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Modeling the Impact of Human Mobility on Influenza Transmission Dynamics in Urban Settings: A Data-Driven SEIR and Time-Varying transmission Analysis

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ABSTRACT

Human mobility is a key driver of infectious disease transmission, yet its role in shaping seasonal influenza dynamics remains insufficiently characterized, particularly in comparison to COVID-19. This study aims to quantify the association between mobility patterns and influenza transmissibility and to evaluate the potential impact of targeted mobility interventions. We conducted a state-level analysis in the United States by integrating mobility data from Google and Apple reports (February 2020 to January 2022) with weekly influenza-like illness data. The time-varying effective reproduction number (Rt) was estimated using a standard epidemiological framework. Cross-correlation analysis was applied to identify lag structures between mobility indicators and RtR_tRt, followed by linear mixed-effects modeling to quantify associations while accounting for spatial heterogeneity. Model performance was evaluated using the Akaike Information Criterion. Regression-derived coefficients were subsequently incorporated into a Susceptible–Exposed–Infectious–Recovered (SEIR) model to simulate intervention scenarios. Influenza transmissibility exhibited clear seasonal variation, with Rt exceeding 1.0 during early-season growth and declining below this threshold in later months. Mobility changes were found to precede fluctuations in Rt by 3 to 6 weeks, with lag patterns varying by activity type. Residential activity and walking were associated with reduced transmission, whereas park visits and grocery-related mobility were identified as significant drivers of increased Rt. The best-performing model achieved the lowest information criteria values and explained a substantial proportion of variability in transmission dynamics. Simulation results indicated that targeted reductions in high-impact mobility activities, particularly park-related mobility, could substantially suppress epidemic growth. Combined moderate interventions across multiple mobility types also demonstrated meaningful effects. Human mobility is a significant and temporally structured determinant of seasonal influenza transmission. Activity-specific mobility patterns provide a predictive window for intervention and offer actionable insights for public health strategies. Targeted, mobility-informed interventions may represent an effective and less disruptive approach to mitigating seasonal influenza outbreaks.

KEYWORDS

Human Mobility; Seasonal Influenza; Public Health Intervention; Influenza Transmissibility.

1. INTRODUCTION

Despite developments in the epidemiological field, influenza is one of the most common forms of infection currently. While yearly changes may be witnessed concerning the level of burden posed by the illness, such changes tend to be significant. According to estimates on influenza-associated morbidity for the years 2010-2023 in the United States by the Centers for Disease Control and Prevention (CDC), annual variations include 9 to 41 million illnesses, 140,000 to 710,000

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hospitalizations, and 12,000 to 52,000 deaths (CDC, 2023). In light of these statistics, therefore, it becomes crucial to consider the determinants affecting its transmission process.

Population density is considered a key determinant in the spread of infectious diseases, although a static variable. It does not account for the movement of people which actually regulates contact opportunity, so human mobility plays an important role in infectious disease dynamics. Incorporating mobility trends into epidemiological models has proven to improve their ability to capture transmission dynamics.

The rise in the availability of digital data pertaining to human movements has made epidemiological researchers use such data more frequently. In particular, mobility proxies based on mobile phones allow estimating mobility and contact patterns within a certain area [1]. Publicly available mobility databases, Google Mobility Reports, are used in numerous studies dealing with the dynamics of infectious diseases [2]. The empirical evidence shows that the spread of respiratory infections depends on specific mobility patterns rather than random walk. Indeed, the study of Charu et al. [3] demonstrates that mobility patterns could explain the timing and location of influenza outbreaks in the US. Similar results were found for COVID-19. Xia et al. [4] show that changes in mobility affect epidemic growth rate and the effective reproduction number in a distance-dependent way. Moreover, in Switzerland, Schläpfer et al. [5] calculated the effect of mobility on infection and proved that for each percent increase in distance traveled, there was a decrease in effective reproduction number of 0.7 to 1.0 percent.

The current pandemic caused by COVID-19 has made significant contributions to the formulation of mobility-based epidemiological models [6]. However, applying the same to seasonal influenza is not yet common practice. Influenza virus differs from SARS-CoV-2 in terms of epidemiological and biological parameters. In particular, serial interval in influenza ranges between 2.6 days while that in COVID-19 – more than 5 days [7,8]. It means that mobility will have a different impact on the infection transmission. Apart from that, the mobility patterns of humans during the time of COVID-19 pandemic could be heavily influenced by measures introduced by authorities. Indeed, people had to follow strict quarantines and social distancing protocols [9,10]. As a result, natural mobility patterns of humans could be different, making mobility-based model unreliable.

With this in mind, the current study aims to determine the influence of human mobility on the transmission dynamics of seasonal influenza in the United States. Time-varying reproductive numbers together with human mobility data will be used in analyzing the correlation between these two factors. The estimation method uses influenza-specific approaches in estimating the effective reproduction number.

2. METHODS

2.1 Data Sources and Preprocessing

Human mobility and influenza data at the state level were used in this study. Human mobility data was obtained from public reports published by Google and Apple between February 15, 2020, and January 26, 2022. As the measure of influenza activity, weekly ILI data were used. In order to achieve temporal consistency, daily observations of mobility were aggregated on a weekly basis. To provide geographic consistency, non-contiguous territories, including Guam and Puerto Rico, were removed from the analysis. In addition to estimating the effective reproduction number (Rt) for each state and each week of the study period, several mobility indicators were used: retail and recreation, grocery and pharmacy, parks, transit stations, workplaces, residential, driving, and walking mobility indicators. For comparing between states, and between mobility indicators, the Z-score normalization approach was utilized for mobility data [11]:

$$Z_{i,t} = \frac{X_{i,t} - \bar{X}_i}{\sigma_i}$$

where $Z_{i,t}$ represents the Z-score for state i and time t of the corresponding indicator and $X_{i,t}$ refers to its observation; $\bar{X}_i$ and σ_i are the mean and standard deviation of the time series.

2.2 Estimation of the Effective Reproduction Number

Weekly ILI incidence data were used as input for estimating the time-varying effective reproduction number (Rt) using the EpiEstim package [7]. Serial interval distribution was assumed to be parametric and characterized by a mean equal to 2.6 days and a standard deviation of 1.5 days [12]. As Rt estimation might have a noise problem during periods of low transmission level of the influenza virus, it seems necessary to limit the study period to the peak period of the influenza month, i.e., from October to March of the next year. Any extreme values of Rt exceeding 5 are regarded as outliers and therefore were omitted from further analysis.

2.3 Lagged Correlation Analysis

As a result of not expecting the effects of mobility on disease transmission to occur instantly, it becomes important to estimate the suitable lag of Rt compared with mobility indicators. Therefore, cross-correlation functions (CCF) method was used for detecting the appropriate lag. Several values between one week and eight weeks between Rt and mobility indicators were tried, and the appropriate lag was identified as that with the maximum correlation.

2.4 Statistical Modeling

In order to estimate the strength of mobility influence on the dynamics of the influenza epidemic taking into account the presence of regional differences, linear mixed-effects models were used [13]. In particular, a random intercept was assumed for each of the states. The general formula of the model can be expressed as follows:

$$R_{t,i} = \beta_0 + \sum_k \beta_k \cdot Mobility_{k,i,t-lag} + u_i + \epsilon_{i,t}$$

where u_i represents the random effect for state i, and $\epsilon_{i,t}$ is the residual error.

Various models were created, considering different combinations of mobility indicators based on data obtained from either Google or Apple, or both of them. For the selection of the best model, an Akaike information criterion [14] was applied.

2.5 Scenario Simulation Using SEIR Model

For analyzing the effects of changes in mobility on the dynamics of the disease spread, the estimated coefficients were applied in combination with the compartmental SEIR model [15]. Transmission rate was calculated as:

$$\beta(t) = \left(R_{t,base} + \sum_k \beta_k \cdot \Delta Mobility_k \right) \cdot \gamma$$

where γ is the recovery rate and $\Delta Mobility_k$ represents hypothetical changes in mobility levels.

The simulations of differential equations were carried out using the deSolve package in R, solving them using the Runge-Kutta method [16]. Intervention scenarios for different levels of reductions in mobility (from 1 to 2 SD below the baseline) were designed, and key outcomes such as maximum infection, epidemic peak time, and total number of infections were assessed.

3. RESULTS

3.1 Time-Lag Spatiotemporal Characteristics of Influenza Rt

In Figure 1 below, the dynamics of the mean Rt have been plotted on a monthly basis from October to March. Specifically, in October, the average Rt attained a value of about 1.17, suggesting a phase of epidemic expansion. Thereafter, a steady decline occurred in November and December, where Rt continued to stay above the epidemic threshold of 1.0. However, from January through February, Rt sharply dropped from 1.03 to about 0.88, achieving the season's low point. Although Rt showed some recovery in March, averaging 0.90, it continued to remain below 1.0, indicating a reduced epidemic growth rate.

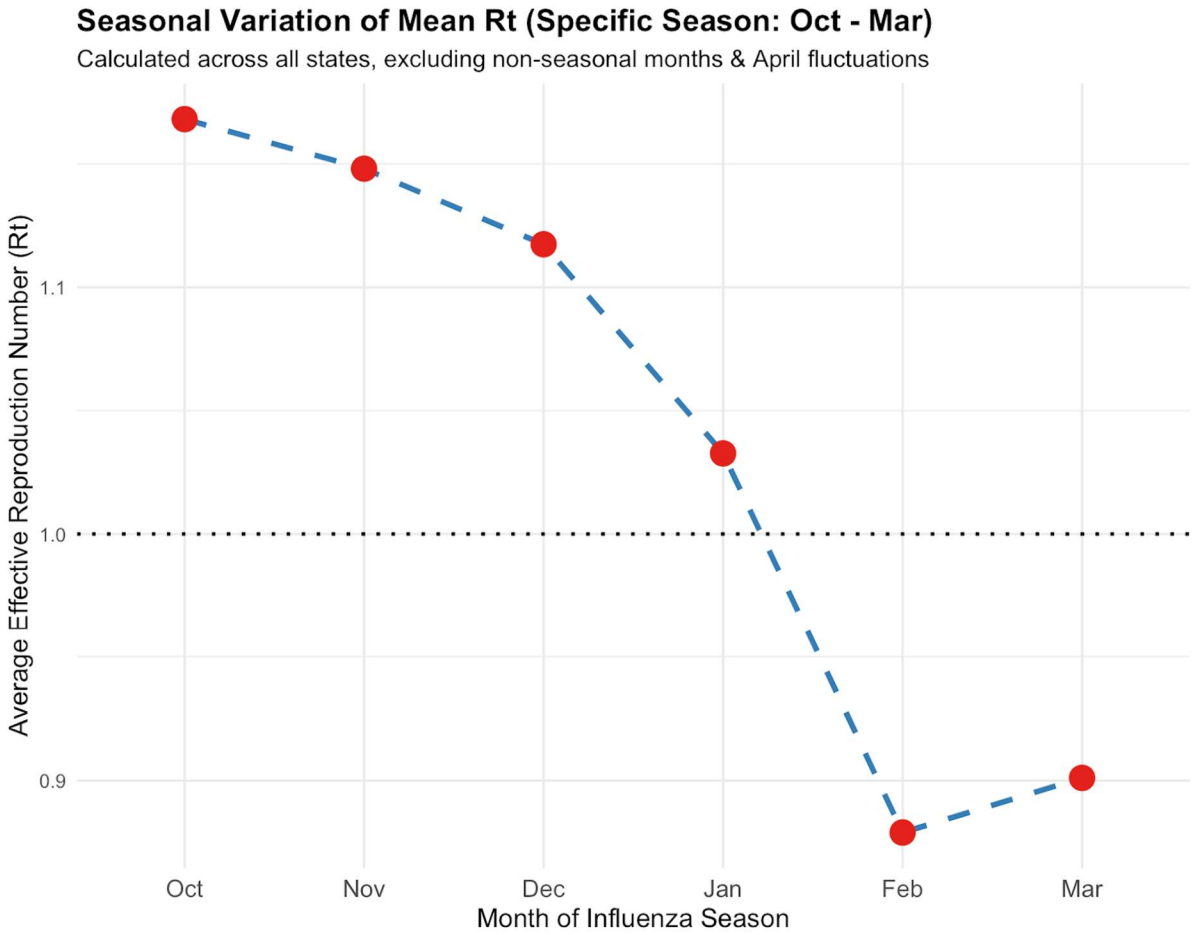


Figure 1. Seasonal dynamics of mean Rt over the Influenza Season (Oct–Mar)

Monthly averages calculated from Rt for all U.S. states, excluding the non-seasonal months. The dashed line is the epidemic threshold (Rt=1.0). The values above the epidemic threshold suggest epidemic expansion, while those below denote a reduction in Rt.

3.2 Differential Effects of Heterogeneous Lag-Time Delays

The results from cross-correlation analyses (CCF) showed that different items exhibit varying time-lag effects on Rt. Specifically, as could be seen in Figure 2 below, most community-based mobility actions, such as driving, retail, and transit, showed high correlation at a 4-week lag, implying that an increase in these activities led to an increment in Rt within four weeks. Importantly, grocery activity and parks had marginally high positive correlation lags of 5 weeks and 6 weeks, respectively. Residential activity, on the other hand, had a strong negative correlation that peaked at a 4-week lag, meaning that spending more time indoors reduces Rt. These findings confirm the distinct lag structures used in the predictive model.

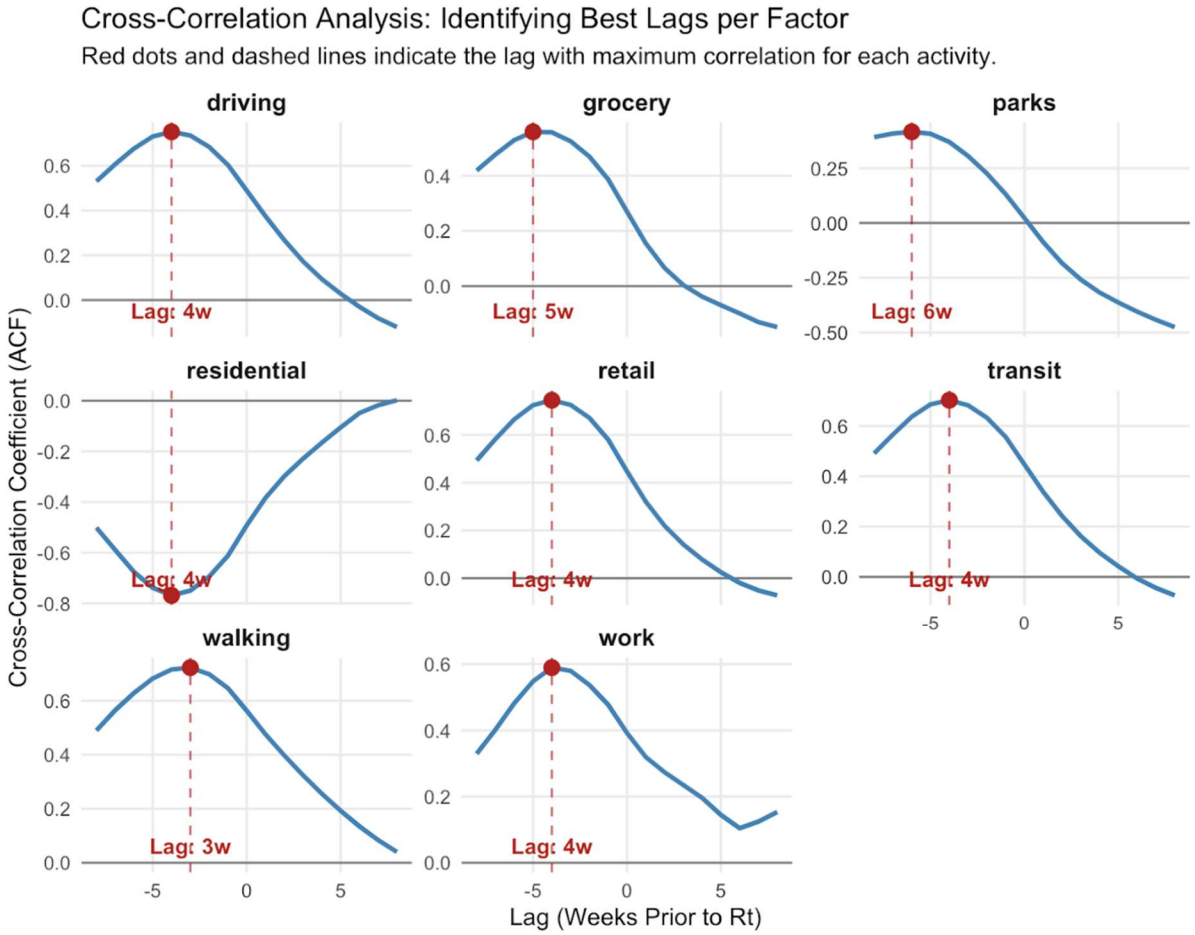


Figure 2. Cross-correlation Functions between Mobility Factors and Rt

Each subplot shows the CCF between a selected mobility factor and Rt with respect to time lags (0 to 8 weeks). The maximum absolute correlation for each plot is marked by red points and vertical dashed lines. Positive correlation means that more mobility increases Rt after a certain lag, whereas a negative correlation implies protection.

3.3 Quantifying Predictors of Transmission (The Best AIC Model)

Model selection results have revealed that the All_Factors model provides the best fit to the data since it has the lowest AIC (-481.60) and BIC (-419.59) values and the highest explained variance (R^2 = 0.193) (Table 1). Four mobility factors that demonstrated a statistically significant influence on influenza Rt ($p < 0.05$) were identified in the multivariable Mixed-Effects Model. Residential activity

and walking were found to be the major protective factors against infection spreading, as seen in Figure 3. Residential activity had the largest negative coefficient with respect to Rt ($\beta = -0.067$, $p < 0.01$), followed by Walking ($\beta = -0.060$, $p < 0.001$). Among the mobility factors contributing to higher rates of transmission, Parks was observed to have the strongest and most significant positive coefficient ($\beta = 0.052$, $p < 0.001$) while Grocery shopping had a considerable influence on Rt as well ($\beta = 0.044$, $p < 0.001$). Driving ($\beta = 0.039$, $p = 0.074$), Transit ($\beta = 0.016$, $p = 0.416$), Work ($\beta = -0.012$, $p = 0.295$), and Retail ($\beta = -0.010$, $p = 0.662$) failed to attain statistical significance.

Table 1. Comparison of candidate mixed-effects models predicting influenza transmission

Model_Name	AIC	BIC	R2_Marginal
All_Factors	-481.6005	-419.5910	0.1929427
No_Residential	-475.5120	-419.1397	0.1897750
Google_Only	-467.0497	-416.3146	0.1859330
Transport_Only	-391.8688	-358.0454	0.1565637
Apple_Only	-384.7745	-356.5884	0.1533336
Outdoor_Active	-382.0178	-342.5572	0.1526199

Models were evaluated using Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC), and marginal R2. The model including all mobility variables demonstrated the best overall performance.

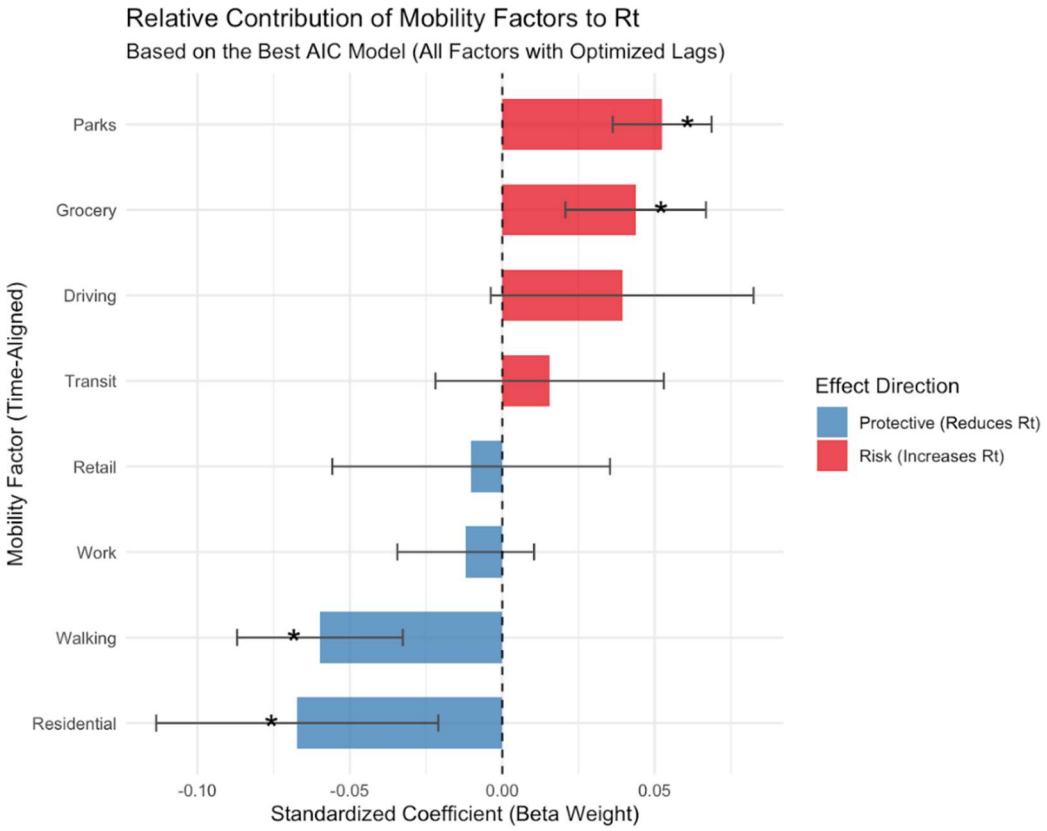


Figure 3. Standardized regression coefficients of mobility factors on influenza Rt

Regression coefficients are displayed on the barplot, while the horizontal line represents 95% confidence interval. Stars represent statistical significance ($p < 0.05$). Coefficients with positive signs stand for increased risk of transmission, while those with negative signs for protective effect.

3.4 Peak Suppression through Scenario Simulations in the SEIR Model

Based on the use of a predictive modeling algorithm, an investigation into the possible effect of lowering activities in "park" and "grocery store" on the scale of an influenza outbreak within a 180-day forecast was conducted using the simulation approach. From Figure 4 below, it is evident that while the baseline scenario led to a rapid exponential increase where an outbreak size reached over 50 infections during its peak, all other scenario simulations resulted in the attenuation of viral transmissions. Comparison of single-factor scenarios showed that an equal reduction in mobility activities had more impact in mitigating the outbreak when the mobility was linked to "parks" rather than "grocery stores." Interestingly, the "Reduced Park Activity (-2SD)" scenario represented by a dark blue curve was found to be the most effective in suppressing the spread of viral infection as it flattened the initial growth curve and maintained the lowest number of infections across the entire simulation duration. Also, the combination scenario involving the slight reduction in mobility factors for both "park" and "grocery store" resulted in an equally good result. In some ways, the combination strategy performed better than any of the single strategies, especially for -1SD reductions.

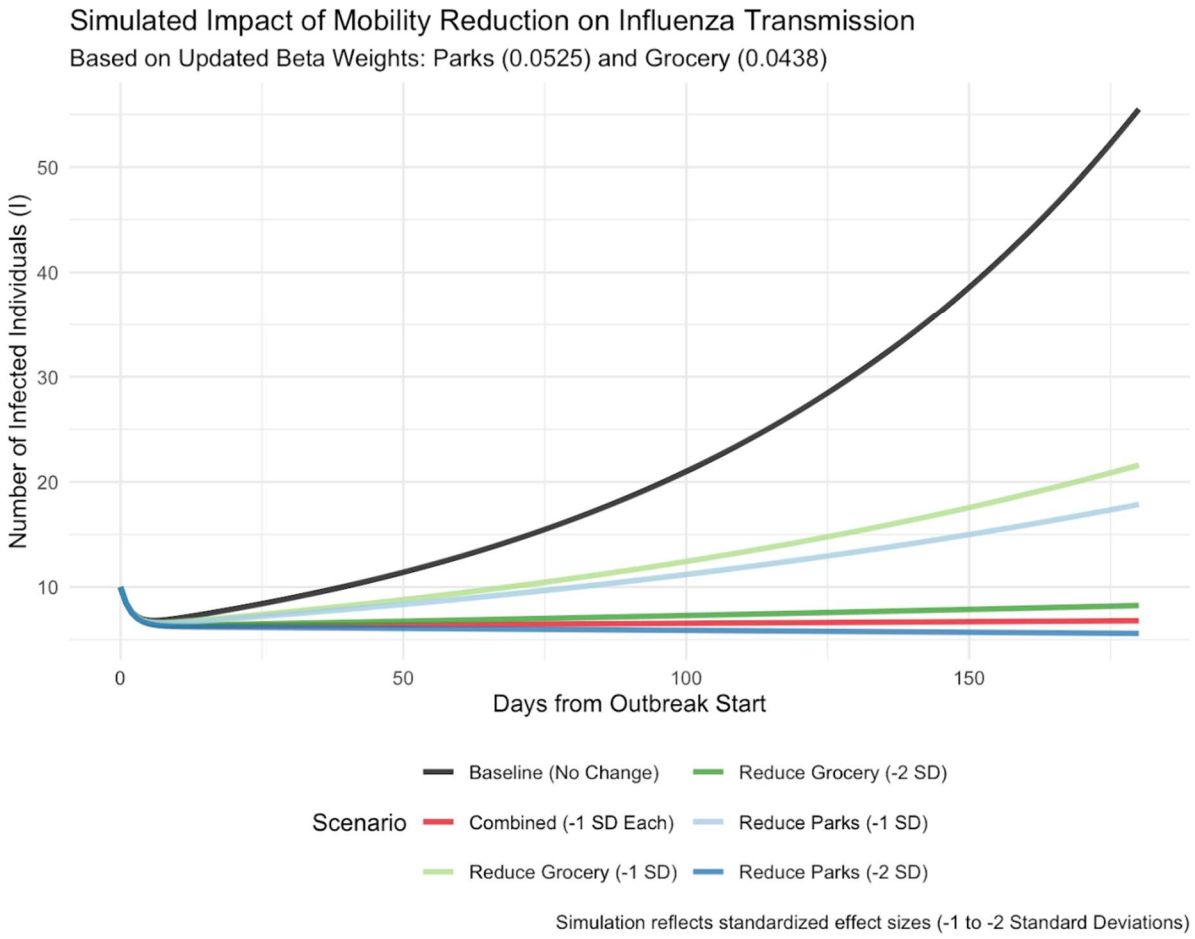


Figure 4. Simulation of mobility reduction scenarios for influenza control

Comparison of epidemic trajectories across baseline and intervention scenarios based on a 180-day simulation.

4. DISCUSSION

This study describes a causal relation between mobility and influenza transmission dynamics at the state level, demonstrating that changes in mobility behavior precede changes in transmission approximately three to six weeks later. This epidemiologically significant relationship specifies a lead-time during which targeted actions can be taken to prevent transmission.

The results obtained also confirm previous findings about heterogeneous mobility patterns, showing that residential mobility always goes hand in hand with decreased transmission. At the same time, however, park mobility and grocery mobility are found to be the main sources of increased transmission. The high importance of park mobility in particular is quite interesting to note, since it demonstrates that the higher risks associated with being outdoors might be counteracted by the specific behavior of people in such an environment – for example, higher levels of social mixing during influenza peaks or the effect of clustering.

The distinctive feature of the results obtained by the authors is their dual relevance for both statistical analysis and mechanistic modeling. Using the regression analysis of the impacts of different mobility categories in the SEIR framework helps go beyond the association and estimate how changing the behaviors will affect epidemic development. Results of simulations show that reductions in park mobility strongly affect the epidemic growth, and even small reductions in intensities of all major mobility categories are highly effective. Overall, results suggest that targeted interventions aimed at relatively modest changes in behavior are possible to reduce influenza transmission.

This paper makes a contribution to the body of epidemiological research using mobility data with particular attention to seasonal influenza. The majority of studies using such approach were devoted to SARS-CoV-2. While the general utility of using mobility data for different viruses may seem obvious, further investigation is still needed to assess the applicability of results from previous research for new cases. According to the results, mobility data seems applicable to assessing transmission regardless of the specific virus studied.

It is important to point out several caveats concerning the interpretation of the study results. First, since the authors focus only on mobility dynamics within 2020-2022, the relationships observed might be driven by pandemic-related changes rather than regular seasonal patterns. Second, because only short-term mobility data were used in the research, it was impossible to observe any seasonal or sub-typing fluctuations that take place throughout the influenza period. Further research using time-series data from several influenza periods is required to address this issue. Finally, despite state-level modeling, the study does not take local climatic, demographic, or economic conditions into account.

5. CONCLUSION

Overall, the findings of this study provide convincing evidence regarding the critical role of human mobility in the development of influenza epidemics. As demonstrated, certain types of mobility exhibit lagged effects driving epidemic dynamics through changes in the effective reproductive rate. In addition, through modeling based on the SEIR framework, the results support the potential for reducing mobility in specific types to control epidemic growth.

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