

MPhil Linear Algebra

Application: COVID-19

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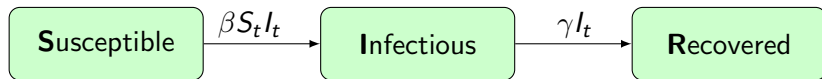
These Notes

- ▶ Background: SIR Model.
- ▶ Local Approximation Using the Jacobian and Spectral Decomposition.
- ▶ This application (SIR model) is non-examinable, but the **methods** (finding a Jacobian/eigenvalues...) are.

Background: SIR Model

Background: SIR Model - Assumptions

- ▶ The population is divided into three **compartments**.



- ▶ Basic version with no reinfection or removal, in discrete time.
- ▶ Classical reference is Kermack and McKendrick (1927), but also see Robert Shiller's 2019 [Marshall Lectures](#).
- ▶ Transition rates given as $\beta S_t I_t$ and γI_t .
- ▶ We will normalise the population such that:

$$S_t + I_t + R_t = 1.$$

Background: SIR Model - Key Equations

- ▶ The model dynamics may be written as:

$$\begin{aligned}S_{t+1} &= S_t - \beta S_t I_t, \\I_{t+1} &= I_t + \beta S_t I_t - \gamma I_t, \\R_{t+1} &= R_t + \gamma I_t.\end{aligned}$$

- ▶ As we have normalised the population, this may be written as a system of (non-linear) equations:

$$\begin{pmatrix} S_{t+1} \\ I_{t+1} \end{pmatrix} = \begin{pmatrix} S_t - \beta S_t I_t \\ I_t + \beta S_t I_t - \gamma I_t \end{pmatrix}.$$

- ▶ Which is of the form (vector-valued function of a vector):

$$\mathbf{x}_{t+1} = \mathbf{f}(\mathbf{x}_t),$$

where $\mathbf{x}_t = \begin{pmatrix} S_t \\ I_t \end{pmatrix}$.

Background: SIR Model - Two Important Questions

1. What are the equilibria?

- ▶ A stationary system requires:

$$\mathbf{x}_{t+1} = \mathbf{f}(\mathbf{x}_t) = \mathbf{x}_t \quad \Rightarrow \quad \begin{pmatrix} -\beta S_t I_t \\ \beta S_t I_t - \gamma I_t \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \end{pmatrix}.$$

- ▶ Two possibilities: **herd immunity** ($S_t = I_t = 0, R_t = 1$) and **disease free** ($S_t = 1, I_t = R_t = 0$).

2. Close to these equilibria, how does the model behave?

- ▶ Does the model display **explosive dynamics** (a pandemic) or does the disease **fade quickly**?

Background: SIR Model - Initial Dynamics

- ▶ Law of motion for I_{t+1} tells us the impact of higher infections:

$$\begin{aligned}I_{t+1} &= \beta S_t I_t + (1 - \gamma) I_t, \\ \Delta I_{t+1} &= (\beta S_t - \gamma) I_t, \\ \Delta I_{t+1} &\approx (\beta - \gamma) I_t.\end{aligned}$$

- ▶ The final line assumed we start “close” to the **disease free** equilibrium with $S_t \approx 1$.
- ▶ Hence if $(\beta - \gamma) > 0$, then I_t **increases** over time (pandemic) and whenever $(\beta - \gamma) < 0$, then I_t **falls** (disease fades).

Background: SIR Model - \mathcal{R}_0 is a Related Concept

- ▶ Much press coverage, see [BBC News](#) or [the Telegraph](#).
- ▶ Defined as the “average number of secondary infections arising from a typical infection in an entirely susceptible population.”
- ▶ To find \mathcal{R}_0 note that (on average):

Number of susceptibles infected by one infectious = β ,

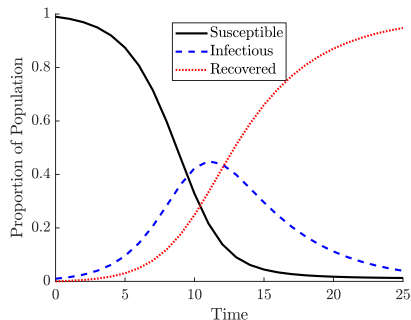
Time until infectious recovers = $1/\gamma$.

Contacts by infectious before removed, $\mathcal{R}_0 \equiv \beta/\gamma$.

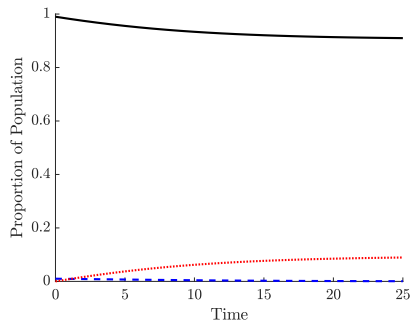
Background: SIR Model - Graphical Example

- ▶ Whenever $\mathcal{R}_0 > 1$, then I increases and an **epidemic** ensues.

Dynamics of SIR Model



(a) Explosive Dynamics, with $\mathcal{R}_0 > 1$.



(b) Fades quickly, with $\mathcal{R}_0 < 1$.

Local Approximation Using the Jacobian and Spectral Decomposition

Local Approximation: Outline

- ▶ We want to know if we are in case (a) or (b).
- ▶ We can find out by **linearising** the system around a given starting point, say the **disease free** equilibrium, $\mathbf{x}_0 = (S_0 \ I_0)' = (1 \ 0)'$.
- ▶ Linearise using the Taylor theorem applied to a vector-valued function of a vector (Hartman–Grobman theorem).

$$\begin{aligned}\mathbf{x}_{t+1} &= \mathbf{f}(\mathbf{x}_t), \\ \mathbf{f}(\mathbf{x}_t) &\approx \mathbf{f}(\mathbf{x}_0) + \frac{d\mathbf{f}(\mathbf{x}_0)}{d\mathbf{x}'}(\mathbf{x}_t - \mathbf{x}_0),\end{aligned}$$

where $\frac{d\mathbf{f}(\mathbf{x}_0)}{d\mathbf{x}'}$ is our **Jacobian matrix** evaluated at $\mathbf{x}_t = \mathbf{x}_0$.

Local Approximation: The Jacobian Matrix

- ▶ Our Jacobian matrix is then given as:

$$\mathbf{f}(\mathbf{x}_t) = \begin{pmatrix} S_t - \beta S_t I_t \\ \beta S_t I_t + (1 - \gamma) I_t \end{pmatrix}$$
$$\Rightarrow \frac{d\mathbf{f}(\mathbf{x}_t)}{d\mathbf{x}'_t} = \begin{pmatrix} \frac{df_1}{dx_1} & \frac{df_1}{dx_2} \\ \frac{df_2}{dx_1} & \frac{df_2}{dx_2} \end{pmatrix} = \begin{pmatrix} 1 - \beta I_t & -\beta S_t \\ \beta I_t & \beta S_t + 1 - \gamma \end{pmatrix}.$$

- ▶ Evaluated at \mathbf{x}_0 this becomes:

$$\frac{d\mathbf{f}(\mathbf{x}_0)}{d\mathbf{x}'_t} = \begin{pmatrix} 1 & -\beta \\ 0 & \beta + 1 - \gamma \end{pmatrix}.$$

- ▶ Plug in to the approximation and we have:

$$\mathbf{x}_{t+1} = \mathbf{f}(\mathbf{x}_t) \approx \mathbf{f}(\mathbf{x}_0) + \frac{d\mathbf{f}(\mathbf{x}_0)}{d\mathbf{x}'_t} (\mathbf{x}_t - \mathbf{x}_0),$$
$$\mathbf{x}_{t+1} \approx \mathbf{x}_t + \begin{pmatrix} 1 & -\beta \\ 0 & \beta + 1 - \gamma \end{pmatrix} (\mathbf{x}_t - \mathbf{x}_0).$$

Local Approximation: Difference Equations

- ▶ Removing \mathbf{x}_0 from each side, the above may be rewritten:

$$\mathbf{x}_{t+1} - \mathbf{x}_0 \approx \begin{pmatrix} 0 & -\beta \\ 0 & \beta - \gamma \end{pmatrix} (\mathbf{x}_t - \mathbf{x}_0).$$

- ▶ This represents a set of **difference equations**:

$$\mathbf{u}_{t+1} = \mathbf{A}\mathbf{u}_t.$$

- ▶ The dynamics are given by the **eigenvalues** of \mathbf{A} .

Local Approximation: Eigenvalues and Eigenvectors

- ▶ Proceed as usual. $\mathbf{Ax} = \lambda\mathbf{x}$, with $\mathbf{x} \neq \mathbf{0}$, infers:

$$\det(\mathbf{A} - \lambda\mathbf{I}) = \det \begin{pmatrix} -\lambda & -\beta \\ 0 & \beta - \gamma - \lambda \end{pmatrix} = -\lambda(\beta - \gamma - \lambda) = 0.$$

- ▶ The eigenvalues are therefore $\lambda_1 = 0$ and $\lambda_2 = \beta - \gamma$.
- ▶ The eigenvectors are therefore $\mathbf{v}_1 = (1 \ 0)'$ and $\mathbf{v}_2 = (-\beta/(\beta - \gamma) \ 1)'$.
- ▶ The diagonalised form of the matrix $\mathbf{A} = \mathbf{Q}\mathbf{\Lambda}\mathbf{Q}^{-1}$ is:

$$\mathbf{A} = \begin{pmatrix} 1 & -\beta/(\beta - \gamma) \\ 0 & 1 \end{pmatrix} \begin{pmatrix} 0 & 0 \\ 0 & \beta - \gamma \end{pmatrix} \begin{pmatrix} 1 & \beta/(\beta - \gamma) \\ 0 & 1 \end{pmatrix}.$$

- ▶ So may quickly compute $\mathbf{u}_{t+k+1} = \mathbf{A}^k \mathbf{u}_t$ since $\mathbf{A}^k = \mathbf{Q}\mathbf{\Lambda}^k\mathbf{Q}^{-1}$.

Final Thought: Why Do We Care So Much?

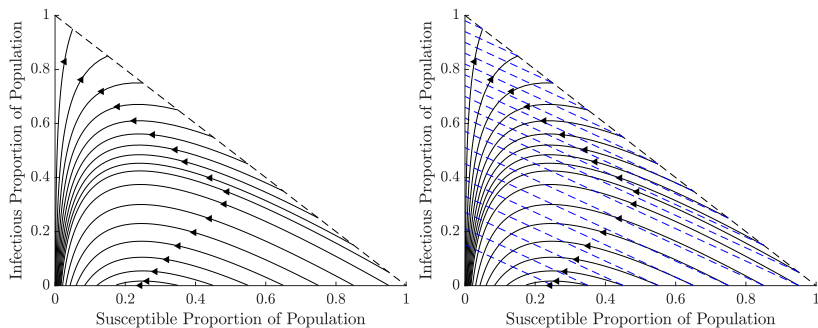
- ▶ The non-zero eigenvalue (and hence \mathcal{R}_0) provides several insights into our system dynamics.
 1. It gives a **threshold** for whether there will be an epidemic.
 2. It gives the initial **rate of increase** of an outbreak (whether explosive or not).
 3. It gives the **final size** of the epidemic (fraction of susceptibles ultimately infected), see Appendix.

Appendix

Appendix: Phase Diagrams

- ▶ If $\mathcal{R}_0 > 1$, proportion of infected initially grows before falling.
- ▶ Linearised solution is a reasonable approximation close to \mathbf{x}_0 .

Phase Diagrams of SIR Model



(a) Explosive Dynamics, with $\mathcal{R}_0 > 1$. (b) Linearised solution added in blue.

Appendix: Does the Epidemic Infect Everyone?

- ▶ Recall the basic model equations (now in continuous time):

$$\frac{\partial S}{\partial t} = -\beta SI, \quad \text{and} \quad \frac{\partial I}{\partial t} = \beta SI - \gamma I.$$

- ▶ Divide these to give:

$$\frac{\partial I}{\partial S} = -1 + \frac{\gamma}{\beta S}.$$

- ▶ Rearrange as:

$$\partial I = \left(-1 + \frac{\gamma}{\beta S}\right) \partial S.$$

- ▶ Integrate:

$$I(t) = -S(t) + \frac{\gamma}{\beta} \ln[S(t)] + C.$$

- ▶ Initial conditions ("close" to the disease free equilibrium), $I(0) \rightarrow 0$ and $S(0) \rightarrow 1$ give $C \rightarrow 1$.

- ▶ Finally, taking the limit when $I(\infty) \rightarrow 0$, such that the pandemic ends:

$$[S_\infty - 1] \frac{\beta}{\gamma} = \ln[S_\infty],$$

$$[S_\infty - 1] \mathcal{R}_0 = \ln[S_\infty].$$