Global Dynamics of an SIR Model with Post-Infection Mortality and Partial Immunity

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Motivation

- There is growing interest in studying epidemiological models that incorporate post-infection mortality and partial immunity. This is because there are diseases, such as COVID, that have both of these properties.
- In this project, we investigate how the choice of transmission term influences disease dyanmics in a model that includes post-infection mortality and partial immunity.
- We are particularly interested in characterizing parameter regions where periodic solutions exist.

Overview

- We incorporate post-infection mortality into the recovered class as an additional death rate, α_R. We incorporate partial immunity a constant ϵ in front of the incidence rate from the recovered to infected class. Our model uses the following compartment diagram:

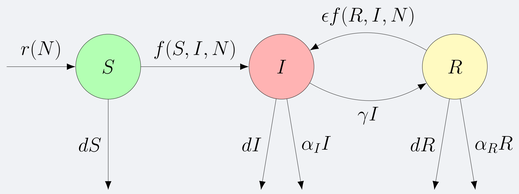


Figure 1. Compartment Diagram

- From this compartment diagram, we have the following system of differential equations.

$$\begin{aligned}\dot{S} &= r(N) - f(S,I,N) - dS\\ \dot{I} &= f(S,I,N) + \epsilon f(R,I,N) - \gamma I - dI - \alpha_I I\\ \dot{R} &= \gamma I - \epsilon f(R,I,N) - dR - \alpha_R R\\ N &= S + I + R\end{aligned}$$

- Our new model uses different recruitment and incidence functions compared to the original model [3].

Model	Recruitment $r(N)$	Incidence $f(S,I,N)$	
Original	Λ	λSI	*"Mass-action Incidence"*
New	bN	$\beta SI/N$	*"Standard Incidence"*

- The incidence rate that a model uses depends on assumptions about how individuals interact and how the infectiousness of the disease depends on population size.

Incidence Rate	Mass Action	Standard
Response to Population Size	$\lambda SI \propto N^2$	$\beta SI/N \propto N$

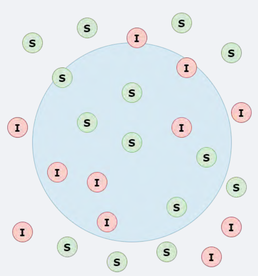


Figure 2. **Standard Incidence:** Spread-out population; assumes that every susceptible individual interacts with a proportion of the infected population.

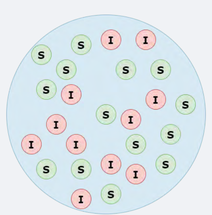
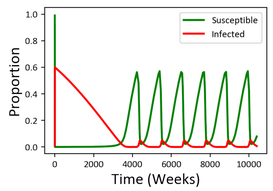
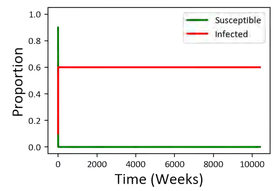
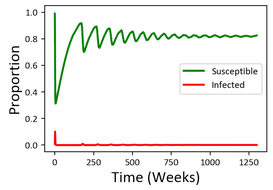
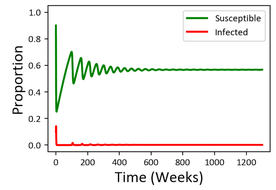


Figure 3. **Mass-action Incidence:** Dense population; assumes that every susceptible individual interacts with every infectious individual.

Numerical Results

Original Model	Parameters	New Model
	$\Lambda = b = d = 0.0004$ $\beta = 2.5$ $\gamma = 1$ $\epsilon = 1$ $\alpha_I = 0$ $\alpha_R = 0.0008$	
	$\Lambda = b = d = 0.005$ $\beta = 5$ $\gamma = 3$ $\epsilon = 0.1$ $\alpha_I = 0.05$ $\alpha_R = 0.01$	

Analytical Results

The new model evolves according to the system of differential equations:

$$\begin{aligned}\dot{S} &= bN - \frac{\beta SI}{N} - dS\\ \dot{I} &= \frac{\beta SI}{N} + \frac{\epsilon\beta RI}{N} - \gamma I - dI - \alpha_I I\\ \dot{R} &= \gamma I - \frac{\epsilon\beta RI}{N} - dR - \alpha_R R\end{aligned}$$

Because of our choice of recruitment and incidence functions, we can make the change of variables $s = S/N$, $i = I/N$, and $r = R/N$ to reduce this model to 2 dimensions.

$$\begin{aligned}\dot{s} &= b - bs - \beta si + \alpha_I si + \alpha_R s(1-s-i)\\ \dot{i} &= \beta si + \epsilon\beta i(1-s-i) - (b + \alpha_I + \gamma)i + \alpha_I i^2 + \alpha_R i(1-s-i)\end{aligned}$$

s, i, and r are population proportions, so we restrict our attention to the feasible set Γ.

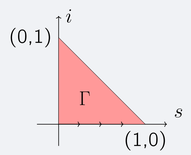


Figure 4. $\Gamma = \{(s,i) : s + i \leq 1,\ s \geq 0,\ i \geq 0\}$

Theorems

Following the next-generation matrix method [1], define the Basic Reproductive Number ($\mathcal{R}_0$) as

$$\mathcal{R}_0 = \frac{\beta}{b + \gamma + \alpha_I}.$$

1. If $\mathcal{R}_0 \leq 1$, the Disease Free Equilibrium is globally stable in Γ.
   - Proof uses a novel Lyapunov Function and modification of Lasalle's Invariance Principle [2].
2. If $\mathcal{R}_0 > 1$, there is a unique Endemic Equilibrium and the Disease Free Equilibrium is unstable.
3. If $\mathcal{R}_0 > 1$ and $\alpha_I \leq \alpha_R + \epsilon\beta$, the Endemic Equilibrium is globally stable in Γ.
   - Proof uses Dulac Criterion and Poincaré-Bendixson Theorem.

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Parameters

Parameter	Biological Meaning	Range
Λ, b	Birth rate	$\Lambda = b > 0$
β, λ	Transmission Coefficient	$\beta = \lambda > 0$
ϵ	Immunity	$0 \leq \epsilon \leq 1$
d	Death rate	$d > 0$
γ	Recovery rate	$\gamma > 0$
α_I	Disease-induced mortality	$\alpha_I \geq 0$
α_R	Post-infectious mortality	$\alpha_R \geq 0$

Conclusions

- From our numerical analysis, we found that the new model does not produce cycles in cases when the original model does; for example, when $\alpha_I = 0$.
- We have analytically shown that the Disease Free Equilibrium is globally stable if $\mathcal{R}_0 \leq 1$, and that cycles cannot occur when $\alpha_I < \alpha_R + \epsilon\beta$.
- Thus, we have shown that the choice of recruitment and incidence functions can have an impact on global dynamics, particularly on the existence of cycles.

Future Research

- We are interested in applying our Lyapunov function to other models. In fact, it can be used to prove the global stability of the disease-free equilibrium in the original model [3].
- We would like to further examine the impact of post-infection mortality on the endemicity. We do not have a mathematical explanation for why the endemicity of each compartment responds to $\mathcal{R}_0$ in the following manner:

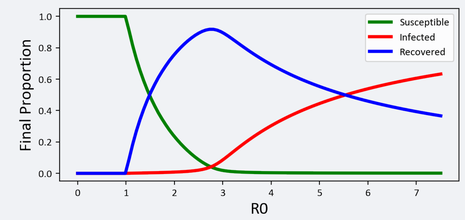

Figure 5. Final proportion of susceptible, infectious, and recovered classes with respect to $\mathcal{R}_0$

References

[1] P. van den Driessche and James Watmough, *Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission*, Mathematical Biosciences. **180** (2002), pp. 29-48, DOI 10.1016/S0025-5564(02)00108-6.

[2] J. P. LaSalle, *Some Extensions of Liapunov's Second Method*, IRE Transactions on Circuit Theory. **7** (1960), 4, pp. 520-527, DOI 10.1109/TCT.1960.1086720.

[3] Chadi M. Saad-Roy, Simon A. Levin, Bryan T. Grenfell, and Mike Books, *Epidemiological Impacts of Post-Infection Mortality*, Royal Society Proceeding B. **290** (2023), 2002, DOI 10.1098/rspb.2023.0343.

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