

CSCI-7000 — Infectious Disease Modeling Final Project

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April 29, 2024

1 Immunosenescence and its Function in Mathematical Modeling of Infectious Disease and Vaccination Modeling

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2 Introduction

Varying factors can contribute to susceptibility to disease among populations. One particular factor to consider is age and the development of immunosenescence. Immunosenescence is the alteration of immune function, typically thymic involution causing the decreased functions of T and B cells, due to aging [?]. [Expand on processes metabolically] ; more lit review. Both of these cell types are involved in the acquisition of antigen-specific immune response such that they are the only cells in an organism that can recognize and respond to that specific antigen epitope [?]. In immunosenescence, the number of memory T and B cells increase, while the response to new antigens decreases. Similarly, this decreases the function of granulocytes, macrophages, and NK cells [?].

2.1 Thesis

The importance of immunosenescence and aging was especially emphasized during the COVID-19 pandemic in 2020. Increased susceptibility to disease due to immunosenescence could play a huge role in the way mathematical and computational methods model disease and immunity as provided by vaccinations. This project seeks to explore how immunosenescence can be mathematically modeled using an SEIRS model, and how this idea can be applied to vaccination models.

3 Method

In order to analyze varying susceptibility among different age groups, an SEIRS model was formed and modified to include variable T. T represents varying loss of immunity due to immunosenescence. This allowed us to form a set of ordinary differential equations (ODEs) with a varied T based on age. Furthermore, a contact matrix was formed for the varying age groups using a total population size of 145 (55 parents, 30 children, and 60 grandparents). We then generated code to compute these varying R_0 values. We then saved these results to a CSV file (`simulation.results.csv`). We then manipulated this data under the influence of a Leaky Vaccination Model with varying Vaccine Efficacy (VE). We analyzed when VE was 0, 1, and 0.8. Each age group was visualized using bar charts generated with the Matplotlib library in Python.

4 Results

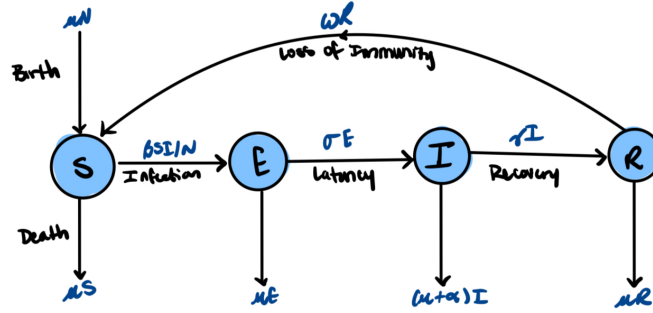


Figure 1: SEIRS Model

As shown in Figure 3, ...
 As shown in Figure 4, ...
 As shown in Figure 5, ...

5 Conclusion

6 Discussion

References

1. Bjørnstad, O.N., Shea, K., Krzywinski, M. et al. The SEIRS model for infectious disease dynamics. Nat Methods 17, 557–558 (2020). <https://doi.org/10.1038/s41592-020-08>

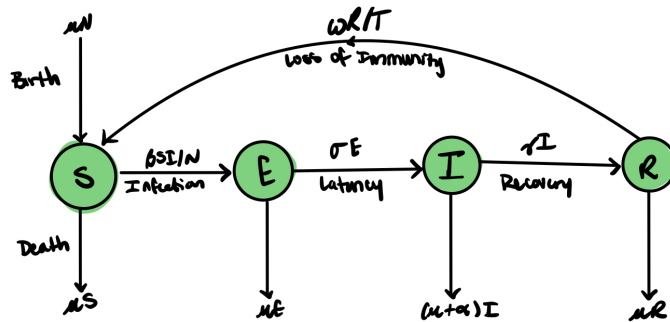


Figure 2: Modified SEIRS Model

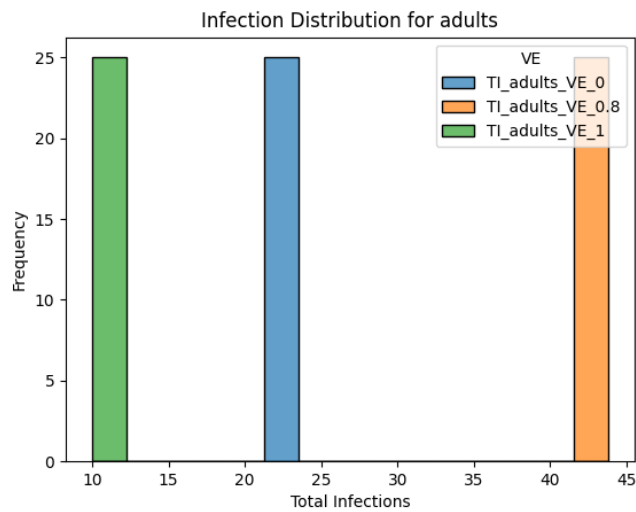


Figure 3: Adults Histogram

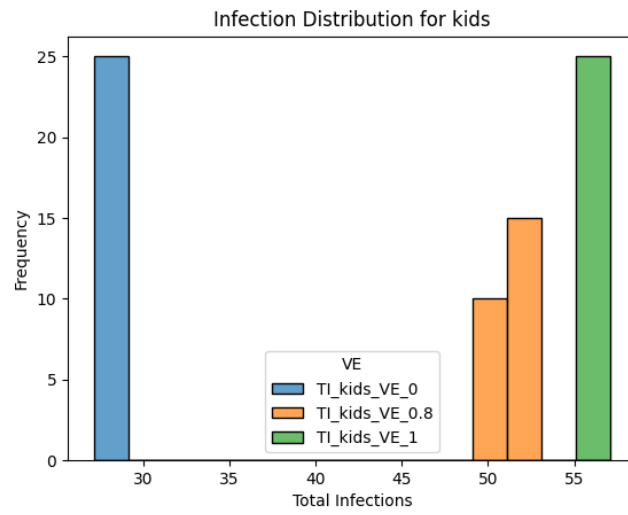


Figure 4: Kids Histogram

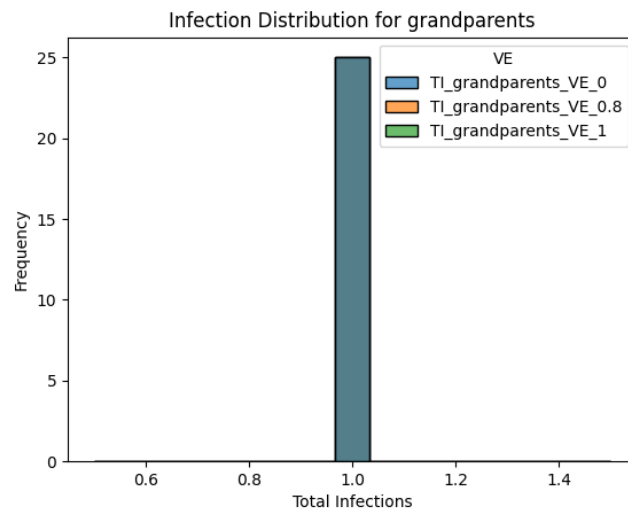


Figure 5: Grandparents Histogram

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