

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

Quick Navigation (Platform Steps)

- ✓ Go to <https://nivedi.res.in/>.
- ✓ Click **NADRESV2** 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
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
S_C — Susceptible Cattle	<i>Do not type.</i> Computed value of animals at risk.	Computed as total cattle minus (Vaccination).	Computed	Non-negative	Computed from $S_C = (N - V_{C1} - V_{C2})$ (dashboard default). If your locale shows an	No need to enter manually, add the requirements asked for

					alternate rule, follow the UI. Do not override.	
E_C — Exposed (Latent)	Animals are exposed but not yet infectious.	Contact-tracing/ field exposure + expected new cases	Count	0–N	Computed using Expected new cases $E_C = S_C \times (1 - e^{\{-(\beta_B + \beta_C) \times I_C2 \times (\Delta t / NC)\}})$ (Stenfeldt et al., 2016). Toggle off to enter manually.	e.g., 350
I_C1 — Asymptomatic Infected	Infected without visible clinical signs.	Lab/sero-survey estimates (% of total Exposed) or counts.	Count or % (see field hint)	0–N	$I_C1 = 0.5 \times E_C$ updates when E_C changes,	e.g., 12% of E_C $=0.12 \times E_C$
I_C2 — Symptomatic Infected	Animals showing clinical symptoms.	Confirmed farm/field reports.	Count	0–N	Count confirmed infected in farms.	e.g., 220
R_C — Recovered	Recovered post-infection (or infected – disease deaths).	Treatment/health records; vaccination ≥ 3 rounds may be counted, disease-induced deaths, if your UI says so.	Count	0–N	Computed using [total infected animals – (disease-induced deaths + V_C2)].	e.g., 480
V_C1 — Vaccinated < 3 rounds	Cattle with partial immunity (1–3 doses).	Vaccination records / NADCP Sero monitoring rounds.	Count	0–N (ensure $V_C1 + V_C2 \leq N$)	Knight et al., 2015. From this, we refer to > 3 and ≤ 3 rounds for vaccination	e.g., 20000
V_C2 — Vaccinated ≥ 3 rounds	Fully immunized cattle (3+ doses).	Vaccination records / NADCP Sero monitoring rounds.	Count	0–N (ensure $V_C1 + V_C2 \leq N$)		e.g., 35000
I_B — Infected Buffalo	Current infectious buffalo.	Active case reports.	Count	≥ 0	If there are cases, enter otherwise 0	e.g., 12

I_P — Infected Pigs	Currently, infectious pigs.	Lab confirmation.	Count	≥ 0	If there are cases, enter otherwise 0	e.g., 0
I_S — Infected Sheep/Goats	Currently, infectious small ruminants.	Field clinical count.	Count	≥ 0	If there are cases, enter otherwise 0	e.g., 4
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%
Prev-S — Symptomatic Prevalence	The percentage of infected animals showing symptoms.	Clinical survey / NADRES.	% (0–100)	0–100%	Percent of infected animals showing symptoms.	e.g., 65%
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 requirement s asked for
Contact-Rate (Computed)- Farm level = Number of animals in contact with the infected animal N_A / Total number of animals in the group N_G						
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 requirement s asked for
Contact-Rate (Computed) District level	Contact-Rate (Computed)- District level $\text{Contact-Rate}_i = \alpha \times \sum_j [w_{ij} \times (I_j / N_j)]$ • $\alpha = (\text{Livestock Density} / \text{Average Density}) \times M$ • $w_{ij} = \text{Active-Inf} + (1 - \text{Vacc-Cov}) + (1 - \text{Monitoring}) + (1 - \text{Biosecurity}) + \text{THI}$ Add the neighbors which is connected to the district that we are concerned					No need to enter manually, add the requirement s asked for
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	$\alpha = (\text{LivestockDensity} / \text{Average Density}) \times M$	150 animals/km ²

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/km ²	> 0	$\alpha = (\text{Livestock Density} / \text{Average Density}) \times M$	300 animals/km ²
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)	$\bullet \alpha = (\text{Livestock Density} / \text{Average Density}) \times M$	1.0
α (Alpha)	Normalized contact potential for this district.	Auto-computed by the panel.	—	≥ 0	$\alpha = (\text{Density} / \text{Average-Density of neighbor districts}) \times M$	$(150/300) \times 1.0 = 0.50$

Neighbor row inputs (for each neighbor/interface j):

Neighbor Name (j)	District or interface name (e.g., border market/check-post).	Adjacency list/trade–interface list.	—	—	—	District A
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
Population (N_j)	Livestock at risk in neighbor j.	Livestock Census/district registry.	animals	> 0	—	50,000
Active-Inf (0–1)	Normalized signal of current outbreak intensity in j.	Scale recent cases, positivity, or R(t>1). Use a consistent scheme.	—	0–1	Active Infection = new cases/total animals.	0.80
Vacc-Cov (0–1)	Vaccination coverage in j (fraction vaccinated).	Vaccination registers; campaign coverage reports.	—	0–1	Animals getting more than 3 vaccination rounds (1) Animals getting less than 3	0.70

					vaccination rounds (0.5) No vaccination (0)	
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
Biosec (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 = $0.2 \times$ how many you picked. Example: pick 3 measures $\rightarrow (0.2 \times 3)$ score 0.6.

Biosecurity Measures:

- ☐ Isolation — separate species/ages(0.2).
- ☐ Feeding — avoid common grazing; sanitize water(0.2).
- ☐ Quarantine — 30 days for new/returning animals(0.2).
- ☐ Surveillance — monitor and report early(0.2).
- ☐ Hygiene — footbaths, clean sheds daily (lime/formalin)(0.2).

THI (0–1)	Temperature-Humidity Index factor scaled 0–1 (stress-prone $\rightarrow$ higher).	IMD/AWS; compute THI then min–max scale 0–1.	—	0–1	Computed THI = $(1.8 \times AT + 32) - [(0.55 - 0.0055 \times RH) \times (1.8 \times AT - 26)]$. (Habeeb, A.A., Gad, A.E., and Atta, M.A., 2018)	No need to enter manually, add the requirements asked for
Composite weight w_{ij}	Composite pressure weight from j onto i.	Auto-computed.	—	≥ 0	$w_{ij} = \text{Active-Inf} + (1 - \text{Vacc-Cov}) + (1 - \text{Monitoring}) + (1 - \text{Biosec}) + \text{THI}$	$0.80 + 0.30 + 0.50 + 0.40 + 0.40 = 2.40$
Infectious ratio	Force component from j due to	Auto-computed.	—	0–1	I_j / N_j	$100 / 50,000 = 0.0020$

	infection prevalence.					
Neighbor contribution	Contribution of j to i's pressure.	Auto-computed.	—	≥ 0	$w_{ij} \times (I_j/N_j)$	$2.40 \times 0.0020 = 0.0048$
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
basicR0 (Computed)	The average new infections caused by one infected.	Contact rate & Infectious days are prerequisites	Computed	> 1 implies growth	Computed: $((I_C1 + I_C2)/N) \times 100 \times \text{contact rate} \times \text{infectious days}$	No need to enter manually, add the requirements asked for
β_C (Computed) — Symptomatic Transmission	Transmission rate from symptomatic cattle.	—	Computed	0–10	Computed: basic R0 $\times$ prev-S $\times$ non-Imm	No need to enter manually, add the requirements asked for
β_B (Computed) — Asymptomatic Transmission	Transmission rate from asymptomatic buffalo/cattle.	—	Computed	0–10	Computed: basic R0 $\times$ prev-A $\times$ non-Imm	No need to enter manually, add the requirements asked for
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
$\alpha_C, \alpha_B, \alpha_P, \alpha_S$ — Vaccination Rates	Proportion vaccinated: total vaccinated / total population (by species).	NADCP Sero monitoring rounds/vaccination registers.	Range (0–1)	0–1 (min suggested 0.4)	Total number of vaccinated cattle / Total cattle population. Vaccination: A minimum	e.g., $\alpha_C = 0.42$

					vaccination rate of 0.4 means 40 % of animals must be vaccinated to reach the herd immunity threshold	
μ_C, μ_B — Natural Mortality Rates	Natural (non-disease) mortality.	Life span references.	Range (0–1)	0–1	Formula: $\mu = 1 / \text{life span}$	E.g., lifespan 10 yrs → $\mu \approx 0.1/\text{yr}$ ($\approx 0.0083/\text{mo}$)
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
Temperature (°C)	Ambient temperature.	Weather station/thermometer.	°C	–10 to 50	Use meteorological data for better analysis	e.g., 28
Humidity (%)	Relative humidity.	Weather station.	%	0–100	Use meteorological data for better analysis	e.g., 72
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
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 $S_C \rightarrow V_C$); 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 $\neq$ total population.

“Results below” = exact values for the selected day

When you hover or move the day slider, the app calls `update All for Day(day)` and updates:

- $scRes$, $ecRes$, $ic1Res$, $ic2Res$, $rcRes$, $ibRes$, $ipRes$, $isRes$ These are rounded counts for that day (the solid vertical line).

How to download the chart

Right-click the chart → Save image as... (works in most browsers since it's a <canvas>).

Quality Checks Before Running Simulation

- **Bounds:** All Ranges are in 0–1, percentages in 0–100, and counts are non-negative integers.
- **Consistency:** $V_{C1} + V_{C2} \leq N$; $I_{C10} + I_{C20} \leq N$; $R_C \leq N$.
- **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.

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