Project 14: Advanced Pandemic Flu Spread Simulation **Plan**

Advanced Pandemic Flu Spread Simulation Using Agent-Based Modeling

Overview

The goal of this project is to simulate the spread of pandemic flu within a large, spatially explicit population using an agent-based approach. The model allows for investigation of infection dynamics, intervention strategies, and vaccination logistics, providing a rigorous platform for quantitative analysis and policy exploration.

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1. Problem Statement

A novel strain of pandemic influenza is introduced into a large, susceptible community. A few infectious individuals enter, and transmission occurs through spatially-localized interactions. Public health measures such as masking, social distancing, and vaccination are possible but may face logistical challenges (such as supply chain delays or partial/late dosing). The goal is to:

- Model infection spread temporally and spatially.
- Evaluate the effects of different interventions and vaccination strategies.
- Quantify outcomes as total infections, deaths, and epidemic duration.

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2. Background and Rationale

Previous flu simulations often focused on small, homogeneous populations (e.g., a single classroom) or employed deterministic population-level models. To capture stochasticity, spatial effects, and heterogeneity in interactions/intervention, an agent-based stochastic simulation on a 2D grid is proposed. This approach reflects modern practices in epidemiological modeling, as seen in recent research and COVID-19 studies.pmc.ncbi.nlm.nih+3

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3. Model Structure

3.1 Spatial and Temporal Setup

- The environment is a 2D grid (e.g., 1000 x 1000 cells), representing a community.
- Each cell may be empty or occupied by at most one agent.
- Time progresses in discrete steps (e.g., one step = one hour or day).

3.2 Agents

- Each agent represents a person and has attributes:
  - Health state: **Susceptible (S), Exposed (E), Infectious (I), Recovered/Removed (R)**
  - Days since state transition (used for incubation/infectious period counters)
  - Vaccination status: unvaccinated, partially vaccinated, fully vaccinated
  - Masking/social distancing behavior (parameterized)

3.3 Movement and Interactions

- Every time step, each agent may move in a random direction within grid boundaries (random walk).
- Upon “contact”—when two agents occupy neighboring (or same) cells—infection may transmit depending on their health/vaccination/mask status and preset probabilities.

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4. Infection Dynamics

- Infection is transmitted when a susceptible agent comes into contact with an infectious agent.
- Upon infection, an agent enters the Exposed state (latent/incubation period).
- After a set number of steps, Exposed becomes Infectious.
- After the infectious period, agents enter the Recovered/Removed state; they cannot be reinfected.
- Death can be modeled as transition to an “inactive” state (optional).

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5. Interventions and Vaccination

- **Masking/Social Distancing:** Reduces movement (for distancing) and/or probability of transmission (for masking).
- **Vaccination:** Agents may be vaccinated at different time points, modeled with:
  - Supply constraints/delays
  - One vs. two dose schedules: single dose provides partial immunity; two doses = full immunity.
  - Probabilities for breakthrough infection
- Can simulate “dose-stretching” strategies by giving wider single doses when supply is tight.

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6. Simulation Outcome Metrics

Evaluate and report:

- Total number of people infected, severe cases, deaths (if modeled)
- Epidemic duration (steps from first to last infection)
- Comparative effect of intervention strategies
- Statistical measures: means, standard deviations/confidence intervals over multiple runs

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7. Monte Carlo and Statistical Analysis

- Each simulation run is stochastic; repeat multiple times per scenario.
- Use output data to construct epidemic curves, estimate means and CIs for key outcomes.
- Hypothesis tests can be run to compare intervention efficacies.

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8. Key Parameters (examples)

- Grid size: 1000 x 1000
- Initial number of infectious: 20
- Incubation period (E→I): 2 days (steps)
- Infectious period (I→R): 5 days (steps)
- Base transmission probability
- Vaccine efficacy (1 or 2 doses)
- Fraction using masks/distancing

- Daily vaccination capacity

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9. Implementation Guide

- **Programming Language:** Python (or language of group preference)
- **Documentation & Usage:** Well-documented code; command-line or graphical input of simulation parameters; plots and statistics of results.

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10. Example Investigations

- How do masking and distancing alter final epidemic size/duration?
- What’s the impact of immediate single-dose vaccination for all versus staggered full dosing with supply lag?
- Sensitivity analysis: impact of changing movement speed, grid density, or dose timing.
