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# NATIONAL ANIMAL DISEASE REFERRAL EXPERT SYSTEM -INTEGRATING DATA-DRIVEN DISEASE SURVEILLANCE AND PREDICTIVE ANALYTICS FOR LIVE-STOCK DISEASES (NADRES V2)

Presenting By
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What is
Early Warning?

**Early Warning** is a **systematic process of hazard monitoring, prediction, and risk forecasting**, combined with the timely dissemination of reliable information to vulnerable populations and institutions, with the objective of enabling **anticipatory actions that reduce disaster risk, protect lives, livelihoods, and ecosystems**.

Floods

Environmental Hazards

Earthquakes & Tsunamis

Cyclones & Hurricanes

Volcanic Eruptions

**Natural Disasters and Other Hazards**

Agriculture & Food Security

zoonotic or livestock diseases

**How Early Warning Helps**

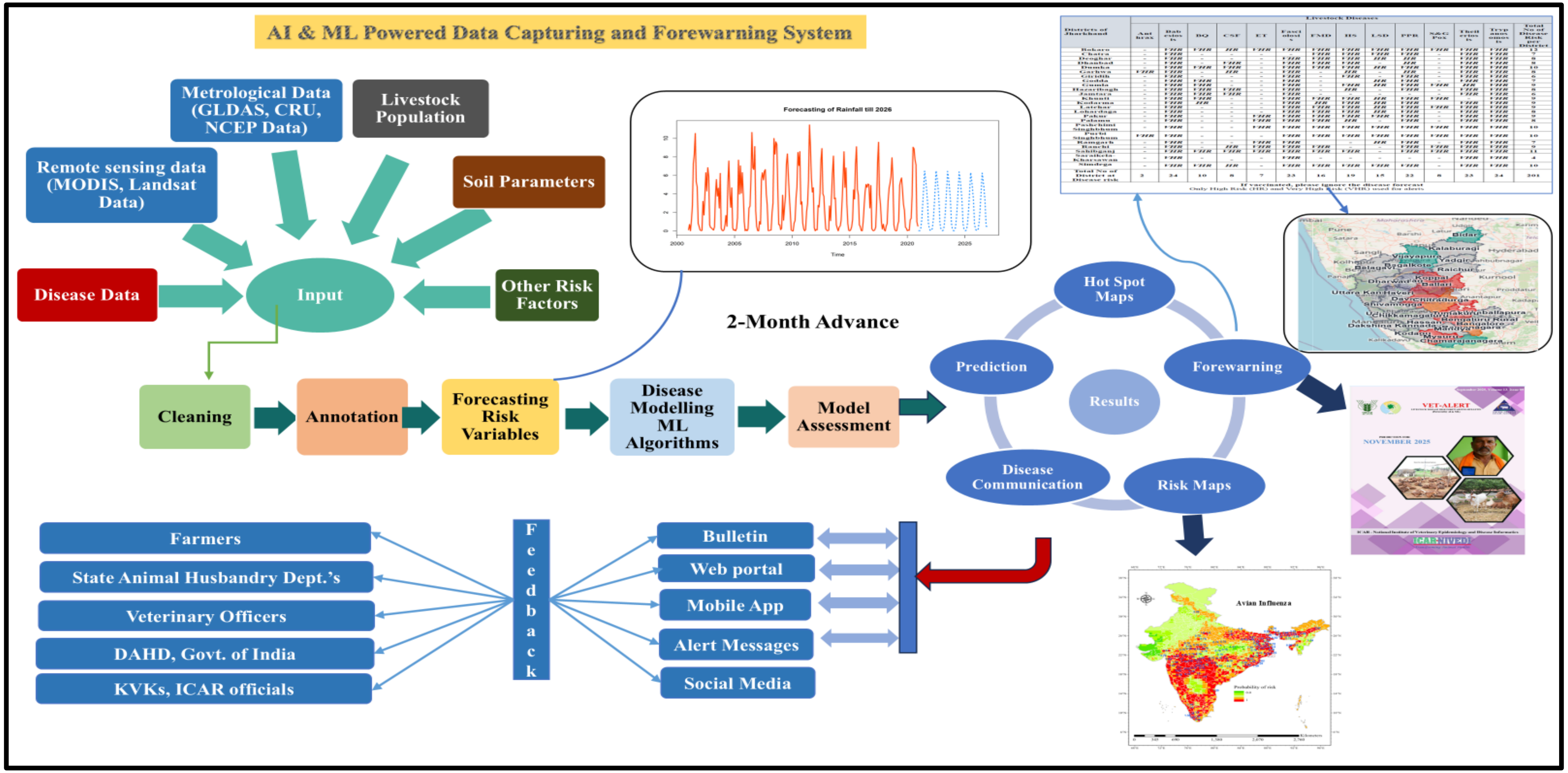
**Risk Reduction:** Provides advance notice to minimize loss of life, livestock, crops, and property.
**Preparedness:** Gives communities and institutions time to plan, evacuate, or safeguard resources.
**Rapid Response:** Ensures that emergency systems (health, rescue, veterinary, disaster management) are activated in time.
**Resilience Building:** Strengthens the capacity of society to withstand and recover from hazards.
**Cost-effectiveness:** Preventive action based on early warning is far less costly than post-disaster recovery.

# Livestock Disease Risk Forewarning Through AI & ML Based Disease Modelling

## NADRES V2- NATIONAL ANIMAL DISEASE REFERRAL EXPERT SYSTEM

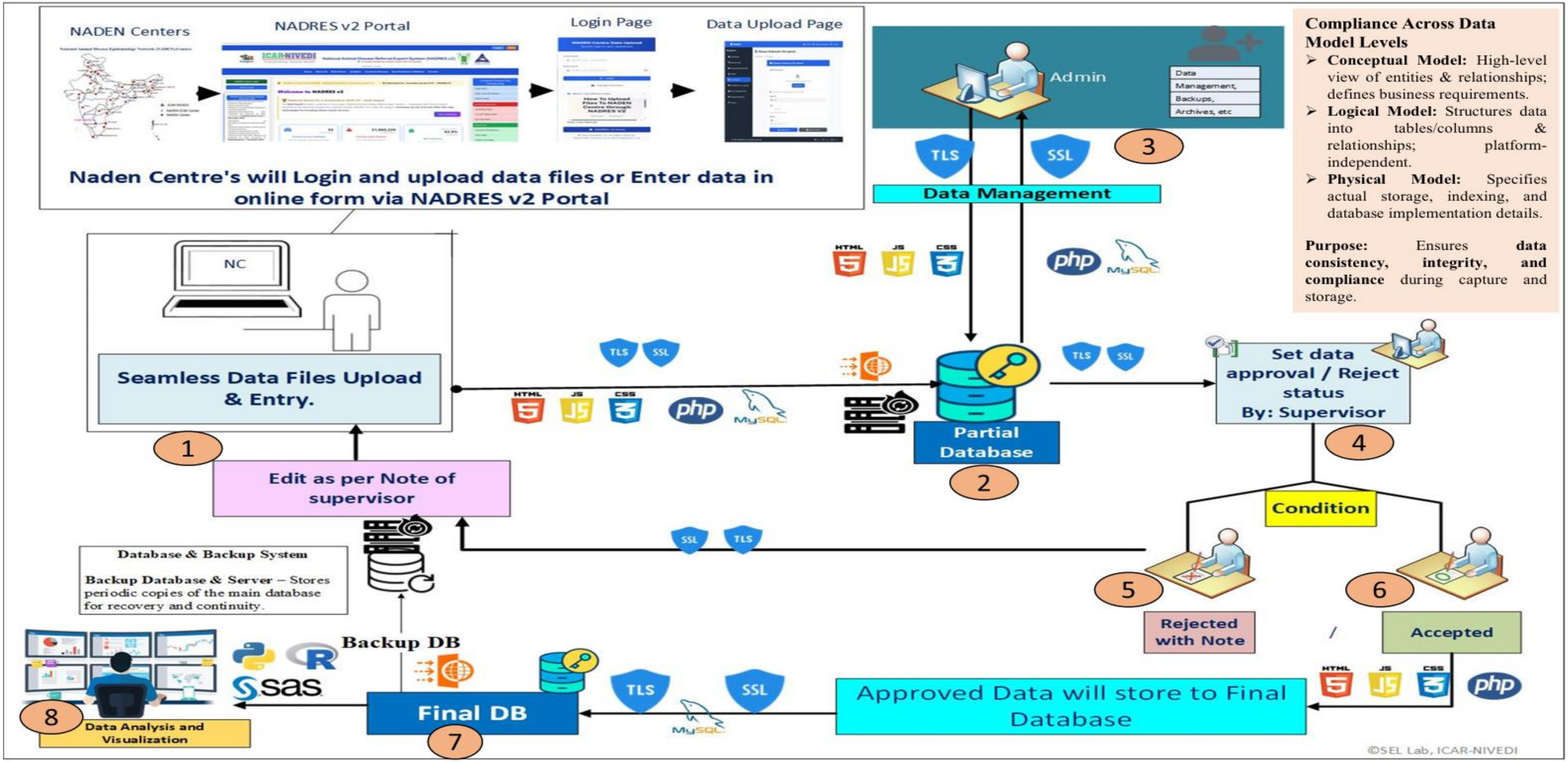
https://nivedi.res.in/Nadres_v2/index.php

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




| Sl. No | List of Diseases |
|---|---|
| 1 | African Swine Fever |
| 2 | Anthrax |
| 3 | Babesiosis |
| 4 | Black Quarter |
| 5 | Bluetongue |
| 6 | Classical swine fever |
| 7 | Enterotoxaemia |
| 8 | Fasciolosis |
| 9 | Foot and mouth disease |
| 10 | Haemorrhagic septicaemia |
| 11 | Lumpy Skin Disease |
| 12 | Peste des petits ruminants |
| 13 | Sheep and Goat pox |
| 14 | Theileriosis |
| 15 | Trypanosomosis |
| **In the pipeline** | |
| Avian Influenza, Anaplasmosis, Mycoplasmosis | |

# Real time/Near Real time Disease Data Capture and Storage Workflow: NADRES V2 Database Flow Diagram




Epidemiological data were compiled at the state, district and village levels from multiple sources, and a subsample of cases was confirmed in the laboratory; the dataset includes information on susceptible populations, attack rates and outbreak-associated mortality

# Real Time Climatic Factors used for Forecasting, Forewarning and Developing Risk maps

## Livestock Population

| Livestock data (Numbers) | |
|---|---|
| Cattle | 19,63,79,000 |
| Buffalo | 11,04,24,984 |
| Sheep | 15,01,13,442 |
| Goat | 7,32,94,702 |
| Pig | 92,94,830 |
| Villages-664369 | |
| Blocks-5564 | |
| Source: 20Th Livestock census, DAHD, GoI | |

## Remote Sensing

| Remote sensing | Units |
|---|---|
| LST | °C |
| NDVI & EVI | -1 to 1 |
| PET | mm |
| LAI | $m^2/m^2$ |
| LST Resolution: 1km | NDVI &EVI, PET, LAI Resolution:500 m. |
| Source: https://ladsweb.modaps.eosdis.nasa.gov/ https://search.earthdata.nasa.gov/ | |

## Meteorological

| Meteorological | Units |
|---|---|
| Air Temperature | k |
| Potential Evaporation Rate | $w/m^2$ |
| Rainfall | $kg/m^2/s$ |
| Soil Moisture | $kg/m^2$ |
| Specific Humidity | kg/kg |
| Surface Pressure | Pa |
| Wind Speed | m/s |
| Source: https://disc.gsfc.nasa.gov/datasets/GLDAS_NOAH025_M_2.1/summary?keywords=GLDAS | |
| Resolution: 0.25 * 0.25 degree | |

| Meteorological | Units |
|---|---|
| Cloud Cover | % |
| Relative Humidity | % |
| Temperature | °C |
| Temperature Max | °C |
| Temperature Min | °C |
| Vapour Pressure | hPa |
| Wet dry Frequency | days |
| Source: https://crudata.uea.ac.uk/cru/data/hrg/cru_ts_4.05/cruts.2103051243.v4.05/ | |
| Resolution: 0.5 degree | |

## Climatic Events

| Climatic event | Criteria |
|---|---|
| Rainfall event | >100mm |
| Maximum Temperature event | >35°C |
| Minimum Temperature event | < 15°C |
| Forest fire | Whole numer |

Limited climatic data were obtained from IMD and NICRA

## Ecological parameters

| Incorporated |
|---|
| Soil PH |
| Elevation (Min, Max, Mean) |
| **Under process** |
| Carbon Emission |
| Water bodies |

★Village populations were aggregated to districts and transformed to population density

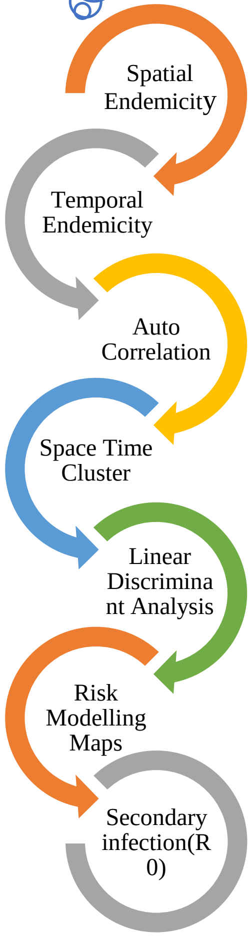
**Delta Weather Parameters:** Represents the difference between two corresponding values, typically between two time periods, **to capture changes or trends**.
**Static Set:** Long-term deltas (2001–2021) showing climatic trends affecting disease patterns.
**Dynamic Set:** Recent deltas (2018–2023 averages) capturing ongoing weather changes for short-term forecasting.

## Remote Sensing Data

ladsweb.modaps.eosdis.nasa.gov ⇒ Select Product ⇒ Select Time period and area ⇒ Download HDF files ⇒ HDF to Geo TIFF Conversion ⇒ Extract Data from GeoTIFF using latl ong ⇒ Data saved in CSV

## Meteorological Data

GLDAS/CRU ⇒ Select Parameters ⇒ Select Time period ⇒ Download NC4 Files ⇒ Extract Data from NC4 files using lat long ⇒ Data saved in CSV




**Seven step approach used for risk Prediction**

# Institutional Collaborations for Climatic Variables and Forecasting

- **Indian Meteorological Department (IMD):** Recently established collaboration to enable **real-time weather data capture** (rainfall, temperature, humidity, wind) from IMD's Automatic Weather Stations (AWS). These datasets are systematically ingested, quality-controlled, and harmonized for seamless integration into **NADRES V2 forecasting pipelines**.

- **Risk Communication and Advisory Dissemination**
- Extension of NADRES V2 advisories through **IMD's farmer outreach platforms** including:
  - **Agromet Advisory Services (AAS)**
  - **Meghdoot Mobile App**
  - **Mausam App**
- Strengthening multi-channel dissemination by integrating with **FRUITS and DLT SMS alerts, NADRES portal, and social media platforms**, thereby ensuring timely, accessible, and actionable early warning for farmers and stakeholders.

- **Indian Space Research Organisation (ISRO):** Partnership to leverage **satellite-based climatic variables** (e.g., land surface temperature, soil moisture, vegetation indices, evapotranspiration) for enhancing the spatio-temporal precision of disease risk prediction models.
- **NICRA (National Innovations on Climate Resilient Agriculture):** Collaboration to utilize selected climatic variables and long-term climate projections for strengthening adaptive capacity and enhancing the accuracy of livestock disease risk forecasting.

**These collaborations strengthen NADRES by improving the accuracy of livestock disease forecasting and expanding risk communication through IMD's outreach platforms for timely, localized advisories.**


**MoU Signed between ICAR-NIVEDI and IMD on 16-09-2025**

# Data Alignment and Data Annotation

**Climate Data**

19 meteorological, 5 remote Sensing, 4 climatic events, 24 Delta parameters, 4 Ecological variables

**Static Dataset**
(Average of 2011 to 2022)

**Dynamic Dataset**
(Average of 2023, 2024, predicted 2025)

**Data Layering**
(First Static & then Dynamic)

**Dimensionality Reduction**

Dimensionality Reduction through Feature extraction technique **Principal Component Analysis (PCA)**. It combines features to capture more of variance

**Lagged Variables**

Incorporating previous months data

**Input climate data**

**Disease Data**

15 Livestock Diseases (2016 to 2025)

**Yearly score**
Disease data from 2016 to 2025 were assigned descending weights, with recent years scoring higher (e.g., 2025 = 10, 2024 = 9, … 2016 = 1).

**Monthly score**
Aggregates 10 years of monthly outbreak data for 15 diseases and scales it from 1–10 to standardize across diseases and months, improving comparability and aiding timely outbreak prediction.

# Integrated Dataset for Disease Outbreak Modeling

**Population Data**

**19 Meteorological variables**

| | state_id | state_name | district_id | district_na | disease_i | disease_name | month | cattle | buaffalo | goat | sheep | pig | d_bovine | d_s_g | d_pig | d_b_s_g | d_all |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2 | 1 | ANDHRA PRADESH | 102 | Anantapu | 189 | Lumpy Skin Disease | 12 | 497102 | 285443 | 884186 | 4926587 | 12767 | 40.9067 | 303.752 | 0.66738 | 344.659 | 345.326 |
| 3 | 1 | ANDHRA PRADESH | 102 | Anantapu | 189 | Lumpy Skin Disease | 12 | 497102 | 285443 | 884186 | 4926587 | 12767 | 40.9067 | 303.752 | 0.66738 | 344.659 | 345.326 |
| 4 | 1 | ANDHRA PRADESH | 103 | Chittoor | 189 | Lumpy Skin Disease | 12 | 950026 | 86680 | 535063 | 1696698 | 3111 | 68.4204 | 147.292 | 0.20532 | 215.712 | 215.917 |
| 5 | 1 | ANDHRA PRADESH | 103 | Chittoor | 189 | Lumpy Skin Disease | 12 | 950026 | 86680 | 535063 | 1696698 | 3111 | 68.4204 | 147.292 | 0.20532 | 215.712 | 215.917 |
| 6 | 1 | ANDHRA PRADESH | 104 | Y.S.R. | 189 | Lumpy Skin Disease | 12 | 137099 | 486581 | 578607 | 1869861 | 3625 | 40.6068 | 159.416 | 0.23602 | 200.023 | 200.259 |
| 7 | 1 | ANDHRA PRADESH | 104 | Y.S.R. | 189 | Lumpy Skin Disease | 12 | 137099 | 486581 | 578607 | 1869861 | 3625 | 40.6068 | 159.416 | 0.23602 | 200.023 | 200.259 |
| 8 | 1 | ANDHRA PRADESH | 105 | East God | 189 | Lumpy Skin Disease | 12 | 396021 | 585246 | 318696 | 316480 | 18646 | 90.7992 | 58.7745 | 1.72536 | 149.574 | 151.299 |
| 9 | 1 | ANDHRA PRADESH | 105 | East God | 189 | Lumpy Skin Disease | 12 | 396021 | 585246 | 318696 | 316480 | 18646 | 90.7992 | 58.7745 | 1.72536 | 149.574 | 151.299 |
| 10 | 1 | ANDHRA PRADESH | 106 | Guntur | 189 | Lumpy Skin Disease | 12 | 95927 | 882347 | 196153 | 704863 | 4128 | 85.8813 | 79.0989 | 0.36239 | 164.98 | 165.343 |
| 11 | 1 | ANDHRA PRADESH | 106 | Guntur | 189 | Lumpy Skin Disease | 12 | 95927 | 882347 | 196153 | 704863 | 4128 | 85.8813 | 79.0989 | 0.36239 | 164.98 | 165.343 |
| 12 | 1 | ANDHRA PRADESH | 110 | Krishna | 189 | Lumpy Skin Disease | 12 | 78846 | 669773 | 196986 | 593007 | 7361 | 85.7819 | 90.5229 | 0.84347 | 176.305 | 177.148 |
| 13 | 1 | ANDHRA PRADESH | 110 | Krishna | 189 | Lumpy Skin Disease | 12 | 78846 | 669773 | 196986 | 593007 | 7361 | 85.7819 | 90.5229 | 0.84347 | 176.305 | 177.148 |
| 14 | 1 | ANDHRA PRADESH | 111 | Kurnool | 189 | Lumpy Skin Disease | 12 | 356122 | 419855 | 610574 | 1985957 | 11482 | 43.9448 | 147.046 | 0.65024 | 190.99 | 191.641 |
| 15 | 1 | ANDHRA PRADESH | 111 | Kurnool | 189 | Lumpy Skin Disease | 12 | 356122 | 419855 | 610574 | 1985957 | 11482 | 43.9448 | 147.046 | 0.65024 | 190.99 | 191.641 |

| | Air_temp | Cloud_cover | Precipitation_rate | Precipitation_water | Precipitation | Pressure | Relative_humidity | Sea_Level_pressure | Soil_moisture | Soil_Temperature | t_max | t_min | Temperat | u_wind | V_wind | wet | Wind_speed | Vapour_pressure | Diurnal_te |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2 | 16893.83007 | 2292.43264 | 1185.700084 | 16.60944466 | 1284.177868 | 155.0745871 | -927.7200328 | -199.611437 | 57.20221397 | -167.8189382 | 85.1603 | -6.6321 | 24.3907 | 9.5354 | -16.1302 | 14.3983 | 13.65470058 | 1.24051003 | -0.10948 |
| 3 | -16436.4469 | 2503.61205 | 2796.14622 | -198.1507603 | -2202.44493 | -1079.51206 | -873.8241509 | 189.7424682 | 24.60903523 | -75.80721605 | -63.6857 | -2.00569 | 33.9836 | -12.8616 | -10.5059 | 4.69859 | 0.854328388 | 0.193514062 | -0.10201 |
| 4 | 16689.26948 | 3904.16852 | 1250.931859 | 0.359429569 | 1417.348009 | -55.9639369 | -155.2797792 | 170.9605899 | -154.1903047 | -49.43091673 | -3.87176 | 28.9984 | -119.288 | 13.3634 | -18.7736 | 14.7335 | 11.80039626 | 2.93800469 | -0.08574 |
| 5 | -16412.3629 | 2495.15364 | 2755.186459 | -205.3458182 | -1892.96346 | -1125.40098 | 390.7676172 | -279.8949087 | -248.0420002 | 37.39723427 | -45.6279 | 44.6898 | -121.329 | -13.5809 | -11.9109 | 7.02289 | -9.87174541 | 2.017000773 | -0.00763 |
| 6 | 16822.43845 | 3564.14616 | 1659.657856 | 7.852598961 | 1313.518666 | 102.740312 | -934.263483 | -185.2889604 | -170.7378163 | -174.757787 | 112.036 | 55.7967 | 0.20935 | 9.92289 | -15.6845 | 19.2504 | 15.38068471 | 1.809760973 | -0.02182 |
| 7 | -16449.9675 | 4109.00105 | 4345.856022 | -215.6903921 | -2055.03711 | -1228.44076 | -354.1737026 | -576.6983128 | -253.8433391 | 60.0271828 | 18.759 | -13.3077 | 8.74958 | -10.765 | -20.8256 | 11.8776 | -1.2745008 | -7.893625307 | -0.00585 |
| 8 | 16833.92384 | 4586.06625 | 3171.649239 | -14.22928355 | 1244.234146 | -187.534076 | -288.4442359 | 122.9994531 | -351.8735011 | -28.44505909 | -37.4145 | 117.95 | -8.75875 | 15.2982 | -28.3671 | 12.5887 | -6.99017465 | -0.182407661 | -0.09474 |
| 9 | -16761.8831 | 4723.79117 | 4927.580363 | -173.2702628 | 1327.985799 | -373.134015 | 103.8310607 | 327.4932807 | -329.6284129 | 110.6221462 | -87.3713 | 101.606 | -1.39381 | -16.426 | -19.6895 | 8.85478 | 12.59619699 | -11.95977787 | -0.23383 |
| 10 | 16913.97094 | 3806.56535 | 3928.246508 | -9.252700358 | 1064.986789 | 439.472011 | -252.7698209 | 106.1647541 | -90.0234869 | -67.57049452 | -39.9865 | 98.4552 | -58.8617 | 9.79177 | -18.4861 | 11.8394 | -4.9127946 | 2.36851291 | -0.00638 |
| 11 | -16766.0738 | 4576.29466 | 4845.946003 | -164.9468427 | 959.4386299 | 213.000361 | -558.1031032 | 527.465182 | -53.9640717 | 26.75528722 | -29.5485 | 91.1627 | -48.3665 | -21.963 | -16.2526 | 6.95991 | 23.88189966 | -4.1800266 | -0.11636 |
| 12 | 16938.13627 | 3473.51293 | 4285.758935 | -5.723996681 | 1039.085627 | 439.7109617 | -703.801798 | -96.02844104 | -106.0940135 | -53.43291299 | -18.0552 | 90.4175 | -52.9716 | 7.65941 | -23.9127 | 15.1347 | 4.018434415 | 3.089694855 | -0.0326 |
| 13 | -16889.7511 | 4636.60377 | 4910.557125 | -165.5129484 | 1037.752134 | 275.3368193 | -391.5601808 | -158.7688348 | -107.5066907 | 67.28701965 | -31.0247 | 93.1335 | -49.6878 | -23.962 | -13.1805 | 10.875 | 53.31814516 | -1.387895505 | -0.1354 |
| 14 | 16854.90339 | 3032.25558 | 1653.683417 | 8.31740242 | 1063.071159 | 236.2757876 | -964.1018954 | -215.2432344 | 17.81676685 | -169.2043594 | 34.1641 | 81.9597 | -3.96981 | 8.45859 | -10.8223 | 14.4766 | 12.95473142 | -1.193173406 | -0.09067 |
| 15 | -16415.6846 | 3941.64904 | 4182.312626 | -159.7020112 | 855.9657218 | -181.835351 | -844.2740694 | 40.38474766 | 42.26513778 | -22.93274968 | 4.1994 | 19.5842 | 7.3802 | -20.2045 | -12.0058 | 9.95874 | 1.42404206 | -10.15634529 | -0.04775 |

**5 Remote Sensing variables**

**24 Delta Parameters**

**4 Climatic Events**

**4 Ecological Parameters**

**52 Lag variables**

**Weightage**

| EVI | LAI | LST | NDVI | PET | Delta_Air | Delta_Clo | Delta_Vap | Delta_Diu | Max_temp_event | Min_temp_event | Rainfall_event | Forest_fire | Soil.PH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 12.9881 | -18.9673 | -10.4377 | 3.569 | 9.41457 | 3.62292 | 1.56881 | 0.69148 | -0.28536 | -0.184186093 | -0.113567553 | 0.104380324 | 0.029935722 | 0.04464 |
| -7.68762 | 11.1341 | -5.2571 | -1.28738 | -4.68017 | 11.1018 | -5.65121 | 0.62684 | -0.19418 | -0.15222836 | -0.170618388 | 0.133832022 | 0.004093454 | 0.0577 |
| -10.7045 | -13.4362 | -3.6083 | -3.60131 | 17.7653 | 2.26936 | 2.83466 | 0.56858 | -0.07617 | -0.220767785 | -0.104802384 | -0.266926432 | -0.01499836 | 0.07207 |
| -3.34075 | 5.27126 | -5.62172 | -0.99314 | -0.27378 | -0.59873 | -2.00046 | 0.6672 | 0.03538 | -0.321506806 | -0.228965054 | -0.052025754 | -0.00375669 | -0.05516 |
| -3.55559 | -16.3153 | -9.96241 | 2.55181 | 6.86125 | 2.65468 | 1.146 | 0.73518 | -0.10514 | -0.139088798 | -0.105839956 | -0.033076333 | -0.00568281 | 0.04519 |
| -12.804 | 11.8091 | -15.3867 | 10.6395 | -2.28695 | 14.8162 | -0.99514 | 0.94849 | -0.21199 | -0.226729534 | -0.21473486 | 0.167036457 | -0.00100344 | 0.02243 |
| 9.66404 | -25.0857 | -16.3558 | 3.28004 | 9.01207 | 13.5266 | 4.93799 | -0.06056 | 0.23808 | -0.372336138 | -0.110260566 | 0.124507901 | -0.04291093 | -0.01053 |
| -6.04899 | 8.49717 | 2.54558 | 8.48913 | 0.78739 | 1.10363 | -4.02632 | -0.04154 | 0.15877 | -0.221953365 | -0.126901217 | 0.268877741 | -0.05028612 | -0.13593 |
| 12.8515 | -25.1727 | -16.0205 | 6.95784 | 7.96015 | 11.0941 | 0.18454 | -0.07586 | 0.11434 | -0.208585098 | -0.182418761 | -0.086432491 | 0.038494831 | -0.01966 |
| 0.4093 | 4.85326 | 0.83931 | 6.31199 | -3.73484 | 7.12044 | -4.59686 | 0.10317 | 0.2219 | -0.076337195 | -0.134844852 | 0.028749108 | -0.03758924 | 0.00759 |
| 12.7733 | -23.4705 | -17.1911 | 7.3678 | 3.93143 | 9.98045 | 2.3509 | -0.13633 | -0.09735 | -0.222310268 | -0.166703912 | 0.008307095 | 0.043491541 | 0.00728 |
| 3.36254 | -0.00335 | 9.52706 | 3.63973 | -6.57298 | 2.2721 | -9.68957 | -0.10823 | 0.0017 | 0.047329319 | -0.087066225 | 0.002918407 | -0.02316855 | -0.13116 |
| 11.4068 | -24.3961 | -11.4941 | 18.6191 | -12.031 | -2.37108 | 9.24575 | 0.5281 | -0.27677 | -0.19255209 | -0.213763043 | 0.107962164 | 0.021885126 | 0.02023 |
| -10.6751 | 4.74387 | -15.0177 | 2.16648 | -5.04211 | 11.7804 | -5.59343 | 0.69902 | -0.14354 | -0.241831879 | -0.289551551 | 0.137944723 | -0.04661712 | 0.05892 |

| Ele_Max | Ele_Mean | Ele_Min | Air_temp_lag | Cloud_cover_lag | Min_temp | Rainfall_event | Forest_fir | Yearly_Score | Month_score | out |
|---|---|---|---|---|---|---|---|---|---|---|
| 0.02712 | 2.70E-05 | -7.43E-06 | 3.622921063 | 2181.255394 | -0.04014 | 0.027172323 | 0.03978 | 0 | 0 | 0 |
| 0.00986 | 1.50E-05 | 3.20E-05 | 11.10178631 | 2121.552889 | -0.05408 | 0.111199262 | -0.01394 | 0 | 0 | 0 |
| 0.01892 | 4.13E-05 | 8.72E-06 | 2.269355864 | 3763.765876 | -0.02331 | -0.24884647 | 0.0109 | 0 | 0 | 0 |
| 0.00302 | 7.65E-06 | 1.45E-05 | -0.598733037 | 2092.921394 | -0.06349 | -0.04471928 | -0.00519 | 0 | 0 | 0 |
| 0.02364 | 3.04E-05 | -1.20E-06 | 2.65468264 | 3425.433702 | -0.05723 | -0.052223917 | -0.01049 | 0 | 0 | 0 |
| 0.0082 | 1.12E-05 | 2.71E-05 | 14.81624438 | 3683.989957 | -0.10913 | 0.165823332 | -0.01674 | 0 | 0 | 0 |
| 0.02834 | 1.57E-06 | -1.36E-05 | 13.52657865 | 4477.328554 | -0.00703 | 0.035557003 | 0.00706 | 0 | 0 | 0 |
| 0.0306 | 1.32E-05 | 8.77E-06 | 1.103625116 | 4442.744038 | -0.06017 | 0.21811646 | -0.04043 | 0 | 0 | 0 |
| -0.00214 | 8.83E-06 | -3.14E-05 | 11.09413844 | 3672.569643 | -0.04137 | -0.116066196 | 0.02902 | 0 | 0 | 0 |
| 0.00657 | 8.45E-06 | 1.20E-05 | 7.120444759 | 4259.31318 | -0.0686 | 0.017546211 | -0.03532 | 0 | 0 | 0 |
| 0.00744 | 1.15E-05 | -2.38E-05 | 9.980445061 | 3343.745903 | -0.07449 | -0.094848073 | 0.02787 | 9 | 2 | 1 |
| 0.00292 | -5.04E-05 | 3.50E-05 | 2.272097932 | 4383.666454 | -0.07776 | -0.149150002 | 0.02009 | 9 | 2 | 1 |
| 0.01938 | 1.79E-05 | -2.28E-05 | -2.371084125 | 2903.223866 | -0.14239 | 0.06464516 | 0.01728 | 0 | 0 | 0 |
| 0.01338 | 7.95E-06 | 1.79E-05 | 11.78039183 | 3577.835583 | -0.2022 | 0.065436832 | -0.02199 | 0 | 0 | 0 |

## Formula

Out ~ Population + Meteorological + Remote Sensing + Delta Parameters + Climatic events +Ecological Parameters + Lag variables+ Yearly score + Monthly Score

**Binary Classification**

If outbreaks >1, then it is 1 or else 0

**Dependent variable (Y): Outbreaks**

# Machine Learning Models: Selection and Evaluation Criteria

## Model Selection Criteria

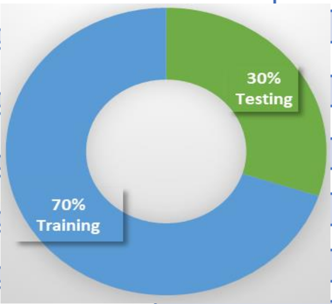
- Akaike information criterion (AIC)
- Bayesian information criterion (BIC)
- Bridge criterion (BCCross-validation
- Deviance information criterion (DIC),
- Likelihood-ratio test
- Mallows's Cp
- Minimum description length
- Minimum message length (MML)
- PRESS statistics
- Stepwise regression

**Key Concepts**

**Goodness of Fit:** How well the model explains the data.
**Model Complexity:** Number of parameters; simpler models preferred.
**Overfitting:** Model fits training data too closely → poor performance on new data.

**Supervised learning models**

1. Generalized Linear Model(GLM)
2. Generalized Additive Model (GAM)
3. Random Forest (RF)
4. Kernal Support Vector Machine (KSVM)
5. Boosted Regression Tree (BRT)
6. Artificial Neural Networks (NN)
7. Multiple Adaptive Regression Splines (MARS)
8. Flexible Discriminant Analysis (FDA)
9. Classification Tree Analysis (CTA)
10. Support Vector Machine (SVM)
11. Decision Trees (Tree_prob)
12. Least Absolute Shrinkage and Selection Operator (Lasso)
13. Gaussian Process (GP)
14. Neural Network (NN)
15. Cubiset
16. Probit Regression
17. Elastic Net
18. Adaptive Boosting
19. Ridge Regression
20. Conditional Random Forest



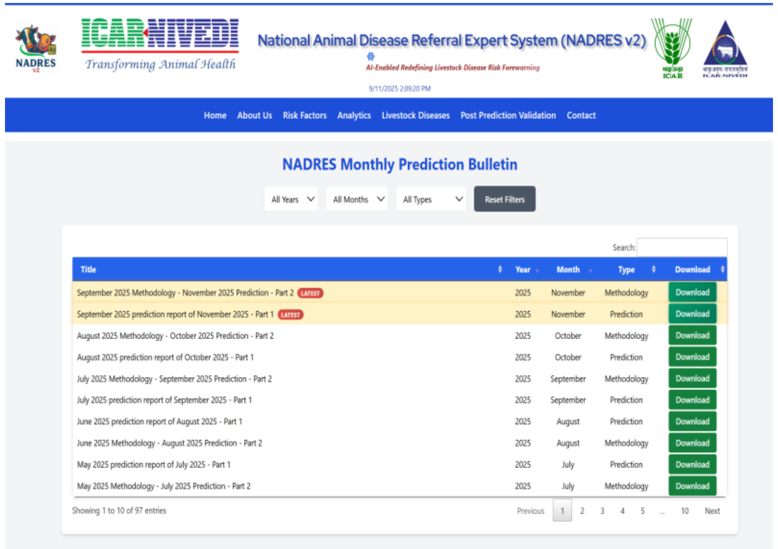

## Model Performance Criteria

1. KAPPA
2. ROC
3. TSS
4. Accuracy
5. Error Rate
6. Precession
7. Sensitivity
8. Specificity
9. F1 Score
10. Log loss
11. Gini Coefficient
12. RMSE
13. MAE

**Using Ensembling Techniques**

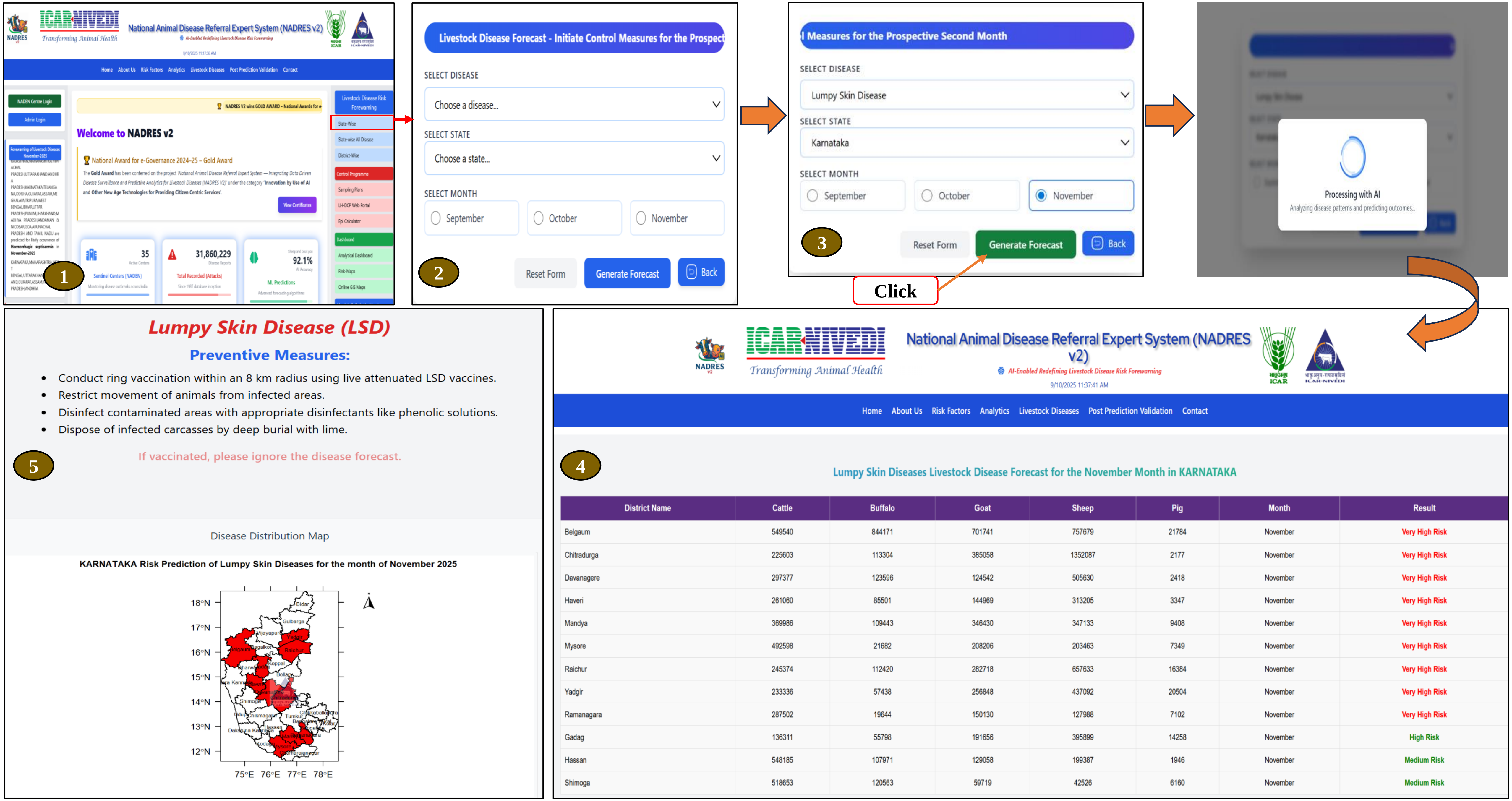
Ensemble models combine multiple machine learning models to improve prediction accuracy, reduce overfitting, and provide more reliable forecasts.

**Types:** Bagging, Boosting, Stacking.
**Methods:** Voting, Averaging, Weighted Averaging.

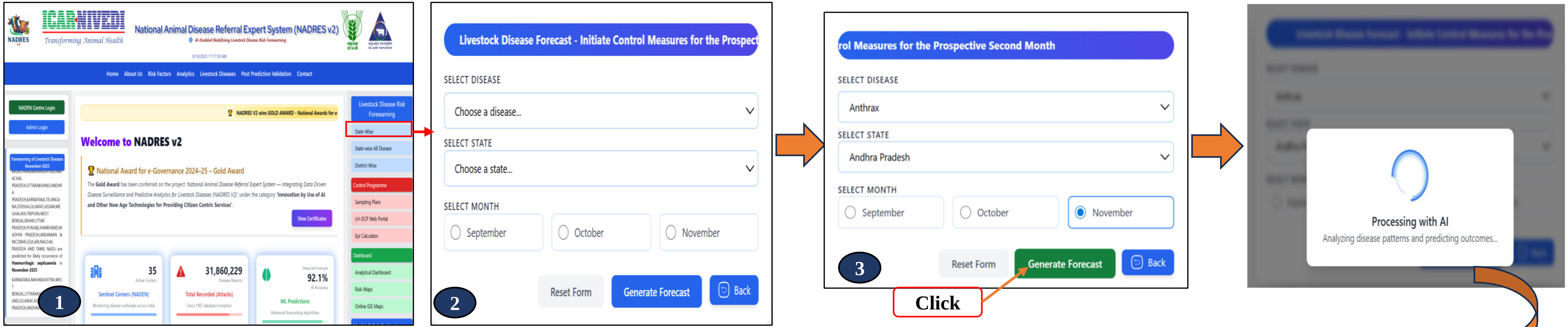


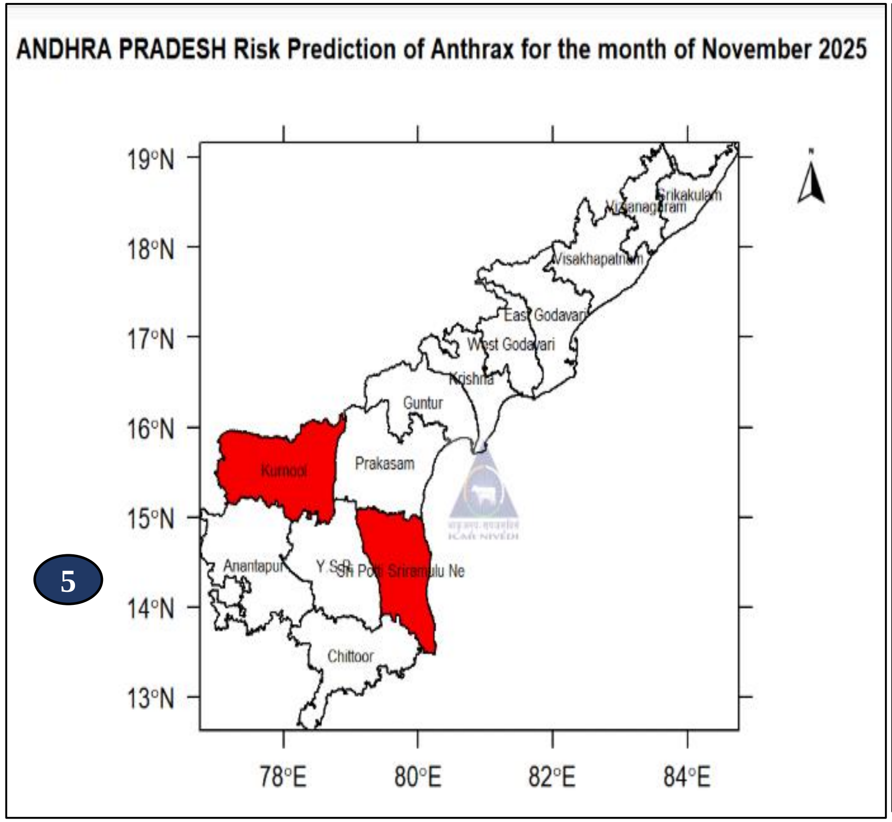

**Vet-Alerts: Livestock Disease Forewarning Bulletin (Web-based Platform)**

# Interactive Visualization of AI-Based Disease Predictions: State, Disease and Month-Specific Insights in NADRES V2



# Interactive Visualization of AI-Based Disease Predictions: Andra Pradesh Insights in NADRES V2




## Anthrax Livestock Disease Forecast for the November Month in ANDHRA PRADESH

| District Name | Cattle | Goat | Sheep | Pig | Month | Result |
|---|---|---|---|---|---|---|
| Kurnool | 356122 | 610574 | 1985957 | 11482 | November | Very High Risk |
| Sri Potti Sriramulu Ne | 107858 | 453820 | 1370812 | 3785 | November | Very High Risk |

4

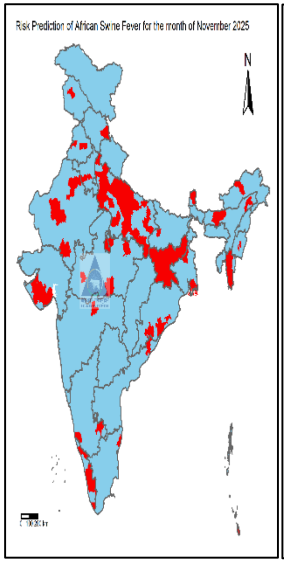
### *Anthrax*

### Preventive Measures:

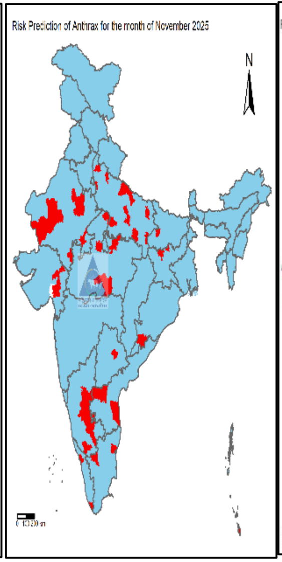
- Ring vaccination and report of disease is advised.
- Vaccination to be done in consultation with veterinarians and as decided by state animal husbandry authorities.
- Strict biosecurity measures may be followed.
- Carcass may be disposed of by deep burying covered with lime powder.
- Contaminated areas may be disinfected with 4% formalin or 10% caustic soda.
- Grazing area may be restricted.

If vaccinated, please ignore the disease forecast.

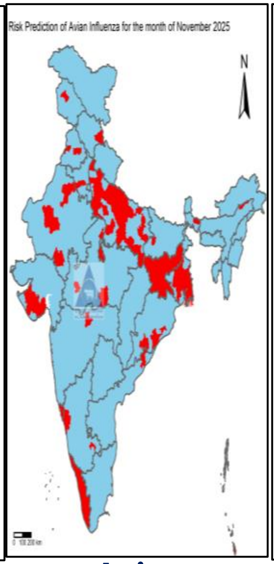
# September 2025 Livestock Disease Risk Maps: Visualizing High and Very High-Risk districts



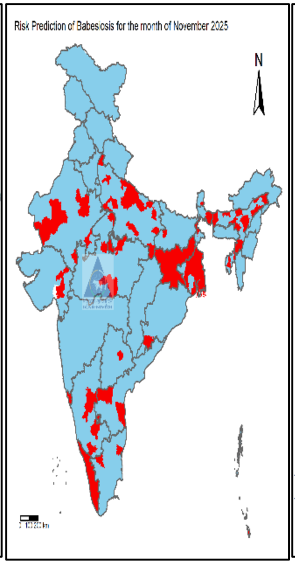

African Swine Fever



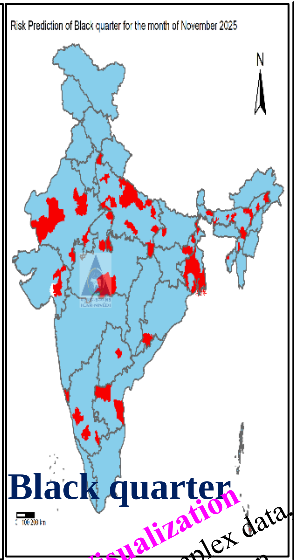

Anthrax



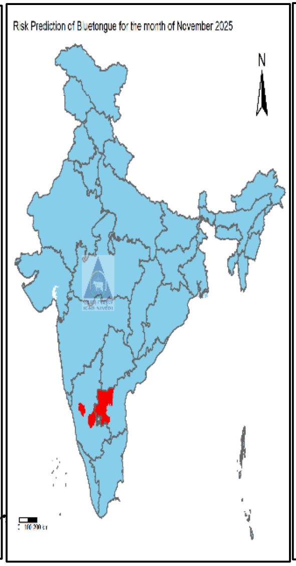

Avian Influenza



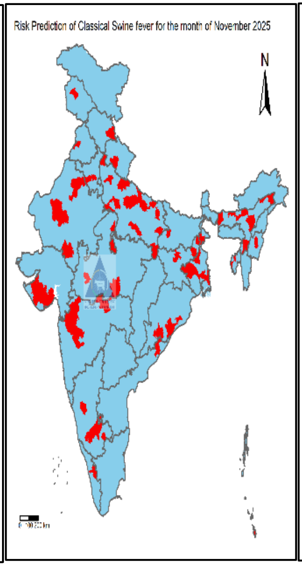

Babesiosis



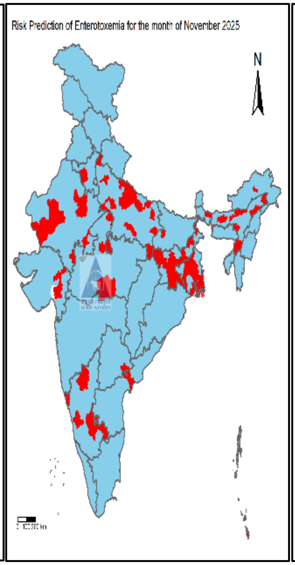

Black quarter



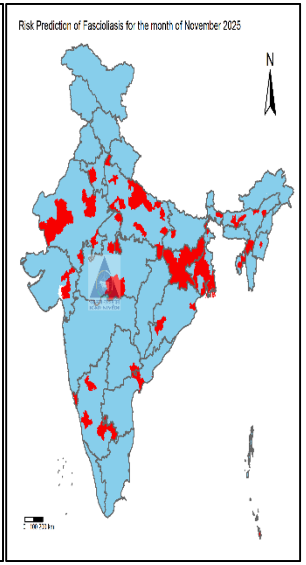

Bluetongue



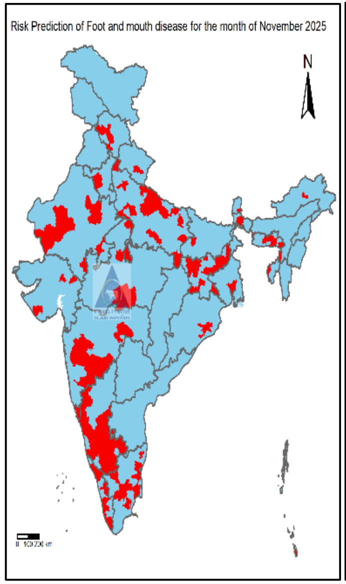

Classical Swine Fever



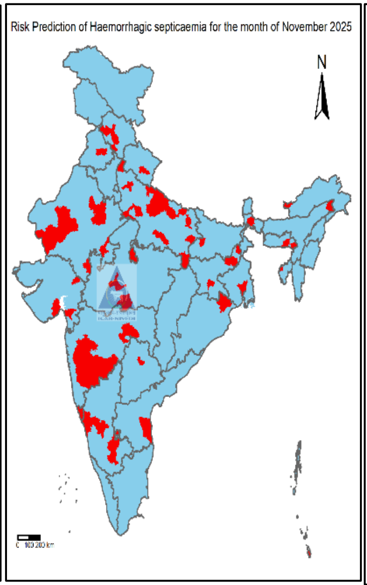

Enterotoxemia



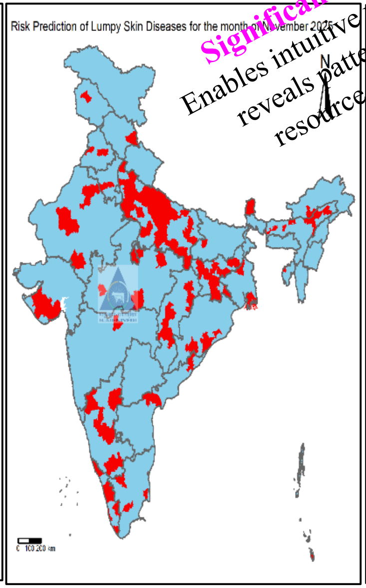

Fascioliasis



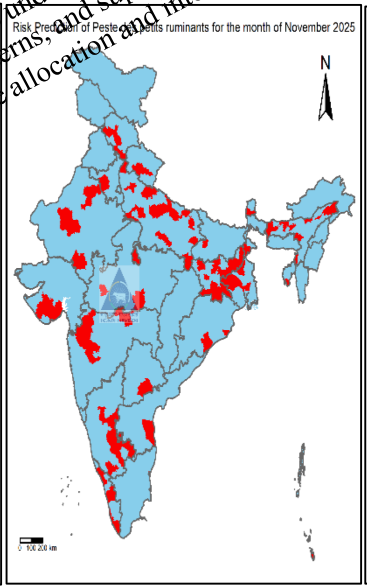

Foot and mouth disease



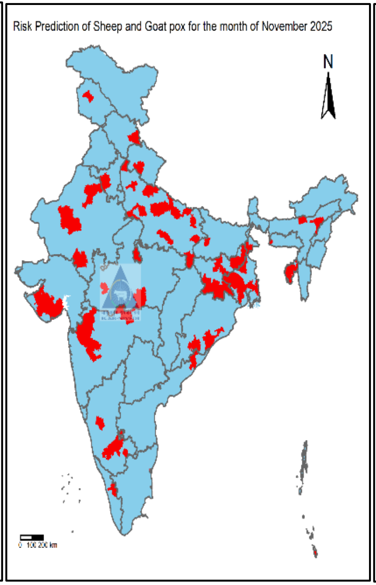

Haemorrhagic septicaemia



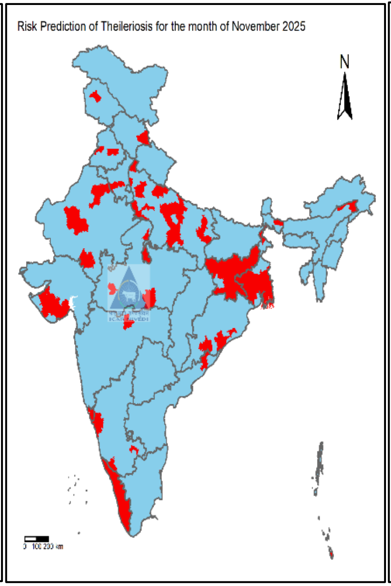

Lumpy Skin disease



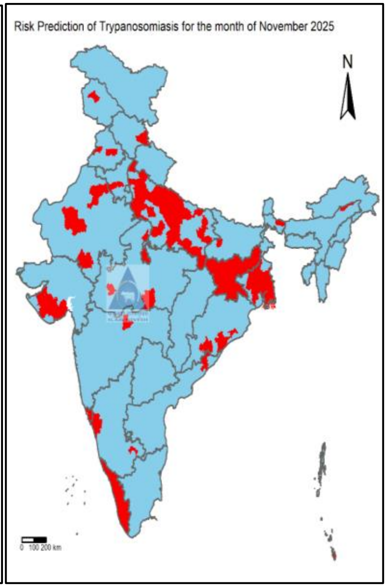

Peste des petits ruminants




Sheep and Goat pox




Theileriosis




Trypanosomiasis

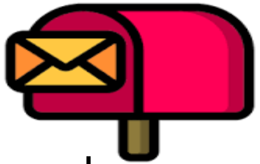
**Significance of Spatial Visualization**

Enables intuitive understanding of complex data, reveals patterns, and supports data-driven resource allocation and interventions.

# End to End Risk Communications

**Monthly Forecasting of 15 Livestock Diseases (Based on AI and ML models) Dissemination to all Stakeholders**

## Hard Copy (Vet-alert, Livestock Diseases Risk Forewarning Bulletin) Dissemination by Post



**DAHD and ICAR officials**

## Soft copy (Vet-alert, Livestock Diseases Risk Forewarning Bulletin) Via emails


**State Veterinary Officials(52), KVKS (731), NADEN centers (55 Including PI &Co-PI)**

## LDF & NER LDF Mobile application


**Real time access by field users (100+ Users)**

- ✓ Veterinary nodal officers use the system to create data-driven sampling plans for targeted surveillance.

## NADRES Website


https://nivedi.res.in/Nadres_v2/index.php

**Total Visitors: 27 Lakh Individuals (as of latest update)**

## Fruits SMS alerts to registered farmers

- ✓ **33.69 lakh** SMS alerts were sent to farmers in September 2025.
- ✓ **35.80 million** SMS alerts disseminated via FRUITS (April 2024 - August 2025).

## DLT SMS to Veterinary Doctors


- ✓ **16,721** SMS alerts sent to veterinarians in September 2025.
- ✓ **2.13 lakh** SMS alerts sent to vets from September 2024 to August 2025.

## Social Media Platforms

**YouTube:** https://www.youtube.com/@icar-nivedi

**Facebook** https://www.facebook.com/icarnivediofficial/

**Instagram** https://www.instagram.com/p/DF5DkqqymcW/?igsh=N2NvZXR5cHp3cXdj

**LinkedIn** https://www.linkedin.com/feed/update/urn:li:share:7294667371829436417/

**X (Twitter)** https://x.com/dilnivedi/status/1888899265411645536

**GitHub:** https://github.com/SEL-NIVEDI/

### Goals

- ✓ **Empowerment:** Facilitate protective and preventive actions.
- ✓ **Trust and Credibility:** Strengthen confidence in expert guidance.
- ✓ **Behavioural Change:** Encourage adoption of risk-mitigating behaviours.
- ✓ **Community Engagement:** Involve communities as active partners in risk management strategies.

**Informed Farming Community & Veterinary Authorities**

- **Early Response**
- **Risk Mitigation**
- **Animal Health Protection**

**Risk Communication:** Real-time, interactive exchange of risk information to enable informed decisions and protective actions.

**Beneficiaries:** Supports farmers, veterinary doctors, and policymakers in prevention, decision-making, and building trust in institutions.

# Field-Level Accuracy of District-Wise Disease Forecasts vs. Reported Cases (2023–2024)

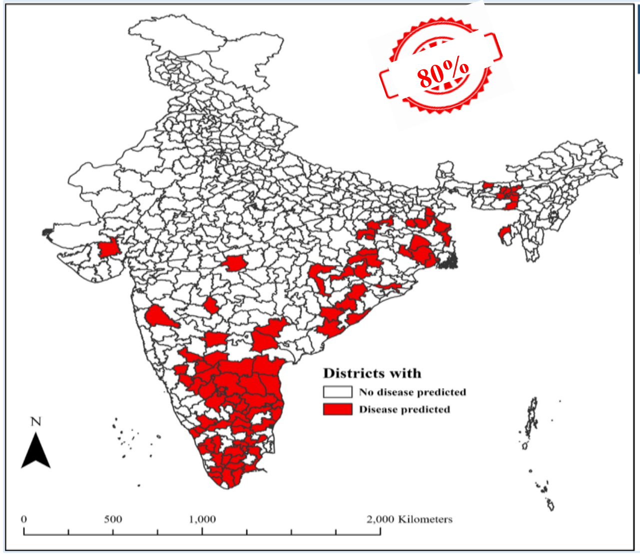
| Sl.NO | Diseases | 2023 | | 2024 | |
|---|---|---|---|---|---|
| | | No. of Districts Forecasted | No. of Districts Reported | No. of Districts Forecasted | No. of Districts Reported |
| 1 | African Swine Fever | - | 153 | 239(from march) | 537 |
| 2 | Anthrax | 257 | 20 | 253 | 38 |
| 3 | Babesiosis | 836 | 488 | 1074 | 473 |
| 4 | Black quarter | 430 | 68 | 592 | 53 |
| 5 | Bluetongue | 45 | 2 | 54 | 22 |
| 6 | Classical Swine Fever | 97 | 27 | 588 | 12 |
| 7 | Enterotoxaemia | 305 | 61 | 418 | 67 |
| 8 | Fascioliasis | 566 | 106 | 572 | 106 |
| 9 | Foot and mouth disease | 664 | 101 | 1001 | 83 |
| 10 | Haemorrhagic septicaemia | 461 | 22 | 872 | 39 |
| 11 | Lumpy Skin Diseases | 30(from oct to dec) | 116 | 508 | 289 |
| 12 | Peste des petits ruminants | 810 | 172 | 968 | 142 |
| 13 | Sheep & Goat pox | 478 | 57 | 526 | 30 |
| 14 | Theileriosis | 793 | 496 | 936 | 501 |
| 15 | Trypanosomiasis | 692 | 325 | 802 | 363 |

**Ground-Truth Observations After Two Months**

**False Negative Error:**
**Districts Reported but Not Forecasted**
In 2024, a total of **24 districts** (approximately **10.76%**) reported at least one disease outbreak, even though they were **not forecasted by the system.**

**False Positive Error:**
**Districts Forecasted but Not Reported**
Meanwhile, **26 districts** (around **3.94%**) were **forecasted** to have outbreaks, but **no cases** were reported from these districts

# Post-Prediction Validation of Livestock Disease Forecasts Using Outbreak




## Anthrax prediction during 2023 for accuracy checking

**NADRES v2** If implemented, could have prevented **93** Anthrax cases from January to March (**=80 %**)

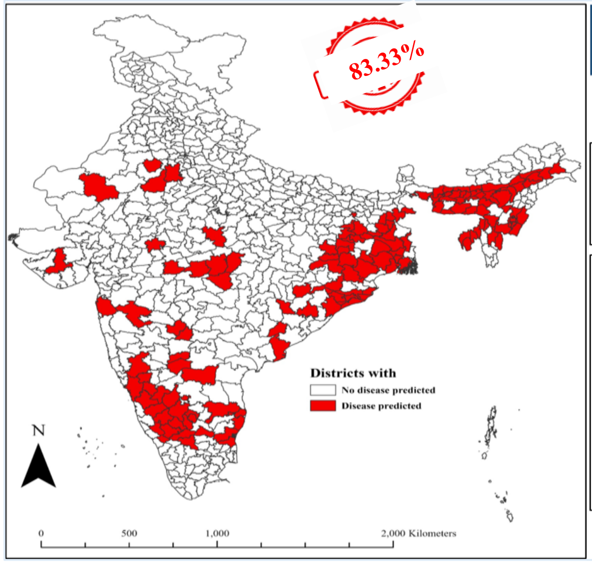
- Total attacks during 2023 : **116**
- Spreads in : **10** districts

NADRES v2 predicted : **8** districts (**=80%**)

- Majority of attacks :**January to March**
- Total attacks in Jan-Mar: **66**
- During Jan-Mar percentage of attacks : **56.9%**
- Spreads in : **5** districts (Jan-Mar)

NADRES v2 predicted : **4** districts (**=80%**)

**Validation of NADRES v2 showed 80% accuracy in predicting Anthrax outbreaks in 2023, highlighting its potential to prevent most cases through early warning.**




## Black Quarter prediction during 2023 for accuracy checking

**NADRES v2** If implemented, could have prevented **542** Black Quarter cases from January to June (**≈ 83.33%**)

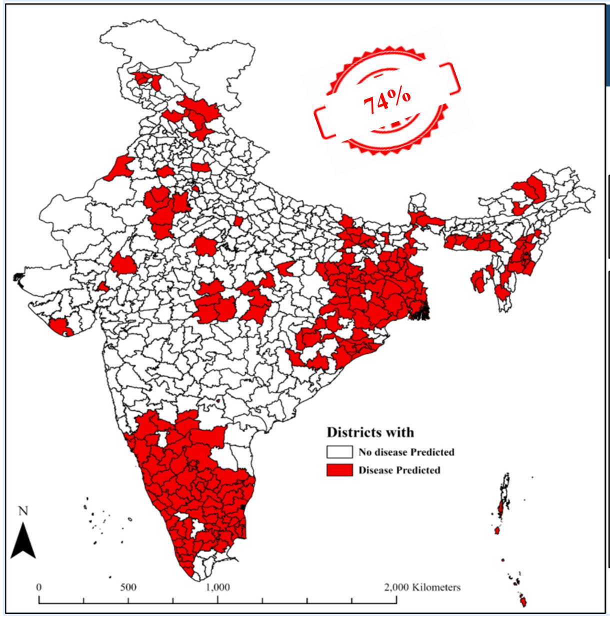
- Total attacks during 2023 : **650**
- Spreads in : **28** districts

NADRES v2 predicted : **23** districts (**≈ 82.14 %**)

- Majority of attacks :**January to June**
- Total attacks in Jan-Jun: **484**
- During Jan-Jun percentage of attacks : **74.46 %**
- Spreads in : **24** districts (Jan-Jun)

NADRES v2 predicted : **20** districts (**≈ 83.33%**)

**Validation of NADRES v2 showed ≈83% accuracy in predicting Black Quarter outbreaks during 2023, underscoring its potential to prevent most cases through timely early warning.**




## FMD prediction during 2021 for accuracy checking

**NADRES v2** If implemented, could have prevented **11,685** FMD cases from June to November (**≈74%**)

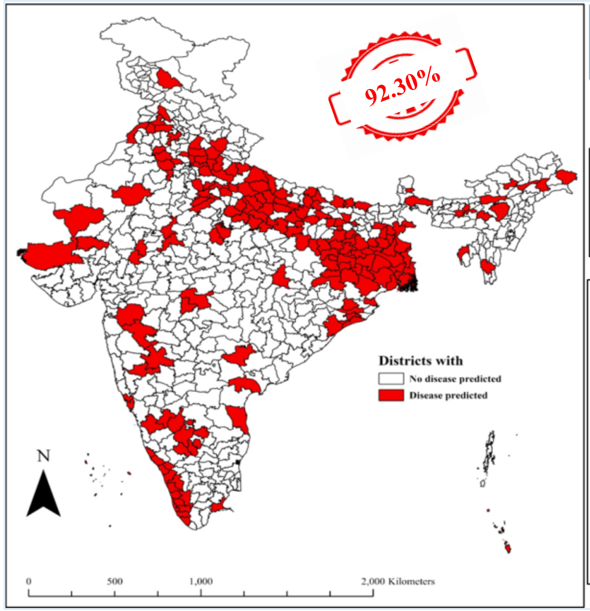
- Total attacks during 2021 : **19363**
- Spreads in : **116** districts

NADRES v2 predicted : **82** districts (**≈71%**)

- Majority of attacks :**June to November**
- Total attacks in June –Nov : **15791**
- During June-Nov percentage of attacks : **81.5 %**
- Spreads in : **104** districts (Jun-Nov)

NADRES v2 predicted : **77** districts (**≈74%**)

**Validation of NADRES v2 showed 74% accuracy in predicting FMD outbreaks in 2021, highlighting its potential to prevent most cases through early warning.**




## Theileriosis prediction during 2023 for accuracy checking

**NADRES v2** If implemented, could have prevented **2907** Theileriosis cases from January to August (**≈ 92.30%**)

- Total attacks during 2023 : **4271**
- Spreads in : **60** districts

NADRES v2 predicted : **54** districts (**= 90.00%**)

- Majority of attacks :**January to August**
- Total attacks in Jan-Aug: **3150**
- During Jan-Aug percentage of attacks : **73.75 %**
- Spreads in : **52** districts (Jan-Aug)

NADRES v2 predicted : **48** districts (**≈ 92.30%**)

**Validation of NADRES v2 showed 92.30% accuracy in predicting Theileriosis outbreaks in 2023, highlighting its potential to prevent most cases through early warning.**

# Post-Prediction Validation Using ProMED Data

We validated our forecasted results for livestock diseases using ProMED outbreak reports.

- Monthly forecasts were compared with actual reported outbreaks to verify whether the predicted diseases occurred in the same month and at the same predicted locations.
- This spatio-temporal validation helped assess the accuracy of the disease timing in our forecasting model.

## African Swine Fever

LAWNGTLAI AND MAMIT (MIZORAM) : PUBLISHED DATE: SAT 29 MAR 2025 : MIZORAM BATTLES FRESH AFRICAN SWINE FEVER OUTBREAK AS OVER 500 PIGS GIE

ProMED INTERNATIONAL SOCIETY FOR INFECTIOUS DISEASES

Click Here: [Mizoram battles fresh African Swine Fever outbreak as over 500 pigs gie - Daijiworld.com]

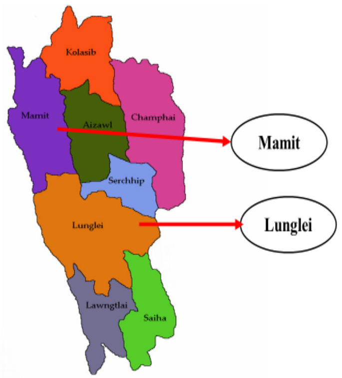
Date: Sat 29 Mar 2025

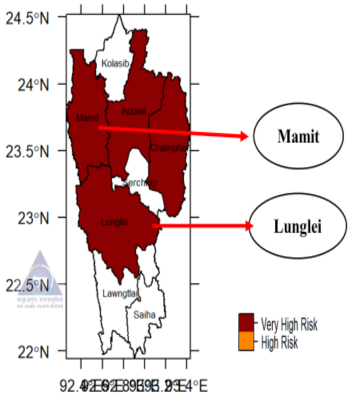
Issue Date: 4/1/2025, 10:45:46 AM GMT+5:30

AFRICAN SWINE FEVER

Mizoram State, India

- A new outbreak of African swine fever (ASF) has struck Mizoram, leading to the deaths of over 510 pigs in just 2 weeks, officials confirmed on Saturday [29 Mar 2025]. The highly contagious disease has spread across 13 villages and localities in Lawngtlai and Mamit districts, prompting urgent containment measures.
- Teams from the Animal Husbandry and Veterinary Department (AHVD) have already culled around 100 pigs and piglets in an effort to prevent further transmission. The fresh outbreak was confirmed on 20 Mar [2025] after testing at the Northeast Regional Disease Diagnostic Laboratory (NERDDL) in Guwahati.
- The outbreak initially surfaced in Lawngtlai district, which shares an unfenced international border with Myanmar and Bangladesh. The infection then spread to Mamit district, which borders Tripura and Bangladesh. Authorities are now closely monitoring the situation to contain the disease and prevent further losses.
- Mizoram has suffered severe financial setbacks due to recurring ASF outbreaks. In 2023 alone, the disease killed over 1100 pigs, while nearly 1000 were culled. The previous year, in 2022, ASF claimed 12 795 pigs, leading to 11 686 cullings. The worst outbreak occurred in 2021, when the state lost 33 417 pigs and was forced to cull 12 568 more, causing a financial loss of INR 334.14 crore [INR 3 341 400 000, approx. USD 39 million].




NIVEDI Prediction Reported February 2025 and Predicted April 2025

| Districts of Mizoram | ASF Preidiction for March 2025 | ASF Preidiction for April 2025 | ASF Preidiction for May 2025 |
|---|---|---|---|
| Aizawl | VHR | VHR | VHR |
| Kolasib | - | - | VHR |
| Lunglei | VHR | VHR | VHR |
| Mamit | VHR | VHR | VHR |
| Saiha | VHR | - | VHR |

## Lumpy Skin Disease

BELAGAVI (KARNATAKA) : PUBLISHED DATE 26-11-2024 : LUMPY SKIN DISEASE STRIKES CALVES IN BELAGAVI

ProMED INTERNATIONAL SOCIETY FOR INFECTIOUS DISEASES

Published Date: 2024-11-26 23:06:36 IST

Subject: PRO/SOAS>Lumpy skin disease - India (02): (Karnataka) cattle, calves

Archive Number: 20241126.8720274

LUMPY SKIN DISEASE - INDIA (02): (KARNATAKA) CATTLE, CALVES

A ProMED-mail post

http://www.promedmail.org

ProMED-mail is a program of the

International Society for Infectious Diseases

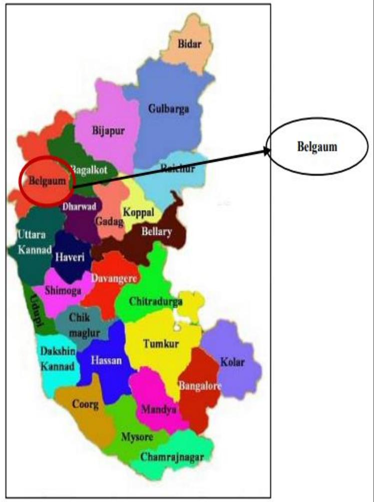
http://www.isid.org

The district [Belagavi, Karnataka state, India] is once again battling lumpy skin disease, a contagious viral disease that a acts cattle, and this time, it is spreading mostly among calves. The department of animal husbandry has commenced vaccination of calves on Monday [25 Nov 2024].

This is the third wave of lumpy skin disease. In the rest phase, the disease a acted local cattle, while the crossbreed cattle were a acted in the second phase. In the third phase, it is a acting the calves, especially the cow calf. However, department sources said the severity of the disease has considerably decreased as compared to the rest phase.

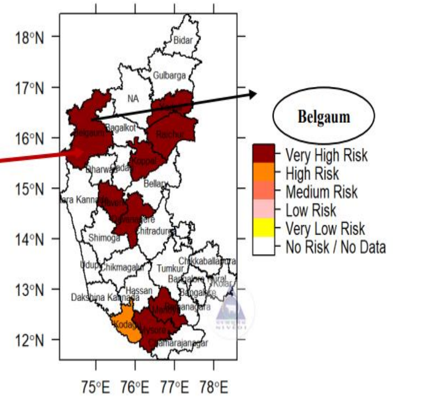
As far as Belagavi district is concerned, the disease has been found in several pockets, mainly in Kittur taluk. Lumpy skin disease is transmitted by blood-feeding insects, such as certain types of flies, mosquitoes, and ticks. It causes fever, nodules on the skin and can lead to death, especially among cattle that were not previously exposed to the virus.

"We started vaccinating calves from Monday [25 Nov 2024]. In the district, there are approximately 70 000 calves, and we have planned to complete their vaccination within a week. We received 1.6akh [160 000] doses of vaccination to vaccinate all calves between 4-12 months. The vaccination is not required for a calf below 4 months because of its naturally strong birth immunity," Rajeev Koler, deputy director of the animal husbandry department told TOI.

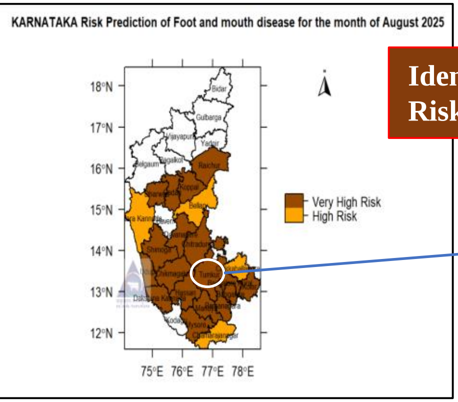



NIVEDI PRECTION Reported September 2024 and Predicted November 2024

| Districts of Mizoram | LSD Preidiction for October 2024 | LSD Preidiction for November 2024 | LSD Preidiction for December 2024 |
|---|---|---|---|
| Belgaum | VHR | VHR | NR |
| Davanagere | NR | VHR | NR |
| Haveri | VHR | VHR | NR |
| Kodagu | NR | VHR | NR |
| Koppal | NR | VHR | NR |



# Integrating Mathematical Modeling Post Disease Risk Forecasting




**Identification High Risk district**

**Tumkur**

**Key Questions Raised**

How will a disease spread within a population, and what factors influence the speed, scale, and peak of an outbreak?

Which combination of interventions (e.g., vaccination, quarantine, and social distancing) is most effective in controlling and epidemic, and what is the optimal timing for their implementation?

What are the economic costs of an epidemic, and which intervention strategies provide the best balance between public health benefits and economic feasibility?

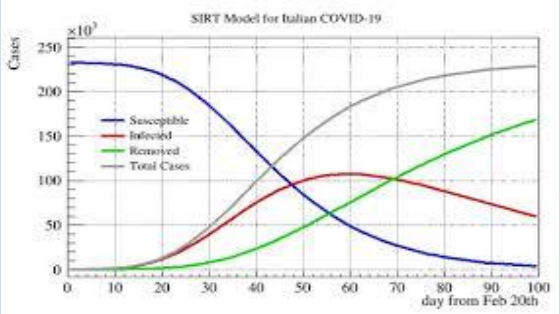
How can mathematical models inform policymakers to prepare for future outbreaks and prevent secondary waves of infection?

## Mathematical Model development

- ✓ Epidemiological Equations (SIR/SEIR Models)
- ✓ Simulations
- ✓ Sensitivity Analysis

E.g., SEIR equations:

$$\frac{dS}{dt} = -\beta SI, \quad \frac{dE}{dt} = \beta SI - \sigma E, \quad \frac{dI}{dt} = \sigma E - \gamma I, \quad \frac{dR}{dt} = \gamma I$$




**Output**

- ✓ Disease transmission curves.
- ✓ Peak infection time and expected case numbers.
- ✓ Estimation of resource needs (e.g., vaccines, isolation units).

## Data Required for Mathematical Modeling

- ✓ Population density of livestock.
- ✓ Movement and contact rates of animals.
- ✓ Vaccination coverage data.
- ✓ Environmental persistence and transmission dynamics.
- ✓ Disease-specific biological parameters (e.g., incubation period, $R_0$).

## Deployment

- ✓ Integration with GIS and prediction outputs.
- ✓ Real-time scenario testing (e.g., effect of vaccination, movement control).
- ✓ Web-based decision support tools for policymakers.
- ✓ Simulation dashboards for field officers and stakeholders.

**Helps in**

- Evidence-based decision-making.
- Efficient resource allocation.
- Designing targeted control strategies (ring vaccination, surveillance).
- Stakeholder communication with scenario simulations.

# Modeling Foot-and-Mouth Disease (FMD) Dynamics Across Multiple Hosts

**Objective:**

1. To develop a multi-host FMD model incorporating cattle, buffalo, sheep/goat, and pigs to capture cross-species transmission and predict outbreak time, duration, infection peak, spread speed, and disease scale under varying population densities.
2. To evaluate the effectiveness of control strategies such as vaccination for host animals and biosecurity measures in reducing FMD spread, and to provide insights for designing optimal intervention policies

## Questions that the model can answer

1. How can mathematical models explain the speed, peak, and overall scale of a disease outbreak in a population, and which parameters (such as transmission rate, recovery, immunity, the role of vaccination, and environmental factors like rainfall, temperature, and $p^H$) most strongly influence these patterns?
2. What combinations and timings of interventions such as vaccination, quarantine/isolation of symptomatically infected animals do models predict as most effective for controlling an epidemic while minimizing social and economic disruption?
3. How can models be used to estimate the risk of disease introduction in a specific region, forecast long-term epidemic dynamics, and guide policymakers in preventing future waves of infection?

## Assumptions

1. Homogeneous Mixing – All host species (cattle, buffalo, sheep, goat, and pigs) are assumed to **mix uniformly, with equal probability of contact across individuals within and between species.**
2. Deterministic Process – The model predicts FMD transmission dynamics based on **fixed parameters and initial conditions**, without incorporating random chance or stochastic events.
3. Constant Rates – Epidemiological parameters such as **recovery rate and natural mortality** are assumed constant over time.
4. Uniform Individual Characteristics – Within each host group, individuals are considered equally **susceptible and equally infectious, without accounting for age, immunity level, or behavioral variation**.
5. Disease-Free or Endemic Equilibria – The model analyzes the conditions under which FMD **either dies out or persists as an endemic infection in the host population.**

## Epidemiology and History of the FMD

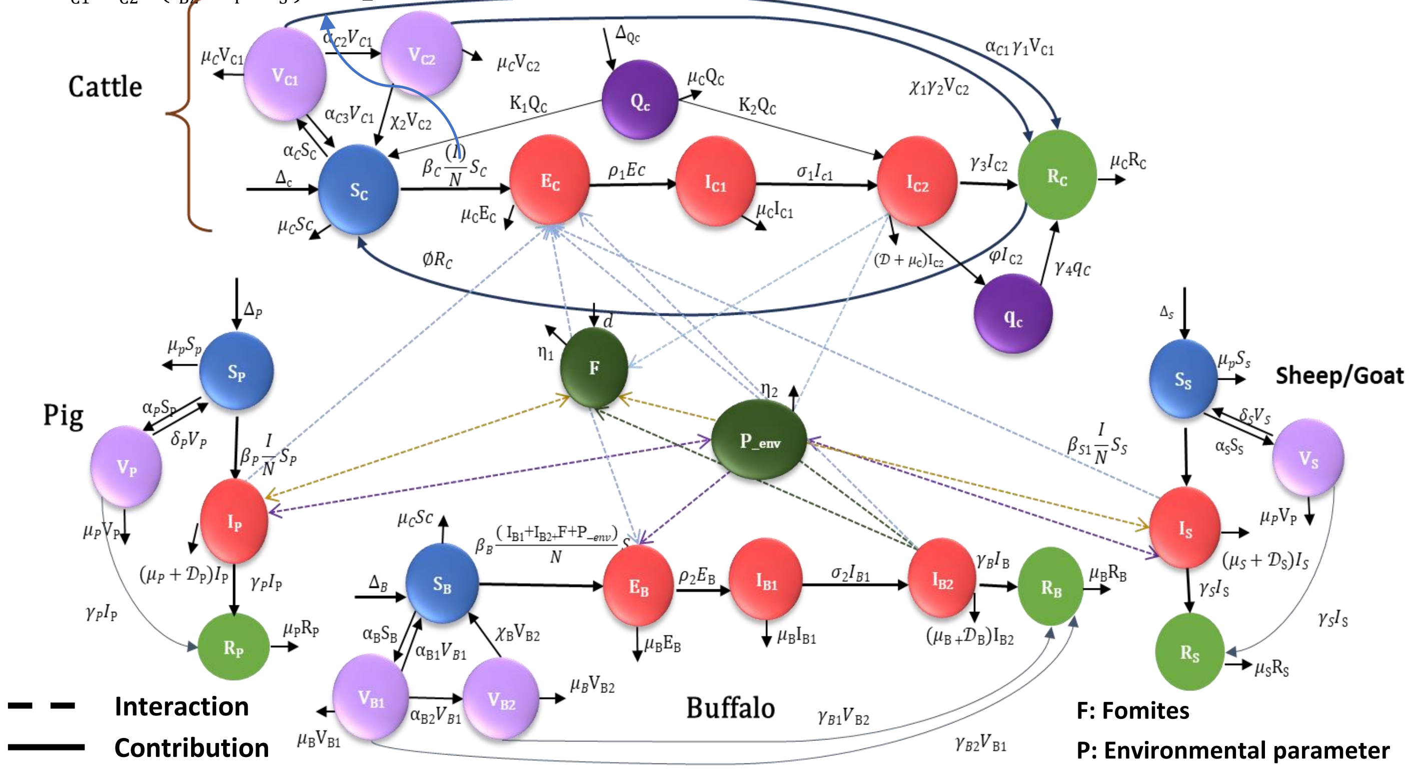
- **Causative agent**: FMDV, genus Aphthovirus, family Picornaviridae. Hosts: Cloven-hooved animals.
- **Transmission:** Direct contact with infected animals or their secretions/excretions, Indirect contact (Fomites, Animal products, and Human), and Wind-borne
- **Morbidity and mortality**: Very highly contagious in susceptible populations.
- **Durations of disease phases in cattle**: Incubation **3.6 days** (2.7–4.8 days); Latent **1.5 days** (1.1–2.1 days); Subclinical infectious **2.2 days** (1.5–3.5 days); Clinical infectious **8.5 days** (6.2–11.6 days); Total infectious phase (Subclinical infectious + Clinical infectious)**10.8 days** (8.2–14.2 days).
- **Serotypes:** Seven types of FMD virus are A, O, C, Southern African Territories (SAT)- 1, 2, and 3, and Asia 1. Only types O, A, and Asia1 are seen in India (Subramaniam *et al.*, 2013).
- **Endemic disease** – FMD has been present in India since the 19th century; serotypes O, A, Asia-1 circulate widely, while C disappeared after the 1990s (Subramaniam et al., 2013).
- **Burden & hosts** – India reports thousands of outbreaks annually, mainly in cattle and buffaloes, but also in sheep and goats. In Karnataka alone, 11,159 outbreaks with ~0.27 million cases were reported between 1977–2012 (Rout et al., 2014).
- **Serotype dominance** – Serotype O causes >80% of outbreaks across India and Karnataka; A and Asia-1 appear sporadically, while C is absent (Rout et al., 2014).
- **Geographic & seasonal trends** – Karnataka's dry zones (Central, Northern, Southern transition) report most cases, with peaks in cool, dry months and cyclic recurrence every 2–3 years (Rout et al., 2014).
- **Control & vaccination** – Preventive vaccination started in 2006–07 (ASCAD) in Karnataka and scaled up under the FMD Control Programme (2004; nationwide 2019) with bi-annual mass vaccination (Govt. of India, 2019).

## Why Mathematical Modeling for FMD

- **Understand disease dynamics:** Models describe how FMD spreads between animals, herds, and regions. They capture factors like transmission rate, incubation, carrier animals, and seasonality.
- **Evaluate control strategies**: Evaluate control strategies: Models assess the impact of vaccination frequency, coverage, and movement restrictions. Biannual vaccination campaigns in India have been designed, and future monitoring can be guided by insights from mathematical modeling.
- **Optimize resource use:** Helps governments decide where to allocate vaccines, manpower, and funds. Reduces wastage by targeting high-risk zones.
- **Policy & decision support:** Provides **evidence-based guidance** for disease eradication programs. Supports India's goal of achieving **FMD-free zones** for livestock trade.
- **Assess the effectiveness of vaccination:** Models measure herd immunity levels and show whether vaccination frequency and coverage are enough to prevent outbreaks.
- **Simulate "what-if" scenarios:** Allows testing of different outbreak situations (e.g., low vs. high vaccination, unrestricted vs. restricted animal movement) without real-world risk.

# Schematic Diagram of SEIRVQq (Cattle), SEIRV (Buffalo), SVIR (Pig), SVIR (Sheep/Goat), Carrier Fomites (F), Environment (P_*env)* Mathematical Model

$I = I_{C1} + I_{C2} + (I_{B2} + I_P + I_S) * F * P\_env$




| Compartment | Description |
|---|---|
| $S_C, S_B$ | Susceptible population of Cattle and Buffalo |
| $E_C, E_B$ | Latent/exposed population of Cattle and Buffalo |
| $I_{C1}, I_{B1}$ | Sub-clinical infectious population of Cattle and Buffalo |
| $I_{C2}, I_{B2}$ | Clinical infectious population of Cattle and Buffalo |
| $R_C, R_B$ | Recovered population of Cattle and Buffalo |
| $V_{C1}, V_{B1}$ | Vaccinated fewer rounds population of Cattle and Buffalo |
| $V_{C2}, V_{B2}$ | Vaccinated more rounds population of Cattle and Buffalo |
| $Q_C$ | Quarantine population of Cattle |
| $q_C$ | Isolated population of Cattle |
| $S_P, S_S$ | Susceptible population of the Pig and Sheep/Goat |
| $V_P, V_S$ | Vaccinated population of pigs and Sheep/Goat |
| $I_P, I_S$ | Infected population of the Pig and Sheep/Goat |
| $R_P, R_S$ | The recovered population of pigs and Sheep/Goat |
| P_env | Environmental parameters includes temperature, humidity and $p^H$ |
| F | Fomites from contaminated feed, water, vehicles or farm workers |

## Factors Influencing the Building of the Mathematical Modeling

**Environmental parameters:** Temperature(<20), Relative Humidity(>55), and $P^H$ (7-7.5) virus will survive in these conditions

| Hosts | Spread factor | Control factor |
|---|---|---|
| Infectious animals (like infected Cattle, Buffalo, Sheep, and Goat) | Reservoir: Direct contact, Indirect contact | Vaccination, Isolation |
| Pig | Amplifier: Airborne | Vaccination and isolation |
| Fomites and Environment | Contact with Infected animals and with emitters of airborne | Isolation of infected animals |

- FMDV spreads mainly through secretions and excretions (breath, milk, semen, etc.) of infected animals.
- Direct transmission occurs via inhalation of virus-laden aerosols or contact with contaminated feed, water, vehicles, or farm workers.
- Indirect transmission happens through ingestion of contaminated animal products (milk, meat) or secondary aerosols.
- The virus survives for days to months in the environment, with survival influenced by temperature, humidity, and $p^H$.

# Model Parameterization

**Why Parameterization:** It is important in mathematical modeling because it assigns realistic biological, ecological, and epidemiological values to the model's variables.

| Sl.No | Parameter | Description |
|---|---|---|
| 1 | $\beta_C$ | Transmission Rate of Cattle |
| 2 | $\beta_B$ | Transmission rate of Buffalo |
| 3 | $\beta_P$ | Transmission rate of Pig |
| 4 | $\beta_S$ | Transmission rate of Sheep/Goat |
| 5 | $\mu_C$ | Death Rate of Cattle |
| 6 | $\mu_B$ | The death rate of Buffalo |
| 7 | $\mu_P$ | Death Rate of Pig |
| 8 | $\mathcal{D}_c$ | Disease-induced mortality rate of cattle |
| 9 | $\rho_1$ | Progression Rate from Exposed Cattle to Asymptomatically Infected Cattle |
| 10 | $\sigma_1$ | Progression rate from Asymptomatic Cattle to symptomatic Cattle |
| 11 | $\rho_2$ | Progression rate from Exposed Buffalo to Infected Buffalo |
| 12 | $\sigma_2$ | Progression rate from Asymptomatic Buffalo to symptomatic Buffalo |
| 13 | $\emptyset$ | Rate of loss of immunity |
| 14 | $\alpha_C$ | Vaccination rate for Cattle |
| 15 | $\alpha_B$ | Vaccination rate for Buffalo |
| 16 | $\varphi$ | Isolated symptomatically infected Cattle |
| 17 | $\chi 2$ | Waning rate of vaccinated animals |
| 18 | $\gamma_3$ | Recovery rate of symptomatic infected |
| 19 | $\gamma_4$ | Isolated Cattle Recovery Rate |
| 20 | $\chi_2$ | Waning rate of vaccinated cattle |
| 21 | $\eta_1$ | Fomites pathogen decay rate |
| 22 | $\eta_2$ | Environment pathogen decay rate |
| 24 | $S_C$ | Susceptible population of Cattle |
| 25 | $E_C$ | Latent/exposed population of Cattle |
| 26 | $I_{C1}$ | Sub-clinical infectious population of Cattle |
| 27 | $I_{C2}$ | Clinical infectious population of Cattle |
| 28 | $R_C$ | Recovered population of Cattle |
| 29 | $V_{C1}$ | Vaccinated fewer rounds population of Cattle |
| 30 | $V^C{}_2$ | Vaccinated more rounds population of Cattle |
| 31 | $Q_C$ | Quarantine population of Cattle |
| 32 | $q_C$ | Isolated population of Cattle |
| 33 | $S_{B,}$ | Susceptible populations of Buffalo |
| 34 | $E_{B,}$ | Exposed populations of Buffalo |
| 35 | $I_{B1,}$ | Subclinical Infected populations of Buffalo, respectively |
| 36 | $I_{B2,}$ | Clinical Infected populations of Buffalo, respectively |
| 37 | $R_B$ | Recovered populations of Buffalo |
| 38 | $V_{B1}$ | Vaccinated population of fewer rounds in Buffalo |
| 39 | $V_{B2}$ | vaccinated more rounds population of Buffalo |
| 40 | $S_P$ | Susceptible population of the Pig |
| 41 | $V_P$ | Vaccinated population of pigs |
| 42 | $I_p$ | Infected population of the Pig |
| 43 | $R_P$ | The recovered population of pigs |
| 44 | $S_{S,}$ | Susceptible populations of Sheep and Goats |
| 45 | $V_S$ | Vaccinated populations of Sheep and Goats |
| 46 | $I_S$ | and Infected populations of Sheep and Goats |
| 47 | $R_S$ | Recovered populations of Sheep and Goats |

# Model Formulation

CATTLE

1. $\frac{dS_c}{dt} = \Delta_C + \alpha_{C3}V_{C1} + \chi_2 V_{C2} + K_1 Q_C + \emptyset RC - [\alpha_C + \mu_C + \beta_C \frac{(IC1 + IC2 + IB2 + f\_env * IP + f\_env * IS)}{N}] S_C$

2. $\frac{dE_c}{dt} = \beta_C \frac{(IC1 + IC2 + IB2 + f\_env * IP + f\_env * IS)}{N} S_C - (\rho_1 + \mu_C)E_C$

3. $\frac{dI_{c1}}{dt} = \rho_1 E_C - (\mu_C + \sigma_1)I_{c1}$

4. $\frac{dI_{c2}}{dt} = \sigma_1 I_{c1} + K_2 Q_C - (\gamma_3 + \mu_C + \varphi + \mathcal{D}_C)I_{C2}$

5. $\frac{dR_c}{dt} = \alpha_{C1}\gamma_1 V_{C1} + \chi_1\gamma_2 V_{C2} + \gamma_3 I_{C2} + \gamma_4 q_C - (\mu_C + \emptyset)R_C$

6. $\frac{dV_{c1}}{dt} = \alpha S_C - (\alpha_{C1}\gamma_1 + \alpha_{C2} + \alpha_{C3} + \mu_C)V_{C1}$

7. $\frac{dV_{c2}}{dt} = \alpha_{C2}V_{C1} - (\chi_1\gamma_2 + \mu_C + \chi_2)V_{C2}$

8. $\frac{dQ_c}{dt} = \Delta_{QC} - [K_1 + K_2 + \mu_C]Q_C$

9. $\frac{dq_c}{dt} = \varphi I_{C2} - (\gamma_4 + \mu_C)q_C$

BUFFALO

1. $\frac{dS_B}{dt} = \Delta_B + \alpha_{B1}V_{B1} + \chi_B V_{C2} - [\alpha_B + \mu_B + \beta_C \frac{(IB1 + IB2 + f\_env * F * IC2)}{N}] S_B$

2. $\frac{dE_B}{dt} = \beta_B \frac{(IB1 + IB2 + f\_env * F * IC2)}{N} S_B - (\rho_2 + \mu_B)E_B$

3. $\frac{dI_{B1}}{dt} = \rho_2 E_B - (\mu_B + \sigma_2)I_{B1}$

4. $\frac{dI_{B2}}{dt} = \sigma_2 I_{B1} - (\mu_B + \mathcal{D}_B)I_{B2}$

5. $\frac{dV_{B1}}{dt} = \alpha_B S_B - (\alpha_{B1} + \alpha_{B2} + \mu_B)V_{B1} - \gamma_{B2}V_{B1}$

6. $\frac{dV_{B2}}{dt} = \alpha_{B2}V_{B1} - (\mu_B + \chi_B)V_{B2} - \gamma_{B1}V_{B2}$

7. $\frac{dR_B}{dt} = \gamma_B I_B - (\mu_B)R_B + \gamma_{B1}V_{B2} + \gamma_{B2}V_{B1}$

SHEEP/GOAT

1. $\frac{dS_S}{dt} = \Delta_S + \delta_S V_S - (\beta_S \frac{(IS)}{N} + \mu_S + \alpha_S)S_S$

2. $\frac{dI_S}{dt} = \beta_S \frac{(IS)}{N} S_S - (\mu_S + \mathcal{D}_S)I_S$

3. $\frac{dV_S}{dt} = \alpha_S S_S - (\delta_S + \mu_S)V_S - \gamma_{S1}V_S$

4. $\frac{dR_S}{dt} = \gamma_S I_S - (\mu_S)R_S + \gamma_{S1}V_S$

PIG

1. $\frac{dS_P}{dt} = \Delta_p + \delta_P V_P - (\beta_P \frac{(IP)}{N} + \mu_P + \alpha_P)S_P$

2. $\frac{dI_P}{dt} = \beta_P \frac{(IP)}{N} S_P - (\mu_P + \mathcal{D}_P)I_P$

3. $\frac{dV_P}{dt} = \alpha_P S_P - (\delta_P + \mu_P)V_P - \gamma_{P1}V_P$

4. $\frac{dR_P}{dt} = \gamma_P I_P - (\mu_P)R_P + \gamma_{P1}V_P$

**Why are differential equations:** Differential equations describe how populations change continuously over time. They provide a precise framework for predicting outbreaks, evaluating interventions, and calculating the basic reproduction number ($R_0$). These equations are essential because they offer a powerful mathematical tool to describe, predict, and analyse how systems evolve, helping us understand natural phenomena, model complex processes, and solve real-world problems

# Equilibrium point

### (1) Disease– free equilibrium point ($E_0$) :

A stable state in an epidemic model where the number of infected individuals in a population is zero, and the disease is no longer circulating.
And Why? Study the DFE to know the disease Can be eradicated? And What conditions (like $R_0 < 1$) ensure elimination?

$$S_C* == \frac{\Delta_c+\alpha_{c3}V_{c1}+\chi_2 V_{C2}+\emptyset RC}{[\alpha_c+\mu_c]}, E_C^* = I_{C1}^* = I_{C2}^* = q_C^* = 0, R_C^* = \frac{\alpha_{c1}\gamma_1 V_{C1}+\chi_1\gamma_2 V_{C2}}{(\mu_c+\emptyset)},$$

$$V_{C1}^* = \frac{\alpha S_C}{(\alpha_{c1}\gamma_1+\alpha_{c2}+\alpha_{c3}+\mu_c)}, V^*_{C2} = \frac{\alpha_{c2}V_{c1}}{(\chi_1\gamma_2+\mu_c+\chi_2)}$$

### (2) Endemic equilibrium point ($E_1$):

An endemic equilibrium point is a stable state in an epidemiological model where an infectious disease persists within a population at a consistent
Why? This study is to understand What happens if the disease cannot be eradicated? And how many people/animals will remain infected long term?

$$S_C* = \frac{\Delta_c+\alpha_{c3}V_{c1}+\chi_2 V_{C2}+K_1 Q_C+\emptyset RC}{\left[\alpha_c+\mu_c+\beta_c\frac{(I_{C1}+IC_2+IB_2+f\_env*IP+f\_env*IS)}{N}\right]},$$

$$E_C* = \frac{\beta_c\frac{(I_{C1}+IC_2+IB_2+f\_env*IP+f\_env*IS)_{sc}}{N}}{(\rho_1+\mu_c)}, I_{C1}* = \frac{\rho_1 EC}{(\mu_c+\sigma_1)}, q_C* = \frac{\varphi I_{C2}}{(\gamma_4+\mu_c)},$$

$$I_{C2}* = \frac{\sigma_1 I_{c1}+K_2 Q_C}{(\gamma_3+\mu_c+\varphi I_{C2}+\mathcal{D}_c)}, Q_C* = \frac{\Delta_{QC}}{[K_1+K_2+\mu_C]}, R_C* = \frac{\alpha_{c1}\gamma_1 V_{C1}+\chi_1\gamma_2 V_{C2}+\gamma_3 I_{C2}+\gamma_4 q_c}{(\mu_c+\emptyset)},$$

$$V_{C1}* = \frac{\alpha S_C}{(\alpha_{c1}\gamma_1+\alpha_{c2}+\alpha_{c3}+\mu_c)}, V_{C2}* = \frac{\alpha_{c2}V_{c1}}{(\chi_1\gamma_2+\mu_c+\chi_2)}$$

# Basic Reproduction Number ($R_0$)

Basic reproduction number: It represents the average number of new infections generated by a single infected person in a completely susceptible population

Steps for finding the next generation matrix (NGM):

Step 1: Identify the infectious compartments (like Exposed "E" and infected "I" compartments)

Step 2: Write the equations for infected compartments

- F: Rate of new infections entering the compartment
- V: Rate of transfer into and out of the compartment (not including the new infections)

Step 3: Compute the Jacobian matrix (Jacobian with respect to E & I)

Step 4: Form the next generation matrix (NGM)

NGM = $FV^{-1}$

Step 5: Compute R0, the basic reproduction number, which is the spectral radius (dominant eigenvalues) of k

R0 = $\rho\ (K)$

$$\boldsymbol{R_0} = \frac{\boldsymbol{S_C\beta_C\rho_1}}{\boldsymbol{2N\ (\mu_C+\rho_1)(D_C+\gamma_3+\mu_C+\varphi)}} + \frac{\boldsymbol{\sqrt{A}}}{\boldsymbol{B}}$$

Here, $A = S_C\beta_C\rho_1(\mu_B+\rho_2+\gamma_B)\Big((4D_CFS_Bf_{env}\beta_B\mu_C)+(4D_CFS_Bf_{env}\beta_B\rho_1)+(4FS_Bf_{env}\beta_B\gamma_3\mu_C)$
$+(4FS_Bf_{env}\beta_B\gamma_3\rho_1)+(4FS_Bf_{env}\beta_B\mu_C^2)+(4FS_Bf_{env}\beta_B\mu_C\rho_1)+(4FS_Bf_{env}\beta_B\varphi\mu_C)$
$+(4FS_Bf_{env}\beta_B\varphi\rho_1)+(S_C\beta_C\gamma_B\rho_1)+(S_C\beta_C\mu_B\rho_1)+(S_C\beta_C\rho_2\rho_1)\Big)$

$B = 2N\ (D_C\gamma_B\mu_C + D_C\gamma_B\rho_1 + D_C\mu_B\mu_C + D_C\mu_B\rho_1 + D_C\mu_C\rho_2 + D_C\rho_2\rho_1 + \gamma_3\gamma_B\mu_C + \gamma_3\mu_B\rho_1 + \gamma_3\mu_B\mu_C$
$+\gamma_B\mu_B\rho_1 + \gamma_3\mu_C\rho_2 + \gamma_3\rho_2\rho_1 + \gamma_B\mu_C^2 + \gamma_B\mu_C\rho_1 + \gamma_B\mu_C\varphi + \gamma_B\rho_1\varphi + \mu_B\mu_C^2 + \mu_B\mu_C\rho_1 + \mu_B\mu_C\varphi$
$+\mu_B\rho_1\varphi + \mu_C^2\rho_2 + \mu_C\rho_2\rho_1 + \mu_C\rho_2\varphi + \rho_2\rho_1\varphi)$

The basic reproduction number $\boldsymbol{R_0}$ serves as a threshold indicator for the control of foot-and-mouth disease (FMD): when $\boldsymbol{R_0} < 1$, the epidemic dies out; when $\boldsymbol{R_0} > 1$, the epidemic persists. Control measures should aim to reduce $\boldsymbol{R_0}$ below 1 to eliminate the disease.

**Herd immunity threshold (HIT):** Minimum proportion of animals that must be immune to stop spread: HIT= $1 - \frac{1}{R_0}$

# Theorem 1: Non-Negativity

Goal: We aim to show that if all the initial conditions are non-negative, then all the state variables remain non-negative for all future time $t \geq 0$.

$S_C(0), E_C(0), I_{C1}(0), I_{C2}(0), R_C(0), V_{C1}(0), V_{C2}(0), Q_C(0), q_C(0) \geq 0$

Proof: We'll prove this for each differential equation using the standard approach:

$$\frac{d\,SC}{dt} = \Delta_C + \alpha_{C3}V_{C1} + \chi_2 V_{C2} + \kappa_1 Q_C + \phi R_C - (\alpha_c + \mu_C + (\beta_C\,(\text{infected})/N)) * Sc$$

(**Note**: infected $I_{C1+}I_{C2+}I_{B2+}I_P+IS+F+P\_env$) All terms are non-negative except the last, which subtracts. The depletion term is proportional to $S_C$, so if $S_C = 0$, this term vanishes. So, $\frac{d\,SC}{dt} \geq 0$ when $S_C = 0 \rightarrow$ no negative flow out of zero.

$\frac{d\,EC}{dt}_{EC=0} = (\beta C(\text{infected})/N) * SC$, If $E_C=0$, the loss term vanishes. Production from $S_C \geq 0$ so $\frac{d\,EC}{dt} \geq 0$.

$\frac{d\,IC1}{dt}_{IC1=0} = \rho_1 E_C$, Again, if $I_{C1}=0$, its depletion stops, $\rho_1 E_C \geq 0$ produces it. So, $I_{C1}(t) \geq 0$.

$\frac{d\,IC2}{dt}_{IC2=0} = \sigma_1 I_{C1} + \kappa_2 Q_C$, Gains from $I_{C1}$ and $Q_C \rightarrow$ both are $\geq 0$, Loss is proportional to $I_{C2} \rightarrow$ stops at 0. So, $I_{C2}(t) \geq 0$.

$\frac{d\,RC}{dt}_{RC=0} = \alpha_{C1}\gamma_1 V_{C1} + \chi_1\gamma_2 V_{C2} + \gamma_3 I_{C2} + \gamma_4 q_C$, All inflow terms $\geq 0$. So, $R_C \geq 0$

$\frac{d\,VC1}{dt}_{VC1=0} = \alpha S_C$, If $V_{C1} = 0$, depletion is zero, Gain from $S_C \geq 0 \rightarrow V$ stays $\geq 0$, Linear ODE with inflow, bounded outflow $\rightarrow$ stays $\geq 0$

$\frac{d\,VC2}{dt}_{VC2=0} = \alpha_{C2}V_{C1}$, If VC2 = 0, depletion is zero, Gain from $S_C \geq 0 \rightarrow V$ stays $\geq 0$

$\frac{d\,QC}{dt}_{QC=0} = \Delta_{QC} \geq 0$

$\frac{dqC}{dt}_{Qc=0} = \Phi\, Ic_2$ Inflow from $I_{C2} \geq 0$, depletion linear in qC, Since the depletion terms vanish at zero for each variable, the inflow terms are always non-negative. The system is well-posed, and all initial conditions are non-negative. By the non-negativity theorem, all state variables remain non-negative for all $t \geq 0$.

**Conclusion: The non-negativity theorem ensures that model solutions never become negative, keeping results biologically meaningful.**

# Theorem 2: Boundedness

Goal: The goal of proving boundedness is to demonstrate that the model's solutions remain finite and well-defined for all time, ensuring that the system does not diverge or exhibit unrealistic, unbounded behavior

The boundedness proof for the model is based on the provided system of differential equations.

Define Total Cattle Population: Let $NC(t)=S_C+E_C+I_{C1}+I_{C2}+R_C+V_{C1}+V_{C2}+Q_C+q_C$

Add All the Equations, Now, compute: $\frac{d\,NC}{dt} = \sum$ all RHS terms

We will notice that many internal transfers cancel each other (e.g., a term leaving one compartment enters another). So, the only non-canceling terms (net sources and sinks) are: Birth/entry terms: $+\Delta_C$, $+\Delta_{QC}$, Natural death terms (all compartments lose μC times their values): Appears in each equation, Disease-related death: $D_C I_{C2}$(only affects one compartment)

$$N_C(t) = \Delta_C + \alpha_{C3}V_{C1} + \chi_2 V_{C2} + K_1 Q_C + \emptyset RC - \alpha_C S_C - \beta_C \frac{(I_{C1+}I_{C2+}I_{B2+}I_P+IS+F+P\_env)}{N}\ ]\ S_C + \beta_C \frac{(I_{C1+}I_{C2+}I_{B2+}I_P+IS+F+P\_env)}{N} S_C - \rho_1 E_C + \rho_1 E_C - \sigma_1 I_{c1} + \sigma_1 I_{c1} + K_2 Q_C - \gamma_3 I_{C2} - \varphi I_{C2} - (\mathcal{D}_C) I_{C2} + \alpha_{C1}\gamma_1 V_{C1} + \chi_1\gamma_2 V_{C2} + \gamma_3 I_{C2} + \gamma_4 q_C - \emptyset RC + \alpha_C S_C - \alpha_{C1}\gamma_1 V_{C1} - \alpha_{C2}V_{C1} - \alpha_{C3}V_{C1} + \alpha_{C2}V_{C1} \_ \chi_1\gamma_2 V_{C2} - \chi_2 V_{C2} + \Delta_{QC} - K_1 Q_C - K_2 Q_C + \varphi I_{C2} - \gamma_4 q_C - \mu_C S_C - E_C\mu_C - \mu_C I_{c1} - \mu_C I_{C2} - \mu_C R_C - \mu_C Q_C - \mu_C q_C - \mu_C V_{C1} - \mu_C V_{C2}$$

$$N_C(t)NC(t) = \Delta_C + \Delta_{QC} - \mu_C S_C - E_C\mu_C - \mu_C I_{c1} - \mu_C I_{C2} - \mu_C R_C - \mu_C Q_C - \mu_C q_C - \mu_C V_{C1} - \mu_C V_{C2} - \mathcal{D}_C I_{C2}$$

$$N_C(t) = \Delta_C + \Delta_{QC} - \mu_C(S_C+E_C+I_{C1}+I_{C2}+R_C+V_{C1}+V_{C2}+Q_C+q_C) - \mathcal{D}_C I_{C2}$$

$$N_C(t) = \Delta_C + \Delta_{QC} - \mu_C N_C - \mathcal{D}_C I_{C2}$$

Therefore: $\frac{d\,NC}{dt} \leq \Delta_C + \Delta_{QC} - \mu_C N_C$ (Why "≤"? Because we ignore disease-related deaths (DC IC2≥0, which would make it smaller).

Step 4: Solve the Differential Inequality Let: $M = \Delta_C + \Delta_{QC}$ Then: $\frac{d\,NC}{dt} \leq M - \mu C\, NC$

This is a standard linear differential inequality. We compare this to: $\frac{d\,Y}{dt} = M - \mu C\, y$

The solution is: $y(t) = (NC(0) - \frac{M}{\mu C})\, e^{-\mu_C t} + \frac{M}{\mu C}$ (Boyce, W. E., & DiPrima, R. C., 2017).

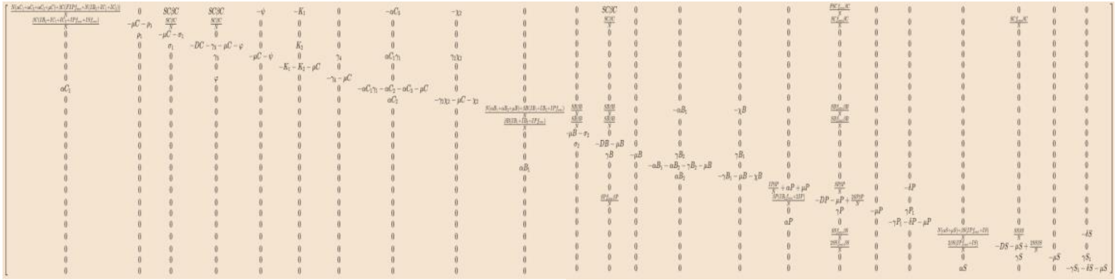
By the comparison theorem: $NC(t) \leq y(t) \leq \max(NC(0), \frac{M}{\mu C})$

Hence, the total population NC(t) is bounded above by: max (NC (0), (ΔC+ΔQC)/μC)), For all t≥0, the total cattle population NC(t) remains bounded above by a constant: $N_C(t) \leq \max(N_C(0), (\Delta_C+\Delta_{QC})/\mu_C)$

The **boundedness theorem** ensures that the total population remains within a finite limit, reflecting real-world constraints and preventing the model from producing unbounded or unrealistic growth.

# Theorem 3: Stability Analysis Around Equilibrium Points

Goal: To determine whether a model's equilibrium points are stable or unstable. Will the system return to equilibrium after a small disturbance (stable), or will it move away and behave differently (unstable).



The Jacobian $J_0$ at the disease-free equilibrium $E_0$ determines the local dynamics of the FMDV model. If all eigenvalues of $J_0$ have negative real parts, $E_0$ is locally asymptotically stable and the infection dies out. If all eigenvalues have positive real parts (as required in this theorem), $E_0$ is unstable, and small perturbations grow. If some eigenvalues are negative and others positive, $E_0$ is a saddle equilibrium, stable along certain directions and unstable along others

$$[\lambda^4(\lambda+\mu_C)(\gamma_4+\lambda+\mu_C)(\alpha_C\alpha_{C1}\gamma_1\gamma_2\chi_2+\alpha_C\alpha_{C1}\gamma_1\lambda+\alpha_C\alpha_{C1}\gamma_1\mu_C+\alpha_C\alpha_{C1}\gamma_1\chi_2+\alpha_C\alpha_{C1}\gamma_2\chi_2+\alpha_C\alpha_{C2}\lambda+\alpha\alpha_C\alpha_{C2}\mu_C+\alpha\alpha_C\alpha_{C2}\psi+\alpha_C\gamma_2\lambda\chi_2+\alpha_C\gamma_2\mu_C\chi_2+\alpha_C\gamma_2\chi_2\psi+\alpha_C\lambda^2+2\alpha_C\lambda\mu_C+\alpha_C\lambda\chi_2+\alpha_C\lambda\psi+\alpha_C{\mu_C}^2+\alpha_C\mu_C\chi_2+\alpha_C\mu_C\psi+\alpha_C\chi_2\psi+\alpha_{C1}\gamma_1\gamma_2\lambda\chi_2+\alpha_{C1}\gamma_1\gamma_2\mu_C\chi_2+\alpha_{C1}\gamma_1\gamma_2\chi_2\psi+\alpha_{C1}\gamma_1\lambda^2+2\alpha_{C1}\gamma_1\lambda\mu_C+\alpha_{C1}\gamma_1\lambda\chi_2+\alpha_{C1}\gamma_1\lambda\psi+\alpha_{C1}\gamma_1{\mu_C}^2+\alpha_{C1}\gamma_1\mu_C\chi_2+\alpha_{C1}\gamma_1\mu_C\psi+\alpha_{C1}\gamma_1\chi_2\psi+\alpha_{C2}\gamma_2\lambda\chi_2+\alpha_{C2}\gamma_2\mu_C\chi_2+\alpha_{C2}\gamma_2\chi_2\psi+\alpha_{C2}\lambda^2+2\alpha_{C2}\lambda\mu C+\alpha_{C2}\lambda\chi_2+\alpha_{C2}\lambda\psi+\alpha_{C2}{\mu_C}^2+\alpha_{C2}\mu_C\chi_2+\alpha_{C2}\mu_C\psi+\alpha_{C2}\chi_2\psi+\alpha_{C3}\gamma_2\lambda\chi_2+\alpha_{C3}\gamma_2\mu_C\chi_2+\alpha_{C3}\gamma_2\chi_2\psi+\alpha_{C3}\lambda^2+2\alpha_{C3}\lambda\mu_C+\alpha_{C3}\lambda\chi_2+\alpha_{C3}\lambda\psi+\alpha_{C3}\mu_C2+\alpha_{C3}\mu_C\chi_2+\alpha_{C3}\mu_C\psi+\alpha_{C3}\chi_2\psi+\gamma_2\lambda^2\chi_2+2\gamma_2\lambda\mu_C\chi_2+\gamma_2\lambda\chi_2\psi+\gamma_2{\mu_C}^2\chi_2+\gamma_2\mu_C\chi_2\psi+\lambda^3+3\lambda^2\mu_C+\lambda^2\chi_2+\lambda^2\psi+3\lambda{\mu_C}^2+2\lambda\mu_C\chi_2+2\lambda\mu_C\psi+\lambda\chi_2\psi+{\mu_C}^3+{\mu_C}^2\chi_2+{\mu_C}^2\psi+\mu_C\chi_2\psi)]=0$$

$$[\lambda^3(\lambda+\mu_B)(\alpha_B\alpha_{B2}\gamma_{B1}+\alpha_B\alpha_{B2}\lambda+\alpha_B\alpha_{B2}\mu_B+\alpha_B\gamma_{B1}\gamma_{B2}+\alpha_B\gamma_{B1}\lambda+\alpha_B\gamma_{B1}\mu_B+\alpha_B\gamma_{B2}\lambda+\alpha_B\gamma_{B2}\mu_B+\alpha_B\gamma_{B2}\chi_B+\alpha_B\lambda^2+2\alpha_B\lambda\mu_B+\alpha_B\lambda\chi_B+\alpha_B{\mu_B}^2+\alpha_B\mu_B\chi_B+\alpha_{B1}\gamma_{B1}\lambda+\alpha_{B1}\gamma_{B1}\mu_B+\alpha_{B1}\lambda^2+2\alpha_{B1}\lambda\mu_B+\alpha_{B1}\lambda\chi_B+\alpha_{B1}{\mu_B}^2+\alpha_{B1}\mu_B\chi_B+\alpha_{B2}\gamma_{B1}\lambda+\alpha_{B2}\gamma_{B1}\mu_B+\alpha_{B2}\lambda^2+2\alpha_{B2}\lambda\mu_B+\alpha_{B2}\lambda\chi_B+\alpha_{B2}{\mu_B}^2+\alpha_{B2}\mu_B\chi_B+\gamma_{B1}\gamma_{B2}\lambda+\gamma_{B1}\gamma_{B2}\mu_B+\gamma_{B1}\lambda^2+2\gamma_{B1}\lambda\mu_B+\gamma_{B1}{\mu_B}^2+\gamma_{B2}\lambda^2+2\gamma_{B2}\lambda\mu_B+\gamma_{B2}\lambda\chi_B+\gamma_{B2}{\mu_B}^2+\gamma_{B2}\mu_B\chi_B+\lambda^3+3\lambda^2\mu_B+\lambda^2\chi_B+3\lambda{\mu_B}^2+2\lambda\mu_B\chi_B+\mu_{B3}+\mu_{B2}\chi_B)]=0$$

$$[\lambda(\lambda+\mu_P)(\alpha_P\gamma_{P1}+\alpha_P\lambda+\alpha_P\mu_P+\gamma_{P1}\lambda+\gamma_{P1}\mu_P+\delta_P\lambda+\delta_P\mu_P+\lambda^2+2\lambda\mu_P+{\mu_P}^2)]=0$$

$$[\lambda(\lambda+\mu_S)(\alpha_S\gamma_{S1}+\alpha_S\lambda+\alpha_S\mu_S+\gamma_{S1}\lambda+\gamma_{S1}\mu_S+\delta_S\lambda+\delta_S\mu_S+\lambda^2+2\lambda\mu S+{\mu_S}^2)]=0$$

**From above, we see that all the characteristic polynomials of the Jacobian matrix are positive. From this, we will obtain negative eigenvalues. If $R_0<1$, then the equilibrium point ($E_0$) is locally asymptotically stable and unstable if $R_0>1$.**

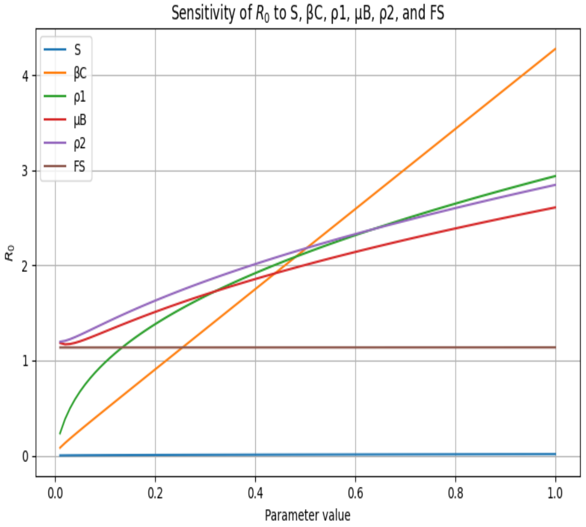
# Sensitivity analysis

Sensitivity analysis on the key parameters to assess their influence on the $R_0$ value and determine which parameter has the greatest impact on the basic reproduction number.

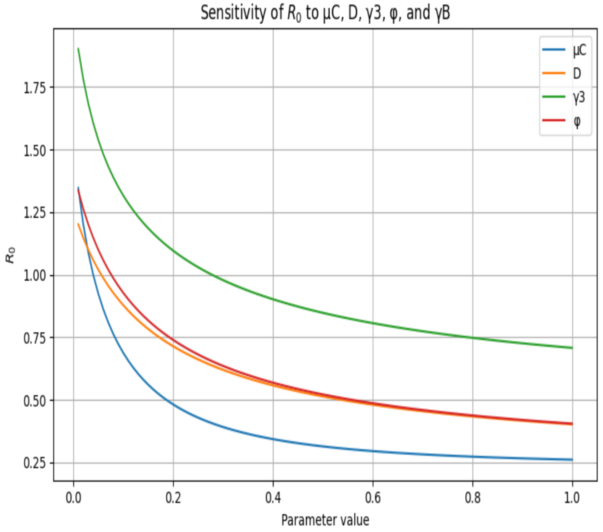
$$\Delta_x^{R_0}=\frac{x}{R_0}*\frac{dR_0}{dx}$$

| Parameter | $\beta_C$ | $\beta_B$ | $D_C$ | $\mu_B$ | $\mu_C$ | $\rho_1$ | $\rho_2$ | $\gamma_3$ | $\varphi$ |
|---|---|---|---|---|---|---|---|---|---|
| description | 0.27 | 0.27 | 0.01 | 0.0057 | 0.02 | 0.15 | 0.0021 | 0.143 | 0.03 |
| Value | 0.27 | 0.27 | 0.01 | 0.0057 | 0.02 | 0.15 | 0.0021 | 0.143 | 0.03 |
| Sensitivity index | 0.99 | 0.2830 | -0.0297 | 0.0831 | -0.1241 | 0.3324 | 0.0369 | -0.4250 | -0.0831 |

| | |
|---|---|
| $\beta_C, \beta_B$ | Transmission rate of Susceptible Cattle and buffalo |
| $\rho_1, \rho_2$ | Progression rate from Exposed Cattle to Infected Cattle and buffalo respectively |
| $D_C$, $\mu_B, \mu_C$, | Disease-induced death rate, natural death rates |
| $\gamma_3, \varphi$ | Recovery rate and isolation rate of cattle |




**Parameters with Positive Contribution to $R_0$: $\beta C$, $\rho_1$, $\mu B$, $\rho_2$, and F S_B**




**Parameters with Negative Contribution to $R_0$: $\mu C$, DC, $\gamma_3$, and $\phi$ on $R_0$**

# Theorem 4: Mathematical analysis of FMD with optimal control

In this section, we analyze the optimality function of the SVVEIIR model using control variables. Our main goal is to reduce the number of infections with vaccination of susceptible animals and isolation of infected animals. The number of infections was minimized while keeping intervention costs under control.

$$\mathbf{J(u_1, u_2)} = \int_0^T \left[ A_1 S_C + A_2 E_C + A_3 I_{C1} + A_4 I_{C2} + \frac{B_1}{2} u_1^2(t) + \frac{B_2}{2} u_2^2(t) \right] dt$$

where $A_1, A_2, A_3$ penalize the cost of minimizing the $S_C$, $E_C$, $I_{C1}$, $I_{C2}$ and $B_1$, $B_2$ are positive weight control costs. Pontryagin's Maximum Principle (PMP) was adopted to determine the optimal solution for the model.

**Apply the Hamiltonian H to obtain the minimum value of PMP, which is given by**

$$H = A_1 S_C + A_2 E_C + A_3 I_{C1} + A_4 I_{C2} + \frac{B_1}{2} u_1^2(t) + \frac{B_2}{2} u_2^2(t) + \lambda_S \{\Delta_c + \alpha_{c3} V_{c1} + \chi_2 V_{C2} + K_1 Q_C + \emptyset R_C - [\alpha_c + \mu_c + (1 - u_1)\beta_C \frac{(IC1 + IC2 + f_{env} * F * IB2 + f_{env} * F * IP + f_{env} * F * IS)}{N}] S_C \} + \lambda_E \{(1 - u_1)\beta_C \frac{(IC1 + IC2 + f_{env} * F * IB2 + f_{env} * F * IP + f_{env} * F * IS)}{N} S_C\} - (\rho_1 + \mu_C) E_C + \{\lambda_{IC1} \{ \rho_1 E_C - (\mu_C + \sigma_1) I_{C1} \} + \lambda_{IC2} \{\sigma_1 I_{C1} + K_2 Q_C - (\gamma_3 + \mu_C + u_2 \varphi + \mathcal{D}_C) I_{C2} \} + \lambda_R \{u_1 \alpha_{C1} \gamma_1 V_{C1} + u_1 \chi_1 \gamma_2 V_{C2} + (1 - u_2)\gamma_3 I_{C2} + u_2 \gamma_4 q_C + u_1 S_C - (\mu C + \emptyset) R_C\} + \lambda_{V1} \{ u_1 \alpha S_C - (\alpha_{C1}\gamma_1 + \alpha_{C2} + \alpha_{C3} + \mu_C) V_{C1} + \lambda_{V2} \{u_1 \alpha_{C2} V_{C1} \_ (u_1 \chi_1 \gamma_2 + \mu_C + \chi_2) V_{C2}\} + \lambda_Q \{\Delta_{QC} - [K_1 + K_2 + \mu_C] Q_C \} + \lambda_q \{u_2 \varphi I_{C2} - (\gamma_4 + \mu_C) q_C\}$$

Theorem. There exists an optimal control $u_1$, $u_2$ and the corresponding solution ($S_C^*$, $V_{C1}^*$, $V_{C2}^*$, $E_C^*$, $I_{C1}^*$, $I_{C2}^*$, $R_C^*$, $Q_C^*$, $Q_C^*$) that minimizes J. For the above statement to be true, there exist adjoint functions $\lambda S_C(t)$, $\lambda E_C(t)$, $\lambda I_{C1}(t)$, $\lambda I_{C2}(t)$, $\lambda R(t)$, $\lambda V_{C1}(t)$, $\lambda V_{C2}(t)$ such that Adjoint functions: $\dot{\lambda} = -\frac{\partial H}{\partial x}$, $\lambda(t) = 0$

Taking $u_1^*$ and $u_2^*$ to be optimal control functions and $S_C^*$, $E_C^*$, $I_{C1}^*$, $I_{C2}^*$, $R_C^*$, $V_{C1}^*$, $V_{C2}^*$, $Q_C^*$, $q_C^*$ are corresponding optimal state variables of the control problem. Here use the Pontryagin Maximum Principle, which requires that the optimal controls maximize the Hamiltonian. The Solving for $u_1$ and $u_2$:

$$u_1 = \frac{(\lambda_S + \lambda_E - \lambda_R) S_C - \lambda_R \{\alpha_{c1}\gamma_1 V_{C1} + \chi_1 \gamma_2 V_{C2}\} - \lambda_{V1} \alpha S_C - \lambda_{V2} (\alpha_{c2} V_{c1} \_ \chi_1 \gamma_2)}{B_1},$$

$$u_2 = \frac{\lambda_{IC2} \varphi + \lambda_R \gamma_3 I_{C2} - \lambda_R \gamma_4 q_c + \lambda_q \varphi I_{C2}}{B_2}$$

Since the controls are constrained by $0 \le u_1 \le u \max 1$ and $0 \le u_2 \le u \max 2$, we apply the projection condition:

$$u_1^* = \max\left(0, \min\left(u_1^{\max}, \frac{(\lambda_S + \lambda_E - \lambda_R) S_C - \lambda_R \{\alpha_{c1}\gamma_1 V_{C1} + \chi_1 \gamma_2 V_{C2}\} - \lambda_{V1} \alpha S_C - \lambda_{V2} (\alpha_{c2} V_{c1} \_ \chi_1 \gamma_2)}{B_1}\right)\right),$$

$$u_2^* = \max\left(0, \min\left(u_2^{\max}, \frac{\lambda_{IC2} \varphi + \lambda_R \gamma_3 I_{C2} - \lambda_R \gamma_4 q_c + \lambda_q \varphi I_{C2}}{B_2}\right)\right)$$

**Conclusion:**

- ✓ $u_1$ represents the optimal level of intervention that is **Vaccination** that **reduces the susceptible population $S_C$ moving into infected states.**
- ✓ $u_2$ represents the **Isolation of symptomatic infected animals** those spreads the FMDV to other susceptible animals and also **reduce FMDV spreads in the environment**.
- ✓ This could include vaccination and isolation measures. Again, it ensures that the control is within the allowed range.

# Purpose of Proving the Theorems

**Theorem 1:** **Positive Invariance**

**Conclusion:** The **non-negativity theorem** ensures that model solutions never become negative, keeping results biologically meaningful.

$S_C(t), E_C(t), I_{C1}(t), I_{C2}(t), R_C(t), V_{C1}(t), V_{C2}(t), Q_C(t), q_C(t) \geq 0, \forall\, t \geq 0$

**Theorem 2:** **Boundness**

The **boundedness theorem** ensures that the total population remains within a finite limit, reflecting real-world constraints and preventing the model from producing unbounded or unrealistic growth.

$N_C(t) \leq \max\left(N_C(0), (\Delta_C+\Delta_{QC})/\mu_C\right)$

**Theorem 3:** The **Jacobian matrix** $\boldsymbol{J_0}$ at the **Disease-Free Equilibrium** $(\boldsymbol{E_0})$, determines whether FMDV will **die out** or **persist** in the population. Stability analysis is used to assess whether the system will return to its equilibrium state over time. A stable disease-free equilibrium suggests that the infection will eventually die out, while an endemic equilibrium indicates that the disease is likely to persist and spread within the population.

**Theorem 4:** **Optimal control problem of the system**

The number of infections was minimized while keeping intervention costs under control. The optimal control strategy cuts infections and costs by blending Isolation of infected animals and vaccination into the most effective shield against disease. Using Pontryagin's Maximum Principle, the model guarantees solutions that are both mathematically sound and cost-efficient. This framework equips policymakers with a powerful toolkit to compare scenarios and choose the ultimate mix of interventions.

# Data collection

1. Total population ($N_C$): District-wise data

| District Name | Cattle | Buffalo | Goat | Sheep | Pig | Reference |
|---|---|---|---|---|---|---|
| Bengaluru Rural | 170722 | 16924 | 95156 | 118788 | 14131 | 20th livestock census |
| Ramanagara | 287502 | 19644 | 150130 | 127988 | 7102 | |

2. Overall, the mean [95% Confidence Interval (CI)] durations of disease phases in cattle (Yadav et al., 2019) were estimated to be: Incubation phase = **3.6** days (2.7–4.8), Latent phase = **1.5** days (1.1–2.1), Subclinical infectious phase = **2.2** days (1.5–3.5), Clinical infectious phase = **8.5** days (6.2–11.6), and Total infectious phase = **10.8** days (8.2–14.2)

***3. (Bradhurst et al., 2015)*** $\boldsymbol{\frac{1}{\mu}} = Average\ natural\ lifespan\ of\ the\ host, (\mu = Natural\ death\ rate)$

| Hosts | Lifespan (min) | Lifespan (max) | Average | Natural death rate |
|---|---|---|---|---|
| Cattle | 15 | 20 | 17.5 | 0.0571 |
| Buffalo | 15 | 20 | 17.5 | 0.0571 |
| Pig | 10 | 15 | 12.5 | 0.0800 |
| Sheep/goat | 12 | 15 | 13.5 | 0.0741 |

- By using pert the natural death range is
- for cattle and buffalo (0.05, 0.0541, 0.0583, 0.0625, 0.0666),
- for pig (0.1, 0.0916, 0.0833, 0.075, 0.066) and
- for sheep/goat is (0.0833, 0.0791, 0.075, 0.0708, 0.066)

4. Progression rate from Exposed Cattle to Asymptomatic Cattle ($\rho$)

$\frac{\mathbf{1}}{\boldsymbol{\sigma}}$ = average duration of latent period, ($\sigma$ = progression rate from exposed to infectious), latent phase = **1.5** days (1.1–2.1), Let it be 1.5

$$\text{Progression Rate (\%)} = \left(\frac{1}{\text{Latent Period}}\right) = \left(\frac{1}{1.5}\right) = 0.66$$

5. Progression rate from Asymptomatic Cattle to symptomatic Cattle ($\sigma$), Incubation 3.6 – latent 1.5 =2.1 average subclinical or asymptomatic infectious period

$$\text{Progression Rate (\%)} = \left(\frac{1}{\text{Incubation} - \text{latent days}}\right) = \left(\frac{1}{2.1}\right) = 0.476$$

6. Rate of Loss of Immunity ($\emptyset$) = $\frac{1}{D}$, D = **duration of immunity** (how long immunity lasts, in days/months): For foot and mouth disease, it's about 6 months or 180 days based on this

$$\emptyset = \frac{1}{180} \approx 0.0056$$

7. The rate at which vaccinated cattle become susceptible $= \frac{\mathbf{1}}{\textbf{duration of immunity for 3 or less vaccination round}}$

$$= \frac{1}{180} \approx 0.0056$$

8. Recovery rate($\gamma$), $\frac{\mathbf{1}}{\boldsymbol{\gamma}}$ = average duration of the infectious period. Let the duration of the infectious period be an average of 7 days

**Recovery rate = 1/7 = 0.143**

9. Transmission rate: From the Risk map, we used $R_0$ for the districts of Bangalore Rural and Ramanagara, Prevalence data from the (Ravindra et al., 2016)

- ***Transmission rate:***

| District | $R_0$ | Recovery rate ($\gamma$) | prevalence | Non-immunnity | Transmission rate $\beta = R_0 * \gamma$* prevalence * (1- immunity) |
|---|---|---|---|---|---|
| Bangalore Rural | 1.1775 | 0.143 | 14 | 0.81 | 1.9095 |
| Ramanagara | 1.3505 | 0.143 | 17 | 0.90 | 2.9548 |

10. Exposed population (E):

$$E = \beta_C(N - V_C.(VE))$$

| State | Vaccination Rounds Covered | Average (Pre) | Average (Post) | $s_0$ | $s_{inf}$ | Vaccine Efficacy |
|---|---|---|---|---|---|---|
| Karnataka | 6 | 72.63 | 92.466667 | 0.273 | 0.0753 | 0.724 |

Transmission rate, let it be 1.9095 and 2.9548, Time let it be 6 months, 0.724

E = Transmission rate (Total population – Vaccination * Vaccination efficacy) -symptomatic infected

For Bangalore Rural is, E = 1.9095 (170722 – (32429 * 0.724 * 6))-699 = **4327.**

**11.** Asymptomatic Infected cattle ($I_1$): Exposed * rate of exposed population change to asymptomatically affected

- Infected population (asymptomatic) = 0

12. Infected symptomatic cattle ($I_2$): Bangalore rural 699, Ramanagara 1075

13. Recovered (R) = Cumulative symptomatic cases* recovery rate + isolated animals * recovery rate of isolated animals

**Bangalore rural**: Recovered from the symptomatically recovered animals =699 * 0.143 = 99, Recovered from the isolated animals =350*0.143 = 50, Total **Recovered animals** =99+50=149

**Ramanagara**: Recovered from the symptomatically recovered animals **= 1075 * 0.143 = 154**, Recovered from the isolated animals **= 537 * 0.143 = 77**, Total **Recovered animals = 153 + 77 = 230**

14. Isolation of animals, let it be 50% that is **350** for Bangalore rural and 537 for Ramanagara

**The total symptomatically infected in Bangalore rural is (699-350-150=199)**

**The total symptomatically infected in Ramanagara is (1075-537-230=306)**

**15. Susceptible** = Total Number of animals – exposed – asymptomatic – symptomatic – recovered – vaccinated – isolated animals

**Bangalore rural Susceptible =** 170722- 4327-0-199-149-32429-350 **= 133268**

**Ramanagara Susceptible =** 287502- 30024-0-306-230-28504-537 **= 227895**

**16. Vaccination rate** $= \frac{\boldsymbol{Vaccinated\ animals}}{\boldsymbol{Total\ animals\ at\ the\ starting}}$

**For cattle =** 229332 / 287502 = 0.7976

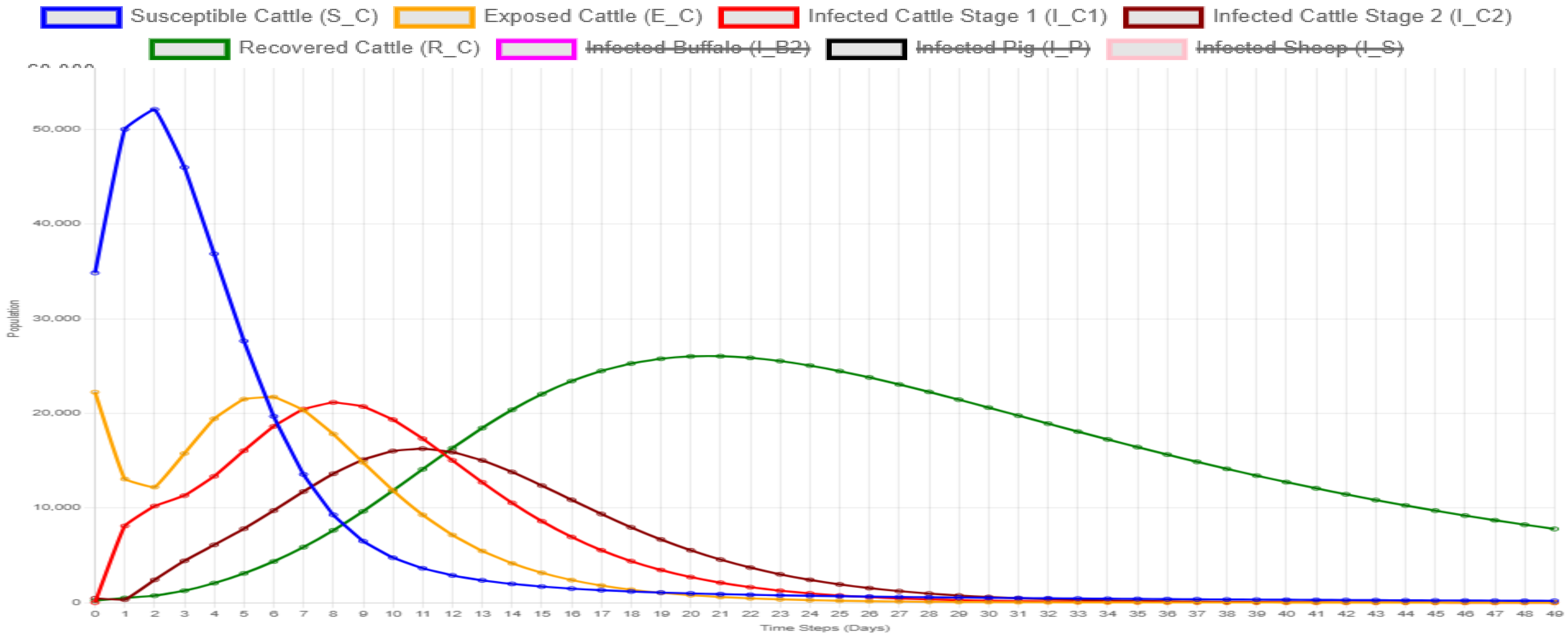
**For buffalo =** 15669/19644 = 0.7976

# Numerical Simulation

## Ramanagara district Scenario-III

$R_0$ **Value: 1.0758**

Data collected from the 20th live stock census and the infection and vaccination data from the NADRES V2, Compartmental data: Susceptible Cattle ($S_C$): 34850, Exposed Cattle ($E_C$): 22245, Infected Cattle Stage 1 ($I_{C1}$): 1, Infected Cattle Stage 2 ($I_{C2}$):449, Recovered Cattle ($R_C$): 208, Vaccination less than 3 doses($V_{C1}$):229330, Vaccination more doses (>3) ($V_{C2}$): 2, Isolated infected Cattle ($q_C$): 416 , Susceptible Buffalo ($S_B$): 2394, Exposed Buffalo ($E_B$): 1554, Temperature (°C): 25 , Humidity (%):60, pH:7




| Days | Key Events | Meaning |
|---|---|---|
| **Rapid Onset (Days 0-10)** | **Blue Line** (Susceptible Cattle) drops fast. **Red Line** (Infected Cattle 1). | **Explosive Outbreak:** The disease is spreading very quickly. Most healthy cattle are now infected. |
| **Peak Infection (Days 7-20)** | **Red Line** (Infected Cattle 1) and **Maroon Line** (Infected Cattle 2) hit their highest points and start to fall. **Green Line** (Recovered Cattle) is rising fast. | **Epidemic Peak:** The maximum number of cattle are sick. Infections are slowing down because animals are starting to recover and become immune. |
| **Decline & Resolution (Days 20-48)** | **Red** and **Maroon Lines** (Infected Animals) fall close to zero. **Green Line** (Recovered Cattle) remains high. | **Outbreak Over:** Implemented isolation of infected animals and vaccination. The epidemic has burned out, leaving most of the initial population immune. |

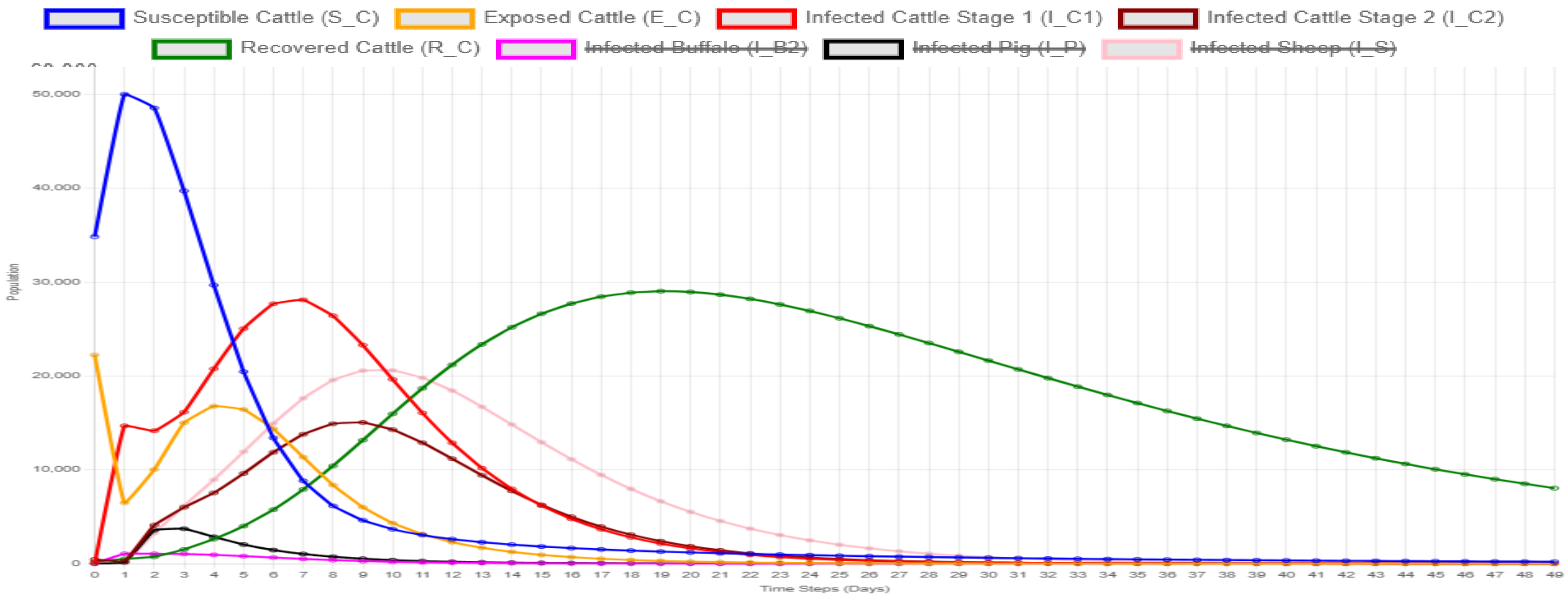
- ✓ **β_C (Cattle Transmission Rate) 2.95,**
- ✓ β_B (Buffalo Transmission Rate)**0.30**,
- ✓ ρ_1 (Cattle Incubation Rate): **0.66**,
- ✓ ρ_2 (Buffalo Incubation Rate): **0.66,**
- ✓ γ_3 (Cattle Recovery Rate): **0.143,**
- ✓ γ_B (Buffalo Recovery Rate): **0.143,**
- ✓ μ_C (Cattle Natural Mortality): **0.0571**,
- ✓ μ_B (Buffalo Natural Mortality): **0.0571**,
- ✓ D_C (Cattle Disease Death Rate): **0.00858,**
- ✓ D_B (Buffalo Disease Death Rate): **0.00858,**
- ✓ **α_B (Buffalo Vaccination Rate): 0.7976,**
- ✓ α_P (Pig Vaccination Rate): **0.06,**
- ✓ **φ (Isolation Rate) 0.173,**
- ✓ F (Environmental Factor): **1,**
- ✓ T_opt (Optimal Temperature): **25,**
- ✓ pH_opt (Optimal pH): **7.4**

# Numerical Simulation

Ramanagara district Scenario-IV

**$R_0$ Value: 0.74**

Data collected from the 20[th] live stock census and the infection and vaccination data from the NADRES V2, Compartmental data: Susceptible Cattle ($S_C$): 34850, Exposed Cattle ($E_C$): 22245, Infected Cattle Stage 1 ($I_{C1}$): 1, Infected Cattle Stage 2 ($I_{C2}$):449, Recovered Cattle ($R_C$): 208, Vaccination less than 3 doses($V_{C1}$):229330, Vaccination more doses (>3) ($V_{C2}$): 2, Isolated infected Cattle ($q_C$): 416 , Susceptible Buffalo ($S_B$): 2394, Exposed Buffalo ($E_B$): 1554, Temperature (°C): 25 , Humidity (%):60, pH:7



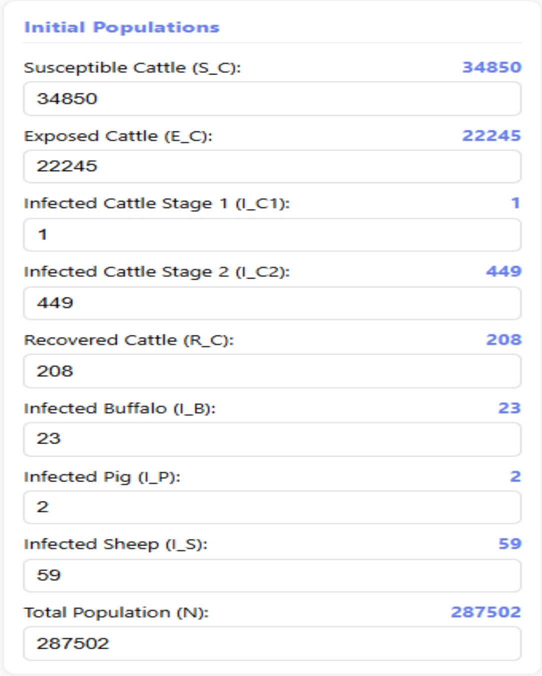

| Feature | Observation from Graph | Interpretation (Effect of Control) |
|---|---|---|
| **Outbreak Severity** | **Infected Cattle (Red/Maroon) peaks are lower** (around 22,000) and less sharp. | **Vaccination** reduced the number of animals that got sick, successfully suppressing the total size of the epidemic. |
| **Speed of Spread** | **Infected Cattle peaks are delayed** (around Days 9-12). | **Isolation/Lower R0** slowed the infection rate, meaning the outbreak took longer to reach its peak. |
| **Exposure Role** | **Exposed Cattle (Orange) line is highly visible** and peaks early. | Effective control measures like vaccination and isolation may delay **the progression** from being exposed to becoming fully infectious. |

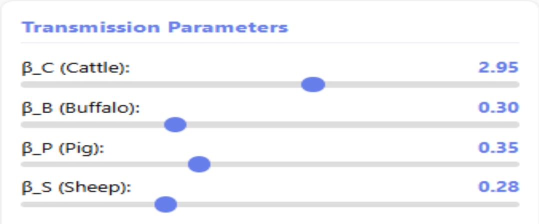
- ✓ β_C (Cattle Transmission Rate) 2.95,
- ✓ β_B (Buffalo Transmission Rate)0.30,
- ✓ ρ_1 (Cattle Incubation Rate): 0.66,
- ✓ ρ_2 (Buffalo Incubation Rate): 0.66,
- ✓ γ_3 (Cattle Recovery Rate): 0.143,
- ✓ γ_B (Buffalo Recovery Rate): 0.143,
- ✓ μ_C (Cattle Natural Mortality): 0.0571,
- ✓ μ_B (Buffalo Natural Mortality): 0.0571,
- ✓ D_C (Cattle Disease Death Rate): 0.00858,
- ✓ D_B (Buffalo Disease Death Rate): 0.00858,
- ✓ **α_B (Buffalo Vaccination Rate): 0.92,**
- ✓ α_P (Pig Vaccination Rate): 0.06,
- ✓ **φ (Isolation Rate) 0.259,**
- ✓ T_opt (Optimal Temperature): 25,
- ✓ pH_opt (Optimal pH): 7.4,

# FMD Simulation (Epidemic Calculator) – Scenario I

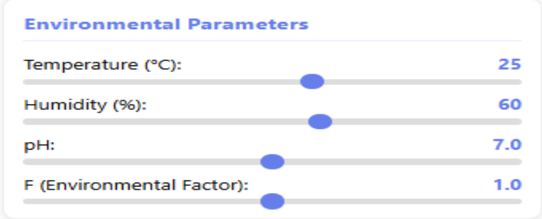
The simulation data is obtained from the 20th Livestock Census (2019) and the NADRES database, with model parameters calculated using the formulas provided in the previous slides.


In this scenario, the number of **susceptible animals** is **48,550**. Control measures are applied at a **low level**, with **isolation at 14.2%** and **vaccination at 79%**, resulting in a **basic reproduction number ($R_0$) of 1.02**, indicating continued disease transmission.

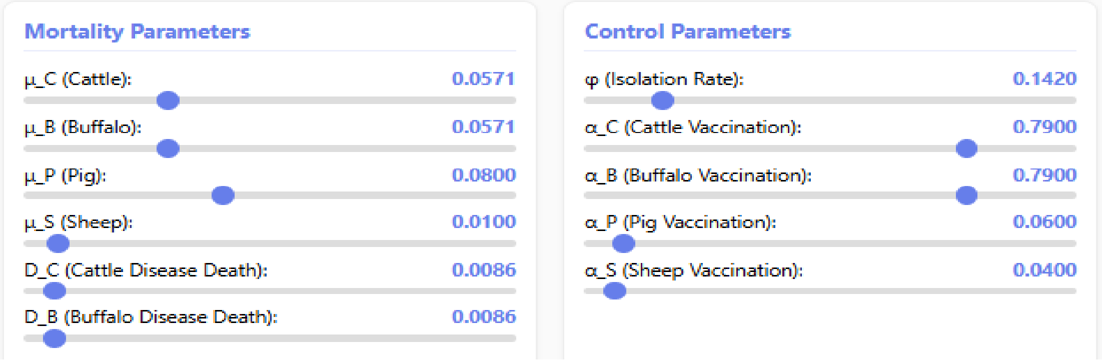



! **UNDER PROGRESS**

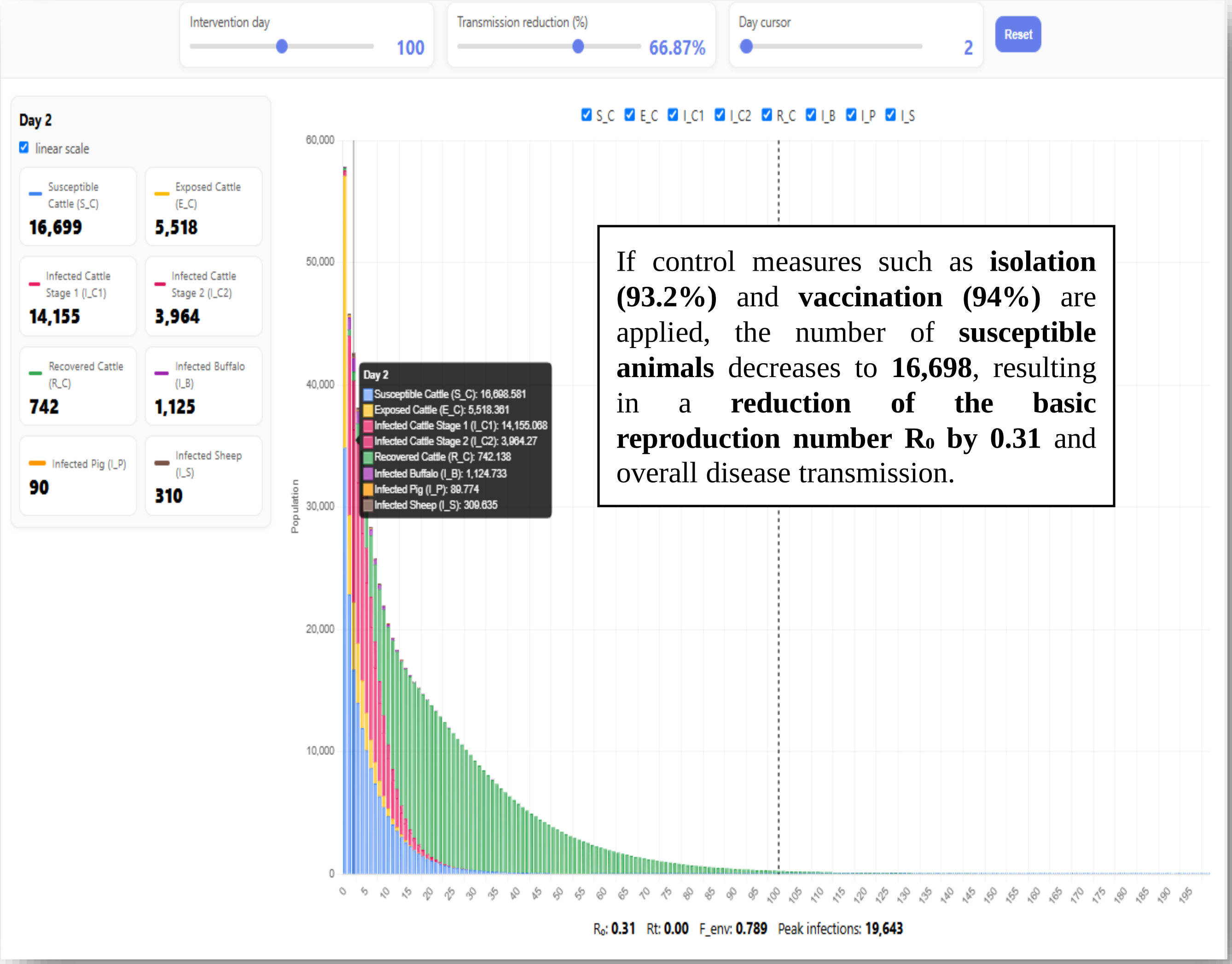



## Data Used for the Simulation

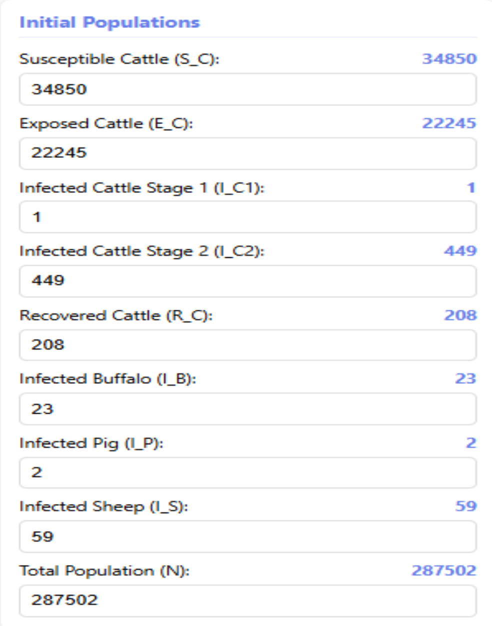


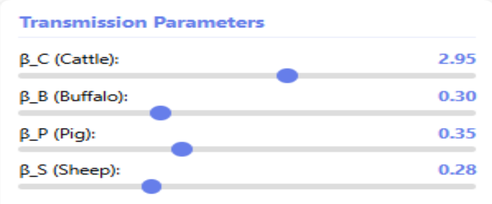
# FMD Simulation (Epidemic Calculator) – Scenario II

The simulation data is obtained from the 20th Livestock Census (2019) and the NADRES database, with model parameters calculated using the formulas provided in the previous slides.

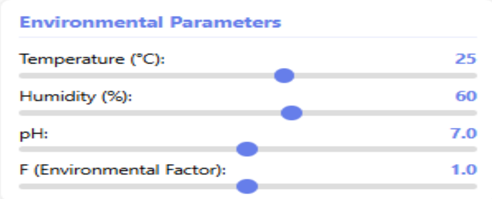



If control measures such as **isolation (93.2%)** and **vaccination (94%)** are applied, the number of **susceptible animals** decreases to **16,698**, resulting in a **reduction of the basic reproduction number $R_0$ by 0.31** and overall disease transmission.

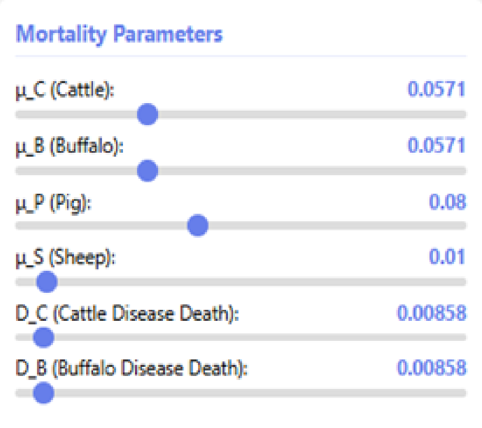


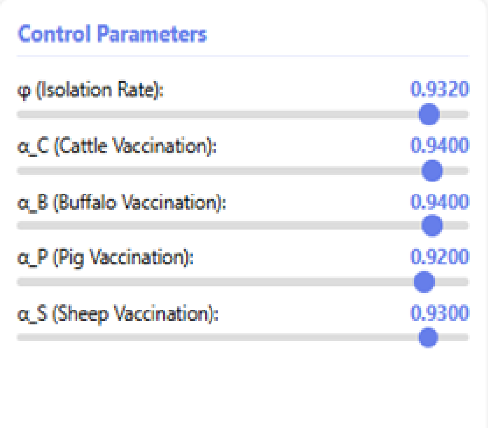




❗UNDER PROGRESS

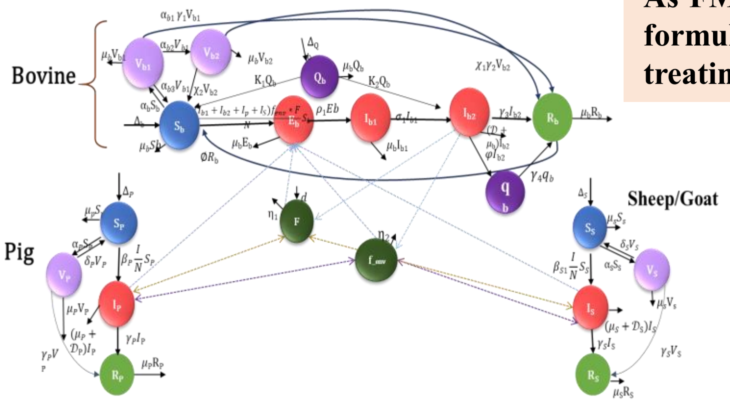



## Data Used for the Simulation



# Schematic Diagram of SEIRVQq (Bovine), SVIR (Pig), SVIR (Sheep/Goat), Carrier Fomites (F), Environment (f_env), FMD Mathematical Modeling




**As FMD vaccination is only available for bovines, the model is formulated using the aggregated 'bovine' population instead of treating cattle and buffalo separately**

The boundedness and non-negativity theorems are proved for the model, demonstrating that all state variables remain non-negative and confined within biologically feasible domains for all.

## Model Formulation

### Bovine

1. $$\frac{dS_b}{dt} = \Delta_b + \alpha_{b3}V_{b1} + \chi_2 V_{b2} + K_1 Q_b + \emptyset Rb - [\alpha_b + \mu_b + \beta_b \frac{(Ib1 + Ib2 + Is + IP) * f\_env * F}{N}] S_b$$

2. $$\frac{dE_b}{dt} = \beta_b \frac{(Ib1 + Ib2 + f\_env * IP + f\_env * IS)}{N} S_b - (\rho_1 + \mu_b) E_b$$

3. $$\frac{dI_{b1}}{dt} = \rho_1 E_b - (\mu_b + \sigma_1) I_{b1}$$

4. $$\frac{dI_{b2}}{dt} = \sigma_1 I_{b1} + K_2 Q_b - (\gamma_3 + \mu_b + \varphi + \mathcal{D}_b) I_{b2}$$

5. $$\frac{dR_b}{dt} = \alpha_{b1}\gamma_1 V_{b1} + \chi_1\gamma_2 V_{b2} + \gamma_3 I_{b2} + \gamma_4 q_b - (\mu_b + \emptyset) Rb$$

6. $$\frac{dV_{b1}}{dt} = \alpha S_b - (\alpha_{b1}\gamma_1 + \alpha_{b2} + \alpha_{b3} + \mu_b) V_{b1}$$

7. $$\frac{dV_{b2}}{dt} = \alpha_{b2} V_{b1} - (\chi_1\gamma_2 + \mu_b + \chi_2) V_{b2}$$

8. $$\frac{dQ_b}{dt} = \Delta_{Qb} - [K_1 + K_2 + \mu_b] Q_b$$

9. $$\frac{dq_b}{dt} = \varphi I_{b2} - (\gamma_4 + \mu_b) q_b$$

## Model Parameterization

| Sl.No | Parameter | Description |
|---|---|---|
| 1-5 | $S_b, E_b, I_{b1}, I_{b2}, R_b$ | Susceptible, Latent, Sub-clinical infectious, clinical infectious and Recovered population of bovine respectively |
| 6-7 | $V_{b1}, V_{b2}$ | Vaccinated fewer rounds, Vaccinated more rounds, population of bovine, respectively |
| 8-10 | $F, f\_env, d$ | Carrier Fomites and Environment, disinfection |
| 11 | $\Delta_b$ | Recruitment rate of bovine population respectively |
| 12 | $\mu_b$ | Death rate of bovine respectively |
| 13 | $\sigma_1$ | Progression rate from Asymptomatic bovine to symptomatic bovine |
| 14 | $\emptyset$ | Rate of loss of immunity |
| 15 | $\alpha_b$ | Vaccination rate for bovine |
| 16 | $\varphi$ | Isolated infected bovine |
| 17-21 | $\alpha_{b1}\gamma_1$, $\chi_1\gamma_2$, $\gamma_3$, $\gamma_4$, $\chi_2$ | Vaccinated fewer rounds, Vaccinated more rounds, Infectious bovine recovery rate, Isolated bovine Recovery rate, Vaccination Waning rate, Respectively |
| 22 | $\mathcal{D}_b$ | Disease Induced mortality rate |
| 23 | $\eta_1$ | Fomites pathogen decay rate |
| 24 | $\eta_2$ | Environment pathogen decay rate |
| 25 | $\beta_b$ | Transmission rate of Susceptible bovine |
| 26 | $\rho_1$ | Progression rate from Exposed Cattle to Infected Cattle |

## $R_0$ Estimation

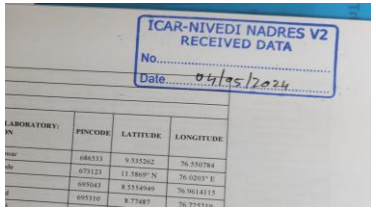
| | | (20th livestock census data Vaccination data) | Environment parameters | Estimated from Serosurveillance and vaccination data | | | Estimated from Seromonitoring data | | | | 20th livestock census data | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **States** | **F** | **Susceptible Bovine** | **fenv** | **Betta** | **Rho 1** | **Db** | **Gamma** | **Mu b** | **Sigma** | **sci** | **Total population** | **R0** |
| **Andaman & Nicobar** | 0.02 | 72696 | 0.049279569 | 5.482389418 | 0.1333333 | 0.003 | 0.2 | 0.01006 | 0.0725406 | 0.004 | 145392 | 0.040577272 |
| **Andhra Pradesh*** | 0.4 | 2558980 | 0.969574083 | 3.444471778 | 0.1333333 | 0.003 | 0.88 | 0.01006 | 0.0725406 | 0.004 | 35498325 | 1.171710704 |
| **Arunachal Pradesh** | 0.18 | 291727 | 0.006776377 | 1.239063245 | 0.1333333 | 0.0082269 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 696264 | 0.007797977 |
| **Assam** | 0.18 | 10087248 | 0.030711705 | 4.652653407 | 0.1333333 | 1.983E-05 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 16159656 | 0.197894544 |
| **Bihar** | 0.205 | 11952388 | 0.559920785 | 5.618202124 | 0.1333333 | 0.003 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 36495801 | 2.602311993 |
| **Chandigarh** | 0.02 | 6706 | 0.29315957 | 0.541556358 | 0.1333333 | 0.003 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 26753 | 0.009807054 |
| **Chhattisgarh** | 0.8 | 1233275 | 0.564388792 | 21.70756815 | 0.1333333 | 0.003 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 10533696 | 14.13931789 |
| **Delhi** | 0.02 | 239947 | 0.107948921 | 1.15399462 | 0.1333333 | 0.003 | 0.04 | 0.01006 | 0.0725406 | 0.004 | 275190 | 0.055543916 |
| **Diu and daman** | 0.02 | 30868 | 0.373364635 | 1.15399462 | 0.1333333 | 0.003 | 0.09 | 0.01006 | 0.0725406 | 0.004 | 51634 | 0.097285177 |
| **Goa*** | 0.8 | 44730 | 0.201802716 | 1.656944174 | 0.1333333 | 0.003 | 0.01 | 0.01006 | 0.0725406 | 0.004 | 132388 | 3.744862217 |
| **Gujarat** | 0.8 | 535644 | 0.416009652 | 5.325217821 | 0.1333333 | 0.0112015 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 22424247 | 0.521148852 |
| **Haryana*** | 0.8 | 2776873 | 0.227084901 | 0.581834922 | 0.1333333 | 0.0018366 | 0.02 | 0.01006 | 0.0725406 | 0.004 | 6805264 | 1.466697609 |
| **Himachal Pradesh** | 0.8 | 1497339 | 0.132619106 | [illegible] | [illegible] | [illegible] | 0.75 | 0.01006 | 0.0725406 | 0.004 | 4376817 | 0.868441056 |
| **Jammu and Kashmir** | 0.02 | 1080969 | 0.095826772 | [illegible] | [illegible] | [illegible] | 0.75 | 0.01006 | 0.0725406 | 0.004 | 8209005 | 0.019025105 |
| **Jharkhand** | 0.205 | 9395332 | 0.541648778 | 9.514074154 | 0.1333333 | 0.0222557 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 23612694 | 5.168382837 |
| **Karnataka*** | 0.4 | 2506583 | 0.042061442 | 6.829163317 | 0.1333333 | 0.0036703 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 28997520 | 0.122368571 |
| **Kerala** | 0.4 | 959846 | 0.41726601 | 8.004002378 | 0.1333333 | 0.0129187 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 2908006 | 5.427214304 |
| **Ladakh** | 0.02 | 84201 | 2.88051E-25 | 1.15399462 | 0.1333333 | 0.003 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 90000 | 7.66386E-26 |
| **Lakshadweep** | 0.02 | 1024 | 1.036640569 | 1.15399462 | 0.1333333 | 0.003 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 45697 | 0.006606083 |
| **Madhya Pradesh** | 0.8 | 6910903 | 0.421329323 | 5.21843904 | 0.1333333 | 0.003 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 40146109 | 3.730898171 |
| **Maharashtra** | 0.8 | 4010255 | 0.021529604 | 13.93042382 | 0.1333333 | 0.0068325 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 32650498 | 0.362957451 |
| **Manipur** | 0.18 | 128439 | 0.01035657 | 4.652653407 | 0.1333333 | 0.0225788 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 540575 | 0.02533757 |
| **Meghalaya** | 0.18 | 426521 | 0.017852858 | 7.204645576 | 0.1333333 | 0.003 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 1476140 | 0.082428144 |
| **Mizoram** | 0.18 | 44233 | 0.018022248 | 4.652653407 | 0.1333333 | 0.003 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 355580 | 0.023134548 |
| **Nagaland** | 0.18 | 82976 | 0.409823529 | 15.03082249 | 0.1333333 | 0.003 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 530608 | 2.136488755 |
| **Odisha** | 0.205 | 4168414 | 1.89396E-30 | 4.852043522 | 0.1333333 | 0.0008396 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 18170057 | 5.32646E-30 |
| **Puducherry** | 0.02 | 74379 | 0.629190429 | 1.369711202 | 0.1333333 | 0.003 | 0.26 | 0.01006 | 0.0725406 | 0.004 | 132222 | 0.137724899 |
| **Punjab** | 0.8 | 5977067 | 0.114054893 | 2.450597842 | 0.1333333 | 0.0094026 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 6542885 | 2.515091822 |
| **Rajasthan** | 0.8 | 25174143 | 0.008436942 | 2.632526062 | 0.1333333 | 0.000719 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 56529814 | 0.097522884 |
| **Sikkim** | 0.18 | 138141 | 0.024940995 | 4.652653407 | 0.1333333 | 0.0043434 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 268996 | 0.132150227 |
| **Tamilnadu** | 0.4 | 1510527 | 0.011501148 | 4.375617606 | 0.1333333 | 0.0001324 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 24493464 | 0.015301337 |
| **Telangana*** | 0.4 | 1434545 | 1.8206E-30 | 1.384890199 | 0.1333333 | 0.003 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 11917048 | 1.49591E-30 |
| **Tripura** | 0.02 | 363710 | 0.795790317 | 15.03082249 | 0.1333333 | 0.0021996 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 697336 | 1.537565101 |
| **Uttar Pradesh*** | 0.8 | 34773917 | 0.071490681 | 4.928680728 | 0.1333333 | 0.0001697 | 0.75 | 0.01006 | 0.0725406 | 0.004 | 65256529 | 1.851434976 |
| **Uttarakhand** | 0.02 | 1531638 | 0.071490681 | 15.03082249 | 0.1333333 | 0.0002612 | 0.06 | 0.01006 | 0.0725406 | 0.004 | 4392686 | 0.16669051 |
| **West Bengal** | 0.205 | 7669880 | 0.731680707 | 5.910376911 | 0.1333333 | 0.003 | 0.13 | 0.01006 | 0.0725406 | 0.004 | 34794476 | 3.28499189 |
| **Total** | | | | | | | | | | | 496289372 | |

**Under Purification**

*Values are still under purification

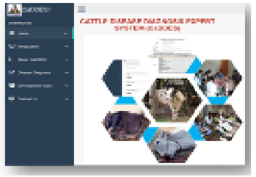
# Integrated Disease Surveillance and Sampling Approaches for Early Warning

| Types of Surveillance | | Sampling Method |
|---|---|---|
| Passive Surveillance | • Not sample based only opportunistic model | Convenience / Opportunistic sampling |
| Event-based Surveillance | • Host factors acts as signal/source early detection of outbreaks | Purposive sampling |
| Risk-based Surveillance | • Risk other than host such as Ecological, environment, trade etc by risk based probability sampling method | Risk-based probability sampling |
| Active surveillance | • systematic or regular recording of cases of a designated disease or a group of diseases by probability sampling method | Probability sampling (Random / 2 stage Stratified / Systematic) |
| Environmental Surveillance model | • Non-invasive method of surveillance that involves the collection of environmental samples by advanced probability sampling methods | Environmental probability sampling |
| Sentinel Surveillance model | •System of disease monitoring in which data are collected from selected reporting sites (called sentinel sites) such as specific hospitals, laboratories, or geographic locations. These sites are chosen purposively to represent a larger population and provide high-quality, continuous information on trends of specific diseases. | Sentinel site sampling (Purposive) |





https://nivedi.res.in/PDDES/



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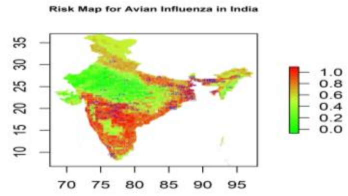
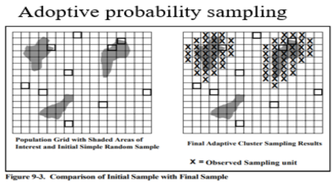
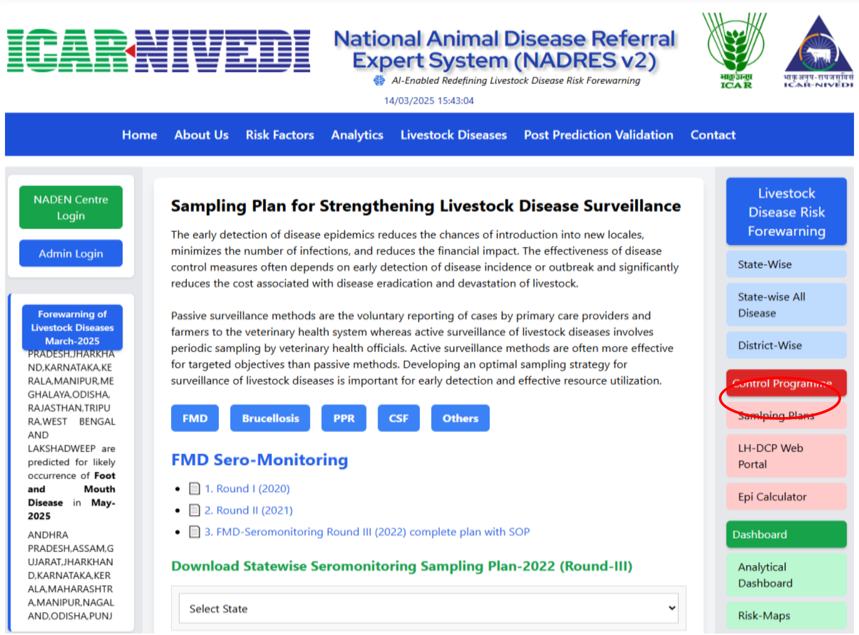



https://www.nivedi.res.in/Nadres_v2/

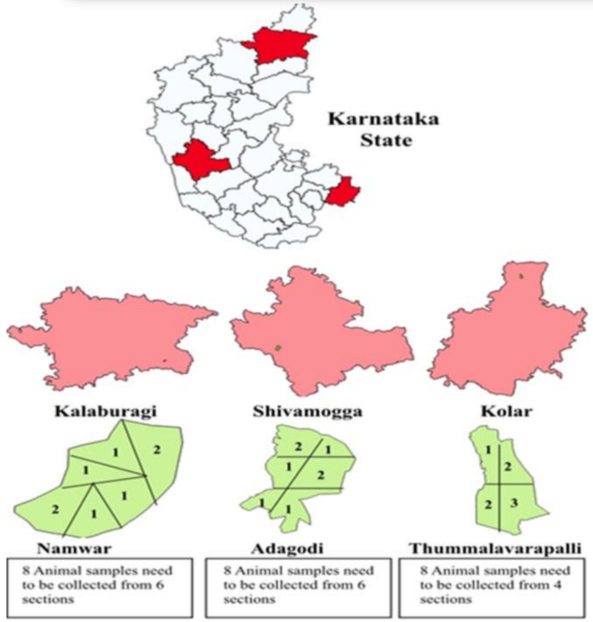



NADRES V2

# Sampling Plan tab under NADRES Website




# Schematic representation of Two-stage stratified random sampling and formula




**LH-DCP Portal : Cloud-Based Digital Platform for Active Livestock Disease Surveillance and Control**

https://nivedi.res.in/Nadres_v2/lhdcp/index


Home Page


Disease Dashboard

# Data Requirements Specifications (DRS)

| DRS of Brucellosis Seromonitoring Phase III - 2023 | | | | | | | | Results | | | Brucellosis Seromonitoring Phase IV - 2024 | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| State id | State | Prevalence | Cluster Level | Sensitivity | Specificity | No of Villages | No of Animals | Phase-I | Phase-II | Phase-III | Average | Protection Level | Prevalence | Cluster Level | Sensitivity | Specificity | No of Villages | No of Animals |
| 1 | Andaman & Nicobar | 0.2 | 0.048 | 0.9 | 0.9 | 68 | 589 | | | | 80.23667 | 32.094667 | 0.32 | 0.04 | 0.9 | 0.9 | 82 | 738 |
| 2 | Andhra Pradesh | 0.2 | 0.024 | 0.9 | 0.9 | 138 | 1794 | 73.25 | 71.51 | 64.52 | 69.76 | 27.904 | 0.28 | 0.04 | 0.9 | 0.9 | 82 | 1066 |
| 3 | Arunachal Pradesh | 0.2 | 0.43 | 0.9 | 0.9 | 75 | 810 | | | | 45.52 | 18.208 | 0.18 | 0.02 | 0.9 | 0.9 | 122 | 1830 |
| 4 | Assam | 0.2 | 0.022 | 0.9 | 0.9 | 150 | 1950 | | 75.67 | 50.76 | 63.215 | 25.286 | 0.25 | 0.03 | 0.9 | 0.9 | 110 | 1210 |
| 5 | Bihar | 0.2 | 0.02 | 0.9 | 0.9 | 165 | 2145 | | 59.93 | | 59.93 | 23.972 | 0.24 | 0.03 | 0.9 | 0.9 | 91 | 1092 |
| 6 | chandigarh | 0.2 | 0.2 | 0.9 | 0.9 | 16 | 193 | 99.49 | 68.68 | 72.54 | 80.23667 | 32.094667 | 0.32 | 0.04 | 0.9 | 0.9 | 82 | 656 |
| 7 | Chhattisgarh | 0.2 | 0.027 | 0.9 | 0.9 | 122 | 1586 | 78.63 | 69.07 | | 73.85 | 29.54 | 0.3 | 0.04 | 0.9 | 0.9 | 82 | 738 |
| 8 | Diu and daman | 0.2 | 0.17 | 0.9 | 0.9 | 18 | 195 | 80.76 | | | 80.76 | 32.304 | 0.32 | 0.04 | 0.9 | 0.9 | 82 | 656 |
| 9 | Delhi | 0.2 | 0.11 | 0.9 | 0.9 | 29 | 334 | 89.47 | 84.17 | | 86.82 | 34.728 | 0.35 | 0.05 | 0.9 | 0.9 | 66 | 528 |
| 10 | Goa | 0.2 | 0.04 | 0.9 | 0.9 | 83 | 916 | 92.12 | 94.8 | | 93.46 | 37.384 | 0.37 | 0.05 | 0.9 | 0.9 | 66 | 462 |
| 11 | Gujarat | 0.2 | 0.024 | 0.9 | 0.9 | 138 | 1794 | 80.12 | | | 80.12 | 32.048 | 0.32 | 0.04 | 0.9 | 0.9 | 82 | 656 |
| 12 | Haryana | 0.2 | 0.031 | 0.9 | 0.9 | 106 | 1378 | 66.84 | 66 | 72.3 | 68.38 | 27.352 | 0.27 | 0.04 | 0.9 | 0.9 | 82 | 820 |
| 13 | Himachal Pradesh | 0.2 | 0.033 | 0.9 | 0.9 | 99 | 1081 | 81.64 | 66.36 | | 74 | 29.6 | 0.3 | 0.04 | 0.9 | 0.9 | 82 | 738 |
| 14 | Jammu and Kashmir | 0.2 | 0.039 | 0.9 | 0.9 | 84 | 1092 | 73.31 | | | 73.31 | 29.324 | 0.29 | 0.04 | 0.9 | 0.9 | 82 | 738 |
| 15 | Jharkhand | 0.2 | 0.028 | 0.9 | 0.9 | 118 | 1534 | 73.95 | 42.41 | | 58.18 | 23.272 | 0.23 | 0.03 | 0.9 | 0.9 | 110 | 1320 |
| 16 | Karnataka | 0.2 | 0.026 | 0.9 | 0.9 | 127 | 1651 | 96.67 | 70.47 | 53 | 73.38 | 29.352 | 0.29 | 0.04 | 0.9 | 0.9 | 82 | 738 |
| 17 | Kerala | 0.2 | 0.036 | 0.9 | 0.9 | 96 | 1020 | 68.78 | 48.64 | | 58.71 | 23.484 | 0.23 | 0.03 | 0.9 | 0.9 | 110 | 1320 |
| 18 | Ladakh | 0.2 | 0.085 | 0.9 | 0.9 | 34 | 394 | 80.18 | 76.48 | | 78.33 | 31.332 | 0.31 | 0.04 | 0.9 | 0.9 | 82 | 738 |
| 19 | Madhya Pradesh | 0.2 | 0.024 | 0.9 | 0.9 | 137 | 1781 | 59.43 | 39.02 | | 49.225 | 19.69 | 0.2 | 0.03 | 0.9 | 0.9 | 165 | 2310 |
| 20 | Maharashtra | 0.2 | 0.027 | 0.9 | 0.9 | 121 | 1435 | | 60.82 | | 60.82 | 24.328 | 0.24 | 0.03 | 0.9 | 0.9 | 110 | 1210 |
| 21 | Manipur | 0.2 | 0.026 | 0.9 | 0.9 | 126 | 1381 | 85.66 | | | 85.66 | 34.264 | 0.34 | 0.05 | 0.9 | 0.9 | 66 | 528 |
| 22 | Meghalaya | 0.2 | 0.038 | 0.9 | 0.9 | 87 | 978 | 45.52 | | | 45.52 | 18.208 | 0.18 | 0.02 | 0.9 | 0.9 | 165 | 2475 |
| 23 | Mizoram | 0.2 | 0.033 | 0.9 | 0.9 | 100 | 733 | 89.36 | | | 89.36 | 35.744 | 0.36 | 0.05 | 0.9 | 0.9 | 66 | 528 |
| 24 | Nagaland | 0.2 | 0.033 | 0.9 | 0.9 | 99 | 693 | | | | 68.38 | 27.352 | 0.27 | 0.04 | 0.9 | 0.9 | 82 | 820 |
| 25 | Odisha | 0.2 | 0.031 | 0.9 | 0.9 | 105 | 1217 | 70.91 | 65.9 | 90.95 | 75.92 | 30.368 | 0.3 | 0.04 | 0.9 | 0.9 | 82 | 738 |
| 26 | Puducherry | 0.2 | 0.043 | 0.9 | 0.9 | 76 | 803 | | | | 84.81 | 33.924 | 0.34 | 0.05 | 0.9 | 0.9 | 66 | 594 |
| 27 | Punjab | 0.2 | 0.031 | 0.9 | 0.9 | 105 | 1365 | | | | 68.38 | 27.352 | 0.27 | 0.04 | 0.9 | 0.9 | 82 | 820 |
| 28 | Rajasthan | 0.2 | 0.043 | 0.9 | 0.9 | 76 | 988 | | | | 68.38 | 27.352 | 0.27 | 0.04 | 0.9 | 0.9 | 82 | 820 |
| 29 | Sikkim | 0.2 | 0.031 | 0.9 | 0.9 | 105 | 1288 | 86.74 | 62.17 | 52.03 | 66.98 | 26.792 | 0.27 | 0.04 | 0.9 | 0.9 | 82 | 820 |
| 30 | Tamilnadu | 0.2 | 0.026 | 0.9 | 0.9 | 126 | 1638 | 88.03 | 77.75 | 88.65 | 84.81 | 33.924 | 0.34 | 0.04 | 0.9 | 0.9 | 66 | 528 |
| 31 | Telangana | 0.2 | 0.024 | 0.9 | 0.9 | 138 | 1794 | 70.76 | 70.71 | | 70.735 | 28.294 | 0.28 | 0.04 | 0.9 | 0.9 | 82 | 820 |
| 32 | Tripura | 0.2 | 0.036 | 0.9 | 0.9 | 91 | 1183 | | | | 45.52 | 18.208 | 0.18 | 0.02 | 0.9 | 0.9 | 122 | 1830 |
| 33 | Uttarakhand | 0.2 | 0.031 | 0.9 | 0.9 | 105 | 1191 | 64.8 | | | 64.8 | 25.92 | 0.26 | 0.03 | 0.9 | 0.9 | 110 | 1210 |
| 34 | Uttar Pradesh | 0.2 | 0.026 | 0.9 | 0.9 | 127 | 1651 | 71.96 | | | 71.96 | 28.784 | 0.29 | 0.04 | 0.9 | 0.9 | 82 | 820 |
| 35 | West Bengal | 0.2 | 0.024 | 0.9 | 0.9 | 138 | 1794 | 86.03 | | | 86.03 | 34.412 | 0.34 | 0.05 | 0.9 | 0.9 | 66 | 528 |
| | **TOTAL** | | | | | **3528** | **42369** | **76.47** | **63.05** | **66.24** | **2485.49** | | | | | | **3153** | **33443** |

# Sampling Plan

| Sample ID | District_Name | Block_Name | Village_Name | Buffaloes | Cattle | Cattle + Buffalo | Number of units to sample | Buffalo Proportion | Cattle Proportion | Probability Value |
|---|---|---|---|---|---|---|---|---|---|---|
| pachmu(1621-1630) | Palakkad | Chittur | Muthalamada(GP)ÔÇôWardNo.9 | 0 | 862 | 862 | 10 | 0 | 10 | 6.20E-07 |
| pamash(1631-1640) | Palakkad | Mannarkad | Sholayur(GP)ÔÇôWardNo.14 | 5 | 924 | 929 | 10 | 0 | 10 | 5.75E-07 |
| pamash(1641-1650) | Palakkad | Mannarkad | Sholayur(GP)ÔÇôWardNo.6 | 0 | 962 | 962 | 10 | 0 | 10 | 5.55E-07 |
| **pachmu(#)** | **Palakkad*** | **Chittur** | **Muthalamada(GP)ÔÇôWardNo.10** | **54** | **1061** | **1115** | **10** | **0** | **10** | **4.79E-07** |
| | | | **Total** | **2634** | **53344** | **55978** | **1660** | **66** | **1594** | **0.000295694** |

*Reserved villages to be used for sampling if any selected village in a given district is not accessible, has logistic problem or any other issues; # The replaced village Sample Numbers are used with the reserved village sample IDs, i.e., if a village with sample id chngng(1015-1027) is replaced with the reserved village then the sample id is replaced with the reserved village id and the sample numbers are same as of replaced village ( gogoda(1015-1027))

# Sampling plan Bulletin

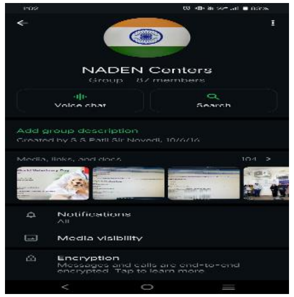

Approximately **5,39,535** samples are allocated annually across India for monitoring and surveillance of four prioritized animal diseases (FMD, Brucellosis, PPR, and CSF) supporting nationwide disease tracking and control initiatives.

# Operational Scale & Response Time Optimization in NADRES V2 via AI/ML Automation

## Data Inputs for Monthly Livestock Disease Forecasting

- ✓ **Total Livestock Population & Animal Species Covered**: **540 million** animals (Cattle, Buffalo, Sheep, Goat, and Pig)
- ✓ **Disease Surveillance Network**: Data collected from 35 NADEN (National Animal Disease Epidemiology Network) Centers

**WhatsApp NADEN Group**




- ✓ **Number of States & Districts Covered: 36** States& UTs, **755** Districts
- ✓ **Number of Target Diseases**: **15** economically important livestock diseases
- ✓ **Climatic Parameters**: **18** key weather and climate variables considered
- ✓ **Remote Sensing Variables**: 5 variables derived from satellite and geospatial data
- ✓ **Delta Variables**: **23** variables capturing changes in climatic trends over time
- ✓ **Forecasting Models**: **20** predictive models used for analysis
- ✓ **Indices**: **13** indices to support decision-making and interpretation

## Operational Scale

| Sl. No. | AI & ML-Driven Operation | Volume of Operations for One year |
|---|---|---|
| 1 | **Data Capturing** | 2,08,380 records(disease data, key risk factors) |
| 2 | **Data Alignment** | 7,61,046 records (additional 23 delta variables) |
| 3 | **Disease Modelling** | Forecasting 15 livestock diseases, over 12 months using 20 models and 13 performance indices across 755 districts and 15 agro climatic zones in India requires approximately **530 million operations per time** |
| 4 | **Risk Communication** | 25 lakh SMS alerts to farmers in 1 year; 17 to 18 thousand DLT SMS alerts to veterinary officials every month |

## Optimized Response Time in NADRES Through AI/ML Automation for Each month

| Process | Before Automation | After Automation | Improvement |
|---|---|---|---|
| **Data Collection + Cleaning** | 10–14 days | < 48 hours | ~90% time saved |
| **Forecasting & Modeling** | 7–10 days | < 10 hours | ~95% faster |
| **Report Preparation** | 10 – 15 days | < 3 days | ~90% time saved |
| **Alert Generation** | Manual dispatch | Instant multi-channel | Real-time communication |
| **Total Response Cycle** | 18–24 days | < 6 days | faster response time |

- ➢ Fully automated pipeline powered by **AI and ML,** Covers the entire workflow from data acquisition through to district-level risk alerts
- ➢ Over **2,346** lines of **R code** implemented across data capture, processing, and modeling stages to automate the NADRES V2 pipeline. ( https://nivedi.res.in/Nadres_v2/ )
- ➢ Nearly **250** CPU hours per month devoted to continuous model execution and risk forecasting.

# NADRES V2: Future Scalability & Strategic Collaborations for Precision Livestock Disease Forecasting

## Scalability Opportunities

- ✓ **Integrated Mathematical and Surveillance Modeling:** Develop mathematical and surveillance models and integrate them with data-driven frameworks for priority livestock diseases such as FMD, PPR, and ASF, enhancing precision and early detection capabilities.
- ✓ **Micro-Level Forecasting**: Expansion from district to **block and village levels**, enabling hyper-localized risk predictions tailored to specific livestock practices and microclimates.
- ✓ **Model and Disease Expansion:** The number of forecasted livestock diseases is projected to increase to 20-30, with a parallel rise in machine learning models to approximately 25-30, improving prediction specificity and robustness.
- ✓ **Offline Accessibility**: Deployment of AI/ML models on mobile devices with **offline capabilities** for remote areas with poor internet.
- ✓ **Multi-Language & Voice Support**: Integration of **AI-driven voice alerts**, SMS, IVR, and community radio in **regional languages** for inclusive communication.

## Strategic Collaborations

- ✓ **NICRA (ICAR)**: Leveraging agro-climatic data to **enhance prediction accuracy** under climate variability (floods, droughts).
- ✓ **IMD Integration:** Real-time meteorological data and **farmer details** across India are integrated to enhance the prediction of climate-sensitive and vector-borne diseases and to enable timely dissemination of alerts to farmers
- ✓ **Government Platforms**: Seamless integration with **NDLM, BSNL, and Digital India** initiatives for unified data exchange and delivery.

**AI & ML Adaptability**: Dynamic model recalibration using real-time feedback and new climate-disease relationships.

## Community-Centric Risk Communication

- ✓ **Global Inter** Engaging **village cooperatives** and **extension workers** as grassroots communication hubs.
- ✓ Dissemination through **SMS**, **IVR**, **local radio**, and **mobile-based tools** to reach digitally underserved areas.
- ✓ We will also **expand SMS alerts to farmers in their local or vernacular languages**, ensuring better understanding and adoption.

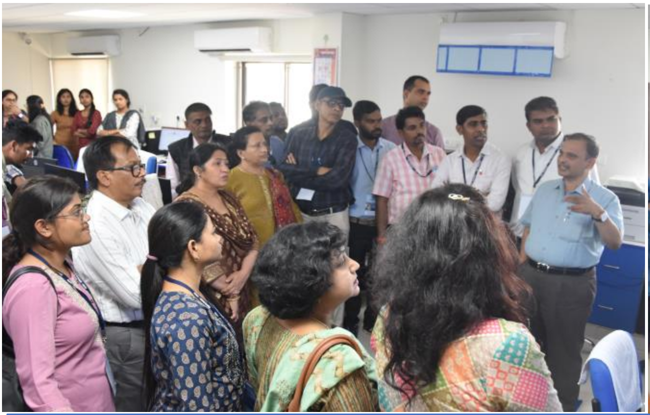
## Global Interest

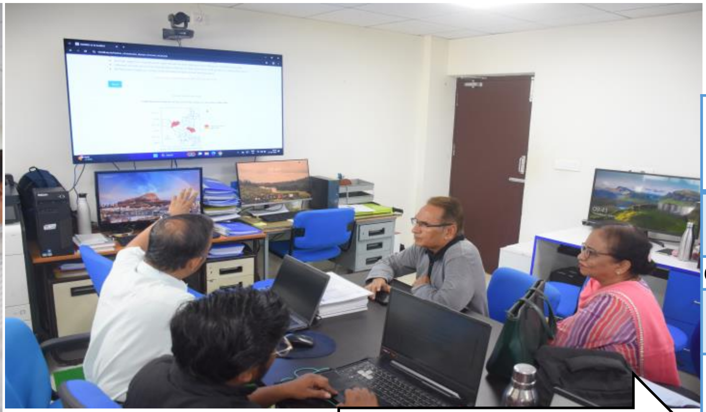
- ✓ FAO experts organized a workshop on community-based early disease detection and reporting systems, and invited the NADRES V2 team to explore expanding its implementation at the community level.

# Officials were oriented on the NADRES V2 workflow during their visit to the SEL Lab



Web Audit Certificate

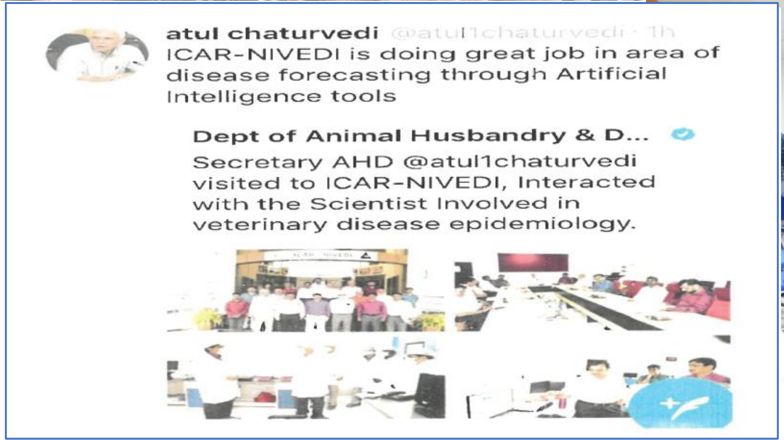




The website is currently under evaluation by the Standards and Quality Compliance Lab (STQCL) for adherence to GIGW guidelines

| Parameter | NADRES v2 Website | ICAR-NIVEDI Website |
|---|---|---|
| Errors | 0 (No critical accessibility errors) | 0 |
| Contrast Errors | 0 (No contrast issues) | 0 |
| Features | 32(Accessibility features implemented) | 55 |
| Structural Elements | 71 | 86 |
| ARIA Attributes | 78 | 46 |

WAVE Tool Accessibility Summary Report


atul chaturvedi @atul1chaturvedi · 1h
ICAR-NIVEDI is doing great job in area of disease forecasting through Artificial Intelligence tools

Dept of Animal Husbandry & D...
Secretary AHD @atul1chaturvedi visited to ICAR-NIVEDI, Interacted with the Scientist Involved in veterinary disease epidemiology.

Message Alert

**NADRES V2** has been conferred with the **National Award for e-Governance 2024–25 (Gold)** under the category **‘Innovation by Use of AI and Other New Age Technologies for Providing Citizen Centric Services’.**



Hesaraghatta Farmer Dairy Farm, Yelahanka, Bengaluru
Thank You