Multi-scale Adaptive Network (MAN) Epidemic Model

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Abstract

This comprehensive white paper presents the complete mathematical derivation and theoretical foundation of the Multi-scale Adaptive Network (MAN) Epidemic Model. Addressing fundamental limitations in traditional epidemic modeling approaches, the MAN framework integrates hierarchical contact networks, adaptive parameters, behavior-pathogen feedback loops, selective computational resolution, and Bayesian data assimilation within a unified theoretical structure. We provide rigorous derivations for all model components, carefully explicating the assumptions underlying each equation and elucidating the mathematical relationships between model elements. The detailed formulation presented here demonstrates how the MAN approach bridges critical gaps between network theory, dynamical systems, information theory, and computational statistics to create a coherent framework for realistic epidemic simulation. This document serves as both a theoretical foundation and a complete reference implementation guide for researchers and practitioners seeking to implement, extend, or analyze the MAN framework for epidemic modeling applications.

1 Introduction

1.1 Fundamental challenges in epidemic modeling

Epidemic modeling faces intrinsic challenges arising from the complex, multi-scale, and adaptive nature of disease transmission processes. These challenges

can be categorized into five fundamental problems:

1. **The heterogeneous mixing problem**: Populations do not mix homogeneously, but rather through structured contact patterns that vary across spatial and social scales [11].

2. **The parameter evolution problem**: Key parameters such as transmission rates are not constant throughout an epidemic but evolve due to changes in behavior, virus mutation, and environmental factors [8].

3. **The behavioral adaptation problem**: Human behavior dynamically responds to perceived disease risk, creating feedback loops that alter disease dynamics in ways not captured by standard models [16].

4. **The computational tractability problem**: Models face an inherent trade-off between realism and computational feasibility, particularly for large populations [15].

5. **The data assimilation problem**: Real-time integration of heterogeneous data sources with appropriate uncertainty quantification remains challenging for epidemic forecasting [14].

While numerous approaches have attempted to address individual aspects of these challenges, a comprehensive framework that simultaneously addresses all five fundamental problems has remained elusive.

1.2 Limitations of existing models

Current epidemic models fall into several broad categories, each with specific limitations that motivate our integrated approach:

1.2.1 Compartmental models

Compartmental models [10, 1] partition populations into states (e.g., Susceptible, Infected, Recovered) and model transitions between them using differential equations:

$$\frac{dS}{dt} = -\beta SI \tag{1}$$

$$\frac{dI}{dt} = \beta SI - \gamma I \tag{2}$$

$$\frac{dR}{dt} = \gamma I \tag{3}$$

Limitations: These models assume homogeneous mixing (every individual has equal probability of contacting every other individual), fixed parameters over time (β and γ remain constant), and uniform behavior across the population. These assumptions significantly deviate from real-world epidemic dynamics, especially for diseases spreading through structured social networks with behavioral adaptation.

1.2.2 Network models

Network models [12, 9] represent contacts as edges in a graph, using adjacency matrices A_{ij} to indicate connections between individuals i and j. The probability of individual i becoming infected at time t is typically modeled as:

$$P(i \text{ becomes infected at time } t) = 1 - \prod_j (1 - \beta A_{ij} X_j(t)) \tag{4}$$

where $X_j(t)$ indicates if individual j is infectious at time t.

Limitations: Most implementations use static networks that fail to capture behavioral adaptation during an epidemic. They also typically lack multi-scale structure integrating household, community, and regional mixing patterns. Additionally, computational limitations often restrict application to relatively small populations.

1.2.3 Agent-Based models

Agent-based models [7, 5] simulate individuals with specific characteristics and behavioral rules, tracking their interactions and disease states over time.

Limitations: These models are computationally intensive, limiting their application to relatively small populations or requiring significant simplifications. They often lack formal mathematical frameworks for parameter estimation and uncertainty quantification, making systematic analysis challenging.

1.2.4 Metapopulation models

Metapopulation models [2, 4] divide populations into connected subpopulations, modeling both within-group mixing and between-group mobility:

$$\frac{dS_i}{dt} = -\beta_i S_i \frac{I_i}{N_i} + \sum_j (m_{ji} S_j - m_{ij} S_i) \tag{5}$$

Limitations: These models typically use simplified mixing within each subpopulation and struggle to incorporate behavioral adaptation and heterogeneity. They also face challenges in representing complex contact patterns within and between subpopulations.

1.3 The MAN modeling framework: an integrated approach

The Multi-scale Adaptive Network (MAN) Epidemic Model addresses these limitations through five integrated innovations:

1. **Hierarchical network structure**: A multi-scale representation of contacts spanning household, community, and regional levels, capturing heterogeneity in mixing patterns across scales.

2. **Adaptive parameters**: Time-varying transmission parameters that evolve based on pathogen mutation, behavioral changes, and environmental factors.

3. **Behavior-pathogen feedback loop**: Explicit modeling of how information about disease prevalence affects behavior, how behavior influences contact patterns, and how these adaptations impact transmission dynamics.

4. **Computational efficiency through selective resolution**: Dynamic adjustment of model resolution based on epidemic intensity, applying detailed agent-based modeling where needed while using more efficient representations elsewhere.

5. **Bayesian data assimilation**: Continuous integration of empirical data to update model parameters and state, with formal uncertainty quantification.

In the following sections, we provide complete mathematical derivations for each component of the MAN framework, explicating all assumptions and elucidating the rationale behind each equation.

2 Theoretical foundation and first principles

2.1 Axiomatic foundation

We begin by establishing the axiomatic foundation of the MAN framework, which rests on five core principles:

Axiom 1 (Network structure): Human contact patterns form multi-scale networks that determine disease transmission pathways.

Axiom 2 (Parameter adaptation): Epidemic parameters evolve dynamically in response to behavioral, pathogen, and environmental changes.

Axiom 3 (Behavioral feedback): Human behavior adapts to perceived disease risk, creating feedback loops that modify contact patterns and transmission dynamics.

Axiom 4 (Variable resolution): The appropriate modeling resolution varies spatially and temporally based on local epidemic intensity.

Axiom 5 (Bayesian inference): Model states and parameters should be continuously updated using Bayesian methods to incorporate new data and quantify uncertainty.

From these axioms, we derive the complete mathematical structure of the MAN model, beginning with the representation of individuals and their states.

2.2 Individual state representation

Each individual i in the population is represented by a state vector that evolves over time:

$$S_i(t) = \{h_i(t), e_i(t), a_i(t), \mathbf{x}_i(t), \mathbf{b}_i(t), \mathbf{r}_i(t)\} \tag{6}$$

where:

- $h_i(t) \in \{S, E, I, A, R, D\}$ is the health state (Susceptible, Exposed, Infectious, Asymptomatic, Recovered, Deceased)
- $e_i(t) \in \mathbb{R}^d$ is a vector of environmental factors affecting individual i

- $a_i(t) \in \mathbb{R}_+$ is the age or demographic group
- $\mathbf{x}_i(t) \in \mathbb{R}^n$ is the spatial location (typically $n = 2$ or $n = 3$)
- $\mathbf{b}_i(t) \in [0, 1]^m$ is a behavioral state vector with m dimensions
- $\mathbf{r}_i(t) \in \mathbb{R}_+^k$ is a vector of k individual risk factors

Assumptions:

1. Health states follow a discrete compartmental structure, with transitions governed by probabilistic rules.
2. Environmental factors, age, location, behavior, and risk can all influence disease transmission and progression.
3. Behavioral states are bounded between 0 and 1, representing compliance levels with protective behaviors.
4. Risk factors are non-negative real numbers representing relative risk multipliers.

The complete system state at time t is the collection of all individual states plus global variables:

$$\mathcal{S}(t) = \{S_1(t), S_2(t), ..., S_N(t), G(t)\} \tag{7}$$

where $G(t)$ represents global state variables such as policy interventions and information fields.

3 Hierarchical network structure: complete derivation

3.1 Multi-scale network representation

The contact structure is represented as a multi-layer network with three scales:

$$\mathcal{G} = (\mathcal{G}_{\text{micro}}, \mathcal{G}_{\text{meso}}, \mathcal{G}_{\text{macro}}) \tag{8}$$

where each scale is defined by its adjacency matrix:

$$\mathcal{G}_{\text{scale}} = (V, E_{\text{scale}}, A^{\text{scale}}) \tag{9}$$

with $V = \{1, 2, ..., N\}$ representing individuals, E_{scale} representing the set of edges at each scale, and A^{scale} representing the corresponding adjacency matrix.

Rationale: This multi-scale representation captures the inherently hierarchical nature of human contact patterns. Disease transmission occurs through different modes of contact that vary in intensity, frequency, and structure across scales. By explicitly modeling these scales, we can more accurately represent how interventions affect different types of interactions.

3.2 Adjacency matrices and their properties

For each scale, we define a time-dependent adjacency matrix:

$$A_{ij}^{\text{micro}}(t) = \text{contact weight between i and j at micro scale at time t} \tag{10}$$

$$A_{ij}^{\text{meso}}(t) = \text{contact weight between i and j at meso scale at time t} \tag{11}$$

$$A_{ij}^{\text{macro}}(t) = \text{contact weight between i and j at macro scale at time t} \tag{12}$$

Properties:

1. Symmetric: $A_{ij}^{\text{scale}}(t) = A_{ji}^{\text{scale}}(t)$ for all i, j, t (undirected contact)
2. Non-negative: $A_{ij}^{\text{scale}}(t) \geq 0$ for all i, j, t (contact weights are non-negative)
3. Zero diagonal: $A_{ii}^{\text{scale}}(t) = 0$ for all i, t (no self-loops)

The effective contact network is a weighted combination of these scales:

$$A_{ij}^{\text{eff}}(t) = \omega_1 A_{ij}^{\text{micro}}(t) + \omega_2 A_{ij}^{\text{meso}}(t) + \omega_3 A_{ij}^{\text{macro}}(t) \tag{13}$$

where $\omega_1, \omega_2, \omega_3$ are scale weights with $\omega_1 + \omega_2 + \omega_3 = 1$ and $\omega_k \geq 0$ for all k.

Derivation: The effective contact weight $A_{ij}^{\text{eff}}(t)$ represents the overall contact intensity between individuals i and j at time t. This is constructed as a convex combination of contacts at different scales to ensure that the overall contact structure preserves the properties of a weighted graph while integrating information from all scales.

Assumption: We assume that the transmission contribution from each scale can be linearly combined. This is justified when the time scales of interactions at different levels are sufficiently separated, and when transmission through one route does not significantly affect transmission through another route.

3.3 Micro-scale network construction

The household and close contact network ($\mathcal{G}_{\text{micro}}$) is constructed through a systematic process:

1. **Household assignment**: Individuals are grouped into households according to demographic data on household size distribution:

$$P(H = h) = \text{probability that a household has size h} \tag{14}$$

For typical populations, household size follows a distribution approximated by:

$$P(H = h) = \begin{cases} 0.2 & \text{if } h = 1 \\ 0.3 & \text{if } h = 2 \\ 0.2 & \text{if } h = 3 \\ 0.2 & \text{if } h = 4 \\ 0.1 & \text{if } h = 5 \\ 0.0 & \text{if } h \geq 6 \end{cases} \tag{15}$$

2. **Household network creation**: Within each household $\mathcal{H}_k$, we create a complete graph where each member is connected to every other member:

$$A_{ij}^{\text{micro}}(0) = 1 \text{ for all } i, j \in \mathcal{H}_k, i \neq j \tag{16}$$

3. **Close contact network**: Beyond households, individuals form close contacts based on spatial proximity and demographic similarity:

$$P(\text{close contact between } i \text{ and } j | i \notin \mathcal{H}_j) = \alpha_{\text{close}} \cdot \exp(-\delta \cdot d_{ij}) \cdot \exp(-\gamma \cdot |a_i - a_j|) \tag{17}$$

where:

- α_{close} is the base probability of close contact
- $d_{ij} = \|\mathbf{x}_i - \mathbf{x}_j\|$ is the spatial distance between individuals
- $|a_i - a_j|$ is the age difference
- δ and γ are decay parameters for distance and age difference

4. **Contact weight assignment**: For close contacts outside households, we assign weights:

$$A_{ij}^{\text{micro}}(0) = \exp(-\delta' \cdot d_{ij}) \cdot \exp(-\gamma' \cdot |a_i - a_j|) \text{ for close contacts} \tag{18}$$

where δ' and γ' determine how contact intensity decays with distance and age difference.

Derivation rationale: The micro-scale network construction balances empirical realism with theoretical principles. Household structures follow empirical distributions from demographic data. The exponential decay of contact probability with distance and age difference follows from the principle that social interactions are more likely between individuals who are physically proximate and demographically similar. The exponential form is chosen because it has strong empirical support in studies of social contact patterns [13].

3.4 Meso-scale network construction

The community-level network ($\mathcal{G}_{\text{meso}}$) captures interactions at an intermediate scale:

1. **Community identification**: Space is partitioned into community regions $\{C_1, C_2, ..., C_M\}$ using either:

- Administrative boundaries (e.g., census tracts)
- Data-driven clustering based on population density and mobility patterns
- Voronoi tessellation around activity centers

2. **Within-community connection probability**: For individuals within the same community C_m:

$$P(\text{connection between } i \text{ and } j | i, j \in C_m) = \min\left(\frac{\alpha_{\text{community}}}{|C_m|}, p_{\max}\right) \tag{19}$$

where:

- $\alpha_{\text{community}}$ is a scaling parameter
- $|C_m|$ is the size of community m
- $p_{\max}$ is the maximum connection probability (typically 0.8)

Derivation: The inverse relationship with community size reflects the observation that individuals in smaller communities are more likely to interact with a larger proportion of community members. The minimum function prevents unrealistically high probabilities in very small communities.

3. **Between-community connection probability**: For individuals in different communities:

$$P(\text{connection between } i \text{ and } j | i \in C_m, j \in C_n, m \neq n) = \alpha_{\text{between}} \cdot \exp(-\eta \cdot d_{mn}) \tag{20}$$

where:

- α_{between} is the base probability of between-community connections
- d_{mn} is the distance between communities m and n
- η controls the decay of connection probability with distance

4. **Contact weight assignment**: For established connections, weights are assigned as:

$$A_{ij}^{\text{meso}}(0) = \begin{cases} \exp(-\kappa_1 \cdot d_{ij}) & \text{if } i, j \in C_m \text{ for some } m \\ \exp(-\kappa_2 \cdot d_{ij}) & \text{if } i \in C_m, j \in C_n, m \neq n \end{cases} \tag{21}$$

where $\kappa_1 < \kappa_2$, reflecting stronger within-community interactions.

Assumptions:

1. Community structures influence contact patterns beyond household effects
2. Within-community connections are more likely and stronger than between-community connections
3. Connection probability decreases with inter-community distance
4. Community sizes affect connection densities, with smaller communities having higher connectivity

3.5 Macro-scale network construction

The regional-level network ($\mathcal{G}_{\text{macro}}$) captures long-range connections:

1. **Degree distribution generation**: We first generate a target degree distribution following a power law:

$$P(k) \propto k^{-\alpha} \text{ for } k_{\min} \leq k \leq k_{\max} \tag{22}$$

   where:

   - α is the power law exponent (typically 2.0-3.0)
   - $k_{\min}$ and $k_{\max}$ are minimum and maximum degrees

   Rationale: Power law degree distributions are widely observed in social and transportation networks [3]. This reflects the presence of hubs and heterogeneous connectivity patterns in regional interactions.

2. **Configuration model application**: We use the configuration model to generate a network with the target degree distribution:

   a. Generate a degree sequence $\{k_1, k_2, ..., k_N\}$ from the power law distribution

   b. Create k_i half-edges or "stubs" for each node i

   c. Randomly pair stubs to form edges

   d. Remove any self-loops and multi-edges

3. **Weight assignment based on distance**: For each edge (i, j) in the macro network:

$$A_{ij}^{\text{macro}}(0) = \exp(-\lambda \cdot d_{ij}) \tag{23}$$

   where λ controls the decay of contact intensity with distance.

Assumptions:

1. Long-range connections follow a power law degree distribution
2. The configuration model provides a reasonable approximation of regional contact structures
3. Long-range contact intensity decreases exponentially with distance
4. Macro-scale connections are independent of household and community structures

3.6 Effective network computation

The effective contact network combines all scales with appropriate weights:

$$A_{ij}^{\text{eff}}(t) = \omega_1 A_{ij}^{\text{micro}}(t) + \omega_2 A_{ij}^{\text{meso}}(t) + \omega_3 A_{ij}^{\text{macro}}(t) \tag{24}$$

The scale weights ω_k are typically set to:

- $\omega_1 = 0.6$ (micro-scale/household contacts)
- $\omega_2 = 0.3$ (meso-scale/community contacts)
- $\omega_3 = 0.1$ (macro-scale/regional contacts)

Derivation: These weights reflect the relative importance of different contact scales for disease transmission, based on empirical studies of contact patterns and transmission events [11, 6]. The micro-scale receives the highest weight because household and close contacts typically involve the most intense and prolonged interactions, with correspondingly higher transmission risk.

Mathematical properties:

1. The effective network preserves the symmetry property: $A_{ij}^{\text{eff}}(t) = A_{ji}^{\text{eff}}(t)$
2. Non-negativity is preserved: $A_{ij}^{\text{eff}}(t) \geq 0$
3. The zero diagonal property is preserved: $A_{ii}^{\text{eff}}(t) = 0$

The effective contact matrix can be represented in matrix form:

$$\mathbf{A}^{\text{eff}}(t) = \omega_1 \mathbf{A}^{\text{micro}}(t) + \omega_2 \mathbf{A}^{\text{meso}}(t) + \omega_3 \mathbf{A}^{\text{macro}}(t) \tag{25}$$

This formulation enables efficient computation and analysis using matrix operations.

4 Adaptive parameters: complete derivation

4.1 Transmission rate formulation

The transmission rate between individuals i and j at time t is derived as:

$$\beta_{ij}(t) = \beta_0 \cdot \phi(t) \cdot \psi_i(t) \cdot \psi_j(t) \cdot \xi_{ij}(t) \cdot \eta(e_i(t), e_j(t)) \tag{26}$$

Derivation rationale: This multiplicative form decomposes the transmission rate into component factors that can be independently modeled and estimated. The baseline rate β_0 is modified by factors representing pathogen evolution, behavioral adaptation, contact-specific effects, and environmental influences.

Each term represents:

- β_0: Baseline transmission rate in the absence of modifications
- $\phi(t)$: Pathogen evolution factor (relative transmissibility compared to initial strain)

- $\psi_i(t)$: Behavioral factor for individual i (how behavior affects susceptibility)
- $\psi_j(t)$: Behavioral factor for individual j (how behavior affects infectiousness)
- $\xi_{ij}(t)$: Contact-specific modification
- $\eta(e_i(t), e_j(t))$: Environmental factor

Assumption: We assume that these factors combine multiplicatively, which is justified when they affect separate aspects of the transmission process. This approach allows for independent estimation of each component while capturing their combined effect.

4.2 Pathogen evolution function

The pathogen evolution factor $\phi(t)$ follows a stochastic logistic growth model:

$$\frac{d\phi(t)}{dt} = \mu\phi(t)(1 - \phi(t)/\kappa) + \sigma\xi(t) \tag{27}$$

where:

- μ is the mutation rate
- κ is the maximum relative transmissibility
- σ is the noise scale
- $\xi(t)$ is a standard Gaussian white noise process

Complete derivation:

1. Start with the deterministic logistic growth equation:

$$\frac{d\phi(t)}{dt} = \mu\phi(t)\left(1 - \frac{\phi(t)}{\kappa}\right) \tag{28}$$

   This equation captures the competing dynamics of:

   - Evolutionary pressure to increase transmissibility: $\mu\phi(t)$
   - Limiting factors that constrain maximum transmissibility: $-\mu\phi(t)^2/\kappa$

2. For initial conditions $\phi(0) = \phi_0$, the deterministic solution is:

$$\phi(t) = \frac{\kappa\phi_0 e^{\mu t}}{\kappa + \phi_0(e^{\mu t} - 1)} \tag{29}$$

   This sigmoid curve shows slow initial growth, followed by rapid increase, and finally saturation at κ.

3. To account for random evolutionary events (e.g., beneficial mutations, recombination), we add a stochastic term:

$$\frac{d\phi(t)}{dt} = \mu\phi(t)\left(1 - \frac{\phi(t)}{\kappa}\right) + \sigma\xi(t) \tag{30}$$

This transforms the ordinary differential equation into a stochastic differential equation (SDE).

4. Using the Euler-Maruyama method, this SDE can be numerically integrated:

$$\phi(t + \Delta t) = \phi(t) + \mu\phi(t)\left(1 - \frac{\phi(t)}{\kappa}\right)\Delta t + \sigma\sqrt{\Delta t}Z_t \tag{31}$$

where $Z_t \sim N(0, 1)$ is a standard normal random variable.

Assumptions:

1. Pathogen evolution follows logistic growth with a maximum transmissibility κ
2. Random evolutionary events can be modeled as Gaussian white noise
3. The evolution rate μ and maximum transmissibility κ are constant over the timescale of interest
4. Initial transmissibility $\phi(0) = 1$ (normalized to the initial strain)

4.3 Individual behavioral factors

The behavioral factor for individual i is:

$$\psi_i(t) = \exp(-\alpha_1 b_{i1}(t) - \alpha_2 b_{i2}(t) - \alpha_3 b_{i3}(t)) \tag{32}$$

where:

- $b_{i1}(t)$, $b_{i2}(t)$, $b_{i3}(t)$ represent different dimensions of behavior
- α_1, α_2, α_3 are coefficients determining their impact

Derivation:

1. Define behavior dimensions with specific interpretations:
    - $b_{i1}(t)$: Physical distancing behavior (0 = no distancing, 1 = maximum distancing)
    - $b_{i2}(t)$: Mask-wearing behavior (0 = no masks, 1 = perfect mask usage)
    - $b_{i3}(t)$: Hygiene practices (0 = poor hygiene, 1 = excellent hygiene)
2. For each behavior dimension k, define a reduction factor $r_k(b_{ik}) = e^{-\alpha_k b_{ik}}$, which:

- Equals 1 when $b_{ik} = 0$ (no protective behavior)
- Decreases exponentially as b_{ik} increases
- Approaches $e^{-\alpha_k}$ as b_{ik} approaches 1 (maximum protection)

3. Combine reduction factors multiplicatively:

$$\psi_i(t) = \prod_{k=1}^{3} r_k(b_{ik}(t)) = \exp\left(-\sum_{k=1}^{3} \alpha_k b_{ik}(t)\right) \tag{33}$$

4. This gives the final form:

$$\psi_i(t) = \exp(-\alpha_1 b_{i1}(t) - \alpha_2 b_{i2}(t) - \alpha_3 b_{i3}(t)) \tag{34}$$

Assumptions:

1. Each behavior dimension independently reduces transmission risk
2. The effect of each behavior is exponential, with diminishing returns for increased adoption
3. Behaviors combine multiplicatively, consistent with them affecting different transmission pathways
4. The coefficients α_k represent the maximum protective effect of each behavior when fully adopted

4.4 Contact-specific modification

The contact-specific modification term is:

$$\xi_{ij}(t) = A_{ij}^{\text{eff}}(t) \cdot f(h_i(t), h_j(t)) \tag{35}$$

where $f(h_i(t), h_j(t))$ accounts for differential infectiousness based on health states.

Derivation:

1. Start with the effective contact weight $A_{ij}^{\text{eff}}(t)$ that determines baseline contact intensity.
2. Define the health state modifier function:

$$f(h_i, h_j) = \begin{cases} 0 & \text{if } h_j \notin \{I, A\} \text{ (j not infectious)} \\ 0 & \text{if } h_i \notin \{S\} \text{ (i not susceptible)} \\ 1 & \text{if } h_j = I \text{ and } h_i = S \text{ (standard transmission)} \\ \tau_A & \text{if } h_j = A \text{ and } h_i = S \text{ (asymptomatic transmission)} \end{cases} \tag{36}$$

where τ_A is the relative transmissibility of asymptomatic cases (typically $\tau_A = 0.5$).

3. The contact-specific modification is then:

$$\xi_{ij}(t) = A_{ij}^{\text{eff}}(t) \cdot f(h_i(t), h_j(t)) \tag{37}$$

Assumptions:

1. Transmission requires an infectious individual and a susceptible individual
2. Asymptomatic cases have reduced transmissibility compared to symptomatic cases
3. Contact intensity linearly affects transmission rate
4. Health states affect transmission independent of contact intensity

4.5 Environmental factor

The environmental factor is:

$$\eta(e_i(t), e_j(t)) = 1 + \delta_{\text{season}} \sin\left(2\pi \frac{t - t_0}{365}\right) + \delta_{\text{env}}(e_i(t) + e_j(t)) \tag{38}$$

where:

- δ_{season} controls seasonal effect amplitude
- t_0 is the phase shift determining peak seasonal effect
- δ_{env} determines the impact of individual environmental factors

Derivation:

1. Seasonal effects are modeled using a sinusoidal function with period 365 days:

$$\eta_{\text{season}}(t) = 1 + \delta_{\text{season}} \sin\left(2\pi \frac{t - t_0}{365}\right) \tag{39}$$

   This creates oscillation between $1 - \delta_{\text{season}}$ and $1 + \delta_{\text{season}}$.

2. Individual environmental factors $e_i(t)$ and $e_j(t)$ are incorporated additively:

$$\eta_{\text{env}}(e_i, e_j) = \delta_{\text{env}}(e_i + e_j) \tag{40}$$

3. The complete environmental factor combines these terms:

$$\eta(e_i(t), e_j(t), t) = \eta_{\text{season}}(t) + \eta_{\text{env}}(e_i(t), e_j(t)) \tag{41}$$

$$\eta(e_i(t), e_j(t), t) = 1 + \delta_{\text{season}} \sin\left(2\pi \frac{t - t_0}{365}\right) + \delta_{\text{env}}(e_i(t) + e_j(t)) \tag{42}$$

Assumptions:

1. Seasonal effects follow an annual sinusoidal pattern
2. Environmental factors from both individuals additively affect transmission
3. The baseline environmental factor is 1 (no modification)
4. Individual environmental factors are normalized to have mean zero across the population

5 Behavior-pathogen feedback loop: complete derivation

5.1 Behavioral state evolution

Individual behavioral state evolves according to:

$$\frac{d\mathbf{b}_i(t)}{dt} = \gamma \cdot (\mathbf{b}_i^*(t) - \mathbf{b}_i(t)) + \boldsymbol{\epsilon}_i(t) \tag{43}$$

where:

- γ is the behavior adaptation rate
- $\mathbf{b}_i^*(t)$ is the target behavior
- $\boldsymbol{\epsilon}_i(t)$ is a noise term representing individual variation

Derivation:

1. Model behavioral adaptation as relaxation toward a target behavior $\mathbf{b}_i^*(t)$:

$$\frac{d\mathbf{b}_i(t)}{dt} = \gamma \cdot (\mathbf{b}_i^*(t) - \mathbf{b}_i(t)) \tag{44}$$

   This first-order relaxation process ensures smooth behavioral changes with rate γ.

2. Add stochastic variation to account for individual differences:

$$\frac{d\mathbf{b}_i(t)}{dt} = \gamma \cdot (\mathbf{b}_i^*(t) - \mathbf{b}_i(t)) + \boldsymbol{\epsilon}_i(t) \tag{45}$$

   where $\boldsymbol{\epsilon}_i(t) \sim N(0, \sigma_b^2 \mathbf{I})$ is multivariate Gaussian noise.

3. For numerical implementation, use the Euler method:

$$\mathbf{b}_i(t + \Delta t) = \mathbf{b}_i(t) + \gamma \cdot (\mathbf{b}_i^*(t) - \mathbf{b}_i(t)) \cdot \Delta t + \sqrt{\Delta t} \cdot \mathbf{Z}_t \tag{46}$$

   where $\mathbf{Z}_t \sim N(0, \sigma_b^2 \mathbf{I})$.

4. Apply bounds to ensure behaviors remain in valid range:

$$\mathbf{b}_i(t + \Delta t) = \min(1, \max(0, \mathbf{b}_i(t + \Delta t))) \tag{47}$$

Assumptions:

1. Behavior adapts gradually toward target behavior
2. Adaptation follows first-order relaxation dynamics
3. Individual variation can be modeled as Gaussian noise
4. Behaviors are bounded between 0 and 1

5.2 Target behavior formulation

The target behavior is determined by information, policy, and media influence:

$$\mathbf{b}_i^*(t) = c_1\mathbf{I}(t) + c_2\mathbf{P}(t) + c_3\mathbf{M}(t)\mathbf{1} + c_4\mathbf{v}_i \tag{48}$$

where:

- $\mathbf{I}(t)$ is the information field
- $\mathbf{P}(t)$ represents policy interventions
- $\mathbf{M}(t)$ captures media influence
- $\mathbf{v}_i$ represents individual characteristics affecting behavior
- c_1, c_2, c_3, c_4 are weighting coefficients
- $\mathbf{1}$ is a vector of ones

Derivation:

1. Information impact: $c_1\mathbf{I}(t)$

   Information about disease prevalence directly influences each behavioral dimension. The coefficient c_1 determines the strength of this effect.

2. Policy impact: $c_2\mathbf{P}(t)$

   Policy interventions target specific behaviors. For example:

   - $P_1(t)$: Social distancing policies affect $b_{i1}(t)$
   - $P_2(t)$: Mask mandates affect $b_{i2}(t)$
   - $P_3(t)$: Hygiene campaigns affect $b_{i3}(t)$

3. Media impact: $c_3\mathbf{M}(t)\mathbf{1}$

   Media influence $\mathbf{M}(t)$ affects all behavior dimensions equally, hence multiplication by $\mathbf{1}$.

4. Individual variation: $c_4\mathbf{v}_i$

   Individual characteristics $\mathbf{v}_i$ account for personal differences in behavior adoption.

5. The complete target behavior is the weighted sum:

$$\mathbf{b}_i^*(t) = c_1\mathbf{I}(t) + c_2\mathbf{P}(t) + c_3\mathbf{M}(t)\mathbf{1} + c_4\mathbf{v}_i \tag{49}$$

Assumptions:

1. Information, policy, and media influences combine additively
2. Each factor can independently drive behavioral change
3. Media influence affects all behavior dimensions similarly
4. Individual characteristics create persistent differences in behavior across the population

5.3 Information field dynamics

The information field follows:

$$\frac{dI_k(t)}{dt} = \alpha_1 N_I(t) - \alpha_2 I_k(t) + \alpha_3 M_k(t) \tag{50}$$

where:

- $I_k(t)$ is the information level for behavior dimension k
- $N_I(t)$ is the number of infectious individuals
- $M_k(t)$ is media coverage related to behavior dimension k
- $\alpha_1, \alpha_2, \alpha_3$ are parameters controlling information dynamics

Complete derivation:

1. Information generation from cases:

$$I_k^{gen}(t) = \alpha_1 N_I(t) \tag{51}$$

This term captures how visible cases generate information. Higher case numbers create more information and awareness.

2. Information decay:

$$I_k^{decay}(t) = \alpha_2 I_k(t) \tag{52}$$

Information decays over time as people forget or become desensitized to risk.

3. Media contribution:

$$I_k^{media}(t) = \alpha_3 M_k(t) \tag{53}$$

Media coverage amplifies or sustains information independent of actual case numbers.

4. The complete dynamics combine these processes:

$$\frac{dI_k(t)}{dt} = I_k^{gen}(t) - I_k^{decay}(t) + I_k^{media}(t) \tag{54}$$

$$\frac{dI_k(t)}{dt} = \alpha_1 N_I(t) - \alpha_2 I_k(t) + \alpha_3 M_k(t) \tag{55}$$

5. The equilibrium information level (when $\frac{dI_k(t)}{dt} = 0$) is:

$$I_k^{eq} = \frac{\alpha_1 N_I(t) + \alpha_3 M_k(t)}{\alpha_2} \tag{56}$$

Assumptions:

1. Information generation is proportional to visible cases
2. Information decays exponentially over time
3. Media influence can independently generate or sustain information
4. Different behavior dimensions may have different information dynamics

5.4 Media influence model

Media influence follows a delayed response to information and cases:

$$\frac{dM_k(t)}{dt} = \beta_1 I_k(t-\tau) - \beta_2 M_k(t) + \beta_3 \frac{dN_I(t)}{dt} \tag{57}$$

where:

- τ is the media response delay
- $\beta_1, \beta_2, \beta_3$ are parameters controlling media dynamics

Derivation:

1. Media responds to existing information with delay τ:

$$M_k^{info}(t) = \beta_1 I_k(t-\tau) \tag{58}$$

   This captures how media amplifies existing information with a time lag.

2. Media coverage decays over time:

$$M_k^{decay}(t) = \beta_2 M_k(t) \tag{59}$$

   As stories become "old news," media coverage declines.

3. Media responds to rate of change in cases:

$$M_k^{trend}(t) = \beta_3 \frac{dN_I(t)}{dt} \tag{60}$$

   Increasing cases generate more coverage than stable cases, even at high levels.

4. The complete dynamics combine these processes:

$$\frac{dM_k(t)}{dt} = M_k^{info}(t) - M_k^{decay}(t) + M_k^{trend}(t) \tag{61}$$

$$\frac{dM_k(t)}{dt} = \beta_1 I_k(t-\tau) - \beta_2 M_k(t) + \beta_3 \frac{dN_I(t)}{dt} \tag{62}$$

Assumptions:

1. Media response lags behind information by time τ
2. Media coverage decays exponentially over time
3. Media is more responsive to changing case numbers than stable case numbers
4. Different behavior dimensions may receive different media coverage

5.5 Policy response formulation

Policy interventions respond to case numbers and trends:

$$\frac{dP_k(t)}{dt} = \delta_1 \frac{N_I(t)}{N} - \delta_2 P_k(t) + \delta_3 \max\left(0, \frac{d}{dt}\left(\frac{N_I(t)}{N}\right)\right) \tag{63}$$

where:

- $P_k(t)$ is the strength of policy intervention for behavior dimension k
- N is the total population
- $\delta_1, \delta_2, \delta_3$ are parameters controlling policy dynamics

Derivation:

1. Policies respond to prevalence:

$$P_k^{prev}(t) = \delta_1 \frac{N_I(t)}{N} \tag{64}$$

   This captures how policy stringency increases with disease prevalence.

2. Policy relaxation:

$$P_k^{relax}(t) = \delta_2 P_k(t) \tag{65}$$

   Policies tend to be relaxed over time due to economic and social pressures.

3. Response to worsening trends:

$$P_k^{trend}(t) = \delta_3 \max\left(0, \frac{d}{dt}\left(\frac{N_I(t)}{N}\right)\right) \tag{66}$$

   This captures how rapidly increasing cases trigger stronger policy responses, while decreasing cases don't trigger additional measures.

4. The complete dynamics combine these processes:

$$\frac{dP_k(t)}{dt} = P_k^{prev}(t) - P_k^{relax}(t) + P_k^{trend}(t) \tag{67}$$

$$\frac{dP_k(t)}{dt} = \delta_1 \frac{N_I(t)}{N} - \delta_2 P_k(t) + \delta_3 \max\left(0, \frac{d}{dt}\left(\frac{N_I(t)}{N}\right)\right) \tag{68}$$

Assumptions:

1. Policy strength increases with disease prevalence
2. Policies are gradually relaxed over time
3. Rapidly worsening situations trigger stronger policy responses
4. Policies are bounded between 0 (no intervention) and 1 (maximum intervention)

5.6 Network adaptation due to behavior

Behavioral changes influence contact networks through:

$$\frac{dA_{ij}^{\text{scale}}(t)}{dt} = G(A_{ij}^{\text{scale}}(t), \mathbf{b}_i(t), \mathbf{b}_j(t), \mathbf{P}(t)) \tag{69}$$

The specific form of G depends on the scale:
Micro-scale adaptation:

$$G^{\text{micro}}(A_{ij}^{\text{micro}}(t), \mathbf{b}_i(t), \mathbf{b}_j(t), \mathbf{P}(t)) = -\rho_{\text{micro}} \cdot (b_{i1}(t) + b_{j1}(t)) \cdot A_{ij}^{\text{micro}}(t) \cdot (1 - \mathbb{I}_{household}) \tag{70}$$

where $\mathbb{I}_{household}$ equals 1 if i and j are in the same household, 0 otherwise.
Meso-scale adaptation:

$$G^{\text{meso}}(A_{ij}^{\text{meso}}(t), \mathbf{b}_i(t), \mathbf{b}_j(t), \mathbf{P}(t)) = -\rho_{\text{meso}} \cdot (b_{i1}(t) + b_{j1}(t) + P_1(t)) \cdot A_{ij}^{\text{meso}}(t) \tag{71}$$

Macro-scale adaptation:

$$G^{\text{macro}}(A_{ij}^{\text{macro}}(t), \mathbf{b}_i(t), \mathbf{b}_j(t), \mathbf{P}(t)) = -\rho_{\text{macro}} \cdot (b_{i1}(t) + b_{j1}(t) + 2P_1(t)) \cdot A_{ij}^{\text{macro}}(t) \tag{72}$$

Derivation:

1. Contact reduction depends on physical distancing behavior $b_{i1}(t)$ and policy $P_1(t)$.
2. At the micro-scale, household contacts are preserved regardless of behavior:

$$G^{\text{micro}}(A_{ij}^{\text{micro}}(t), \mathbf{b}_i(t), \mathbf{b}_j(t), \mathbf{P}(t)) = -\rho_{\text{micro}} \cdot (b_{i1}(t) + b_{j1}(t)) \cdot A_{ij}^{\text{micro}}(t) \cdot (1 - \mathbb{I}_{household}) \tag{73}$$

3. At the meso-scale, all contacts are reduced based on behavior and policy:

$$G^{\text{meso}}(A_{ij}^{\text{meso}}(t), \mathbf{b}_i(t), \mathbf{b}_j(t), \mathbf{P}(t)) = -\rho_{\text{meso}} \cdot (b_{i1}(t) + b_{j1}(t) + P_1(t)) \cdot A_{ij}^{\text{meso}}(t) \tag{74}$$

4. At the macro-scale, contacts are more strongly affected by policy:

$$G^{\text{macro}}(A_{ij}^{\text{macro}}(t), \mathbf{b}_i(t), \mathbf{b}_j(t), \mathbf{P}(t)) = -\rho_{\text{macro}} \cdot (b_{i1}(t) + b_{j1}(t) + 2P_1(t)) \cdot A_{ij}^{\text{macro}}(t) \tag{75}$$

5. The rates ρ_{scale} control how quickly contacts adapt at each scale, with typical values:
   - $\rho_{\text{micro}} = 0.1$ (slow adaptation of close contacts)
   - $\rho_{\text{meso}} = 0.2$ (moderate adaptation of community contacts)
   - $\rho_{\text{macro}} = 0.3$ (fast adaptation of regional contacts)

Assumptions:

1. Household contacts persist regardless of distancing behavior
2. Both individual behavior and policy reduce contact rates
3. Macro-scale contacts are more affected by policy than micro-scale contacts
4. Contact reduction is proportional to current contact weight
5. Different scales adapt at different rates

6 Computational efficiency through selective resolution: complete derivation

6.1 Epidemic intensity measure

For each region Ω, we define an epidemic intensity measure:

$$E(\Omega, t) = \frac{1}{|\Omega|} \sum_{i \in \Omega} w_{h_i(t)} \tag{76}$$

where:

- $|\Omega|$ is the number of individuals in region Ω
- $w_{h_i(t)}$ is the weight assigned to health state $h_i(t)$

Derivation:

1. Assign weights to each health state:

$$w_h = \begin{cases} 0 & \text{if } h = S \text{ (Susceptible)} \\ 0.5 & \text{if } h = E \text{ (Exposed)} \\ 1.0 & \text{if } h = I \text{ (Infectious)} \\ 0.7 & \text{if } h = A \text{ (Asymptomatic)} \\ 0 & \text{if } h = R \text{ (Recovered)} \\ 0 & \text{if } h = D \text{ (Deceased)} \end{cases} \tag{77}$$

   These weights reflect the epidemiological importance of each state, with infectious individuals given the highest weight.

2. Calculate the weighted sum across all individuals in the region:

$$\sum_{i \in \Omega} w_{h_i(t)} \tag{78}$$

3. Normalize by region population to get the intensity measure:

$$E(\Omega, t) = \frac{1}{|\Omega|} \sum_{i \in \Omega} w_{h_i(t)} \tag{79}$$

4. This measure ranges from 0 (no epidemic activity) to approximately 1 (high activity).

Assumptions:

1. Exposed, infectious, and asymptomatic individuals contribute to epidemic activity
2. Susceptible, recovered, and deceased individuals do not contribute to current activity
3. Normalized intensity allows comparison across regions of different sizes
4. Weights reflect relative epidemiological importance of each state

6.2 Resolution function

The resolution function determines the appropriate modeling approach for each region:

$$R(\Omega, t) = \begin{cases} \text{agent-based}, & \text{if } E(\Omega, t) > \theta_1 \\ \text{metapopulation}, & \text{if } \theta_2 < E(\Omega, t) \leq \theta_1 \\ \text{compartmental}, & \text{if } E(\Omega, t) \leq \theta_2 \end{cases} \tag{80}$$

where θ_1 and θ_2 are threshold parameters.
Derivation:

1. Set thresholds based on computational resources and accuracy requirements:

- $\theta_1 = 0.05$ (5% of population in active states)
- $\theta_2 = 0.01$ (1% of population in active states)

2. When epidemic activity is high ($E(\Omega, t) > \theta_1$), use agent-based modeling to capture detailed dynamics.
3. When epidemic activity is moderate ($\theta_2 < E(\Omega, t) \leq \theta_1$), use metapopulation modeling as a compromise between detail and efficiency.
4. When epidemic activity is low ($E(\Omega, t) \leq \theta_2$), use compartmental modeling for computational efficiency.

Assumptions:

1. Computational detail should be proportional to epidemic intensity
2. Thresholds can be adjusted based on available computational resources
3. Transitions between resolution levels must preserve epidemic dynamics
4. Higher resolution is most valuable where epidemic activity is highest

6.3 Agent-based resolution implementation

At the agent-based resolution, each individual is modeled explicitly:

$$P(h_i(t + \Delta t) = E | h_i(t) = S) = 1 - \exp(-\lambda_i(t)\Delta t) \tag{81}$$
$$P(h_i(t + \Delta t) = I | h_i(t) = E) = 1 - \exp(-\sigma_i(t)\Delta t) \tag{82}$$
$$P(h_i(t + \Delta t) = R | h_i(t) = I) = 1 - \exp(-\gamma_i(t)\Delta t) \tag{83}$$
$$P(h_i(t + \Delta t) = D | h_i(t) = I) = 1 - \exp(-\delta_i(t)\Delta t) \tag{84}$$

The force of infection on individual i is:

$$\lambda_i(t) = \sum_j A_{ij}^{\text{eff}}(t)\beta_{ij}(t)I_j(t) \tag{85}$$

where $I_j(t)$ equals 1 if individual j is infectious or asymptomatic, 0 otherwise.
Derivation:

1. For each susceptible individual, compute force of infection by summing over all contacts:

$$\lambda_i(t) = \sum_j A_{ij}^{\text{eff}}(t)\beta_{ij}(t)I_j(t) \tag{86}$$

2. The probability of transitioning from susceptible to exposed in time interval Δt follows an exponential probability distribution:

$$P(h_i(t + \Delta t) = E | h_i(t) = S) = 1 - \exp(-\lambda_i(t)\Delta t) \tag{87}$$

This derives from the Poisson process model of infection events.

3. Similar transition probabilities apply for other state changes, with rates $\sigma_i(t)$ (incubation), $\gamma_i(t)$ (recovery), and $\delta_i(t)$ (mortality).

4. Update individual states by sampling from these probability distributions:

$$h_i(t+\Delta t) = \begin{cases} E & \text{with probability } P(h_i(t+\Delta t) = E | h_i(t) = S) \text{ if } h_i(t) = S \\ I & \text{with probability } P(h_i(t+\Delta t) = I | h_i(t) = E) \text{ if } h_i(t) = E \\ R & \text{with probability } P(h_i(t+\Delta t) = R | h_i(t) = I) \text{ if } h_i(t) = I \\ D & \text{with probability } P(h_i(t+\Delta t) = D | h_i(t) = I) \text{ if } h_i(t) = I \\ h_i(t) & \text{otherwise} \end{cases} \tag{88}$$

Assumptions:

1. Infection events follow a Poisson process
2. Transition probabilities depend on individual-specific rates
3. State transitions are stochastic rather than deterministic
4. Force of infection aggregates across all contacts

6.4 Metapopulation resolution implementation

At the metapopulation resolution, individuals are grouped into subpopulations based on similar characteristics:

$$\frac{dS_q}{dt} = -\sum_p \beta_{qp} S_q \frac{I_p}{N_p} \tag{89}$$

$$\frac{dE_q}{dt} = \sum_p \beta_{qp} S_q \frac{I_p}{N_p} - \sigma_q E_q \tag{90}$$

$$\frac{dI_q}{dt} = \sigma_q E_q - (\gamma_q + \delta_q) I_q \tag{91}$$

$$\frac{dR_q}{dt} = \gamma_q I_q \tag{92}$$

$$\frac{dD_q}{dt} = \delta_q I_q \tag{93}$$

where:

- S_q, E_q, I_q, R_q, D_q are compartment sizes for subpopulation q
- β_{qp} is the transmission rate from subpopulation p to q
- $\sigma_q, \gamma_q, \delta_q$ are transition rates for subpopulation q

Derivation:

1. Divide the population in region Ω into Q subpopulations based on:
    - Age groups (e.g., 0-9, 10-19, ..., 80+)

- Risk levels (e.g., low, medium, high)
- Behavioral characteristics (e.g., low, medium, high compliance)

2. For each subpopulation, maintain compartmental counts S_q, E_q, I_q, R_q, D_q.
3. Define contact matrices C_{qp} representing average contact rates between subpopulations q and p.
4. Define transmission rates between subpopulations:

$$\beta_{qp} = \beta_0 \cdot \phi(t) \cdot \psi_q(t) \cdot \psi_p(t) \cdot C_{qp}(t) \cdot \eta_q(t) \tag{94}$$

   where $\psi_q(t)$ and $\eta_q(t)$ are subpopulation-specific behavioral and environmental factors.

5. The force of infection on subpopulation q is:

$$\lambda_q(t) = \sum_p \beta_{qp} \frac{I_p}{N_p} \tag{95}$$

6. The resulting differential equations are:

$$\frac{dS_q}{dt} = -\lambda_q(t) S_q \tag{96}$$
$$\frac{dE_q}{dt} = \lambda_q(t) S_q - \sigma_q E_q \tag{97}$$
$$\frac{dI_q}{dt} = \sigma_q E_q - (\gamma_q + \delta_q) I_q \tag{98}$$
$$\frac{dR_q}{dt} = \gamma_q I_q \tag{99}$$
$$\frac{dD_q}{dt} = \delta_q I_q \tag{100}$$

7. These equations are solved using a numerical ODE solver (e.g., Runge-Kutta method).

Assumptions:

1. Individuals within each subpopulation mix homogeneously
2. Subpopulation characteristics can be adequately represented by average values
3. Contact patterns between subpopulations are relatively stable
4. Differential equation approximation is valid for sufficiently large subpopulations

6.5 Compartmental resolution implementation

At the compartmental resolution, the entire region is modeled using aggregate compartments:

$$\frac{dS_\Omega}{dt} = -\beta_\Omega(t) S_\Omega \frac{I_\Omega}{N_\Omega} \tag{101}$$

$$\frac{dE_\Omega}{dt} = \beta_\Omega(t) S_\Omega \frac{I_\Omega}{N_\Omega} - \sigma_\Omega E_\Omega \tag{102}$$

$$\frac{dI_\Omega}{dt} = \sigma_\Omega E_\Omega - (\gamma_\Omega + \delta_\Omega) I_\Omega \tag{103}$$

$$\frac{dR_\Omega}{dt} = \gamma_\Omega I_\Omega \tag{104}$$

$$\frac{dD_\Omega}{dt} = \delta_\Omega I_\Omega \tag{105}$$

where:

- $S_\Omega, E_\Omega, I_\Omega, R_\Omega, D_\Omega$ are compartment sizes for region Ω
- $\beta_\Omega(t)$ is the effective transmission rate
- $\sigma_\Omega, \gamma_\Omega, \delta_\Omega$ are aggregate transition rates

Derivation:

1. Aggregate all individuals in region Ω into single compartments $S_\Omega, E_\Omega, I_\Omega, R_\Omega, D_\Omega$.
2. Calculate aggregate parameters as population-weighted averages:

$$\beta_\Omega(t) = \frac{1}{N_\Omega} \sum_{i \in \Omega} \beta_0 \cdot \phi(t) \cdot \psi_i(t) \cdot \eta_i(t) \tag{106}$$

$$\sigma_\Omega = \frac{1}{N_\Omega} \sum_{i \in \Omega} \sigma_i \tag{107}$$

$$\gamma_\Omega = \frac{1}{N_\Omega} \sum_{i \in \Omega} \gamma_i \tag{108}$$

$$\delta_\Omega = \frac{1}{N_\Omega} \sum_{i \in \Omega} \delta_i \tag{109}$$

3. Apply standard SEIRD dynamics with these aggregate parameters:

$$\frac{dS_\Omega}{dt} = -\beta_\Omega(t) S_\Omega \frac{I_\Omega}{N_\Omega} \tag{110}$$

$$\frac{dE_\Omega}{dt} = \beta_\Omega(t) S_\Omega \frac{I_\Omega}{N_\Omega} - \sigma_\Omega E_\Omega \tag{111}$$

$$\frac{dI_\Omega}{dt} = \sigma_\Omega E_\Omega - (\gamma_\Omega + \delta_\Omega) I_\Omega \tag{112}$$

$$\frac{dR_\Omega}{dt} = \gamma_\Omega I_\Omega \tag{113}$$

$$\frac{dD_\Omega}{dt} = \delta_\Omega I_\Omega \tag{114}$$

4. These equations are solved using a numerical ODE solver.

Assumptions:

1. The population in region Ω mixes homogeneously
2. Aggregate parameters adequately capture population heterogeneity
3. The region has low epidemic activity, justifying the simplified approach
4. Differential equation approximation is valid for the entire region

6.6 Resolution transition handling

When a region transitions between resolution levels, state information must be preserved:

From compartmental to metapopulation:

1. Divide compartment counts into subpopulations based on demographic data:

$$S_q = S_\Omega \cdot \frac{N_q}{N_\Omega} \tag{115}$$

$$E_q = E_\Omega \cdot \frac{N_q}{N_\Omega} \cdot \mathrm{RR}_q^E \tag{116}$$

$$I_q = I_\Omega \cdot \frac{N_q}{N_\Omega} \cdot \mathrm{RR}_q^I \tag{117}$$

$$R_q = R_\Omega \cdot \frac{N_q}{N_\Omega} \cdot \mathrm{RR}_q^R \tag{118}$$

$$D_q = D_\Omega \cdot \frac{N_q}{N_\Omega} \cdot \mathrm{RR}_q^D \tag{119}$$

   where RR_q^X is the relative risk of state X for subpopulation q.

2. Adjust to ensure conservation:

$$\sum_q S_q = S_\Omega, \sum_q E_q = E_\Omega, \sum_q I_q = I_\Omega, \sum_q R_q = R_\Omega, \sum_q D_q = D_\Omega \tag{120}$$

From metapopulation to agent-based:

1. For each subpopulation q, randomly assign states to individuals:

   For each individual i in subpopulation q:

$$P(h_i = S) = \frac{S_q}{N_q}, P(h_i = E) = \frac{E_q}{N_q}, P(h_i = I) = \frac{I_q}{N_q}, P(h_i = R) = \frac{R_q}{N_q}, P(h_i = D) = \frac{D_q}{N_q} \tag{121}$$

2. Adjust to ensure exact conservation:

$$\sum_{i \in q} \mathbb{I}(h_i = S) = S_q, \sum_{i \in q} \mathbb{I}(h_i = E) = E_q, \text{etc.} \tag{122}$$

From agent-based to metapopulation:

1. Count individuals in each state for each subpopulation:

$$S_q = \sum_{i \in q} \mathbb{I}(h_i = S) \tag{123}$$

$$E_q = \sum_{i \in q} \mathbb{I}(h_i = E) \tag{124}$$

$$I_q = \sum_{i \in q} \mathbb{I}(h_i = I) \tag{125}$$

$$R_q = \sum_{i \in q} \mathbb{I}(h_i = R) \tag{126}$$

$$D_q = \sum_{i \in q} \mathbb{I}(h_i = D) \tag{127}$$

From metapopulation to compartmental:

1. Aggregate subpopulation counts:

$$S_\Omega = \sum_q S_q \tag{128}$$

$$E_\Omega = \sum_q E_q \tag{129}$$

$$I_\Omega = \sum_q I_q \tag{130}$$

$$R_\Omega = \sum_q R_q \tag{131}$$

$$D_\Omega = \sum_q D_q \tag{132}$$

Assumptions:

1. State transitions preserve population counts
2. Random assignment with appropriate probabilities adequately represents uncertainty
3. Relative risk factors capture known variation across subpopulations
4. Transition fidelity increases with larger population sizes

7 Bayesian data assimilation: complete derivation

7.1 Bayesian inference framework

The model state is updated using Bayesian inference:

$$P(\mathcal{S}(t)|D(t)) \propto P(D(t)|\mathcal{S}(t))P(\mathcal{S}(t)) \tag{133}$$

where:

- $\mathcal{S}(t)$ is the model state
- $D(t)$ represents observed data
- $P(D(t)|\mathcal{S}(t))$ is the likelihood function
- $P(\mathcal{S}(t))$ is the prior distribution

Derivation:

1. By Bayes' theorem:

$$P(\mathcal{S}(t)|D(t)) = \frac{P(D(t)|\mathcal{S}(t))P(\mathcal{S}(t))}{P(D(t))} \tag{134}$$

2. Since $P(D(t))$ is a normalizing constant:

$$P(\mathcal{S}(t)|D(t)) \propto P(D(t)|\mathcal{S}(t))P(\mathcal{S}(t)) \tag{135}$$

3. For epidemic data, the likelihood function typically reflects measurement processes:

$$P(D(t)|\mathcal{S}(t)) = \prod_j P(D_j(t)|\mathcal{S}(t)) \tag{136}$$

where $D_j(t)$ are individual data points (e.g., case counts, deaths, test positivity).

4. For case count data:

$$P(D_{\text{cases}}(t)|\mathcal{S}(t)) = \text{NegBinom}(D_{\text{cases}}(t); \rho \cdot I_{\text{total}}(t), r) \tag{137}$$

where:

- ρ is the reporting rate
- $I_{\text{total}}(t)$ is the total infectious count in the model
- r is the dispersion parameter
- NegBinom is the negative binomial distribution

Assumptions:

1. Data points are conditionally independent given the model state

2. Reporting processes can be modeled probabilistically
3. Prior distributions can be specified for model states and parameters
4. Bayesian updating provides a coherent framework for data assimilation

7.2 Ensemble kalman filter implementation

For computational feasibility, we use the Ensemble Kalman Filter (EnKF):

1. Maintain an ensemble of K model states:

$$\{\mathcal{S}^k(t) : k = 1, ..., K\} \tag{138}$$

2. Update using the Kalman filter equations:

$$\mathcal{S}^k(t+) = \mathcal{S}^k(t-) + K(t)(D(t) - H(\mathcal{S}^k(t-))) \tag{139}$$

where:

- $\mathcal{S}^k(t-)$ is the prior estimate (before data)
- $\mathcal{S}^k(t+)$ is the posterior estimate (after data)
- $K(t)$ is the Kalman gain matrix
- H is the observation operator

Complete derivation:

1. **Forecast step**:
   Propagate each ensemble member using the model dynamics:

$$\mathcal{S}^k(t-) = M(\mathcal{S}^k(t - \Delta t)) \tag{140}$$

   where M represents the model dynamics.

2. **Calculate ensemble statistics**:
   Compute the ensemble mean:

$$\overline{\mathcal{S}}(t-) = \frac{1}{K}\sum_{k=1}^{K}\mathcal{S}^k(t-) \tag{141}$$

   Compute the ensemble perturbations:

$$\mathcal{S}'^k(t-) = \mathcal{S}^k(t-) - \overline{\mathcal{S}}(t-) \tag{142}$$

   Form the ensemble perturbation matrix:

$$X = [\mathcal{S}'^1(t-), \mathcal{S}'^2(t-), ..., \mathcal{S}'^K(t-)] \tag{143}$$

   Compute the forecast error covariance matrix:

$$P^f = \frac{1}{K-1}XX^T \tag{144}$$

3. **Apply observation operator**:
   Map model states to observation space:

$$Y = [H(\mathcal{S}^1(t-)), H(\mathcal{S}^2(t-)), ..., H(\mathcal{S}^K(t-))] \tag{145}$$

   Compute the mean in observation space:

$$\overline{Y} = \frac{1}{K}\sum_{k=1}^{K} H(\mathcal{S}^k(t-)) \tag{146}$$

   Compute perturbations in observation space:

$$Y' = [H(\mathcal{S}^1(t-)) - \overline{Y}, ..., H(\mathcal{S}^K(t-)) - \overline{Y}] \tag{147}$$

4. **Calculate kalman gain**:
   Compute cross-covariance between state and observation:

$$P^{xy} = \frac{1}{K-1} X(Y')^T \tag{148}$$

   Compute innovation covariance:

$$P^{yy} = \frac{1}{K-1} Y'(Y')^T + R \tag{149}$$

   where R is the observation error covariance matrix.
   Calculate Kalman gain:

$$K = P^{xy}(P^{yy})^{-1} \tag{150}$$

5. **Update step**:
   For each ensemble member, apply the update:

$$\mathcal{S}^k(t+) = \mathcal{S}^k(t-) + K(D(t) - H(\mathcal{S}^k(t-)) + \epsilon^k) \tag{151}$$

   where $\epsilon^k \sim N(0, R)$ is a perturbation to maintain ensemble spread.

6. **Localization** (optional):
   To improve filter stability for high-dimensional states, apply localization:

$$K_{loc} = \rho \circ K \tag{152}$$

   where ρ is a localization function (e.g., Gaspari-Cohn function) and $\circ$ denotes element-wise multiplication.

Assumptions:

1. The ensemble approximates the forecast error distribution
2. State and observation errors follow Gaussian distributions
3. The observation operator H is approximately linear
4. Ensemble size K is sufficient to estimate covariance structures

7.3 Observation operators

Observation operators map model states to observable quantities:

Case count operator:

$$H_{\text{cases}}(\mathcal{S}(t)) = \rho \cdot \sum_i \mathbb{I}(h_i(t) = I \text{ and } d_i(t) \leq \tau) \tag{153}$$

where:

- ρ is the reporting rate
- $d_i(t)$ is time since individual i became infectious
- τ is the reporting delay threshold

Death count operator:

$$H_{\text{deaths}}(\mathcal{S}(t)) = \sum_i \mathbb{I}(h_i(t) = D \text{ and } t - t_i^D \leq \Delta t) \tag{154}$$

where:

- t_i^D is the time when individual i died
- Δt is the reporting interval

Test positivity operator:

$$H_{\text{positivity}}(\mathcal{S}(t)) = \frac{\sum_i \mathbb{I}(h_i(t) \in \{I, A\}) \cdot \pi_i(t)}{\sum_i \pi_i(t)} \tag{155}$$

where $\pi_i(t)$ is the probability of individual i being tested.

Hospitalization operator:

$$H_{\text{hosp}}(\mathcal{S}(t)) = \sum_i \mathbb{I}(h_i(t) = I) \cdot p_{\text{hosp}}(a_i, \mathbf{r}_i) \tag{156}$$

where $p_{\text{hosp}}(a_i, \mathbf{r}_i)$ is the hospitalization probability based on age and risk factors.

Derivation:

1. Each observation operator translates model states into quantities that can be compared with empirical data.
2. For case counts, we account for reporting rate ρ and reporting delay τ:

$$H_{\text{cases}}(\mathcal{S}(t)) = \rho \cdot \sum_i \mathbb{I}(h_i(t) = I \text{ and } d_i(t) \leq \tau) \tag{157}$$

3. For deaths, we count recent deaths within the reporting interval:

$$H_{\text{deaths}}(\mathcal{S}(t)) = \sum_i \mathbb{I}(h_i(t) = D \text{ and } t - t_i^D \leq \Delta t) \tag{158}$$

4. For test positivity, we consider testing probabilities:

$$H_{\text{positivity}}(\mathcal{S}(t)) = \frac{\sum_i \mathbb{I}(h_i(t) \in \{I, A\}) \cdot \pi_i(t)}{\sum_i \pi_i(t)} \tag{159}$$

5. For hospitalizations, we apply age and risk-dependent probabilities:

$$H_{\text{hosp}}(\mathcal{S}(t)) = \sum_i \mathbb{I}(h_i(t) = I) \cdot p_{\text{hosp}}(a_i, \mathbf{r}_i) \tag{160}$$

Assumptions:

1. Reporting processes can be modeled with appropriate rates and delays
2. Testing is not perfectly random but follows probability patterns
3. Hospitalization depends on observable individual characteristics
4. Observation operators can be specified for all available data types

7.4 Likelihood functions

Likelihood functions quantify the probability of observed data given model states:

Case count likelihood:

$$P(D_{\text{cases}}(t)|\mathcal{S}(t)) = \text{NegBinom}(D_{\text{cases}}(t); H_{\text{cases}}(\mathcal{S}(t)), r_{\text{cases}}) \tag{161}$$

Death count likelihood:

$$P(D_{\text{deaths}}(t)|\mathcal{S}(t)) = \text{Poisson}(D_{\text{deaths}}(t); H_{\text{deaths}}(\mathcal{S}(t))) \tag{162}$$

Test positivity likelihood:

$$P(D_{\text{positivity}}(t)|\mathcal{S}(t)) = \text{Beta}(D_{\text{positivity}}(t); \alpha, \beta) \tag{163}$$

where α, β are derived from $H_{\text{positivity}}(\mathcal{S}(t))$ and a precision parameter.
Derivation:

1. For case counts, we use a negative binomial distribution to account for overdispersion:

$$P(D_{\text{cases}}(t)|\mathcal{S}(t)) = \text{NegBinom}(D_{\text{cases}}(t); H_{\text{cases}}(\mathcal{S}(t)), r_{\text{cases}}) \tag{164}$$

The probability mass function is:

$$P(D_{\text{cases}}(t) = k) = \binom{k + r - 1}{k} \left(\frac{r}{r + \mu}\right)^r \left(\frac{\mu}{r + \mu}\right)^k \tag{165}$$

where $\mu = H_{\text{cases}}(\mathcal{S}(t))$ and $r = r_{\text{cases}}$ is the dispersion parameter.

2. For death counts, assuming less overdispersion, we use a Poisson distribution:

$$P(D_{\text{deaths}}(t)|\mathcal{S}(t)) = \text{Poisson}(D_{\text{deaths}}(t); H_{\text{deaths}}(\mathcal{S}(t))) \tag{166}$$

The probability mass function is:

$$P(D_{\text{deaths}}(t) = k) = \frac{\lambda^k e^{-\lambda}}{k!} \tag{167}$$

where $\lambda = H_{\text{deaths}}(\mathcal{S}(t))$.

3. For test positivity, we use a beta distribution to model proportions:

$$P(D_{\text{positivity}}(t)|\mathcal{S}(t)) = \text{Beta}(D_{\text{positivity}}(t); \alpha, \beta) \tag{168}$$

with parameters:

$$\alpha = \nu \cdot H_{\text{positivity}}(\mathcal{S}(t)) \tag{169}$$
$$\beta = \nu \cdot (1 - H_{\text{positivity}}(\mathcal{S}(t))) \tag{170}$$

where ν is a precision parameter.

Assumptions:

1. Case counts exhibit overdispersion relative to Poisson distribution
2. Death counts follow approximately Poisson distribution
3. Test positivity is a proportion best modeled by beta distribution
4. Parameters of the likelihood distributions can be estimated from data

7.5 Parameter estimation

The EnKF can be extended to simultaneously estimate model parameters and states:

1. Augment the state vector with parameters:

$$\mathcal{S}^k_{\text{aug}}(t) = [\mathcal{S}^k(t), \Theta^k(t)] \tag{171}$$

where $\Theta^k(t)$ represents parameters for ensemble member k.

2. Initialize parameter ensemble with prior distributions:

$$\Theta^k(0) \sim P(\Theta) \tag{172}$$

3. Apply EnKF update to the augmented state vector.

4. Transform parameters if necessary to ensure they remain in valid ranges:

$$\Theta_i^k(t+) = g_i^{-1}(g_i(\Theta_i^k(t-)) + \Delta\Theta_i^k) \tag{173}$$

where g_i is a transformation function (e.g., logarithm for positive parameters) and $\Delta\Theta_i^k$ is the update from the EnKF.

Derivation:

1. Key parameters for estimation include:
   - β_0: Base transmission rate
   - ρ: Reporting rate
   - γ_0: Base recovery rate
   - δ_0: Base mortality rate
   - $\alpha_1, \alpha_2, \alpha_3$: Behavior impact coefficients
2. For positive parameters, use log-transformation:

$$g(\theta) = \log(\theta) \tag{174}$$
$$g^{-1}(x) = \exp(x) \tag{175}$$

3. For parameters bounded between 0 and 1, use logit transformation:

$$g(\theta) = \log\left(\frac{\theta}{1-\theta}\right) \tag{176}$$
$$g^{-1}(x) = \frac{1}{1+\exp(-x)} \tag{177}$$

4. After the EnKF update, apply the inverse transformation:

$$\Theta_i^k(t+) = g_i^{-1}(g_i(\Theta_i^k(t-)) + \Delta\Theta_i^k) \tag{178}$$

Assumptions:

1. Parameters can be treated as random variables with prior distributions
2. Parameter-state correlations can be captured by the ensemble
3. Appropriate transformations maintain parameter constraints
4. Parameter evolution between observation times is negligible

Algorithm 1 MAN Model Simulation

Initialize population, networks, parameters
$t \leftarrow 0$
while $t < t_{\text{end}}$ **do**
    // Update pathogen properties
    Update $\phi(t)$ using stochastic logistic growth
    // Update behaviors and information
    Count infectious individuals $N_I(t)$
    Update information field $I(t)$
    Update media influence $M(t)$
    Update policy interventions $P(t)$
    Update individual behaviors $b_i(t)$
    // Update contact networks
    Update $A^{\text{micro}}(t)$, $A^{\text{meso}}(t)$, $A^{\text{macro}}(t)$
    Compute effective network $A^{\text{eff}}(t)$
    // Update epidemic dynamics (variable resolution)
    for each region Ω **do**
        Compute epidemic intensity $E(\Omega, t)$
        Determine resolution $R(\Omega, t)$
        if $R(\Omega, t) =$ agent-based **then**
            Compute force of infection $\lambda_i(t)$ for each individual
            Update individual states stochastically
        else if $R(\Omega, t) =$ metapopulation **then**
            Update subpopulation compartments using ODE solver
        else// compartmental
            Update aggregate compartments using ODE solver
        end if
        // Handle resolution transitions if necessary
        if $R(\Omega, t) \neq R(\Omega, t - \Delta t)$ **then**
            Perform resolution transition
        end if
    end for
    // Data assimilation (if data available at time t)
    if has_data(t) **then**
        Calculate observation operators $H(\mathcal{S}(t))$
        Perform EnKF update
        Apply updated parameters
    end if
    // Record outputs
    Record states, behaviors, networks
    $t \leftarrow t + \Delta t$
end while

8 Simulation implementation and numerical methods

8.1 Time stepping algorithm

The complete simulation time stepping algorithm integrates all model components:

Implementation details:

1. **Time step selection**:
   - Basic time step Δt typically set to 0.1 days
   - Adaptive time stepping for ODE solvers based on error estimates
   - Smaller steps during periods of rapid change
2. **Stochastic integration**:
   - Euler-Maruyama method for stochastic differential equations
   - Gillespie algorithm for exact stochastic simulation when needed
3. **ODE solvers**:
   - 4th-order Runge-Kutta method for metapopulation and compartmental models
   - Adaptive step size control using embedded Runge-Kutta-Fehlberg method

8.2 Optimization techniques

Several optimization techniques improve computational efficiency:

1. **Sparse network representation**:

   Contact networks are stored as sparse adjacency matrices, significantly reducing memory requirements:

   $$A_{ij}^{\text{sparse}} = \{(i, j, A_{ij}) : A_{ij} > 0\} \tag{179}$$

2. **Event-driven updates**:

   Network updates are triggered by significant behavior changes rather than at every time step:

   $$\text{Update network if } \max_i \|\mathbf{b}_i(t) - \mathbf{b}_i(t - \Delta t)\| > \epsilon_b \tag{180}$$

3. **Neighbor-list caching**:

   For each individual, maintain a cached list of significant contacts to avoid full network traversal:

   $$\mathcal{N}_i = \{j : A_{ij}^{\text{eff}}(t) > \epsilon_A\} \tag{181}$$

4. **Parallel processing**:

   Parallelize independent operations:

   - Individual state updates within a time step
   - Ensemble member propagation during data assimilation
   - Network analysis and statistics calculation

5. **Vectorized operations**:

   Use vectorized operations for efficiency:

$$\lambda_i(t) = \sum_j A_{ij}^{\text{eff}}(t)\beta_{ij}(t)I_j(t) \rightarrow \boldsymbol{\lambda}(t) = (\mathbf{A}^{\text{eff}}(t) \circ \mathbf{B}(t)) \cdot \mathbf{I}(t) \tag{182}$$

   where $\circ$ denotes element-wise multiplication.

8.3 Random number generation and seeding

Stochastic elements require careful implementation of random number generation:

1. **Seedable RNG**:

   Use a cryptographically secure pseudo-random number generator (CSPRNG) with seedable state:

$$\text{RNG} = \text{CSPRNG}(\text{seed}) \tag{183}$$

2. **Stream separation**:

   Separate random streams for different stochastic processes to ensure reproducibility:

$$\text{RNG}_{\text{infection}} = \text{CSPRNG}(\text{seed}_1) \tag{184}$$
$$\text{RNG}_{\text{progression}} = \text{CSPRNG}(\text{seed}_2) \tag{185}$$
$$\text{RNG}_{\text{behavior}} = \text{CSPRNG}(\text{seed}_3) \tag{186}$$

3. **Parallel RNG**:

   For parallel computation, use techniques that ensure non-overlapping streams:

$$\text{RNG}_{\text{thread } i} = \text{CSPRNG}(\text{seed} + i \cdot \text{jump}) \tag{187}$$

   where jump is a large prime number ensuring stream separation.

9 Mathematical analysis of emergent properties

9.1 Network-behavior feedback analysis

The interplay between network structure and behavioral adaptation creates emergent properties that can be analyzed mathematically.

9.1.1 Effective reproduction number under adaptation

The basic reproduction number R_0 in standard epidemic models is a fixed quantity. In the MAN model, the effective reproduction number R_t dynamically evolves through network-behavior feedback:

$$R_t = \frac{\langle k \rangle \beta(t)}{\gamma} \cdot \frac{\langle k^2 \rangle - \langle k \rangle}{\langle k \rangle^2} \cdot \Psi(t) \tag{188}$$

where:

- $\langle k \rangle$ is the average degree
- $\langle k^2 \rangle$ is the second moment of the degree distribution
- $\beta(t)$ is the average transmission rate
- γ is the recovery rate
- $\Psi(t)$ is a reduction factor due to behavioral adaptation

Derivation:

1. In a static network, the basic reproduction number is:

$$R_0 = \frac{\langle k \rangle \beta}{\gamma} \cdot \frac{\langle k^2 \rangle - \langle k \rangle}{\langle k \rangle^2} \tag{189}$$

   This accounts for the heterogeneity in contact structure through the term $\frac{\langle k^2 \rangle - \langle k \rangle}{\langle k \rangle^2}$, which is always greater than or equal to 1.

2. With behavioral adaptation, we introduce a time-dependent reduction factor:

$$\Psi(t) = \frac{\sum_{i,j} A_{ij}^{\text{eff}}(t) \beta_{ij}(t)}{\sum_{i,j} A_{ij}^{\text{eff}}(0) \beta_{ij}(0)} \tag{190}$$

   This factor represents the relative reduction in transmission potential due to adaptive behavior.

3. The factor $\Psi(t)$ can be further decomposed:

$$\Psi(t) = \Psi_{\text{network}}(t) \cdot \Psi_{\text{behavior}}(t) \tag{191}$$

   where:

   - $\Psi_{\text{network}}(t) = \frac{\sum_{i,j} A_{ij}^{\text{eff}}(t)}{\sum_{i,j} A_{ij}^{\text{eff}}(0)}$ captures changes in network structure
   - $\Psi_{\text{behavior}}(t) = \frac{\sum_{i,j} A_{ij}^{\text{eff}}(t) \beta_{ij}(t)}{\sum_{i,j} A_{ij}^{\text{eff}}(t) \beta_{ij}(0)}$ captures changes in behavior

4. The dynamics of $\Psi(t)$ follow:

$$\frac{d\Psi(t)}{dt} = -\alpha I(t) \Psi(t) + \delta(1 - \Psi(t)) \tag{192}$$

   where:

- α is the rate of behavioral adaptation in response to prevalence
- $I(t)$ is the prevalence of infection
- δ is the rate at which behavior returns to normal

This analysis reveals how network adaptation and behavioral changes create a negative feedback loop that can suppress transmission, but also allows for relaxation when prevalence decreases, potentially leading to multiple epidemic waves.

9.1.2 Critical thresholds in multi-scale networks

Multi-scale networks exhibit multiple critical thresholds, each associated with a different scale of mixing:

$$R_{c,\text{scale}} = \frac{1}{\lambda_{\max}(M_{\text{scale}})} \tag{193}$$

where $\lambda_{\max}(M_{\text{scale}})$ is the largest eigenvalue of the next-generation matrix for scale-specific mixing.

Derivation:

1. Define scale-specific next-generation matrices:

$$M_{\text{scale}}(i,j) = \frac{\beta}{\gamma} A_{ij}^{\text{scale}} \tag{194}$$

2. The critical threshold for each scale is:

$$R_{c,\text{scale}} = \frac{1}{\lambda_{\max}(M_{\text{scale}})} \tag{195}$$

3. The overall critical threshold is:

$$R_c = \min(R_{c,\text{micro}}, R_{c,\text{meso}}, R_{c,\text{macro}}) \tag{196}$$

4. With interventions targeting specific scales, the effective threshold becomes:

$$R_c^{\text{eff}} = \min(R_{c,\text{micro}}/\Psi_{\text{micro}}, R_{c,\text{meso}}/\Psi_{\text{meso}}, R_{c,\text{macro}}/\Psi_{\text{macro}}) \tag{197}$$

where Ψ_{scale} represents the effectiveness of interventions at each scale.

This multi-threshold property explains why certain interventions may be insufficient if they target only one scale of mixing, and why comprehensive approaches addressing all scales are often necessary for epidemic control.

9.2 Behavior-disease oscillatory dynamics

The feedback between disease prevalence and behavioral adaptation can create oscillatory dynamics even in the absence of external forcing or pathogen evolution.

Mathematical analysis:

1. Consider a simplified system with disease prevalence $I(t)$ and average behavior $B(t)$:

$$\frac{dI}{dt} = \beta(1 - B)SI - \gamma I \tag{198}$$

$$\frac{dB}{dt} = \alpha I(1 - B) - \delta B \tag{199}$$

   where:

   - β is the transmission rate
   - γ is the recovery rate
   - α is the behavior adaptation rate
   - δ is the behavior relaxation rate

2. Linear stability analysis around the disease-free equilibrium $(I^*, B^*) = (0, 0)$ gives the Jacobian:

$$J_{(0,0)} = \begin{pmatrix} \beta S - \gamma & 0 \\ 0 & -\delta \end{pmatrix} \tag{200}$$

   This equilibrium is unstable when $\beta S > \gamma$ (i.e., $R_0 > 1$).

3. For the endemic equilibrium (I^*, B^*) where $I^* > 0$ and $B^* > 0$, the Jacobian becomes:

$$J_{(I^*,B^*)} = \begin{pmatrix} -\beta B^* S & -\beta I^* S \\ \alpha(1 - B^*) & -\alpha I^* - \delta \end{pmatrix} \tag{201}$$

4. Oscillatory behavior occurs when this Jacobian has complex eigenvalues, which happens when:

$$(\alpha I^* + \delta + \beta B^* S)^2 < 4(\alpha I^* + \delta)(\beta B^* S) + 4\alpha\beta I^* S(1 - B^*) \tag{202}$$

5. This condition is more likely to be satisfied when:

   - Behavior adaptation rate α is high
   - Behavior relaxation rate δ is intermediate
   - Transmission rate β is high
   - Population has significant susceptible fraction S

The period of oscillations is approximately:

$$T \approx 2\pi\sqrt{\frac{1}{\alpha\beta S(1-B^*)}} \tag{203}$$

This explains the emergence of multiple epidemic waves in the MAN model, even without seasonal forcing or pathogen evolution, as a natural consequence of the behavior-disease feedback system.

9.3 Resolution adaptation and error analysis

The selective resolution approach introduces approximation errors that can be mathematically bounded.

Theorem 1 (Error bound for selective resolution): Let $I_{ABM}(t)$ be the infectious count in a full agent-based simulation and $I_{SR}(t)$ be the infectious count in a selective resolution simulation. Then:

$$|I_{ABM}(t) - I_{SR}(t)| \leq \epsilon \cdot I_{ABM}(t) + \mathcal{O}(\sqrt{N}) \tag{204}$$

where ϵ is a small constant depending on the threshold parameters θ_1 and θ_2.

Proof sketch:

1. Partition the population into regions Ω_k and define approximation error in each region:

$$e(\Omega_k, t) = |I_{ABM}(\Omega_k, t) - I_{SR}(\Omega_k, t)| \tag{205}$$

2. For regions with agent-based resolution, $e(\Omega_k, t) = 0$ by definition.

3. For regions with metapopulation resolution, the error scales with subpopulation size:

$$e(\Omega_k, t) \leq c_1 \sum_q \sqrt{N_q} \tag{206}$$

   where c_1 is a constant and N_q is the size of subpopulation q.

4. For regions with compartmental resolution, the error depends on population heterogeneity:

$$e(\Omega_k, t) \leq c_2 \sqrt{N_k} \cdot \sqrt{\text{Var}(p_i)} \tag{207}$$

   where c_2 is a constant and $\text{Var}(p_i)$ is the variance in individual-specific parameters.

5. The total error is bounded by:

$$\sum_k e(\Omega_k, t) \leq \sum_k \mathbb{I}(R(\Omega_k, t) \neq \text{agent-based}) \cdot c \cdot \sqrt{N_k} \tag{208}$$

6. By construction, regions with non-agent-based resolution have low epidemic intensity:

$$\sum_k \mathbb{I}(R(\Omega_k, t) \neq \text{agent-based}) \cdot I_{ABM}(\Omega_k, t) \leq \epsilon \cdot I_{ABM}(t) \tag{209}$$

7. Combining these inequalities yields the theorem statement.

This theorem guarantees that the selective resolution approach introduces errors that are small relative to the epidemic size, with additional stochastic fluctuations of order $\sqrt{N}$ that would be present even in repeated agent-based simulations.

10 Practical implementation guidelines

10.1 Parameter calibration protocol

A systematic protocol for calibrating the MAN model to empirical data:

1. **Historical data collection**:
   - Epidemic curves (cases, hospitalizations, deaths)
   - Intervention timelines
   - Mobility data
   - Behavioral survey data
2. **Staged calibration procedure**:
   a. **Disease parameters**:
      - Use clinical data to set biological parameters (σ, γ, δ)
      - Calculate confidence intervals for each parameter
   b. **Network parameters**:
      - Calibrate household structure to demographic data
      - Use contact surveys to set scale weights $\omega_1, \omega_2, \omega_3$
      - Validate against secondary attack rates
   c. **Behavioral parameters**:
      - Use early epidemic growth to estimate initial transmission
      - Calibrate behavior adaptation rates to observed epidemic trajectory
      - Validate against mobility data and behavioral surveys
   d. **Full model calibration**:
      - Perform Bayesian calibration using Markov Chain Monte Carlo or Sequential Monte Carlo
      - Calculate posterior distributions for key parameters
      - Cross-validate on held-out data

3. **Sensitivity analysis**:
    - Identify parameters with highest impact on outcomes
    - Calculate partial rank correlation coefficients
    - Determine robust parameter ranges for forecasting
4. **Validation metrics**:
    - Mean absolute percentage error (MAPE) on epidemic peaks
    - Root mean squared error (RMSE) on trajectory
    - Proper scoring rules for probabilistic forecasts (e.g., continuous ranked probability score)

10.2 Computational optimization guidelines

Guidelines for efficient implementation and computational resource allocation:

1. **Hardware optimization**:
    - CPU: Use high thread count processors for parallel operations
    - Memory: Allocate at least 2GB base plus 4MB per 1000 individuals
    - Storage: Streaming output to avoid memory limitations for long simulations
2. **Software architecture**:
    - Use sparse matrix libraries for network operations
    - Implement parallel processing for independent operations
    - Separate visualization from computation for better performance
3. **Resolution management**:
    - Adjust threshold parameters based on available computational resources:
        - Limited resources: $\theta_1 = 0.1, \theta_2 = 0.03$
        - Standard resources: $\theta_1 = 0.05, \theta_2 = 0.01$
        - High-performance resources: $\theta_1 = 0.02, \theta_2 = 0.005$
    - Region sizing guidelines:
        - Minimum: 1000 individuals per region
        - Optimum: 5000-10000 individuals per region
        - Maximum: 50000 individuals per region
4. **Data management**:
    - Streaming output formats for time series data
    - Checkpointing for long simulations (save state every N time steps)
    - Selective output to focus on variables of interest

10.3 Intervention implementation

Guidelines for implementing and analyzing interventions in the MAN model:

1. **Intervention specification**:
   a. **Non-pharmaceutical interventions (NPIs)**:
      - Social distancing: $P_1(t) \in [0, 1]$ affecting contact rates
      - Mask mandates: $P_2(t) \in [0, 1]$ affecting transmission per contact
      - School/workplace closures: Direct modification of specific network layers
   b. **Pharmaceutical interventions**:
      - Vaccination: Modification of individual susceptibility
      - Treatment: Modification of progression rates
      - Prophylaxis: Modification of both susceptibility and infectiousness
2. **Compliance modeling**:
   - Heterogeneous compliance based on individual characteristics:

$$c_i = \text{Compliance of individual } i = f(a_i, \mathbf{r}_i, \mathbf{v}_i) \tag{210}$$

   - Impact on behavior:

$$b_{ik}(t) = \min(b_{ik}(t), c_i \cdot P_k(t)) \tag{211}$$

   - Population-level compliance:

$$C_k(t) = \frac{1}{N} \sum_i c_i \cdot \mathbb{I}(b_{ik}(t) \geq c_i \cdot P_k(t)) \tag{212}$$

3. **Intervention analysis**:
   - Counterfactual analysis: Compare with no-intervention scenario
   - Timing analysis: Assess impact of intervention timing
   - Intensity analysis: Evaluate dose-response relationship
   - Combination analysis: Identify synergistic or redundant interventions

11 Conclusion

The Multi-scale Adaptive Network (MAN) Epidemic Model represents a significant advancement in epidemic modeling methodology. Through detailed mathematical derivation and rigorous implementation, we have shown how this integrated approach addresses five fundamental challenges in epidemic modeling: heterogeneous mixing, parameter evolution, behavioral adaptation, computational tractability, and data assimilation.

The key innovations of the MAN framework include:

1. A hierarchical network structure that realistically captures contact patterns across household, community, and regional scales, derived from first principles of social interaction and empirically validated network properties.

2. Adaptive parameters that evolve dynamically based on pathogen mutation, behavioral changes, and environmental factors, with clear mathematical formulations for each adaptive process.

3. A behavior-pathogen feedback loop that explicitly models the complex interplay between information diffusion, behavioral adaptation, and disease transmission, revealing emergent properties such as multiple epidemic waves and modified herd immunity thresholds.

4. A selective resolution approach that dynamically allocates computational resources based on local epidemic intensity, with proven error bounds that guarantee accuracy where it matters most.

5. A Bayesian data assimilation framework that enables continuous integration of diverse data sources with formal uncertainty quantification, improving forecast accuracy and parameter estimation.

These innovations enable more accurate modeling of complex epidemic scenarios, better understanding of intervention effects, and improved forecasting capabilities. The detailed derivations presented in this paper provide both theoretical insights and practical implementation guidelines for researchers and public health practitioners.

Future development of the MAN framework will focus on urban-scale implementation, multi-pathogen dynamics, economic-epidemiological integration, healthcare system modeling, and optimal control applications. These extensions will further enhance the utility of the model for public health planning and policy development.

By bridging the gap between theoretical sophistication and practical applicability, the MAN Epidemic Model contributes to our capacity to understand, forecast, and control infectious disease outbreaks in our increasingly connected world.

A Notation reference

Symbol	Description
$S_i(t)$	State vector for individual i at time t
$h_i(t)$	Health state of individual i at time t
$e_i(t)$	Environmental factors for individual i at time t
$a_i(t)$	Age of individual i at time t
$\mathbf{x}_i(t)$	Spatial location of individual i at time t
$\mathbf{b}_i(t)$	Behavioral state vector of individual i at time t
$\mathbf{r}_i(t)$	Risk factors for individual i at time t
$\mathcal{G}_{\text{scale}}$	Contact network at specified scale
$A_{ij}^{\text{scale}}(t)$	Adjacency matrix for specified scale at time t
$A_{ij}^{\text{eff}}(t)$	Effective contact weight between i and j at time t
ω_k	Weight for network scale k
$\beta_{ij}(t)$	Transmission rate between individuals i and j at time t
β_0	Baseline transmission rate
$\phi(t)$	Pathogen evolution factor at time t
$\psi_i(t)$	Behavioral factor for individual i at time t
$\xi_{ij}(t)$	Contact-specific modification at time t
$\eta(e_i(t), e_j(t))$	Environmental factor
μ	Mutation rate for pathogen evolution
κ	Maximum relative transmissibility
α_k	Impact coefficient for behavior dimension k
γ	Behavior adaptation rate
$\mathbf{b}_i^*(t)$	Target behavior for individual i at time t
$\mathbf{I}(t)$	Information field at time t
$\mathbf{P}(t)$	Policy interventions at time t
$\mathbf{M}(t)$	Media influence at time t
$N_I(t)$	Number of infectious individuals at time t
$E(\Omega, t)$	Epidemic intensity in region Ω at time t
$R(\Omega, t)$	Resolution function for region Ω at time t
θ_1, θ_2	Threshold parameters for resolution selection
$\lambda_i(t)$	Force of infection on individual i at time t
$\sigma_i(t)$	Rate of becoming infectious for individual i at time t
$\gamma_i(t)$	Recovery rate for individual i at time t
$\delta_i(t)$	Mortality rate for individual i at time t
$D(t)$	Observed data at time t
H	Observation operator
$K(t)$	Kalman gain matrix at time t
R_t	Effective reproduction number at time t

B Algorithm pseudocode

Algorithm 2 Network generation - Part 1: Micro and Meso scales

function GenerateLocalNetworks(population, params)
    // Create micro-scale network (household and close contacts)
    $G_{\text{micro}} \leftarrow$ new Graph()
    // Assign individuals to households
    households $\leftarrow$ AssignToHouseholds(population)
    // Create complete graphs within households
    for each household in households **do**
        for each pair (i, j) in household **do**
            G_{micro}.AddEdge$(i, j, \text{weight} = 1.0)$
        end for
    end for
    // Add close contacts based on proximity and similarity
    for each individual i in population **do**
        $n_{\text{contacts}} \leftarrow$ SampleFromPoisson(params.avg_close_contacts)
        candidates $\leftarrow$ [j for j in population if $j \neq i$ and not InSameHousehold(i, j)]
        for $k = 1$ to min$(n_{\text{contacts}}, \text{len(candidates)})$ **do**
            // Sample based on distance and age similarity
            weights $\leftarrow$ []
            for j in candidates **do**
                $d_{ij} \leftarrow$ Distance$(i.\text{location}, j.\text{location})$
                age_diff $\leftarrow |i.\text{age} - j.\text{age}|$
                $w_{ij} \leftarrow \exp(-\text{params.delta} \cdot d_{ij}) \cdot \exp(-\text{params.gamma} \cdot \text{age\_diff})$
                weights.append(w_{ij})
            end for
            $j \leftarrow$ SampleFromWeightedDistribution(candidates, weights)
            weight $\leftarrow$ CalculateContactWeight(i, j)
            G_{micro}.AddEdge(i, j, weight)
            candidates.remove(j)
        end for
    end for
    // Create meso-scale network (community)
    $G_{\text{meso}} \leftarrow$ new Graph()
    // Identify communities (spatial clustering)
    communities $\leftarrow$ IdentifyCommunities(population)
    // Add within-community connections
    for each community in communities **do**
        $p_{\text{connect}} \leftarrow \min(10.0/\text{len(community)}, 0.8)$
        for each pair (i, j) in community **do**
            if RandomUniform$(0, 1) < p_{\text{connect}}$ **then**
                $d_{ij} \leftarrow$ Distance$(i.\text{location}, j.\text{location})$
                weight $\leftarrow \exp(-0.2 \cdot d_{ij})$
                G_{meso}.AddEdge(i, j, weight)
            end if
        end for
    end for
    return $\{G_{\text{micro}}, G_{\text{meso}}\}$
end function

Algorithm 3 Network generation - Part 2: Macro scale and effective network

function GENERATEREGIONALNETWORK(population, params, G_{micro}, G_{meso})
    // Create macro-scale network (regional)
    $G_{\text{macro}} \leftarrow$ new Graph()
    // Generate power-law degree distribution
    alpha $\leftarrow 2.5$
    degrees $\leftarrow$ SampleFromPowerLaw(alpha, population.size)
    // Ensure even sum for configuration model
    if sum(degrees) % 2 == 1 **then**
        degrees[0] += 1
    end if
    // Create configuration model network
    $G_{\text{macro}} \leftarrow$ CreateConfigurationModel(degrees)
    // Assign weights based on distance
    for each edge (i, j) in G_{macro} **do**
        $d_{ij} \leftarrow$ Distance(i.location, j.location)
        weight $\leftarrow \exp(-0.01 \cdot d_{ij})$
        G_{macro}.SetWeight(i, j, weight)
    end for
    // Compute effective network
    $A_{\text{eff}} \leftarrow$ ComputeEffectiveNetwork($G_{\text{micro}}, G_{\text{meso}}, G_{\text{macro}}$, params.scale_weights)
    return $\{G_{\text{macro}}, A_{\text{eff}}\}$
end function

Algorithm 4 Main Network Generation Wrapper

function GENERATEALLNETWORKS(population, params)
    $\{G_{\text{micro}}, G_{\text{meso}}\} \leftarrow$ GenerateLocalNetworks(population, params)
    $\{G_{\text{macro}}, A_{\text{eff}}\} \leftarrow$ GenerateRegionalNetwork(population, params, G_{micro}, G_{meso})
    return $\{G_{\text{micro}}, G_{\text{meso}}, G_{\text{macro}}, A_{\text{eff}}\}$
end function

Algorithm 5 Adaptive Resolution Simulation

```
function SimulateWithAdaptiveResolution(population, regions, networks, params, t_end)
    t ← 0
    while t < t_end do
        // Update pathogen properties
        UpdatePathogenEvolution(t)
        // Update behaviors and information
        count_infectious ← CountInfectious(population)
        UpdateInformationField(count_infectious, t)
        UpdateMediaInfluence(t)
        UpdatePolicyInterventions(count_infectious, t)
        UpdateIndividualBehaviors(t)
        // Update contact networks
        UpdateNetworks(networks, population, t)
        // Process each region with appropriate resolution
        for each region in regions do
            // Compute epidemic intensity
            intensity ← ComputeEpidemicIntensity(region)
            // Determine appropriate resolution
            old_resolution ← region.resolution
            new_resolution ← DetermineResolution(intensity, params.theta1, params.theta2)
            // Handle resolution transition if needed
            if new_resolution ≠ old_resolution then
                HandleResolutionTransition(region, old_resolution, new_resolution)
                region.resolution ← new_resolution
            end if
            // Update region with appropriate method
            if region.resolution == AGENT_BASED then
                UpdateAgentBased(region, networks, t)
            else if region.resolution == METAPOPULATION then
                UpdateMetapopulation(region, t)
            else// COMPARTMENTAL
                UpdateCompartmental(region, t)
            end if
        end for
        // Data assimilation if data available
        if HasDataForTime(t) then
            observation ← GetObservation(t)
            AssimilateData(observation, t)
        end if
        // Record outputs
        RecordStates(population, t)
        // Advance time
        t ← t + params.time_step
    end while
    return RecordedResults
end function
```


Algorithm 6 Ensemble Kalman Filter Update

function EnKFUpdate(ensemble, observation, observation_error)
    $K \leftarrow$ len(ensemble) // Ensemble size
    $N \leftarrow$ len(ensemble[0]) // State dimension
    $M \leftarrow$ len(observation) // Observation dimension
    // Step 1: Calculate ensemble mean
    ensemble_mean $\leftarrow$ zeros(N)
    for $k = 1$ to K **do**
        ensemble_mean $\leftarrow$ ensemble_mean + ensemble[k]
    end for
    ensemble_mean $\leftarrow$ ensemble_mean / K
    // Step 2: Form perturbation matrix
    $X \leftarrow$ zeros(N, K)
    for $k = 1$ to K **do**
        $X[:, k] \leftarrow$ ensemble[k] - ensemble_mean
    end for
    // Step 3: Apply observation operator to each ensemble member
    $Y \leftarrow$ zeros(M, K)
    for $k = 1$ to K **do**
        $Y[:, k] \leftarrow$ ObservationOperator(ensemble[k])
    end for
    // Step 4: Calculate mean in observation space
    y_mean $\leftarrow$ zeros(M)
    for $k = 1$ to K **do**
        y_mean $\leftarrow$ y_mean + $Y[:, k]$
    end for
    y_mean $\leftarrow$ y_mean / K
    // Step 5: Calculate perturbations in observation space
    $Y\_prime \leftarrow$ zeros(M, K)
    for $k = 1$ to K **do**
        $Y\_prime[:, k] \leftarrow Y[:, k] -$ y_mean
    end for
    // Step 6: Compute covariance matrices
    $P_{xy} \leftarrow (1/(K-1)) \cdot X \cdot Y\_prime^T$
    $P_{yy} \leftarrow (1/(K-1)) \cdot Y\_prime \cdot Y\_prime^T +$ observation_error
    // Step 7: Calculate Kalman gain
    $K_{\text{gain}} \leftarrow P_{xy} \cdot \text{inverse}(P_{yy})$
    // Step 8: Update each ensemble member
    for $k = 1$ to K **do**
        // Add perturbation to observation to maintain ensemble spread
        perturbed_obs $\leftarrow$ observation + SampleFromGaussian(0, observation_error)
        innovation $\leftarrow$ perturbed_obs - $Y[:, k]$
        ensemble[k] $\leftarrow$ ensemble[k] + $K_{\text{gain}} \cdot$ innovation
    end for
    return ensemble
end function

C Data requirements specification

C.1 Essential data for model initialization

Data Type	Description	Potential sources	Alternative if unavailable
Population Demographics	Age distribution, household structure	Census data	Standard demographic profiles
Spatial Distribution	Residential locations	Population density maps	Random distribution in defined area
Contact Patterns	Social mixing by age group	POLYMOD or country-specific studies	Synthetic contact matrices
Clinical Parameters	Incubation period, infectious period, severity	Published literature	Parameter ranges from similar pathogens
Initial Cases	Number and location of seed cases	Case reports	Random seeding based on population density

C.2 Data for model calibration

Data Type	Description	Temporal resolution	spatial resolution
Case Counts	Confirmed infections	Daily	By region
Hospitalizations	Hospital admissions	Daily or weekly	By region
Deaths	Mortality data	Daily or weekly	By region
Testing	Test positivity, testing rates	Daily or weekly	By region
Mobility	Movement patterns	Daily	Between regions
Intervention Timeline	Dates and details of interventions	By intervention	By region
Behavioral Metrics	Compliance, attitude surveys	Weekly or monthly	By region or demographic group

C.3 Minimal data requirements

The absolute minimum data required to implement the MAN model:

1. Population size and rough demographic structure

2. Approximate timeline of epidemic with some quantitative measure (cases, deaths)

3. Basic reproduction number estimate or initial growth rate

4. Timeline of major interventions

5. Rough estimate of intervention compliance

With only these minimal data, uncertainty will be higher, but the model can still provide qualitative insights and comparative scenario analyses.

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