Flu Virus Simulation Analysis Report

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1 Introduction

The global impact of influenza viruses continues to present significant public health challenges, particularly in urban environments where population density and movement patterns can accelerate disease spread. This study examines the effectiveness of local isolation measures and various intervention strategies in controlling flu epidemics within a city environment. Our research specifically addresses how local isolation can reduce the diffusion of an epidemic, incorporating factors such as population movement patterns, family structures, and virus mutations. The simulation model developed for this study integrates geographical information system (GIS) data of buildings and roads to create a realistic urban environment for epidemic modeling. The primary objectives of this research include:

- Evaluating the effectiveness of local isolation strategies
- Analyzing the impact of family structures on disease transmission
- Assessing vaccination programs and their effectiveness
- Understanding the dynamics of virus mutations and variant evolution
- Determining optimal vaccination coverage rates

2 Model Design and Features

2.1 Base Model Implementation

The simulation uses GIS-based city environment with buildings and road networks. Key features include:

- Environment: City layout with buildings connected by road networks
- Population Movement: Daily patterns between homes and workplaces
- Disease Transmission: Base infection probability 33% upon contact
- Testing Protocol: Daily testing of 1% of population
- Isolation Measures: 12-day isolation period for positive cases

2.2 Extension 1: Family Structure

Added family dynamics for realistic social clustering:

- Family size: 3-6 members per household
- Children: 0-2 per family
- School: Largest building designated as central school
- Movement: Adults to workplaces, children to school

2.3 Extension 2: Vaccination System

Implemented vaccination program:

- Daily rate: 0.05% of unvaccinated population
- Effectiveness: Reduces infection probability by a factor of 3
- Targets: Non-infected, non-isolated individuals

Vaccination impact:

- Tracked vaccination coverage over time
- Measured effect on infection rates
- Analyzed population immunity development

2.4 Extension 3: Variant Evolution

Dynamic variant system modeling virus mutation:

- Mutation chance: 0.1% per infected per day
- Variant features:
  - Infection rate varies from parent ($0.5\times$ to $1.5\times$)
  - Vaccine 50% less effective against new variants
  - Immunity to previously encountered variants

Variant analysis:

- Tracked new variant emergence
- Studied variant competition
- Evaluated vaccine adaptation effectiveness
- Observed infection rate changes across variants

2.5 Core Model Parameters

- Time Step: 1 hour
- Work Hours: 8:00-17:00
- Population: 4000 families
- Mutation Rate: 0.1%
- Test Rate: 1%

This model design creates a realistic framework for studying epidemic spread in urban environments. Each extension adds complexity while maintaining analytical clarity, allowing us to study how different factors influence disease transmission and control measures. The experiments were designed to isolate and understand the impact of each new feature, while also observing their combined effects on the overall epidemic dynamics. Results from these experiments provide insights into effective control strategies and the challenges of managing evolving pathogens.

3 Simulation Results and Analysis

3.1 Extension 1

The simulation is configured with key parameters that shape the disease spread dynamics in a family-structured environment. The population consists of 4,000 families with varying sizes (3-6 members), resulting in a total population of 17,908 individuals and an average family size of 4.48. The demographic distribution shows 80.4% adults (14,386) and 19.6% children (3,522). Movement patterns are governed by an 8 AM to 5 PM schedule, with adults traveling between homes and workplaces while children commute to the central school. The disease transmission probability is set at 33% for general contacts, with a 1.5x multiplier (49.5%) for within-family transmission. The control measure includes daily testing of 1% of the population with a 12-day isolation period for positive cases and their family members.

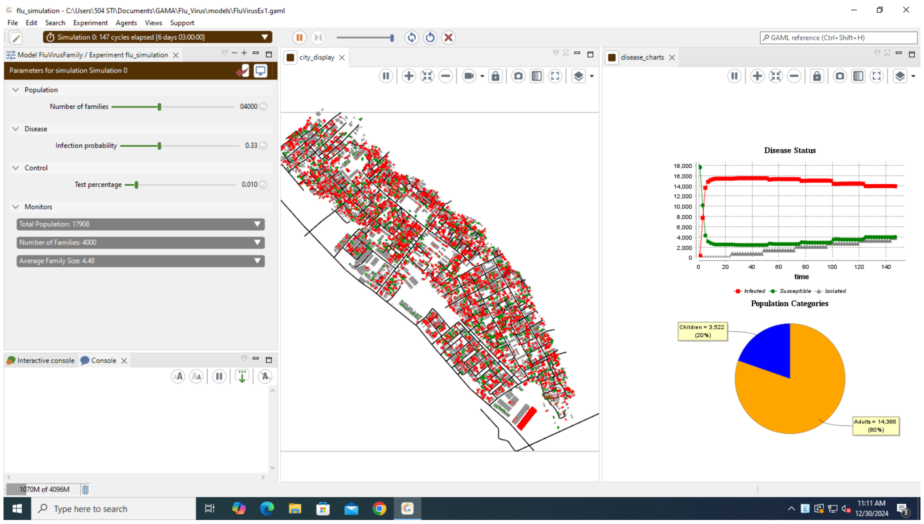

Figure 1: Simulation with initialized parameters

The simulation results reveal three distinct phases in the epidemic progression. The initial phase shows a rapid increase in infections, with the number of cases rising sharply in the first 50 time units. During the peak phase (50-200 time units), infections reach approximately 15,000 cases, followed by a gradual decline and stabilization.

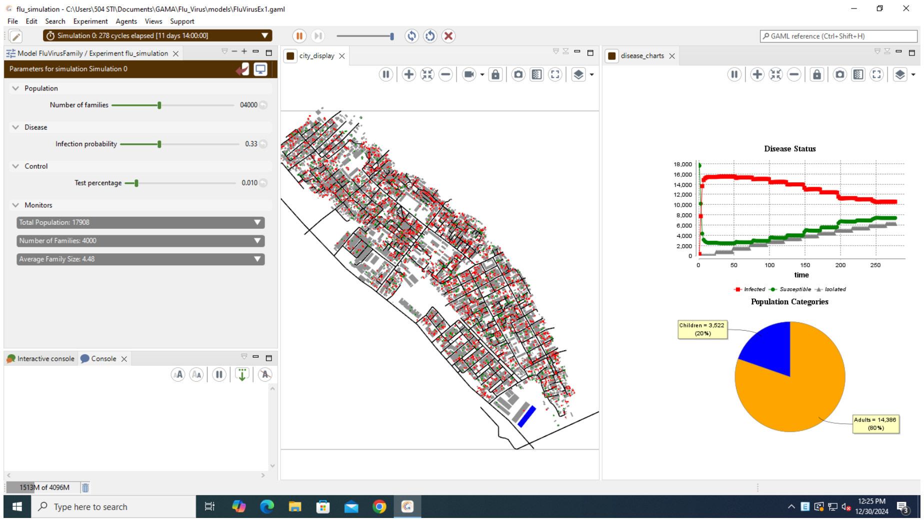

Figure 2: Result after 6 days

In the final phase (beyond 200-time units), the system reaches an equilibrium with about 11,000 infected, 6,000 isolated, and 7,000 susceptible individuals. The school emerges as a significant transmission hub, while family units act as both transmission accelerators and containment units when isolated. The family-based isolation strategy proves effective in controlling the spread, though the interconnected nature of the population through school and workplace interactions maintains a persistent level of transmission in the community.

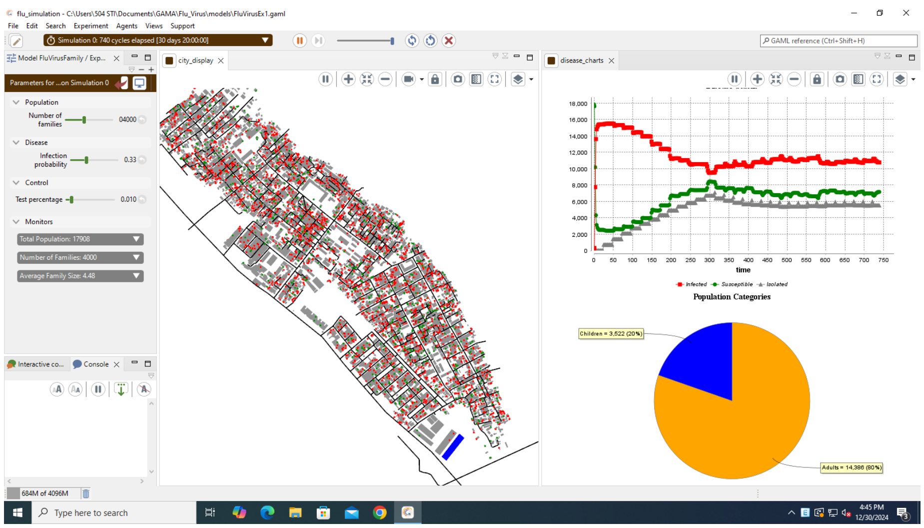

Figure 3: Result after 30 days

Insight:

- Family Impact - Getting sick at home is very likely due to close contact. But when a family stays home together after finding a sick member, it helps stop the virus from spreading to others.

- School Risk - The school is a major spreading point even with few children (20% of population). Daily gathering of all children makes the virus spread easily between families.

- Testing Strategy - Daily testing 1% of people plus family isolation works to control the outbreak. Cases stay around 11,000 instead of growing endlessly.

- Movement Pattern - Regular travel between home, work and school creates fixed paths for virus spread. This leads to quick early spread followed by stable case numbers.

- Social Groups - Using natural groups like families makes control easier. Testing plus family isolation, with focus on risky places like schools, helps manage the outbreak better.

3.2 Extension 2

The simulation models 4,000 families with a total population of 18,024 people in a city environment. Disease parameters include a 33% base infection probability balanced by control measures of 1% daily testing rate with 12-day isolation periods. The key new feature is vaccination, implemented with a 3% daily vaccination rate of the unvaccinated population and providing triple protection against infection by reducing infection probability to one-third of the original rate. These parameters create a balanced system of disease spread and control mechanisms.

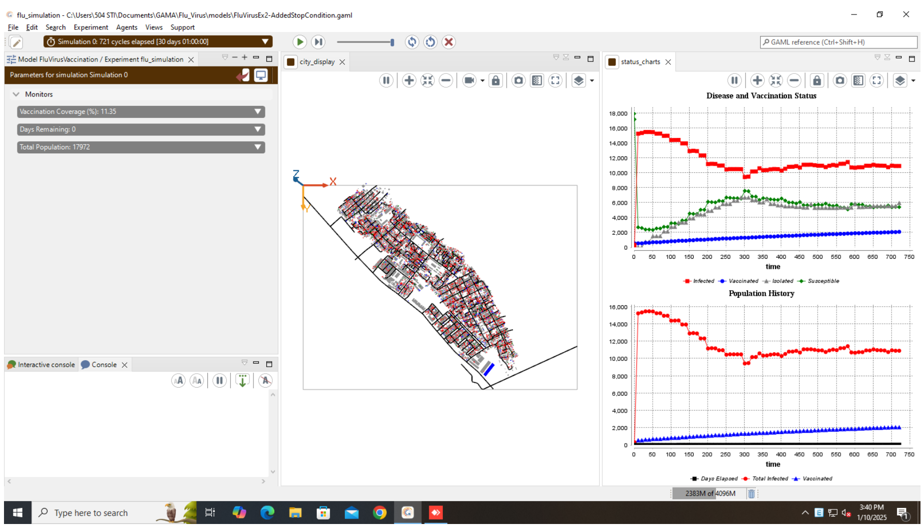

Figure 4: Result after 30 days

The city map visualization shows a mixed population where vaccinated individuals (blue dots) gradually appear among infected (red) and isolated (gray) cases, with a notable concentration around residential areas and the school positioned at the city edge. The disease and vaccination status graph reveals four key trends: an initial spike in infections followed by a gradual decline, a steady but slow increase in vaccinated population, isolation cases mirroring infection patterns, and fluctuating susceptible population. The population statistics demonstrate limited vaccination success, reaching only 12.62% coverage (blue) while 87% remain unvaccinated (orange), suggesting the vaccination rate might be insufficient for effective disease control.

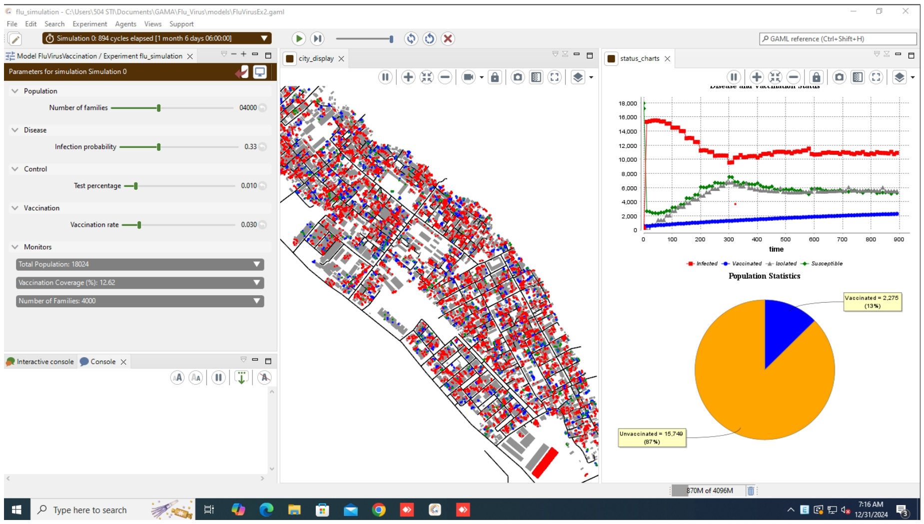

Figure 5: Caption

Insights

- Vaccination Effect - Vaccine's 3x protection helps reduce cases, but slow 3% daily rate means limited coverage (only 12.62%).
- Disease Pattern - Despite vaccination, infection still maintains around 11,000 cases, suggesting higher vaccination rate needed.
- Population Mix - With 87% still unvaccinated, virus keeps spreading. Shows current vaccination rate too low to achieve herd immunity.
- Timing Impact - Gradual buildup of vaccinated population shows in city map (blue dots), but too slow to prevent ongoing transmission.

3.3 Extension 3 + 4 - completed simulations

The simulation expands upon previous models by introducing virus variants with a 2% mutation probability and complex vaccine effectiveness mechanics. The base setup includes 4,000 families (approximately 18,000 people) with a high base infection rate of 0.5. The model introduces three vaccination scenarios: low (0.05%), medium (0.11%), and high (1%) daily vaccination rates. Variant dynamics include mutation probability, varying infection rates for new variants, and reduced vaccine effectiveness against new variants (50% reduction). The simulation runs for a fixed 30-day period to allow consistent comparison between scenarios.

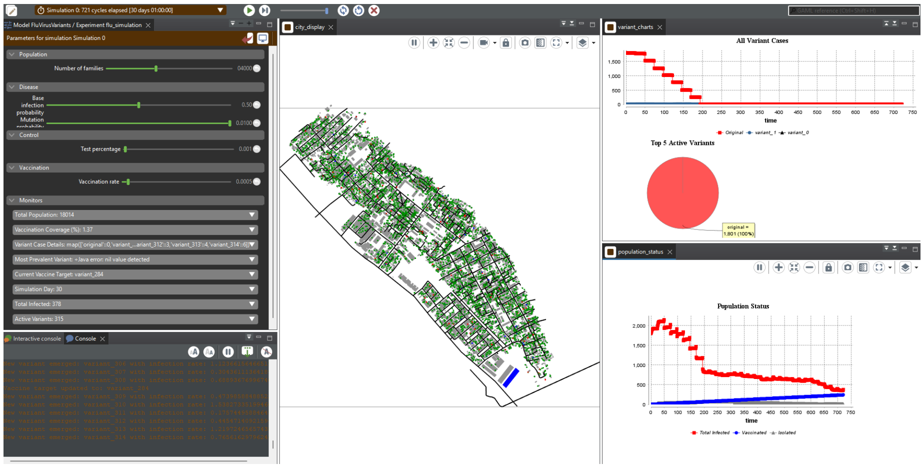

Figure 6: Result with vaccination rate = 0.05%

With a low vaccination rate, we can see the results:

- Population reached only 1.37% vaccination coverage
- 315 active variants emerged
- Total infected peaked at 2,000 and stabilized around 400
- Map shows mostly green (susceptible) and red (infected)
- Very low presence of blue (vaccinated) individuals
- Weak impact on controlling variant spread

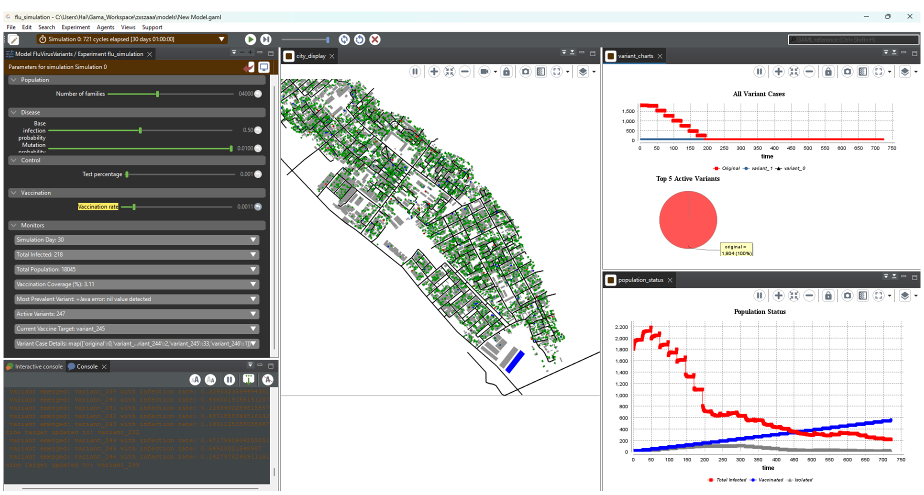

Figure 7: Result with vaccination rate = 0.11%

With a higher vaccination rate (0.11%), the result was becoming better with:

- Achieved 3.11% vaccination coverage
- 247 active variants detected
- Total infected initially peaked at 2,200, declined to 600
- More visible blue dots in population map
- Better distribution of infection patterns
- Variant numbers reduced compared to low rate
- Blue line (vaccinated) shows steady but slow growth

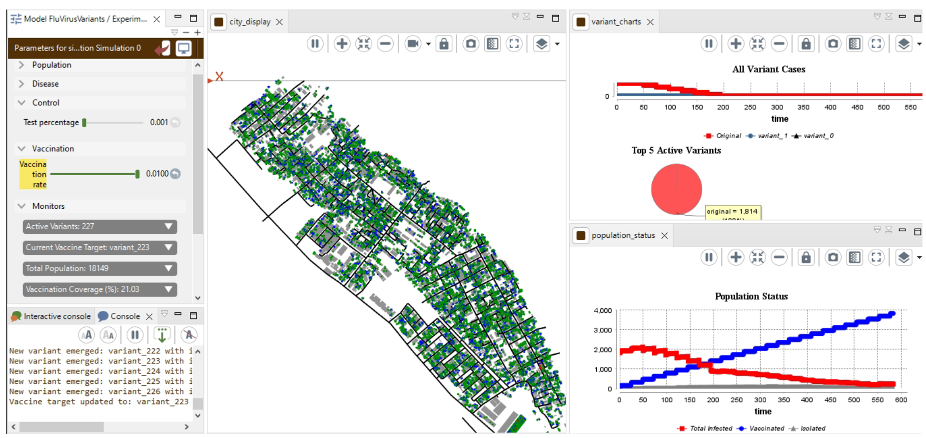

Figure 8: Result with vaccination rate = 1%

In the case of the highest vaccination rate (1%), we observe:

- Reached 21.03% vaccination coverage
- Only 227 active variants - lowest among all scenarios
- Initial infection peak 2,000, dropped below 500
- Significant blue presence in population map
- Strong growth in vaccination line (blue)
- Clear crossover point where vaccinated exceeds infected
- Most effective at controlling both original and variant cases
- Shows potential for long-term epidemic control

Insights:

- Vaccination Rate Impact
  - Higher vaccination rate (1%) significantly reduces total infections and variant emergence
  - Low vaccination rate (0.05%) allows continued high transmission and variant development
  - Critical threshold appears between 0.11% and 1% daily vaccination rate
- Variant Evolution Patterns
  - More variants emerge under low vaccination scenarios
  - High vaccination reduces both variant numbers and their survival rate
  - Original variant maintains dominance regardless of vaccination rate
- Population Protection
  - 17.85% vaccination coverage (high rate) shows best disease control
  - Lower rates (1.37% and 3.11%) insufficient to prevent variant spread
  - Vaccination helps even with reduced effectiveness against variants
- Mutation-Vaccination Balance
  - 2% mutation rate creates constant variant pressure
  - Higher vaccination rates better contain both original and variant cases
  - Vaccine targeting system adapts but struggles with low coverage

A daily vaccination rate of 1% proves significantly more effective than lower rates of 0.05% or 0.11%, achieving 21.03% population coverage versus just 1.37% and 3.11% respectively. Higher vaccination rates not only reduce total infections but also limit variant emergence, with the number of variants dropping from 315 (at 0.05% rate) to 227 (at 1% rate). This shows that reaching a critical vaccination threshold is essential - too low a rate (below 0.11%) barely impacts the epidemic, while a substantial rate (1%) can effectively control disease spread and variant evolution. With the increase in vaccination rate, the simulation not only reduced the possibility of infection but also reduced the number of variants. The number of patients can be decreased and the epidemic is controlled.

4 Conclusion

This project developed a comprehensive GAMA-based simulation model for analyzing urban flu epidemics. The GIS-integrated environment allowed realistic modeling of city dynamics, incorporating buildings, road networks, and natural movement patterns. Through three progressive extensions, the model evolved to include family structures, vaccination systems, and variant evolution mechanics, creating a robust framework for epidemic analysis. The simulation results demonstrate the critical importance of vaccination rates in epidemic control. Testing three different vaccination scenarios (0.05%, 0.11%, and 1% daily rates) revealed a clear threshold effect. The 1% daily vaccination rate proved significantly more effective, achieving 21.03% population coverage and reducing variant counts to 227, compared to 315 variants with the 0.05% rate. This higher vaccination rate also demonstrated superior control of both original and variant strains, despite reduced vaccine effectiveness against new variants. These simulation outcomes provide valuable insights for real-world epidemic management. The ability to model complex interactions between social structures, vaccination programs, and virus evolution in a realistic urban setting helps bridge the gap between theoretical epidemiology and practical public health planning. This research shows that computer simulations can effectively predict intervention outcomes and guide policy decisions, particularly in determining optimal vaccination strategies for urban populations.