What are the key differences between the SEIRD model with deterministic parameters observed during COVID-19 and the SEIRD model with stochastic parameters, particularly in how they differ in the peak number of infections throughout the simulation?

A ModSim Computational Essay - Project 3

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Abstract SEIRD models are mathematical models of the spread of an infectious disease. Every individual in a population is in one of five states—they are either susceptible (S) to the disease, exposed (E) to the disease, infected (I) by the disease, or have recovered (R) or died (D) from the disease. Using SEIRD to predict COVID-19 spread, we are comparing the peak infectivity presented when using deterministic parameters obtained from data gathered during COVID-19 with the peak infectivity presented when using stochastic parameters that represent the real world as reasonably as possible.

Modeling and Simulation of the Physical World

Submitted to *Modeling and Simulation of the Physical World*.

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1 Question

1.1 Modeling Question and Categorization

What are the key differences between the SEIRD model with deterministic parameters observed during COVID-19 and the SEIRD model with stochastic parameters, particularly in how they differ in the peak number of infections throughout the simulation? - Our modeling question is an explanatory question because it assesses how the difference between the state of parameters as deterministic or random in the SEIRD model affects the modeling results.

1.2 Importance/Interest

This exciting modeling question can help us determine how pandemics could have a very distinctive pattern of disease transmission that would not necessarily be the same as observed during COVID-19. It would be crucial for epidemiologists to better prepare for any scenarios that may arise due to randomness observed in future pandemics, building upon the data from COVID-19.

1.3 Background Information and References

Explanatory Questions of this type compare the advantages and disadvantages of specific model-building decisions, such as deterministic vs stochastic parameters. Our research is summarized in the Research Synthesis Matrix below (All cited in References section):

Stochastic vs Deterministic Parameters

	("1.3.6.6.17. Beta Distribution"), ("Beta Distribution - Definition, Formulas, Properties, Applications"), (Kim), (Weisstein)	(Ala'raj et al.), (Korolev), (Loli Piccolomini and Zama), (Menda et al.)	("Difference between Deterministic and Non-Deterministic Algorithms - GeeksforGeeks"), (Hastings et al.), (Lande), (Shoemaker et al.), (Stephanie), ("Stochasticity - an Overview | ScienceDirect Topics")	
SEIRD Model		Expert models serve as validation for our models, and also provide guidance and structure for any modeling decision we make. These sources also helped us decide which parameters we can make stochastic and why.		
Stochasticity & Determinism			Our modeling question was looking at stochastic vs deterministic parameters, and the effects they have on the results of an SEIRD model. Understanding these concepts first was critical before making any modeling decisions. The clarity these sources gave us also helped with determining the parameters we randomized and the reasons for doing so.	
Beta Distribution	These sources gave us great insight into the nature and usefulness of Beta Distributions. The distribution's properties made sense to utilize as the probability distribution for the stochastic parameters of our model (infectivity and recovery rate). We also learned the differences between using discrete and continuous distributions through these sources.			

Figure 1 Research Synthesis Matrix

What are the key differences between the SEIRD model with deterministic parameters observed during COVID-19 and the SEIRD model with stochastic parameters, particularly in how they differ in the peak number of infections throughout the simulation?

2 Methodology/Model

2.1 Description

Our model is a state-based SEIRD model that categorizes people into 1 of 5 different states: Susceptible, Exposed, Infected, Recovered, and Dead.

Our model is displayed below:

```
% SEIRD (deterministic) parameters
alpha = 0.3;                                % Infection rate
beta  = 0.037;                              % Exposure rate
gamma = 0.25;                               % Recovery rate
δ = 0.033;                                  % Death rate
sigma = 0.015;                              % Re-susceptible rate

% Time period
timestep = 100;

% Initial number of people
i_0 = 2;
s_0 = 100 - i_0;
r_0 = 0;
e_0 = 6;
d_0 = 0;


% SEIRD simulation
[S, E, I, R, D, W] = simulate_seird(s_0 - e_0, e_0, i_0, r_0, ...
    ↪ d_0, alpha, beta, gamma, δ, sigma, timestep);


% Conditions
assert(all(abs(S + E + I + R + D - 100) < 1e-3), ...
    ↪ "Conservation of People Violated!")

assert(all(S≥0)||all(E≥0)||all(I≥0)||all(R≥0)||all(D≥0), ...
    ↪ "Negative People!")

assert(all(S≤100)||all(E≤100)||all(I≤100)||all(R≤100)|| ...
    ↪ all(D≤100), "Extra People Found!")

assert(all((D(2:end)-D(1:(end-1)))≥0), "Dead People decreasing!")


% Plot SEIRD
plot(W, S, 'b-', 'LineWidth', 1, 'DisplayName', 'Susceptible');
hold on;
plot(W, E, 'g-', 'LineWidth', 1, 'DisplayName', 'Exposed');
plot(W, I, 'm-', 'LineWidth', 1, 'DisplayName', 'Infectious');
plot(W, R, 'c-', 'LineWidth', 1, 'DisplayName', 'Recovered');
plot(W, D, 'k-', 'LineWidth', 1, 'DisplayName', 'Dead');
hold off;
xlabel("Week")
ylabel("Persons")
legend()
```

```
title("SEIRD (deterministic)")

% SEIRD (stochastic) parameters
alpha_n = 0.3;                                  % Infection rate
beta_n  = 0.037;                                % Exposure rate
gamma_n = 0.25;                                 % Recovery rate
ᐞ_n = 0.033;                                   % Death rate
sigma_n = 0.015;                                % Re-susceptible rate

% Infectivity (beta) parameter stochasticity
x_beta = 0.0005:0.0005:0.05;
beta_pdf = betapdf(x_beta,5,20);
plot(x_beta,beta_pdf)
title("Infectivity (\beta) stochasticity - Beta distribution")

% Recovery (gamma) parameter stochasticity
x_gamma = 0.1:0.002:0.3;
gamma_pdf = betapdf(x_gamma,10,8);
plot(x_gamma,gamma_pdf)
title("Recovery (\gamma) stochasticity - Beta distribution")

% Verification for stochastic parameter values
for i=1:length(beta_pdf)
    assert(all(beta_pdf(i) ≥ 0 & beta_pdf(i) ≤ 1), "Error in ...
        ↪ stochastic beta parameter value!")
    assert(all(gamma_pdf(i) ≥ 0 & gamma_pdf(i) ≤ 1), "Error ...
        ↪ in stochastic gamma parameter value!")
end

% Time period
timestep = 100;

% Initial number of people
i_0 = 2;
s_0 = 100 - i_0;
r_0 = 0;
e_0 = 6;
d_0 = 0;

rng(101)

I_ensemble = zeros(timestep, length(beta_pdf));

for i=1:length(beta_pdf)

    beta_pdf_temp = beta_pdf(i);
    gamma_pdf_temp = gamma_pdf(i);

    % SEIRD simulation
    [Sn, En, In, Rn, Dn, Wn] = simulate_seird(s_0 - e_0, e_0, ...
        ↪ i_0, r_0, d_0, alpha_n, beta_pdf_temp, ...
        ↪ gamma_pdf_temp, ᐞ_n, sigma_n, timestep);

    I_ensemble(:, i) = sum(In, 1);

end

I_mean = mean(I_ensemble, 2);
```

What are the key differences between the SEIRD model with deterministic parameters observed during COVID-19 and the SEIRD model with stochastic parameters, particularly in how they differ in the peak number of infections throughout the simulation?

```
98
99  % Conditions
100 assert(all(abs(Sn + En + In + Rn + Dn - 100) < 1e-3), ...
        ↪ "Conservation of People Violated!")
101
102 assert(all(Sn≥0)||all(En≥0)||all(In≥0)||all(Rn≥0)||all(Dn≥0), ...
        ↪ "Negative People!")
103
104 assert(all(Sn≤100)||all(En≤100)||all(In≤100)||all(Rn≤100)|| ...
        ↪ all(Dn≤100), "Extra People Found!")
105
106 assert(all((Dn(2:end)-Dn(1:(end-1)))≥0), "Dead People ...
        ↪ decreasing!")
107
108
109 % Plot SEIRD (stochastic) infections
110 plot(Wn, I_ensemble, 'b-', 'LineWidth', 0.1, 'DisplayName', ...
        ↪ 'Infectious');
111 hold on;
112 plot(Wn, I_mean, 'r-', 'LineWidth', 5, 'DisplayName', ...
        ↪ 'Infectious');
113 hold off;
114 xlabel("Week")
115 ylabel("Infected Persons")
116 title("SEIRD (stochastic)")
117
118
119 % Plot SEIRD (stochastic) infections for takeoff simulations ...
        ↪ vs all simulations
120
121 I_ensemble_high = zeros(timestep, length(beta_pdf));
122
123 for i=1:100
124
125     if (max(I_ensemble(:,i)) > 50) && (30≤i) && (i≤100)
126
127         I_ensemble_high(:,i) = I_ensemble(:,i);
128
129         plot(Wn, I_ensemble(:,i), 'y-', 'LineWidth', 0.1, ...
                ↪ 'HandleVisibility','off');
130         hold on;
131
132     end
133
134 end
135
136 I_mean_high = mean(I_ensemble_high(:,30:86), 2);
137
138 plot(Wn, I_mean_high, 'k-', 'LineWidth', 5, 'DisplayName', ...
        ↪ 'Mean Infections - Takeoff simulations');
139 plot(Wn, I_mean, 'r-', 'LineWidth', 5, 'DisplayName', 'Mean ...
        ↪ Infections - All simulations');
140 hold off;
141 xlabel("Week")
142 ylabel("Infected Persons")
143 legend()
144 title("SEIRD (stochastic) maximum infections - Takeoff vs All ...
        ↪ simulations")
```

```
145
146 % Plot SEIRD (stochastic)
147 plot(Wn, Sn, 'b-', 'LineWidth', 1, 'DisplayName', 'Susceptible');
148 hold on;
149 plot(Wn, En, 'g-', 'LineWidth', 1, 'DisplayName', 'Exposed');
150 plot(Wn, I_mean, 'r-', 'LineWidth', 1, 'DisplayName', ...
        ↪ 'Infectious');
151 plot(Wn, Rn, 'c-', 'LineWidth', 1, 'DisplayName', 'Recovered');
152 plot(Wn, Dn, 'k-', 'LineWidth', 1, 'DisplayName', 'Dead');
153 hold off;
154 xlabel("Week")
155 ylabel("Persons")
156 legend()
157 title("SEIRD (stochastic)")
158
159 % Plot SEIRD (Deterministic) vs SEIRD (Stochastic)
160 plot(W, I, 'b-', 'LineWidth', 1, 'DisplayName', 'SEIRD ...
        ↪ (Deterministic)');
161 hold on;
162 plot(Wn, I_mean, 'r-', 'LineWidth', 1, 'DisplayName', 'SEIRD ...
        ↪ (Stochastic)');
163 hold off;
164 xlabel("Week")
165 ylabel("Infected Persons")
166 legend()
167 axis([0,100,ylim()]);
168 title("SEIRD (Deterministic) vs SEIRD (Stochastic)")
```

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Stock-and-Flow diagram of SEIRD model:

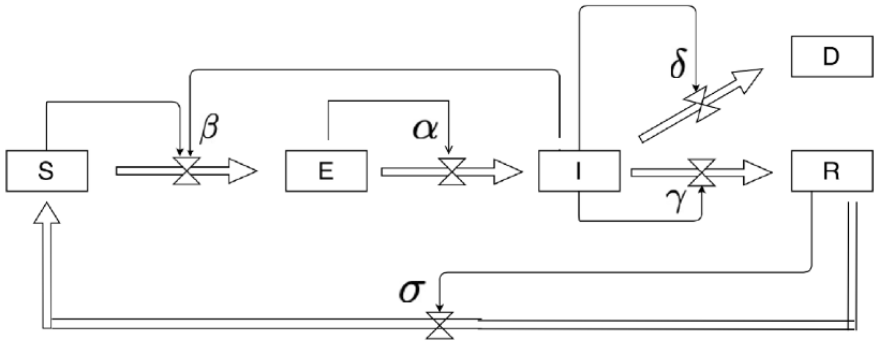

Figure 2 SEIRD Model represented in stock-and-flow form

Update Equations of SEIRD model:

$S_{n+1} = S_n - \beta IS + \sigma R$
$E_{n+1} = E_n - \alpha E + \beta IS$
$I_{n+1} = I_n - \gamma I - \delta I + \alpha E$
$R_{n+1} = R_n - \sigma R + \gamma I$
$D_{n+1} = D_n + \delta I$

Stocks in the SEIRD model:

- S represents the number of Susceptible people in the model
- E represents the number of Exposed people in the model
- I represents the number of Infectious people in the model
- R represents the number of Recovered people in the model
- D represents the number of Dead people in the model

Flows in the SEIRD model:

- The flow from S to E represents susceptible people getting exposed
- The flow from E to I represents exposed people becoming infectious
- The flow from I to D represents infectious people dying
- The flow from I to R represents infectious people recovering
- The flow from R to S represents recovered people becoming re-susceptible

2.2 Abstractions

The SEIRD model has multiple abstractions, but the greatest being that natural births and deaths cancel out leaving only the deaths by the disease itself. This is an acceptable assumption because natural births and deaths are relatively balanced within the short-term across which the model is simulated. The models also assume that keeping the re-susceptibility parameter the same across both, albeit chosen arbitrarily, does not influence the visible differences in behavior holistically. This assumption is acceptable because the modeling question looks at overall trends in model results and infectivity sensitivity rather than disease-specific characteristics.

2.3 Development

The parameters of the deterministic SEIRD model were set by taking into account the following:
α **(incubation time)** - The incubation time of COVID is, on average 8 days, according to the CDC. A person starts at 100% health and is considered infectious at 25% health. With each passing week, a person's current health is multiplied by alpha to calculate their new health. This calibration was used to find a value of 30/100 for alpha where after 8 days, a person is considered infectious.
β **(infectivity)** - The parameter beta is within the range of 0.005 and 0.2. These values were chosen as bounds because below 0.005, the simulation time frame is insufficient to produce results, and above 0.2, the metrics measured become almost entirely linear for the SEIRD model.
γ **(recovery**) - The recovery time for COVID was found to be approximately one week. A person starts at 100% infectiousness and is considered recovered at 25% infectiousness. With each passing week, a person's current infectiousness is multiplied by gamma to calculate their new infectiousness. This calibration was used to find a value of 1/4, where after 7 days, a person is considered healthy and non-infectious.
δ **(death)** - The death rate of COVID is 1/30.
σ **(re-susceptibility)** - This parameter is arbitrary such that the models produce results within the simulation window.

The stochastic parameters of the stochastic SEIRD model were set by taking into account the following:
β_n **(infectivity)** - The Exposure Rate of stochastic SEIRD models we looked at in published research models determined β_n **(infectivity)** to be between 0.03 and 0.04, and our models achieve the closest results when using the value of 0.037.
γ_n **(recovery)** - The Recovery Rate of stochastic SEIRD models we looked at in published research models determined γ_n **(recovery)** to be between 0.2 and 0.3, and our models achieve the closest results when using the value of 0.25.

2.4 Verification

There are four verification facts used to ensure that the SEIRD model functions as expected:

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- Conservation of People Violated: The total number of people has either exceeded or fallen below the starting value.
- Negative People: A stock is experiencing negative people.
- Extra People found: A stock has more than the initial number of people in the simulation.
- Dead People decreasing: The Dead stock is decreasing.

```
assert(all(abs(S + E + I + R + D - 100) < 1e-3), ...
    ↪ "Conservation of People Violated!")
assert(all(S≥0)||all(E≥0)||all(I≥0)||all(R≥0)||all(D≥0), ...
    ↪ "Negative People!")
assert(all(S≤100)||all(E≤100)||all(I≤100)||all(R≤100)|| ...
    ↪ all(D≤100), "Extra People found!")
assert(all((D(2:end)-D(1:(end-1)))≥0), "Dead People decreasing!")
```

The verification facts used to ensure that the stochastic probability distribution and the parameter values function as expected are:

- Beta distribution bounds violated: In the SEIRD (stochastic) model, we draw values for the stochastic parameters from the Beta Probability Distribution function, and the bounds cannot exceed the interval [0,1]

```
for i=1:length(beta_pdf)
    assert(all(beta_pdf(i) ≥ 0 & beta_pdf(i) ≤ 1), "Beta ...
        ↪ distribution bounds violated!")
    assert(all(gamma_pdf(i) ≥ 0 & gamma_pdf(i) ≤ 1), "Beta ...
        ↪ distribution bounds violated!")
end
```

2.5 Validation

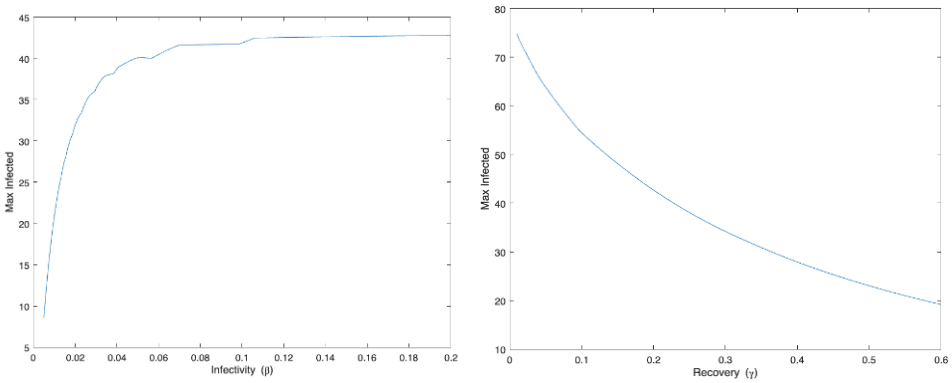
The beta distribution is a family of continuous probability distributions set on the interval [0, 1] having two positive shape parameters, expressed by α and β. These two parameters appear as exponents of the random variable and manage the shape of the distribution. In comparison to a binomial distribution, beta distributions model the probability of success instead of the number of successes (hence the axis labels in Figures 4d & 4e). Think of α-1 as the number of successes and β-1 as the number of failures. Thus, Beta distributions are appropriate for our stochastic parameters since they are a continuous distribution that models the 'probability of a probability' of the stochastic parameters, i.e., what are the odds of infectivity having a value of X? As a contributor on Towards Data Science (cited in section 5) writes, "The Beta distribution is the conjugate prior for the Bernoulli, binomial, negative binomial and geometric distributions (seems like those are the distributions that involve success & failure) in Bayesian inference. Computing a posterior using a conjugate prior is very convenient because you can avoid expensive numerical computation involved in Bayesian Inference." This essentially means that since we know we are using a Beta distribution prior to running the model, we already know that post-run, we will still

get a Beta distribution, which eases the task from both a computational and model design standpoint.

What are the key differences between the SEIRD model with deterministic parameters observed during COVID-19 and the SEIRD model with stochastic parameters, particularly in how they differ in the peak number of infections throughout the simulation?

3 Result

3.1 Metrics and Sweeps



(a) Parameter Sweep for Infectivity Rate β **(b)** Parameter Sweep for Recovery Rate γ

We conducted a sensitivity analysis using parameter sweeps for the SEIRD model. The metric we chose to help answer our question is: how does the peak number of infections differ with the use of deterministic vs stochastic parameters? This metric is appropriate because it allows us to observe the degree of difference in using deterministic vs stochastic parameters in our model.

```
% Time
timestep = 100;

% Parameters
alpha_middle = 0.3;
beta_middle  = 0.037;
gamma_middle = 0.25;
ฮ”_middle = 0.033;
sigma_middle = 0.015;

% Initial number of people
i_0 = 2;
s_0 = 100 - i_0;
r_0 = 0;
e_0 = 6;
d_0 = 0;

% Parameter sweep for infectivity (beta)

beta_start = 0.005;
beta_end = 0.2;
Beta_all = linspace(beta_start, beta_end, 500);

% Reserve space for the resulting metric values
Max_all = zeros(size(Beta_all));

% Loop over all beta values
```

```
for i = 1 : length(Beta_all)

    % Simulate with the desired beta
    beta_temp = Beta_all(i);

    [S, E, I, R, D, W] = simulate_seird(s_0 - e_0, e_0, i_0, ...
        ↪ r_0, d_0, alpha_middle, beta_temp, gamma_middle, ...
        ↪ _middle, sigma_middle, timestep);

    % Compute and store the metric value
    Max_all(i) = max(I);

end

% Visualize the results
figure()
plot(Beta_all, Max_all)
xlabel('Infectivity (\beta)')
ylabel('Max Infected')

% Parameter sweep for recovery (gamma)

gamma_start = 0.01;
gamma_end = 0.6;
Gamma_all = linspace(gamma_start, gamma_end, 500);

% Reserve space for the resulting metric values
Max_all = zeros(size(Gamma_all));

% Loop over all beta values
for i = 1 : length(Gamma_all)

    % Simulate with the desired beta
    gamma_temp = Gamma_all(i);

    [S, E, I, R, D, W] = simulate_seird(s_0 - e_0, e_0, i_0, ...
        ↪ r_0, d_0, alpha_middle, beta_middle, gamma_temp, ...
        ↪ _middle, sigma_middle, timestep);

    % Compute and store the metric value
    Max_all(i) = max(I);

end

% Visualize the results
figure()
plot(Gamma_all, Max_all)
xlabel('Recovery (\gamma)')
ylabel('Max Infected')
```

What are the key differences between the SEIRD model with deterministic parameters observed during COVID-19 and the SEIRD model with stochastic parameters, particularly in how they differ in the peak number of infections throughout the simulation?

3.2 Analysis

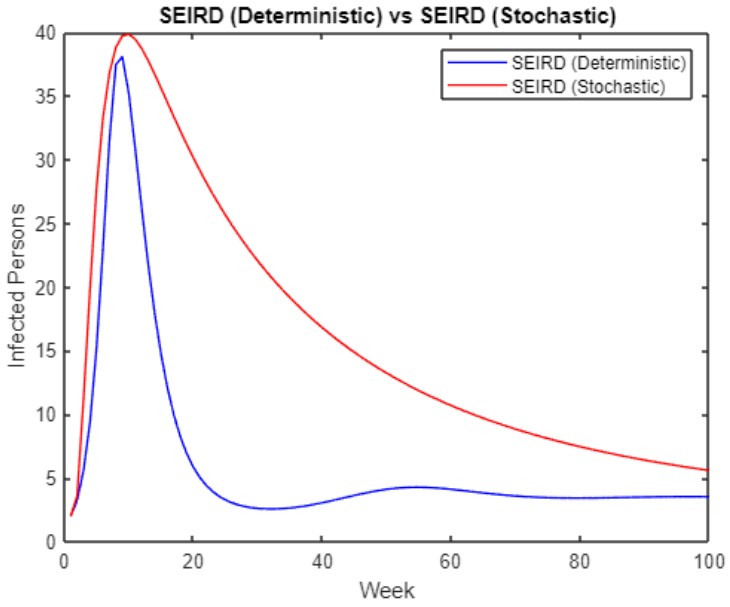
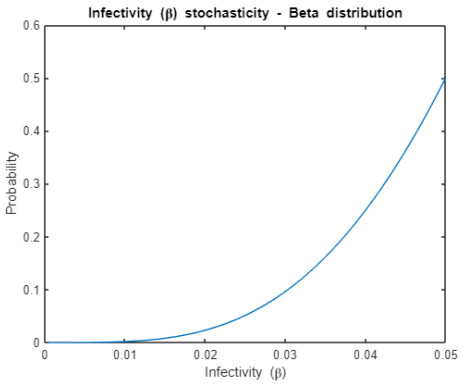
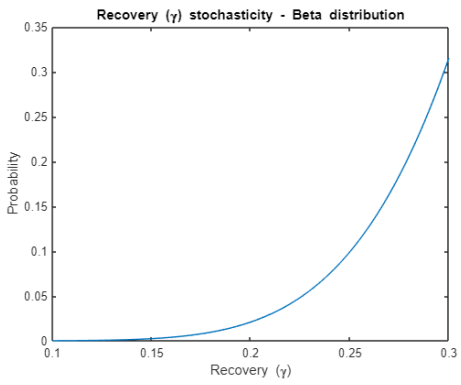


Figure 4 Graphing Our Results

Our results show a similar peak in Infectivity (around 37-40) for both the Deterministic and Stochastic versions of our SEIRD model. However, there is one clear difference, as seen in Figure 3: The Stochastic curve has a gradual decrease in infectivity over time, unlike the Deterministic curve. Other models in the field corroborate that the former is far more reflective of the real world, with infectivity slowly decreasing instead of suddenly falling in a matter of weeks.
Parameter sweeps for Infectivity and Recovery indicate the nature of our Beta distribution implementation, with an upward curve in probability for increased values of each.



(a) Stochastic Infectivity (β) Distribution



(b) Stochastic Recovery (γ) Distribution

The SEIRD (stochastic) model is run for a total of 100 simulations with different parameter values in each simulation set according to their beta distribution values. We plot the simulations and a mean infections curve for all the simulations to have a better visual and understanding of the total number of infections across the simulation.

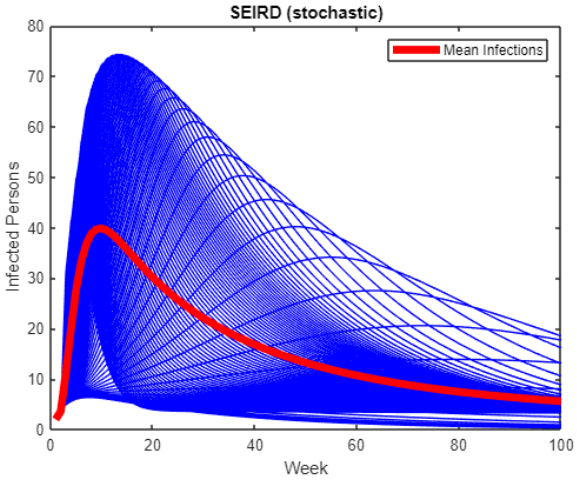


Figure 6 100-simulations 100-person Stochastic SEIRD Model Result

We also compare the results of the SEIRD (stochastic) model for takeoff simulations to all simulations in Figure 6. The simulations that are being classified as "takeoff" have the following two conditions: the peak number of infections should be more than or equal to 60 throughout at least one timestep and should occur before 20 weeks into the simulation.

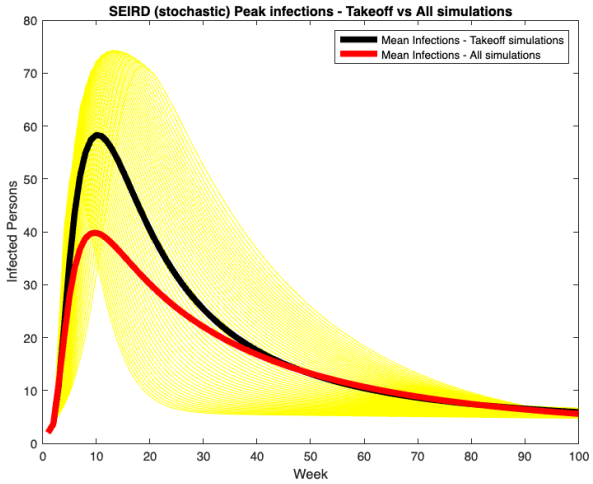
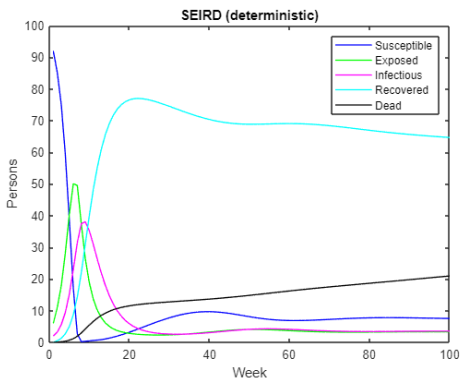


Figure 7 100-person Stochastic SEIRD Model Result for Takeoff simulations vs All simulations

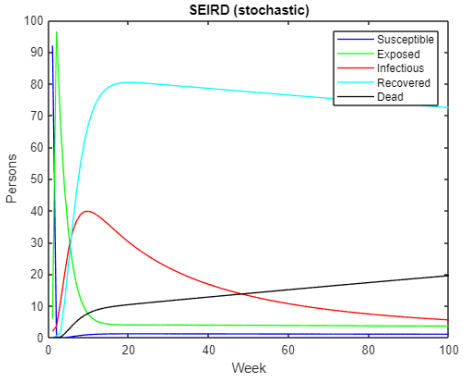
We observe that computing the mean infections curve using just the takeoff simulation gives a higher peak number of cases at around Week 10 than compared to the mean infections curve for all simulations. Also, the curves stayed aligned and

overlapped each other before week 5 (approx.) and after week 45 (approx.) in the simulation.

In the following plots, both the SEIRD (deterministic) and SEIRD (stochastic) models with all of the stocks are simulated.



(a) 100-person SEIRD (Deterministic) Model Result



(b) 100-person SEIRD (Stochastic) Model Result

In the deterministic SEIRD model, we see a symmetrical increase and decrease in the maximum number of infections at the peak and then a stable constant number of maximum infections throughout the rest of the simulation. In the stochastic SEIRD model, we see a steep increase in the maximum number of infections, but we see a longer-lasting peak (gradual decrease) in the maximum number of infections after the peak. A major difference that can be observed is the number of exposed individuals throughout the simulation between the two models. In the SEIRD (deterministic) model, the total number of exposed individuals reaches a maximum value of 50 throughout the simulation. However, the total number of exposed individuals increases rapidly and also reaches a maximum value of more than 90 in the SEIRD (stochastic) model. Similarly, we see a very sharp decrease in the maximum number of susceptible individuals in the stochastic SEIRD model compared to the deterministic SEIRD model. We can also observe that the curves are much smoother in the stochastic SEIRD model, whereas there are slight variations in the deterministic SEIRD model at a few timesteps.

4 Interpretation

4.1 Therefore

The results indicate that randomizing the infectivity and recovery parameters in the stochastic model majorly contributes to the different behavior of the maximum number of infections throughout the simulation between the deterministic SEIRD and stochastic SEIRD models. Although we observe a similar peak number of infections in both models, but also see a distinct curve for the increase and decrease in the total number of infections throughout the simulation. We also observe different curve patterns for susceptible and exposed stocks between the two models in terms of peak intensity and time period of simulation.

4.2 Limitations and Future Work

A few limitations of the stochastic SEIRD model include:

- Mean infection curve: To easily compare the differences between the two models, we take the mean curve over the total of 100 simulations in the SEIRD stochastic model. However, this leads to critical observations about other scenarios/simulations being missed out because we focus on an ideal 'average' value. This leads to a bias because many simulations do not reflect the data observed during COVID-19, and it heavily affects the overall mean curve.
- Stochastic Beta distribution (infectivity and recovery): We observed that the two positive shape parameters, α and β, already discussed earlier in section 2.5, are responsible for the shape of the distribution. Hence, modifying these two parameters even by a very low value would result in massive changes in the stochastic SEIRD model's simulation. This would give inaccurate results, and therefore, choosing an optimal value for these shape parameters was challenging and arbitrary.

The next steps to further test the stochastic SEIRD model could involve randomizing other parameters as well to observe the differences among the models being discussed in this computational essay. Also, there is potential to test out different "takeoff simulations" cases by modifying the conditions that were set above. We could also observe differences in the peak behavior and occurrence of further peaks in the deterministic and stochastic SEIRD models by simulating them for a longer period of time.

What are the key differences between the SEIRD model with deterministic parameters observed during COVID-19 and the SEIRD model with stochastic parameters, particularly in how they differ in the peak number of infections throughout the simulation?

5 References

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What are the key differences between the SEIRD model with deterministic parameters observed during COVID-19 and the SEIRD model with stochastic parameters, particularly in how they differ in the peak number of infections throughout the simulation?

6 Appendix

6.1 *simulate_seird.m*

```
function [S, E, I, R, D, W] = simulate_seird(s_0, e_0, i_0, ...
    ↪ r_0, d_0, alpha, beta, gamma, ∆, sigma, num_steps)
% Simulate a SEIRD model
%
% Usage
%   [S, E, I, R, D, W] = simulate_seird(s_0, e_0, i_0, r_0, ...
    ↪ d_0, alpha, beta, gamma, ∆, sigma, num_steps)
%
% Arguments
%   s_0 = initial number of susceptible individuals
%   e_0 = initial number of exposed individuals
%   i_0 = initial number of infected individuals
%   r_0 = initial number of recovered individuals
%   d_0 = initial number of dead individuals
%
%   alpha = infection rate parameter
%   beta  = exposure rate parameter
%   gamma = recovery rate parameter
%   ∆ = death rate parameter
%   sigma = re-susceptible rate parameter
%
%   num_steps = number of simulation steps to simulate
%
% Returns
%   S = simulation history of susceptible individuals; vector
%   E = simulation history of exposed individuals; vector
%   I = simulation history of infected individuals; vector
%   R = simulation history of recovered individuals; vector
%   D = simulation history of dead individuals; vector
%   W = simulation week; vector

% Setup
S = zeros(1, num_steps); S(1) = s_0;
E = zeros(1, num_steps); E(1) = e_0;
I = zeros(1, num_steps); I(1) = i_0;
R = zeros(1, num_steps); R(1) = r_0;
D = zeros(1, num_steps); D(1) = d_0;
W = 1 : num_steps;

% Run simulation
for step = 1 : (num_steps - 1)
    [S(step+1), E(step+1), I(step+1), R(step+1), D(step+1)] = ...
        ↪ action_seird(S(step), E(step), I(step), R(step), ...
        ↪ D(step), alpha, beta, gamma, ∆, sigma);
end

end
```

6.2 *action_seird.m*

```
function [s_n, e_n, i_n, r_n, d_n] = action_seird(s, e, i, r, d, alpha, beta, gamma, ∆, sigma)
% Advance a SEIRD model one timestep
%
% Usage
%   [s_n, e_n, i_n, r_n, d_n] = action_seird(s, e, i, r, d, alpha, beta, gamma, ∆, sigma)
%
% Arguments
%   s = current number of susceptible individuals
%   e = current number of exposed individuals
%   i = current number of infected individuals
%   r = current number of recovered individuals
%   d = current number of death individuals
%
%   alpha = infection rate parameter
%   beta  = exposure rate parameter
%   gamma = recovery rate parameter
%   ∆ = death rate parameter
%   sigma = re-susceptible rate parameter
%
% Returns
%   s_n = next number of susceptible individuals
%   e_n = next number of exposed individuals
%   i_n = next number of infected individuals
%   r_n = next number of recovered individuals
%   d_n = next number of dead individuals


% compute new infections and recoveries
susceptible = min(sigma*r,r);
exposed     = min(beta * i * s,s);
infectious  = min(alpha * e,e);
recovered   = min(gamma * i,i);
dead        = min(∆*i,i);

% Update state
s_n = s - exposed     + susceptible;
e_n = e - infectious  + exposed;
i_n = i - recovered   - dead        + infectious;
r_n = r - susceptible + recovered;
d_n = d + dead;

% Enforce invariants; necessary since we're doing a discrete approx.
s_n = max(s_n, 0);
e_n = max(e_n, 0);
i_n = max(i_n, 0);
r_n = max(r_n, 0);
d_n = max(d_n, 0);

end
```