Epidemiological Modelling of Coronavirus Infection in Quarantined Population
A Outline of Project for MATH371 Wi2020

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2020

Outline

Objectives

- ▶ to explore the SIRD model and its stability points
- ▶ to develop methodology to estimate parameters for data without assumption of population
- ▶ to estimate parameters of the SIR model given COVID-19 epidemiological data from Wuhan of China
- ▶ to explore SIRD models that embed quarantining of population, and age distribution

COVID-19

The COVID-19 pandemic is caused by a novel virus named SARS-CoV-2 that found its first confirmed case in December 2020. By March 2020, $780,000$ cases of COVID-19 have been confirmed around the world, and it is still developing.

SIRD Model

The fraction of individuals susceptible to contract COVID-19 in a population, $\frac{S}{N} = s$, fraction of infected individuals, $\frac{I}{N} = i$, fraction of removed individuals, $\frac{R}{N} = r$ and fraction of dead, $\frac{D}{N} = d$ change in dynamic described in the following system of differential equations:

$$
\begin{aligned}
\dot{s} &= -\beta s i & s(0) &= s_0 \\
\dot{i} &= \beta s i - (\alpha + \mu)i & i(0) &= i_0 \\
\dot{r} &= \alpha i & r(0) &= r_0 \\
\dot{d} &= \mu i & d(0) &= 0
\end{aligned}
\tag{1}
$$

where:

β = infection rate; $\qquad \frac{1}{\beta}$ = average days to be infected

α = recovery rate; $\qquad \frac{1}{\alpha}$ = average days to recover

μ = death rate

R_0 = basic reproduction number, $\frac{\beta}{\alpha + \mu}$

Stability Analysis of the SIRD

Taking out $d = 1 - s - i - d$, the system in (1) can be rewritten as

$$\dot{\mathbf{x}} = \mathbf{F}(\mathbf{x})$$

where $\mathbf{x}^T = [s \ i \ r]$.

$\dot{\mathbf{x}}^T = 0$ at steady state. This implies $\mathbf{x}^T = \hat{\mathbf{x}}^T = [s_{ss} \ 0 \ r_{ss}]$
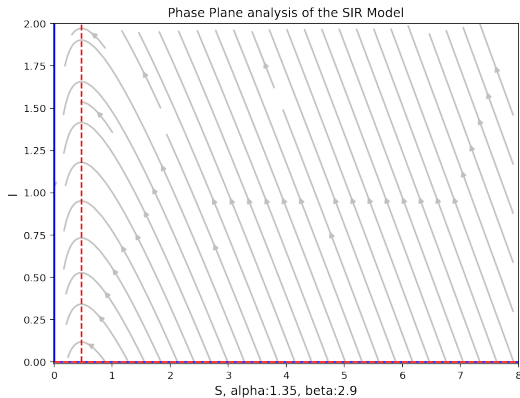where s_{ss} and r_{ss} are s and r at steady state, respectively.
The linearized system around steady state has Jacobian matrix

$$J\hat{\mathbf{x}} = \begin{pmatrix} 0 & \beta s_{ss} & 0 \\ 0 & \beta s_{ss} - (\alpha + \mu) & 0 \\ 0 & \alpha & 0 \end{pmatrix} \tag{2}$$

and eigenvalues $\lambda_1, \lambda_2 = 0, \lambda_3 = bs - (\alpha + \mu) < 0$ since s_{ss} is less
than s when i is maximum

Phase Plane Analysis

Figure: Phase plane plot obtained from Jay Newby 2020 lecture materials
The phase plane plot reveals that $i = 0$, $s = 0$ is a stable point.

SIRD with Quarantine

The SIRD model with quarantine adds a compartment $\dot{q} = \frac{Q}{N}$, where Q represents the quarantined infected individuals. Infected individuals are quarantined at rate γ, recover at rate α, and perish at rate μ.

$$
\begin{aligned}
\dot{s} &= -\beta s i & s(0) &= s_0 \\
\dot{i} &= \beta s i - (\alpha + \mu + \gamma)i & i(0) &= i_0 \\
\dot{r} &= \alpha(i + q) & r(0) &= r_0 \\
\dot{q} &= \gamma i - (\mu + \alpha)q & q(0) &= 0 \\
\dot{d} &= \mu(i + q) & d(0) &= 0
\end{aligned} \tag{3}
$$

Replacing i with i $+$ q in the linearized system of the SIRD in Eq(2) yields the same stable point $(s, i) = (0, 0)$.

Assumptions

The SIR family of models assume:

▶ instantaneous infection, recovery of individuals

▶ no delay in any effect, including death

▶ i has reached a peak and has started decreasing

which are not captured in the publicly available data.

Motivation of Methods

The SIR models do not provide a way to decide N, value of which often distorts total error, and requires assumption by the researcher.

In the following methods, N is included in the parameter estimation without loss of system behaviour. Specifically, the SIR model is fitted on the data yielding estimated $\hat{\alpha}, \hat{\mu}, \hat{N}$. β is assumed 1 since it's linked in the change in time, dt.

Minimisation Problem

To estimate parameters from data from regions that **have reached** the maximum number of confirmed cases (i), we solve the following problem:

$$\underset{\alpha,\beta=1,\mu,N}{\text{minimize}} \quad \left(\frac{I_{max} - \widehat{I}_{max}}{I_{max}}\right)^2 + \frac{1}{T}\sum_{t=1}^{T}\left(\frac{R_t - \widehat{R_t}}{R_{max}}\right)^2 + \left(\frac{D_t - \widehat{D_t}}{D_{max}}\right)^2$$

$$\text{subject to} \quad 0 \leq \frac{\alpha + \mu}{\beta} \leq \left(\frac{N - (I + R + D)}{N}\right)\bigg|_{I=I_{max}}$$

$$(4)$$

Time Scale of Estimated Data

Using Euler's method, a differential form $\dot{s} = -\beta s i$ can be expressed as

$$s_{t+1} = s_t + dt(-\beta s_t i_t)$$

Which we consider as

$$s_{t+1} = s_t + \beta dt(-s_t i_t)$$

Thus, a change in β leads to a change in the timescale. In Eq(4) we assumed $\beta = 1$.

The Time-scale constant

The estimated data has time scale t'. It is scaled to match the timescale used by the data in t time scale. We obtain

$$k = \frac{t_m}{t'_m} \tag{5}$$

where t_m is the time at which $i(t)$ is maximum and t'_m is the time when $\hat{i}(t')$ is maximum.

Eq(5) implies $t' = \frac{t}{k}$. Thus, to match timescales, $\hat{s}(t') = \hat{s}(\frac{t}{k})$. In addition, since $\beta = 1$ in Eq(4), the estimated parameters are scaled i.e.

$$\alpha = \frac{\hat{\alpha}}{k}, \beta = \frac{1}{k}, \mu = \frac{\hat{\mu}}{k}, N = \hat{N}$$

.

Result & Discussion

- solution to the SIR model is unique by the Picard-Lindelöf theorem (**F** is Lipschitz continuous),
- the estimation methods avoids assumption of the population N.
- the methods are not robust to different initial guess in N fed to the solver (shown in Fig 2, 3).
- the SIRDQ model gives better estimates The estimated R_0's

  are larger than the values in the literature (1.4 to 6.49[1]). This may be because the number of people infected and recovered quickly (e.g. in 2 days), which is shown by the model, are not reported in the data.
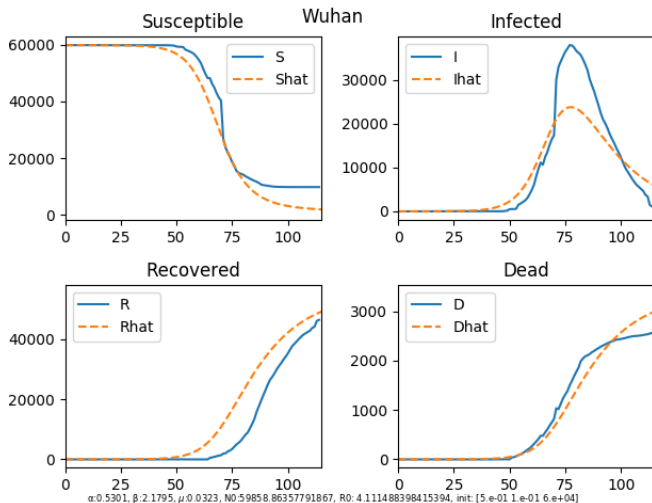
SIRD Fit 1
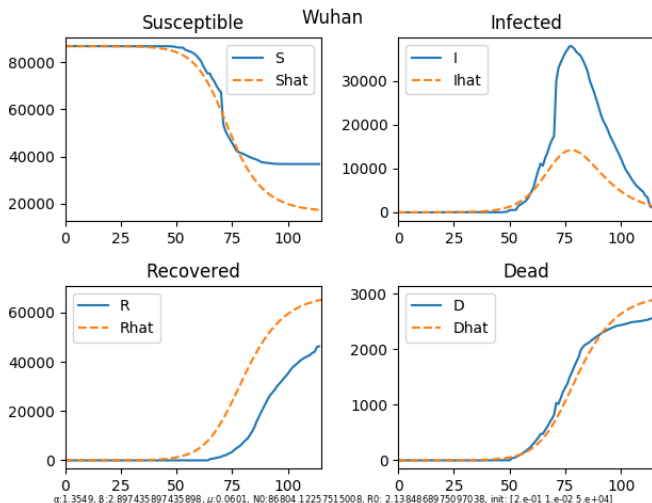
Figure: Estimated s, i, r, d from Wuhan epidemiological data. $R_0 \approx 2.138$

Using initial guess $N_0 = 5 \times 10^4$, the estimated $\alpha \approx 1.35$, $\beta \approx 2.9$, $\mu \approx 0.06$, $N_0 \approx 9 \times 10^4$

SIRD Fit 2

Figure: Estimated s, i, r, d from Wuhan epidemiological data. $R_0 \approx 4.111$

Using initial guess $N_0 = 6 \times 10^4$, the estimated $\alpha \approx 0.53$, $\beta \approx 2.18$, $\mu \approx 0.03$, $N_0 \approx 6 \times 10^4$
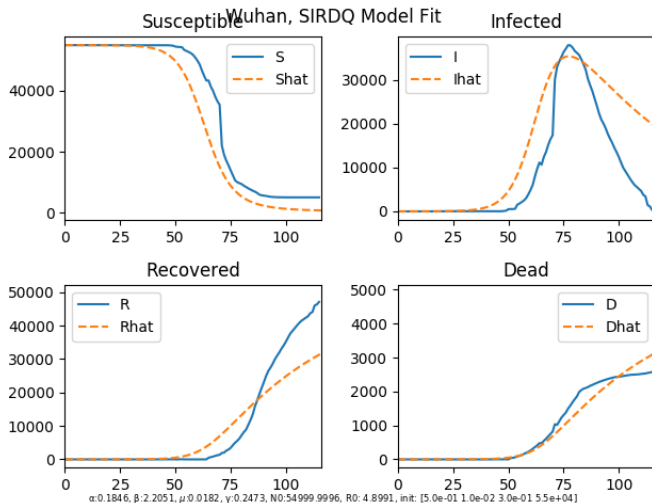
SIRDQ Fit 1

Figure: Estimated s, i, r, d from Wuhan epidemiological data. $R_0 \approx 4.9$

Using initial guess $N_0 = 5.5 \times 10^4$, the estimated $\alpha \approx 0.18$, $\beta \approx 2.2$, $\mu \approx 0.01$, $\gamma \approx 0.25$, $N_0 \approx 6 \times 10^4$

Appendix and Reference

1. Liu, Y., Gayle A A., Wilder-Smith, A., Rocklov, J. (2020). The reproductive number of COVID-19 is higher compared to SARS coronavirus. *Journal of Travel Medicine*, 4-10.

2. The code and data used for estimation is published here: Github/NatashaTing/covid19-modelling.