

Disease Eradication if $\mathcal{R}_0 < 1$?
It's Not That Simple
(Math 747 Weekly Update)

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- “Occurrence of backward bifurcation and prediction of disease transmission with imperfect lockdown: A case study on COVID-19” by Sk Shahid Nadim & Joydev Chattopadhyay.
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7430254/>
- Topic: Develop and analyze compartmental model for COVID-19 to account for lockdown efficacy and success rate.

Discussion overview

- 1 Introduce model
- 2 Key insights and findings
- 3 Conclusions and takeaways

Introducing model

The model proposed by Nadim and Chattopadhyay is a compartmental model. Unlike the standard SEIR model with vital dynamics, here, we divide the population into 6 mutually exclusive groups:

S - Susceptible,

L - Lockdown,

E - Exposed,

I - Infected (un-notified),

J - Hospitalized/Isolated,

R - Recovered,

Total population $N(t) = S(t) + L(t) + E(t) + I(t) + J(t) + R(t)$.

System Parameters

The model includes several additional parameters. We pay close attention to r , l , and $1/\psi$; key differences from the SEIR model with vital dynamics.

Π — Recruitment rate of human population (source of new susceptibles)

$1/\mu$ — Average life expectancy at birth

β — Transmission rate of infected individuals

r — Lockdown efficacy (perfect $\implies r = 0$, imperfect $\implies 0 < r < 1$)

$1/\gamma$ — COVID-19 incubation period (estimate range 1 - 14 days)

l — Lockdown success rate (range 0 - 1)

$1/\psi$ — Lockdown period

η — Rate at which symptomatic infected become hospitalized/notified

δ — Death rate of hospitalized/notified population

τ_1 — Recovery rate for symptomatic infected

τ_2 — Recovery rate for hospitalized/notified individuals

The model is a deterministic one, and it's implemented via the following system of ordinary differential equations.

$$\frac{dS}{dt} = \Pi + \psi L - \frac{\beta SI}{N - J} - (\mu + l)S,$$

$$\frac{dL}{dt} = lS - \frac{r\beta LI}{N - J} - (\mu + \psi)L,$$

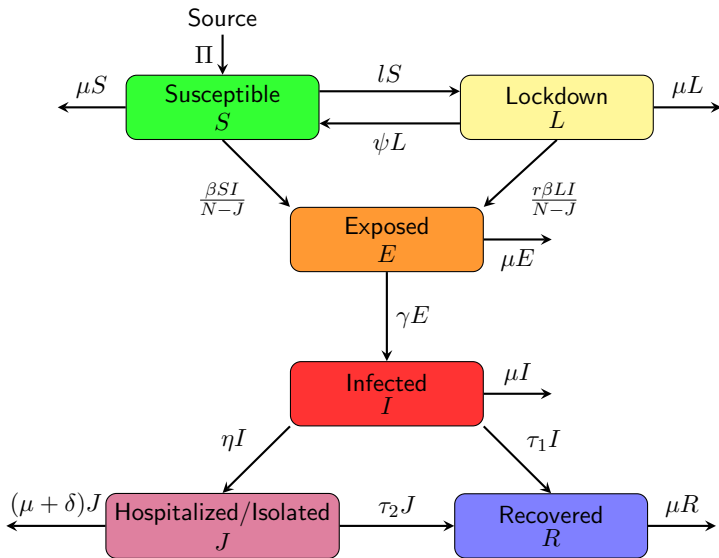
$$\frac{dE}{dt} = \frac{\beta SI}{N - J} + \frac{r\beta LI}{N - J} - (\gamma + \mu)E,$$

$$\frac{dI}{dt} = \gamma E - (\eta + \tau_1 + \mu)I,$$

$$\frac{dJ}{dt} = \eta I - (\tau_2 + \delta + \mu)J,$$

$$\frac{dR}{dt} = \tau_1 I + \tau_2 J - \mu R.$$

Flow Chart



Well-posedness

The model is biologically well posed by Theorem 3.1, which guarantees two fundamental properties.

- 1 For $t > 0$, solutions with positive initial data remain positive.
- 2 The biologically feasible region Ω , a subset of six-dimensional Euclidean space is positively invariant and globally attracting.

$$\Omega = \left\{ (S, L, E, I, J, R) \in \mathbb{R}_+^6 : S + L + E + I + J + R \leq \frac{\Pi}{\mu} \right\}$$

What is \mathcal{R}_0 ?

- 1 \mathcal{R}_0 is defined as “the number of new infections produced by a typical infective individual in a population at a disease free equilibrium (DFE)”.
- 2 More formally, it's the spectral radius of the next generation operator at disease free equilibrium (DFE).
- 3 The authors define \mathcal{R}_0 using the FV^{-1} approach described in class.

Calculating \mathcal{R}_0

- $\varepsilon_0 = \left(\frac{\Pi(\mu+\psi)}{\mu(\mu+\psi+l)}, \frac{\Pi l}{\mu(\mu+\psi+l)}, 0, 0, 0, 0 \right)$ (Calculate DFE)
- $X = (E(t), I(t), J(t))$ (Identify the infected classes)
- $\dot{X} = \mathcal{F} - \mathcal{V}$ (Decompose \dot{X})
- Linearize \mathcal{F} and \mathcal{V} at ε_0

$$F = \begin{pmatrix} 0 & \frac{\beta(\mu+\psi+rl)}{\mu+\psi+l} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} \gamma + \mu & 0 & 0 \\ -\gamma & \eta + \tau_1 + \mu & 0 \\ 0 & -\eta & \tau_2 + \delta + \mu \end{pmatrix}$$

- $\mathcal{R}_0 = \rho(FV^{-1}) = \frac{\beta\gamma(\mu + \psi + rl)}{(\mu + \gamma)(\eta + \tau_1 + \mu)(\mu + \psi + l)}$

Insights from \mathcal{R}_0

- What can we say about ε_0 ?

Lemma 3.1

The DFE is LAS whenever $\mathcal{R}_0 < 1$ and unstable whenever $\mathcal{R}_0 > 1$.

- How about endemic equilibria (EE)?

Theorem 3.2

Let P_1 , P_2 and P_3 denote sets of certain parameter conditions. The model has

- 1 a unique EE if $P_1 \iff \mathcal{R}_0 > 1$,
- 2 a unique EE if P_2 ,
- 3 two EEs if P_3 ,
- 4 no EEs otherwise.

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- Take another look at case 3.
- What could having two EEs mean?
- To analyze this, we pick a 'nice' quantity to play with.
- Let $\varepsilon^* = (S^*, L^*, E^*, I^*, J^*, R^*)$ be any EE.
- Define $\lambda_h^* = \frac{\beta I^*}{N^* - J^*}$ (the 'force of infection')

Super Unfortunate Result

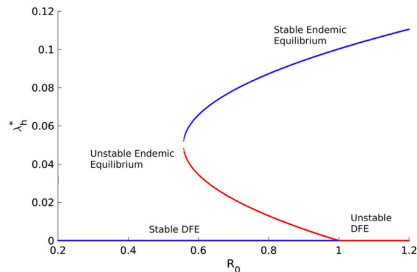


Fig. 2. Backward bifurcation diagram for the force of infection (λ_b^c) of the model (2.1). Using the parameter values: $\psi = 0.000246$, $\mu = 0.0049$, $r=0.09$, $\gamma = 0.0016$, $\eta = 0.0159$, $\beta=5.905$, $\tau_1 = 0.0101$, $\tau_2 = 0.0094$, $\delta = 0.0332$, $l=0.09$.

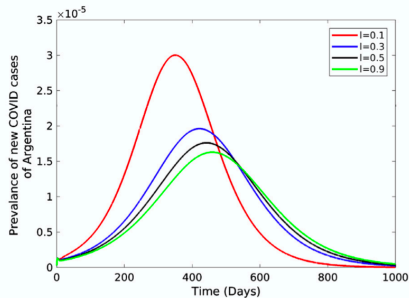
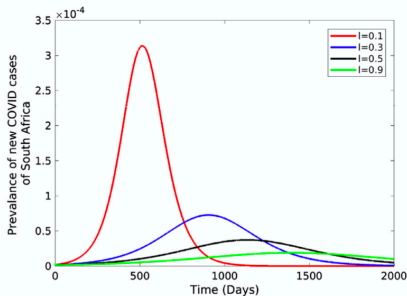
- (WOAH!) Stable DFE and stable EE can coexist with $\mathcal{R}_0 < 1!$
- Need to get $\mathcal{R}_0 < \mathcal{R}_0^c$ (\mathcal{R}_0^c point of saddle node bifurcation).
- How?

How to decrease \mathcal{R}_0 ?

- We start by highlighting an important result in the paper.

$$\frac{\partial \mathcal{R}_0}{\partial l} = -\frac{(1-r)\beta\gamma(\mu+\psi)}{(\gamma+\mu)(\eta+\tau_1+\mu)(\mu+\psi+l)^2} < 0$$

- Increases in lock down success (l) always reduce \mathcal{R}_0 .
- Not particularly enlightening (as we defined l to have that effect), but still good to see that the model makes sense.



What else can be done?

- Aim for perfect lockdown efficacy ($r = 0$). Set $r = 0$ in ODEs.
- Obtain a reduced model M with $\mathcal{R}_0^* = \frac{\beta\gamma(\mu+\psi)}{(\mu+\gamma)(\eta+\tau_1+\mu)(\mu+\psi+1)}$.

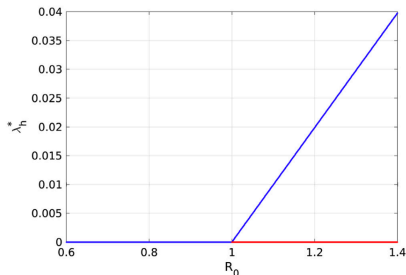


Fig. 3. Transcritical bifurcation for the force of infection (λ_h^*) of the model (2.1). Using the parameter values: $\psi = 0.000246$, $\mu = 0.0049$, $r=0$, $\gamma = 0.0016$, $\eta = 0.0159$, $\tau_1 = 0.0101$, $\beta=0.5905$, $\tau_2 = 0.0094$, $\delta = 0.0332$, $l=0.09$.

Theorem 3.4

The DFE of M is GAS in Ω whenever $\mathcal{R}_0^* \leq \frac{\mu+\psi}{\mu+\psi+l} < 1$.

Recruitment into lockdown

- In model, recruited humans (Π) feed susceptible pool only.
- However Π is defined as the immigration or birth rate.
- Most countries during the COVID-19 crisis have travel advisories in place that restrict entirely, or severely limit the inflow of incoming travellers.
- If travellers are permitted into a country like Canada for instance, they're told to self isolate from the moment they step foot into the country to 14 days after that day.
- It would be more realistic to have the travel rate flow to the lock down population, or to split incoming travellers into a proportion that do self isolate and those that don't, and adjust the flow accordingly.

Final Takeaways

- Not always safe to strictly aim for $\mathcal{R}_0 < 1$,
- Bifurcation analysis is critical in understanding complex dynamics,
- Lockdowns **DO** help.