Foot-and-Mouth Disease (FMD)
Simulation Parameter Entry User Manual

Quick Navigation (Platform Steps)

- ✓ Go to https://nivedi.res.in/.
- ✓ Click **NADRES**V2 or open https://nivedi.res.in/Nadres_v2/.
- ✓ Click on **Disease Simulation** or open https://nivedi.res.in/simulation/.
- ✓ **Click on Start Exploring.**
- ✓ Select the **disease** (e.g., choose **FMD**).
- ✓ Click **Open Dashboard**.
- ✓ Review **Theorems & Analysis** (summary of model and assumptions).
- ✓ Click **Simulation** to reach the **Simulation Dashboard** and start entering parameters.

Before You Start

- ✓ Keep the latest district-level counts: animals, vaccination (round-wise), infected (symptomatic/asymptomatic), recovered, and deaths due to disease.
- ✓ If your dashboard supports languages (English-EN/Hindi-HI/Kannada-KN), the *titles/desc/how/range* texts mirror the on-screen help bubbles.
- ✓ Use whole numbers for counts, decimals (0–1) for ranges, and 0–100 for percentages (unless the field explicitly expects 0–1).

Recommended Data-Entry Order before the automatic computation

- ✓ **Population & Vaccination:** N Total population (Cattle-N_C, Buffalo-N_B, Pig-N_P, Sheep & goat -N_S) → V_C1 → V_C2
- ✓ **Infection & Recovery:** I_C1 (Asymptomatic) → I_C2 (Symptomatic) → I_B → I_P → I_S → R_C
- ✓ **Prevalence (if used):** Prev Asymptomatic → Prev Symptomatic
- ✓ **Control/Program rates:** φ (phi), α_C, α_B, α_P, α_S
- ✓ **Mortality:** μ_C, μ_B, D (disease-induced)
- ✓ **Environment:** Temperature, Humidity, pH (Env Computed)
- ✓ **Infectiousness:** Infectious Days (contact Rate Computed)

Parameter-by-Parameter Guidelines

	Parameter	What to Enter	Where to Get It	Units / Format	Range / Checks	Computed / Formula	Example
1.	N — Total Population	Total animals included in this model.	Field census or NADRES livestock data.	Count (whole number)	Positive integer	Adding all the individual species count (N_C, N_B, N_P, N_S)	e.g., 125000

2.	S_C — Susceptible Cattle	*Do not type*. Computed value of animals at risk.	Computed as total cattle minus (Vaccination).	Computed	Non-negative	Computed from S_C0 = NC − (V_C10 + V_C20 + E_C0 + I_C10 + I_C20 + R_C0) (dashboard default). If your locale shows an alternate rule, follow the UI.	No need to enter manually, add the requirements asked for
3.	E_C — Exposed (Latent)	Animals are exposed but not yet infectious.	Multiplier (M) = {Mode of transmission + Duration & proximity +Stage of illness	Computed or enter manually	0–N	**Computed using** E_C = $\frac{\beta\, S\, I}{N}$ *M	-
4.	Multiplier (M) = Mode of transmission + Duration & proximity + Stage of illness. Mode of transmission: Direct contact (1), Indirect (0.5), No route (0). Duration & proximity: High contact (1), Medium (0.5), Low (0). Stage of illness: Peak infectious (1), Moderate (0.5), Not infectious (0).						
5.	I_C1 — Asymptomatic Infected	Infected without visible clinical signs.	1/ Total subclinical period (1.5-2 days)	Compute	0–N	I_C1 = 0.66 × E_C updates when E_C changes,	e.g.,0.66* E_C
6.	I_C2 — Symptomatic Infected	Animals showing clinical symptoms.	Confirmed farm/field reports.	Count	0–N	Count confirmed infected in farms.	e.g., 220
7.	R_C — Recovered	Recovered post-infection (or infected −	Treatment/health records; vaccination >= 3 rounds may be counted,	Count	0–N	Computed using [total infected animals – (disease-	e.g., 480

		disease deaths).	disease-induced deaths, if your UI says so.			induced deaths +V_C2)].	
8.	V_C1 — Vaccinated < 3 rounds	Cattle with partial immunity (1–3 doses).	Vaccination records / NADCP Sero monitoring rounds.	Count	0–N (ensure V_C1+V_C2 ≤ N)	Knight et al., 2015. From this, we refer to > 3 and ≤ 3 rounds for vaccination	e.g., 20000
9.	V_C2 — Vaccinated ≥ 3 rounds	Fully immunized cattle (3+ doses).	Vaccination records / NADCP Sero monitoring rounds.	Count	0–N (ensure V_C1+V_C2 ≤ N)	—	e.g., 35000
10.	I_B — Infected Buffalo	Current infectious buffalo.	Active case reports.	Count	≥ 0	If there are cases, enter otherwise 0	e.g., 12
11.	I_P — Infected Pigs	Currently, infectious pigs.	Lab confirmation.	Count	≥ 0	If there are cases, enter otherwise 0	e.g., 0
12.	I_S — Infected Sheep/Goats	Currently, infectious small ruminants.	Field clinical count.	Count	≥ 0	If there are cases, enter otherwise 0	e.g., 4
13.	Prev-A — Asymptomatic Prevalence	The percentage of sub-clinically or asymptomatically infected animals	Past Sero-surveillance or literature evidence.	% (0–100)	0–100%	Estimated using past Sero-surveillance records or evidence from published literature	e.g., 35%
14.	Incidence (%)	Percentage of newly infected animals within a	Confirmed farm/field reports. and Census data	Auto (≥0).	Typical values: 0–100 per 1000 (depends on	Computed as incidence = (I_C20 / NC) × 1000.	e.g,833/287502*1000=2.89

		specific time period.			outbreak intensity).		
15.	Prev-S — Symptomatic Prevalence	The percentage of infected animals showing symptoms.	Clinical survey / NADRES.	% (0–100) = Incidence * average duration of the disease(i.e 7)	0–100%	Percent of infected animals showing symptoms.	e.g., 65%
16.	Non-Imm — Non-Immunity (Computed)	Portion of animals without immunity.	Vaccinated animals are immunized	Computed (0–1)	0–1	**Computed:** [1 − (V_C1+V_C2)/N]	No need to enter manually, add the requirements asked for
	Contact-Rate (Computed)- Farm level = Number of infected animal N_A / Total number of animals in the group N_G						
17.	Contact-Rate (Computed) Farm level	Average fraction of animals contacted by one infected.	—	Computed (0–1)	0–1	**Computed:** N_A / N_G	No need to enter manually, add the requirements asked for
18.	Contact-Rate (Computed) District level	Contact-Rate (Computed)- District level $\text{Contact-Rate}_i = \alpha \times \Sigma_j [w_{ij} \times (I_j / N_j)]$ • α = (Livestock Density / Average Density) × M • w_{ij} = (1 – Vacc-Cov) + (1-Monitoring) + (1 − Biosecurity) + THI Add the neighbors that are connected to the district that we are concerned about					No need to enter manually, add the requirements asked for
19.	Livestock Density	Current livestock density for this district (total livestock ÷ district area).	Livestock Census (GoI/state AH&VS) or your GIS census layer.	animals/km^2	≥ 0	Livestock Density = Total population / KM^2	150 animals/km^2

20.	Average Density (comparison set)	Average livestock density across neighbors or state (pick one set and keep consistent).	Same source as above; compute mean across chosen set.	animals/km²	> 0	Average = sum of all the densities / total number of densities *Average density from neighboring districts only if they are infectious.*	300 animals/km²
21.	Modifier (M)	Contextual adjustment for contact potential (mobility, fairs/markets, terrain, season).	Expert judgement; mobility/market intel; seasonal flags.	Based on mobility or environmental context.	0–1 (1 = neutral, 0= no mobility)	Based on mobility and markets, give value for the modifier	1.0
22.	α (Alpha)	Normalized contact potential for this district.	Auto-computed by the panel.	—	≥ 0	α = (Density / Average-Density of neighbor districts) × M	(150/300) × 1.0 = 0.50
	Neighbor row inputs (for each neighbor/interface j): if u don't want the neighbor, put zero to Infected (I_j) if u need another, please click on "add neighbor"						
23.	Neighbor Name (j)	District or interface name (e.g., border market/check-post).	Adjacency list/trade–interface list.	—	—	—	District A
24.	Infected (I_j)	Current active infectious count in neighbor j (confirmed/ best estimate).	NADRES line list; state/institute outbreak sheets; field intel.	animals	≥ 0	—	100

25.	Population (N_j)	Livestock at risk in neighbor j.	Livestock Census/district registry.	animals	> 0	—	50,000
26.	Vacc-Cov (0–1)	Vaccination coverage in j (fraction vaccinated).	Vaccination registers; campaign coverage reports.	—	0–1	Animals getting > 3 vaccination rounds (1.0) Animals getting less than 3 vaccination rounds (0.5) No vaccination (0)	0.70
27.	Monitoring (0–1)	Surveillance intensity (sampling %, inspections per 10k head), normalized.	Field ops logs; lab throughput.	—	0–1	Sero-monitoring specifically looks for the presence of FMDV-specific antibodies in the blood.	0.50
28.	Biosecurity (0–1)	Biosecurity score (higher = better), normalized from checklists.	Field biosecurity audits.	—	0–1	Add suitable values for each parameter based on site conditions Use the help and enter the values	0.60

	Pick the biosecurity measures you're using. There are 5 measures; each gives 0.2 points. Your score = 0.2 × how many you picked. Example: pick 3 measures → (0.2*3) score 0.6. Biosecurity Measures: 1. Isolation — separate species/ages (0.2). 2. Feeding — avoid common grazing; sanitize water (0.2). 3. Quarantine — 30 days for new/returning animals (0.2). 4. Surveillance — monitor and report early (0.2). 5. Hygiene — footbaths, clean sheds daily (lime/formalin) (0.2).						
29.	THI (0–1)	Temperature-Humidity Index factor scaled 0–1 (stress-prone → higher).	IMD/AWS; compute THI then min–max scale 0–1.	—	0–1	Computed THI = (1.8×AT+32) – [(0.55−0.0055×RH) × (1.8×AT−26)]. **(**Habeeb, A.A., Gad, A.E., and Atta, M.A., 2018)	No need to enter manually, add the requirements asked for
30.	Composite weight w_{ij}	Composite pressure weight from j onto i.	Auto-computed.	—	≥ 0	w_{ij} = (1−Vacc-Cov) + (1-Monitoring) + (1−Biosec) + THI	0.80 + 0.30 + 0.50 + 0.40 + 0.40 = 2.40
31.	Infectious ratio	Force component from j due to infection prevalence.	Auto-computed.	—	0–1	I_j / N_j	100 / 50,000 = 0.0020
32.	Neighbor contribution	Contribution of j to i's pressure.	Auto-computed.	—	≥ 0	$w_{ij} \times (I_j/N_j)$	2.40 × 0.0020 = 0.0048
33.	Infectious days	The duration an animal remains infectious.	Lab/clinical evidence, or if u observed, u can edit	Days	0–100	Usually 7 days (Yadav et al., 2019)	e.g., 7

34.	basicR0 (Computed)	The average new infections caused by one infected.	Contact rate & Infectious days are prerequisites	Computed	> 1 implies growth	**Computed:** ((I_C1+I_C2)/N) × 100 × contact rate × infectious days	No need to enter manually, add the requirements asked for
35.	β_C (Computed) — Symptomatic Transmission	Transmission rate from symptomatic cattle.	—	Computed	0–10	**Computed:** basic R0 × prev-S × non-Imm	No need to enter manually, add the requirements asked for
36.	β_B (Computed) — Asymptomatic Transmission	Transmission rate from asymptomatic buffalo/cattle.	—	Computed	0–10	**Computed:** basic R0 × prev-A × non-Imm	No need to enter manually, add the requirements asked for
37.	φ (phi) — Isolation Rate	Proportion of infected effectively isolated or with reduced contact.	Biosecurity practice/isolation records.	Range (0–1)	0–1 (min suggested 0.2)	A minimum isolation rate of **0.2** means **20%** of infected animals must be separated or have reduced contact to limit disease spread.	e.g., 0.25
38.	α_C, α_B, α_P, α_S — Vaccination Rates	Proportion vaccinated: total vaccinated / total population (by species).	NADCP Sero monitoring rounds/vaccination registers.	Range (0–1), Vaccination: A minimum vaccination rate of **0.4** to get HIT	0–1 (min suggested 0.4)	Total number of vaccinated cattle / Total cattle population. immunity threshold	e.g., α_C = 0.42, means **40 %** of animals must be vaccinated to reach the herd immunity

39.	μ_C, μ_B — Natural Mortality Rates	Natural (non-disease) mortality.	Life span references.	Range (0–1)	0–1	**Formula:** μ = 1 / life span	E.g., lifespan 10 yrs → μ≈0.1/yr (≈0.0083/mo)
40.	D — Disease-Induced Death Rate	Deaths caused by the disease among the infected.	Case records — deaths & total infected.	Range (0–1)	Typical 0.005–0.02	**Computed hint:** D = deaths / Total Infected	E.g., 12 deaths / 1800 infected = 0.0067
41.	Temperature (°C)	Ambient temperature.	Weather station/thermometer.	°C	−10 to 50	Use meteorological data for better analysis	e.g., 28
42.	Humidity (%)	Relative humidity.	Weather station.	%	0–100	Use meteorological data for better analysis	e.g., 72
43.	pH	Environmental pH affects viral stability.	pH meter / soil kit.	0–14	0–14 (7 = neutral)	Use meteorological data for better analysis	e.g., 6.8
44.	F (Fomites Multiplier)	The transmission of the FMD virus via contact with contaminated inanimate objects or substances.	—	Computed (0.0–1.0)	0.0–1.0	**Computed:** Add suitable values for each parameter based on site conditions	—
	Add suitable values for each parameter based on site conditions 1. **Fomites: vehicles, tools, surfaces, contaminated feed (0.30)** 2. **Environmental: Cool, moist conditions, shaded or water-present areas (0.25)** 3. **Human-mediated: Many handlers, poor hygiene, and no personal protective equipment (0.25)**						

	4. **Carrier species: Free access to wildlife, birds, and rodents (0.10)** 5. **Biological materials: Unverified or contaminated biological products (0.10)**

What the graph lets you spot

- Peak symptomatic burden (**I_C2**, red): the tallest red segment pinpoints the day of max clinical cases—useful for surge planning.
- Silent spread (**I_C1**, purple) vs clinical (I_C2, red): compare purple vs red height to see if transmission is mostly subclinical or clinical.
- Incubation pressure (**E_C**, orange): rising orange while red is still low signals cases are about to rise (lead indicator).
- Susceptible depletion (**S_C**, blue): steep blue decline shows strong transmission or high vaccination (since S_C→V_C1); a flat blue line means low force of infection.
- Recovery accumulation (**R_C**, green): growth here tracks natural + vaccine-induced immunity; plateaus mean epidemic tailing off.
- Cross-species timing: yellow (**I_B**), cyan (**I_P**), grey (I_S) show spillover pace relative to cattle; if they rise only after red/purple spike, environment/contacts are driving it.
- Pre/post marker check: the dashed line (intervention day) is your reference marker; look for slope/height changes after this day (e.g., vaccination, movement control). *(Note: the line is a visual marker—any actual change depends on your inputs.)*
- Low-level persistence: switch Y to log to see lingering small counts that a linear scale hides.

Tip: this stack shows S_C, E_C, I_C1, I_C2, R_C, I_B, I_P, I_S only. It doesn't include V_C1/V_C2, Q_C, or q_C, so the stack height ≠ total population.
"Results below" = exact values for the selected day

How to download the chart?

Download Options and use **HTML report** for a complete printable and editable report.

- **Download PNG:** Saves the **chart + summary footer** (R_0, HIT, F_env, day cursor, key compartments, peak/epidemic markers, equilibrium S*/R*/I_C2*/q_C*).
- **Download Results (CSV):** Saves **day-wise simulation data** (S_C, E_C, I_C1, I_C2, R_C, I_B, I_P, I_S, q_C, I_total, R0, HIT, F_env).
- **Download Parameters (CSV):** Saves **all input settings** (parameter name/id/value + sliders/checkbox).
- **Download Report (HTML):** Saves a **full report** (summary + current day values + equilibrium + embedded charts + all parameters). Open in browser and **Print → Save as PDF**.
- **Right-click the chart → Download image**

Quality Checks Before Running Simulation

- **Bounds:** All Ranges are in 0–1, percentages in 0–100, and counts are non-negative integers.
- **Consistency:** V_C1 + V_C2 ≤ N; I_C10 + I_C20 ≤ N; R_C ≤ N.

- **Units:** Confirm whether the field expects % (0–100) or proportion (0–1); convert accordingly.

Time base: If your model tick is monthly, convert annual rates (e.g., μ) to per-month.

The **Endemic Equilibrium** feature estimates the **steady-state ("long-run") levels** of key cattle compartments when the system settles and stops changing rapidly.

It gives the equilibrium point:

- **S*** = Susceptible cattle at equilibrium
- **R*** = Recovered cattle at equilibrium
- **I_C2*** = Symptomatic infected cattle at equilibrium
- **q_C*** = compartment at equilibrium (linked to I_C2 through φ and γ_4)

This is useful to answer:

- "If this disease persists, what levels will it stabilize around?"
- "If I change symptomatic infections (I_C2) or rates, how does equilibrium shift?"

How equilibrium is calculated

1) It uses the model equations: The equilibrium point is computed from the **equilibrium formulas** (steady-state equations).

At equilibrium, each compartment satisfies: **inflow = outflow**, so the compartment stays constant.

How to use it (what the user should do)

Basic workflow: Run the simulation or enter realistic initial values.

- Open **Endemic Equilibrium Parameters** (tap to expand): Adjust only if needed: If you know typical disease durations, tune γ_3 (recovery), σ_1 (progression), etc.

- The equilibrium point auto-updates and shows: **S***, **R***, **I_C2***, **q_C***

How "Advanced" inputs affect equilibrium (quick meaning guide)

- **Δ_C (delta_C)**: higher → increases S* (more recruitment)
- **θ (theta)**: higher → reduces R* and increases S* (faster waning)
- **β_C (beta_C)**: higher → increases infections → lowers S*, raises I*
- **ρ_1 (rho_1)**: higher → faster E→I_C1, shifts equilibrium toward infectious chain
- **σ_1 (sigma_1)**: higher → more I_C2*
- **γ_3 (gamma_3)**: higher → reduces I_C2*, increases R*
- **φ (phi)**: higher → increases q_C*, can reduce I_C2 depending on other rates
- **γ_4 (gamma_4)**: higher → clears q_C faster → increases R*
- **α_C, α_C1/2/3, χ_1/χ_2**: shape vaccination routing between S and R
- **K_1/K_2 + Δ_QC**: affect quarantine size and how much leaks into I_C2

What-If Symptomatic infected cases (I_C20) changes and Equilibrium tiles

- **What it does:** Compares outbreak curves for different **initial symptomatic cattle (I_C20)** and shows key markers (**epidemic start/end, peak, endemic start**) on the same plot.
- **Lines:**
  - **Solid curves:** Different runs for different **I_C20** (e.g., 500/1000/2000). Higher I_C20 usually gives a bigger/faster outbreak.
- **Markers:**
  - **Epidemic start:** first day **I_total > 1**
  - **Peak:** maximum point (red)
  - **Endemic start:** after peak, first 14-day window stable within **±2%** and mean > 1 (green)
  - **Epidemic end:** last day **I_total > 1**
- **What-If controls:** Enter **I_C20 → View curve** to add a scenario; **Clear** resets.

Run & Interpret

1. If validation errors appear, correct the field as per the ranges above.
2. On the outputs page, note that **R_0 > 1** indicates expanding outbreak; check **β_C** and **β_B** to see symptomatic vs asymptomatic contributions.
3. Use the control sliders (**φ**, vaccination rates α_*) to test intervention scenarios.

Based on the entered data, the system will calculate the basic reproduction number (R_0). If R_0 is greater than 1, it indicates a higher potential for disease spread and possible endemic conditions. The output will also provide the Herd Immunity Threshold (HIT), which represents the percentage of the population that needs to be vaccinated to achieve immunity against Foot-and-Mouth Disease.