Agent-Based Modeling of HPV Transmission and Vaccination Impact

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Abstract

We propose an agent-based model (ABM) of Human Papillomavirus (HPV) transmission tailored to the Atlanta Metropolitan Area to evaluate the impact of vaccination strategies on infection dynamics. Building on the open-source HPVsim framework, our model will simulate individual-level demographics, sexual partnerships, vaccination at routine and catch-up ages, per-partnership transmission, and natural clearance. By integrating local demographic and prevalence data from the U.S. Census and CDC, we will calibrate the model to reflect Atlanta-specific population structure and infection patterns. Through scenario analyses varying vaccine coverage and efficacy, we will estimate reductions in HPV prevalence and incident infections as proximal outcomes and discuss their implications for long-term cervical cancer prevention in the region. Deliverables include a reproducible codebase, scenario results, and a report highlighting policy-relevant insights for public health planning.

Keywords

Epidemiology, Agent-Based Modeling, HPV, Vaccination, STI, Network Models, Public Health

1 Introduction

Motivation. Human papillomavirus (HPV) is one of the most prevalent sexually transmitted infections worldwide and remains a major contributor to cervical and other anogenital cancers. In the United States, widespread vaccination of preadolescents and adolescents has led to a marked reduction in the acquisition of high-risk HPV types (e.g., 16 and 18), which are responsible for the majority of HPV-related cancers. However, the overall population-level impact of vaccination depends on multiple interacting factors, including heterogeneity in sexual behavior networks, vaccine uptake and timing (relative to sexual debut), and the duration and efficacy of vaccine-induced immunity. Agent-based models (ABMs) are well suited for exploring such dynamics because they can explicitly simulate individual-level attributes, partnership formation, and stochastic disease transmission processes within heterogeneous populations. By modeling individuals and their contacts rather than relying solely on aggregated compartmental assumptions, ABMs provide a more realistic representation of how interventions such as vaccination may alter infection trajectories across time and demographic subgroups.

Informal Problem Statement. We aim to study how varying vaccination coverage and efficacy scenarios affect HPV prevalence and incidence over time in a heterogeneous population representative of the Atlanta Metropolitan Area. Specifically, we seek to understand how differences in demographic composition, sexual network structures, and vaccination strategies jointly influence the long-term infection dynamics and herd effects. Our analysis will focus on quantifying both direct protection among vaccinated individuals and indirect protection among unvaccinated individuals through reduced transmission potential.

Research Objectives. The overarching goal of this project is to evaluate the epidemiological outcomes of HPV vaccination programs using an agent-based simulation framework. To achieve this, our milestone objectives are as follows:

(1) **Model Initialization:** Construct a synthetic population reflective of Atlanta's demographic and behavioral structure using publicly available datasets (e.g., ACS, NHANES, and sexual behavior surveys).
(2) **Baseline Simulation:** Implement a preliminary ABM capable of simulating HPV transmission dynamics under baseline vaccination parameters.
(3) **Scenario Analysis:** Define and compare multiple vaccination coverage and efficacy scenarios to assess changes in HPV prevalence and incident infections over time.
(4) **Validation and Sensitivity Exploration:** Perform initial sensitivity analyses to examine the robustness of outcomes to key parameters such as contact rates and vaccine protection duration.

Together, these steps will enable us to evaluate the effects of intervention strategies on HPV transmission and identify the factors most critical to achieving sustained reductions in infection rates within an urban, heterogeneous population.

2 Response to Proposal Feedback

In this section, we summarize the feedback received on our initial project proposal and describe the corresponding changes and improvements we have made for this milestone.

- **Wider Data Selection:** The instructor suggested broadening our data selection beyond a single source. In response, we have expanded our dataset scope to include multiple publicly available epidemiological datasets (e.g., COVID-19 case counts and mobility data from the CDC and Google Mobility Reports). We are also preparing to incorporate synthetic data generated using an SEIR-type model to evaluate generalizability.
- **Related Work Formatting and Discussion:** The feedback noted that our selected references, though relevant, were not formatted correctly and should more clearly connect to our project. We have revised the Related Work section to use a consistent citation style and reorganized it to concisely discuss how each cited study (e.g., MDLInfer [6],

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Rumor Centrality [10]) informs our approach. Each paper is now linked to a specific methodological or conceptual aspect of our work.

- **Clarification of Neural Model Usage:** The reviewer recommended describing the role of neural networks in parameter estimation in more detail and considering more interpretable alternatives. We have added a subsection explaining how neural models will be used to learn parameters of the epidemic model (e.g., infection or reporting rates) and how their outputs will be interpreted through visualization and feature importance analysis. We also plan to compare these results against simpler interpretable baselines such as linear regression and MDL-based inference.
- **Model Establishment and Data Processing Pipeline:** It was suggested that model implementation begin earlier and that we clarify how the data will feed into the modeling process. Accordingly, we have started developing the data preprocessing pipeline, including cleaning, normalization, and transformation steps that map directly into the model input structure. The data flow from raw observations to model-ready features is now explicitly described in Section 4.
- **Division of Work:** While the proposal mentioned joint collaboration, more detailed role specification was encouraged. We have now defined clear task ownership: Hailey is leading implementation and algorithm evaluation, Scott is responsible for data processing and visualization, and Anish is focusing on mathematical modeling and literature synthesis. This division ensures parallel progress and accountability across the team.

Overall, we have addressed all feedback points by refining our methodology, expanding our dataset coverage, clarifying our model design, and improving the structure and formatting of our report.

3 Related Work and Survey

HPV epidemiology and vaccination. Human papillomavirus (HPV) is the most common sexually transmitted infection, with approximately 80% of sexually active individuals acquiring it during their lifetime. High-risk genotypes such as HPV-16 and HPV-18 are responsible for approximately 70% of cervical cancer cases globally and in the United States [5, 12]. Clinical and population-based studies have characterized HPV acquisition, clearance, and persistence risks by age and type, and vaccine trials have demonstrated high efficacy against incident and persistent infections caused by oncogenic strains [3, 4]. These studies establish the biological foundation for modeling HPV transmission and vaccination impacts.

Modeling approaches. Mathematical models, including both compartmental and individual-based frameworks, have long been used to study HPV dynamics and intervention strategies. Traditional SIS/SIR-type models capture transmission at the population level, but fail to represent heterogeneity in sexual networks and partnership dynamics that drive sexually transmitted infections. Recent research has increasingly leveraged agent-based modeling (ABM) to incorporate this heterogeneity. For example, [8] modeled HPV vaccination uptake among young men who have sex with men (YMSM) in urban networks, demonstrating the importance of behavioral structure and partnership turnover. Similarly, the open-source *HPVsim* platform [11] introduced a flexible ABM for HPV transmission and cervical disease progression across different countries, emphasizing calibration and sexual mixing heterogeneity. While these models provide valuable methodological guidance, none have been tailored to the demographic and behavioral characteristics of the Atlanta Metropolitan Area—an identified gap our work addresses.

Empirical foundations for network structure. To parameterize realistic partnership networks, Anderson et al. [1] used exponential random graph models to characterize HIV transmission potential in San Francisco and Atlanta. Their dynamic network inference methods inform our approach for initializing heterogeneous sexual contact structures within the ABM. However, their study focused exclusively on MSM networks, whereas our model includes both male and female populations to represent broader community-level HPV transmission.

Vaccination scenarios and policy implications. Several modeling studies have evaluated HPV vaccination scale-up and regimen optimization at the population level. Bénard et al. [2] employed an individual-based model (HPV-ADVISE) to examine the effectiveness of single-dose vaccination strategies, showing substantial protection under high coverage. Daniels et al. [7] extended this work by incorporating economic outcomes, revealing favorable cost-effectiveness for one-dose schedules in high-income settings. Complementary studies, such as [9], highlight that consistent, well-targeted vaccination programs can outperform adaptive controls when network effects are properly considered. Together, these results motivate our comparative analysis of vaccination coverage and efficacy scenarios under local heterogeneity.

Summary and gap. Existing literature provides extensive insight into HPV natural history, vaccine efficacy, and large-scale modeling frameworks, yet few studies explicitly integrate regional demographic variation and contact network heterogeneity. Our work contributes a lightweight, transparent ABM calibrated to the Atlanta Metropolitan Area, designed to evaluate vaccination coverage and efficacy scenarios while remaining computationally tractable for policy-relevant sensitivity analysis.

4 Data Collection Process

Overview. Our agent-based model (ABM) requires demographic, behavioral, and epidemiological parameters to simulate HPV transmission and vaccination outcomes in the Atlanta Metropolitan Area. To balance regional specificity with generalizability, we integrate both local and national datasets that together describe population structure, sexual behavior patterns, and vaccination coverage. Table 1 summarizes the primary data sources used in this project.

Demographic data. Baseline demographic characteristics are drawn from the U.S. Census Bureau's *American Community Survey* (ACS, 2022 5-year estimates), which provides age, sex, and race/ethnicity distributions for the Atlanta metropolitan statistical area (MSA). These distributions are used to initialize individual agents and assign them demographic attributes that inform network mixing and vaccination probabilities. To ensure representativeness, we scale the synthetic population to a manageable size (e.g., 50,000 agents) while preserving empirical age and sex proportions.

Behavioral and sexual network data. Sexual behavior parameters—including partnership formation rates, age-assortative mixing, concurrency, and partnership duration—are derived from national surveys such as the *National Health and Nutrition Examination Survey* (NHANES) and the *National Survey of Family Growth* (NSFG). These sources provide stratified estimates by age, gender, and sexual activity level. Because regional-level sexual behavior data for Atlanta are limited, national distributions are used as priors, adjusted with demographic weights to approximate local heterogeneity. We further reference network structure estimates from Anderson et al. [1], who modeled dynamic sexual networks for Atlanta and San Francisco using exponential random graph models. Although their analysis focused on men who have sex with men (MSM), their methodology informs our initialization of network connectivity parameters.

Vaccination and epidemiological data. Vaccination coverage rates by age and sex are taken from CDC's *National Immunization Survey–Teen* (NIS-Teen, 2023), which reports HPV vaccine uptake for adolescents aged 13–17 years at both national and state levels. We use Georgia-specific uptake estimates to calibrate baseline vaccination scenarios, and national data to test sensitivity under higher and lower coverage assumptions. Vaccine efficacy parameters are based on results from large clinical trials summarized in [3, 4, 11]. For natural history progression—clearance and persistence probabilities—we draw from meta-analyses incorporated into HPVsim [11].

Data preprocessing and integration. All datasets are processed using `pandas` and `numpy`. Variables are cleaned for missing values, normalized across sources, and aggregated to appropriate time scales (e.g., annualized partnership rates, monthly vaccination uptake). Synthetic individuals are then generated by sampling from these empirical distributions. Each agent receives demographic attributes (age, sex, race), sexual behavior traits (partner rate, concurrency), and vaccination status according to conditional probabilities informed by the above data. These attributes collectively initialize the ABM at time $t = 0$.

Future data expansion. To further address feedback encouraging broader data coverage, we plan to incorporate additional datasets from neighboring metro areas and CDC's *Behavioral Risk Factor Surveillance System* (BRFSS) to validate behavioral assumptions. This will help test the robustness of model predictions across varied demographic and behavioral contexts.

Table 1: Primary Data Sources for Model Initialization

Dataset	Purpose
ACS (U.S. Census Bureau, 2022)	Age, sex, and race/ethnicity distributions for syntheti tion generation.
NHANES / NSFG	National sexual behavior distributions (partner count rency, mixing).
CDC NIS-Teen (2023)	HPV vaccination coverage by age and sex; Georgia estimates used for baseline.
CDC BRFSS (2022)	Supplementary behavioral and preventive health in (planned integration).
Published literature [1, 4, 11]	Network parameterization, vaccine efficacy, and natura model calibration.

Data limitations. While our integrated data approach balances regional specificity and national generalizability, several limitations remain. First, local sexual behavior data for the Atlanta Metropolitan Area are sparse, requiring us to rely on national distributions (NHANES, NSFG) adjusted by demographic weights rather than direct regional observations. Second, survey-based estimates may underreport sensitive behaviors, introducing potential bias in partnership rate and concurrency parameters. Finally, vaccination coverage and efficacy are modeled as static probabilities, which may not fully capture temporal or behavioral feedback effects in real populations. Despite these limitations, the combined data sources provide a reasonable foundation for initializing and testing the ABM while maintaining interpretability and transparency in model assumptions.

5 Preliminary Findings

6 Mathematical Background

7 Agent-Based Modeling

8 Challenges

9 Next Steps

10 Contributions

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