A survey of compartmental disease models for predicting the progression of COVID-19

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Abstract

We start out with SIRD, a simple extension of the SIR model, adding D compartment on the same level as R in order to account for disease deaths. Then we explore on a more complicated model, SEIRD. We shall design a more complicated model, SEEAIRD.

Introduction

The Covid-19 pandemic has progressed in different ways across the various US states. Each state has its own set of policies and guidelines, and these guidelines can differ greatly between states. Policy makers depend on epidemiologists and data driven evidence to inform their decisions about local laws and public statements.

In this paper, we discuss the use of epidemiological compartment models for understanding the progression of the Covid-19 pandemic. These models focus on capturing the dynamics of an outbreak given a set of parameters related to how the virus spreads. With that said, there are several factors have and continue to play a role in the evolution of Covid-19 cases and deaths within each state. These include:

- Transmission rate
- External exposure
- Population demographics
- Population density
- Medical infrastructure
- State policies and guidelines
- Federal policies and guidelines
- Media coverage
- Public sentiment
- Social dynamics

Although these factors vary from state to state, we work under the assumption that the incubation period and viral progression are constant between states. It is important to note that the effects of many of the factors above aren't accounted for by epidemiological compartment models. As we introduce each model, we will be careful to point out which factors are taken into account. We hope that this survey will help inform leaders on the use of these models for policy decisions. We will point out the benefits as well as the drawbacks of using compartment based models for predicting the progression of cases and fatalities.

1 Data

We primarily used the *US Coronavirus Cases and Deaths* datasets from usafacts.org for our analysis. Specifically, we utilized the datasets containing information about known cases and deaths at the county level were utilized for our work.

- covid_confirmed_usafacts
- covid_deaths_usafacts
- covid_county_population_usafacts

A detailed discussion on the methodology for data collection and cleaning can be found at:

https://usafacts.org/articles/detailed-methodology-covid-19-data/.

The detail provided by these data sets allowed our group to explore model performance at a county level, at a state level, and national level. This ability is vital to understanding the role that epidemiological models can play in forecasting case counts and confirmed deaths due to the virus.

If we look at a national level or even at a state level, we quickly see that the epidemiological models don't capture the trends that we see in the data. We believe this happens for two reasons. Firstly, changes in policies and social dynamics will affect transmission rates. Secondly, the time lag between outbreaks in geographically different regions causes the aggregated behavior to deviated from the typical progression which is predicted by an epidemiological model.

2 Epidemiological Models

2.1 SIR model

The epidemiological compartmental SIR model is created by W. O. Kermack and A. G. McKendrick in 1927. It is formulated as Markov chains. The SIR model includes three compartments in a fixed population:

- Susceptible, **S(t)**. It represents the individuals who are susceptible but not yet infected with the disease at time **t**.
- Infected, **I(t)**. It represents the individuals who have already been infected with the diseases and are capable of spreading the disease to **S(t)** at time **t**.
- Removed, **R(t)**. It represents the individuals who were previously in **I(t-i) (, where i represents any time interval)** compartment, but have been permanently removed from **I(t)** at time **t**, due to recovery, immunization or death. And those individuals in **R(t)** are not be able to transmit to any other compartments.

The flow of this model could be describe as The formulation of the ordinary differential equation of the

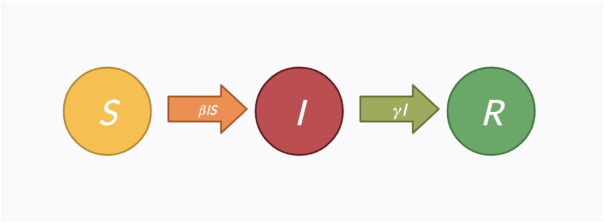

Figure 1: The transition flow of the SIR model

SIR model following the transition flow is:

$$\frac{dS}{dt} = -\beta I \frac{S}{N}$$
$$\frac{dI}{dt} = \beta I \frac{S}{N} - \gamma I$$
$$\frac{dR}{dt} = \gamma I$$

In this formulation, we assume that the value N is fixed and remain constant within the simulation. Which means: $N = S(t) + I(t) + R(t) = c$, where c could be any positive integer. The flow model updates the three variables for every time point with β and γ. For the first equation, β represents the transmission probability of each individual times the contact rate of each individual, where the transmission probability of each individual in N should be as equal as every others in N and the contact

rate of each person in N is the average number of people that an individual makes contact with. In those individuals makes contact with others, only S/N of them are susceptible. For the second and third equations, the population leaving the Susceptible compartment should be the same as the population entering the Infected compartment. γ represents the mean recovery and death rate. In other word, $1/\gamma$ represents the infected period. And there are γI infections are leaving Infected compartment and entering the Removed compartment. Those parameters would be updated with each cycle of time period of epidemic.

In our cases, we are not considering birth and death rate, since the rate of infection and recovery is much faster than the birth and death rate in a same time interval.

2.2 SIRD model

The SIRD model is short for Susceptible- Infectious- Recovered- Deceased- Model. The differences between SIR model and SIRD model is that the latter one differentiates the Recovered compartment in the former one into two different compartments: Recovered and Deceased. So in SIRD model the R and D have different meanings:

- Recovered, **R(t)**. It represents the individuals who have recovered from the disease and have been immune at time **t**.
- Deceased, **D(t)**. It represents the individuals who have already died from the disease at time **t**.

The flow of SIRD model could be describe as

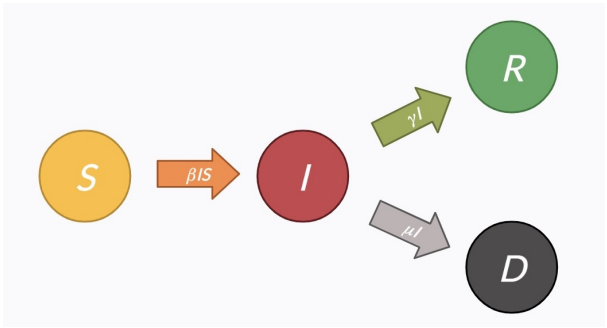

Figure 2: The transition flow of the SIRD model

We cannot guarantee that all the people in the susceptible compartment are well. For COVID-19 pandemic, there is an incubation period for people just being infected. To know the exact number of infections we need to identify how many people are in the incubation stage.

2.3 SEIRD model

Which means that there is a small number of people in the susceptible compartment who are actually infected but are not yet infectious. To identify those people we introduced the E compartment to separate those incubated infected people and those people who are truly well.

- Exposed, **E(t)**. It represents the individuals who have been infected but have not yet became infectious(either not been identified or have no capability to infect others) at time **t**.

The flow of SEIRD model could be describe as

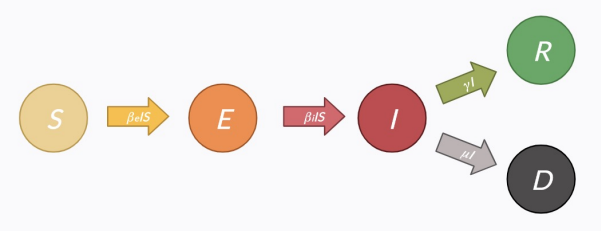

Figure 3: The transition flow of the SEIRD model

2.4 SEEAIRD model

Next, we further refine the Exposed compartment into two groups by considering that those exposed people are in the incubation stage and have not go through the infected stage and those people have already go through the infected stage but have not been detected by a test.

Second, considered about the appearance of the asymptomatic carriers of COVID-19 infections, they may exist in the Susceptible compartment or the Exposed compartment, determined by whether or not those people have been detected or not.

Thus, we further separate the Exposed compartment into the initial Exposed compartment and the final Exposed compartment. And we introduced the Asymptomatic compartment into the model.

- Incubation, $E_i(\mathbf{t})$. It represents the individuals who have been exposed to infections and actually been infected but they are still in the incubation stage and have not became infectious at time $\mathbf{t}$.
- Final Exposed, $E_f(\mathbf{t})$. It represents the individuals who have been infected and have became infectious but they are not identified by test either due to not have not tested or they are asymptomatic at time $\mathbf{t}$.
- Asymptomatic, $\mathbf{A(t)}$. It represents the individuals who have been an infections but does not have the symptom of an infection at time $\mathbf{t}$.

The flow of SEEAIRD model could be describe as

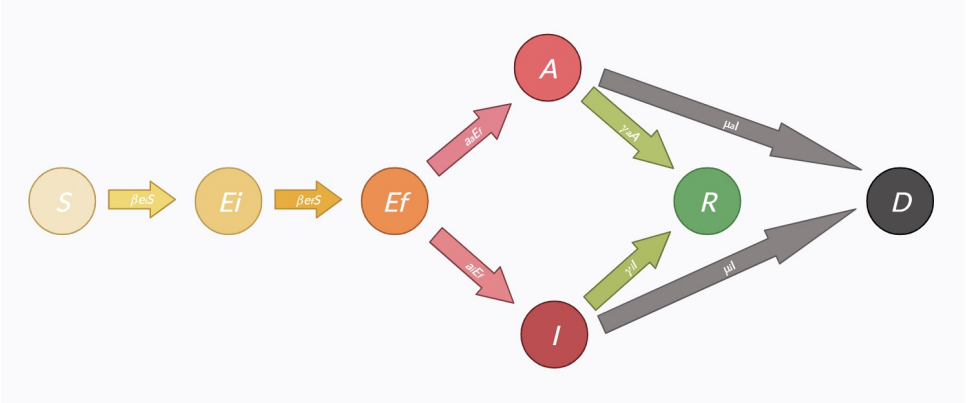

Figure 4: The transition flow of the SEEAIRD model

3 Model derivation

3.1 SIRD model derivation

The ODE version of this model is:

$$\begin{aligned}\frac{dS}{dt} &= -\beta I \frac{S}{N} \\ \frac{dI}{dt} &= \beta I \frac{S}{N} - (\gamma + \mu) I \\ \frac{dR}{dt} &= \gamma I \\ \frac{dD}{dt} &= \mu I\end{aligned}$$

with the assumption that $N = S + I + R + D$

3.1.1 Transition probabilities

$(\Delta S, \Delta I, \Delta R)$	Probability
$(-1, +1, 0)$	$\beta i \frac{s}{N} \Delta t$
$(0, -1, +1)$	$\gamma i \Delta t$
$(0, -1, 0)$	$\mu i \Delta t$

3.1.2 System of SDEs

Let $\Delta X(t) = (\Delta S(t), \Delta I(t), \Delta R(t))^T$, the expectation of ΔX, $\mathbb{E}(\Delta X)$, to the order Δt is:

$$\mathbb{E}(\Delta X) = \begin{bmatrix} -\beta I \frac{S}{N} \\ \beta I \frac{S}{N} - (\gamma + \mu) I \\ \gamma I \end{bmatrix} \Delta t = f \Delta t$$

and the covariance matrix of ΔX, $CV(\Delta X)$, to the order of Δt, is:

$$\begin{aligned} CV(\Delta X) &= \mathbb{E}(\Delta X (\Delta X)^T) \\ &= \mathbb{E} \begin{bmatrix} (\Delta S)^2 & \Delta S \Delta I & \Delta S \Delta R \\ \Delta S \Delta I & (\Delta I)^2 & \Delta I \Delta R \\ \Delta S \Delta I & \Delta I \Delta R & (\Delta R)^2 \end{bmatrix} \\ &= \begin{bmatrix} \beta I \frac{S}{N} & -\beta I \frac{S}{N} & 0 \\ -\beta I \frac{S}{N} & \beta I \frac{S}{N} + (\gamma + \mu) I & -\gamma I \\ 0 & -\gamma I & \gamma I \end{bmatrix} \Delta t \\ &= C \Delta t \end{aligned}$$

Cholesky decomposing C such that $C = GG^T$ (I did the math so you don't have to):

$$G = \begin{bmatrix} \sqrt{\beta I \frac{S}{N}} & 0 & 0 \\ -\sqrt{\beta I \frac{S}{N}} & \sqrt{(\gamma + \mu) I} & 0 \\ 0 & \frac{-\gamma I}{\sqrt{(\gamma + \mu) I}} & \sqrt{\frac{\gamma \mu I}{(\gamma + \mu)}} \end{bmatrix}$$

Our system of SDEs, in the form of $dX(t) = f(X(t))dt + G(X(t))dW(t)$, is:

$$
\begin{aligned}
dS(t) &= -\beta I(t)\frac{S(t)}{N}dt + \sqrt{\beta I(t)\frac{S(t)}{N}}dW_1(t) \\
dI(t) &= [\beta I(t)\frac{S(t)}{N} - (\gamma+\mu)I(t)]dt - \sqrt{\beta I(t)\frac{S(t)}{N}}dW_1(t) + \sqrt{(\gamma+\mu)I(t)}dW_2(t) \\
dR(t) &= \gamma I(t)dt - \frac{\gamma I(t)}{\sqrt{(\gamma+\mu)I(t)}}dW_2(t) + \sqrt{\frac{\gamma\mu I(t)}{(\gamma+\mu)}}dW_3(t) \\
dD(t) &= \mu I(t)dt - \frac{\mu I(t)}{\sqrt{(\gamma+\mu)I(t)}}dW_2(t) - \sqrt{\frac{\gamma\mu I(t)}{(\gamma+\mu)}}dW_3(t)
\end{aligned}
$$

where $dW_i(t) \sim \mathcal{N}(0, dt)$.

3.1.3 Numerical Simulation

We use the Euler-Maruyama method to simulate sample paths of the SDEs:

$$
\begin{aligned}
S(t_{k+1}) &= S(t_k) - [\beta I(t_k)\frac{S(t_k)}{N}]\delta t + \sqrt{\beta I(t_k)\frac{S(t_k)}{N}}\sqrt{\delta t}\eta_1 \\
I(t_{k+1}) &= I(t_k) + [\beta I(t_k)\frac{S(t_k)}{N} - (\gamma+\mu)I(t_k)]\delta t - \sqrt{\beta I(t_k)\frac{S(t_k)}{N}}\sqrt{\delta t}\eta_1 + \sqrt{(\gamma+\mu)I(t_k)}\sqrt{\delta t}\eta_2 \\
R(t_{k+1}) &= R(t_k) + \gamma I(t_k)\delta t - \frac{\gamma I(t_k)}{\sqrt{(\gamma+\mu)I(t_k)}}\sqrt{\delta t}\eta_2 + \sqrt{\frac{\gamma\mu I(t_k)}{(\gamma+\mu)}}\sqrt{\delta t}\eta_3 \\
D(t_{k+1}) &= N - S(t_{k+1}) - I(t_{k+1}) - R(t_{k+1})
\end{aligned}
$$

3.1.4 Parameters estimation

Minimizing sum of squared residuals A naive approach Bayesian Inference Let $\boldsymbol{\theta} = (\beta, \gamma, \mu)^T$ be the vector of parameters. We have the likelihood function for $\boldsymbol{\theta}$ given the data as

$$
L(\boldsymbol{\theta}; \boldsymbol{X}) = \prod_{k=1}^{n} p(X(t_k) \mid X(t_{k-1}); \boldsymbol{\theta})
$$

where $X(t_k) = (S(t_k), I(t_k), R(t_k))^T$; $p(X(t_k) \mid X(t_{k-1}); \boldsymbol{\theta})$ is the transition probability of $X(t_k)$ starting from $X(t_{k-1})$ given the vector $\boldsymbol{\theta}$. With the Euler-Maruyama approximation above, this transition probability is implied to be

$$
p(X(t_k) \mid X(t_{k-1}); \boldsymbol{\theta}) \approx \frac{\exp\left(-\frac{1}{2}(X(t_k) - \boldsymbol{\mu}(X(t_{k-1}), \boldsymbol{\theta}))^T \boldsymbol{\Sigma}(X(t_{k-1}), \boldsymbol{\theta})^{-1}(X(t_k) - \boldsymbol{\mu}(X(t_{k-1}), \boldsymbol{\theta}))\right)}{\sqrt{(2\pi)^3 |\boldsymbol{\Sigma}(X(t_{k-1}), \boldsymbol{\theta})|}}
$$

because

$$
X(t_k) \mid X(t_{k-1}); \boldsymbol{\theta} \sim \mathcal{N}\left(\boldsymbol{\mu}(X(t_{k-1}), \boldsymbol{\theta}), \boldsymbol{\Sigma}(X(t_{k-1}), \boldsymbol{\theta})\right)
$$

where

$$
\begin{aligned}
\boldsymbol{\mu}(X(t_{k-1}), \boldsymbol{\theta}) &= \begin{bmatrix} S(t_{k-1}) \\ I(t_{k-1}) \\ R(t_{k-1}) \end{bmatrix} + \begin{bmatrix} -\beta I(t_{k-1})\frac{S(t_{k-1})}{N} \\ \beta I(t_{k-1})\frac{S(t_{k-1})}{N} - (\gamma+\mu)I(t_{k-1}) \\ \gamma I(t_{k-1}) \end{bmatrix}\delta t \\
\boldsymbol{\Sigma}(X(t_{k-1}), \boldsymbol{\theta}) &= \begin{bmatrix} \beta I(t_{k-1})\frac{S(t_{k-1})}{N} & -\beta I(t_{k-1})\frac{S(t_{k-1})}{N} & 0 \\ -\beta I(t_{k-1})\frac{S(t_{k-1})}{N} & \beta I(t_{k-1})\frac{S(t_{k-1})}{N} + (\gamma+\mu)I(t_{k-1}) & -\gamma I(t_{k-1}) \\ 0 & -\gamma I(t_{k-1}) & \gamma I(t_{k-1}) \end{bmatrix}\delta t
\end{aligned}
$$

The resulting log-likelihood function follows easily:

$$\begin{aligned}\log L(\boldsymbol{\theta}; \boldsymbol{X}) &:= l(\boldsymbol{\theta}; \boldsymbol{X}) \\ &= \sum_{k=1}^{n} \log(p(X(t_k) \mid X(t_{k-1}); \boldsymbol{\theta}))\end{aligned}$$

where:

$$\begin{aligned}\log(p(X(t_k) \mid X(t_{k-1}); \boldsymbol{\theta})) = &-\frac{1}{2}(X(t_k) - \boldsymbol{\mu}(X(t_{k-1}), \boldsymbol{\theta}))^T \boldsymbol{\Sigma}(X(t_{k-1}), \boldsymbol{\theta})^{-1}(X(t_k) - \boldsymbol{\mu}(X(t_{k-1}), \boldsymbol{\theta})) \\ &- \log(\sqrt{(2\pi)^3 |\boldsymbol{\Sigma}(X(t_{k-1}), \boldsymbol{\theta})|})\end{aligned}$$

so that:

$$\begin{aligned}l(\boldsymbol{\theta}; \boldsymbol{X}) = &\sum_{k=1}^{n} -\frac{1}{2}(X(t_k) - \boldsymbol{\mu}(X(t_{k-1}), \boldsymbol{\theta}))^T \boldsymbol{\Sigma}(X(t_{k-1}), \boldsymbol{\theta})^{-1}(X(t_k) - \boldsymbol{\mu}(X(t_{k-1}), \boldsymbol{\theta})) \\ &+ \sum_{k=1}^{n} - \log(\sqrt{(2\pi)^3 |\boldsymbol{\Sigma}(X(t_{k-1}), \boldsymbol{\theta})|})\end{aligned}$$

In reality, we only have data on cumulative "Confirmed Cases", cumulative "Fatalities", and cumulative "Recoveries". In light of this, we can make the following assumptions:

$$\begin{aligned}I(t) = &\#\text{"daily cumulative Confirmed Cases"} - (\#\text{"daily cumulative Fatalities"} + \\ &\#\text{"daily cumulative Recoveries"})\end{aligned}$$

What is left is the data of susceptible population over time, which are not readily available from data. We can proceed as follows:

1. **Imputing series of S from I and R:**

$$S(t_k)|I(t_k), R(t_k) \sim \mathcal{N}(\bar{\boldsymbol{\mu}}, \bar{\boldsymbol{\Sigma}})$$

where:

$$\begin{aligned}\bar{\boldsymbol{\mu}} &= \boldsymbol{\mu}_1 + \boldsymbol{\Sigma}_{12}\boldsymbol{\Sigma}_{22}^{-1}(a - \boldsymbol{\mu}_2) \\ \bar{\boldsymbol{\Sigma}} &= \boldsymbol{\Sigma}_{11} - \boldsymbol{\Sigma}_{12}\boldsymbol{\Sigma}_{22}^{-1}\boldsymbol{\Sigma}_{21} \\ \boldsymbol{\mu}_1 &= S(t_{k-1}) - \beta I(t_{k-1})\frac{S(t_{k-1})}{N}\delta t \\ a &= (I(t_k), R(t_k))^T \\ \boldsymbol{\mu}_2 &= \begin{bmatrix}\beta I(t_{k-1})\frac{S(t_{k-1})}{N} - (\gamma + \mu)I(t_{k-1}) \\ \gamma I(t_{k-1})\end{bmatrix}\delta t \\ \boldsymbol{\Sigma}_{11} &= \beta I(t_{k-1})\frac{S(t_{k-1})}{N}\delta t \\ \boldsymbol{\Sigma}_{12} &= \begin{bmatrix}-\beta I(t_{k-1})\frac{S(t_{k-1})}{N} & 0\end{bmatrix}\delta t \\ \boldsymbol{\Sigma}_{21} &= \begin{bmatrix}-\beta I(t_{k-1})\frac{S(t_{k-1})}{N} \\ 0\end{bmatrix}\delta t \\ \boldsymbol{\Sigma}_{22} &= \begin{bmatrix}\beta I(t_{k-1})\frac{S(t_{k-1})}{N} + (\gamma + \mu)I(t_{k-1}) & -\gamma I(t_{k-1}) \\ -\gamma I(t_{k-1}) & \gamma I(t_{k-1})\end{bmatrix}\delta t\end{aligned}$$

as a result:

$$\hat{S}(t_k) \approx \mathbb{E}[S(t_k)|I(t_k), R(t_k)]$$

Usually we would need to sample from this distribution and compute the average if its p.d.f. is something heinous, but here we are spared that work because multivariate Gaussian is just that nice. What I wrote for $\bar{\boldsymbol{\Sigma}}$ was probably redundant, except for completeness' sake.

2. **Let $S(t_0)$ be another parameter to be estimated:**
   In this case, our vector of parameters would be $\boldsymbol{\theta} = (\beta, \gamma, \mu, S(t_0))^T$. We can observe above that $S(t_k)$ is one giant recursive computation as k is large, with $S(t_0)$ as its base case!

- **Maximizing the log-likelihood:** or minimizing the negative log-likelihood with good ol' algorithms like Nelder-Mead, for instance.
- **Markov Chain Monte Carlo:** with objective priors for our parameters:

$$\pi(\beta) \propto \frac{1}{\beta}$$
$$\pi(\gamma) \propto \frac{1}{\gamma}$$
$$\pi(\mu) \propto \frac{1}{\mu}$$
$$\pi(S(t_0)) \propto \frac{1}{S(t_0)}$$

Assume these are independent, we have the prior distribution of $\boldsymbol{\theta} = (\beta, \gamma, \mu, S(t_0))^T$ as:

$$\pi(\beta, \gamma, \mu, S(t_0)) \propto \frac{1}{\beta}\frac{1}{\gamma}\frac{1}{\mu}\frac{1}{S(t_0)}$$

and the posterior distribution follows as

$$\pi(\beta, \gamma, \mu, S(t_0)|\boldsymbol{X}) \propto \pi(\beta, \gamma, \mu, S(t_0))L(\boldsymbol{\theta}; \boldsymbol{X})$$

One of the most common MCMC scheme is Metropolis-Hastings. The proposal distribution can be a multivariate Gaussian distribution $\mathcal{N}(\mathbf{0}, \sigma^2\mathbf{I}_4)$, in which case it is known as Random Walk Metropolis-Hastings (RWMH). The following is "borrowed" from *Introduction to Bayesian Estimation and Copula Models of Dependence*:

1. Define the ratio:
$$R_g(\theta_1, \theta_2) = \frac{f(\theta_1)}{f(\theta_2)}$$
where $f(\theta) \propto \pi(\theta|\mathbf{X})$
2. For $t = 0$, choose any z_0 from Θ.
3. For $t = 1, \ldots, N$:
   - Generate a random proposal $y_t \sim \mathcal{N}(z_{t-1}, \sigma^2\mathbf{I}_4)$.
   - Generate a random $u_t \sim Unif[0, 1]$;
   - Define
$$z_t = \begin{cases} y_t & \text{if } R_g(y_t, z_{t-1}) \geq u_t \text{ (accept)}; \\ z_{t-1} & \text{otherwise (reject)} \end{cases}$$

The obtained Markov chain z_t will have posterior $\pi(\theta|\mathbf{X})$ as its stationary distribution. An important "parameter" that needs to be fine-tuned is σ

3.1.5 Paths simulation of pandemic progress

One of the benefits of using the stochastic model (over its deterministic counterpart) is that we can simulate potential paths that the pandemic might take and estimate our confidence intervals. The time interval is first discretized. Define $\Delta t = \frac{T}{L}$ for some positive integer L and let $\tau_j = j\Delta t$.

3.2 SEIRD-Model Derivation

The ODE of this model is:

$$\begin{aligned}
\frac{dS}{dt} &= -\beta_i I\frac{S}{N} - \beta_e E\frac{S}{N} \\
\frac{dE}{dt} &= \beta_e E\frac{S}{N} + \beta_i I\frac{S}{N} - aE \\
\frac{dI}{dt} &= aE - I(\gamma+\mu) \\
\frac{dR}{dt} &= \gamma I \\
\frac{dD}{dt} &= \mu I
\end{aligned}$$

with the assumption that $N = S + E + I + R + D$

3.2.1 Transition probabilities

$(\Delta S, \Delta E, \Delta I, \Delta R)$	Probability
$(-1, +1, 0, 0)$	$\beta_i i\frac{s}{N}\Delta t$
$(-1, -1, 0, 0)$	$\beta_e e\frac{s}{N}\Delta t$
$(0, -1, 1, 0)$	aet
$(0, 0, -1, 1)$	$\mu i\Delta t$
$(0, 0, -1, 0)$	$\gamma i\Delta t$

3.2.2 System of SDEs

Let $\Delta X(t) = (\Delta S(t), \Delta E(t), \Delta I(t), \Delta R(t))^T$, the expectation of ΔX, $\mathbb{E}(\Delta X)$, to the order Δt is:

$$\mathbb{E}(\Delta X) = \begin{bmatrix} -\beta_i I\frac{S}{N} - \beta_e E\frac{S}{N} \\ \beta_i I\frac{S}{N} + (\beta_e\frac{S}{N} - a)E \\ aE - (\gamma+\mu)I \\ \gamma I \end{bmatrix}\Delta t = f\Delta t$$

and the co variance matrix of ΔX, $CV(\Delta X)$, to the order of Δt, is:

$$\begin{aligned}
\mathbb{CV}(\Delta X) &= \mathbb{E}(\Delta X(\Delta X)^T) \\
&= \mathbb{E}\begin{bmatrix} (\Delta S)^2 & \Delta S\Delta E & \Delta S\Delta I & \Delta S\Delta R \\ \Delta E\Delta S & (\Delta E)^2 & \Delta E\Delta I & \Delta E\Delta R \\ \Delta I\Delta S & \Delta I\Delta E & (\Delta I)^2 & (\Delta I\Delta R) \\ \Delta R\Delta S & \Delta R\Delta E & \Delta R\Delta I & (\Delta R)^2 \end{bmatrix} \\
&= \begin{bmatrix} \beta_i I\frac{S}{N} + \beta_e E\frac{S}{N} & -\beta_i I\frac{S}{N} - \beta_e E\frac{S}{N} & 0 & 0 \\ -\beta_i I\frac{S}{N} - \beta_e E\frac{S}{N} & \beta_i I\frac{S}{N} + (\beta_e\frac{S}{N} + a)E & -aE & 0 \\ 0 & -aE & aE + I(\gamma+\mu) & -\gamma I \\ 0 & 0 & -\gamma I & \gamma I \end{bmatrix}\Delta t \\
&= C\Delta t
\end{aligned}$$

Cholesky decomposing C such that $C = GG^T$:

$$G = \begin{bmatrix} \sqrt{\beta_i I\frac{S}{N} + \beta_e E\frac{S}{N}} & 0 & 0 & 0 \\ -\sqrt{\beta_i I\frac{S}{N} + \beta_e E\frac{S}{N}} & \sqrt{aE} & 0 & 0 \\ 0 & -\sqrt{aE} & -\sqrt{I(\gamma+\mu)} & 0 \\ 0 & 0 & \frac{\gamma I}{\sqrt{I(\gamma+\mu)}} & \frac{I\sqrt{\gamma\mu}}{\sqrt{\gamma+\mu}} \end{bmatrix}$$

Our system of SDEs, in the form of $dX(t) = f(X(t))dt + G(X(t))dW(t)$, is:

$$
\begin{aligned}
dS(t) &= -\beta I(t)\frac{S(t)}{N}dt + \sqrt{\beta I(t)\frac{S(t)}{N}}dW_1(t) \\
dI(t) &= [\beta I(t)\frac{S(t)}{N} - (\gamma+\mu)I(t)]dt - \sqrt{\beta I(t)\frac{S(t)}{N}}dW_1(t) + \sqrt{(\gamma+\mu)I(t)}dW_2(t) \\
dR(t) &= \gamma I(t)dt - \frac{\gamma I(t)}{\sqrt{(\gamma+\mu)I(t)}}dW_2(t) + \sqrt{\frac{\gamma\mu I(t)}{(\gamma+\mu)}}dW_3(t)
\end{aligned}
$$

where $dW_i(t) \sim \mathcal{N}(0, dt)$.

3.3 SEEAIRD-model derivation

The ODE of this model is:

$$
\begin{aligned}
\frac{dS}{dt} &= -\beta_i I\frac{S}{N} - \beta_e E_f\frac{S}{N} - \beta_a A\frac{S}{N} \\
\frac{dE_i}{dt} &= \beta_i I\frac{S}{N} + \beta_e E_f\frac{S}{N} + \beta_a A\frac{S}{N} - aE_i \\
\frac{dE_f}{dt} &= aE_i - a_f E_f - a_a E_f \\
\frac{dA}{dt} &= a_a E_f - \gamma_a A - \mu_a A \\
\frac{dI}{dt} &= a_i E_f - \gamma_i I - \mu_i I \\
\frac{dR}{dt} &= \gamma_i I + \gamma_a A \\
\frac{dD}{dt} &= \mu_i I + \mu_a A
\end{aligned}
$$

with the assumption that $N = S + E_i + E_f + A + I + R + D$

3.3.1 Transition probabilities

$(\Delta S, \Delta E_i, \Delta E_f, \Delta A, \Delta I, \Delta R)$	Probability
$(-1, +1, 0, 0, 0, 0)$	$\beta_i i\frac{s}{N}\Delta t$
$(-1, +1, 0, 0, 0, 0)$	$\beta_e e_f\frac{s}{N}\Delta t$
$(-1, +1, 0, 0, 0, 0)$	$\beta_a a\frac{s}{N}\Delta t$
$(0, -1, +1, 0, 0, 0)$	$ae_i\Delta t$
$(0, 0, -1, +1, 0, 0)$	$a_f e_f\Delta t$
$(0, 0, -1, 0, +1, 0)$	$a_a e_f\Delta t$
$(0, 0, 0, -1, 0, +1)$	$\gamma_a a\Delta t$
$(0, 0, 0, -1, 0, 0)$	$\mu_a a\Delta t$
$(0, 0, 0, 0, -1, +1)$	$\gamma_a a\Delta t$
$(0, 0, 0, 0, -1, 0)$	$\mu_i i\Delta t$

3.3.2 System of SDEs

Let $\Delta X(t) = (\Delta S(t), \Delta E_i(t), \Delta E_f(t), \Delta A(t), \Delta I(t), \Delta R(t))^T$, the expectation of ΔX, $\mathbb{E}(\Delta X)$, to the order Δt is:

$$
\mathbb{E}(\Delta X) = \begin{bmatrix}
-\beta_i I\frac{S}{N} - \beta_e E_f\frac{S}{N} - \beta_a A\frac{S}{N} \\
\beta_i I\frac{S}{N} + \beta_e E_f\frac{S}{N} + \beta_a A\frac{S}{N} - aE_i \\
aE_i - a_f E_f - a_a E_f \\
a_a E_f - \gamma_a A - \mu_a A \\
a_i E_f - \gamma_i I - \mu_i I \\
\gamma_i I + \gamma_a A
\end{bmatrix}\Delta t = f\Delta t
$$

4 References

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