

Human Spillover Model

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## SEIR MODEL FOR RIFT VALLEY FEVER (RVF)
## Humans (Abattoir Staff - Namisindwa District)
## Spillover-driven transmission with decaying seasonality

## LOAD LIBRARIES
library(deSolve)
library(rootSolve)
library(ggplot2)
library(dplyr)

## POPULATION
N <- 283 # Total abattoir staff (closed population)

## Define initial susceptible pool
S0 <- 30 # actively exposed abattoir workers

## DEMOGRAPHY
mu <- 1 / (60 * 365) # Natural death/replacement rate (per day)

## DISEASE PARAMETERS (HUMANS)
eh <- 1 / 4 # Incubation rate (mean 4 days)
ch <- 1 / 10 # Recovery rate (mean 10 days infectious)
lh <- 0.01 # Disease-induced mortality (per day)

## WANING IMMUNITY
omega <- 1 / (3 * 365) # Immunity wanes after ~3 years

## LIVESTOCK-TO-HUMAN SPILLOVER
Il <- 20 # Infected livestock
L <- 100 # Total livestock
klh <- 0.03 # Spillover transmission coefficient

## Mean (constant) force of infection from livestock
lambda_mean <- klh * (Il / L)

## SEASONAL FORCING (DECAYING)
amp <- 0.6 # Initial seasonal amplitude
period <- 365 # Annual seasonality (days)
tau <- 5 * 365 # Decay timescale (5 years)

## Compute spillover reproductive number
R0_spill <- (lambda_mean * S0 * eh) /
  ((eh + mu) * (mu + lh + ch))
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R0_spill
## [1] 1.635386

## ENDEMIC EQUILIBRIUM (NO SEASONALITY)
seir_equilibrium <- function(x) {

  S <- x[1]
  E <- x[2]
  I <- x[3]
  R <- x[4]

  # Population replacement balances natural + disease mortality
  Ph <- mu * N + lh * I

  dS <- Ph - lambda_mean * S - mu * S + omega * R
  dE <- lambda_mean * S - (eh + mu) * E
  dI <- eh * E - (mu + lh + ch) * I
  dR <- ch * I - mu * R - omega * R

  c(dS, dE, dI, dR)
}

## Solve for endemic equilibrium
EE <- multiroot(
  f = seir_equilibrium,
  start = c(50, 5, 5, 223)
)$root

names(EE) <- c("S", "E", "I", "R")

## Check population balance
EE

##           S           E           I           R
## 41.842713  1.004042  2.280966 237.872183

sum(EE) # ≈ 283

## [1] 282.9999

## FULL SEIR MODEL WITH TIME-VARYING FORCE OF INFECTION
seir_model <- function(time, state, parameters) {

  with(as.list(c(state, parameters)), {

    ## Decaying seasonal force of infection
    lambda_t <- lambda_mean *
      (1 + amp * exp(-time / tau) *

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    sin(2 * pi * time / period))

lambda_t <- max(lambda_t, 0) # Ensure non-negative

## Effective surveillance-driven removal
detect <- screen * Se

## Population replacement
Ph <- mu * N + lh * I

dS <- Ph - lambda_t * S - mu * S + omega * R
dE <- lambda_t * S - (eh + mu) * E
dI <- eh * E - (mu + lh + ch + detect) * I
dR <- ch * I + detect * I - mu * R - omega * R

list(c(dS, dE, dI, dR))
})
}

## SURVEILLANCE SCENARIOS
scenarios <- list(
  Status_Quo = list(
    Se = 0.74,
    screen = 0.00
  ),
  Improved_Surveillance = list(
    Se = 0.90,
    screen = 0.80
  )
)

## SIMULATION SETTINGS
times <- seq(0, 365 * 50, by = 1) # 50 years
burnin <- 365 * 20 # 20-year burn-in

## INITIAL CONDITIONS (PERTURBED EQUILIBRIUM)
initial_state <- EE * c(1.05, 0.95, 1.10, 0.90)

## RUN SIMULATIONS
results <- list()

for (sc in names(scenarios)) {

  params <- c(
    mu = mu,
    eh = eh,
    ch = ch,
    lh = lh,

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    lambda_mean = lambda_mean,
    omega = omega,
    amp = amp,
    tau = tau,
    period = period,
    Se = scenarios[[sc]]$Se,
    screen = scenarios[[sc]]$screen
  )

  out <- ode(
    y = initial_state,
    times = times,
    func = seir_model,
    parms = params
  )

  df <- as.data.frame(out)
  df$Scenario <- sc
  results[[sc]] <- df
}

results_all <- bind_rows(results)

## PLOT: TRANSIENT OSCILLATIONS → ENDEMIC EQUILIBRIUM
ggplot(results_all,
  aes(x = time / 365, y = I, color = Scenario)) +
  geom_line(linewidth = 1.2) +
  geom_vline(xintercept = burnin / 365,
    linetype = "dashed", color = "black") +
  labs(
    title = "RVF Dynamics Among Abattoir Staff",
    subtitle = "Transient Seasonal Oscillations Around a Stable Endemic
Equilibrium",
    x = "Time (years)",
    y = "Infectious Individuals"
  ) +
  theme_minimal()

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RVF Dynamics Among Abattoir Staff
Transient Seasonal Oscillations Around a Stable Endemic Equilibrium

