Modeling and Analysis of Seasonal Flu (H3N2) Dynamics in Türkiye

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Abstract

Seasonal flu causes morbidity and mortality issues affecting all parts of the world. Understanding the transmission dynamics of the disease is crucial for implementing effective public health measures. This study aims to gain insights on the transmission dynamics of the influenza type H3N2 in Türkiye by using an age stratified compartmental SEIR model. Upon verification and validation of the model using the surveillance data from Türkiye, the effects of different public health policies on key variables of disease burden such as infections, hospitalizations, and deaths are analyzed. These policy scenarios include increased vaccination rates, adoption of healthy behaviors like physical distancing, mask use, hand hygiene, and increased isolation of symptomatic school age children. The experiments with different scenarios showed the intricate relationship between the age groups and that one healthy behavior adopted by an age group often also significantly benefits the other groups.

1. Introduction

Seasonal outbreak of influenza occurs annually in many regions of the world leading to productivity losses and even deaths, especially in high-risk individuals such as immune-compromised people, elderly, and people with chronic conditions. There are 4 types of influenza viruses (types A, B, C, and D), two of which (types A and B) causes seasonal epidemics. Influenza A is subdivided in various subtypes according to the protein combinations on the surface of the virus [1]. Among them, the H3N2 type is of particular importance and the focused type in this study due to its relative dominance across seasons and its association with more severe flu seasons [2].

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The pathogen's specific features as well as local settings and behavioral patterns of the susceptible and infected people play an important role in the dynamics of the epidemics. The transmission dynamics of the disease is unique to the country in which it spreads because of the different lifestyles and health measures in different countries. Additionally, people interact at different rates based on the groups which they belong such as their age groups, professions, and socio-economic status. That is why, any attempt to analyze the dynamics of the disease spread should be both country and at least a sub-group specific. Analyzing the transmission dynamics is essential for implementing cost-effective health policies specific for the disease. This study aims to model and analyze the seasonal flu spread in Türkiye with respect to the age groups and symptom-status of the infected people.

2. Model Description

The model is built on the classical SEIR (Susceptible-Exposed-Infected-Recovered) framework. It includes the *Symptomatic* and *Asymptomatic* stock variables to account for the differing behavioral patterns and infectivity of these individuals as well as the *Hospitalized* and *Infected at Home* stock variables to address the epidemic burden and isolation of the people from the general population. The *Immune* stock variable represents both the people who are effectively vaccinated and the people who recovered. The population is stratified by their age since people in different age groups interact at different contact rates with each other. Age groups **0-19**, **20-64**, and **65+** are used in the model. Figure 2.1 shows the Stock-Flow Diagram of the model.

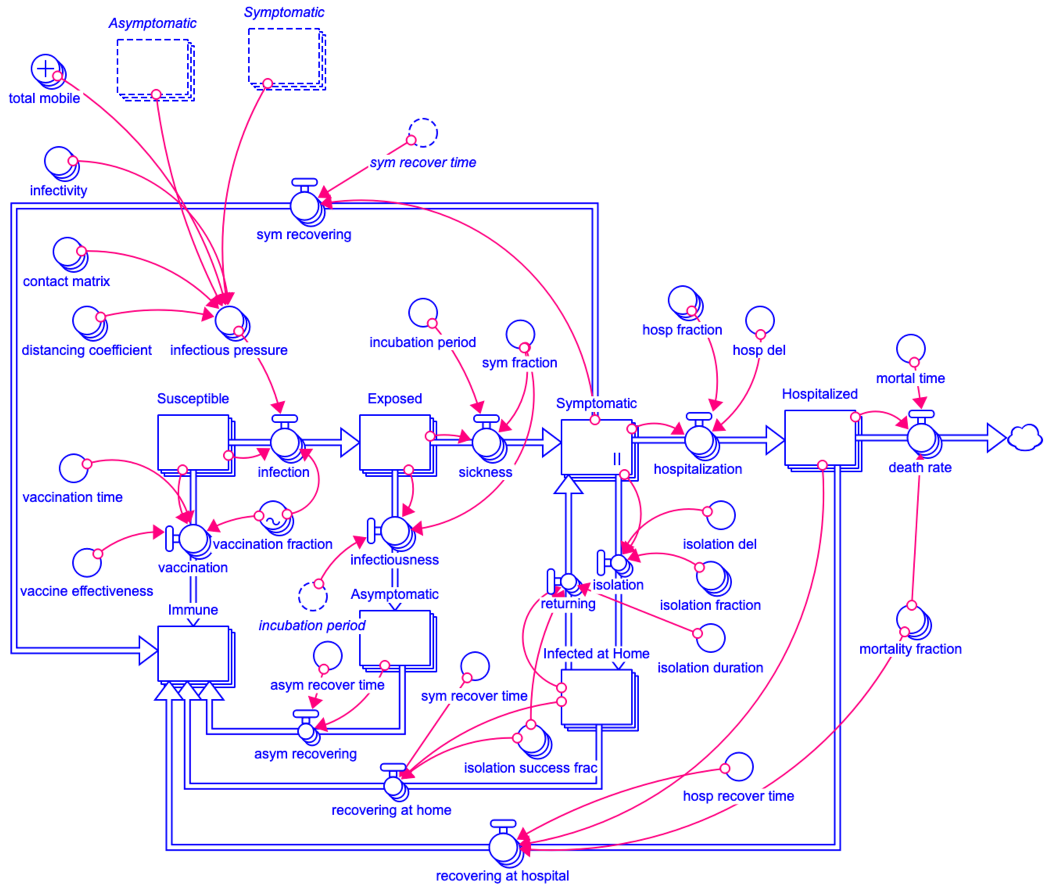


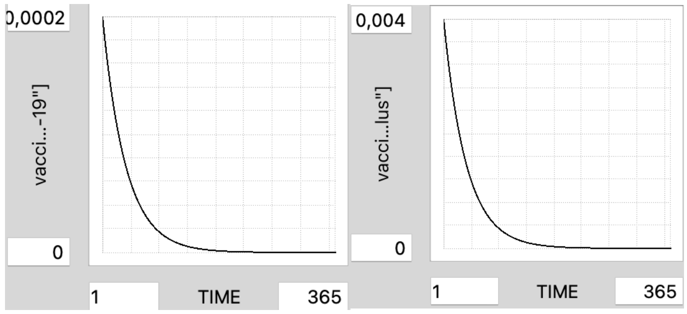
Figure 2.1 The Stock-Flow Diagram

2.1 Model Variables and Formulations

Some of the key variables and their formulations are listed below (the units are given in parentheses):

vaccination fraction: A graphical function representing the fraction of people who are getting vaccinated over time, arrayed by age groups. (dmnl)

The flu vaccine takes about 2 weeks to confer immunity [3]. For this reason, the flu vaccination usually starts 2 weeks before the influenza season to prevent infections during this period. Therefore, most people who are eventually going to get the vaccine do so, just before or at the beginning of the season. And since the most inclined people will get the vaccine earlier, less people will get the vaccine later in the season. Figure 2.2 shows the graphical functions.



(a) (b)

Figure 2.2 *vaccination fraction* over time; (a) for age groups 0-19 and 20-64, (b) for age group 65+

infectivity: The probability of becoming infected after a close contact with an infectious individual took place, arrayed by infection type to reflect the different infectivity values of *Symptomatic* and *Asymptomatic* people (dmnl).

contact matrix: A 2D array variable which shows the average number of contacts between the age groups per day (1/day). The variable is arrayed by age group and age group. There is a study that provides the contact matrix estimations for 152 countries, including Türkiye [4].

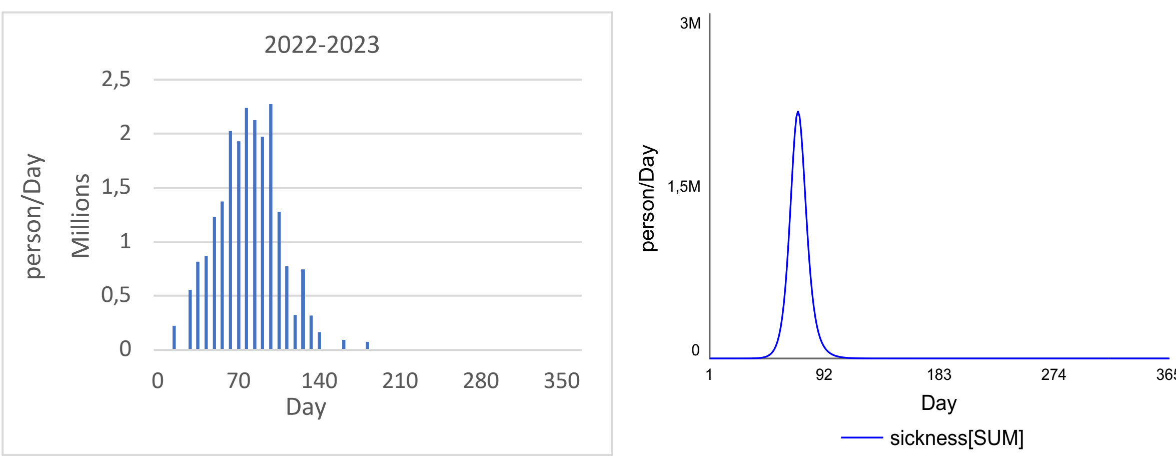
***distancing coefficient*:** A behavioral variable which reflects the different contact patterns of *Symptomatic* and *Asymptomatic* people (dmnl). It can be defined as the coefficient which excludes people who will not transmit the disease because they took distancing measures (e.g., physical distancing, mask use, hand hygiene etc.). The variable can take a value from 0 to 1 for each infectious group—with 0 meaning the utmost caution took place and 1 meaning no distancing measures took place at all.

infectious pressure: A derived variable representing the risk of infection that individuals in a specific age group are exposed to per day (1/day). The equation showing the total *infectious pressure* on a person in the Age Group 'a' is as follows:

$$
\begin{aligned}
& infectious\ pressure[a] \\
& = \sum_{b \in AgeGroup} contact\ matrix[b;a] \\
& * \frac{distancing\ coef[Symptomatic] * Symptomatic[b] + distancing\ coef[Asymptomatic] * Asymptomatic[b]}{total\ mobile[b]} \\
& * infectivity
\end{aligned}
$$

3. Model Validation

The values of the parameters and variables are grounded from the literature if there are addressing studies and the others are calibrated. However, obtaining high-quality data for the calibration is difficult due to several reasons. Firstly, only a fraction of the *Symptomatic* people will have a chance to and be willing to consult a physician. Secondly, in clinical practice, people are not tested to check for the viral strain since the diagnosis is made clinically and the treatment is generally "supportive", meaning no specific drug is recommended unless the flu is so severe and usually only NSAIDs, bed rest, and fluid intake are recommended. Thirdly, only a minute fraction of the physicians is reporting test results for surveillance. The surveillance system is mostly concerned with detecting the major strains to decide which strains should be included in the annual vaccine. Although the data has its limitations, we can make use of it by adjusting it to obtain a comparable data with the model output [5]. This can be achieved by finding the percentages of the positive H3N2 cases in the samples to infer an approximation to the incidence ratio, and eventually to the daily incidence of the *Symptomatic* people. The respective comparable output from the model is the *sickness* flow in Figure 2.1. Figure 3.1 shows the adjusted daily incidence data and the total *sickness* graph from the model.



(a) (b)

Figure 3.1 (a) The adjusted daily incidence data for the 2022-2023 flu season,
(b) The graph of the sum of the *sickness* flows

4. Results

The baseline results for the key stock variables are given in Figure 4.1. The *Susceptible* graph shows the classical S-shaped epidemic pattern. The epidemic reaches a peak at around day 68 depicted in the *Symptomatic* graph.

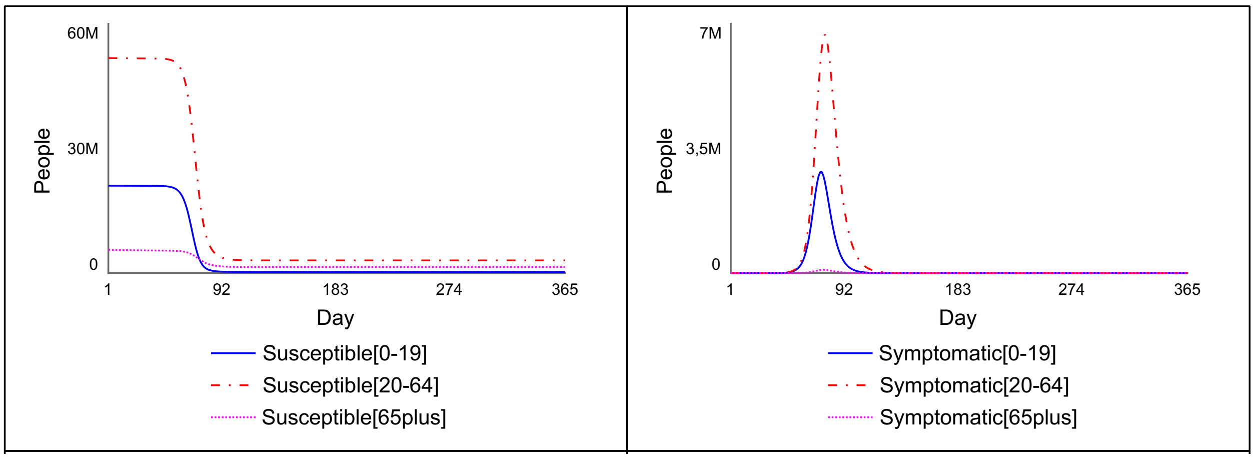


Figure 4.1 Baseline results for the *Susceptible* (left) and *Symptomatic* (right) variables, arrayed by age groups.

5. Scenario and Policy Experiments

Possible public health measures could lead to behavioral changes among the population. These changes may include increasing *vaccination fraction*, *isolation fraction*, and decreased *distancing coefficient*. Among the many simulation experiments with changes in these variables the most notable ones regarding gaining new insights are given in this section.

5.1 Increased *vaccination fraction* for the Age Groups 0-19 and 20-64

In the baseline run, the initial maximum *vaccination fraction* for the Age Groups 0-19 and 20-64 were estimated as 0.0002, a significantly low fraction. If we were to increase this fraction to 0.02, all age groups will have less disease burden, including the elderly people who did not change their vaccination status. The total number of symptomatic people, hospitalizations, and deaths will be lowered in all age groups. Figure 5.1 shows the effects of this scenario on the age group 65+.

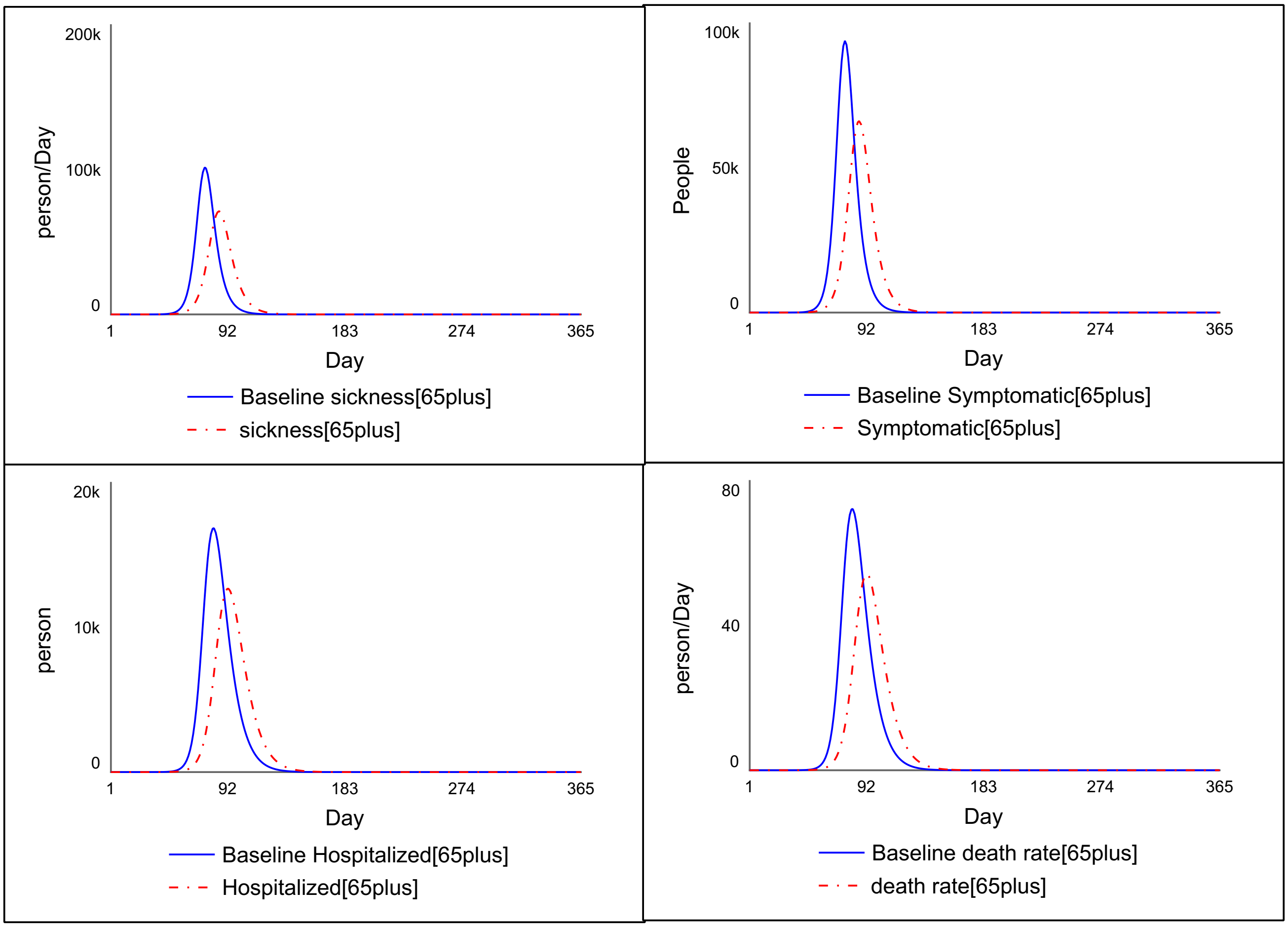


Figure 5.1 Key outputs of the age group 65+ comparing the baseline with the increased *vaccination fraction* for age groups 0-19 and 20-64.

5.2 Decreased *distancing coefficient* for *Symptomatic* People

If symptomatic people were more cautious and were to take more distancing measures such as physical distancing, use of mask, hand hygiene etc. (in this scenario it is analyzed 0.5 *distancing coefficient* for the *Symptomatic*, instead of the initial 0.75) there would be less disease burden in all the age groups, similar to the effects of increased vaccination numbers. Figure 5.2 shows some of the key outputs representing this scenario vs. the baseline results.

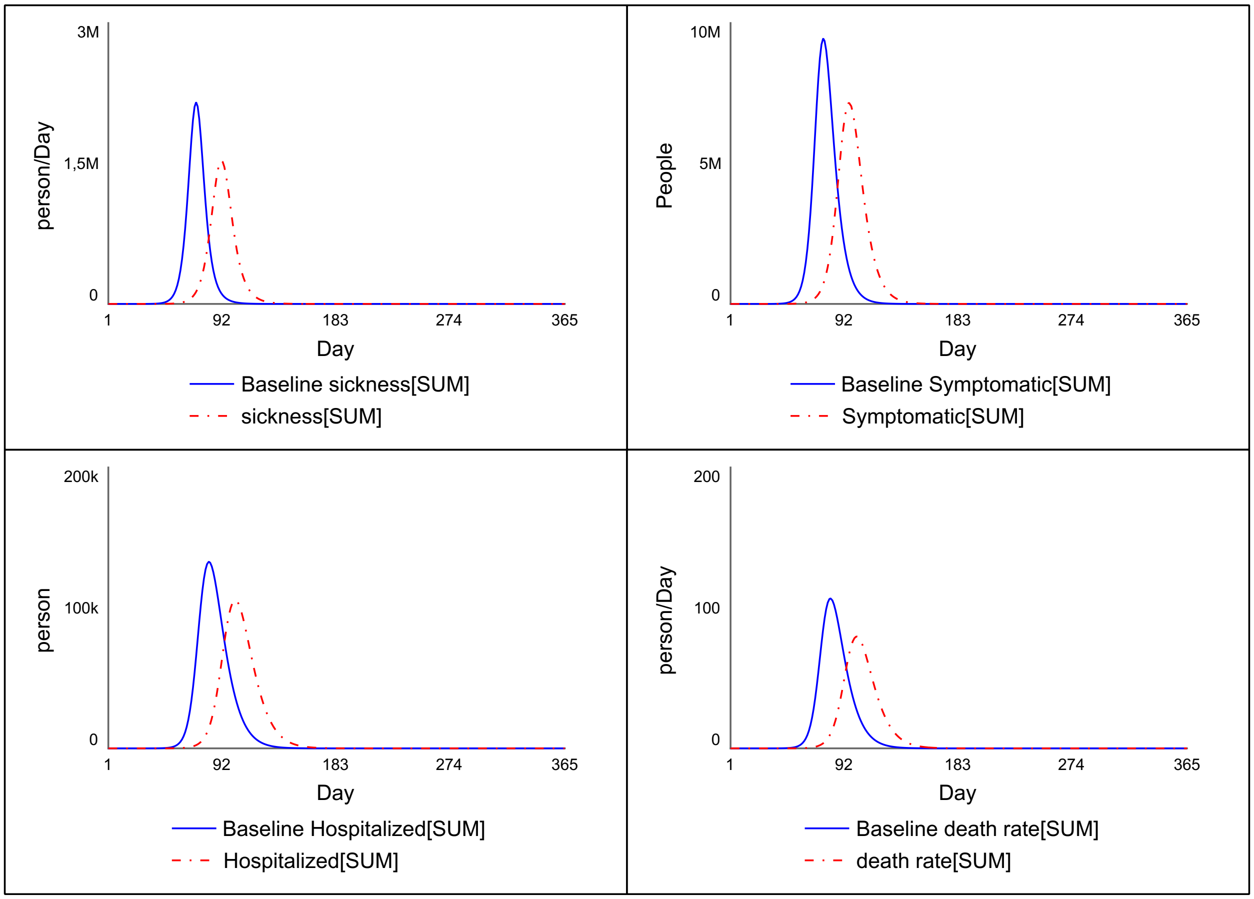


Figure 5.2 Key outputs representing the *distancing coefficient* 0.5 for *Symptomatic* people vs. the baseline with 0.75 *distancing coefficient*.

6. Conclusion and Future Work

Modeling the disease spread aims to alleviate the unavailability of the high-quality data in order to gain insights on public health measures. But the model also suffers from this data unavailability in the validation process. Upon (limited) output validation, different scenarios which can be achieved by setting realistic public health policies are analyzed. Promoting healthy behaviors of the symptomatic people and decreasing the *distancing coefficient* are almost as equally effective as increasing the *vaccination fraction*. It is also observed that one public health measure for one age group positively affects the spread of the disease for all the age groups, including the death rates of the elderly population.

This initial research can be extended in the future in two dimensions. First, by obtaining more data on certain type of influenza dynamics in a selected city, the model can be custom-tailored and validated for the given city. Policy analysis can then be carried out to assist the city's health managers. Secondly, the model structure can be used to build models to address other epidemic problems with similar structures that may be important for the nation in different years and/or regions.

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