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

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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 [1].
- The pathogen's specific features as well as local settings and behavioral patterns of the susceptible and infected people both 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. People in a given society interact at different rates based on the groups which they belong such as their age groups, professions, and socio-economic status. In addition to the different contact rates among different sub-groups in a society, the nature of this contacts changes with the cultural conventions such as different regarding towards handshake or hugging.

MODEL DESCRIPTION

- The model is built on the classical SEIR framework with the addition of key stock variables:
  - *Symptomatic* and *Asymptomatic* people
  - People who take bed rest (*Infected at Home*)
  - *Hospitalized* people
  - *Immune* people (either recovered from the disease or vaccinated effectively)
- And key auxiliary variables for different behavioral patterns:
  - *distancing coefficient* (reflecting the different behavioral patterns related to symptom status)
  - *contact matrix* [2] (reflecting the differing daily contact rates of the age groups with each other)
- The age groups **0-19**, **20-64**, and **65+** are used in the model.

RESULTS

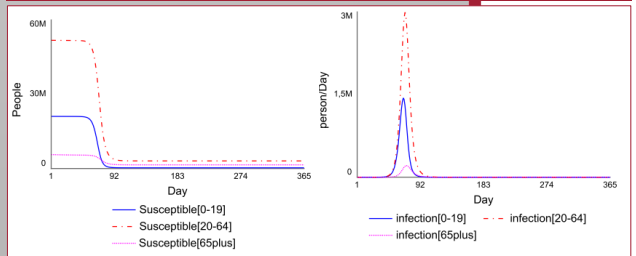


Figure 4. The model outputs of the key variables depicting the epidemic's behavior

- Although we have no dynamic data against which we can evaluate the dynamics of all the stock and flow variables, their dynamics are meaningful and explainable.

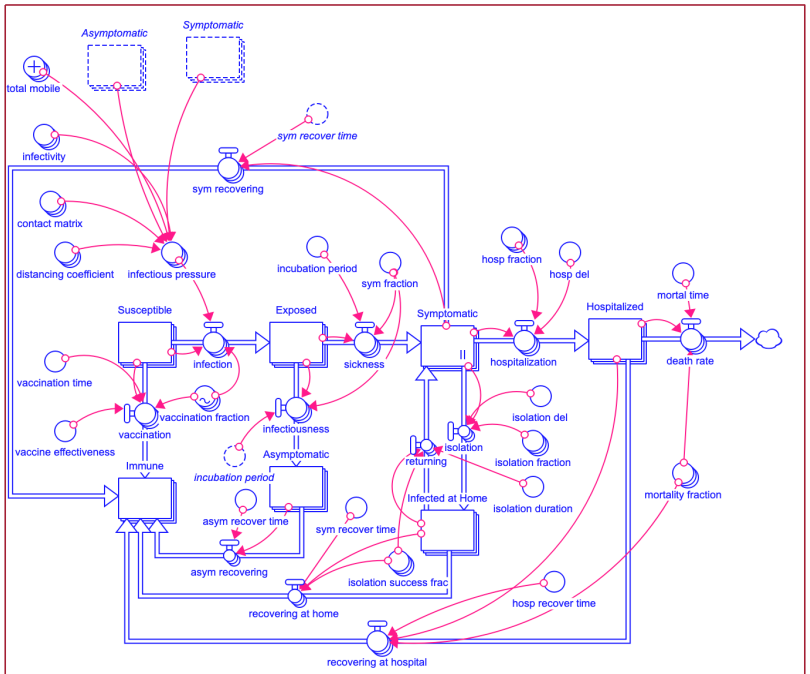


Figure 1. The Stock-Flow Diagram

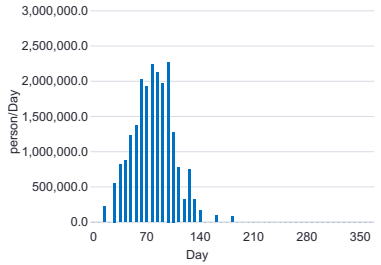


Figure 2. The adjusted daily incidence data of the 2022-2023 flu season

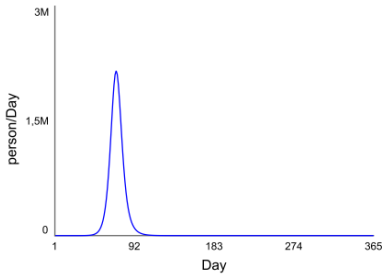


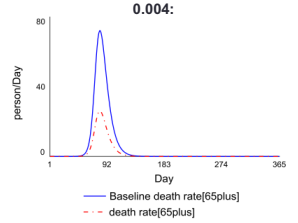
Figure 3. The graph showing the sum of *sickness* flow for all ages from the base run

- Modeling the disease spread aims to alleviate the unavailability of high-quality data and to gain insights on public health measures, while it also suffers from this in the validation process. In order to overcome this, we tried to generalize from the surveillance data which is collected in limited settings for the whole country [3]. Figure 2 shows adjusted data from surveillance data for comparison, while Figure 3 shows the comparable respective output from our model with the data, that is, the *sickness* flow.

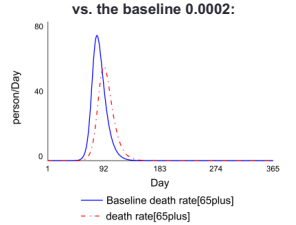
SCENARIO AND POLICY EXPERIMENTS

- **Increased Initial Maximum *vaccination fraction*;**

- for the age group 65+ 0.1 vs. the baseline 0.004:

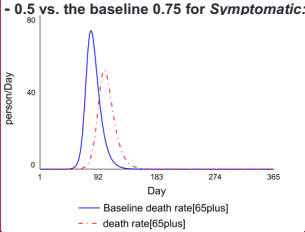


- for the age groups 0-19 and 20-64 0.02 vs. the baseline 0.0002:



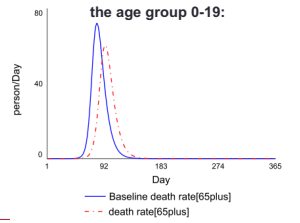
- **Decreased *distancing coefficient*;**

- 0.5 vs. the baseline 0.75 for *Symptomatic*:



- **Increased *isolation fraction*;**

- 0.3 vs. the baseline 0.05 for the age group 0-19:



CONCLUSION AND FUTURE WORK

- Promoting healthy behaviors such as increased *isolation fraction* and increased distancing for symptomatic people is almost as effective as increasing *vaccination fraction*.
- A healthy behavior adopted by one age group often also benefits the other age groups.
- The data used in the calibration and validation of the model was limited especially due to the nature of the influenza. Not many people seek healthcare for the flu unless it is severely progressing and/or they have a special reason to be concerned. Also, even when they seek healthcare, the flu cases are not highly reported since the diagnosis is often made clinically, and routine influenza testing is not recommended.
- The model can be extended in the future:
  - –By obtaining more spatially controlled data for a selected region or city
  - –To build similar epidemic's models tailored for the country

ACKNOWLEDGEMENT

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2. Prem, K., Cook, A. R., & Jit, M. (2017). *Projecting social contact matrices in 152 countries using contact surveys and demographic data. PLoS Computational Biology*, 13(9), e1005697. https://doi.org/10.1371/journal.pcbi.1005697

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