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Pandemic Modeling Final Report

Introduction

During the start of the COVID pandemic, there was a challenge in the U.S. concerning the lack of data that was available for effective pandemic modeling to take place in predicting and implementing enough health resources to curb. [1,2] SIR modeling was resorted to due to previous successful cases of using compartmental models in predicting the trend of disease transmission in the 2002 SARS pandemic.[1] The SIR model is one of the most referenced, used models for simulating the spread of infectious diseases in a population. It breaks down the population into three compartments: Susceptible (S), representing those who can contract the disease; Infected (I), representing those currently carrying and spreading the disease; and Recovered (R), representing those who were infected but have now gained immunity.
From the inspiration of utilizing the simple SIR model, this project delves into an extension of the SIR model with the SIRD model, which incorporates the possibility of deceased (D), representing individuals who succumb to the disease and are permanently removed from the population dynamics. In addition, we also included other variables such as age cohorts, reinfection, and vaccinations, which we believed to provide a more realistic representation of the impact of severe diseases on populations. We aimed to simulate and refine the SIRD model to accurately represent disease spread and real-world age group interactions.

Background

The study of infectious disease dynamics dates back to the early 20th century, with foundational work by Kermack and McKendrick in 1927, who introduced the original SIR model.[3] The initial model only included two ordinary differential equations for susceptible (S') and infected classes (I'):

$$S' = -\beta SI$$
$$I' = (\beta S - a) I$$

For their initial model, the following three assumptions had to be made: 1) that the average member of the population makes sufficient contact for transmission; 2) infected individuals leave the infected compartment at rate *a*; and 3) there is no departure or entry into the population besides death from the disease. Their model revolutionized the understanding of epidemic behavior by successfully fitting data from many former epidemics, showing how diseases can be easily analyzed quantitatively effectively.[3] However, there were certain limitations regarding this model, solely that many subjective values were put under one value. One clear example is the assumption of interactions fitting perfectly at a rate *a* per time, which does not accommodate the varying interaction levels between different aged peoples. Over time, researchers extended this model to include additional compartments like exposed individuals (SEIR), vaccinated individuals (SIRV), and deceased individuals (SIRD) to better reflect the complexities of real-world epidemics to accommodate the shortcomings and absolute assumptions from the initial model.

Studies leveraging the SIRD framework have been instrumental in guiding public health policies, including lockdown measures, vaccination campaigns, and healthcare resource allocation. By simulating different scenarios, researchers and policymakers have been able to predict potential outcomes and adjust strategies to reduce the overall impact of infectious diseases on communities. Another important feature of a pandemic is reinfection, or the possibility that recovered individuals may return to the susceptible pool, which occurs due to the rapid adaptive changes of the disease or natural waning of the body's immune system. The SEIRS (Susceptible-Exposed-Infected-Recovered-Susceptible repeat) model incorporates reinfection by introducing a second transition from the Recovered population back to the Susceptible population, accounting for immunity loss over time. This model is particularly useful when studying diseases with varying immunity durations, such as events like seasonal influenza or emerging pathogens.

Implementation

In MATLAB, the original SIR model is implemented by solving a system of differential equations that represent the change between compartments or population sub-groupings: Susceptible (S), Infected (I), and Recovered (R).

The parameter **beta** represents the infection rate, which governs how quickly susceptible individuals become infected through contact with infected individuals. The parameter **gamma** represents the recovery rate, which determines how quickly infected individuals recover and move to the recovered compartment. The equations are modeled based on the principle of mass balance: the change in each compartment over time reflects the interactions between the compartments.

The rate of change for the susceptible population (dS/dt) decreases as individuals move from susceptible to infected based on the equation:

$$\mathbf{dS/dt} = \beta \mathbf{* S * I / N}$$

where N is the total population size. Similarly, the rate of change for the infected population (dI/dt) increases due to new infections but decreases as individuals recover, based on:

$$\mathbf{dI/dt = \beta * S * I / N - \gamma * I}$$

and the recovered population increases at the rate:

$$\mathbf{dR/dt = \gamma * I}$$

which represents the individuals leaving the infected compartment.

The model is solved numerically using MATLAB's ode45 function, which calculates these rates of change per time step given the parameters, and integrates them over the specified time interval. The results are stored in a matrix, where each column corresponds to one compartment (S, I, or R). The solutions are then plotted to visualize the dynamics of the disease over time, showing how the infection spreads, peaks, and eventually diminishes as individuals recover and immunity builds in the population. To attain a proper SIRD model, we then implemented an additional differential equation that calculates the rate of change concerning death. When adding the death compartment, the differential or rate of change of the amount of people dead would be:

$$\mathbf{dD/dt = \mu * I}$$

with mu (μ) being the death rate, which when multiplied with the infected population yields the total population of dead individuals.

With our basic SIRD model complete, we then decided to implement other factors, such as age cohorts, vaccination rate, and reinfection. In our implementation of age, we utilized a contact matrix as well as different greek letter parameters for three distinct age cohorts of young, middle aged, and old people. The contact matrix dimension was 3x3, with the young age cohort starting in the left most column and topmost row. The first value in either the column or row would be the interaction between young first, then middle, and then old age cohorts. For the addition of the contact matrix, the ordinary differential equation concerning infected had to be changed to:

$$\mathbf{dI/dt = \lambda S - \beta *(\gamma + \mu)}$$

The purpose in adding lambda (λ) or the force of infection would be that it quantifies the rate at which the specified cohort of individuals become infected. In context of the contact matrix, our three distinct age cohorts would have three respective lambda values for each to represent the total risk of infection for that specific cohort. Each lambda value for its respective cohort then is influenced by all 9 contact matrix elements in the 3x3, with the value in each matrix element corresponding to a interaction intensity between one cohort with another.

Having implemented a contact matrix, we began to tinker with the system of ODEs so as to simulate events such as vaccination and reinfection as parameters. To do so, we added onto our SIRD model susceptible and recovered differential equations:

$$\begin{aligned} &\mathbf{dS/dt} \;= \mathbf{-}\beta * S * I / N \; \underline{\mathbf{- (\nu * S) - (\rho * P)}} \\ &dI/dt = \beta * S * I / N - \gamma * I \\ &\mathbf{dR/dt} = \gamma * I + \underline{\mathbf{(\nu * S) - (\rho * P)}} \\ &dD/dt = \mu * I \end{aligned}$$

In introducing specifically the rate of vaccination (ν) and rate of reinfection (ρ) within only the susceptible and recovered population equations, we simulated the phenomenon of vaccination –where people move from the susceptible to recovered population– and reinfection –where people can move from recovered back to susceptible population. In figure 1, the lefthand model was the basic SIRD model whilst the righthand model, SIRDVR, incorporated the two parameters of vaccination and reinfection,

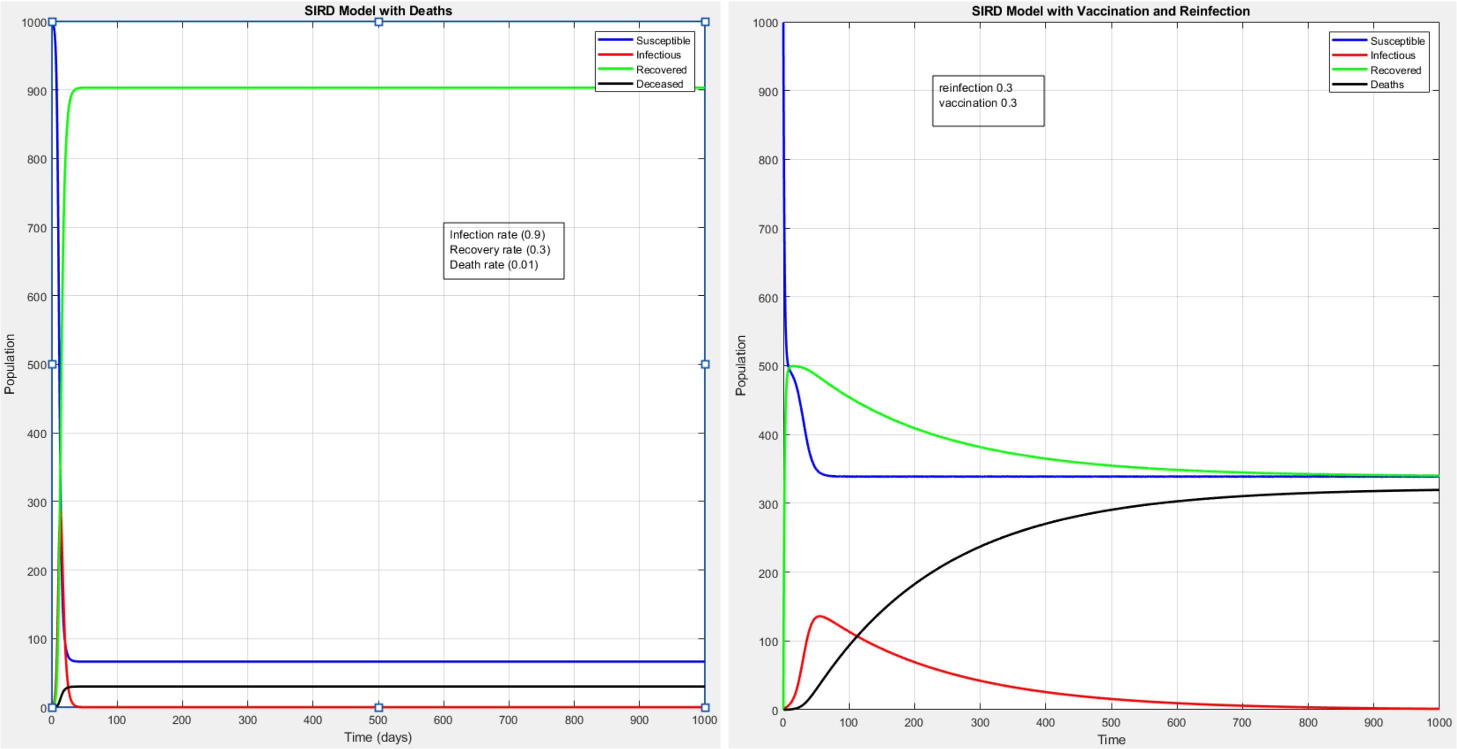
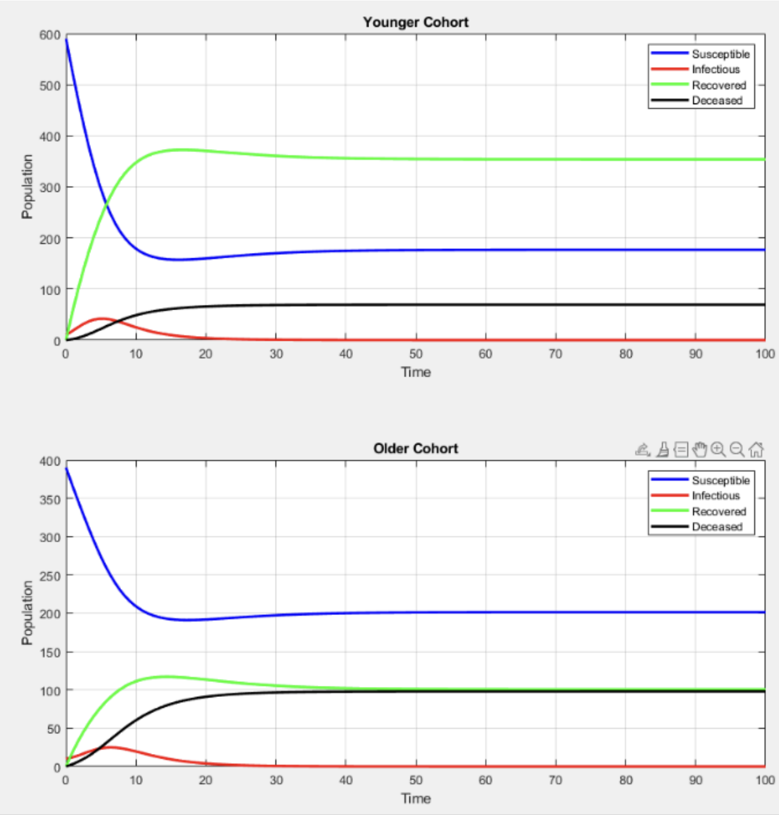
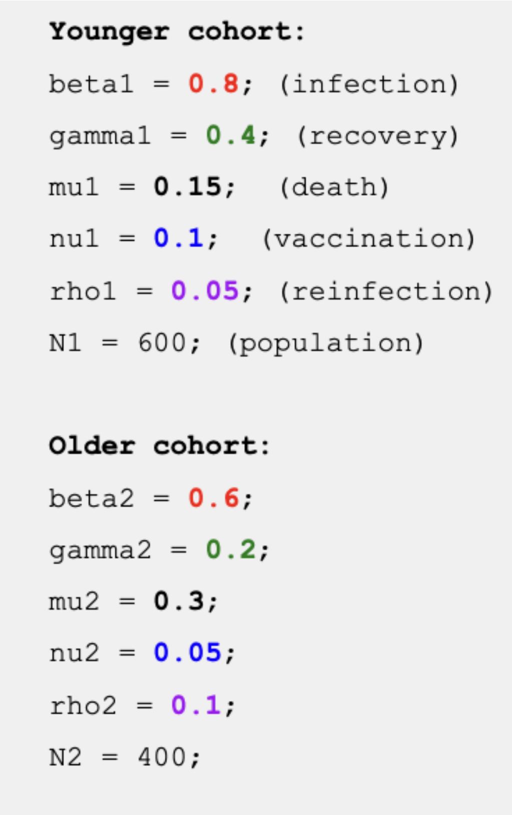


Figure 1. SIRD model(left) vs SIRDVRmodel (right) comparison

Of note would be the change in pace of plateaus occurring, with the implementation of additional parameters drawing out the plateau to occur later in comparison with the basic SIRD model. The reasons plateaus occur within these plots is due to the constant rates we are assigning eventually depleting infected people, leaving a final balance amongst all other population compartments. In adding more complexity to the SIRD model, we then proceeded to observe how the trends would change if putting the ODES through a contact matrix.





```
Younger cohort:

beta1 = 0.8; (infection)

gamma1 = 0.4; (recovery)

mu1 = 0.15;  (death)

nu1 = 0.1;  (vaccination)

rho1 = 0.05; (reinfection)

N1 = 600; (population)


Older cohort:

beta2 = 0.6;

gamma2 = 0.2;

mu2 = 0.3;

nu2 = 0.05;

rho2 = 0.1;

N2 = 400;
```

Figure 2. Use of contact matrix to simulate age group interactions, between younger and older people. The right shows the different parameter values assigned to each cohort, with the younger having double the recovery rate and half the death rate compared to the older.

A simple contact matrix of 2x2 was generated, with interactions between young and older populace being similar, whilst the only difference is that interactions amongst young people was at 1 while for older people it was 0.8. When comparing older cohorts of different contact matrix, it seemed that driving interaction scores down in general seemed to indicate a lower deceased population compared with increasing interaction scores (fig 3).

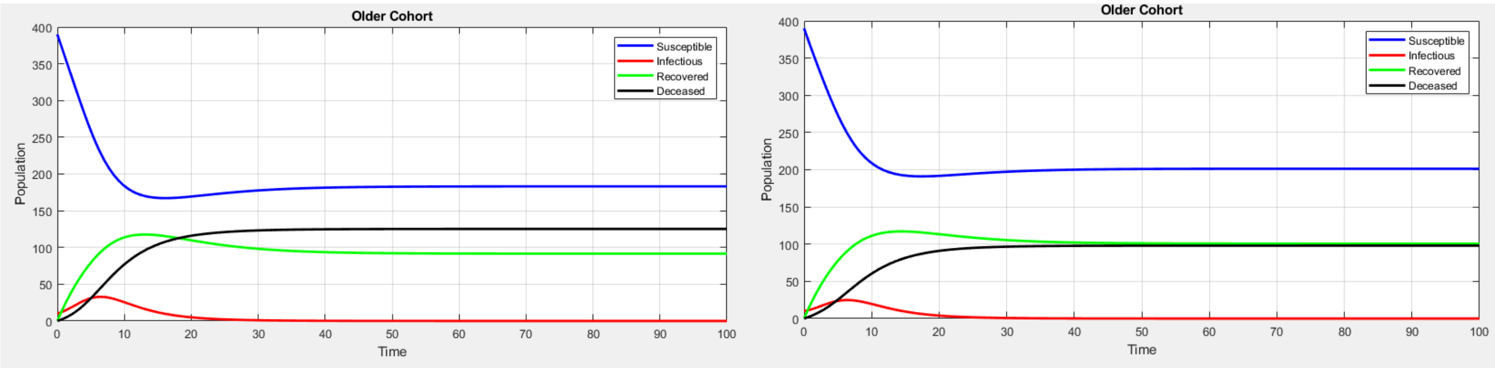


Figure 3. Older Cohort Interaction Comparison. Interaction score of 0.8 with aged (right) vs Interaction score of 1 with aged (left). Note that the deceased population rose when interaction score rose.

One additional change with SIRDVR we experiment with was eliminating the death coefficient but retaining the contact matrix. We can see that by doing so, the number of infected individuals plateaus at a higher value as the population does not automatically dwindle to zero due to their being a death rate. No changes were observed in the shape of each parameters curve when comparing with (left) and without (right) the death coefficient, but simply that the infected populace rose.

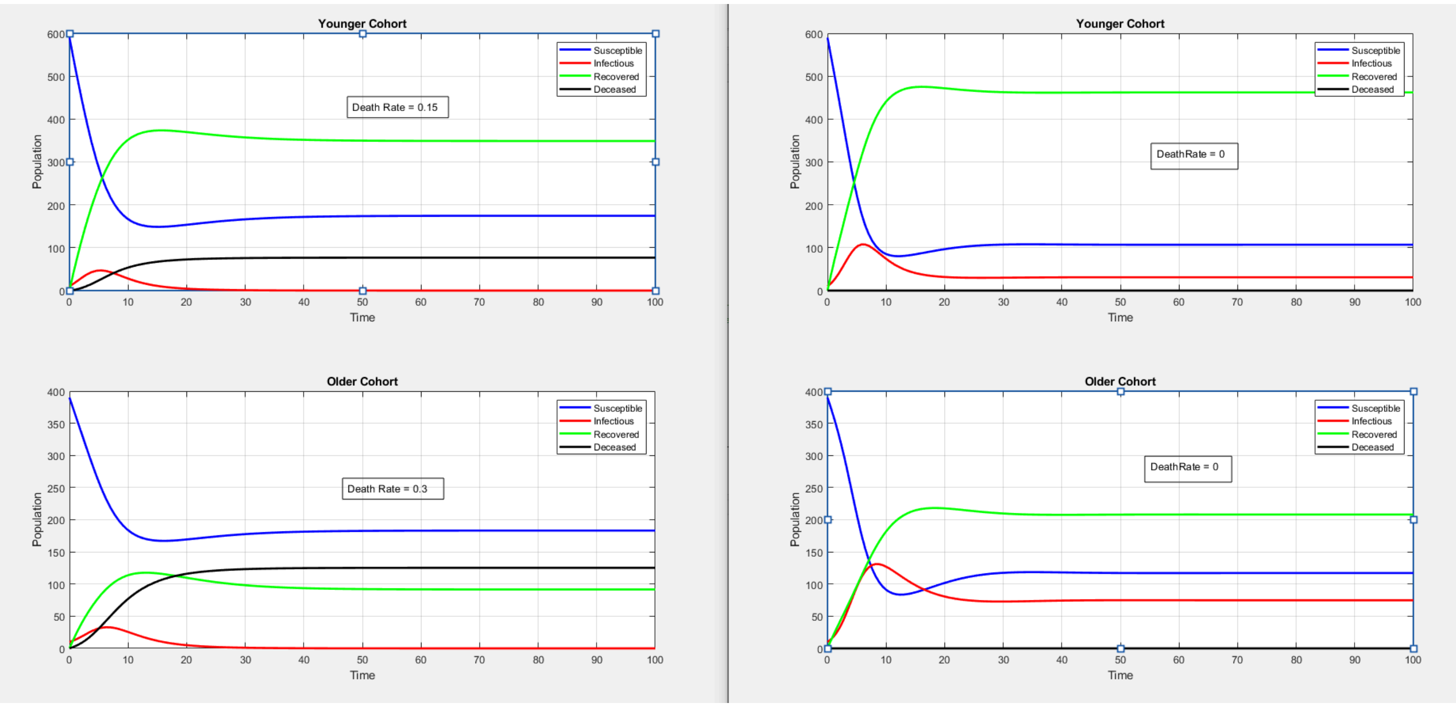


Figure 4. Age Cohorts with Death rate (left) and Age Cohorts without Death rate (right).

Another change we observed was the elimination of reinfection (Figure 5). In doing so, both cohorts seemed to exhibit high levels of recovered individuals due to removing the path for recovered individuals to become infected again. One major change is that all individuals essentially became recovered, which accounts for having reinfection maintaining a constant population of susceptible individuals. The recovered curve seems to also be heavily affected by reinfection, as the slight bump or negative tick of recovered individuals with reinfection never occurs when it is absent from the SIRDVR ODEs. It seems that the curves are also less dynamic because vaccination rate stabilizes and accelerates the plateuing effect onto each compartment's curve.

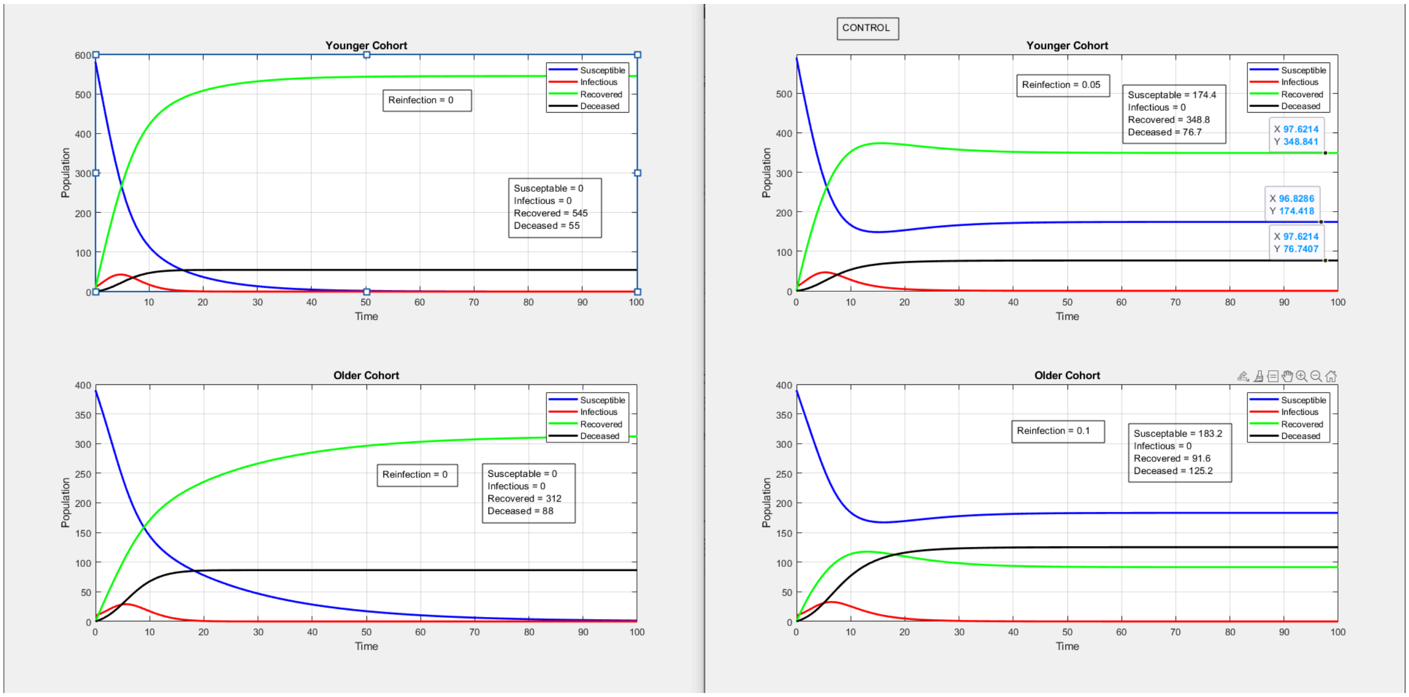


Figure 5. Age Cohorts without Reinfection (left) and Age Cohorts with Reinfection (right)

The last parameter we were interested in observing changes to each compartment's curves was to eliminate vaccination rate within the SIRDVR model (Figure 6). Elimination of vaccination seemed to bring the greatest drastic change compared to other parameter eliminations. Noticeably, the curves of susceptible and deceased populations took longer to reach plateau compared to the other curves. Looking at it by cohort, the younger cohort usually has a rise in recovered population, as vaccination seems to accelerate the plateau effect of reaching individuals immune to reinfection. With vaccination eliminated, the curve of recovered individuals noticeably decreases naturally as that balance attained between vaccination and reinfection is lost, subsequently not resulting in a plateau but decline to zero. Within the curves for the no vaccination cohorts, one can see that there now exists a sudden pop back up in "susceptible" after the typical drop in the susceptible group right before plateau that one can find on the control plot. As vaccination has been eliminated, this allows reinfection to convert recovered individuals into susceptible. The new increase in population then slows after all recovered have become susceptible again, explaining the upwards “bump.” What’s new would be the gradual increase in deceased individuals, which could be explained by a higher peak of infected individuals occurring without the vaccination parameter. In having a higher peak of infected, there’s a higher likelihood for deaths to occur, thereby explaining the longer time to plateau for the deceased population.

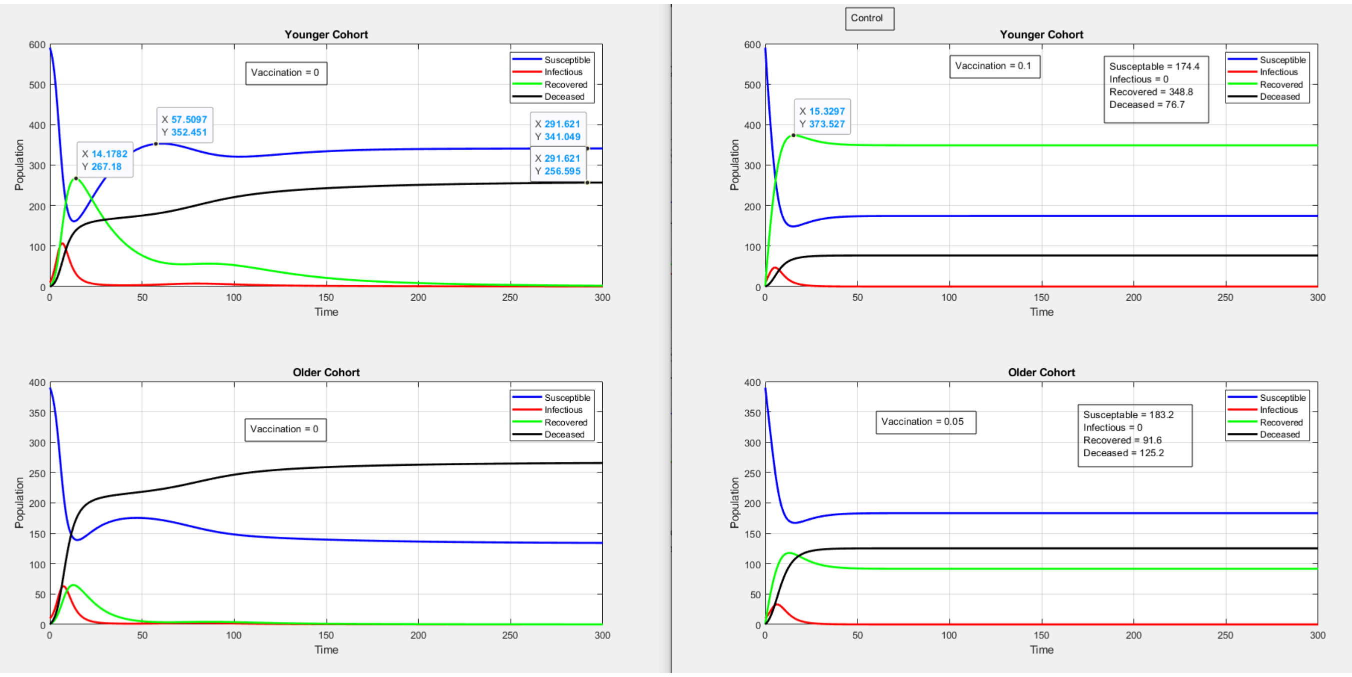


Figure 6. Age Cohorts without Vaccination Rate (left) vs with Vaccination Rate (right).

Conclusion

We successfully demonstrated the progression from the basic SIR model to a more complex SIRDVR framework, incorporating critical factors such as vaccination, reinfection, and age-cohort-specific dynamics through a contact matrix. The added parameters allowed for a closer representation of real-world behaviors, and the results of disease spread. In changing the critical parameters of vaccination rates, and reinfection rates, we demonstrated how the dynamics or characteristics of the spread of disease changes within the subgroup compartments affect the overall population. By modifying individual parameters, we also provided insights into the critical balance required for effective pandemic management, as the absence of a parameter can drastically change the progression and behavior of individual compartments which will affect the overall health of the population.

However, the model is not without its limitations. Our reliance on fixed contact intensities for the contact matrix may limit its applicability to a highly heterogeneous population, or thinking of different dynamics globally. Additionally, our exclusion of spatial dynamics and potential interactions with external factors, such as healthcare capacity or socioeconomic influences, can be seen to constrain the model’s ability to help provide a better understanding of epidemic trajectories. A possible next step for this model project would be to integrate spatial dynamics to better examine localized outbreaks. The introduction of spatial components can be done with a multiagent approach, which further breaks down our established age cohorts into different risk groups along with assigning each group their own level of susceptibility, infectivity, and mortality rates. The model would then involve visualization of the spatial dynamics of the population's different risk groups by occupying them in a 3D grid that becomes dictated by each group's predefined rules and patterns to emulate real world counterparts. From what we've learned in class, heatmaps could be used to display the density of groups across the grid. In utilizing multiple heatmaps to measure for a given time period, we can make a stop-motion movie which would theoretically capture the movements of each group, as well as look at the corresponding intensity of infection rates based off of those movements for a time step.

Nonetheless, if one were to try and maintain the current model's relative simplicity, there are additional improvements that could be made to increase accuracy without sacrificing ease of use. One such idea is to add seasonality. This would require a "calendar" to be built into the model instead of having a time set to a select number of days. Then probably similarly to the cohorts, different times of the years would affect the various pandemic parameters and potentially even the interaction matrix. An even simpler addition is the inclusion of an "exposed"population, a group where people could latently host the disease. This would more accurately represent the real world and allows for more interesting interactions.

Citations

1. Liu, T., Huang, J., He, Z. *et al.* A real-world data validation of the value of early-stage SIR modelling to public health. *Sci Rep* 13, 9164 (2023). https://doi.org/10.1038/s41598-023-36386-9
2. Tsai, P.-C., Tsai, S.-H., Lian, I.-S., Young, T.-P., Kuo, J.-C., Chen, P.-W., Hsueh, P.-R., Chang, S.-C., Lin, C.-H., Lee, C.-G., Chang, S.-H., Chen, C.-K., Chan, T.-H., Wang, S.-Y., Chen, H.-H., Chen, S.-F., Lee, P.-H., Lee, C.-T., Shih, S.-R., & Wang, J.-R. (2022). Rapid displacement of SARS-CoV-2 variant Delta by Omicron reveals immune modulation and escape strategies. *International Journal of Molecular Sciences, 23*(13), Article 7289. https://doi.org/10.3390/ijms23137289
3. Brauer, F. (2005). The Kermack–McKendrick epidemic model revisited. *Mathematical Biosciences, 198*(2), 119–131. https://doi.org/10.1016/j.mbs.2005.07.006

Appendix

1.1 SIR model simulation

```
% SIR Model Simulation
%Params (CHANGE THESE)
beta = 0.3;    % Transmission rate (probability of contact rates and
transmission
gamma = 0.1;   % Recovery rate
N = 1000000;   % Total population
I0 = 1000;     % Initial number of infected individuals
R0 = 0;        % Initial number of recovered individuals
S0 = N - I0 - R0; % Initial number of susceptible individuals
days = 100;    % Duration of simulation (days)
tspan = [0 days]; % Time Span
% Initial Conditions
y0 = [S0; I0; R0];
% Differential equations of SIR Model
function dydt = sir_model(t, y, beta, gamma, N)
   S = y(1); % Susceptible
   I = y(2); % Infected
   R = y(3); % Recovered
   dS = -beta * S * I / N;            % Rate of change of Susceptible
   dI = beta * S * I / N - gamma * I; % Rate of change of Infected
   dR = gamma * I;                    % Rate of change of Recovered
   dydt = [dS; dI; dR];
end
% Solve the ODEs
[t, y] = ode45(@(t, y) sir_model(t, y, beta, gamma, N), tspan, y0);
% Extract Results
S = y(:, 1); % Susceptible
I = y(:, 2); % Infected
R = y(:, 3); % Recovered
% Plot the Results
figure;
hold on;
plot(t, S, 'b', 'LineWidth', 2); % Susceptible
plot(t, I, 'r', 'LineWidth', 2); % Infected
plot(t, R, 'g', 'LineWidth', 2); % Recovered
hold off;
% Customize Plot
title('SIR Model Simulation');
xlabel('Time (days)');
ylabel('Population');
legend('Susceptible', 'Infected', 'Recovered');
grid on;
```

1.2 Immunization implement

```
% Parameters
% beta = 0.8;   % Infection rate
% gamma = 0.001;  % Recovery rate
% mu = 0.1;    % Death rate
% nu = 0.9;    % Vaccination rate
% rho = 0.8;   % Reinfection rate
% N = 10000;     % Total population
% Initial conditions
S0 = 5000;     % Initial susceptible population
I0 = 100;      % Initial infectious population
```

```
R0 = 10;       % Initial recovered population
D0 = 100;       % Initial deaths
initial_conditions = [S0, I0, R0, D0];
% Time vector
tspan = [0 1000];
% Solve the system of ODEs
[t, Pop] = ode45(@sirvd_ode, tspan, initial_conditions);
% Extract results
S = Pop(:, 1);
I = Pop(:, 2);
R = Pop(:, 3);
D = Pop(:, 4);
% Plotting elements
figure;
plot(t, S, 'b', 'LineWidth', 2); hold on;
plot(t, I, 'r', 'LineWidth', 2);
plot(t, R, 'g', 'LineWidth', 2);
plot(t, D, 'k', 'LineWidth', 2);
xlabel('Time');
ylabel('Population');
legend('Susceptible', 'Infectious', 'Recovered', 'Deaths');
title('SIRD Model with Vaccination and Reinfection');
grid on;
% ODE function
function dPop = sirvd_ode(~, Pop, tspan)
   % Parameters
   beta = 0.8 * (1 + 0.2 * sin(0.01 * tspan));    % Infection rate
   gamma = 0.1;  % Recovery rate
   mu = 0.1;    % Death rate
   nu = 0.6 + 0.2 * exp(-0.005 * tspan);     % Vaccination rate
   rho = 0.8;   % Reinfection rate
   N = 10000;     % Total population
   % Population compartments (SIRD)
   S = Pop(1);
   I = Pop(2);
   R = Pop(3);
   D = Pop(4);
   % ODE system
   dS = -beta * S * I / N - nu * S + rho * R;
   dI = beta * S * I / N - gamma * I - mu * I;
   dR = gamma * I + nu * S - rho * R;
   dD = mu * I;
   dPop = [dS; dI; dR; dD];
end
```

1.3 Age Cohort Basic implementation (Young vs Old)

```
function sirvd_cohorts

 %Parameters for younger cohort (cohort 1)
   beta1 = 0.4;  % Infection rate for younger
   gamma1 = 0.1; % Recovery rate for younger
   mu1 = 0.005;  % Death rate for younger
   nu1 = 0.05;   % Vaccination rate for younger
   rho1 = 0.02;  % Reinfection rate for younger
   % Parameters for older cohort (cohort 2)
   beta2 = 0.3;  % Infection rate for older
   gamma2 = 0.08; % Recovery rate for older
   mu2 = 0.02;   % Death rate for older
   nu2 = 0.04;   % Vaccination rate for older
   rho2 = 0.01;  % Reinfection rate for older
   % Interaction between cohorts (contact rates)
   contact_matrix = [0.8, 0.5;  % Younger interacting with younger and older
                     0.5, 0.7]; % Older interacting with younger and older
%Total population
   N1 = 600; % Population size of younger cohort
   N2 = 400; % Population size of older cohort

%Initial conditions
   S1_0 = 590; I1_0 = 10; R1_0 = 0; D1_0 = 0; % Younger cohort
   S2_0 = 390; I2_0 = 10; R2_0 = 0; D2_0 = 0; % Older cohort
   initial_conditions = [S1_0, I1_0, R1_0, D1_0, S2_0, I2_0, R2_0, D2_0];

%Time vector
   tspan = [0 100];


%System of ODEs
   params = struct('beta1', beta1, 'gamma1', gamma1, 'mu1', mu1, 'nu1', nu1,
'rho1', rho1, ...
                   'beta2', beta2, 'gamma2', gamma2, 'mu2', mu2, 'nu2', nu2,
'rho2', rho2, ...
                   'contact_matrix', contact_matrix, 'N1', N1, 'N2', N2);
[t, Pop] = ode45(@(t, Pop) sirvd_ode(t, Pop, params), tspan,
initial_conditions);
   % Extract results
   S1 = Pop(:, 1); I1 = Pop(:, 2); R1 = Pop(:, 3); D1 = Pop(:, 4);
   S2 = Pop(:, 5); I2 = Pop(:, 6); R2 = Pop(:, 7); D2 = Pop(:, 8);
   % Plot results
   figure;
   subplot(2, 1, 1);
   plot(t, S1, 'b', 'LineWidth', 2); hold on;
   plot(t, I1, 'r', 'LineWidth', 2);
   plot(t, R1, 'g', 'LineWidth', 2);
   plot(t, D1, 'k', 'LineWidth', 2);
   xlabel('Time');
   ylabel('Population');
   legend('S1 (Younger)', 'I1 (Younger)', 'R1 (Younger)', 'D1 (Younger)');
   title('Younger Cohort');
   grid on;
   subplot(2, 1, 2);
   plot(t, S2, 'b--', 'LineWidth', 2); hold on;
   plot(t, I2, 'r--', 'LineWidth', 2);
   plot(t, R2, 'g--', 'LineWidth', 2);
   plot(t, D2, 'k--', 'LineWidth', 2);
   xlabel('Time');
   ylabel('Population');
   legend('S2 (Older)', 'I2 (Older)', 'R2 (Older)', 'D2 (Older)');
   title('Older Cohort');
   grid on;
end


% ODE Function
```

```
function dPop = sirvd_ode(~, Pop, params)
   % Extract parameters
   beta1 = params.beta1; gamma1 = params.gamma1; mu1 = params.mu1; nu1 =
params.nu1; rho1 = params.rho1;
   beta2 = params.beta2; gamma2 = params.gamma2; mu2 = params.mu2; nu2 =
params.nu2; rho2 = params.rho2;
   contact_matrix = params.contact_matrix; N1 = params.N1; N2 = params.N2;
   % Population compartments
   S1 = Pop(1); I1 = Pop(2); R1 = Pop(3); D1 = Pop(4);
   S2 = Pop(5); I2 = Pop(6); R2 = Pop(7); D2 = Pop(8);
   % Force of infection (interaction between cohorts)
   lambda1 = beta1 * (contact_matrix(1, 1) * I1 / N1 + contact_matrix(1, 2) *
I2 / N2);
   lambda2 = beta2 * (contact_matrix(2, 1) * I1 / N1 + contact_matrix(2, 2) *
I2 / N2);
   % Younger cohort ODES
   dS1 = -lambda1 * S1 - nu1 * S1 + rho1 * R1;
   dI1 = lambda1 * S1 - gamma1 * I1 - mu1 * I1;
   dR1 = gamma1 * I1 + nu1 * S1 - rho1 * R1;
   dD1 = mu1 * I1;
   % Older cohort ODES
   dS2 = -lambda2 * S2 - nu2 * S2 + rho2 * R2;
   dI2 = lambda2 * S2 - gamma2 * I2 - mu2 * I2;
   dR2 = gamma2 * I2 + nu2 * S2 - rho2 * R2;
   dD2 = mu2 * I2;
   % Combine results
   dPop = [dS1; dI1; dR1; dD1; dS2; dI2; dR2; dD2];
end
```