

# R shiny APP: an Agent Based Model - SEIR Simulation Platform

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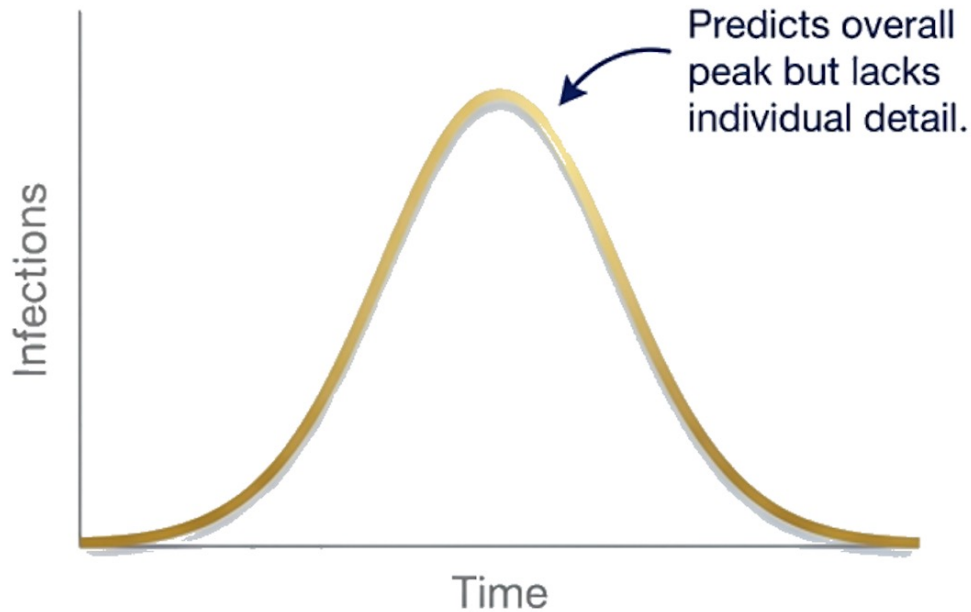


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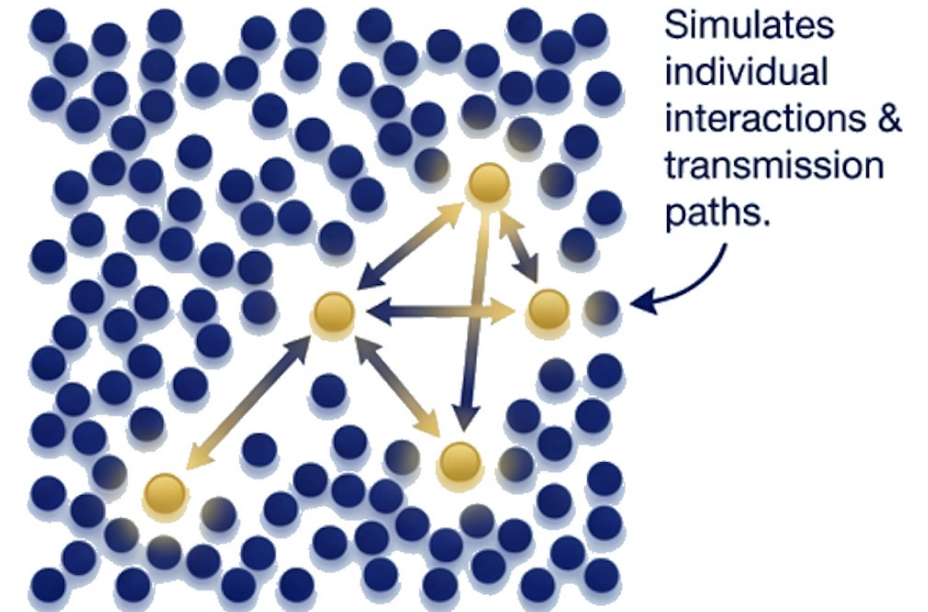
# Step 1. Background & Methods

## Aggregate Models



Aggregate equation-based models treat the population as a uniform whole. They are useful for broad trends but miss the granular, real-world dynamics that emerge from individual interactions.

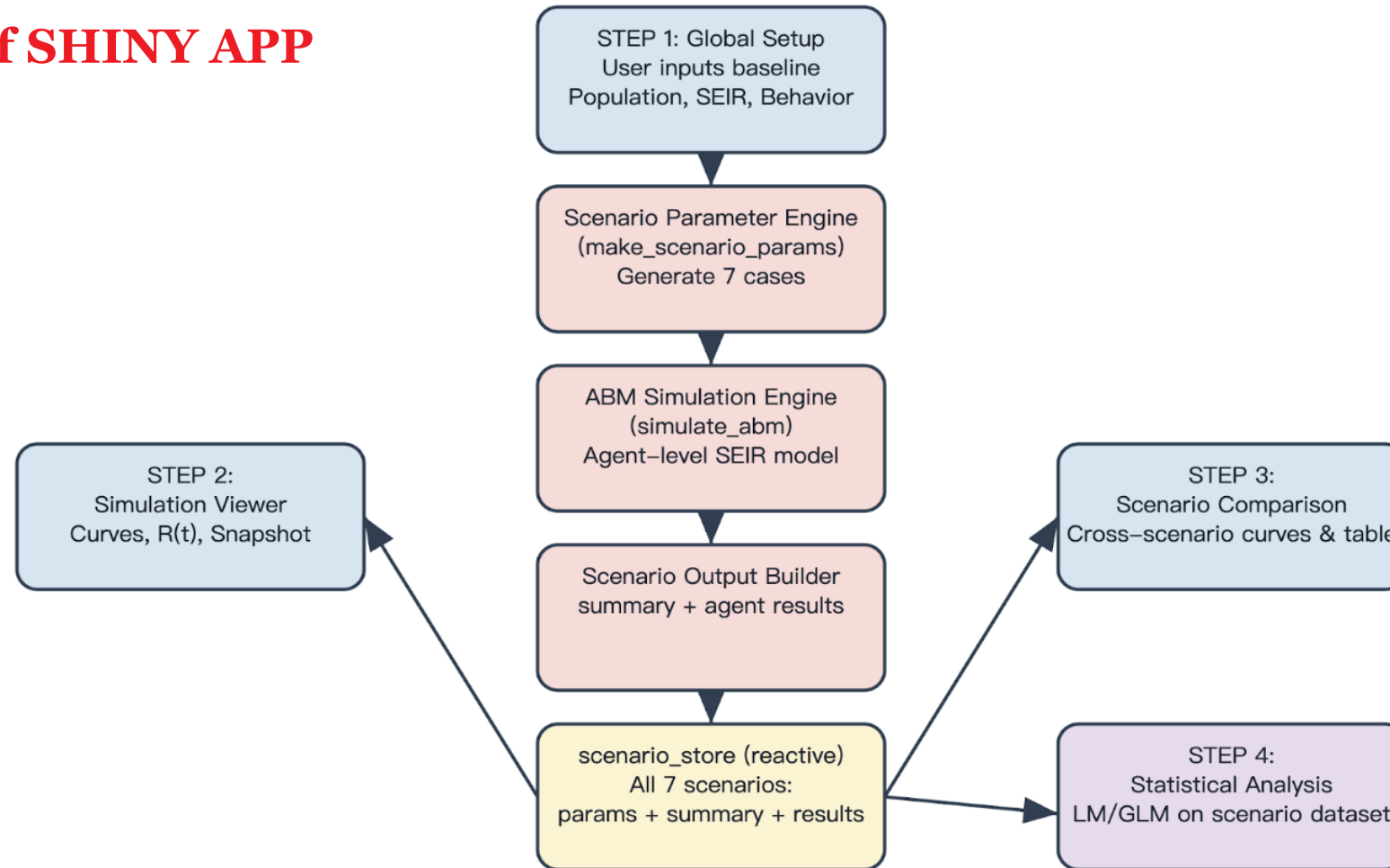
## Our Approach: Agent-Based Models



Our framework simulates thousands of individual agents, each with unique states and interactions. This bottom-up approach creates more realistic, emergent patterns, moving beyond simple curves to capture complexity.

# Step 1. Background & Methods

## Workflow of SHINY APP



# Step 2. Key Concepts & Parameters

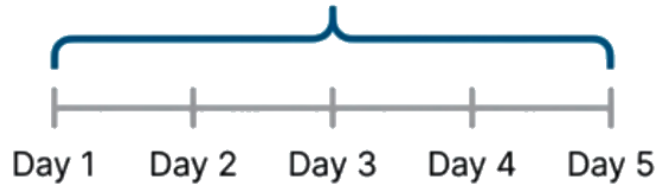
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## Epidemiological Compartments

- **Susceptible (S):** Vulnerable individuals.  
Probability of infection depends on local prevalence.
- **Exposed (E):** Infected but not yet infectious (Latent period).
- **Infected (I):** Infectious individuals capable of transmitting the virus.
- **Recovered (R):** Immune individuals removed from the transmission chain.

## Step 2. Key Concepts & Parameters

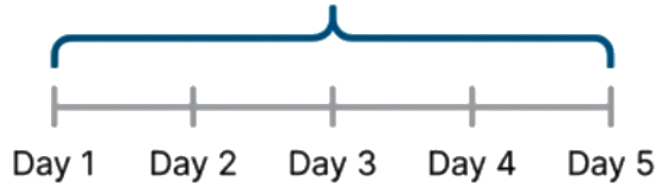
Incubation Period



$$\text{Incubation Rate } (\sigma) = \frac{1}{T_{\text{inc}}} = \frac{1}{5} = 0.2$$

A 20% daily probability of an Exposed agent becoming Infectious.

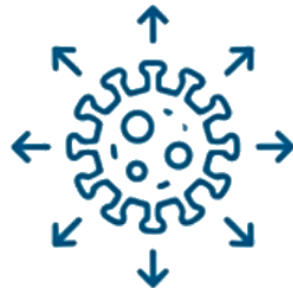
Infectious Period



$$\text{Recovery Rate } (\gamma) = \frac{1}{T_{\text{inf}}} = \frac{1}{5} = 0.2$$

A 20% daily probability of an Infectious agent Recovering.

Transmission



Transmission Rate ( $\beta$ )

The core driver of spread. Related to  $R_0$  by  $R_0 = \frac{\beta}{\gamma}$ .  
This is the parameter interventions will modify.

# Step 3. Mathematical Framework

## Stochastic SEIR Foundations (Discrete-Time Model)

- SEIR as Individual-Level Stochastic Transitions

Each individual evolves independently through the states:

$$S \rightarrow E \rightarrow I \rightarrow R$$

- Biological Durations  $\rightarrow$  Rates  $\rightarrow$  Daily Transition Probabilities

Empirical epidemiological durations are mapped into per-day transition rates, then converted into probabilities used in simulation.

### Incubation (Latent) Transition

Average incubation period:  $T_{\text{inc}}$

$$\sigma = \frac{1}{T_{\text{inc}}}$$

Daily probability that an Exposed agent becomes Infectious:

$$P(E \rightarrow I) = 1 - e^{-\sigma \Delta t}$$

### Infectious (Recovery) Transition

Average infectious period:  $T_{\text{inf}}$

$$\gamma = \frac{1}{T_{\text{inf}}}$$

Daily probability that an Infectious agent recovers:

$$P(I \rightarrow R) = 1 - e^{-\gamma \Delta t}$$

# Step 3. Mathematical Framework

## Transmission Dynamics: Effective $\beta$ & Force of Infection

- Effective Transmission Rate ( $\beta_{\text{eff}}$ ) Under Interventions

Interventions (masking, distancing) do not alter SEIR structure, but directly reduce transmissibility.

Baseline transmission rate:  $\beta$

Intervention-adjusted rate:  $\beta_{\text{eff}} = \beta(1 - \text{MaskEffect})(1 - \text{SocialDistancing})$

- Force of Infection ( $\lambda$ ): Linking Exposure to Prevalence

For each susceptible agent, infection risk depends on:

- effective transmissibility  $\beta_{\text{eff}}$
- average contact rate  $c$
- current infection prevalence  $I/N$
- The instantaneous force of infection:

$$\lambda = \beta_{\text{eff}} c \frac{I}{N}$$

- Daily Probability of Infection for Susceptible Agents

Using the exponential survival form:  $P(S \rightarrow E) = 1 - e^{-\lambda \Delta t}$



# Step 3. Mathematical Framework

## Stochastic Transition Kernel & Emergent Dynamics

- Summary of Transition Probabilities

Transition	Formula	Meaning
$S \rightarrow E$	$1 - e^{-\lambda}$	Infection probability
$E \rightarrow I$	$1 - e^{-\sigma}$	End of incubation
$I \rightarrow R$	$1 - e^{-\gamma}$	Recovery probability

- From Micro-Level Stochasticity to Macro-Level Epidemic Waves

Aggregating thousands of agents produces:

- epidemic curves
- peak prevalence
- timing of outbreak
- scenario differences driven by  $\beta_{\text{ef}}$

Monte Carlo repetitions further estimate **mean trajectories and confidence intervals**.

## Step 4. Statistical Analysis

$$Y = \beta_0 + \underbrace{\beta_1 SD + \beta_2 Mask + \beta_3 Lockdown}_{\text{Main Effects}} + \underbrace{\beta_{ij}(X_i \times X_j)}_{\text{Interaction Terms}} + \epsilon$$

### Model Fitting

- Fitting **linear regression model** to the aggregate dataset ( $N = \text{Scenarios} \times \text{Repetitions}$ ). Outcome Variables includes *`Peak Prevalence`* and *`Day of Peak`*.
- To capture the potential effects of combined interventions, the model includes pairwise interaction terms between all selected **predictors (Social Distancing, Mask Usage, and Lockdown)**.

## Step 4. Statistical Analysis

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### Notes for Interaction Terms

- **Baseline Trap:** In models with interactions, the main effect coefficient represents the outcome only when the interacting variable is zero.
- **Avoid Isolated Interpretation:** When an interaction term is significant, coefficients cannot be interpreted in isolation.
- **Focus on Net Effect:** Evaluate true effectiveness based on the net effect under specific conditions.

## 5. Limitations & Future Work

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**While this simulation provides valuable insights, the following limitations should be considered and may improved in future:**

- **Computational Constraints (Population Size):** Agent-Based Models require significant memory. To ensure this app runs smoothly in the browser, we limited the simulation to a maximum of 5,000 individuals.

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- **Limited Scenarios & Data:** Our simulation follows the setting in Silva et al. (2020). This means we are limited to the 7 specific scenarios and parameters defined in that paper, resulting in a relatively small dataset.

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- **Limited Scenarios & Data:** Our simulation follows the setting in Silva et al. (2020). This means we are limited to the 7 specific scenarios and parameters defined in that paper, resulting in a relatively small dataset.
- **Modeling Assumptions:** We used a basic linear regression model to analyze the results. While useful for general trends, a more advance model might be needed to capture the complicated details of viral transmission.

## 6. Resources & References

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### Our Project Resource:

- **GitHub:** <https://github.com/fan-zhongyu/ABM-SEIR-Simulation>
- **R shiny APP:** <https://zhongyu.shinyapps.io/2560FinalProject/>

### Other Interesting Related Resources:

- **Epidemic Calculator by Goh:** [https://gabgoh.github.io/COVID/?utm\\_source=catalyzex.com](https://gabgoh.github.io/COVID/?utm_source=catalyzex.com)
- **Interactive Agent-Based Model Visualization for COVID-19 Masking:** <https://dek.ai/masksim/>

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## 6. Resources & References

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# R Shiny APP Demonstration



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# Thank You



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