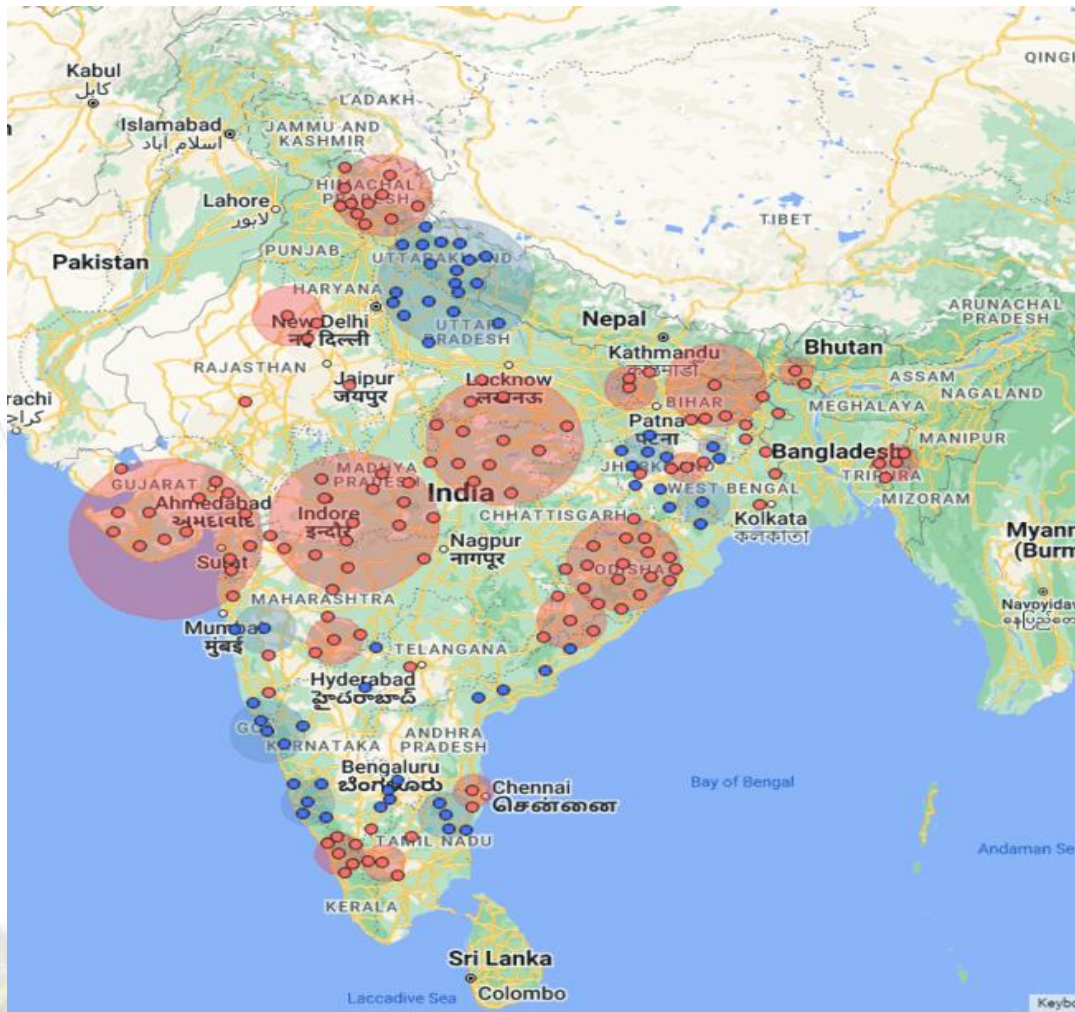
- **Retrospective Analysis: Space-Time**
- **Probability Model: Space-Time Poisson Model**
  - With the Space-Time Poisson model, the number of cases in each location is Poisson-distributed.
  - The model requires case and population counts for a set of data locations and geographical coordinates for 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)



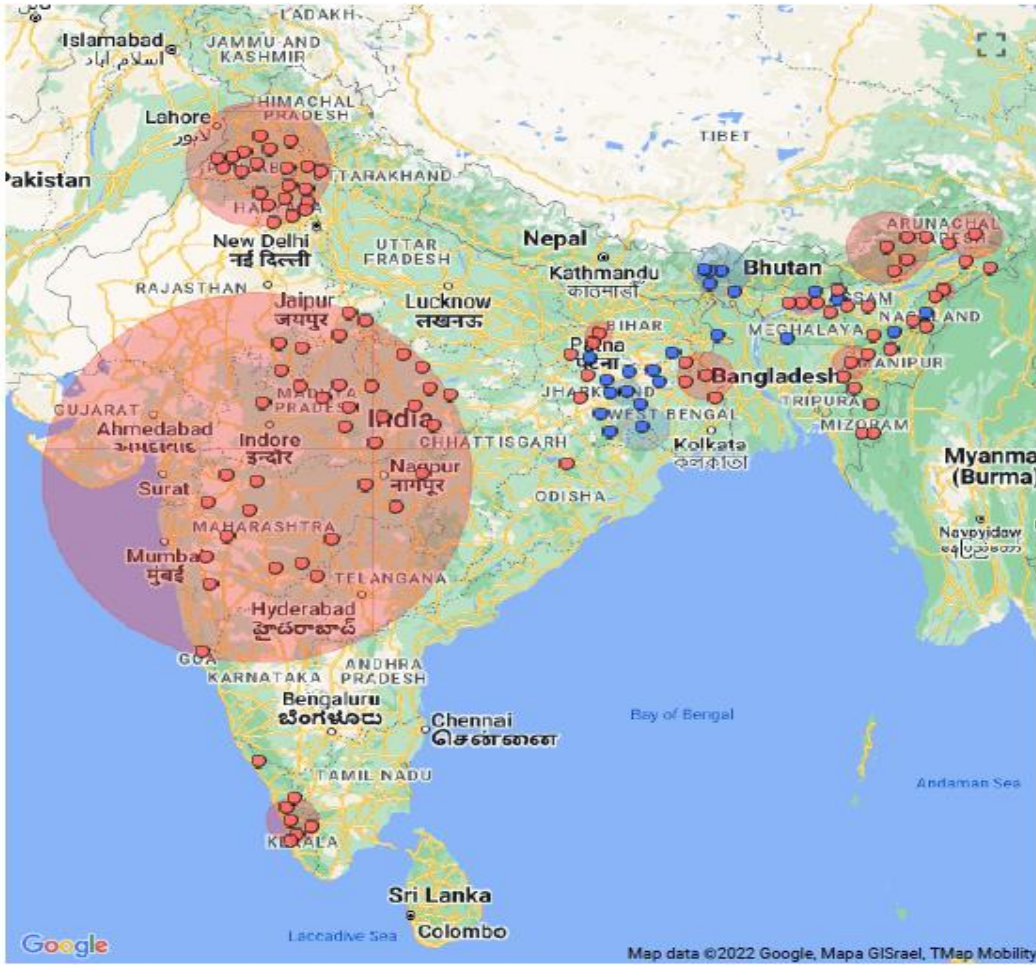
### Model Specifications

- **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)



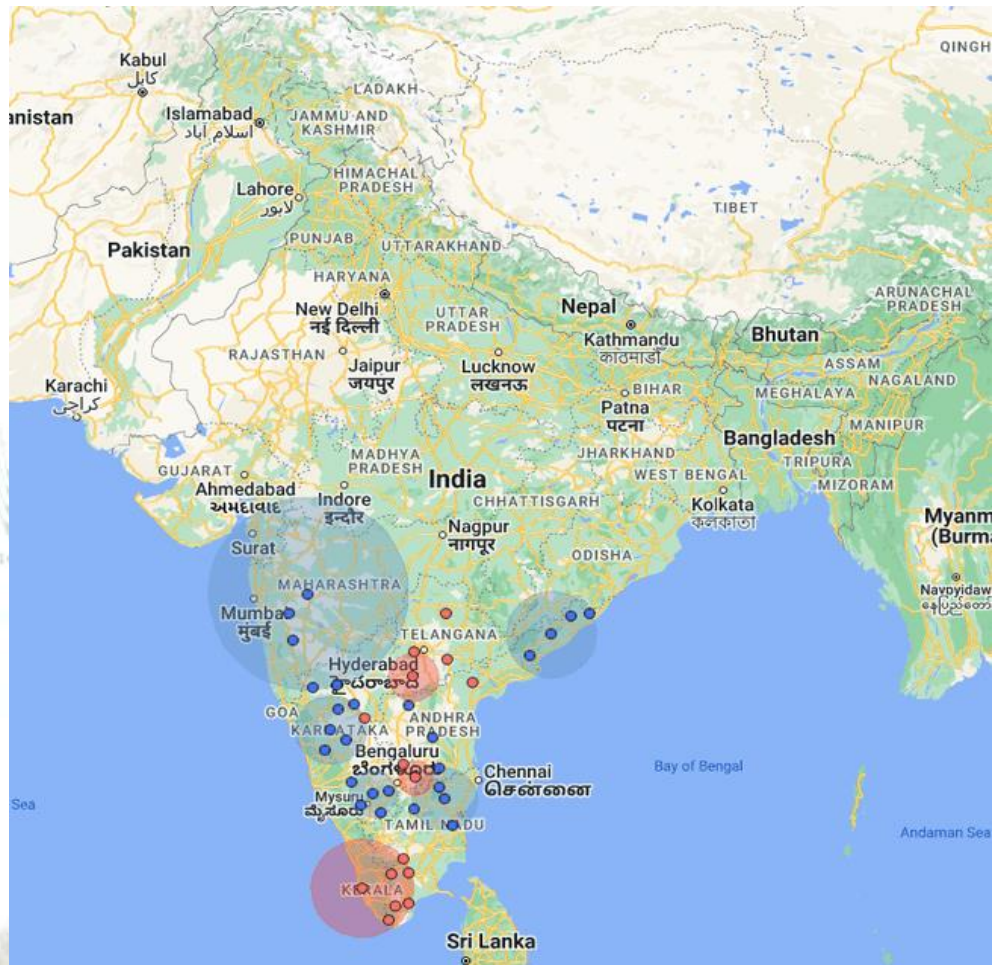
### Model Specifications

- **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)



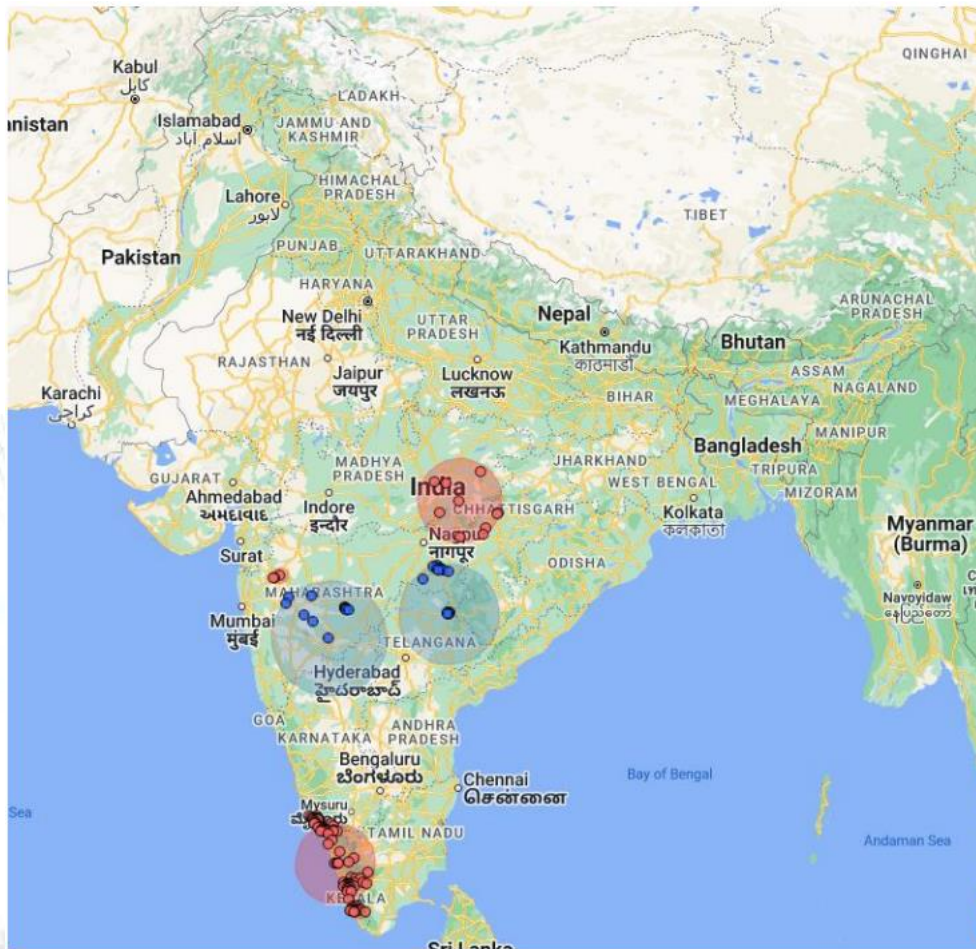
#### Model Specifications

- **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)**



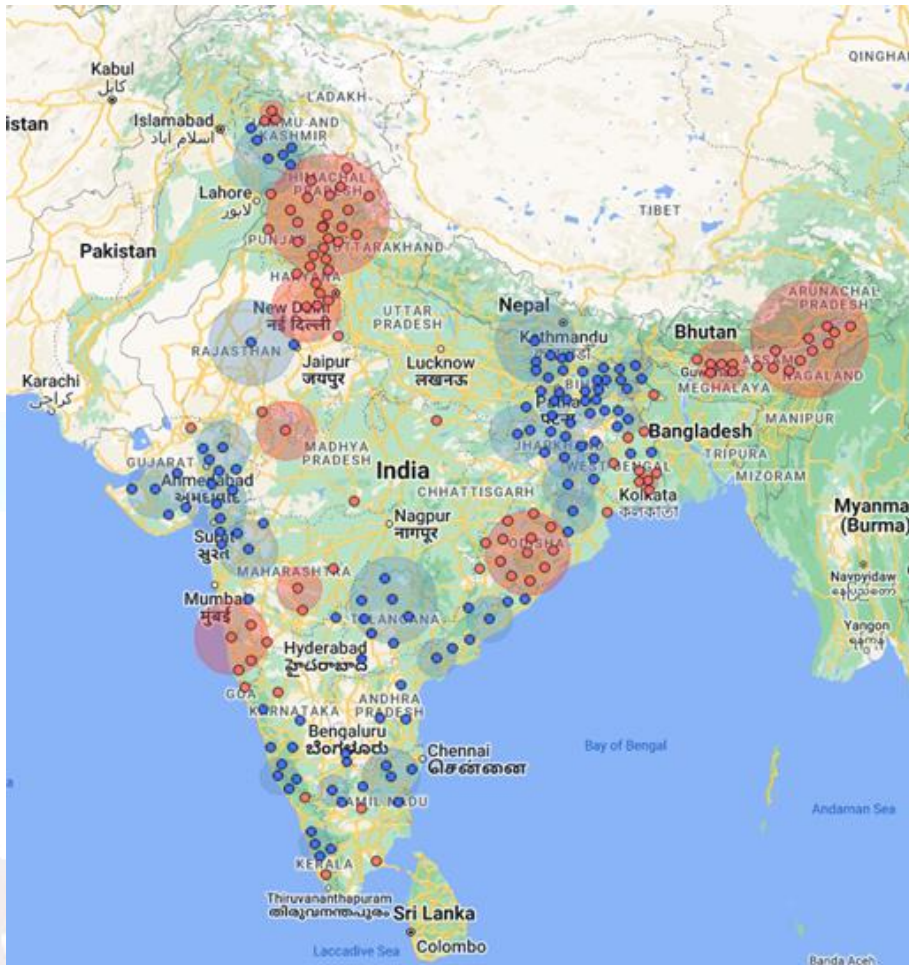
**Model Specifications**

- **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. a) FMD Hotspot by Poisson Model – FMD in India (2000-2004)



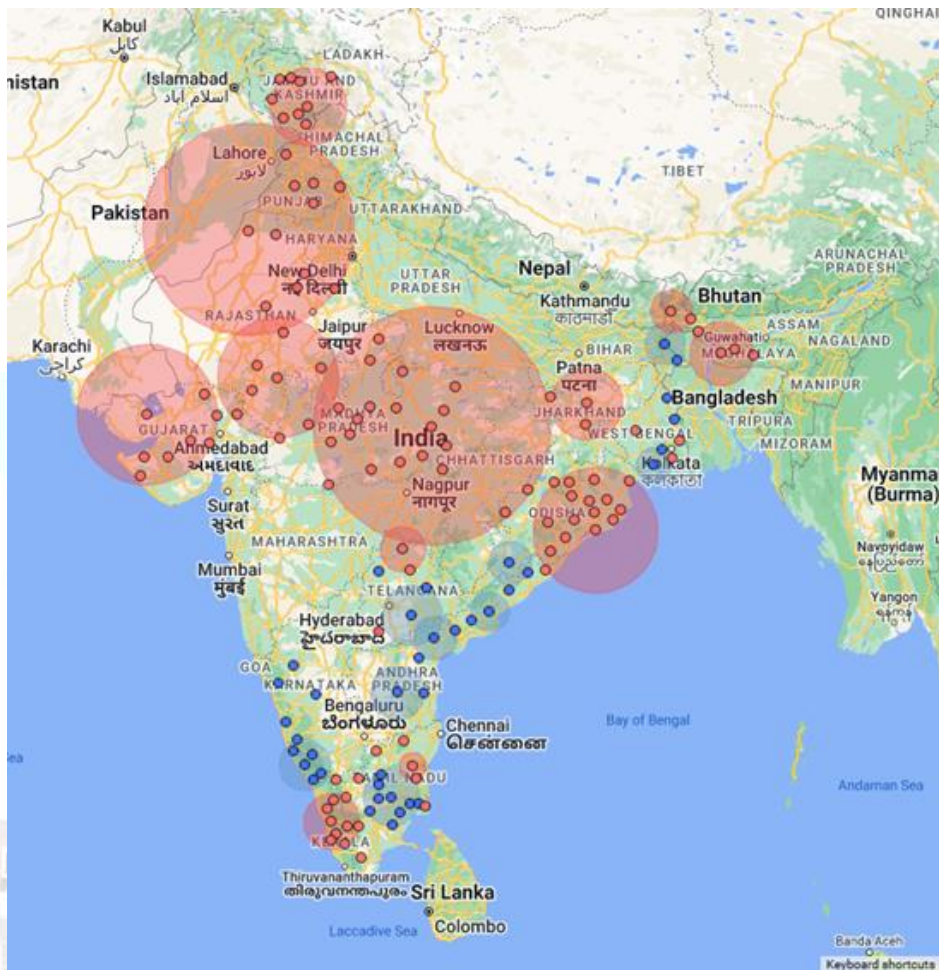
### Model Specifications

- **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– Hotspot: 1 km, 72 clusters, 29 high, 43 low
  - The output is generated using **SaTScan v9. 6.**

**Note: Red Dot: High Disease Cluster**

**Blue Dot: Low Disease Cluster**

## b) FMD Hotspot by Poisson Model – FMD in India (2005-2009)



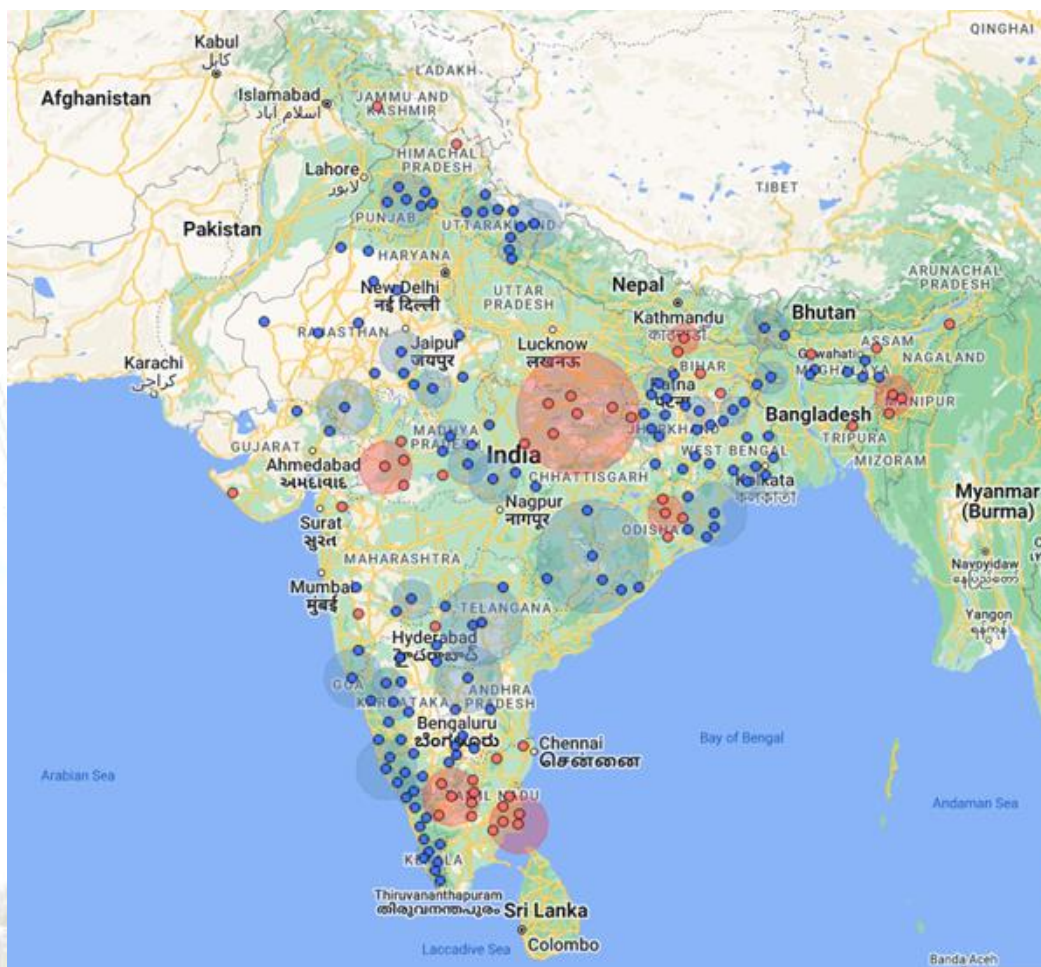
### Model Specifications

- **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– Hotspot: 1 km, 41 clusters, 23 high, 18 low
  - The output is generated using SaTScan v9. 6.

**Note: Red Dot: High Disease Cluster**

**Blue Dot: Low Disease Cluster**

## C) FMD Hotspot by Poisson Model – FMD in India (2010-2014)



### Model Specifications

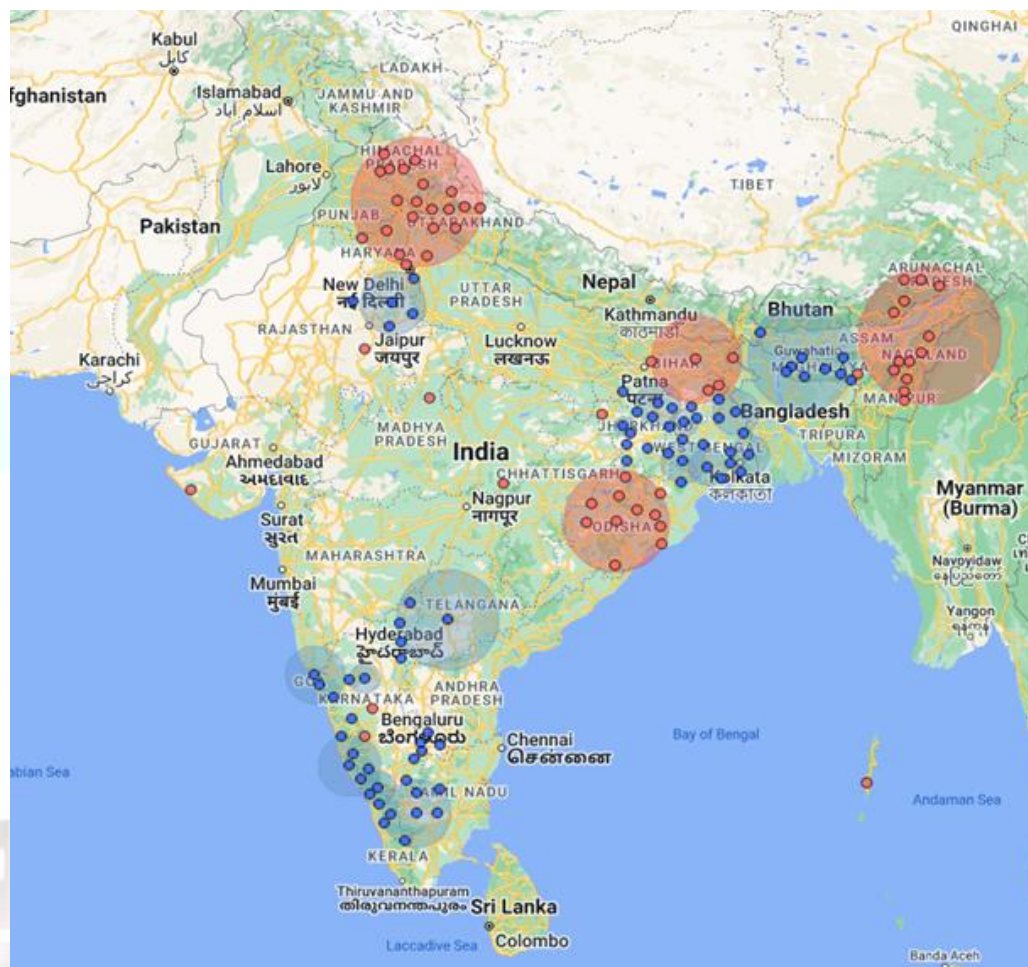
- **Retrospective Analysis:** Space-Time
- **Probability Model:** Space-Time Poisson Model
  - **With the Space-Time Poisson model,** the number of cases in each location is Poisson-distributed.
  - The model requires case and population counts for a set of data locations and geographical coordinates 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– Hotspot: 1 km, 103 clusters, 24 high, 79 low
  - The output is generated using **SaTScan v9. 6.**

**Note: Red Dot: High Disease Cluster**

**Blue Dot: Low Disease Cluster**



## D)FMD Hotspot by Poisson Model – FMD in India (2015-2019)



### Model Specifications

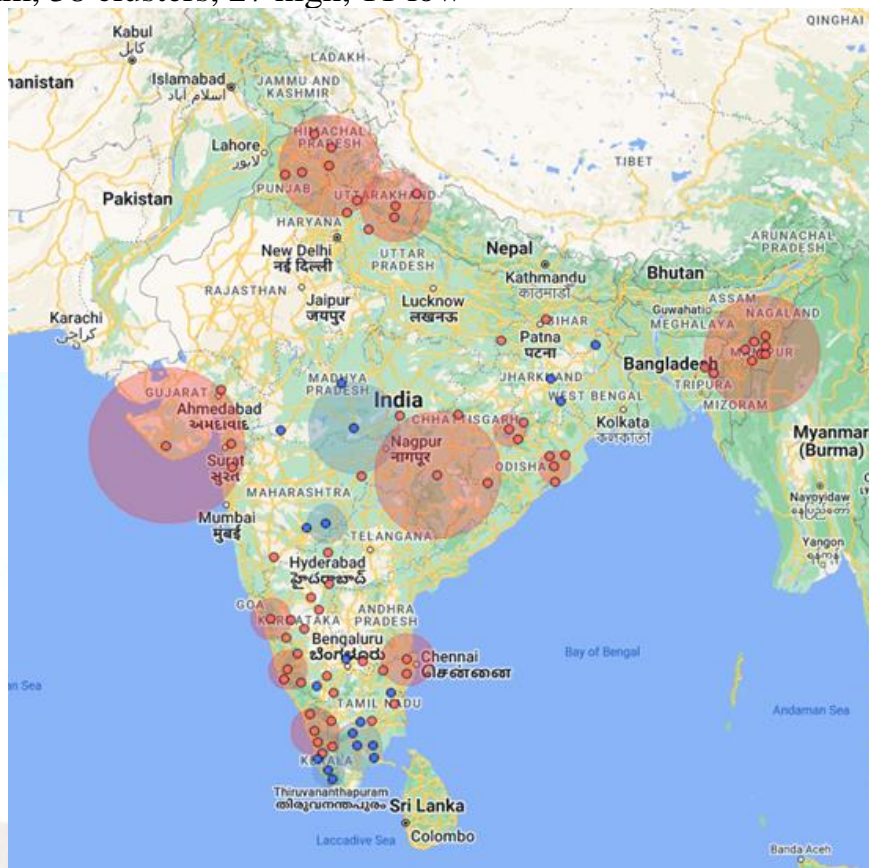
- **Retrospective Analysis:** Space-Time
- **Probability Model:** Space-Time Poisson Model
  - **With the Space-Time Poisson model**, the number of cases in each location is Poisson-distributed.
  - The model requires case and population counts for a set of data locations and geographical coordinates 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:** 2 km.
  - **Time Aggregation:** 1 year.
  - **Output obtained with no geographical overlap-** Total Hotspots-Hotspot: Hotspot: 2 km, 43 clusters, 13 high, 30 low
  - The output is generated using **SaTScan v9.6**.

**Note: Red Dot: High Disease Cluster**

**Blue Dot: Low Disease Cluster**

## E)FMD Hotspot by Poisson Model – FMD in India (2020-2023)

Hotspot: 1 km, 38 clusters, 27 high, 11 low



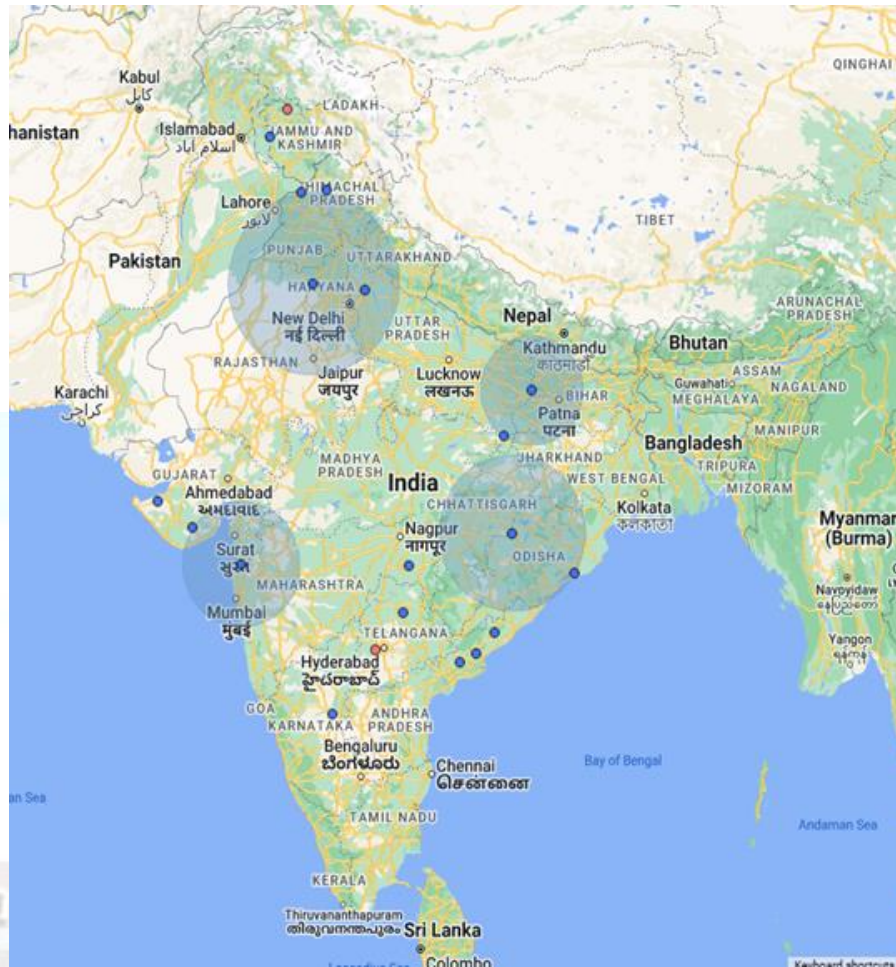
### Model Specifications

- **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-Hotspot: 1 km, 38 clusters, 27 high, 11 low
  - The output is generated using **SaTScan v9. 6**.

**Note: Red Dot: High Disease Cluster**

**Blue Dot: Low Disease Cluster**

### 11.3. Foot rot district wise Risk map (2001-2019)



#### Model Specifications

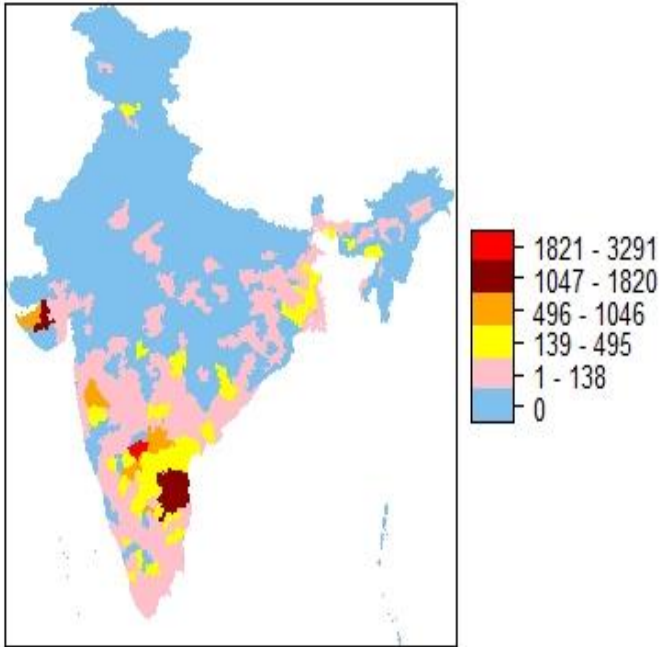
- **Retrospective Analysis:** Space-Time
- **Probability Model:** Space-Time Poisson Model
  - **With the Space-Time Poisson model**, the number of cases in each location is Poisson-distributed.
  - The model requires case and population counts for a set of data locations and geographical coordinates 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-Hotspot: Hotspot: 1 km, 15 clusters, 2 high, 13 low
  - The output is generated using **SaTScanv9. 6**.

**Note: Red Dot: High Disease Cluster**

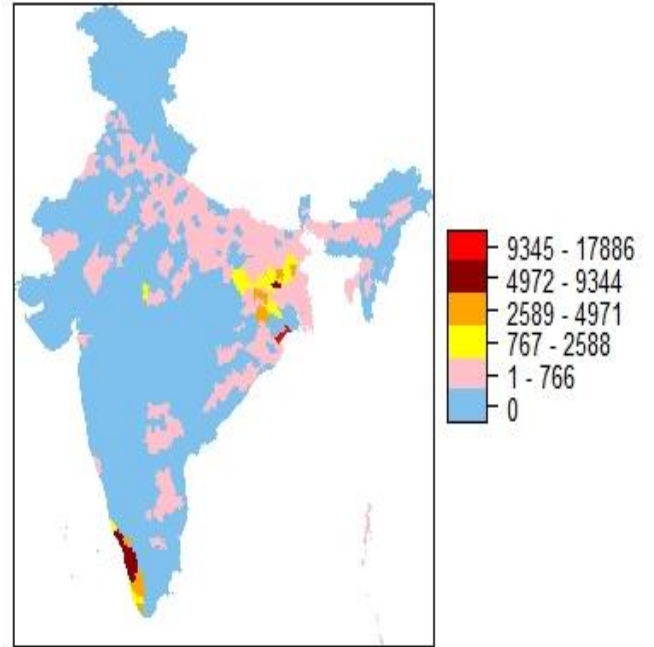
**Blue Dot: Low Disease Cluster**

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

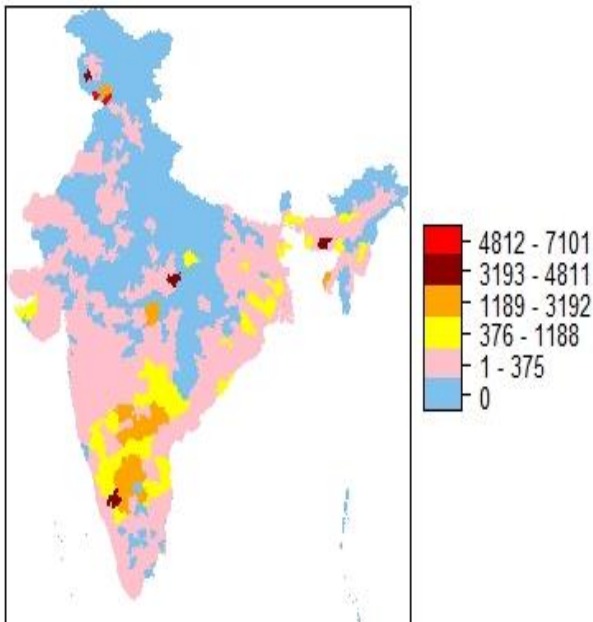
Outbreaks/Incidence- Anthrax(1990-2022)



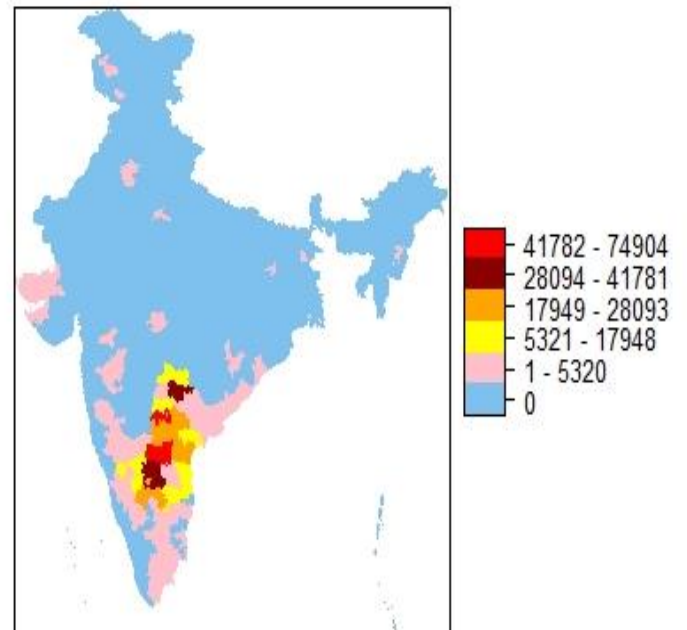
Outbreaks/Incidence- Babesiosis(1990-2022)



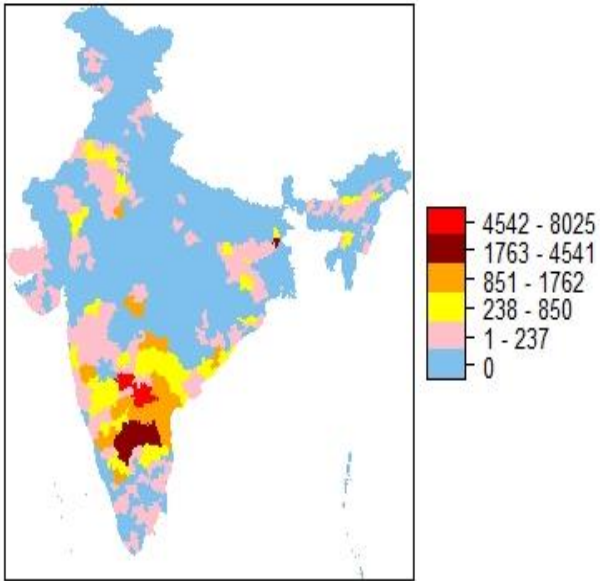
Outbreaks/Incidence- Blackquarter(1990-2022)



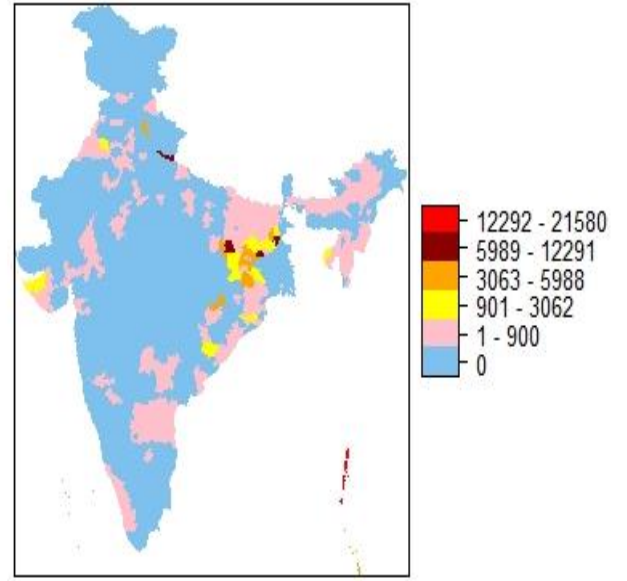
Outbreaks/Incidence- Bluetongue(1990-2022)



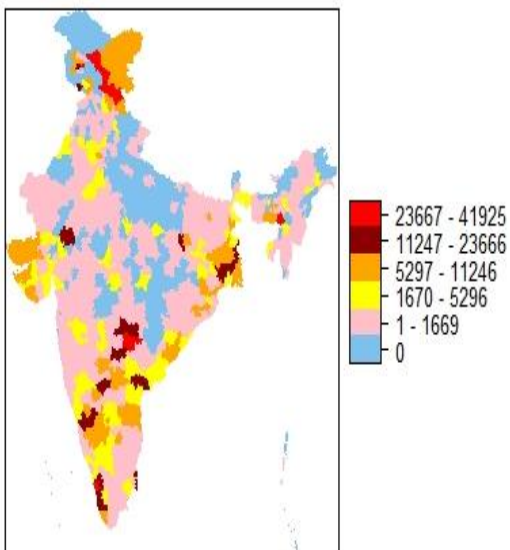
**Outbreaks/Incidence- Enterotoxaemia(1990-2022)**



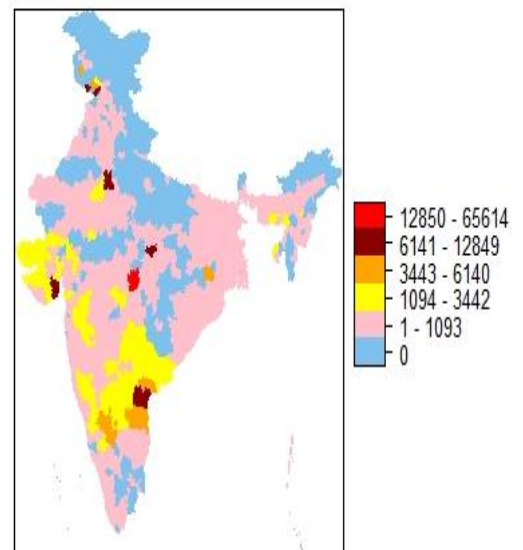
**Outbreaks/Incidence- Fascioliasis(1990-2022)**



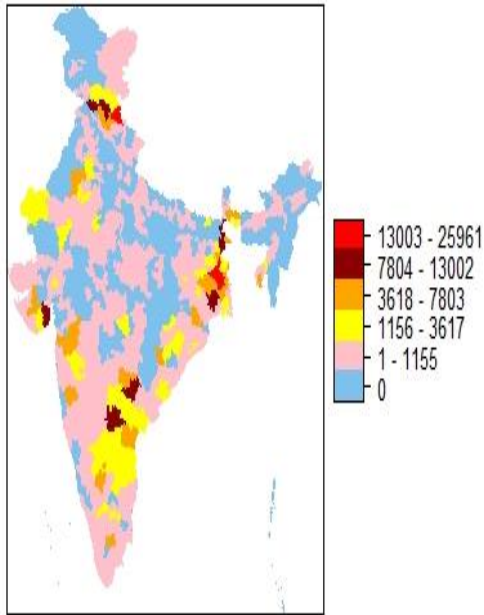
**Outbreaks/Incidence-Foot and Mouth Disease(1990-2022)**



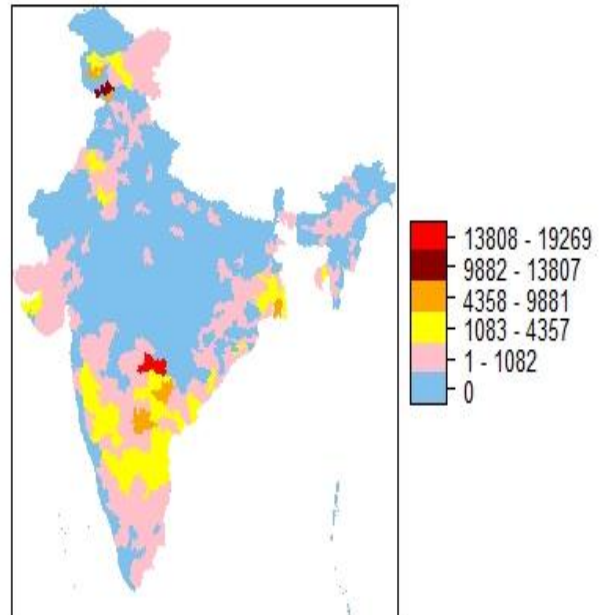
**Outbreaks/Incidence-Haemorrhagic Septicaemia(1990-2022)**



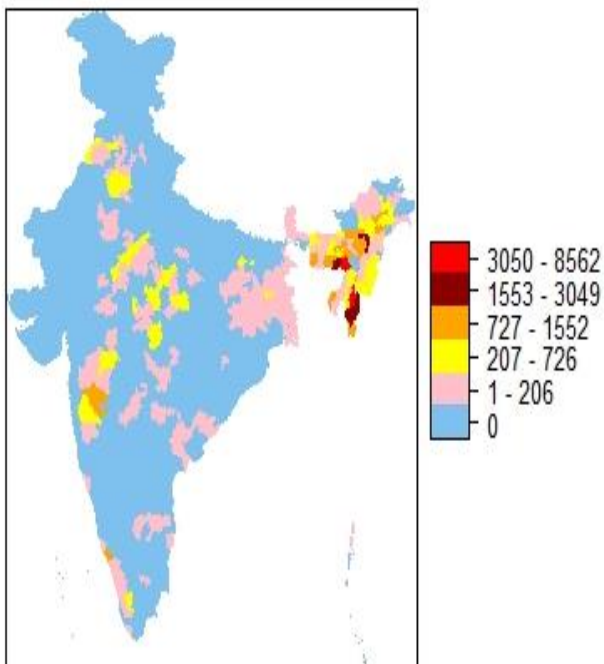
Outbreaks/Incidence-Peste des petits Ruminants(1990-2022)



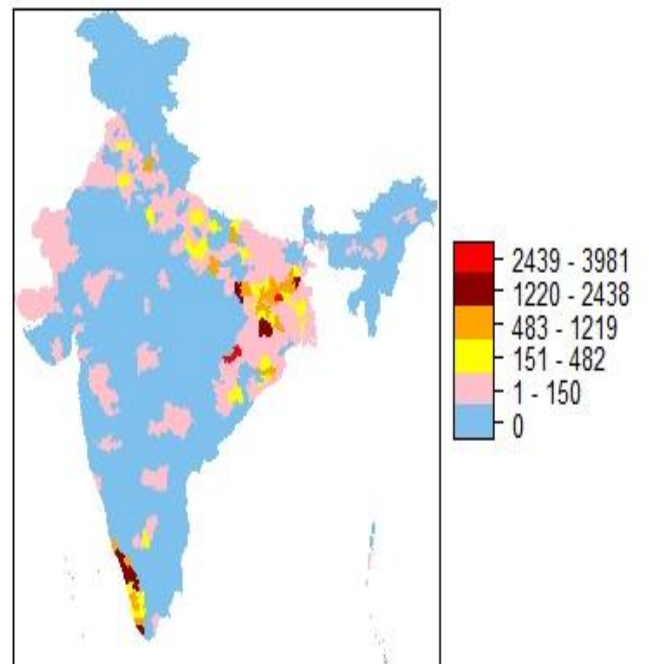
Outbreaks/Incidence-Sheep & Goat Pox(1990-2022)



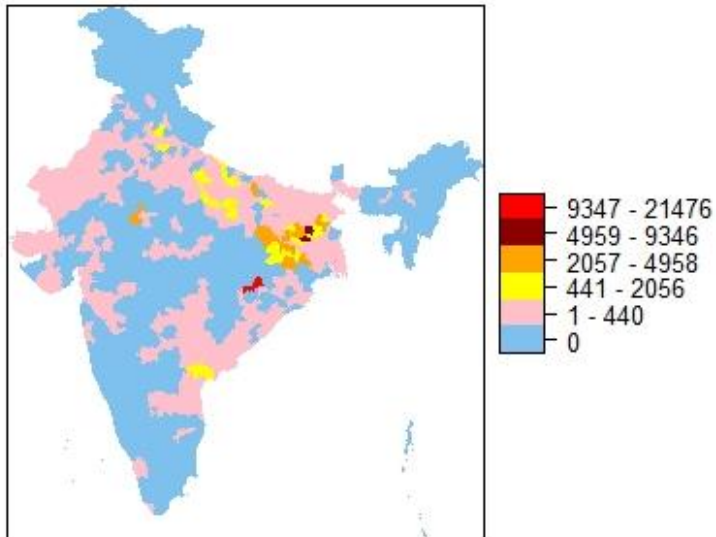
Outbreaks/Incidence-Swine Fever(1990-2022)



Outbreaks/Incidence-Theileriosis(1990-2022)

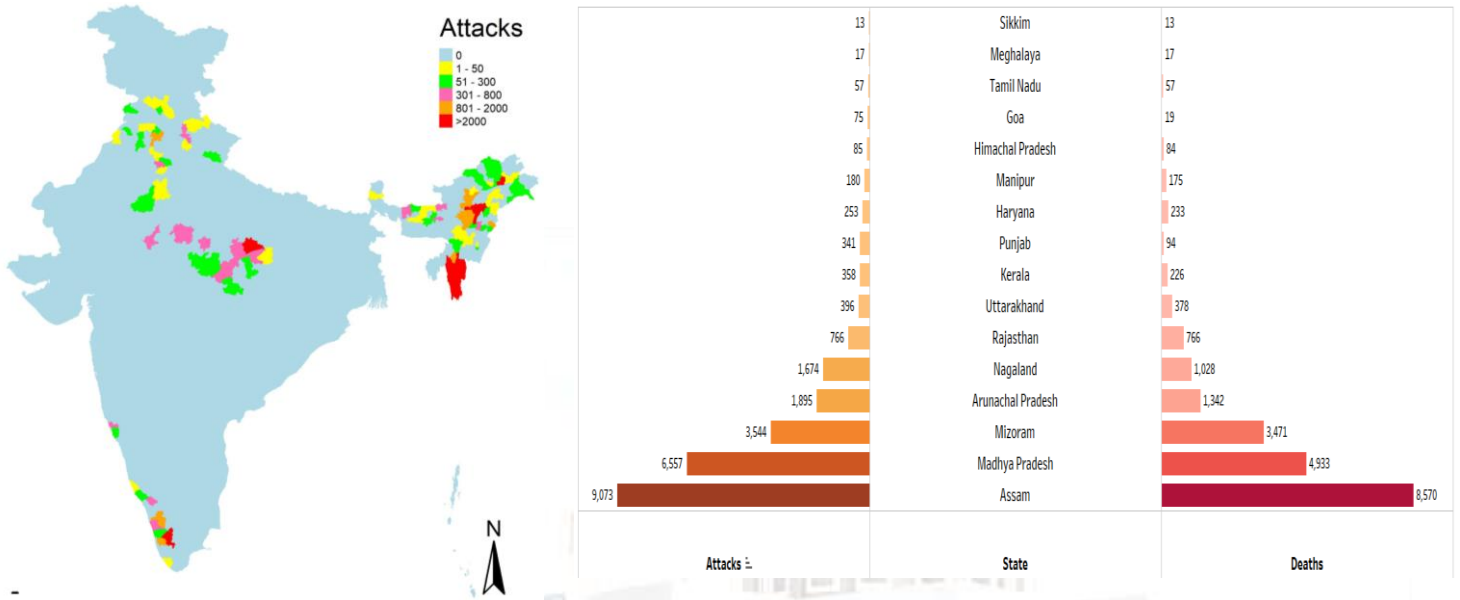


## Outbreaks/Incidence-Trypanosomiasis(1990-2022)



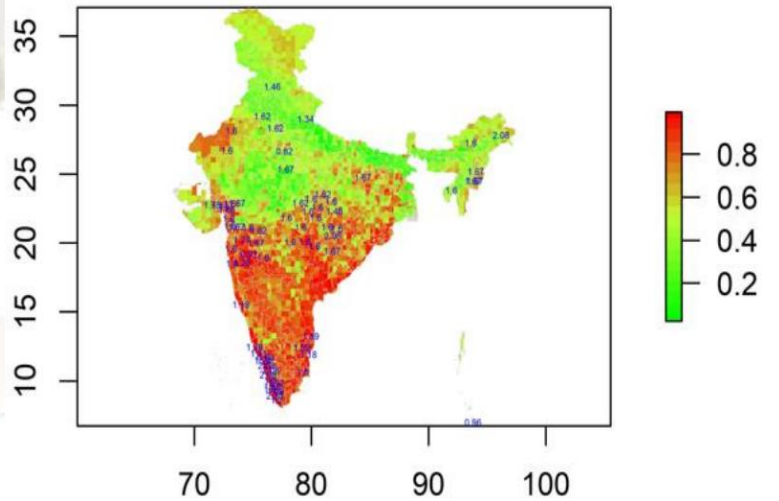
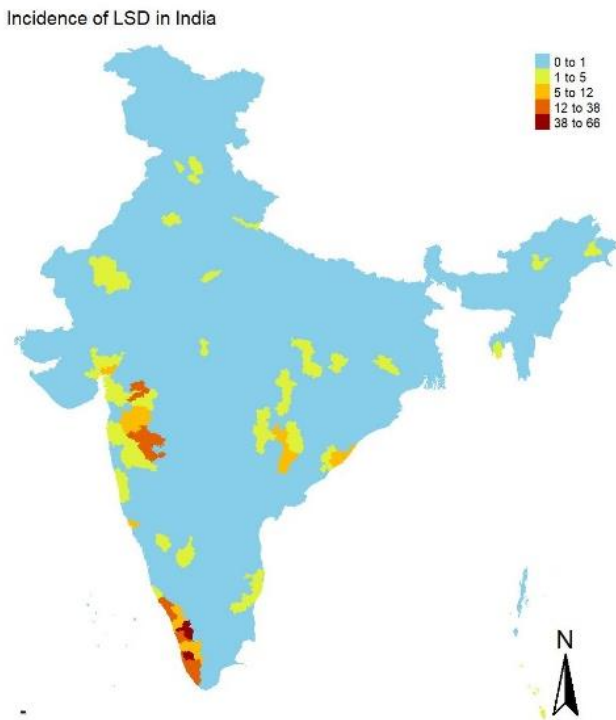
# 11.5. MODEL BASED RISK MAPS OF LIVESTOCK INFECTIOUS DISEASES IN INDIA

## Disease map considering attacks of ASFV in India



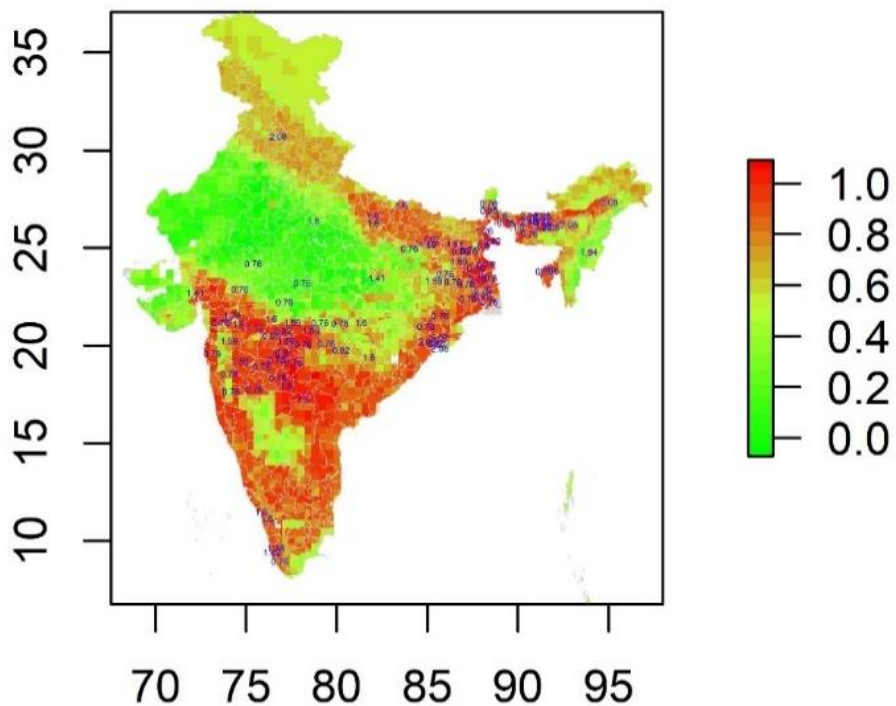
## Incidence of LSD in India

## Risk map for LSD in India

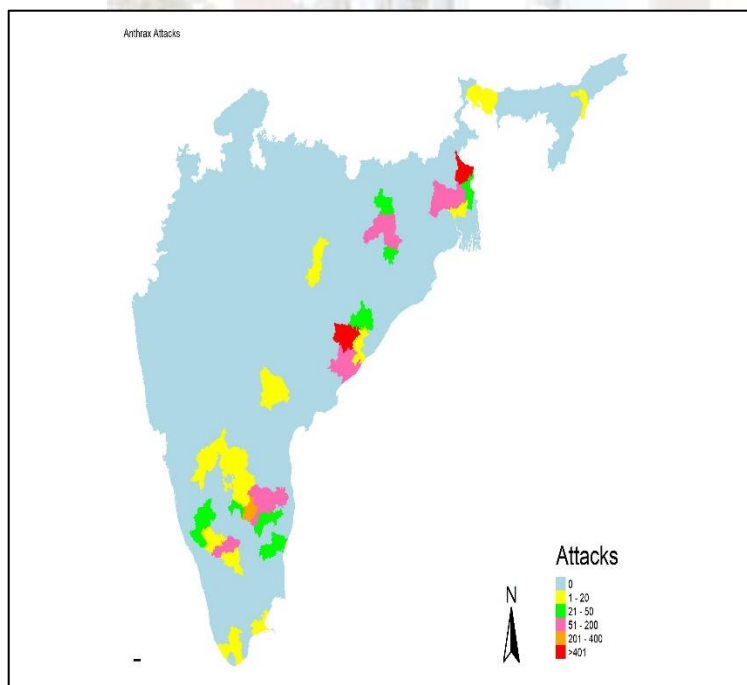




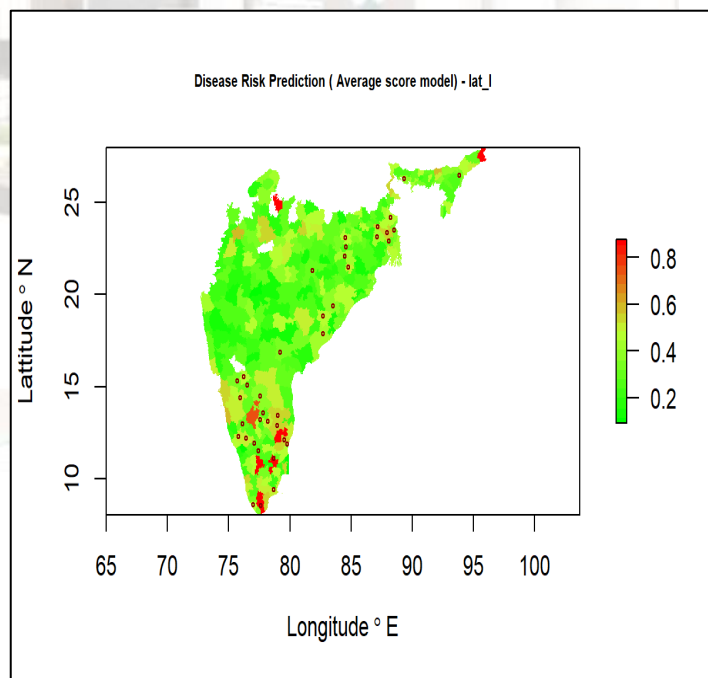
**Risk map for Avian Influenza in India**



**Disease Map for Anthrax on Attacks**

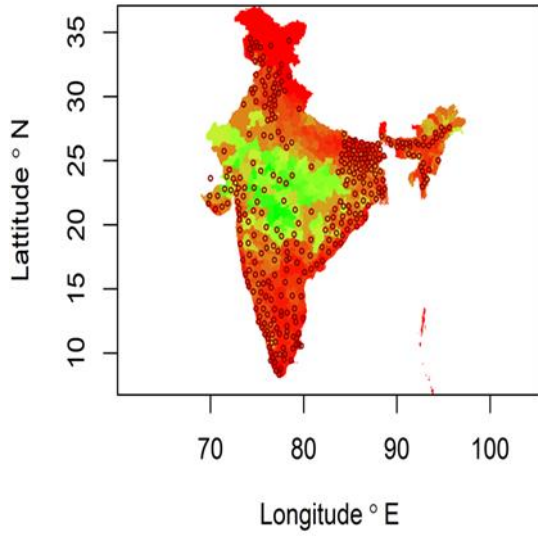


**Risk map for Anthrax in India**

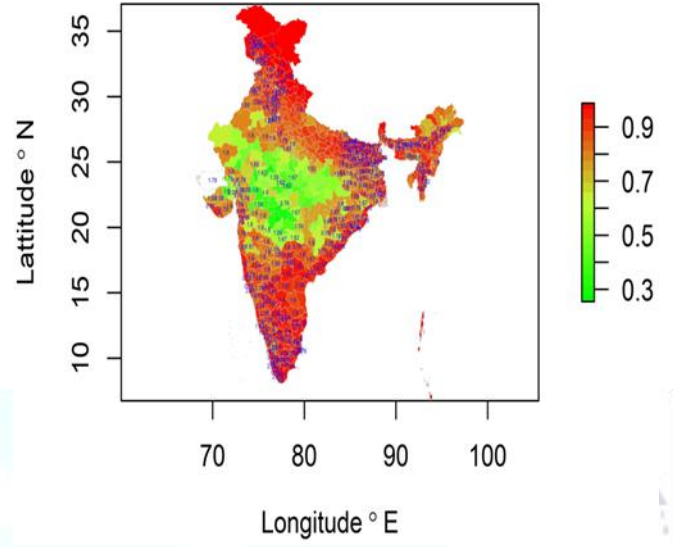


**FMD district wise Risk map (2000-2004)**

**Without R0**

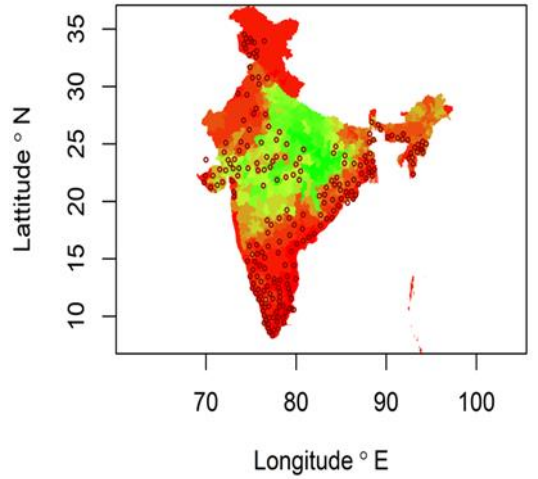


**With R0**

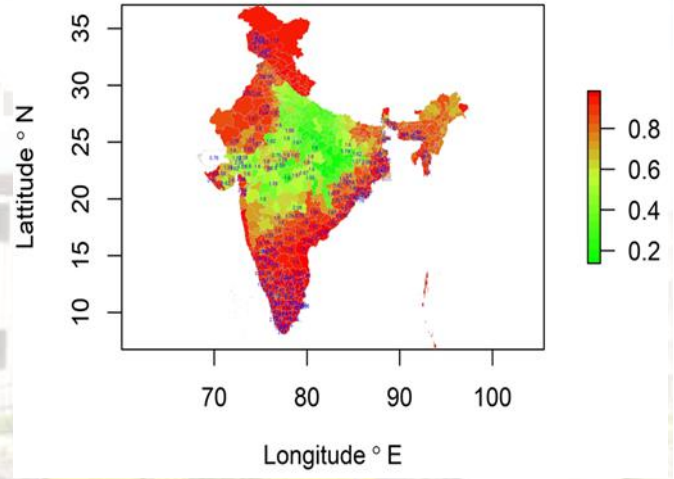


**FMD district wise Risk map (2005-2009)**

**Without R0**

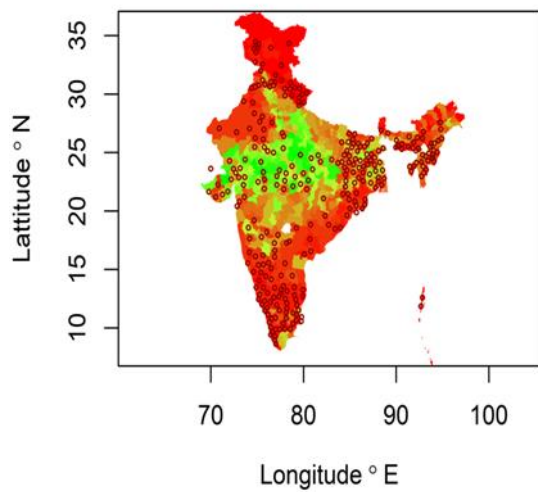


**With R0**

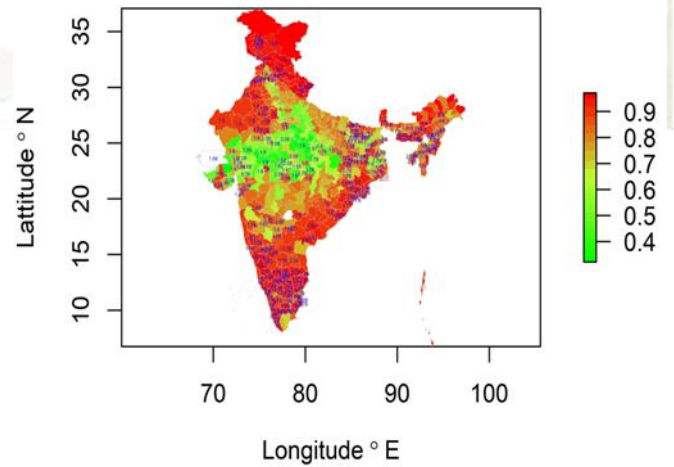


**FMD district wise Risk map (2010-2014)**

**Without R0**

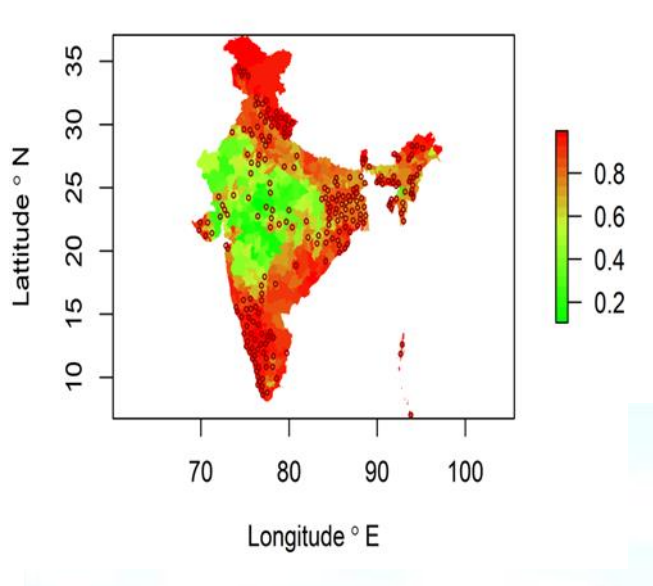


**With R0**

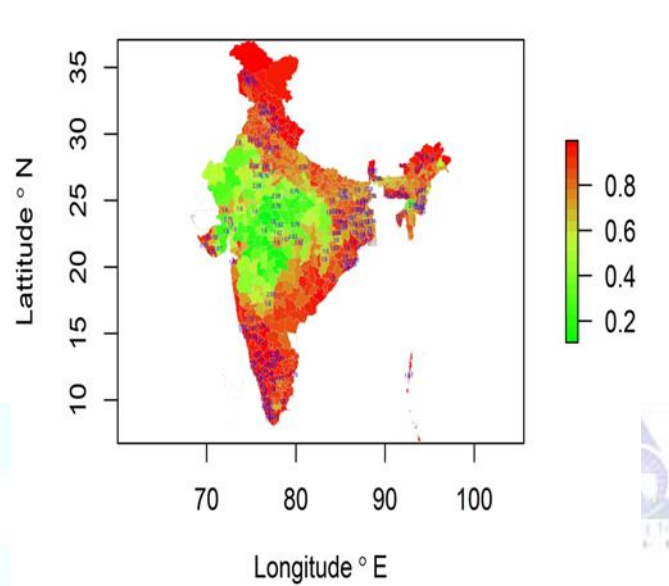


**FMD district wise Risk map (2015-2019)**

**Without R0**

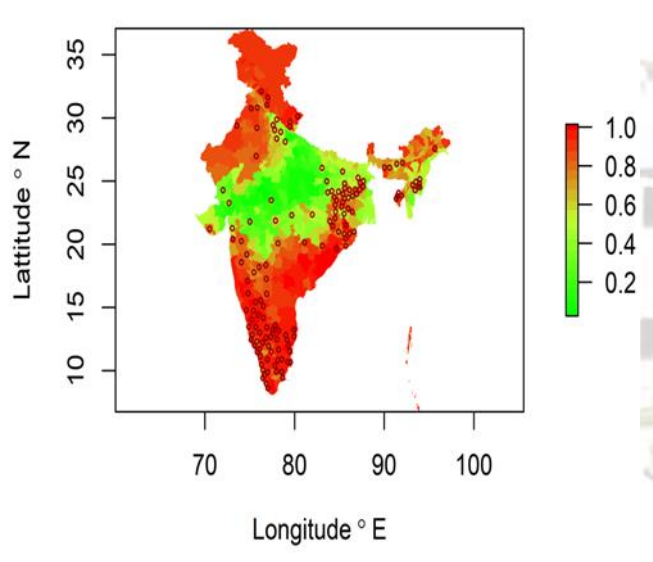


**With R0**

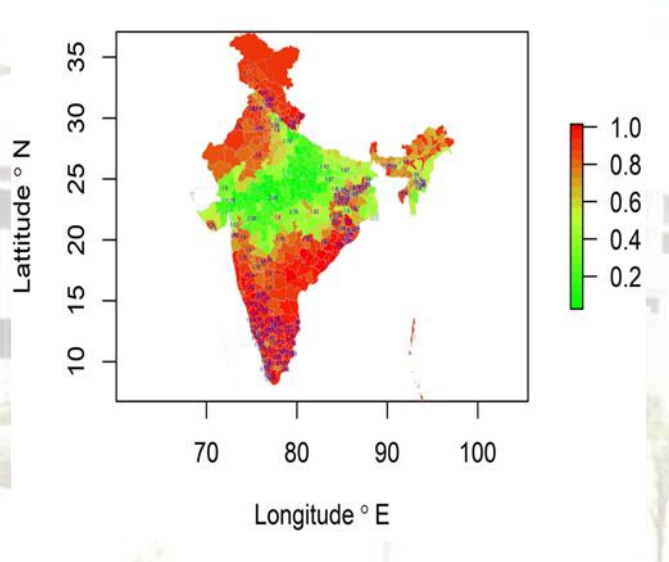


**FMD district wise Risk map (2020-2023)**

**Without R0**

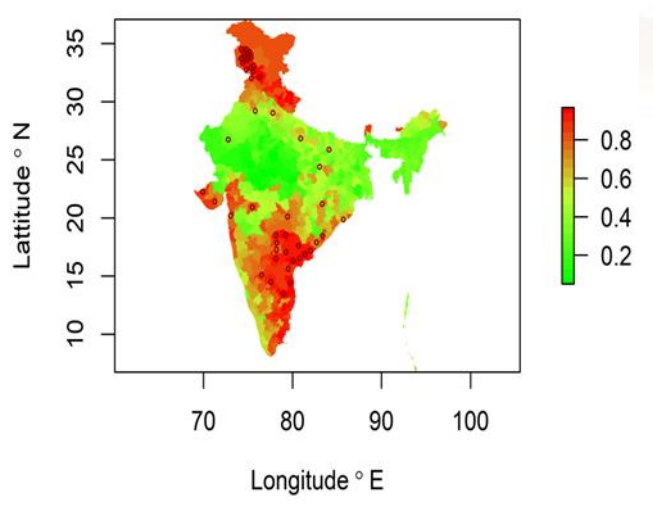


**With R0**

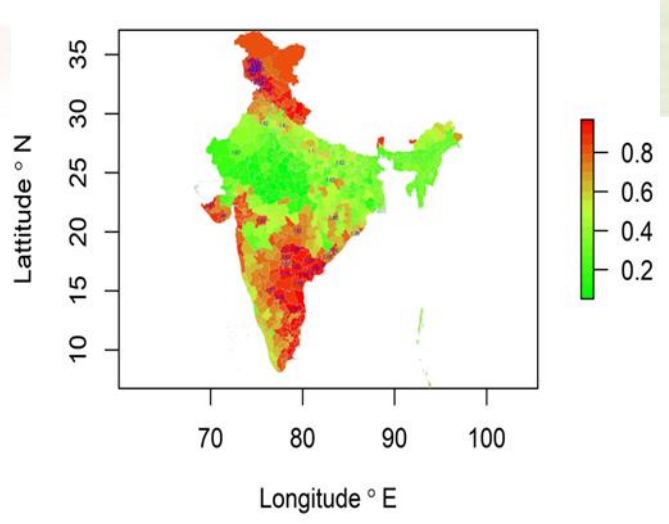


**Foot rot district wise Risk map (2001-2019)**

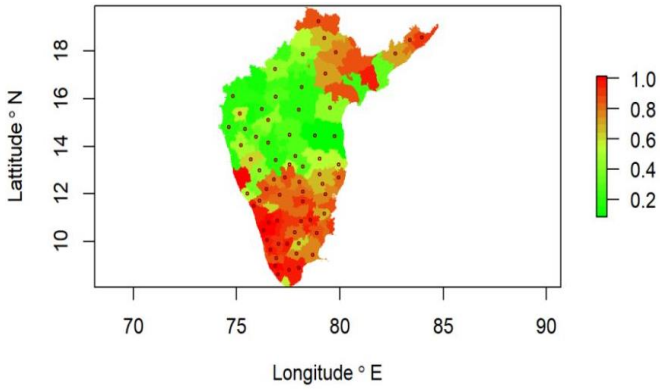
**Without R0**



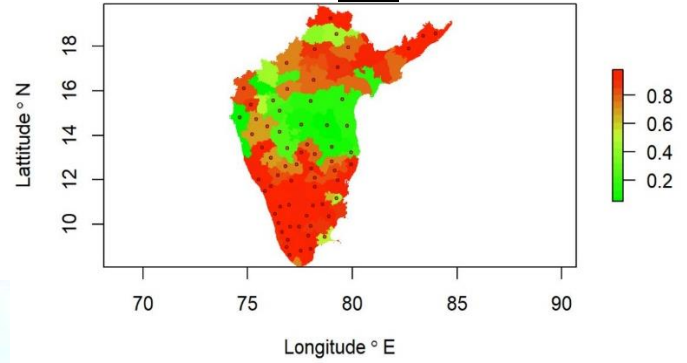
**With R0**



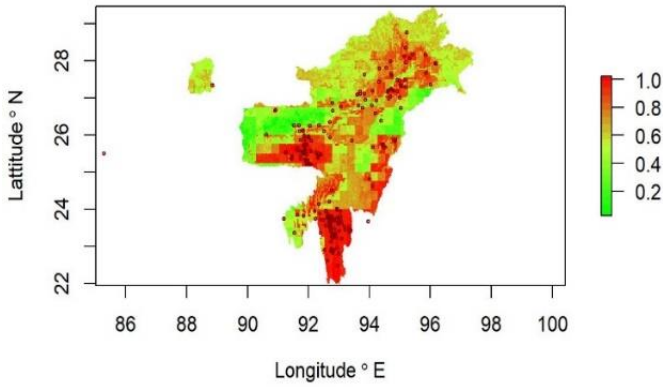
**Risk prediction for Anthrax Disease for Southern India**



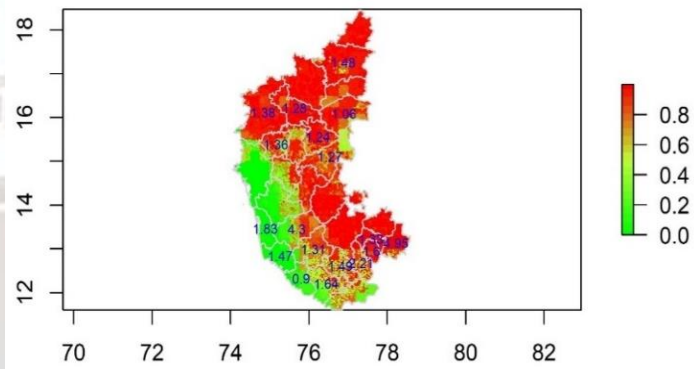
**Risk prediction for Enterotoxaemia Disease for Southern India**



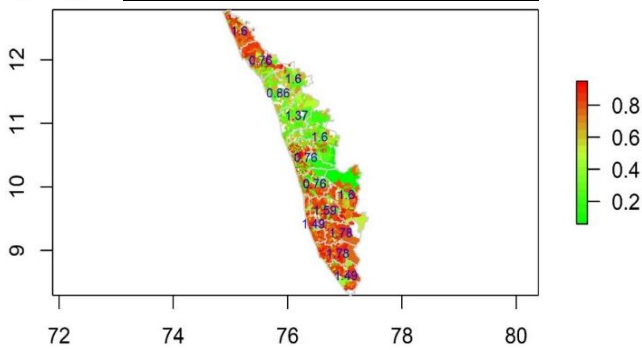
**Risk prediction for ASF for North Eastern India**



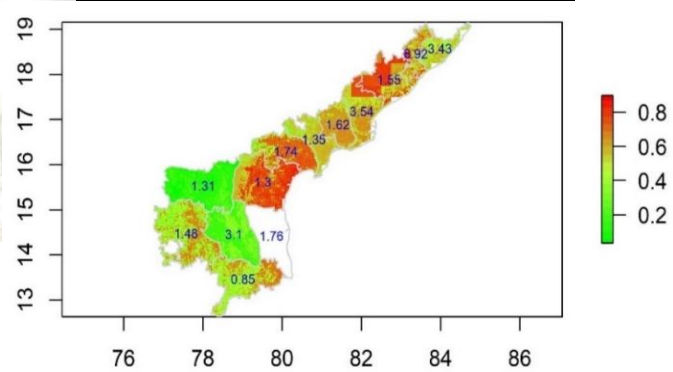
**Karnataka Risk map Bluetongue**



**Risk map of Anaplasmosis in Kerala**

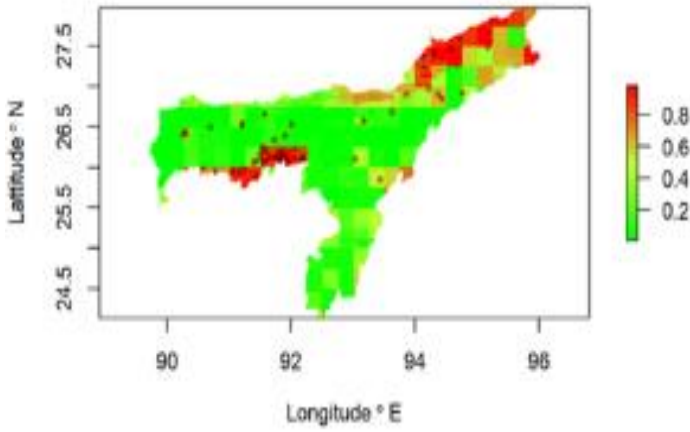


**Risk map of Bluetongue in Andhra Pradesh**

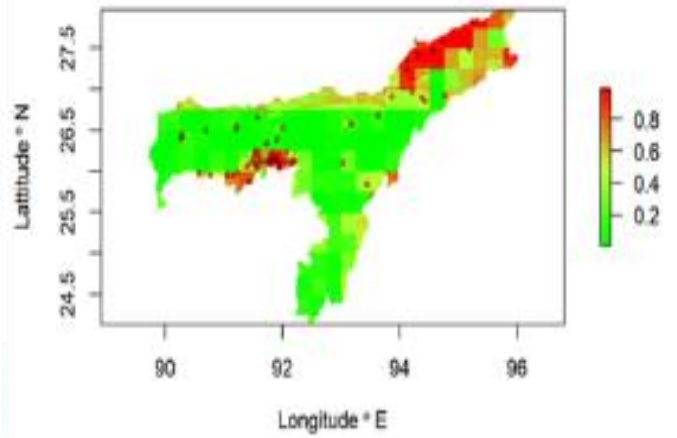


**Forecasted risk maps for Classical Swine Fever disease in Assam**

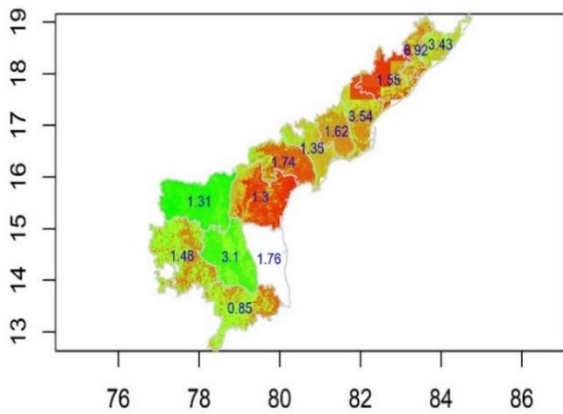
Disease Risk Prediction (Average score model) - Classical Swine Fever 2019-20



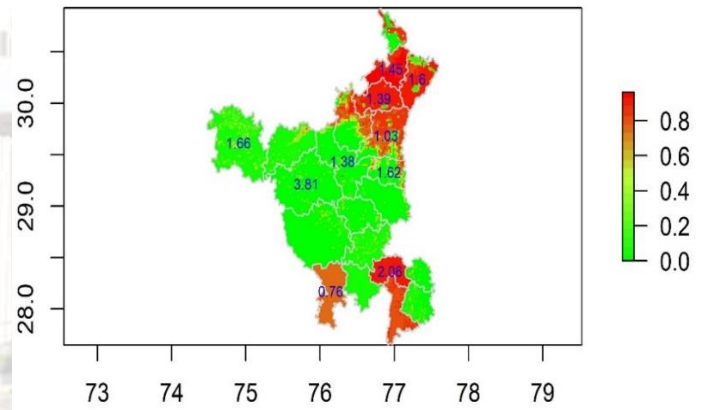
Disease Risk Prediction (Average score model) - Classical Swine Fever 2021-23



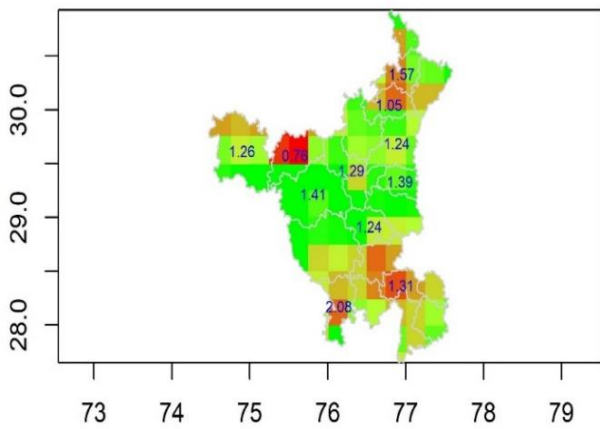
**Risk map for Bluetongue in Andhra Pradesh**



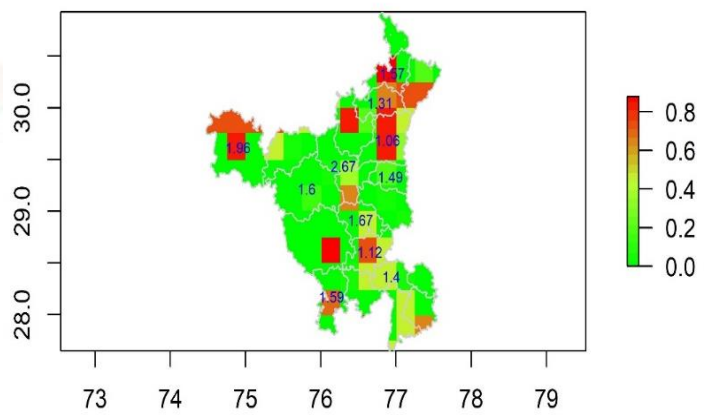
**Risk map for Babesiosis in Har yana**



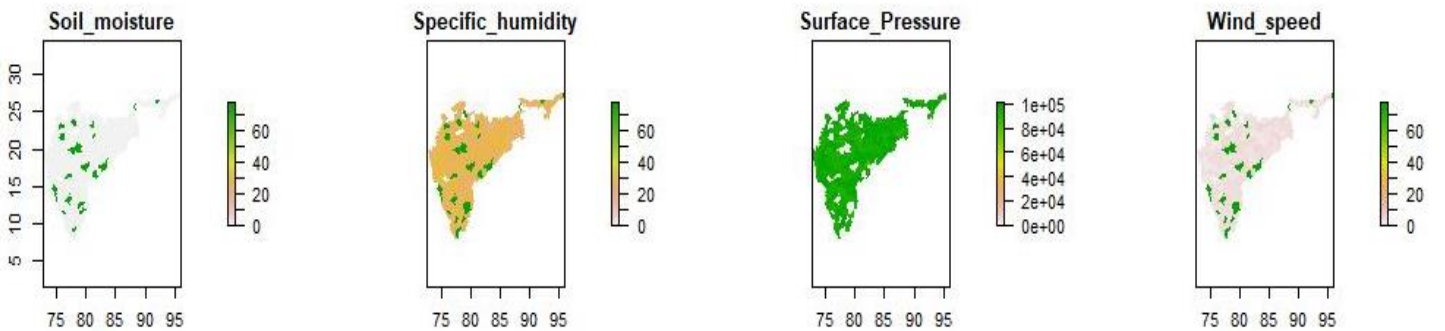
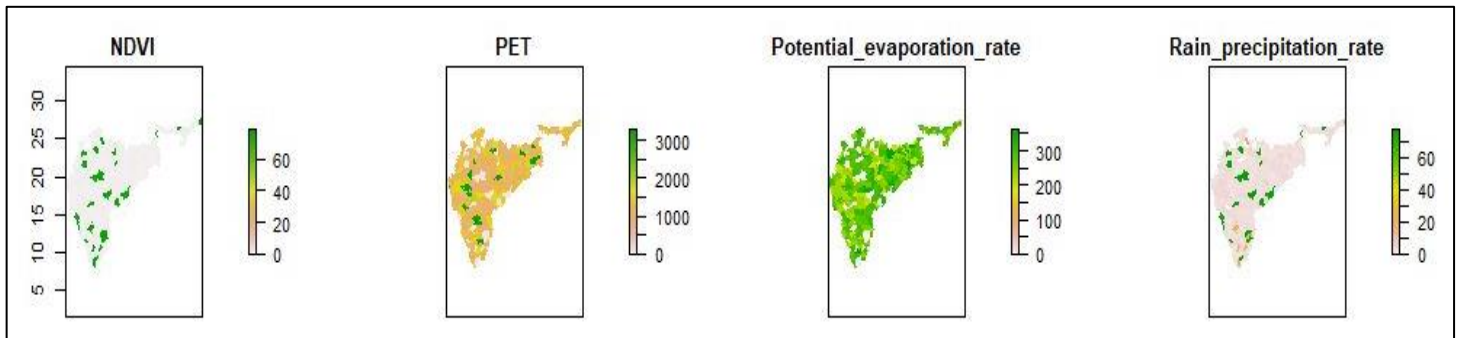
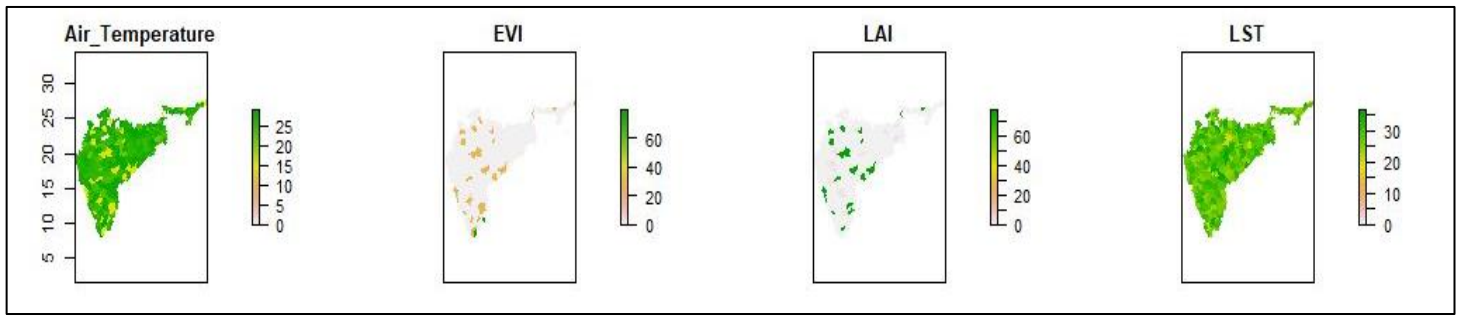
**Risk map for Theileriosis in Har yana**



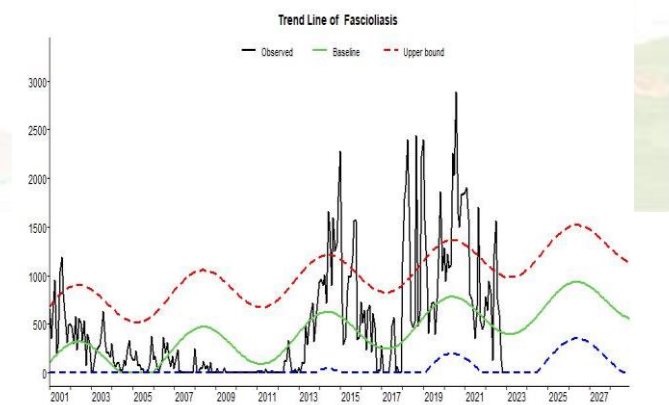
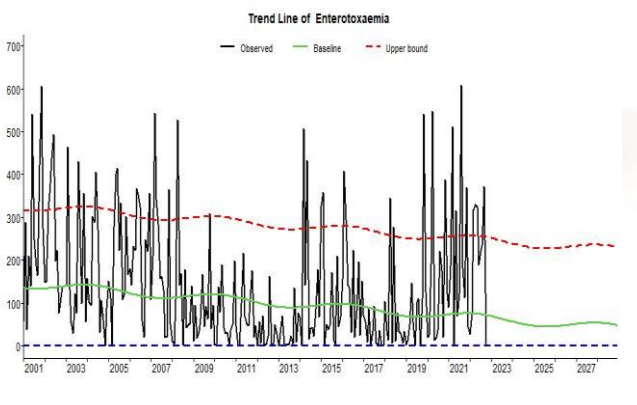
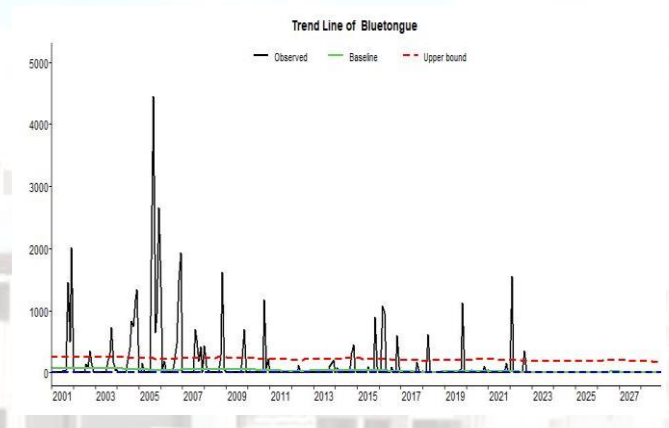
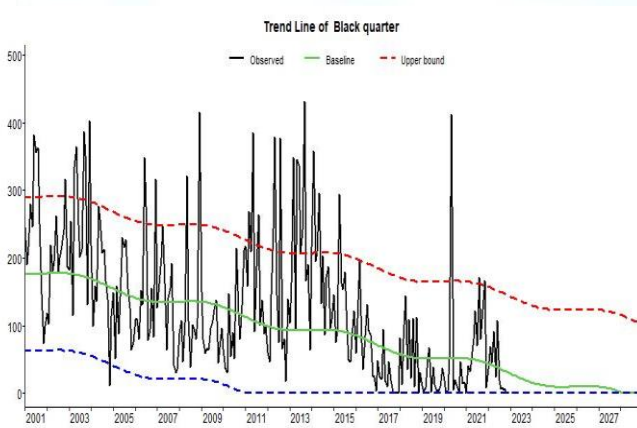
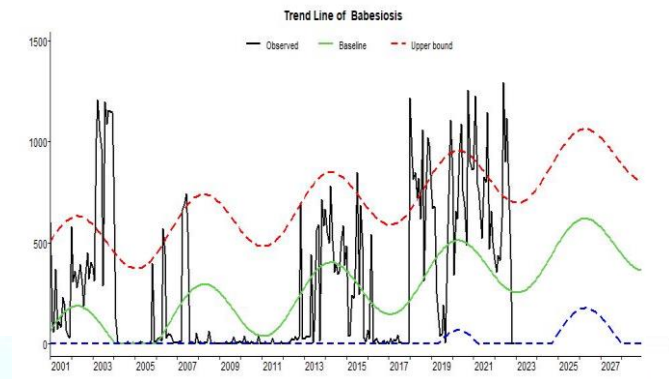
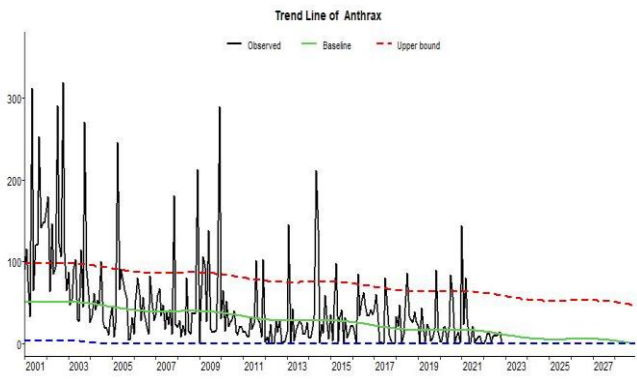
**Risk map for Trypanosomiasis in Har yana**

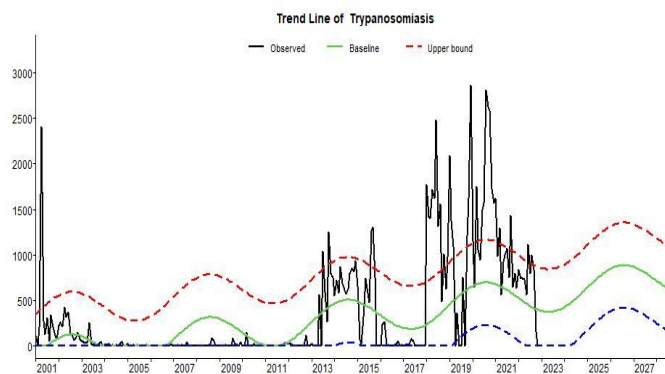
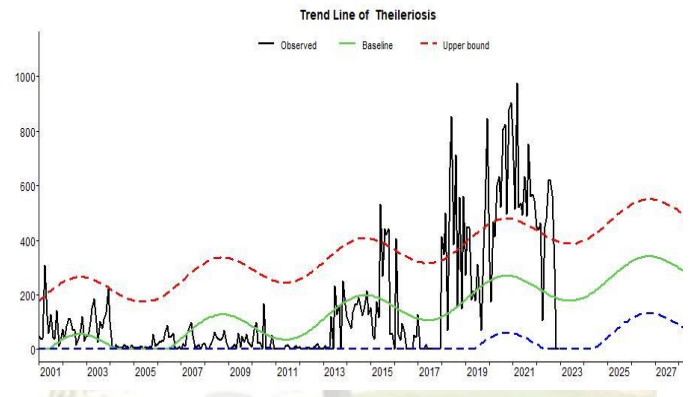
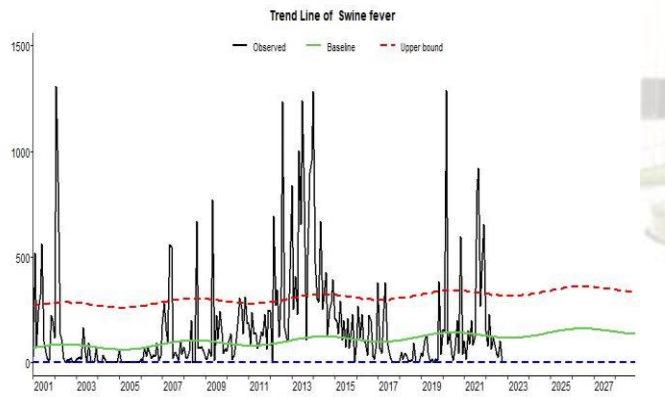
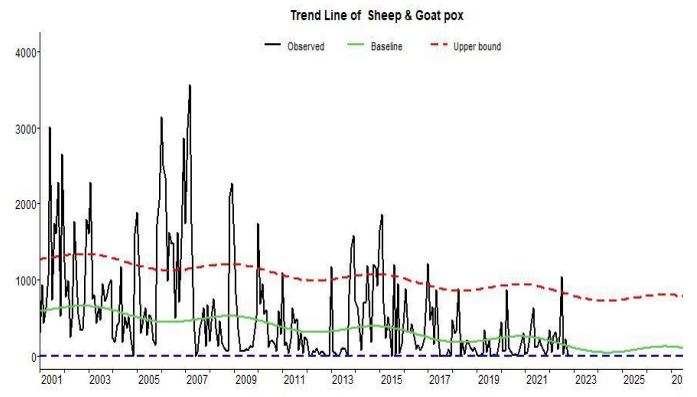
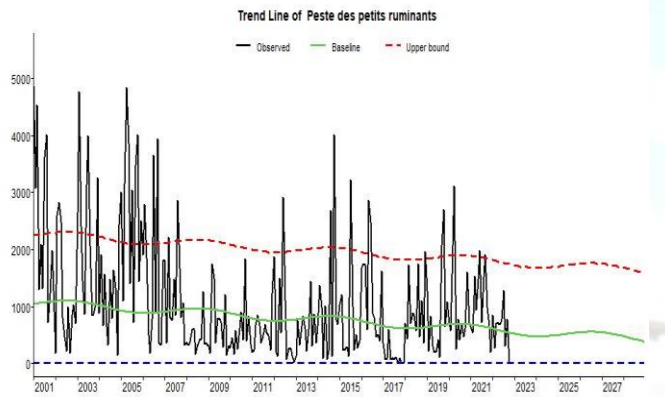
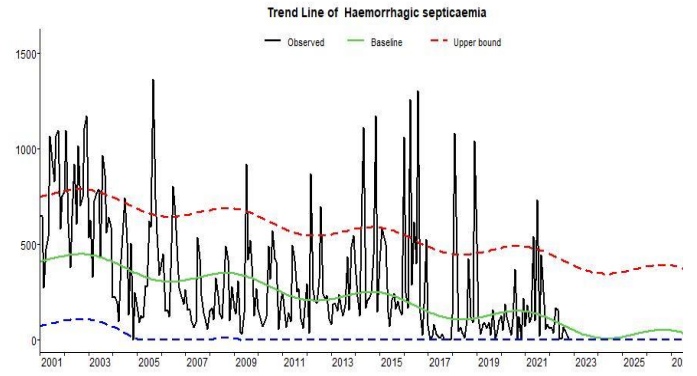
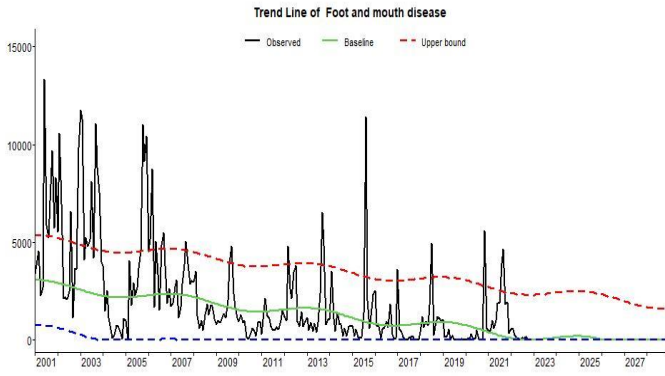


## Effects of different parameters on Anthrax disease



# 11.6. Model based Periodic Regression Model 2023







## 12. APPLICATION OF META ANALYSIS FOR UNDERSTANDING THE DISEASE PREVALENCE

Veterinary World, EISSN: 2231-0916  
Available at [www.veterinaryworld.org/Vol.11/March-2018/7.pdf](http://www.veterinaryworld.org/Vol.11/March-2018/7.pdf)

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

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**Received:** 18-11-2017, **Accepted:** 18-01-2018, **Published online:** 13-03-2018

**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

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Kempanahalli M. Ranjitha<sup>2</sup>, Channappagowda Shivaranjini<sup>2</sup>, Parimal Roy<sup>4</sup> and Kuralayanapalya P. Suresh<sup>3</sup>

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**Corresponding author:** Kuralayanapalya P. Suresh, e-mail: [sureshkp97@gmail.com](mailto:sureshkp97@gmail.com)

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**Received:** 26-07-2019, **Accepted:** 22-11-2019, **Published online:** 11-01-2020

**doi:** [www.doi.org/10.14202/vetworld.2020.80-91](http://www.doi.org/10.14202/vetworld.2020.80-91) **How to cite this article:** Barman NN, Patil SS, Kurli R, Deka P, Bora DP, Deka G, Ranjitha KM, Shivaranjini C, Roy P, Suresh KP (2020) Meta-analysis of the prevalence of livestock diseases in North Eastern region of India, *Veterinary World*, 13(1): 80-91.

### 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<sup>1,2</sup>, Bhavya, A. P<sup>1</sup>, Akshata, N<sup>1</sup>, Kumar, K, V<sup>1</sup>, Bokade, P. P<sup>1</sup>, Suresh,  
K. P<sup>1</sup>, Shome, B. R<sup>1</sup>, Balamurugan, V<sup>1</sup> \****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*

Received 18 November 2021; Accepted 14 December 2021

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](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**

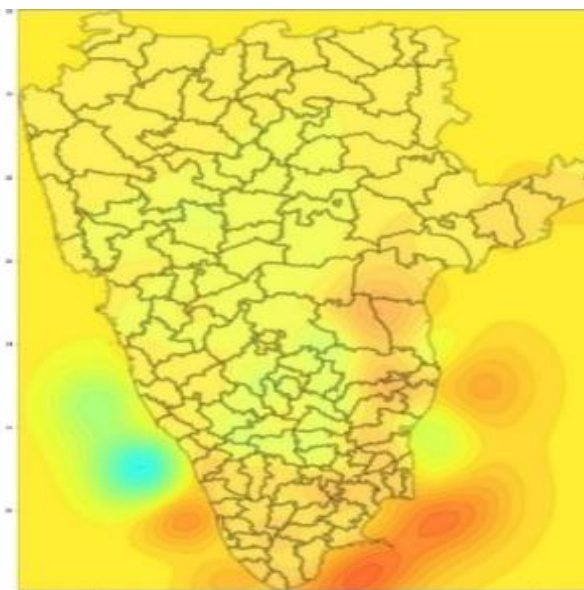
**Abstract**

*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.

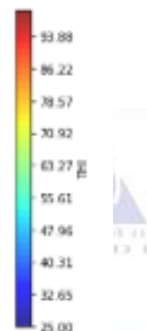
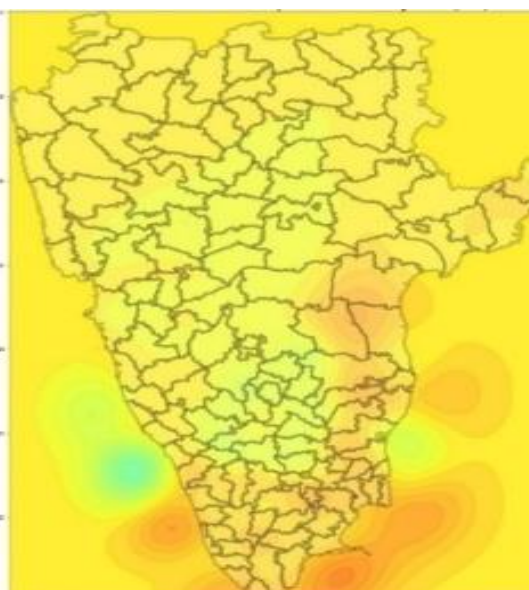
# 14. IMPACT OF CLIMATE CHANGE ON LIVESTOCK DISEASE INCIDENCE

## 14.1 Southern States Temperature Humidity Index (THI) 2001-2021

THI for 2001



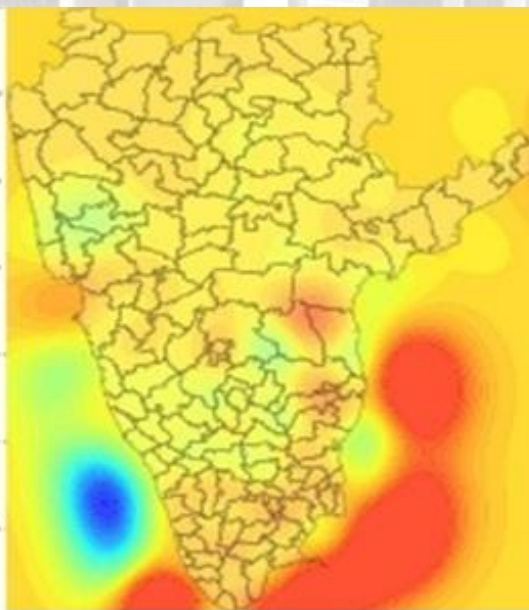
THI for 2011



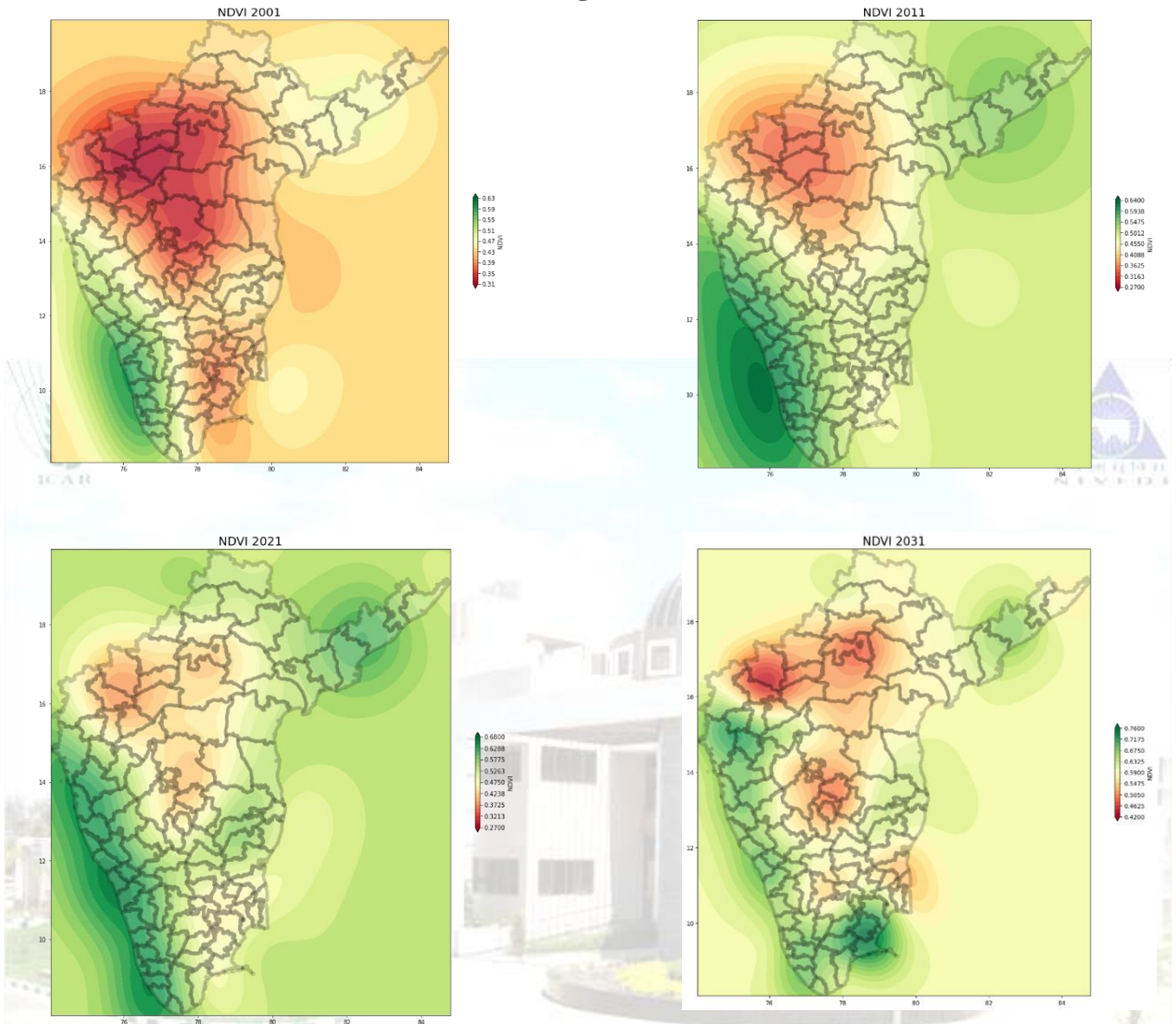
THI for 2021



THI for 2023 (Predicted)

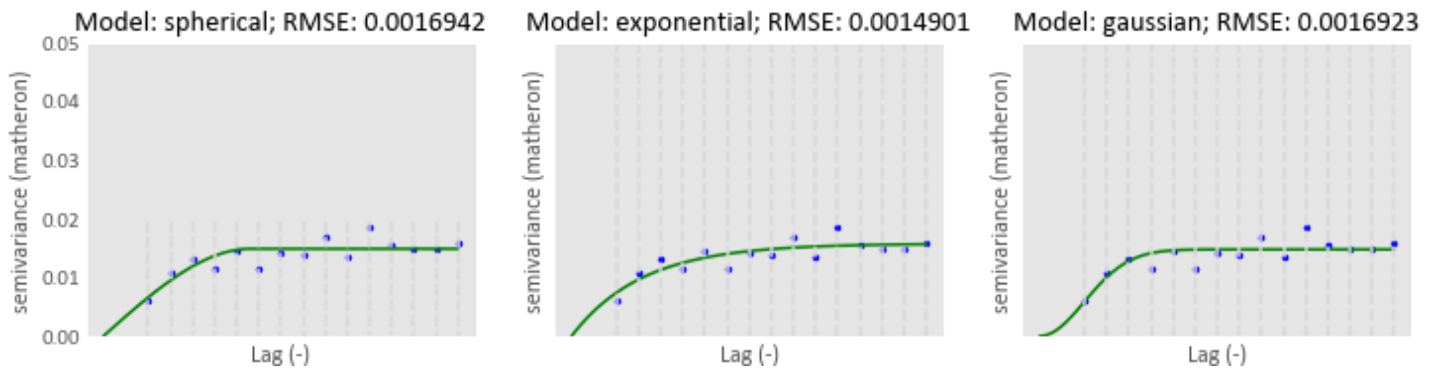


## 14.2. Southern States Normalized Difference Vegetation Index (NDVI)

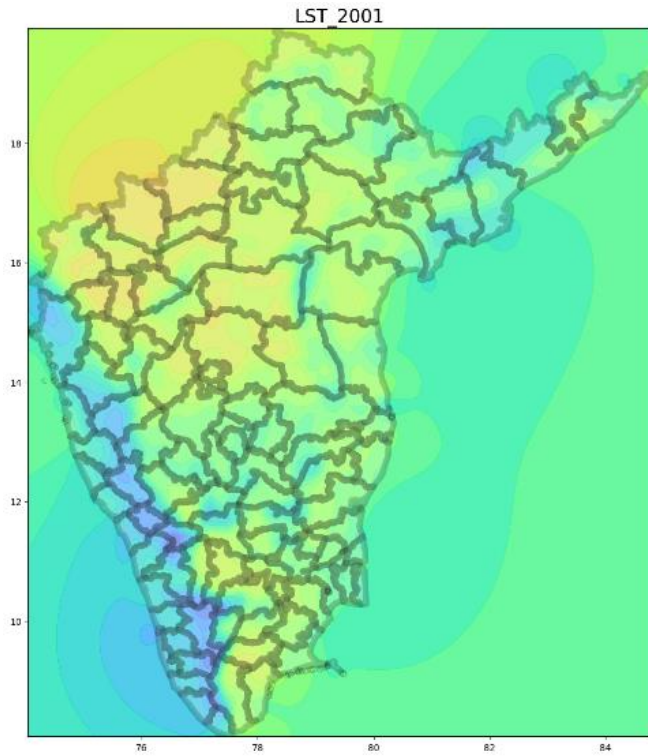


### Best fit Variogram model for NDVI:

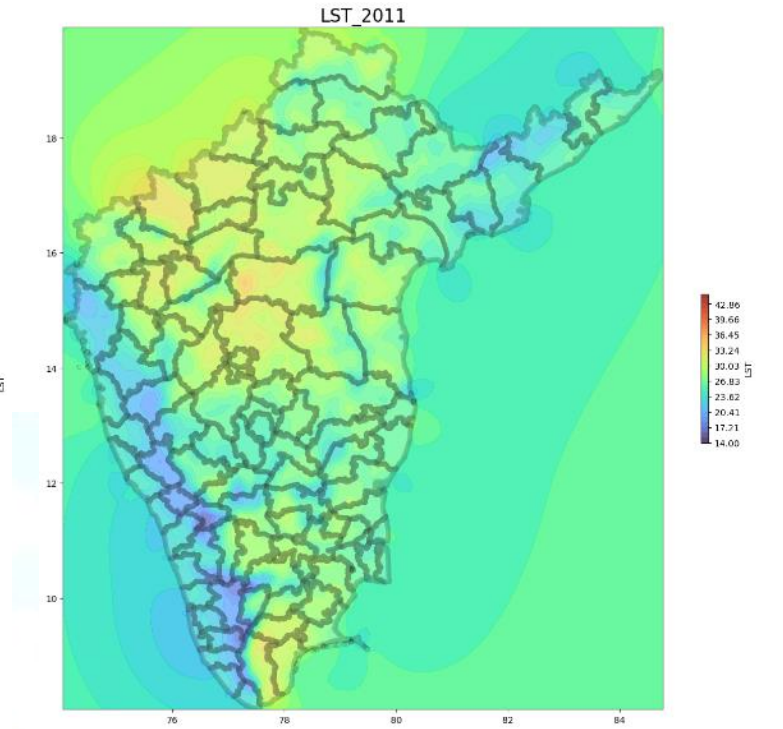
After comparing various variogram models, we could choose the one that would fit kriging the best based on the RMSE value. Based on the result with the lowest RMSE, we may say that the exponential model was best specified.



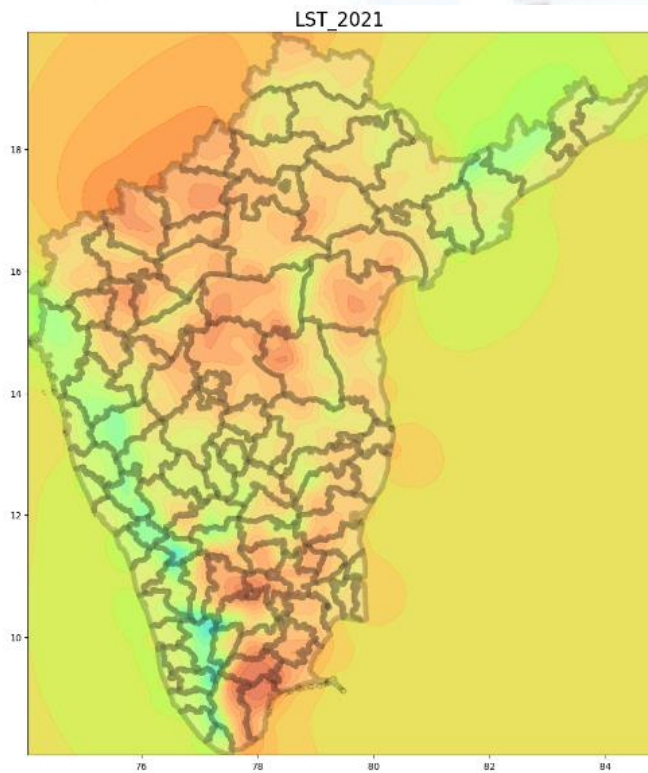
# 14.3 Land Surface Temperature (LST) - 2001-2031



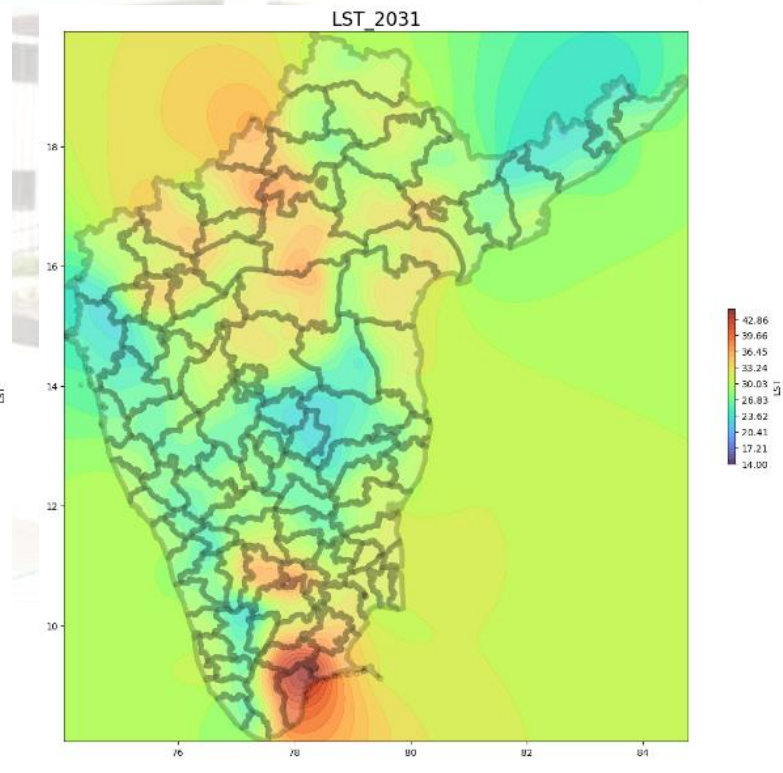
LST-2001



LST-2011



LST-2021

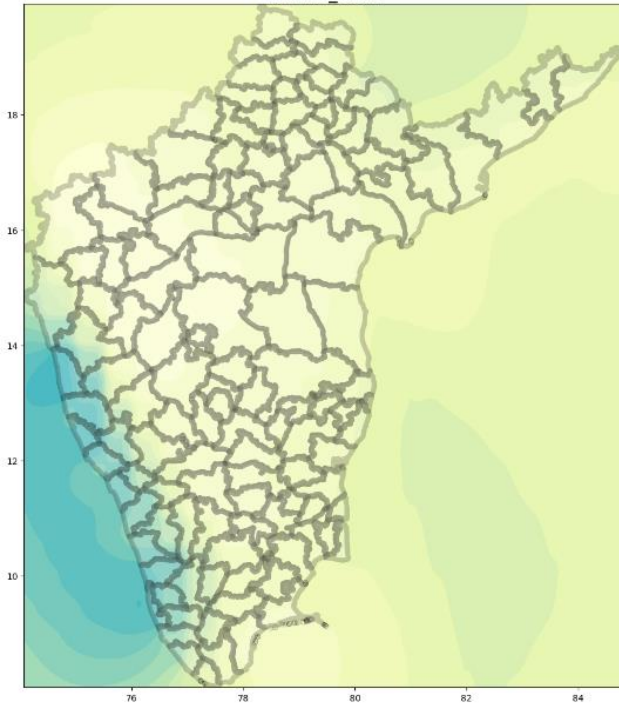


LST-2031(Predicted)



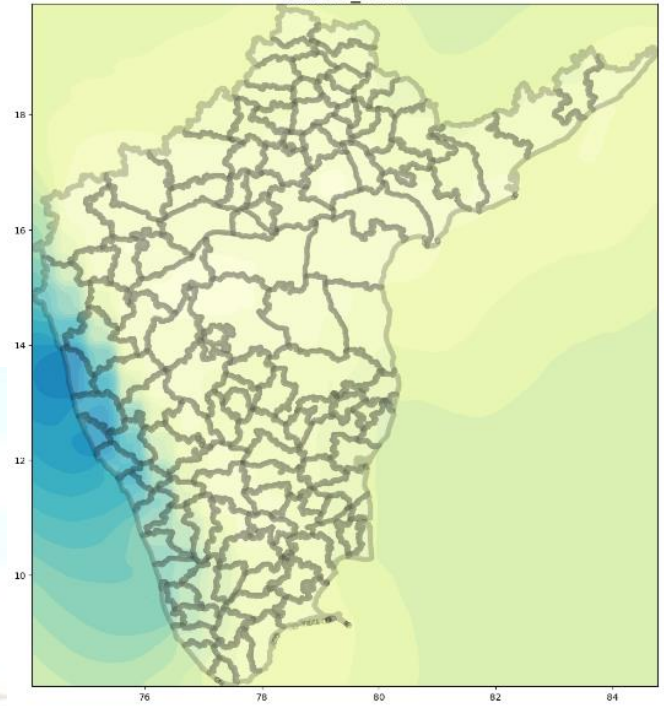
# 14.4 Rainfall - 2001-2031

Rainfall\_2001



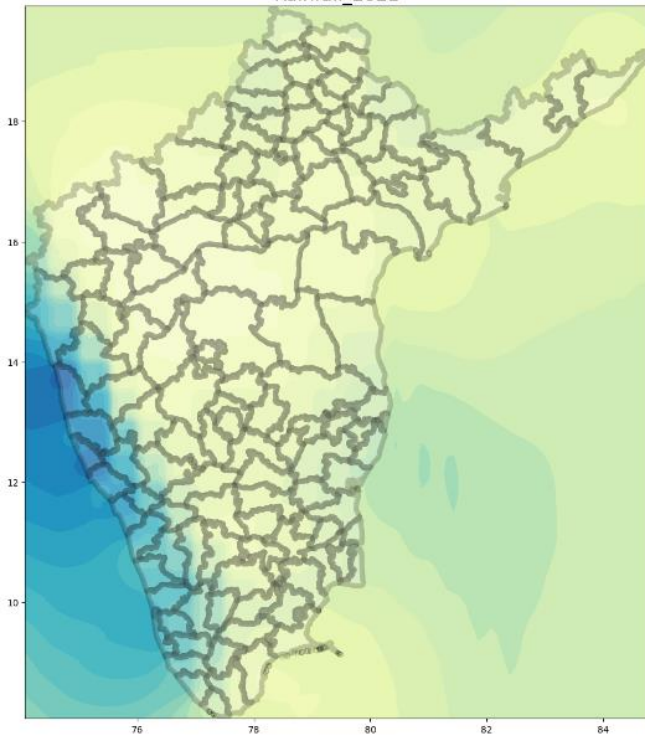
**Rainfall 2001**

Rainfall\_2011



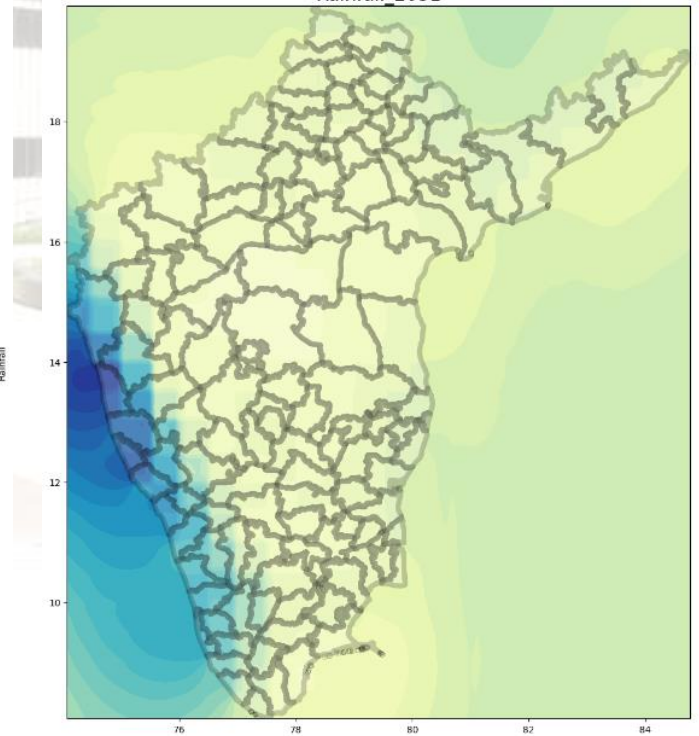
**Rainfall 2011**

Rainfall\_2021



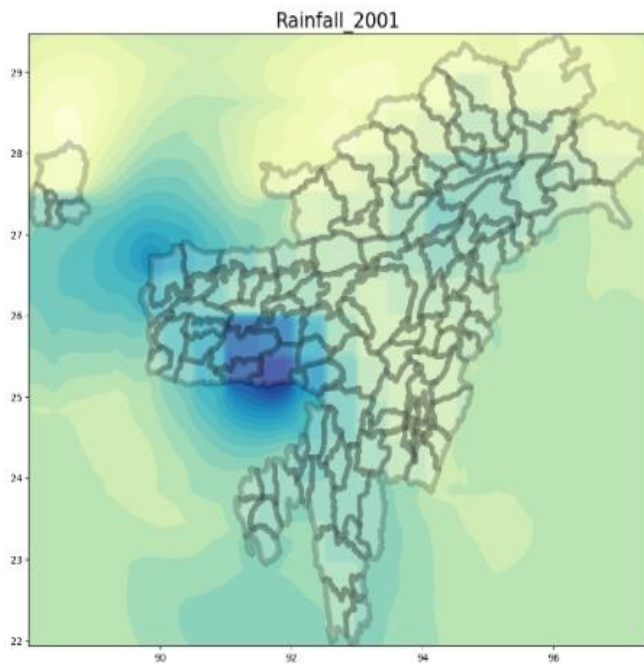
**Rainfall 2021**

Rainfall\_2031

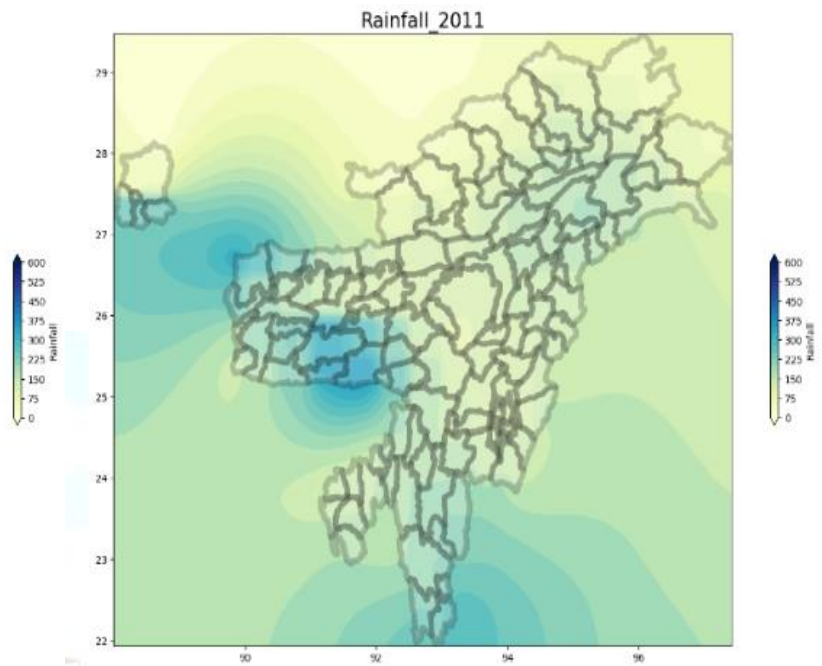


**Rainfall 2031 (Predicted)**

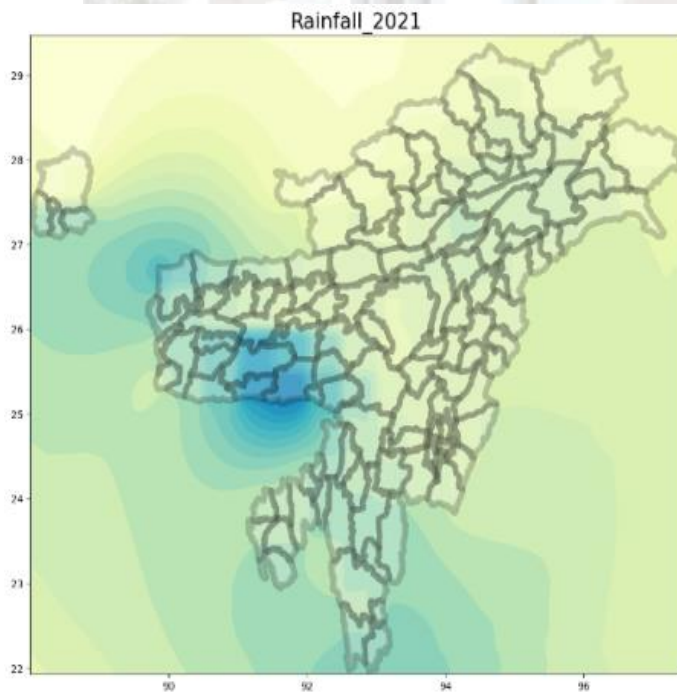
# 14.5 Rainfal NER 2001-2031



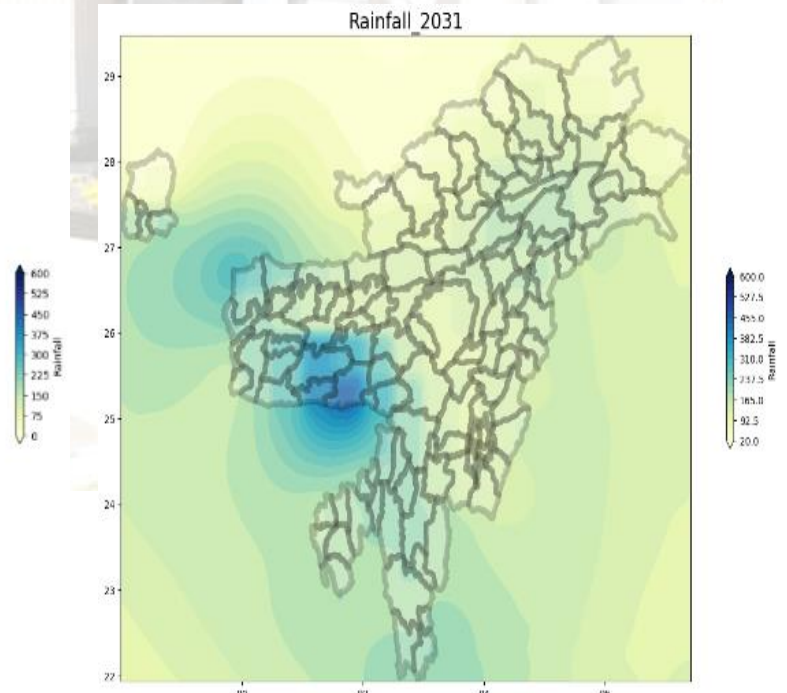
**Rainfall 2001**



**Rainfall 2011**

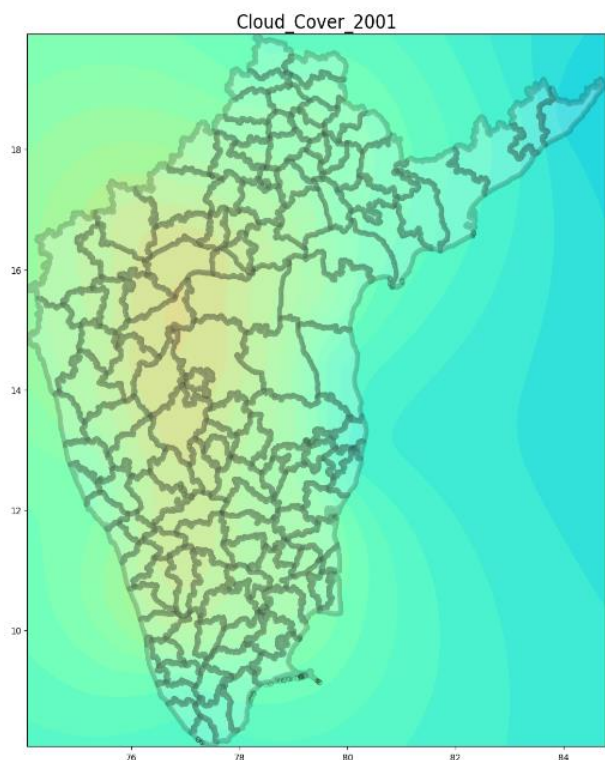


**Rainfall 2021**

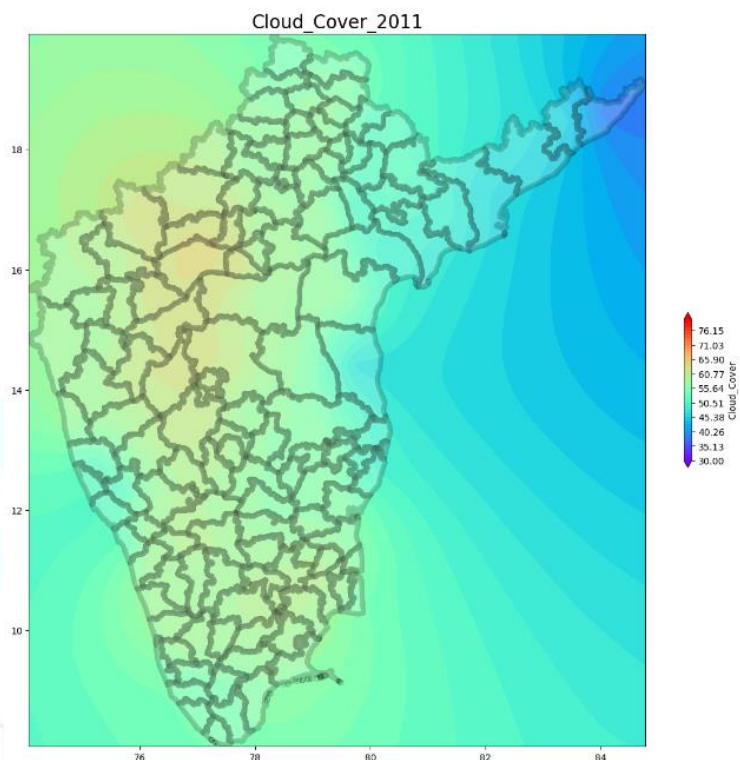


**Rainfall 2031(Predicted)**

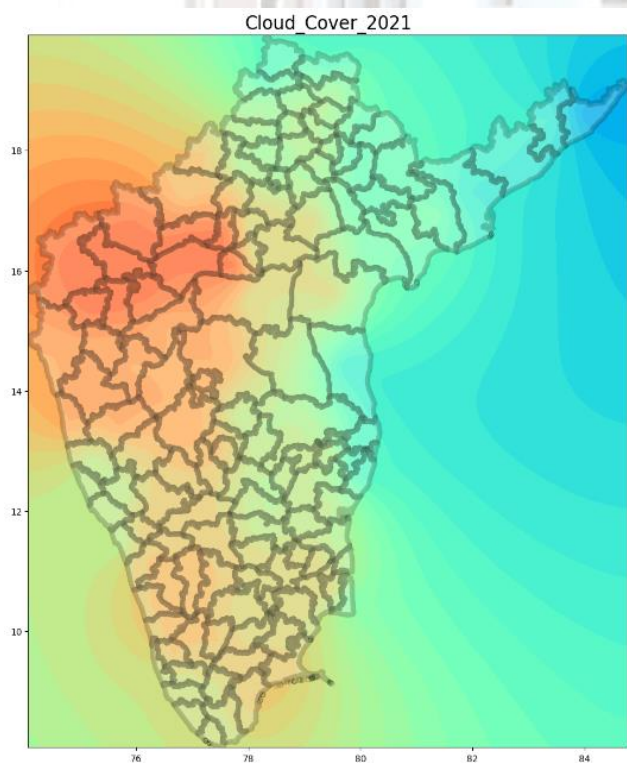
## 14.6 Cloud cover – 2001-2031



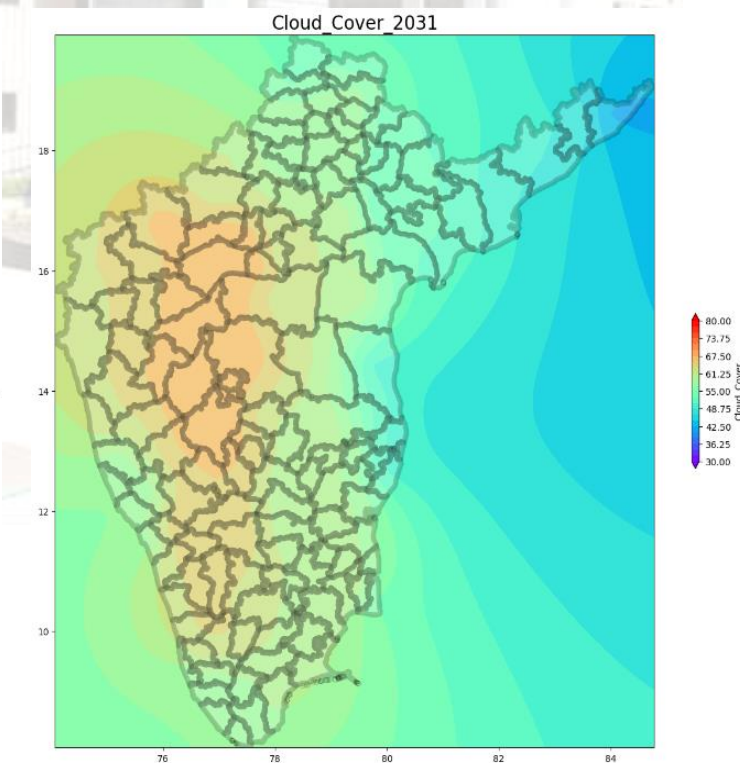
**Cloud cover 2001**



**Cloud cover 2011**

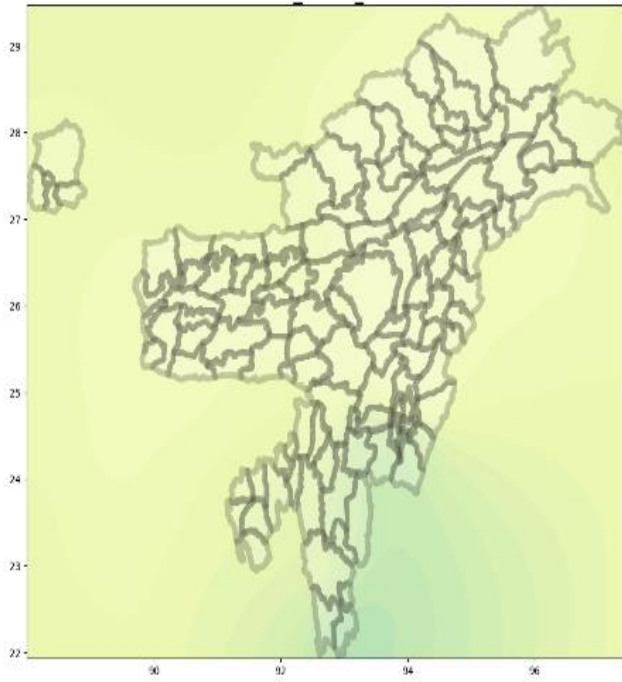


**Cloud cover 2021**

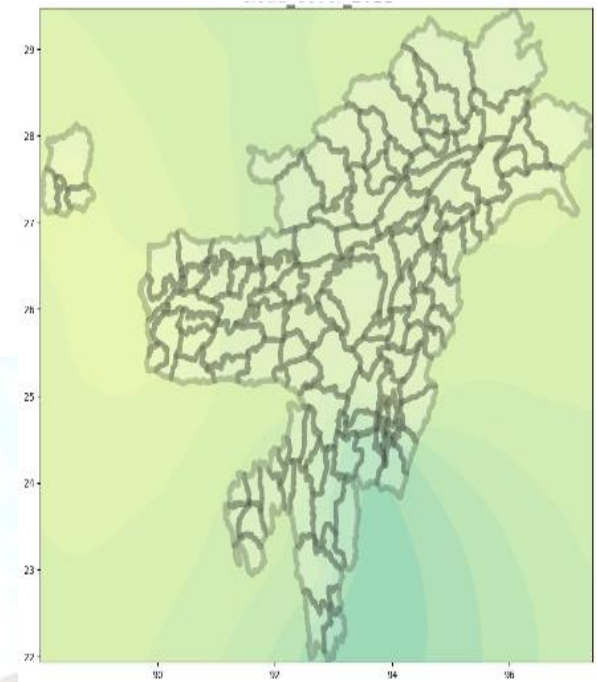


**Cloud cover 2031**

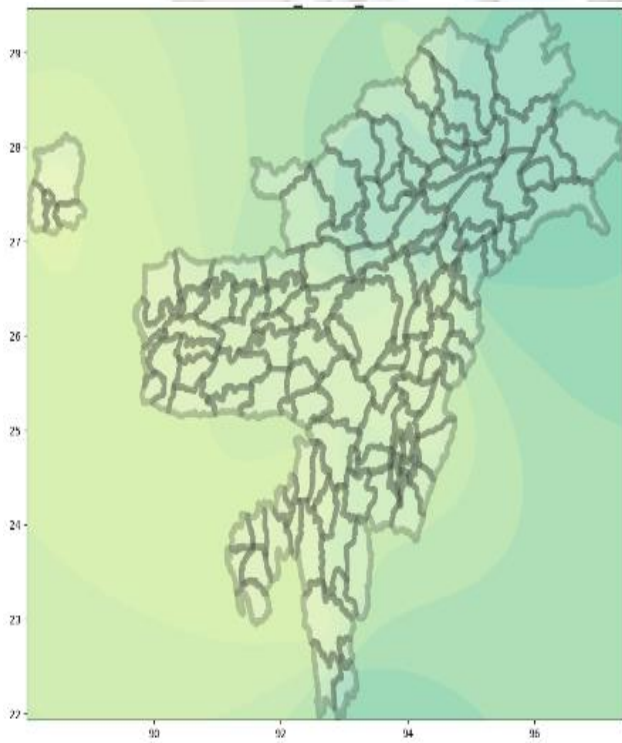
### 14.7 Cloud cover NER 2001-2031



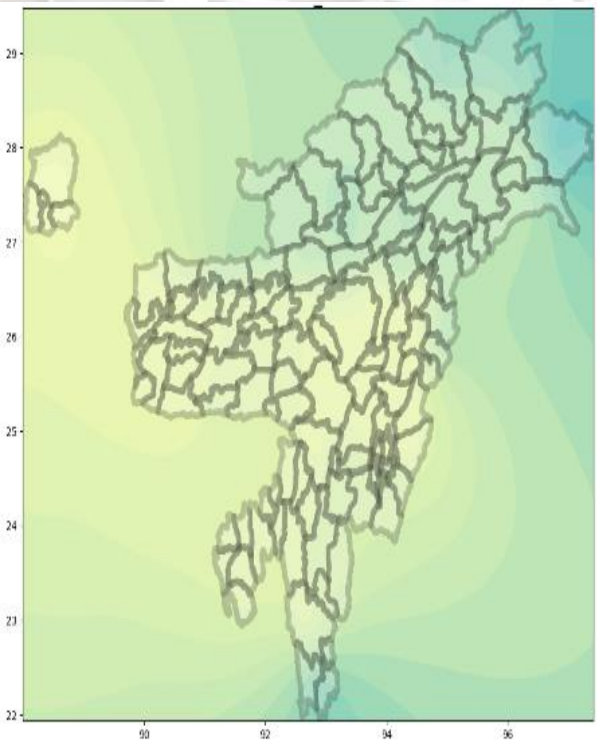
**Cloudcover – 2001**



**Cloudcover - 2011**

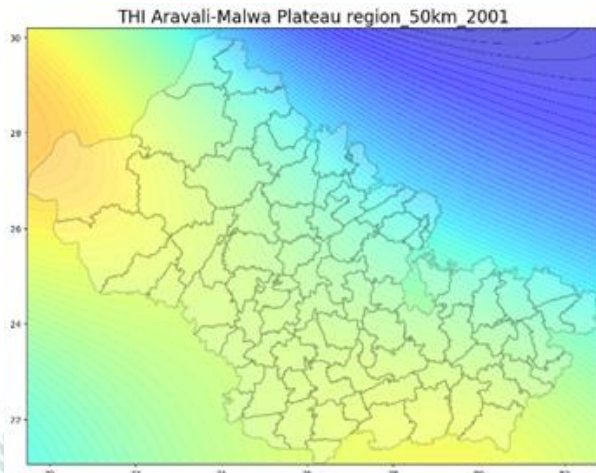


**Cloudcover- 2021**

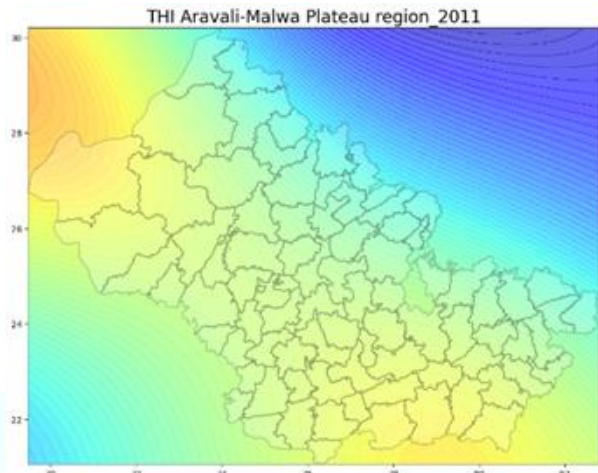


**Cloudcover- 2031**

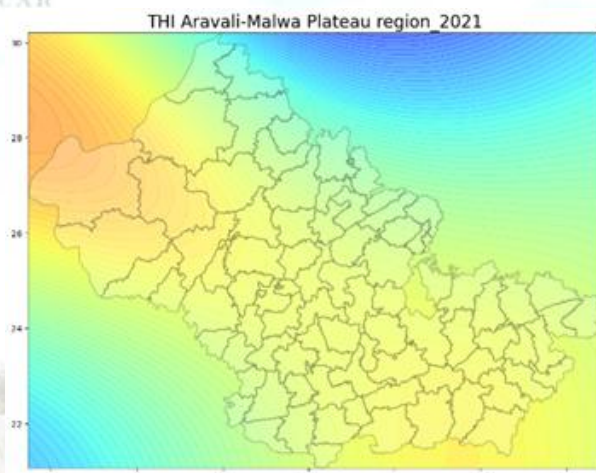
## 14.8 THI for Aravalli Central Plateau & Hills 2001-2033 (Predicted)



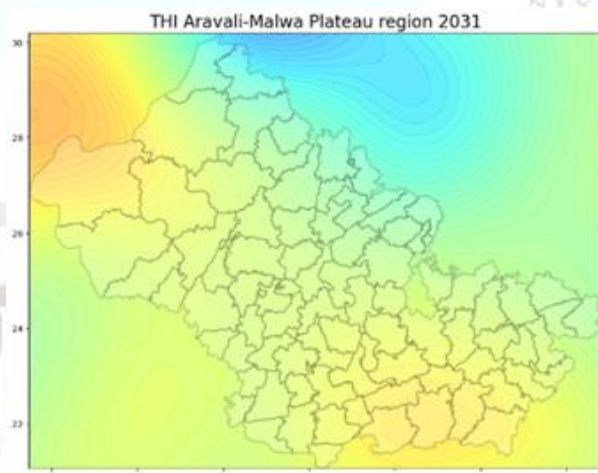
THI for Aravalli Central Plateau & Hills 2001



THI for Aravalli Central Plateau & Hills 2011



THI for Aravalli Central Plateau & Hills 2021



THI for Aravalli Central Plateau & Hills 2031 (predicted)

**Zone Name:** Aravalli Central Plateau & Hills

**Zone No:** 08

**States:** Madhya Pradesh, Rajasthan

**No of Districts:** 83

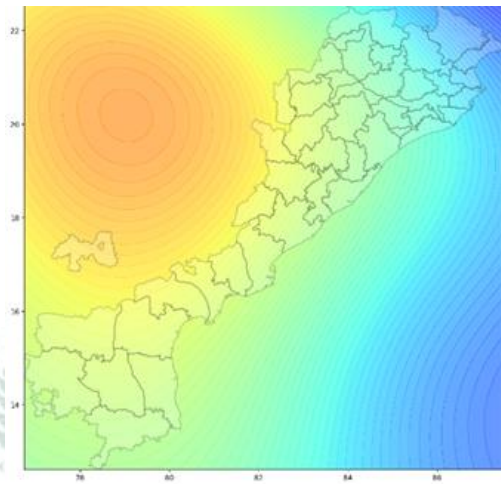
**50 KM grids of 0.08 size:** No of grids 963

**Total Number of Data Points:** 374607

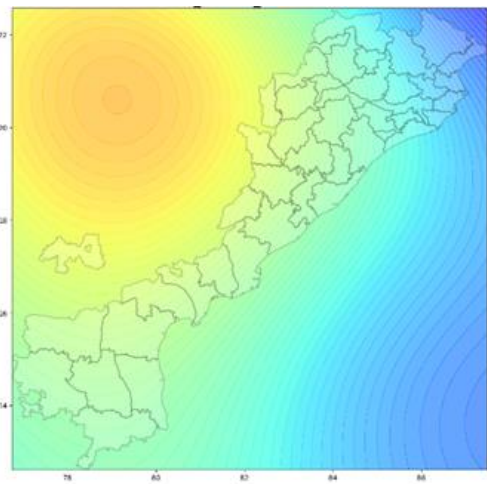
**Variogram best fit (least RMSE)** Gaussian

**Predicted Data:** Predicted for next 10 years (2023 to 2033)

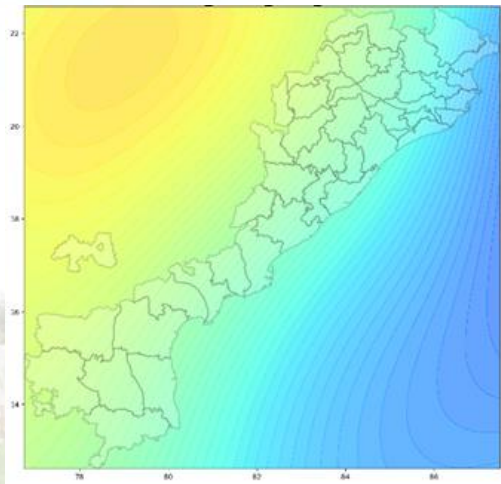
## 14.9 THI for Eastern Central Plains and Hills 2001-2033 (Predicted)



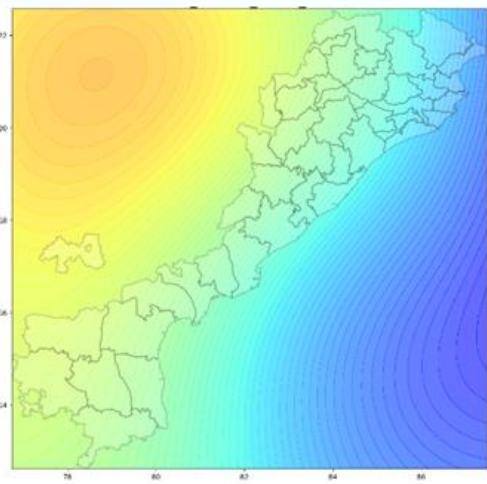
THI for Eastern Central Plains and Hills 2001



THI for Eastern Central Plains and Hills 2011



THI for Eastern Central Plains and Hills 2021



THI for Eastern Central Plains and Hills 2031(Prediction)

**Zone Name:** Eastern central plains & Hills

**Zone No:** 11

**States:** Andhra Pradesh, Odisha

**No of Districts:** 44

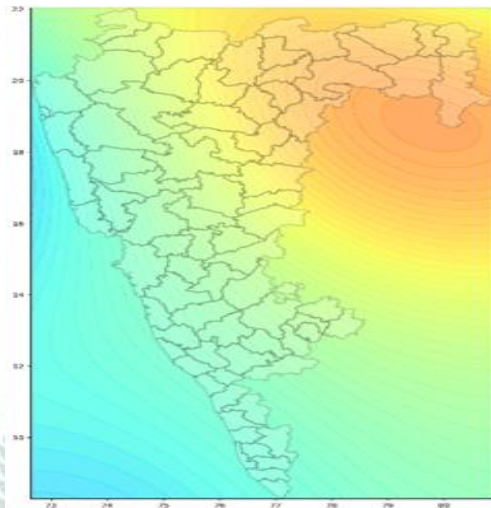
**50 KM grids of 0.08 size:** No of grids 484

**Total Number of Data Points:** 188276

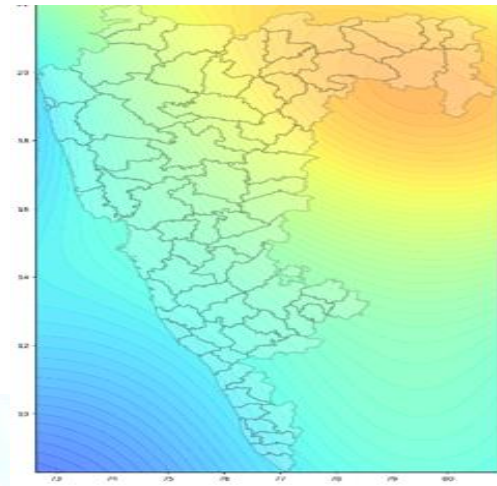
**Variogram best fit (least RMSE) Gaussian**

**Predicted Data:** Predicted for the next 10 years (2023 to 2033)

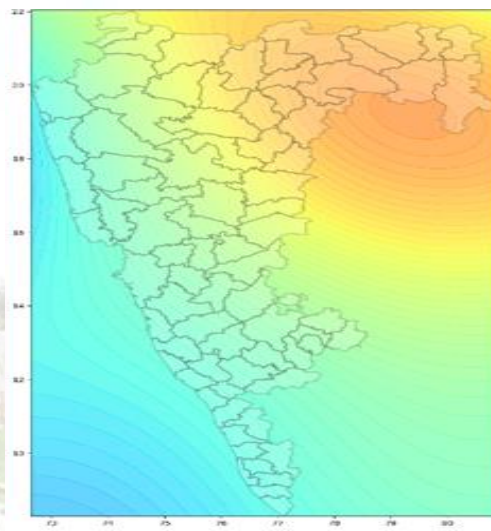
## 14.10 THI for Western Coastal Plains and Ghats 2001-2033 (Predicted)



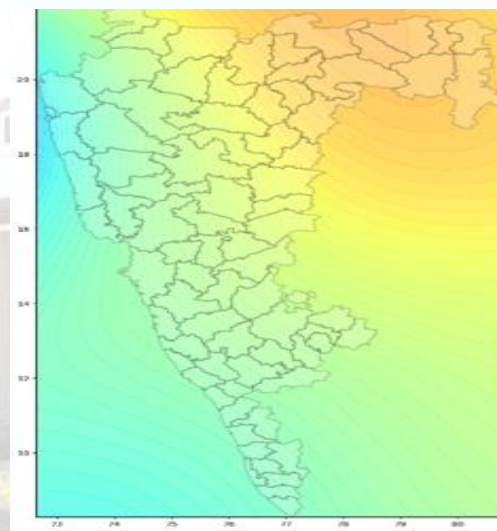
THI for Western Coastal Plains and Ghats 2001



THI for Western Coastal Plains and Ghats 2011



THI for Western Coastal Plains and Ghats 2021



THI for Western Coastal Plains and Ghats 2031(Predicted)

**Zone Name:** Western Coastal Plains & Ghats

**Zone No:** 12

**States:** Karnataka, Kerala, Maharashtra

**No of Districts:** 80

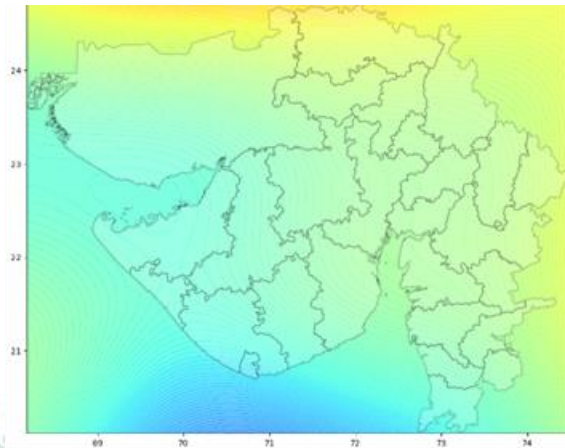
**50 KM grids of 0.08 size:** No of grids 816

**Total Number of Data Points:** 317424

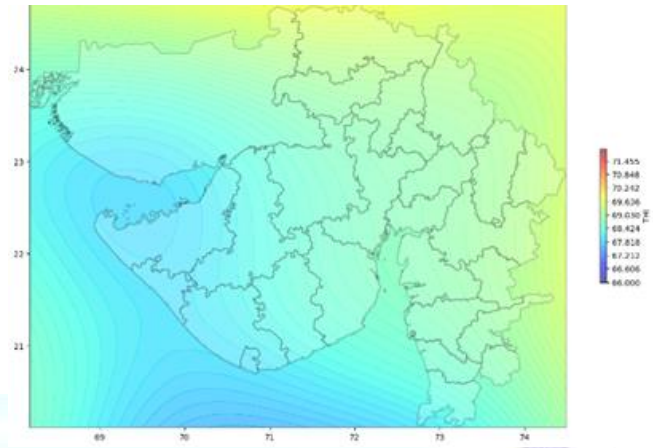
**Variogram best fit (least RMSE) Gaussian**

**Predicted Data:** Predicted for the next 10 years (2023 to 2033)

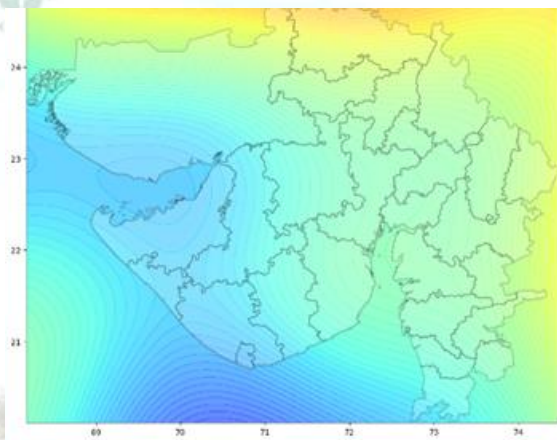
### 14.11. THI for Gujarat Plains and Hills 2001-2033 (Predicted)



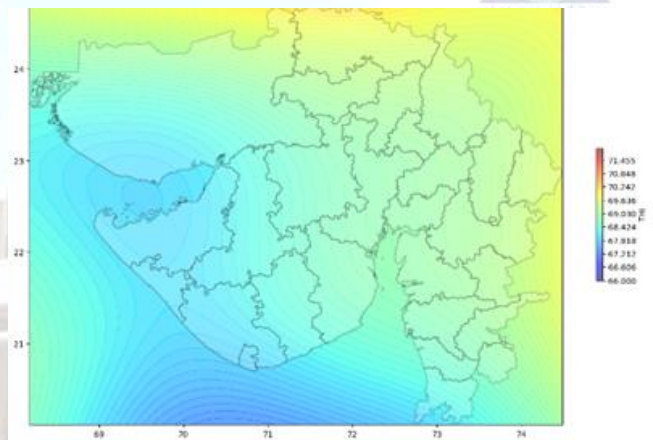
THI for Gujarat Plains and Hills 2001



THI for Gujarat Plains and Hills 2011



THI for Gujarat Plains and Hills 2021



THI for Gujarat Plains and Hills 2031(Predicted)

**Zone Name:** Gujarat Plains & Hills

**Zone No:** 13

**States:** Gujarat

**No of Districts:** 26

**50 KM grids of 0.08 size:** No of grids 289

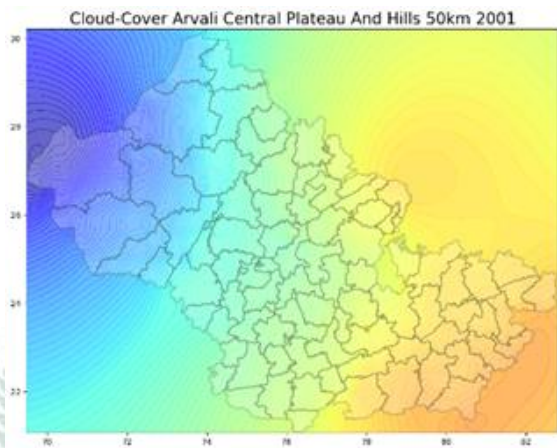
**Total Number of Data Points:** 112810

**Variogram best fit (least RMSE):** Gaussian

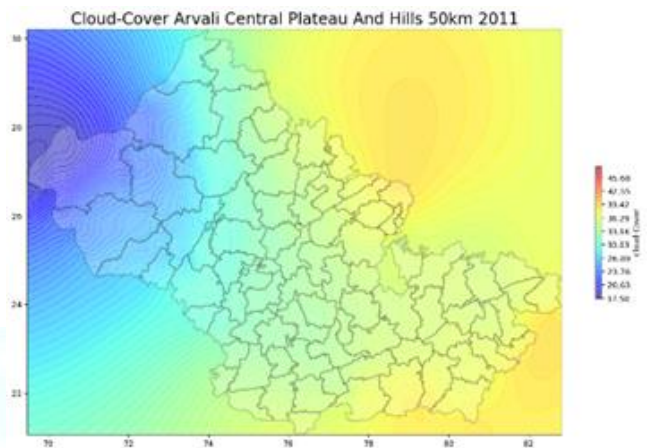
**Predicted Data:** Predicted for the next 10 years (2023 to 2033)



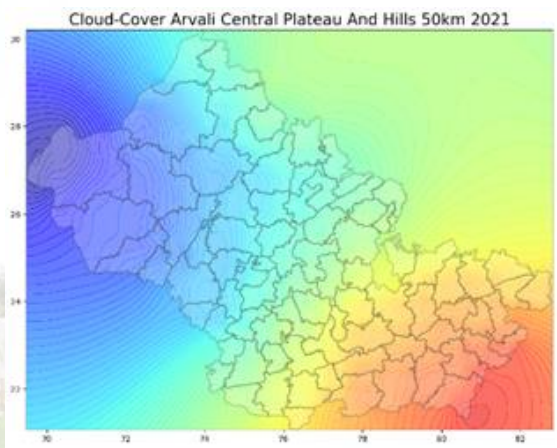
## 14.12. Cloud-Cover for Aravalli Central Plateau & Hills 2001-2033 (Predicted)



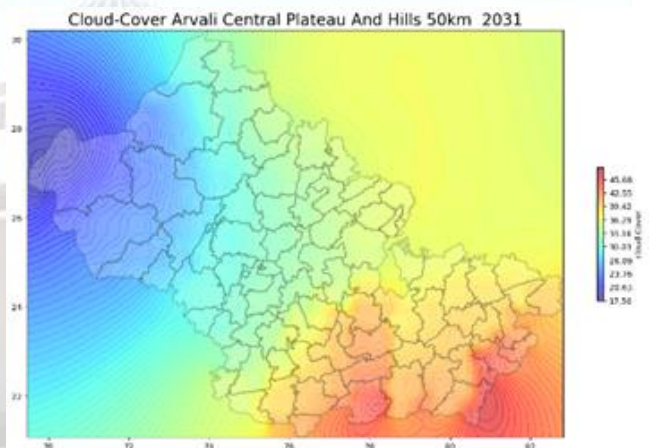
Cloud-Cover for Aravalli Central Plateau & Hills 2001



Cloud-Cover for Aravalli Central Plateau & Hills 2001



Cloud-Cover for Aravalli Central Plateau & Hills 2001



Cloud-Cover for Aravalli Central Plateau & Hills 2031 (predicted)

**Zone Name:** Aravalli Central Plateau & Hills

**Zone No:** 08

**States:** Madhya Pradesh, Rajasthan

**No of Districts:** 83

**50 KM grids of 0.08 size:** No of grids 963

**Total Number of Data Points:** 358236

**Variogram best fit (least RMSE):** Spherical

**Predicted Data:** Predicted for next 10 years (2023 to 2033)

## 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

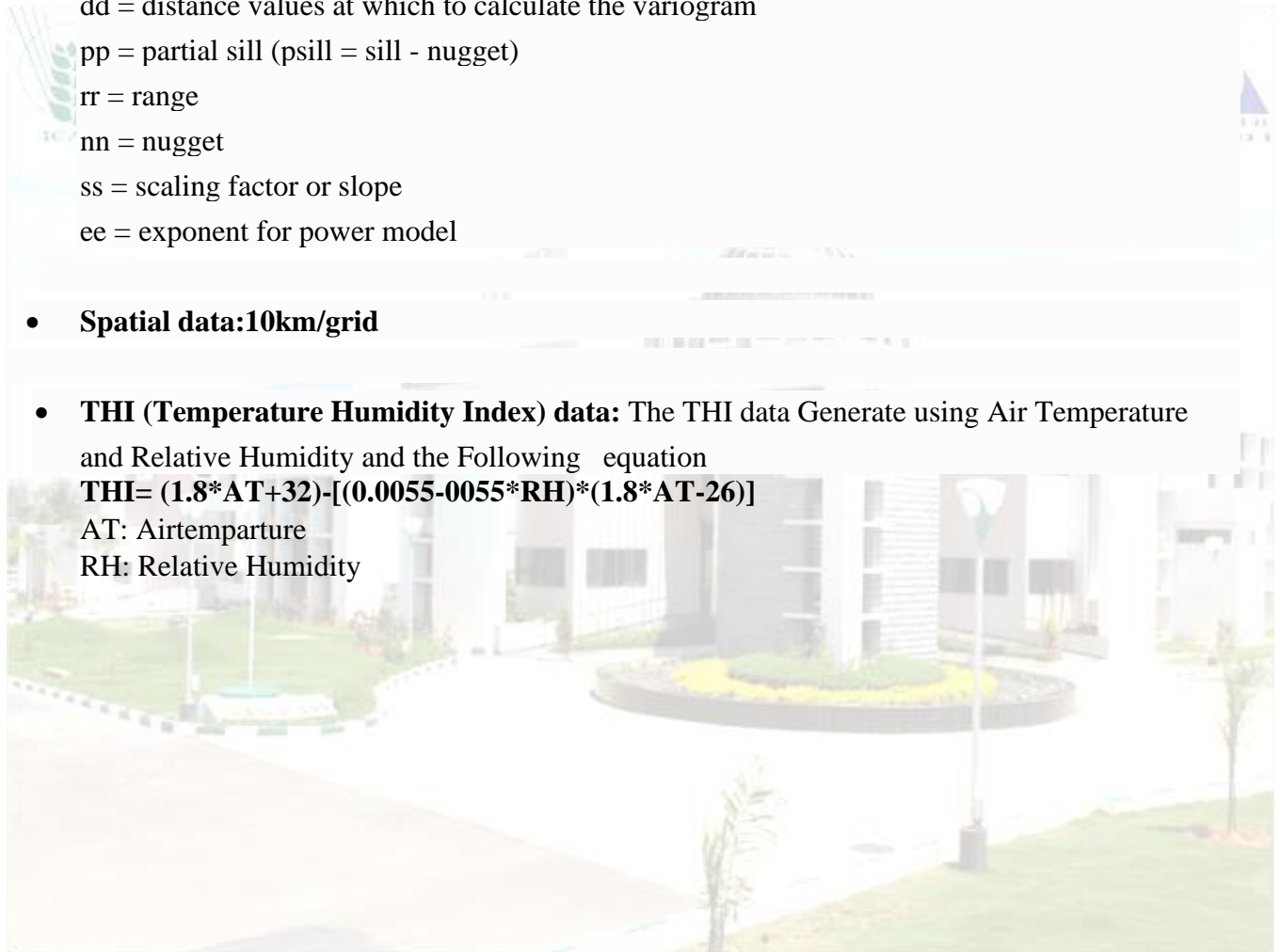
- **Spatial data:10km/grid**

- **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

**ASF** : African Swine Fever

**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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