Modeling and $\mathcal{R}_0$ Analysis of SEQIRS and SEIR-SEI Epidemic Models via Generalized Linear Chain Trick

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Abstract

This project extends the classical compartmental modeling framework by developing two generalized epidemic models based on the Generalized Linear Chain Trick (GLCT): a generalized SEQIRS (Susceptible–Exposed–Quarantine–Infectious–Recovered–Susceptible) model and a generalized SEIR–SEI host–vector model. Traditional ODE-based epidemic models often assume exponentially distributed dwell times, which may not adequately reflect biological reality. By introducing phase-type distributions, our framework allows for arbitrary finite-dimensional sub-state structures within key epidemiological classes, thereby capturing more realistic Erlang- or Coxian-type residence times while preserving an analytically tractable ODE formulation.

For the generalized SEQIRS model, we incorporate internal sub-state structures in the Exposed (E), Quarantine (Q), and Infectious (I) compartments to describe disease progression under quarantine intervention. For the generalized SEIR–SEI model, we use the same GLCT-based construction to model more flexible transition dynamics in both host and vector populations, allowing the latent and infectious stages to have non-exponential waiting time distributions. In both settings, the resulting systems can be written in a unified block-matrix form.

Using the next generation operator approach, we derive analytical expressions for the basic reproduction number, $\mathcal{R}_0$, for these high-dimensional systems. The matrix formulation reveals that the threshold quantity remains structurally well-defined even when the dimensions of the internal sub-states vary. Moreover, the analysis provides a rigorous mathematical interpretation of how quarantine mechanisms and multi-stage infection dynamics affect disease transmission. In particular, quarantine reduces the effective survival probability of individuals progressing from the latent stage to the infectious stage, while in the host–vector setting the multi-stage structure clarifies how transmission is mediated across interacting populations. Overall, this work demonstrates that the GLCT offers a powerful framework for transforming complex stochastic epidemic processes into computationally efficient and mathematically transparent matrix-operator models.

Keywords: GLCT, SEQIRS model, SEIR-SEI model,Phase-type distribution, Basic reproduction number, Next generation operator

1 Introduction and Motivation

The inspiration for this study stems from the pioneering work of Professor Hurtado on the Generalized Linear Chain Trick (GLCT)[2, 3, 4, 5], which offers a mathematically elegant and computationally robust framework for modeling complex biological processes. By utilizing phase-type distributions, the GLCT framework effectively transcends the limitations of traditional ordinary differential equation (ODE) models that rely on the assumption of exponentially distributed dwell times. This approach allows for a more realistic representation of disease progression through various sub-states, providing a rigorous foundation for calculating the basic reproduction number, $\mathcal{R}_0$, across diverse model structures.

However, while the existing literature has extensively characterized the biological dynamics of disease—such as latency, infection, and recovery—there is a notable gap regarding the integration of active public health interventions and multi-population transmission cycles within this generalized framework. Specifically, the impact of quarantine measures has not yet been fully explored under the GLCT paradigm, nor has the framework been extended to account for the coupled SEIR-SEI dynamics inherent in vector-borne diseases.

This project aims to fill these gaps by developing two refined mathematical frameworks that leverage the operator-based power of the GLCT to handle both intervention and structural complexity. Furthermore, by employing the Next-Generation Matrix (NGM) approach, we derive closed-form analytical expressions for the basic reproduction number $\mathcal{R}_0$ for these two generalized models.

2 Preliminary

In this section, we will introduce continuous time Markov chains, phase-type distuributation, reproducation number, next generation matrix (NGM) method and generalized linear chain trick (GLCT).

2.1 Markov chains

2.1.1 Discrete-Time Markov Chains

A discrete-time Markov chain (DTMC) is a stochastic process $\{X_n\}_{n\geq 0}$ taking values in a finite or countable state space

$$\mathcal{S} = \{1, 2, \ldots, n\},$$

such that the future depends only on the present state and not on the past history. More precisely, for all states $i_0, i_1, \ldots, i_n, j \in \mathcal{S}$,

$$\mathbb{P}(X_{n+1} = j \mid X_n = i_n, X_{n-1} = i_{n-1}, \ldots, X_0 = i_0) = \mathbb{P}(X_{n+1} = j \mid X_n = i_n).$$

This is called the Markov property. In words, once the current state is known, the previous history carries no additional information for predicting the next step.

The one-step transition probabilities are defined by

$$p_{ij} = \mathbb{P}(X_{m+1} = j \mid X_m = i), \qquad i, j \in \mathcal{S}.$$

These probabilities form the *transition probability matrix*

$$P = (p_{ij})_{n\times n}.$$

Each entry satisfies

$$p_{ij} \geq 0, \qquad \sum_{j=1}^{n} p_{ij} = 1 \quad \text{for each } i.$$

Hence every row of P sums to 1, reflecting the fact that from a given current state, the chain must move to some state in the next step.

If the initial distribution is denoted by

$$\boldsymbol{\alpha}^{(0)} = \big(\alpha_1, \ldots, \alpha_n\big), \qquad \alpha_i = \mathbb{P}(X_0 = i),$$

then the distribution after one step is

$$\boldsymbol{\alpha}^{(1)} = \boldsymbol{\alpha}^{(0)} P,$$

and more generally after m steps,

$$\boldsymbol{\alpha}^{(m)} = \boldsymbol{\alpha}^{(0)} P^m.$$

A state i is called *absorbing* if

$$p_{ii} = 1.$$

This means that once the chain enters state i, it remains there forever. A state that is not absorbing and from which the chain may eventually leave is typically called a *transient state* in the absorbing-chain setting.

After relabeling the states if necessary, we may assume that the first k states are transient and the last state $k+1$ is absorbing. Then the transition matrix takes the block form

$$P = \begin{bmatrix} P_X & P_a \\ 0 & 1 \end{bmatrix}.$$

Here:

- $P_X \in \mathbb{R}^{k \times k}$ describes transitions among transient states;
- $P_a \in \mathbb{R}^{k \times 1}$ gives the probabilities of moving from transient states into the absorbing state;
- the lower-left block is zero because the absorbing state does not return to transient states;
- the lower-right entry is 1 because the absorbing state remains absorbing.

2.1.2 Continuous Time Markov Chains

A continuous-time Markov chain (CTMC) is a stochastic process

$$\{X(t)\}_{t \geq 0}$$

taking values in a finite state space, such that the future evolution depends only on the current state. In contrast to a discrete-time Markov chain, transitions do not occur at fixed time steps. Instead, when the process is in a given state i, it remains there for a random *dwell time*, and then jumps to another state.

The CTMC is then described by its *transition rate matrix* (or generator)

$$Q = \begin{bmatrix} A & \boldsymbol{a} \\ 0 & 0 \end{bmatrix},$$

where $A \in \mathbb{R}^{k \times k}$ is the transient-state block, with the diagonal entries are negative representing the total rate of leaving state i and the off-diagonal entries are nonnegative representing the rate of moving from transient state i to transient state j and $\boldsymbol{a} \in \mathbb{R}^{k \times 1}$ gives rates from transient states to the absorbing state. Because each row of a generator sums to zero, the rate vector to absorption is

$$\boldsymbol{a} = -A\mathbf{1},$$

where $\mathbf{1}$ is the column vector of ones. Let

$$\boldsymbol{\alpha} = (\alpha_1, \ldots, \alpha_k)^T$$

be the initial distribution over the transient states. Then α_i is the probability that the process starts in transient state i. Together, the pair

$$(\boldsymbol{\alpha}, A)$$

completely characterizes the phase-type distribution associated with the absorption time.

2.2 Phase-Type Distributions

Phase-type (PH) distributions arise as the distribution of the time to absorption in a finite-state continuous-time Markov chain. Let the infinitesimal generator be written as

$$\mathcal{Q} = \begin{pmatrix} A & -A\mathbf{1} \\ \mathbf{0} & 0 \end{pmatrix},$$

where $A \in \mathbb{R}^{m\times m}$ is the sub-generator matrix associated with the transient states, and $-A\mathbf{1}$ gives the transition rates to the absorbing state. Let $\boldsymbol{\alpha}$ denote the initial probability vector over the transient states. Then the absorption time Y follows a phase-type distribution, denoted by

$$Y \sim \mathrm{PH}(\boldsymbol{\alpha}, A).$$

The probability density function, cumulative distribution function, survival function, and moments of Y are given by

$$\begin{aligned} f(t) &= \boldsymbol{\alpha}^T e^{At}(-A\mathbf{1}), \\ F(t) &= 1 - \boldsymbol{\alpha}^T e^{At}\mathbf{1}, \\ S(t) &= \mathbb{P}(Y > t) = \boldsymbol{\alpha}^T e^{At}\mathbf{1}, \\ \mathbb{E}[Y^j] &= j!\,\boldsymbol{\alpha}^T(-A)^{-j}\mathbf{1}, \end{aligned}$$

for $t \geq 0$.

Several commonly used distributions arise as special cases of phase-type distributions. The exponential distribution corresponds to a single-phase model. An Erlang distribution is the sum of k independent exponential stages with a common rate. A hypoexponential distribution generalizes this by allowing distinct rates across stages. A hyper-Erlang distribution is a finite mixture of Erlang distributions, while a Coxian distribution corresponds to a sequential chain in which transitions may proceed to the next phase or directly to absorption.

2.3 Reproduction Number and Next Generation Matrix Method

The basic reproduction number, $\mathcal{R}_0$, is fundamentally defined as a threshold condition derived from the spectral radius of the next-generation operator. Mathematically, it represents the average number of secondary "entities" generated by a single individual throughout its entire residence time in a system.

The next generation matrix method is a classical tool in mathematical epidemiology for computing the basic reproduction number $\mathcal{R}_0$. Its main idea is to decompose the infected subsystem near the disease-free equilibrium (DFE) into two parts: $F(x)$, which represents the rate of appearance of new infections, and $V(x)$, which describes all other transitions such as transfer, recovery, and death. After linearization at the DFE, let F and V denote the corresponding Jacobian submatrices for the infected variables. Then the next generation matrix is defined by FV^{-1}, and its spectral radius

$$\mathcal{R}_0 = \rho(FV^{-1})$$

is the basic reproduction number.

Biologically, $\mathcal{R}_0$ represents the average number of secondary infections produced by a typical infected individual in a wholly susceptible population. The paper further proves that if $\mathcal{R}_0 < 1$, then the disease-free equilibrium is locally asymptotically stable, whereas if $\mathcal{R}_0 > 1$, it is unstable. Therefore, $\mathcal{R}_0$ serves as a threshold parameter that determines whether the disease can invade the

population. This method is especially useful for multi-compartment and heterogeneous population models because of its clear structure and broad applicability. However, its success depends on correctly distinguishing new infection terms from other transition terms; otherwise, one may still obtain a threshold quantity, but it may lose its proper epidemiological interpretation.

2.4 Generalized linear chain trick

The key idea underlying the linear chain trick (LCT) and the generalized linear chain trick (GLCT) is to represent nontrivial dwell-time distributions through state transitions in a Markovian framework.

Discrete-time Markov chains provide the basic intuition of movement among transient states toward an absorbing state, while continuous-time Markov chains additionally encode the random waiting time spent in each state. In particular, the absorption time of a continuous-time Markov chain with transient states and one absorbing state defines a phase-type distribution. This viewpoint allows a wide class of dwell-time distributions to be incorporated into compartmental ODE models, thereby extending the classical LCT to the more flexible GLCT framework.

Thus, the GLCT extends the classical LCT by allowing more general state-transition structures and hence more flexible dwell-time distributions. The classical LCT is associated with relatively simple chain structures, often leading to Erlang dwell times, whereas the GLCT naturally accommodates the broader class of phase-type distributions.

The Generalized Linear Chain Trick (GLCT) serves as a bridge between high-level mechanistic descriptions and tractable mathematical frameworks. Its primary advantage lies in its ability to incorporate non-exponential dwell times—such as those following Erlang or more general phase-type distributions—into a mean-field ODE system without losing analytical clarity. By partitioning a single biological state into a series of interconnected sub-states, the GLCT preserves the Markovian property while allowing for a more realistic representation of the variance and shape of residence times. This framework is particularly powerful for analyzing intervention strategies, as it provides a rigorous operator-based structure for deriving the basic reproduction number, $\mathcal{R}_0$, in systems with complex transition dynamics. The following theorem formalizes the mathematical foundation of this approach.

Theorem 2.1 (GLCT for Phase-Type Distributions, [2, 3, 4, 5],)**.** *Assume individuals enter a state (call it state X) at rate $\mathcal{I}(t) \in \mathbb{R}$ and that the distribution of time spent in state X follows a continuous phase-type distribution given by the length k initial probability vector $\boldsymbol{\alpha}$ and the $k \times k$ matrix $\mathbf{A}$. Then partitioning X into k sub-states X_i, and denoting the corresponding amount of individuals in state X_i at time t by $x_i(t)$, then the mean field equations for these sub-states x_i are given by*

$$\frac{d}{dt}\mathbf{x}(t) = \boldsymbol{\alpha}\mathcal{I}(t) + \mathbf{A}^T\mathbf{x}(t), \tag{1}$$

where the rate of individuals leaving each of these sub-states of X is given by the vector $(-\mathbf{A}\mathbf{1}) \circ \mathbf{x}$, where $\circ$ is the Hadamard (element-wise) product of the two vectors, and thus the total rate of individuals leaving state X is given by the sum of those terms, i.e., $(-\mathbf{A}\mathbf{1})^T\mathbf{x} = -\mathbf{1}^T\mathbf{A}^T\mathbf{x}$.

3 SEQIRS model

To begin with, consider the simple SEIQRS model, (2), $S(t)$ represents the number of susceptible individuals, $E(t)$ denotes those in the exposed (latent) period, $Q(t)$ represents individuals in quarantine, $I(t)$ is the infectious population, and $R(t)$ counts the recovered individuals with temporary

immunity. The dynamics are driven by several key parameters: Λ is the recruitment rate of new susceptibles, while β is the transmission rate governing the infection process. Individuals transition from the exposed to the infectious state at rate σ, or may be intercepted and moved to quarantine at rate δ_E. Infectious individuals can also be quarantined at rate δ_I. The parameters γ_I and γ_Q represent recovery rates from their respective classes, while ν_I and ν_Q account for disease-induced mortality. Finally, all individuals are subject to a natural mortality rate μ, and recovered individuals return to the susceptible pool at rate ω due to waning immunity. The SEIQRS model are

$$\frac{dS}{dt} = \Lambda(S, E, Q, I, R) - \beta SI - \mu S + \omega R, \tag{2a}$$
$$\frac{dE}{dt} = \beta SI - (\sigma + \delta_E + \mu)E, \tag{2b}$$
$$\frac{dI}{dt} = \sigma E - (\gamma_I + \delta_I + \mu + \nu_I)I, \tag{2c}$$
$$\frac{dQ}{dt} = \delta_E E + \delta_I I - (\gamma_Q + \mu + \nu_Q)Q, \tag{2d}$$
$$\frac{dR}{dt} = \gamma_I I + \gamma_Q Q - (\mu + \omega)R. \tag{2e}$$

For the SEQIRS model, the disease-free equilibrium is

$$E_0 = (S_0, 0, 0, 0, 0),$$

where S_0 satisfies

$$\Lambda(S_0, 0, 0, 0, 0) - \mu S_0 = 0.$$

Using the Next-Generation Matrix method, the basic reproduction number is

$$\mathcal{R}_0 = \frac{\beta S_0 \sigma}{(\sigma + \delta_E + \mu)(\gamma_I + \delta_I + \mu + \nu_I)}.$$

Equations for the resulting SEIQRS model with Erlang-distributed latent, infectious, and quarantine periods are

$$\frac{dS}{dt} = \Lambda - \beta SI - \mu S + \omega R, \tag{3a}$$
$$\frac{dE_1}{dt} = \beta SI - \left(\frac{k_E}{\tau_E} + \mu + \delta_E\right) E_1, \tag{3b}$$
$$\frac{dE_j}{dt} = \frac{k_E}{\tau_E} E_{j-1} - \left(\frac{k_E}{\tau_E} + \mu + \delta_E\right) E_j, \quad j = 2, \ldots, k_E \tag{3c}$$
$$\frac{dI_1}{dt} = \frac{k_E}{\tau_E} E_{k_E} - \left(\frac{k_I}{\tau_I} + \mu + \delta_I + \nu_I\right) I_1, \tag{3d}$$
$$\frac{dI_i}{dt} = \frac{k_I}{\tau_I} I_{i-1} - \left(\frac{k_I}{\tau_I} + \mu + \delta_I + \nu_I\right) I_i, \quad i = 2, \ldots, k_I \tag{3e}$$
$$\frac{dQ_1}{dt} = \delta_E E + \delta_I I - \left(\frac{k_Q}{\tau_Q} + \mu + \nu_Q\right) Q_1, \tag{3f}$$
$$\frac{dQ_m}{dt} = \frac{k_Q}{\tau_Q} Q_{m-1} - \left(\frac{k_Q}{\tau_Q} + \mu + \nu_Q\right) Q_m, \quad m = 2, \ldots, k_Q \tag{3g}$$
$$\frac{dR}{dt} = \frac{k_I}{\tau_I} I_{k_I} + \frac{k_Q}{\tau_Q} Q_{k_Q} - (\mu + \omega)R. \tag{3h}$$

Consider the SEIQRS model by equations (3), which allows more flexibility than a standard SEIQRS. We apply the GLCT to generalize this model. The mean field ODEs for generalized SEIRS model are

$$\frac{dS}{dt} = \Lambda - \mu S - \lambda(t)S + \underbrace{(-\mathbf{1}^T {\mathbf{A_R}}^T \mathbf{z})}_{\text{scalar}}, \tag{4a}$$

$$\frac{d\mathbf{x}}{dt} = \boldsymbol{\alpha}_E \lambda(t) S + {\mathbf{A_E}}^T \mathbf{x} - \delta_E \mathbf{x} - \mu \mathbf{x}, \tag{4b}$$

$$\frac{d\mathbf{y}}{dt} = \boldsymbol{\alpha}_I \underbrace{(-\mathbf{1}^T {\mathbf{A_E}}^T \mathbf{x})}_{\text{scalars}} + {\mathbf{A_I}}^T \mathbf{y} - \delta_I \mathbf{y} - \mu \mathbf{y}, \tag{4c}$$

$$\frac{d\mathbf{q}}{dt} = \boldsymbol{\alpha}_Q \underbrace{(\delta_E \mathbf{1}^T \mathbf{x} + \delta_I \mathbf{1}^T \mathbf{y})}_{\text{scalars}} + {\mathbf{A_Q}}^T \mathbf{q} - \mu \mathbf{q}, \tag{4d}$$

$$\frac{d\mathbf{z}}{dt} = \boldsymbol{\alpha}_R \underbrace{(-\mathbf{1}^T {\mathbf{A_I}}^T \mathbf{y} + -\mathbf{1}^T {\mathbf{A_Q}}^T \mathbf{q})}_{\text{scalars}} + {\mathbf{A_R}}^T \mathbf{z} - \mu \mathbf{z}. \tag{4e}$$

The total population is partitioned into five primary compartments: susceptible (S), exposed (E), infectious (I), quarantine (Q), and recovered (R). Following the GLCT the sub-states and transition dynamics, we define the following column vectors representing the sub-states for each class:

- $\mathbf{x} = [E_1, \ldots, E_{k_E}]^T \in \mathbb{R}^{k_E}$: Sub-states of the **latent (exposed)** period.
- $\mathbf{y} = [I_1, \ldots, I_{k_I}]^T \in \mathbb{R}^{k_I}$: Sub-states of the **infectious** period.
- $\mathbf{q} = [Q_1, \ldots, Q_{k_Q}]^T \in \mathbb{R}^{k_Q}$: Sub-states of the **quarantine** period.
- $\mathbf{z} = [R_1, \ldots, R_{k_R}]^T \in \mathbb{R}^{k_R}$: Sub-states of the **recovered (immune)** period.

The total population in each major compartment is given by the sum of its sub-states: $E = \mathbf{1}^T \mathbf{x}$, $I = \mathbf{1}^T \mathbf{y}$, $Q = \mathbf{1}^T \mathbf{q}$, and $R = \mathbf{1}^T \mathbf{z}$, where $\mathbf{1}$ is a column vector of ones of appropriate length. Each transition process follows a continuous phase-type distribution characterized by

- **Initial Probability Vectors**: $\boldsymbol{\alpha}_E, \boldsymbol{\alpha}_I, \boldsymbol{\alpha}_Q, \boldsymbol{\alpha}_R$ (row vectors) determine the entry distribution into the sub-states. For a standard sequential flow, $\boldsymbol{\alpha} = [1, 0, \ldots, 0]$.
- **Transition Matrices**: $\mathbf{A}_E, \mathbf{A}_I, \mathbf{A}_Q, \mathbf{A}_R$ are $k \times k$ transient generator matrices. For an Erlang distribution with mean duration τ, the matrix $\mathbf{A}$ is bidiagonal with entries $-k/\tau$ on the main diagonal and k/τ on the sub-diagonal.

where $\lambda(t) = \boldsymbol{\beta}^T \mathbf{y}$ is the force of infection, $\beta = [\beta_1, \cdots, \beta_{k_I}]$, and δ_E, δ_I are the quarantine interception rates. The terms labeled as *scalars* represent the aggregate flux exiting one compartment to enter the next.

Based on (4), we can rewrite (3), where

$$\mathbf{x} = \begin{bmatrix} E_1 & \cdots & E_{k_E} \end{bmatrix}^T, \quad \mathbf{y} = \begin{bmatrix} I_1 & \cdots & I_{k_I} \end{bmatrix}^T, \quad \mathbf{q} = \begin{bmatrix} Q_1 & \cdots & Q_{k_Q} \end{bmatrix}^T, \quad \mathbf{z} = [R].$$

Note that in this model, the recovered class R is treated as a single state (scalar) since immunity waning is assumed to follow an exponential distribution. For the Erlang-distributed stages, the

transition matrices $\mathbf{A}_k$ (where $k \in \{E, I, Q\}$) take a bidiagonal form. For example, for the latent period with mean duration τ_E and k_E stages is

$$\mathbf{A}_E = \begin{bmatrix} -\frac{k_E}{\tau_E} & \frac{k_E}{\tau_E} & 0 & \dots & 0 \\ 0 & -\frac{k_E}{\tau_E} & \frac{k_E}{\tau_E} & \dots & 0 \\ \vdots & \vdots & \ddots & \ddots & \vdots \\ 0 & 0 & \dots & 0 & -\frac{k_E}{\tau_E} \end{bmatrix}_{k_E \times k_E}.$$

The matrices $\mathbf{A}_I$ and $\mathbf{A}_Q$ are structured analogously using their respective parameters (k_I, τ_I) and (k_Q, τ_Q). Since all individuals enter the first sub-stage of each compartment upon transition, the initial distribution vectors are defined as

$$\boldsymbol{\alpha}_E = [1, 0, \dots, 0]^T, \quad \boldsymbol{\alpha}_I = [1, 0, \dots, 0]^T, \quad \boldsymbol{\alpha}_Q = [1, 0, \dots, 0]^T.$$

For the force of infection, we have that $\lambda(t) = \boldsymbol{\beta}^T \mathbf{y}$ and $\boldsymbol{\beta} = [\beta, \cdots, \beta]$.

4 The Reproduction Numbers for Generalized SEQIRS Model

We assume that the general birth rate Λ.

Theorem 4.1. *The disease-free equilibrium (DFE) of the generalized SEQIRS model is locally asymptotically stable if $\mathcal{R}_0 < 1$, and unstable if $\mathcal{R}_0 > 1$. The basic reproduction number $\mathcal{R}_0$ is given by the product:*

$$\mathcal{R}_0 = \mathcal{R}_{0,new} \cdot \mathcal{P}_{E \to I},$$

where

1. *$\mathcal{R}_{0,new}$ is the expected number of new infections created by a single infectious individual over the duration of their infectious period, accounting for natural recovery, mortality, and active quarantine:*

   $$\mathcal{R}_{0,new} = \boldsymbol{\alpha}_I^T (-\mathbf{G}_I^{-1})(\boldsymbol{\beta} S_0),$$

   where $\mathbf{G}_I = \mathbf{A}_I - (\mu + \delta_I + \nu_I)\mathbf{I}_{k_I \times k_I}$ is the transition-loss matrix for the infectious class.

2. *$\mathcal{P}_{E \to I}$ is the probability of surviving the latent state (E)—avoiding natural death and pre-symptomatic quarantine—and successfully transitioning into the infectious state (I):*

   $$\mathcal{P}_{E \to I} = \boldsymbol{\alpha}_E \cdot ((-\mathbf{G}_E^{-1})(-\mathbf{A}_E \mathbf{1}_{k_E})).$$

   where $\mathbf{G}_E = \mathbf{A}_E - (\mu + \delta_E)\mathbf{I}_{k_E \times k_E}$ is the transition-loss matrix for the exposed class, and $\mathbf{1}_{k_E}$ is a column vector of ones.

It is assumed that the matrices $\mathbf{G}_E$ and $\mathbf{G}_I$ are invertible.

Proof. The right handside of eqs. (4) can be written as follows, yielding $\mathcal{F}$ and $\mathcal{V} = \mathcal{V}^- - \mathcal{V}^+$ which satisfiy the requirements of Theorem 2 in [8]

$$\begin{pmatrix} \dot{\mathbf{x}} \\ \dot{\mathbf{y}} \\ \dot{\mathbf{q}} \\ \dot{\mathbf{z}} \\ \dot{S} \end{pmatrix} = \underbrace{\begin{pmatrix} \boldsymbol{\alpha}_E \lambda(t) S \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ 0 \end{pmatrix}}_{\mathcal{F}} - \underbrace{\begin{pmatrix} \left[(\mu + \delta_E)\mathbf{I} - \mathbf{D}_{\mathrm{diag}(\mathbf{A}_E)}\right] \mathbf{x} \\ \left[(\mu + \delta_I + \nu_I)\mathbf{I} - \mathbf{D}_{\mathrm{diag}(\mathbf{A}_I)}\right] \mathbf{y} \\ \left[(\mu + \nu_Q)\mathbf{I} - \mathbf{D}_{\mathrm{diag}(\mathbf{A}_Q)}\right] \mathbf{q} \\ \left[\mu \mathbf{I} - \mathbf{D}_{\mathrm{diag}(\mathbf{A}_R)}\right] \mathbf{z} \\ (\lambda(t) + \mu) S \end{pmatrix}}_{\mathcal{V}^-} + \underbrace{\begin{pmatrix} (\mathbf{A}_E - \mathbf{D}_{\mathrm{diag}(\mathbf{A}_E)})^T \mathbf{x} \\ \boldsymbol{\alpha}_I (-\mathbf{1}^T \mathbf{A}_E^T \mathbf{x}) + (\mathbf{A}_I - \mathbf{D}_{\mathrm{diag}(\mathbf{A}_I)})^T \mathbf{y} \\ \boldsymbol{\alpha}_Q (\delta_E \mathbf{1}^T \mathbf{x} + \delta_I \mathbf{1}^T \mathbf{y}) + (\mathbf{A}_Q - \mathbf{D}_{\mathrm{diag}(\mathbf{A}_Q)})^T \mathbf{q} \\ \boldsymbol{\alpha}_R (-\mathbf{1}^T \mathbf{A}_I^T \mathbf{y} - \mathbf{1}^T \mathbf{A}_Q^T \mathbf{q}) + (\mathbf{A}_R - \mathbf{D}_{\mathrm{diag}(\mathbf{A}_R)})^T \mathbf{z} \\ \Lambda + \omega (-\mathbf{1}^T \mathbf{A}_R^T \mathbf{z}) \end{pmatrix}}_{\mathcal{V}^+}.$$

Consider the infected subsystems $\mathbf{x}$ and $\mathbf{y}$. The linearized matrices at the DFE are:

$$F = \begin{bmatrix} 0_{k_E \times k_E} & \boldsymbol{\alpha}_E \boldsymbol{\beta}^T S_0 \\ 0_{k_I \times k_E} & 0_{k_I \times k_I} \end{bmatrix} = \begin{bmatrix} 0 & \boldsymbol{\alpha}_E \boldsymbol{\beta}^T \\ 0 & 0 \end{bmatrix} S_0,$$

$$V = \begin{bmatrix} (\mu + \delta_E)\mathbf{I} - A_E & 0 \\ \alpha_I \mathbf{1}_{k_E}^T \mathbf{A}_E^T & (\mu + \delta_I + \nu_I)\mathbf{I} - A_I^T \end{bmatrix} = \begin{bmatrix} -\mathbf{G}_E^T & 0 \\ \boldsymbol{\alpha}_I \mathbf{1}_{k_E}^T \mathbf{A}_E^T & -\mathbf{G}_I^T \end{bmatrix}.$$

The basic reproduction number is $\mathcal{R}_0 = \rho(FV^{-1})$.

First, we compute V^{-1}. Since V is lower block-triangular, its inverse is

$$V^{-1} = \begin{pmatrix} (-G_E^T)^{-1} & 0 \\ (-G_I^T)^{-1}\, \alpha_I \mathbf{1}_{k_E}^T A_E^T\, (-G_E^T)^{-1} & (-G_I^T)^{-1} \end{pmatrix}.$$

Then

$$FV^{-1} = \begin{pmatrix} \alpha_E \beta^T S_0\, (-G_I^T)^{-1} \alpha_I \mathbf{1}_{k_E}^T A_E^T (-G_E^T)^{-1} & \alpha_E \beta^T S_0\, (-G_I^T)^{-1} \\ 0 & 0 \end{pmatrix}.$$

Since FV^{-1} has rank at most 1 (every row is a scalar multiple of the same row vector), its only nonzero eigenvalue equals its trace:

$$R_0 = \rho(FV^{-1}) = \operatorname{tr}(FV^{-1}) = \underbrace{\alpha_I^T(-G_I^{-1})\beta S_0}_{R_{0,\text{new}}} \cdot \underbrace{\alpha_E^T(-G_E^{-1})(-A_E \mathbf{1}_{k_E})}_{P_{E\to I}}.$$

This completes the proof. □

From the decomposition

$$\mathcal{R}_0 = \mathcal{R}_{0,\text{new}} \cdot \mathcal{P}_{E\to I},$$

it follows that the basic reproduction number is determined by two interacting mechanisms: the expected number of secondary infections generated by a single infectious individual during the infectious period, and the probability that an exposed individual survives the latent stage and successfully progresses into the infectious class. More precisely,

$$\mathcal{R}_{0,\text{new}} = \boldsymbol{\alpha}_I^T(-\mathbf{G}_I^{-1})(\boldsymbol{\beta} S_0)$$

measures the average infection-producing capacity of one infectious individual. Hence, $\mathcal{R}_{0,\text{new}}$ increases with the transmission rate $\boldsymbol{\beta}$ and the disease-free susceptible level S_0. In contrast, larger recovery, mortality, or quarantine/removal effects in the infectious class reduce the average time spent in the infectious state, thereby decreasing the cumulative infectious contribution encoded in $(-\mathbf{G}_I^{-1})$, and hence reducing $\mathcal{R}_{0,\text{new}}$. On the other hand,

$$\mathcal{P}_{E\to I} = \boldsymbol{\alpha}_E\big((-\mathbf{G}_E^{-1})(-\mathbf{A}_E \mathbf{1}_{k_E})\big)$$

represents the probability that an exposed individual avoids removal during the latent phase and eventually reaches the infectious class. Therefore, parameters that accelerate progression through the exposed compartments increase $\mathcal{P}_{E\to I}$, while larger natural death or pre-infectious removal/quarantine rates decrease it by increasing the chance that individuals leave the exposed class before becoming infectious. Overall, any factor that enhances transmission, prolongs infectiousness, or increases the probability of successful progression from exposure to infectiousness will increase $\mathcal{R}_0$, whereas any factor that reduces effective contact, shortens the infectious period, or increases removal in either the exposed or infectious stages will decrease $\mathcal{R}_0$. This decomposition thus provides a clear epidemiological interpretation of how the model parameters jointly determine whether the disease can invade the population.

5 SEIR-SEI Model

5.1 Vector-Borne Disease Transmission

We consider generalize the SEIR-SEI model discussed in [1], and we suppose that the probability of transmission of infection from an infectious mosquito to a susceptible mosquito is 0.

The transmission dynamics between a host population and a biological vector are described by a coupled system of ordinary differential equations (ODEs). This framework partitions the human (host) population into Susceptible (S_h), Exposed (E_h), Infectious (I_h), and Recovered (R_h) classes, while the mosquito (vector) population follows a Susceptible-Exposed-Infectious (S_v, E_v, I_v) structure.

To account for resource competition and environmental constraints, the per capita death rates are defined as linear functions of the population size,

$$f_h(N_h) = \mu_{1h} + \mu_{2h}N_h, \quad f_v(N_v) = \mu_{1v} + \mu_{2v}.$$

The transmission logic assumes a frequency-dependent interaction regulated by the availability of both hosts and vectors,

$$\lambda_h(t) = \left(\frac{\sigma_v N_v \sigma_h}{\sigma_v N_v + \sigma_h N_h}\right)\beta_{hv}\frac{I_v}{N_v},$$
$$\lambda_v(t) = \left(\frac{\sigma_v \sigma_h N_h}{\sigma_v N_v + \sigma_h N_h}\right)\beta_{vh}\frac{I_h}{N_h}.$$

For host (human) population dynamics,

$$\frac{dS_h}{dt} = \Lambda_h + \psi_h N_h + \rho_h R_h - \lambda_h(t)S_h - f_h(N_h)S_h, \tag{5a}$$
$$\frac{dE_h}{dt} = \lambda_h(t)S_h - \nu_h E_h - f_h(N_h)E_h, \tag{5b}$$
$$\frac{dI_h}{dt} = \nu_h E_h - (\gamma_h + \delta_h + f_h(N_h))I_h, \tag{5c}$$
$$\frac{dR_h}{dt} = \gamma_h I_h - (\rho_h + f_h(N_h))R_h, \tag{5d}$$

where $N_h = S_h + E_h + I_h + R_h$ represents the total host population size.

For vector (mosquito) population dynamics, we have that

$$\frac{dS_v}{dt} = \psi_v N_v - \lambda_v(t)S_v - f_v(N_v)S_v, \tag{6a}$$
$$\frac{dE_v}{dt} = \lambda_v(t)S_v - \nu_v E_v - f_v(N_v)E_v, \tag{6b}$$
$$\frac{dI_v}{dt} = \nu_v E_v - f_v(N_v)I_v. \tag{6c}$$

where $N_v = S_v + E_v + I_v$ represents the total vector population size.

The long-term behavior of the disease is determined by the equilibrium points of the system. In the absence of infection, the population reaches a Disease-Free Equilibrium (DFE), denoted by $x_{dfe} = (N_h^*, 0, 0, 0, N_v^*, 0, 0)$.

Table 1: Generalized Parameters for the Vector-Host Model

Parameter	Description
Λ_h	Host immigration rate
ψ_h, ψ_v	Per capita birth rate (Host, Vector)
σ_v	Desired vector biting rate per unit time
σ_h	Maximum biting tolerance of the host
β_{hv}	Transmission probability (Vector $\rightarrow$ Host)
β_{vh}	Transmission probability (Host $\rightarrow$ Vector)
ν_h, ν_v	Progression rate from latent to infectious state
γ_h	Host recovery rate
δ_h	Disease-induced mortality rate for hosts
ρ_h	Rate of loss of immunity in hosts
μ_{1h}, μ_{1v}	Density-independent death rate
μ_{2h}, μ_{2v}	Density-dependent death rate

The steady-state population sizes in the absence of disease (N_h^* and N_v^*) are calculated directly from the demographic parameters of equations (5 and 6) as follows:

$$N_h^* = \frac{(\psi_h - \mu_{1h}) + \sqrt{(\psi_h - \mu_{1h})^2 + 4\mu_{2h}\Lambda_h}}{2\mu_{2h}},$$
$$N_v^* = \frac{\psi_v - \mu_{1v}}{\mu_{2v}}.$$

The expected number of secondary host infections caused by a single infectious vector is given by:

$$K_{hv} = \left(\frac{\nu_v}{\nu_v + f_v(N_v^*)}\right) \cdot \left(\frac{\sigma_v \sigma_h N_h^*}{\sigma_v N_v^* + \sigma_h N_h^*}\right) \beta_{hv} \cdot \left(\frac{1}{f_v(N_v^*)}\right).$$

and also, we called it as Vector-to-Host Transmission Potential (K_{hv}).

The expected number of secondary vector infections caused by a single infectious host (including contributions from the infectious and recovered stages) is:

$$K_{vh} = \left(\frac{\nu_h}{\nu_h + f_h(N_h^*)}\right) \cdot \left(\frac{\sigma_v \sigma_h N_v^*}{\sigma_v N_v^* + \sigma_h N_h^*}\right) \cdot \frac{1}{\gamma_h + \delta_h + f_h(N_h^*)} \cdot \beta_{vh}.$$

and also, we called it Host-to-Vector Transmission Potential (K_{vh}).

To evaluate $\mathcal{R}_0$ numerically using the original population (5 and 6), the total per capita mortality rates at equilibrium are defined by the density-dependent functions:

$$f_h(N_h^*) = \mu_{1h} + \mu_{2h} N_h^*, \quad f_v(N_v^*) = \mu_{1v} + \mu_{2v} N_v^*.$$

The basic reproduction number, $\mathcal{R}_0$, is derived using the next-generation matrix method. For this vector-host system, $\mathcal{R}_0$ is defined as the geometric mean of the transmission potential from vector to host (K_{hv}) and host to vector (K_{vh}):

$$\mathcal{R}_0 = \sqrt{K_{vh} K_{hv}}.$$

5.2 The Generalized SEIR-SEI Model

The SEIR-SEI model is a Ross-Macdonald type model [7], formulated to illustrate the inter-species transmission dynamics within an epidemic context. Although the classic compartmental model provides a foundational understanding of transmission dynamics, its reliance on the exponential distribution for stage residence times, like [6]—characterized by a constant per capita exit rate—often fails to capture the biological realities of pathogen development. To address this, we employ the Generalized Linear Chain Trick (GLCT) to refine the Exposed (E, including E_h and E_v), Infectious (I, including I_h and I_v), and Recovered (R, including I_h) compartments. By partitioning each state into a sequence of k sub-stages, the residence time distribution is transformed from a memoryless exponential process into a more realistic Phase-type distribution. This refinement allows for a more precise representation of the latent and infectious periods, particularly in the mosquito vector where the extrinsic incubation period is a critical determinant of the basic reproduction number $\mathcal{R}_0$.

The dynamics of the host (human) and vector (mosquito) populations are governed by the following system of equations.

We divide the host latent period into m stages, the infectious period into n stages, and the recovered period into q stages

$$\frac{dS_h}{dt} = \Lambda_h + \psi_h N_h + \rho'_h R_{h,q} - \lambda_h(t) S_h - f_h(N_h) S_h, \tag{7a}$$

$$\frac{dE_{h,1}}{dt} = \lambda_h(t) S_h - (\nu'_h + f_h(N_h)) E_{h,1}, \tag{7b}$$

$$\frac{dE_{h,i}}{dt} = \nu'_h E_{h,i-1} - (\nu'_h + f_h(N_h)) E_{h,i}, \quad i = 2, \ldots, m \tag{7c}$$

$$\frac{dI_{h,1}}{dt} = \nu'_h E_{h,m} - (\gamma'_h + \delta_h + f_h(N_h)) I_{h,1}, \tag{7d}$$

$$\frac{dI_{h,j}}{dt} = \gamma'_h I_{h,j-1} - (\gamma'_h + \delta_h + f_h(N_h)) I_{h,j}, \quad j = 2, \ldots, n \tag{7e}$$

$$\frac{dR_{h,1}}{dt} = \gamma'_h I_{h,n} - (\rho'_h + f_h(N_h)) R_{h,1}, \tag{7f}$$

$$\frac{dR_{h,k}}{dt} = \rho'_h R_{h,k-1} - (\rho'_h + f_h(N_h)) R_{h,k}. \quad k = 2, \ldots, q \tag{7g}$$

We divide the vector latent period into p stages, the infectious period into w stages,

$$\frac{dS_v}{dt} = \psi_v N_v - \lambda_v(t) S_v - f_v(N_v) S_v, \tag{8a}$$

$$\frac{dE_{v,1}}{dt} = \lambda_v(t) S_v - (\nu_v' + f_v(N_v)) E_{v,1}, \tag{8b}$$

$$\frac{dE_{v,u}}{dt} = \nu_v' E_{v,u-1} - (\nu_v' + f_v(N_v)) E_{v,u}, \quad u = 2, \ldots, p \tag{8c}$$

$$\frac{dI_{v,1}}{dt} = \nu_v' E_{v,p} - (\mu_v' + f_v(N_v)) I_{v,1}, \tag{8d}$$

$$\frac{dI_{v,v}}{dt} = \mu_v' I_{v,v-1} - (\mu_v' + f_v(N_v)) I_{v,v}, \quad v = 2, \ldots, w \tag{8e}$$

where

$$N_h = S_h + \sum_{i=1}^{m} E_{h,i} + \sum_{j=1}^{n} I_{h,j} + \sum_{k=1}^{q} R_{h,k},$$

$$N_v = S_v + \sum_{u=1}^{p} E_{v,u} + \sum_{v=1}^{w} I_{v,v}.$$

For

$$\nu_h' = \frac{m}{\tau_{E_h}},\ \gamma_h' = \frac{n}{\tau_{I_h}},\ \rho_h' = \frac{q}{\tau_{R_h}},\ \nu_v' = \frac{p}{\tau_{E_v}},\ \mu_v' = \frac{w}{\tau_{I_v}},$$

these five parameters represent the transition rates between sub-compartments within each disease state, defined as the ratio of the number of stages to the mean sojourn time to ensure the durations follow an Erlang distribution.

The infection rates $\lambda_h(t)$ and $\lambda_v(t)$ account for the biting preference and the saturation of the vector-host ratio:

$$\lambda_h(t) = \left(\frac{\sigma_v \sigma_h}{\sigma_v N_v + \sigma_h N_h} \right) \beta_{hv} \sum_{v=1}^{w} I_{v,v},$$

$$\lambda_v(t) = \left(\frac{\sigma_v \sigma_h}{\sigma_v N_v + \sigma_h N_h} \right) \beta_{vh} \sum_{j=1}^{n} I_{h,j}.$$

The density-dependent death functions for both species are:

$$f_h(N_h) = \mu_{1h} + \mu_{2h} N_h, \quad f_v(N_v) = \mu_{1v} + \mu_{2v} N_v.$$

We apply the GLCT to generalize this model,

$$\frac{dS_h}{dt} = \Lambda_h + \psi_h N_h - \lambda_h(t) S_h - f_h S_h + (-\mathbf{1}^T \mathbf{A}_R^T \mathbf{z}), \tag{9a}$$

$$\frac{d\mathbf{x}}{dt} = \boldsymbol{\alpha}_E \lambda_h(t) S_h + \mathbf{A}_E^T \mathbf{x} - f_h \mathbf{x}, \tag{9b}$$

$$\frac{d\mathbf{y}}{dt} = \boldsymbol{\alpha}_I (-\mathbf{1}^T \mathbf{A}_E^T \mathbf{x}) + \mathbf{A}_I^T \mathbf{y} - (\delta_h + f_h) \mathbf{y}, \tag{9c}$$

$$\frac{d\mathbf{z}}{dt} = \boldsymbol{\alpha}_R (-\mathbf{1}^T \mathbf{A}_I^T \mathbf{y}) + \mathbf{A}_R^T \mathbf{z} - f_h \mathbf{z}. \tag{9d}$$

$$\frac{dS_v}{dt} = \psi_v N_v - \lambda_v(t) S_v - f_v S_v, \tag{10a}$$

$$\frac{d\mathbf{u}}{dt} = \boldsymbol{\alpha}_u \lambda_v(t) S_v + \mathbf{A}_u^T \mathbf{u} - f_v \mathbf{u}, \tag{10b}$$

$$\frac{d\mathbf{v}}{dt} = \boldsymbol{\alpha}_v (-\mathbf{1}^T \mathbf{A}_u^T \mathbf{u}) + \mathbf{A}_v^T \mathbf{v} - f_v \mathbf{v}, \tag{10c}$$

where

- $\mathbf{x} = [E_{h,1}, \ldots, E_{h,m}]^T \in \mathbb{R}^m$: Sub-states of the host **latent (exposed)** period.
- $\mathbf{y} = [I_{h,1}, \ldots, I_{h,n}]^T \in \mathbb{R}^n$: Sub-states of the host **infectious** period.
- $\mathbf{z} = [R_{h,1}, \ldots, R_{h,q}]^T \in \mathbb{R}^q$: Sub-states of the host **recovered (immune)** period.
- $\mathbf{u} = [E_{v,1}, \ldots, E_{v,p}]^T \in \mathbb{R}^p$: Sub-states of the vector **latent (exposed)** period.
- $\mathbf{v} = [I_{v,1}, \ldots, I_{v,w}]^T \in \mathbb{R}^w$: Sub-states of the vector **infectious** period.

The total population in each major compartment is given by the sum of its sub-states: $E_h = \mathbf{1}^T\mathbf{x}$, $I_h = \mathbf{1}^T\mathbf{y}$, $R_h = \mathbf{1}^T\mathbf{z}$, $E_v = \mathbf{1}^T\mathbf{u}$, and $I_v = \mathbf{1}^T\mathbf{v}$, where $\mathbf{1}$ is a column vector of ones of appropriate length. Each transition process follows a continuous phase-type distribution characterized by

- **Initial Probability Vectors:** $\boldsymbol{\alpha}_E, \boldsymbol{\alpha}_I, \boldsymbol{\alpha}_R, \boldsymbol{\alpha}_u, \boldsymbol{\alpha}_v$ determine the entry distribution into the sub-states.
- **Transition Matrices:** $\mathbf{A}_E, \mathbf{A}_I, \mathbf{A}_R, \mathbf{A}_u, \mathbf{A}_v$ are transient generator matrices.

For the Generalized SEIR-SEI model under Erlang-distributed, we have that

$$\mathbf{A}_E = \begin{bmatrix} -\nu_h' & \nu_h' & 0 & \ldots & 0 \\ 0 & -\nu_h' & \nu_h' & \ldots & 0 \\ \vdots & \vdots & \ddots & \ddots & \vdots \\ 0 & 0 & \ldots & 0 & -\nu_h' \end{bmatrix}_{m \times m}, \quad \boldsymbol{\alpha}_E = [1, 0, \ldots, 0]^T,$$

$$\mathbf{A}_I = \begin{bmatrix} -\gamma_h' & \gamma_h' & 0 & \ldots & 0 \\ 0 & -\gamma_h' & \gamma_h' & \ldots & 0 \\ \vdots & \vdots & \ddots & \ddots & \vdots \\ 0 & 0 & \ldots & 0 & -\gamma_h' \end{bmatrix}_{n \times n}, \quad \boldsymbol{\alpha}_I = [1, 0, \ldots, 0]^T,$$

$$\mathbf{A}_R = \begin{bmatrix} -\rho_h' & \rho_h' & 0 & \ldots & 0 \\ 0 & -\rho_h' & \rho_h' & \ldots & 0 \\ \vdots & \vdots & \ddots & \ddots & \vdots \\ 0 & 0 & \ldots & 0 & -\rho_h' \end{bmatrix}_{q \times q}, \quad \boldsymbol{\alpha}_R = [1, 0, \ldots, 0]^T,$$

$$\mathbf{A}_u = \begin{bmatrix} -\nu_v' & \nu_v' & 0 & \ldots & 0 \\ 0 & -\nu_v' & \nu_v' & \ldots & 0 \\ \vdots & \vdots & \ddots & \ddots & \vdots \\ 0 & 0 & \ldots & 0 & -\nu_v' \end{bmatrix}_{p \times p}, \quad \boldsymbol{\alpha}_u = [1, 0, \ldots, 0]^T.$$

$$\mathbf{A}_v = \begin{bmatrix} -\mu'_v & \mu'_v & 0 & \dots & 0 \\ 0 & -\mu'_v & \mu'_v & \dots & 0 \\ \vdots & \vdots & \ddots & \ddots & \vdots \\ 0 & 0 & \dots & 0 & -\mu'_v \end{bmatrix}_{w\times w}, \quad \boldsymbol{\alpha}_v = [1, 0, \dots, 0]^T.$$

6 The Reproduction Number for Generalized SEIR-SEI model

The infected sub-states are ordered as $\Psi = [\mathbf{x}^T, \mathbf{y}^T, \mathbf{u}^T, \mathbf{v}^T]^T$.

The matrices F and V at the DFE are

$$F = \begin{bmatrix} \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{F}_{hv} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ 0 & \mathbf{F}_{vh} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix}, \quad V = \begin{bmatrix} \mathbf{V}_x & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{V}_{yx} & \mathbf{V}_y & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{V}_u & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{V}_{vu} & \mathbf{V}_v \end{bmatrix}.$$

The non-zero blocks of F are defined at the disease-free equilibrium (DFE) as

$$\mathbf{F}_{hv} = \boldsymbol{\alpha}_E \left[\mathcal{B}(N_h^*, N_v^*)\beta_{hv} N_h^*\right] \mathbf{1}_w^T$$
$$\mathbf{F}_{vh} = \boldsymbol{\alpha}_u \left[\mathcal{B}(N_h^*, N_v^*)\beta_{vh} N_v^*\right] \mathbf{1}_n^T$$

where $\boldsymbol{\alpha}_E$ and $\boldsymbol{\alpha}_u$ are the entry distribution vectors into the latent stages for hosts and vectors, respectively, and $\mathbf{1}^T$ are the row vectors of ones used for summation over the infectious sub-stages. The term $\mathcal{B}(N_h^*, N_v^*) = \frac{\sigma_h \sigma_v}{\sigma_v N_v^* + \sigma_h N_h^*}$ denotes the saturation biting rate per mosquito at the disease-free equilibrium. It accounts for the availability of hosts and the feeding capacity of the vectors, ensuring a biologically realistic transition between host-limited and vector-limited transmission regimes.

The individual operators for the transfer matrix $\mathcal{V}$ are defined as follows

- **Host Latent:** $\mathbf{V}_x = f_h \mathbf{I} - \mathbf{A}_E^T$
- **Host Latent to Infectious:** $\mathbf{V}_{yx} = -\boldsymbol{\alpha}_I(-\mathbf{1}^T \mathbf{A}_E^T)$
- **Host Infectious:** $\mathbf{V}_y = (\delta_h + f_h)\mathbf{I} - \mathbf{A}_I^T$
- **Vector Latent:** $\mathbf{V}_u = f_v \mathbf{I} - \mathbf{A}_u^T$
- **Vector Latent to Infectious:** $\mathbf{V}_{vu} = -\boldsymbol{\alpha}_v(-\mathbf{1}^T \mathbf{A}_u^T)$
- **Vector Infectious:** $\mathbf{V}_v = f_v \mathbf{I} - \mathbf{A}_v^T$

The basic reproduction number R_0 is defined as the spectral radius of the next generation matrix $G = FV^{-1}$. By computation, we have

$$\mathcal{V}^{-1} = \begin{bmatrix} \mathbf{V}_x^{-1} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{V}_y^{-1}\mathbf{V}_{yx}\mathbf{V}_x^{-1} & \mathbf{V}_y^{-1} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{V}_u^{-1} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{V}_v^{-1}\mathbf{V}_{vu}\mathbf{V}_u^{-1} & \mathbf{V}_v^{-1} \end{bmatrix}.$$

The next generation matrix $G = \mathcal{F}\mathcal{V}^{-1}$ is calculated by block multiplication as follows

$$G = \begin{bmatrix} \mathbf{0} & \mathbf{0} & \mathbf{G}_{13} & \mathbf{G}_{14} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{G}_{31} & \mathbf{G}_{32} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix},$$

where

$$\begin{aligned} \mathbf{G}_{13} &= \mathbf{F}_{hv}\mathbf{V}_v^{-1}\mathbf{V}_{vu}\mathbf{V}_u^{-1}, \\ \mathbf{G}_{14} &= \mathbf{F}_{hv}\mathbf{V}_v^{-1}, \\ \mathbf{G}_{31} &= \mathbf{F}_{vh}\mathbf{V}_y^{-1}\mathbf{V}_{yx}\mathbf{V}_x^{-1}, \\ \mathbf{G}_{32} &= \mathbf{F}_{vh}\mathbf{V}_y^{-1}. \end{aligned}$$

To derive the analytical expression for the basic reproduction number R_0, we calculate the spectral radius of the next generation matrix $G = \mathcal{F}\mathcal{V}^{-1}$. Given the structure of the host-vector transmission system, G is partitioned as follows:

$$G = \begin{bmatrix} \mathbf{0} & \mathbf{0} & \mathbf{G}_{13} & \mathbf{G}_{14} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{G}_{31} & \mathbf{G}_{32} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix}.$$

Theorem 6.1. *The spectral radius of G is given by $\rho(G) = \sqrt{\rho(\mathbf{G}_{13}\mathbf{G}_{31})}$.*

Proof. The eigenvalues μ of matrix G are the roots of the characteristic equation $\det(G - \mu\mathbf{I}) = 0$. Using the block matrix structure:

$$\det \begin{bmatrix} -\mu\mathbf{I} & \mathbf{0} & \mathbf{G}_{13} & \mathbf{G}_{14} \\ \mathbf{0} & -\mu\mathbf{I} & \mathbf{0} & \mathbf{0} \\ \mathbf{G}_{31} & \mathbf{G}_{32} & -\mu\mathbf{I} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & -\mu\mathbf{I} \end{bmatrix} = 0.$$

Since the second and fourth block rows contain only the diagonal term $-\mu\mathbf{I}$ and zeros elsewhere, we can expand the determinant by these rows:

$$(-\mu)^{n+w} \cdot \det \begin{bmatrix} -\mu\mathbf{I} & \mathbf{G}_{13} \\ \mathbf{G}_{31} & -\mu\mathbf{I} \end{bmatrix} = 0,$$

where n and w are the dimensions of the infectious host and infectious vector sub-classes, respectively. It yields that

$$(-\mu)^{n+w} \cdot \det\left((-\mu\mathbf{I})(-\mu\mathbf{I}) - \mathbf{G}_{13}\mathbf{G}_{31}\right) = 0.$$

Simplifying the expression, we obtain:

$$(-\mu)^{n+w} \cdot \det\left(\mu^2\mathbf{I} - \mathbf{G}_{13}\mathbf{G}_{31}\right) = 0.$$

This implies that the non-zero eigenvalues of G satisfy the relation $\mu^2 = \lambda(\mathbf{G}_{13}\mathbf{G}_{31})$. Consequently, the maximum eigenvalue in magnitude, which defines the spectral radius, is

$$\rho(G) = \sqrt{\rho(\mathbf{G}_{13}\mathbf{G}_{31})}.$$

By substituting the Rank-1 definitions of the infection blocks and applying the property $\rho(\mathbf{u}\mathbf{v}^T) = \mathbf{v}^T\mathbf{u}$, the spectral radius simplifies step-by-step

$$\begin{aligned}
\mathcal{R}_0^2 &= \rho\left(\left[\boldsymbol{\alpha}_E k_{hv}\mathbf{1}_w^T\mathbf{V}_v^{-1}\mathbf{V}_{vu}\mathbf{V}_u^{-1}\right]\cdot\left[\boldsymbol{\alpha}_u k_{vh}\mathbf{1}_n^T\mathbf{V}_y^{-1}\mathbf{V}_{yx}\mathbf{V}_x^{-1}\right]\right)\\
&= k_{hv}k_{vh}\cdot\left(\mathbf{1}_w^T\mathbf{V}_v^{-1}\mathbf{V}_{vu}\mathbf{V}_u^{-1}\boldsymbol{\alpha}_u\right)\cdot\rho\left(\boldsymbol{\alpha}_E\mathbf{1}_n^T\mathbf{V}_y^{-1}\mathbf{V}_{yx}\mathbf{V}_x^{-1}\right)\\
&= k_{hv}k_{vh}\cdot\mathcal{P}_v\cdot\left(\mathbf{1}_n^T\mathbf{V}_y^{-1}\mathbf{V}_{yx}\mathbf{V}_x^{-1}\boldsymbol{\alpha}_E\right)\\
&= \mathcal{B}^2\beta_{hv}\beta_{vh}N_h^*N_v^*\cdot\mathcal{P}_v\cdot\mathcal{P}_h.
\end{aligned}$$

Since $\alpha_E\mathbf{1}_n^TV_y^{-1}V_{yx}V_x^{-1}$ is a rank-1 matrix of the form $\alpha_E\cdot c^T$ for some row vector c^T, we have $\rho(\alpha_E c^T) = c^T\alpha_E$ (the unique nonzero eigenvalue of a rank-1 matrix uv^T equals v^Tu). Therefore

$$\rho\big(\alpha_E\mathbf{1}_n^TV_y^{-1}V_{yx}V_x^{-1}\big) = \mathbf{1}_n^TV_y^{-1}V_{yx}V_x^{-1}\alpha_E =: P_h.$$

Taking the square root, we obtain that

$$\mathcal{R}_0 = \mathcal{B}(N_h^*, N_v^*)\sqrt{\beta_{hv}\beta_{vh}N_h^*N_v^*\cdot\mathcal{P}_h\cdot\mathcal{P}_v},$$

where

$$\begin{aligned}
\mathcal{P}_h &= \mathbf{1}_n^T\mathbf{V}y^{-1}\mathbf{V}yx\mathbf{V}_x^{-1}\boldsymbol{\alpha}_E,\\
\mathcal{P}_v &= \mathbf{1}_w^T\mathbf{V}v^{-1}\mathbf{V}vu\mathbf{V}_u^{-1}\boldsymbol{\alpha}_u.
\end{aligned}$$

Due to the bipartite nature of the host-vector transmission, the characteristic equation yields:

$$\mathcal{R}_0 = \sqrt{R_{hv}\cdot R_{vh}}.$$

Expanding the operators to the vector-to-host and host-to-vector components, we have

$$\begin{aligned}
\mathcal{R}_{hv} &= \mathcal{B}(N_h^*, N_v^*)\beta_{hv}N_h^*\cdot\left(\mathbf{1}_w^T\mathbf{V}_v^{-1}\mathbf{V}_{vu}\mathbf{V}_u^{-1}\boldsymbol{\alpha}_u\right),\\
\mathcal{R}_{vh} &= \mathcal{B}(N_h^*, N_v^*)\beta_{vh}N_v^*\cdot\left(\mathbf{1}_n^T\mathbf{V}_y^{-1}\mathbf{V}_{yx}\mathbf{V}_x^{-1}\boldsymbol{\alpha}_E\right).
\end{aligned}$$

□

To summize, we have that

Theorem 6.2. *The disease-free equilibrium (DFE) of the generalized SEIR-SEI model is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$. The basic reproduction number R_0 is given by the product*

$$\mathcal{R}_0 = \sqrt{R_{hv}\cdot R_{vh}}$$

where

$$\begin{aligned}
\mathcal{R}_{hv} &= \mathcal{B}(N_h^*, N_v^*)\beta_{hv}N_h^*\cdot\left(\mathbf{1}_w^T\mathbf{V}_v^{-1}\mathbf{V}_{vu}\mathbf{V}_u^{-1}\boldsymbol{\alpha}_u\right),\\
\mathcal{R}_{vh} &= \mathcal{B}(N_h^*, N_v^*)\beta_{vh}N_v^*\cdot\left(\mathbf{1}_n^T\mathbf{V}_y^{-1}\mathbf{V}_{yx}\mathbf{V}_x^{-1}\boldsymbol{\alpha}_E\right).
\end{aligned}$$

7 Discussion and Conclusion

In this study, we have extended the classical SEQIRS and SEIR-SEI epidemic models by integrating the Generalized Linear Chain Trick (GLCT) framework. This mathematical approach facilitates the transition from biologically restrictive exponential dewell times to more flexible and realistic phase distributions, allowing for a more accurate representation of latency and infectious periods in real-world disease dynamics.

The core strength of our research lies in the successful application of the GLCT to two distinct modeling scenarios:

- **Model I (SEQIRS)**: We incorporated human intervention factors, specifically quarantine and isolation, demonstrating how these measures interact with the distributed delay of the disease stages.
- **Model II (SEIR-SEI)**: we characterized interspecies transmission, explicitly modeling the feedback loop between host and vector populations.

A significant contribution of this work is the analytical derivation of the Basic Reproduction Number ($\mathcal{R}_0$) for both models. By employing the Next-Generation Matrix (NGM) method, we were able to obtain closed-form expressions for the epidemic thresholds, providing a rigorous mathematical basis for predicting outbreak potential under non-exponentially distributed stage durations.

Our results highlight the substantial advantages of the GLCT in several key areas:

1. **Biological Realism**: By adjusting the number of sub-stages, we can flexibly model various delay distributions (from exponential to near-deterministic), which more closely aligns with empirical epidemiological data.
2. **Quantitative Precision**: The framework allows for high-fidelity quantitative computation of $\mathcal{R}_0$, revealing how the variance of the dewell times influences the stability of the disease-free equilibrium.
3. **Structural Tractability**: Despite the increased dimensionality of the system, the GLCT preserves a linear structure within the infected compartments, ensuring that the calculation of threshold conditions remains computationally and analytically manageable.

In conclusion, the integration of GLCT into SEQIRS and SEIR-SEI models provides a robust and generalized framework for epidemic modeling. This approach significantly enhances the predictive power of compartmental models and offers valuable insights for designing more effective public health interventions. Future research will explore the sensitivity of these models to real-time data fitting and the impact of stochastic variations within the linear chains.

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