Covid-19 SIR Model Analysis

By: Caleb Traxler, Minh Ton, Nameer Ahmed, Sasha Prostota, Annie Cheng

Our Model and Variables

$$dS/dt = \mu N - \frac{\beta I(t)S(t)}{N} - \mu S(t)$$

$$dI/dt = \frac{\beta I(t)S(t)}{N} - \gamma I(t) - \mu I(t)$$

$$dR/dt = \gamma I(t) - \mu R(t)$$

S: Number of **S**usceptible Individuals
I: Number of **I**nfectious Individuals
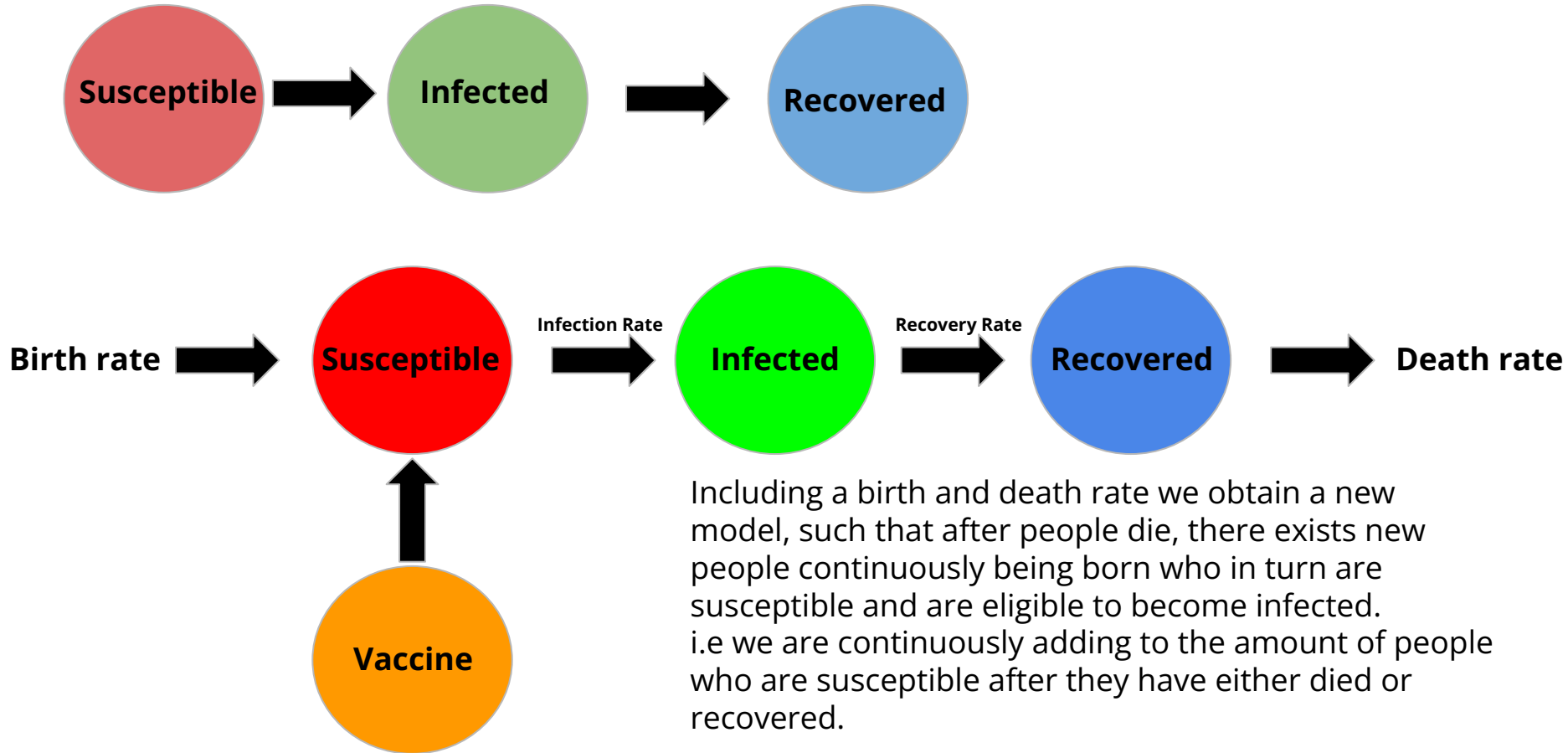R: Number of **R**emoved (and Immune) or Deceased Individuals

N: Population Size
μ: Birth and Death Rate (Assumed to be Equal)
β: Infection Rate
γ: Relative Recovery Rate

Question: How is our model different from the Kermack Mckendrick Model?

Susceptible → Infected → Recovered

Birth rate → Susceptible → (Infection Rate) → Infected → (Recovery Rate) → Recovered → Death rate

Vaccine → Susceptible

Including a birth and death rate we obtain a new model, such that after people die, there exists new people continuously being born who in turn are susceptible and are eligible to become infected.
i.e we are continuously adding to the amount of people who are susceptible after they have either died or recovered.

Our Model

For our convenience we define, $s(t) = S(t)/N,\ i(t) = I(t)/N,\ r(t) = R(t)/N$

so,

$$ds/dt = \mu - \beta i(t)s(t) - \mu s(t)$$
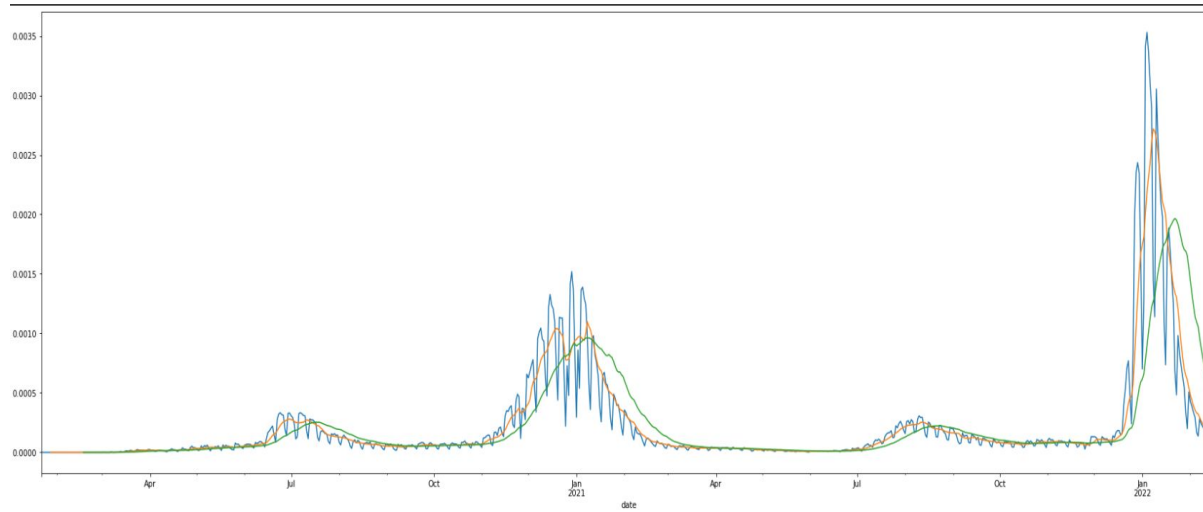$$di/dt = \beta i(t)s(t) - \gamma i(t) - \mu i(t)$$
$$dr/dt = \gamma i(t) - \mu r(t)$$

since, $r(t) = 1 - s(t) - i(t)$

We will only be looking at ds/dt and di/dt in our analysis.

Our Data & Determining Infection/Recovery Rates

Data: January 2020 - March 2022 - COVID Data - Four Waves

Wave 1:
$\beta = 1.8$
$\gamma = 1.677$

Wave 2:
$\beta = 2.6$
$\gamma = 2.285$

Wave 3:
$\beta = 1.82$
$\gamma = 1.702$

Wave 4:
$\beta = 4.35$
$\gamma = 3.52$

Conservation of Mass

Since birth rate and death rate are the same, the population stays constant:

$$s(t) + i(t) + r(t) = 1$$

$$ds/dt + di/dt + dr/dt = \mu - \beta i(t)s(t) - \mu s(t) + \beta i(t)s(t) - \gamma i(t) - \mu i(t) + \gamma i(t) - \mu r(t) = 0$$

therefore, $s(t) + i(t) + r(t)$ is a conservation of mass and invariant. Therefore, we only focus on the first quadrant of the system.

Invariance of Our Model

Because our model is conservative, so

$$s(t) + i(t) + r(t) = 1$$

Our model is invariant on the simplex:

$$\Omega = \{(s(t), i(t)) \in R_+^2 \,|\, s(t) + i(t) \leq 1\}$$
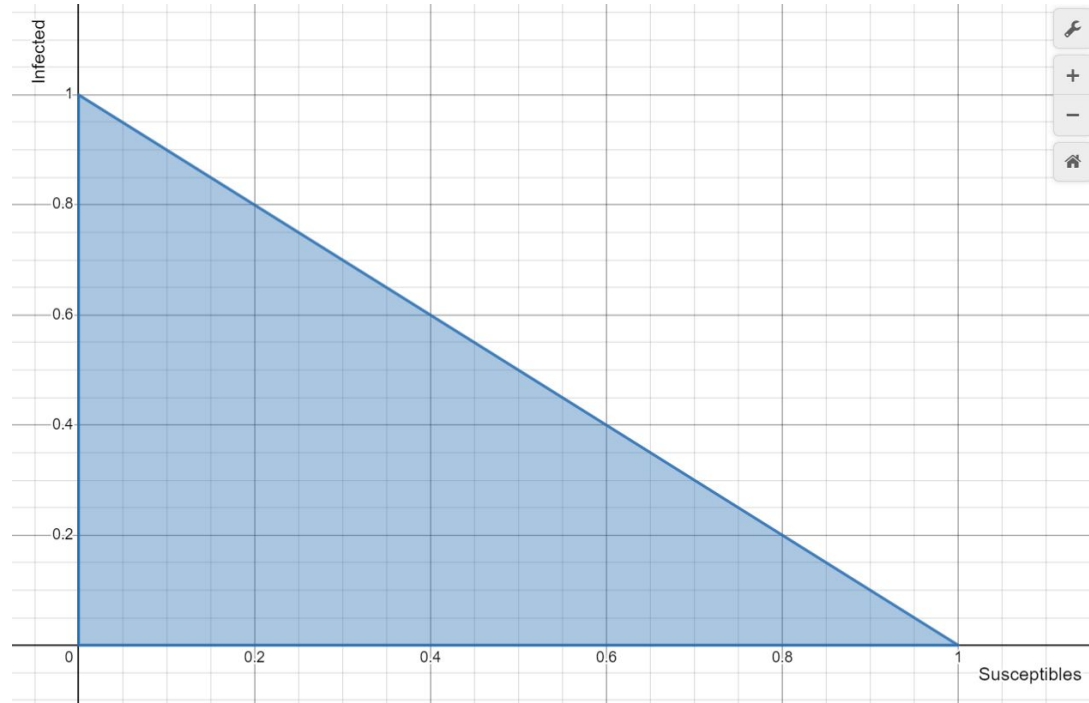
Along the s-Axis (i.e. $i = 0$):

$$\begin{pmatrix} \dot{s} \\ \dot{i} \end{pmatrix} = \begin{pmatrix} \mu(1 - s) \\ 0 \end{pmatrix}$$

Since $\dot{i} = 0$, does not cross S-axis

Along the i-axis (i.e. $s = 0$):

$$\begin{pmatrix} \dot{s} \\ \dot{i} \end{pmatrix} = \begin{pmatrix} \mu \\ -(\gamma + \mu)i \end{pmatrix}$$

Since $\dot{s} = \mu > 0$, does not cross i-axis

Linearization

There are 2 possible fixed points:

1. Disease-Free Equilibrium Point: $(s^*, i^*) = (1,0)$

2. Endemic Equilibrium Points: $(s^*, i^*) = \left(\dfrac{\gamma+\mu}{\beta} , \dfrac{\mu(\beta-\gamma-\mu)}{\beta(\gamma+\mu)} \right)$

Whether the fixed point of our model will be the disease-free equilibrium point or the endemic equilibrium point will be determined by R_0

R_0 is the reproduction number (ie the number of infections caused by an initial infection). It is found by: $\quad R_0 = \dfrac{\beta}{\gamma+\mu}$

Using bifurcation analysis, we will observe the behavior of our model at different R_0 values.

Jacobian of the System

$$J_{(s,i)} = \begin{pmatrix} -\beta - \mu & -\beta s \\ -\beta i & \beta - \gamma - \mu \end{pmatrix}$$

At (1,0):

At E*:

$$J_{(1,0)} = \begin{pmatrix} -\mu & -\beta \\ 0 & \beta - \gamma - \mu \end{pmatrix}$$

$$J_{\left(\frac{\gamma+\mu}{\beta}, \frac{\mu(\beta-\gamma-\mu)}{\beta(\gamma+\mu)}\right)} = \begin{pmatrix} -\beta - \mu & -\gamma - \mu \\ \frac{-\gamma(\beta-\gamma-\mu)}{\beta(\gamma+\mu)} & \beta - \gamma - \mu \end{pmatrix}$$

$$\lambda_1 = -\mu, \ \lambda_2 = \beta - \gamma - \mu$$

$$\lambda = \frac{1}{2}[-\mu R_0 \pm \sqrt{\mu^2 R_0^2 - 4\mu(\beta - \gamma - \mu)}]$$

Linearization of Wave #1

$$\mathrm{Ja} = \begin{bmatrix} -1.8I - 0.046 & -1.8S \\ 1.8I & 1.8S - 1.723 \end{bmatrix}$$

Examine (1,0)

Examine (0.957.0.00114)

$$Ja_{(1,0)} = \begin{bmatrix} -0.046 & -1.8 \\ 0 & 0.077 \end{bmatrix}$$

$$Ja_{\left(\frac{1723}{1800}, \frac{1771}{1550700}\right)} = \begin{bmatrix} -0.048 & -1.723 \\ 0.002 & 0 \end{bmatrix}$$

Eigenvalue: -0.046 and -1.8

(1,0) is a saddle point

Eigenvalue: -0.024 + i(0.054) and -0.024 - i(0.054)

(0.957,0.00114) is stable spiral

Linearization of Wave #2

$$Ja = \begin{bmatrix} -2.6I - 0.046 & -2.6S \\ 2.6I & 2.6S - 2.331 \end{bmatrix}$$

Examine (1,0)

Examine (0.897,0.00204)

$$Ja_{(1,0)} = \begin{bmatrix} -0.046 & -2.6 \\ 0 & 0.27 \end{bmatrix}$$

$$Ja_{(\frac{2331}{2600}, \frac{6187}{3030300})} = \begin{bmatrix} -0.051 & -2.331 \\ 0.0053 & 0 \end{bmatrix}$$

Eigenvalue: -0.046 and 0.27

Eivengalue: -0.026 + i(0.11) and -0.026-i(0.11)

(1,0) is a saddle point

(0.897,0.00204) is a stable spiral

Linearization of Wave #3

$$Ja = \begin{bmatrix} -1.82I - 0.046 & -2.6S \\ 1.82I & 1.82S - 1.748 \end{bmatrix}$$

Examine (1,0)

Examine (0.96,0.00105)

$$Ja_{(1,0)} = \begin{bmatrix} -0.046 & -2.6 \\ 0 & 0.27 \end{bmatrix}$$

$$Ja_{(0.96,0.00105)} = \begin{bmatrix} -0.0479 & -2.496 \\ 0.0019 & -0.0008 \end{bmatrix}$$

Eigenvalue : 0.27 and -0.046

Eigenvalue: -0.0244+i(0.065) and -0.0244- i(0.065)

(1,0) is saddle point

(0.96,0.00105) is stable spiral

Linearization of Wave #4

$$Ja = \begin{bmatrix} -4.35I - 0.046 & -4.35S \\ 4.35I & 4.35S - 3.566 \end{bmatrix}$$

Examine (1,0)

Examine (0.8198, 0.00232)

$$Ja_{(1,0)} = \begin{bmatrix} -0.046 & -4.35 \\ 0 & 0.784 \end{bmatrix}$$

$$Ja_{\left(\frac{1783}{2175}, \frac{9016}{3878025}\right)} = \begin{bmatrix} -0,056 & -3.566 \\ 0.0101 & 0 \end{bmatrix}$$

Eigenvalue: -0.046 and 0.784

Eigenvalue: -0.028 + i(0.19) and -0.028 - i(0.19)

(1,0) is a saddle point

(0.8198,0.00232) is a stable spiral

Hartman Grobman Theorem

Wave 1:

(1,0) is a saddle point. Hartman Grobman Theorem holds because saddle point is hyperbolic

 (0.957.0.00114) is a stable spiral. Hartman Grobman Theorem holds because stable spiral is hyperbolic.

Wave 1 satisfies existence and uniqueness of fixed point

Since **wave 2**, **wave 3**, and **wave 4** have similar differential equations as wave 1. Therefore, all the fixed points in **wave 2**, **wave 3**, and **wave 4** satisfies existence and uniqueness of fixed point since Hartman Grobman Theorem holds.

Phase Portraits

Wave 1
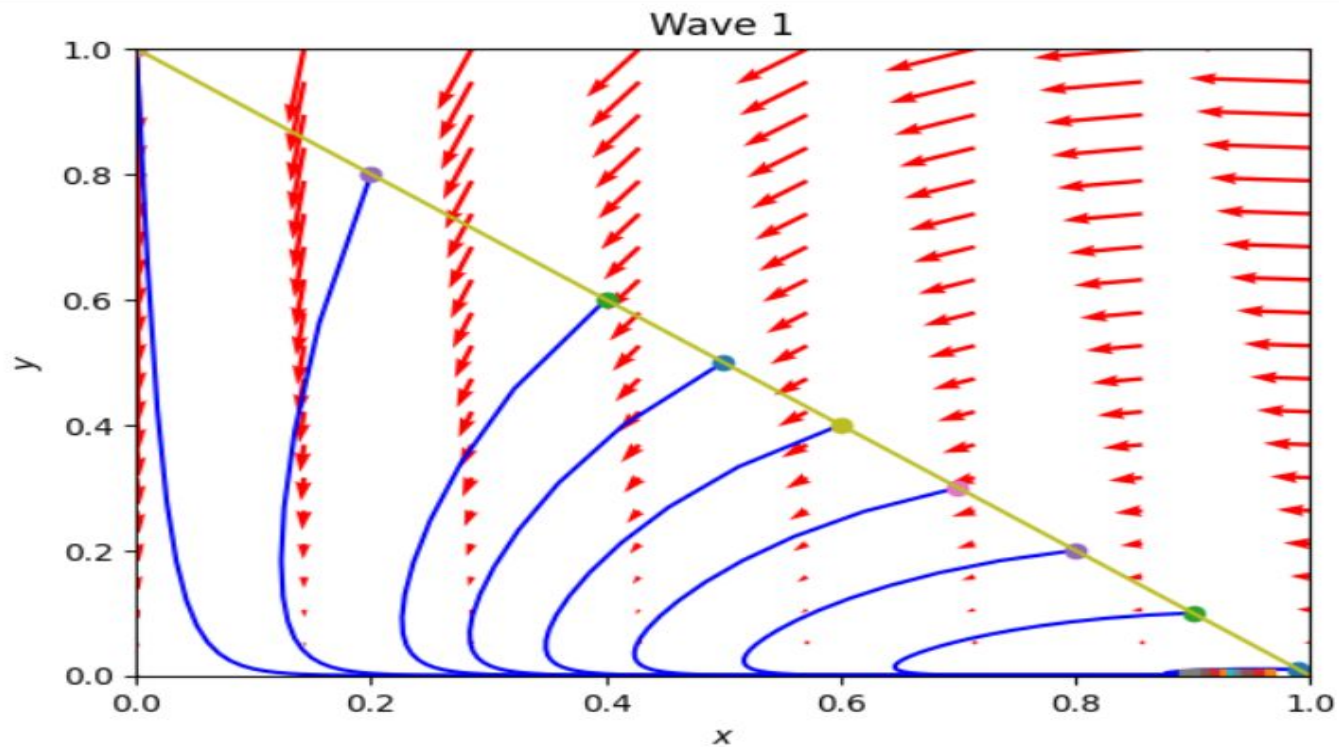
Biological Interpretation

A. if $R_0 < 1$, either hasn't occurred or end
. Trajectories approaches S - axis
. Susceptible population increases
. Infection population decreases

B. $R_0 = 1$ represents a threshold between epidemic and not epidemic

C. If $R_0 > 1$, epidemic occurs
. Trajectories rise high from the right to left
. Susceptible population decreases
. Infection population increases

Bifurcation Analysis

Bifurcation Analysis for SIR Models:

I want to vary the reproduction number, R_0
$R_0 > 1, \quad R_0 < 1, \quad R_0 = 1$

$$R_0 = \frac{\beta}{\gamma + \mu}$$

For the case $R_0 > 1$, we have already performed four variations using the obtained data, such that:

Wave 1: $R_0 = 1.045$
Wave 2: $R_0 = 1.118$
Wave 3: $R_0 = 1.0412$
Wave 4: $R_0 = 1.22$

Thus, upon plugging in the coefficients, I obtain the fixed points:

1.) Wave 1 endemic fixed point is $(\frac{1.677+0.046}{1.8}, \frac{0.046(1.8-1.677-0.046)}{1.8(1.677+0.046)}) = (0.9572, 0.00114206)$

2.) Wave 2 endemic fixed point is $(\frac{2.285+0.046}{2.6}, \frac{0.046(2.6-2.285-0.046)}{2.6(2.285+0.046)}) = (0.8965, 0.00204)$

3.) Wave 3 endemic fixed point is $(\frac{1.702+0.046}{1.82}, \frac{0.046(1.82-1.702-0.046)}{1.82(1.702+0.046)}) = (0.96044, 0.00104106)$

4.) Wave 4 endemic fixed point is $(\frac{3.52+0.046}{4.35}, \frac{0.046(4.35-3.52-0.046)}{4.35(3.52+0.046)}) = (0.819, 0.00232)$

After careful analysis, we found that for the case, $R_0 > 1$, all waves classified the fixed point, $(\frac{\gamma+\mu}{\beta}, \frac{\mu(\beta-\gamma-\mu)}{\beta(\gamma+\mu)})$ as a stable spiral.

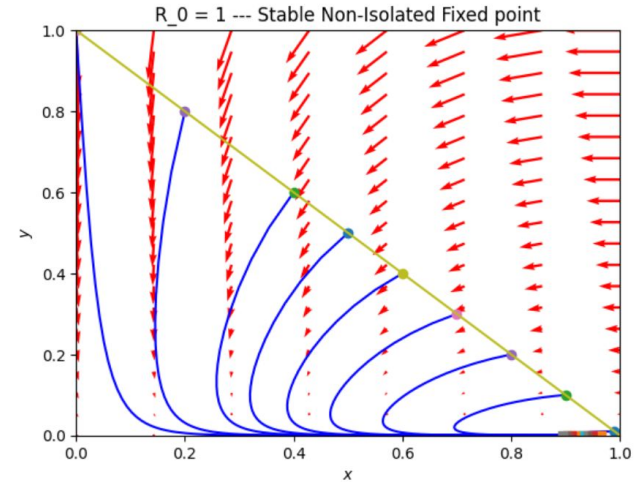Also note that the fixed point, (1,0) is classified to be a saddle.
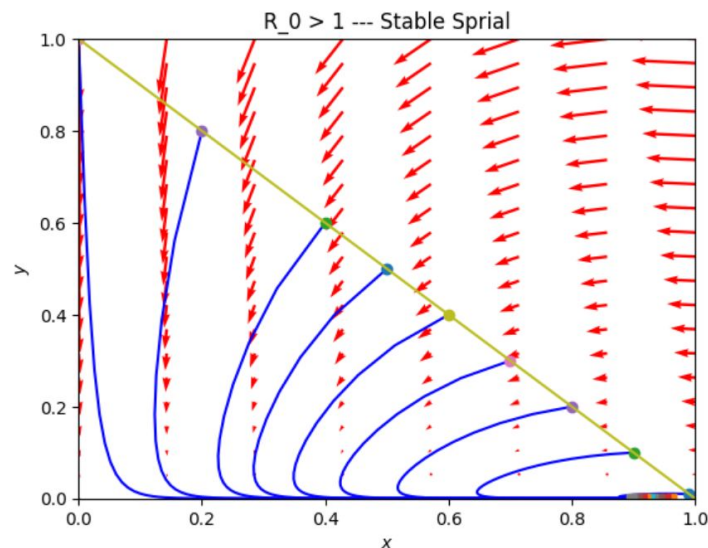
To perform the bifurcation, choose $\beta = 1$ and $\gamma = 0.954$, so that $R_0 = 1$.

$$S' = 0.046 - IS - 0.046S$$
$$I' = IS - 0.954I - 0.046I$$

$$J_{(1,0)} = \begin{bmatrix} -y - 0.046 & -x \\ y & x - 0.954 - 0.046 \end{bmatrix} = \begin{bmatrix} -0.046 & -1 \\ 0 & 0 \end{bmatrix}$$

R_0 = 1 --- Stable Non-Isolated Fixed point

The eigenvalues are $\lambda = -0.046$ and $\lambda = 0$. Thus, (1,0) is a non-isolated fixed point when $R_0 = 1$. Stability cannot be determined by H-G theorem since it is non-hyperbolic.

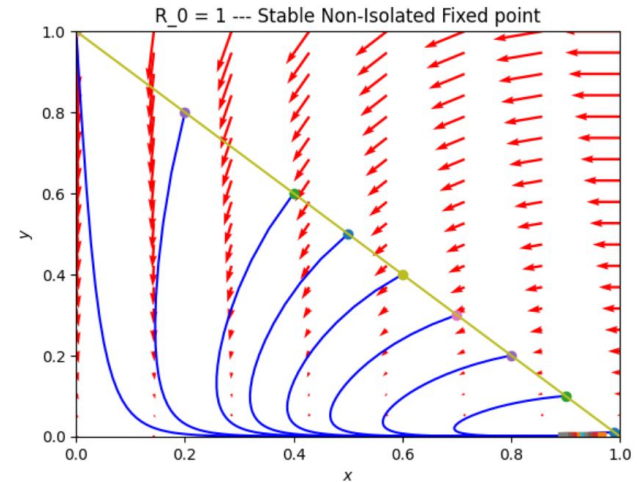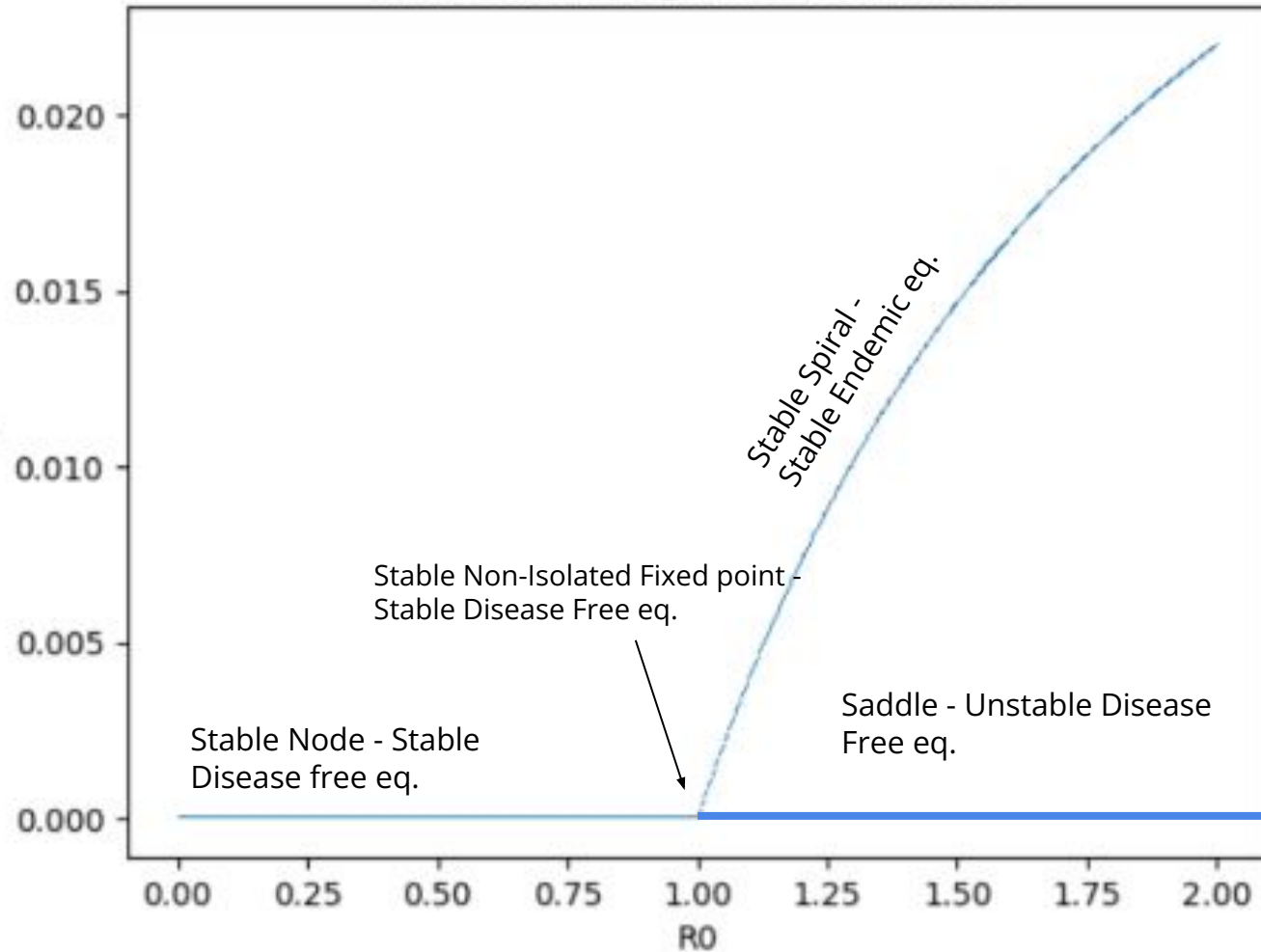To perform the bifurcation, choose β = 1.5 and γ = 3, so that $R_0 < 1$.

$$S' = 0.046 - 1.5IS - 0.046S$$
$$I' = 1.5IS - 3I - 0.046I$$

$$J_{(1,0)} = \begin{bmatrix} -1.5y - 0.046 & -1.5x \\ 1.5y & 1.5x - 3 - 0.046 \end{bmatrix} = \begin{bmatrix} -0.046 & -1.5 \\ 0 & -2.546 \end{bmatrix}$$

The eigenvalues are λ = -0.046 and λ = -2.546. Thus, (1,0) is a stable node.

Bifurcation Diagram for SIR Model

This bifurcation is called a transcritical bifurcation, such that the stability changes after some point.

In this case, the stability changes after

For R0 < 1, there exists a single disease free fixed point, (1,0) classified as a stable node.

At R0 = 1, there exists a single, nonhyperbolic fixed point (1,0).

For R0 > 1, there exists an endemic fixed point and a disease free fixed point, however the disease free fixed point is now unstable. The endemic fixed point is classified as a stable spiral.

Stable Spiral - Stable Endemic eq.

Stable Non-Isolated Fixed point - Stable Disease Free eq.

Stable Node - Stable Disease free eq.

Saddle - Unstable Disease Free eq.

Endemic Fixed Point

Endemic fixed point is a stable spiral for all four waves:

- Satisfies attracting because some of trajectories are approaching endemic fixed point.

- Satisfies Lyapunov stable because all trajectories are close to the fixed point.

- Since Endemic fixed point is attracting and Lyapunov stable, so Endemic fixed point is global asymptotically stable

SIR Model with Vaccine Parameter (p != 0)

If we include vaccinations, we get the following equations:

$$\frac{ds}{dt} = (1-p)\mu - \beta is - \mu s$$

$$\frac{di}{dt} = \beta is - \gamma i - \mu i$$

$$\frac{dr}{dt} = \gamma i - \mu r$$

$$\frac{dv}{dt} = p\mu - \mu v$$

s, i, r, and γ are the same as before
μ is the mortality rate
v is the group of vaccinated people
p is the vaccination rate

s + i + r + v = 1

Again, we can leave out the r equation
because r = 1 - s - i - v

Assume p = 0.74

Domain:

$$\Omega_1 = \{(s(t), i(t), v(t)) \in R^3_+, s(t) + i(t) + v(t) \le 1\}.$$

Equilibrium Points of Vaccine Model

Disease-free equilibrium point E_0 = (s = 1-p, i = 0, v = p)

Endemic equilibrium point E_e = (s = $(\gamma+\mu)/\beta$, i = $\mu(\beta(1-p)-\gamma-\mu) / \beta(\gamma+\mu)$, v = p)

New reproductive number R_v = R_0(1-p)

The endemic equilibrium point only exists if R_v > 1. For our model, R_v<1, so we only have the disease-free equilibrium point.

Linearization of Equilibrium Points of Vaccine Model

The introduction of vaccines, restricts our R_v value to be less than one, so there is no longer an endemic fixed point.

The linearization for the model gives us:

$$Ja_{(S^\star,I^\star)}= \begin{bmatrix} -1.8I - 0.046 & -1.8S \\ 1.8I & 1.8S - 1.723 \end{bmatrix}$$

$$Ja_{(\frac{13}{50},0)}= \begin{bmatrix} -0.046 & -0.0468 \\ 0 & 1.255 \end{bmatrix}$$

So, the disease-free equilibrium point is stable. Thus, as time goes to infinity, the number of infected will go to 0.
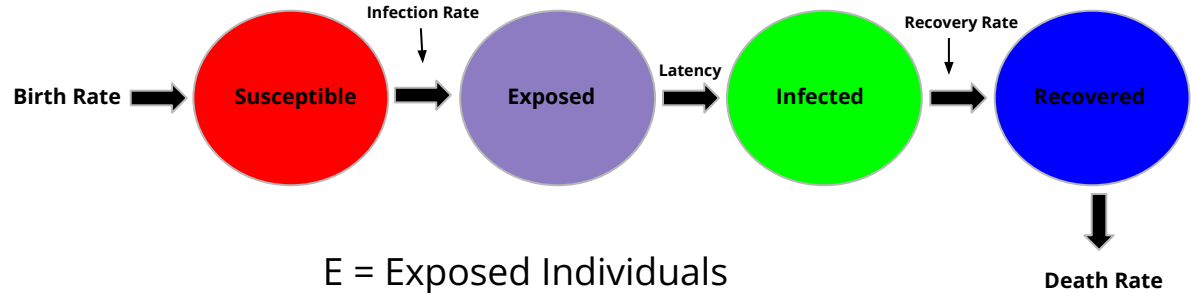
Adding Complexity

We want to analyze a system that doesn't assume that the birth rate equals to the death rate.

The best way to do this is to analyze the **SEIR model**, such that we introduce an exposed parameter.

Thus, we need to introduce a latency period.

Note that we will only analyze wave one data.

SEIR Model

$$\frac{dS}{dt} = -\beta SI + \lambda - \mu S$$

$$\frac{dE}{dt} = \beta SI - (\mu + k)E$$

$$\frac{dI}{dt} = kE - (\gamma + \mu)I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

$$R_0 = \frac{k\beta\lambda}{\mu(k+\mu)(\gamma+\mu)}$$

E = Exposed Individuals

$\lambda = 0.046$ birth rate

$\mu = 0.011$ death rate

$k = 5.6 = 1/5.6 = 0.178$ day latency period

We obtained that during the time period of 2020 - 2022, there was a death rate of 1.1%
The latency period from 2020 - 2022 was about 5.6 days. This means that COVID symptoms did not appear 5.6 days after a person has been exposed.

Linearization

Wave 1

$$\dot{S} = -1.8SI + 0.046 - 0.011S$$
$$\dot{E} = 1.8SI - 0.189E$$
$$\dot{I} = 0.178E - 1.688I$$

$$Ja = \begin{bmatrix} -1.8S - 0.011 & 0 & -1.8S \\ 1.8I & -0.189 & 1.8S \\ 0 & 0.178 & -1.688 \end{bmatrix}$$

$$Ja_{(-0.938, -0.316, -0.03)} = \begin{bmatrix} 0.043 & 0 & 1.6884 \\ -0.054 & -0.189 & -1.6884 \\ 0 & 0.178 & -1.688 \end{bmatrix}$$

$\tau = -1,834 < 0$
$\det = 0.0104 > 0$
$\tau^2 - 4\det = -1.876 < 0$
$(-0.938, -0.316, -0.03)$ is stable spiral

$$Ja_{(\frac{46}{11}, 0, 0)} = \begin{bmatrix} -0.011 & 0 & -7.53 \\ 0 & -0.189 & 7.53 \\ 0 & 0.178 & -1.688 \end{bmatrix}$$

$\tau = -1.888 > 0$
$\det = -0.011 < 0$
$(\frac{46}{11}, 0, 0)$ is a saddle point

References

1. Census Reporter for Orange County. Available at:
https://censusreporter.org/profiles/05000US06059-orange-county-ca/
2. M. A. Taneco-Hernández and C. Vargas-De-León. "Stability and Lyapunov functions for systems with Atangana–Baleanu Caputo derivative: an HIV/AIDS epidemic model." Chaos Solit. Fractals, 132:109586, 2020.
3. ResearchGate. "Stability Analysis of SIR Model with Vaccination." Available at:
https://www.researchgate.net/publication/261252884_Stability_Analysis_of_SIR_Model_with_Vaccination
4. Stanford University. "Jones-on-R0.pdf." Available at:
https://web.stanford.edu/~jhj1/teachingdocs/Jones-on-R0.pdf
5. WebMD. "Coronavirus Incubation Period: How Long and When Most Contagious." Available at:
https://www.webmd.com/lung/coronavirus-incubation-period