A Brief Study of the SIERS Model in Epidemiology

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Contents

Chapter 1

Background

1.1 Compartmental Modelling

To build an epidemiological model for a given population and a given pathogen, we may begin with compartmentalising the population on the basis of their absolute health with respect to this pathogen under study. We ignore exceptional circumstances and any behaviour on the microscopic level. Hence, broadly speaking, we wish to only study the variation of the population in each compartment with respect to an independent variable, here taken as time.

In this report, we consider exactly four components to divide the population into: Susceptible (S), Exposed (E), Infected (I), Recovered (R) and assume no vaccination.

1.2 Definitions

Susceptible Population (S): The compartment of the population not infected, but likely to catch the pathogen soon enough.

Exposed Population (E): The compartment of the population with the pathogen in their body, but for whom the symptoms haven't kicked in yet.

Infected Population (I): The compartment of the population infected and suffering due to the pathogen.

Recovered Population (R): The compartment of the population immunised against the pathogen after recovering from infection. Note that it is possible to lose immunity and become susceptible again.

1.3 Parameters

Parameter	**Comments**
μ	Natural Birth/Death Rate
α	Death Rate due to infection
β	Rate of spread of infection due to contact
γ	Rate of recovery
σ	Inverse of latency period between exposure and infection
ω	Rate of immunity loss

1.4 Assumed Mechanism of the Dynamics

1.4.1 Susceptible Population

Babies born into the population are assumed susceptible to the pathogen.

The more susceptible people exist, higher is the interaction between the infected and susceptible. So we may expect an interaction term appearing as a product of I and S.

Previously recovered people may become susceptible again.

People may just naturally die, at a rate taken to be equal to birth rate

1.4.2 Exposed Population

Susceptible people who interacted with the infected now qualify as exposed.

The exposed become infected after a brief latency period.

People may just naturally die, at a rate taken to be equal to birth rate.

1.4.3 Infected Population

The exposed qualify as infected after the latency period.

People may recover and exit this compartment.

People may just naturally die, at a rate taken to be equal to birth rate, but this time they may die due to the infection as well.

1.4.4 Recovered Population

Infected people may recover.

One may even lose immunity and become susceptible again.

People may just naturally die, at a rate taken to be equal to birth rate.

All these facts can be expressed mathematically, as shown in the next chapter.

Chapter 2

System Dynamics

2.1 Forming the Differential Equations

$$\frac{dS}{dt} = \mu N - \beta \frac{IS}{N} + \omega R - \mu S$$

$$\frac{dE}{dt} = \beta \frac{IS}{N} - \sigma E - \mu E$$

$$\frac{dI}{dt} = \sigma E - \gamma I - \mu I - \alpha I$$

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

Observe that we have simply translated the mechanism in the previous chapter to a system of ordinary differential equations using the parameters we defined in the table earlier, with N being the total population number at any given time.

2.2 Conversion to Population Fractions

Instead of working with absolute population numbers let's divide by N and work with population fractions s, e, i and r. So the ODEs now look like:

$$\frac{ds}{dt} = \mu - \beta is + \omega r - \mu s$$

$$\frac{de}{dt} = \beta is - \sigma e - \mu e$$

$$\frac{di}{dt} = \sigma e - \gamma i - \mu i - \alpha i$$

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

2.3 Analysis

Analysing a 4-dimensional ODE system is not as straightforward. Since there is no obvious constant of dynamics or symmetry, we could not find a change of variables to reduce dimensions. Hence what follows is a very basic analysis.

Firstly, why is total population not a constant of dynamics (because usually it is)? The answer is easily observed if one sums up all the ODEs to obtain:

$$\frac{dn}{dt} = -\alpha i$$

This suggests that if we take the limit of

$$\frac{\alpha}{\mu} << 1$$

then we may reduce dimensions to 3 (from 4).

Let's find the fixed points of this system. Recall that these are found by setting each derivative to 0 and solving the corresponding equations we get. After a little algebra, we get

$$s^* = \frac{1}{R_0}$$

$$e^* = \frac{\beta R_0}{\sigma + \mu}\mu(1 - R_0)\frac{\omega + \mu}{\omega\gamma R_0 - \beta(\omega + \mu)}$$

$$i^* = \mu(1 - R_0)\frac{\omega + \mu}{\omega\gamma R_0 - \beta(\omega + \mu)}$$

$$r^* = \frac{\gamma}{\omega + \mu}\mu(1 - R_0)\frac{\omega + \mu}{\omega\gamma R_0 - \beta(\omega + \mu)}$$

where the basic reproduction number R_0 is defined as

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

If $R_0 > 1$, the epidemic expands else it dies out soon enough. The above ODEs can be suitably solved once we fix our set of parameters.

Chapter 3

Coding it up in Julia

3.1 Epidemic 1: No Deaths

```
using DifferentialEquations
using Plots

function seirs!(du, u, p, t)
    du[1] = μ-β*u[3]*u[1]+ω*u[4]-μ*u[1]
    du[2] = β*u[3]*u[1]-σ*u[2]-μ*u[2]
    du[3] = σ*u[2]-γ*u[3]-(μ+α)*u[3]
    du[4] = γ*u[3]-ω*u[4]-μ*u[4]
    nothing
end

μ=0.013/365
α=0
β=0.214
ω=1/365
σ=0.143
γ=0.071

u0 = [0.4; 0.1; 0.2; 0.3]
tspan = (0.0, 1000.0)
prob = ODEProblem(seirs!, u0, tspan)
sol = solve(prob);

plot(sol, idxs=[1,2,3,4], xlabel="Time", ylabel="Population", label=["s(t)" "e(t)" "i(t)" "r(t)"])
```

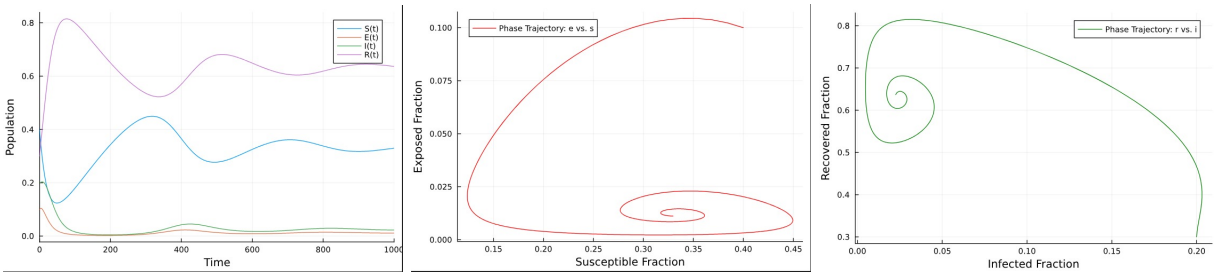

Figure 3.1: (a) s, e, i, r vs. time; (b) e vs. s; (c) r vs. i

The above code in Julia is a straightforward implementation of Julia's DifferentialEquations package. The parameters chosen [1] are typical for a pathogen with very low death rate (taken to be 0 here). Observe how the phase trajectories exhibit limit cycles in general. Let's also try to find the fixed points from 2.3 and verify that they agree with the graphs above.

$$s^* = \frac{1}{R_0} = 0.332025$$

$$e^* = \frac{\beta R_0}{\sigma + \mu}\mu(1 - R_0)\frac{\omega + \mu}{\omega\gamma R_0 - \beta(\omega + \mu)} = 0.0122536$$

$$i^* = \mu(1 - R_0)\frac{\omega + \mu}{\omega\gamma R_0 - \beta(\omega + \mu)} = 0.0246675$$

$$r^* = \frac{\gamma}{\omega + \mu}\mu(1 - R_0)\frac{\omega + \mu}{\omega\gamma R_0 - \beta(\omega + \mu)} = 0.631054$$

With $s^* + e^* + i^* + r^* = 1$ as expected since α is 0. Note that the graphs shown end up spiralling to the numbers we found just above. The R_0 value here is approximately 3 (one person spreads the pathogen to 3 other people on average).

3.2 Epidemic 2: Diminished Population

Chapter 4

Conclusion

4.1

Chapter 5

Bibliography

[1] Bjørnstad, O.N., Shea, K., Krzywinski, M. et al. The SEIRS model for infectious disease dynamics. Nat Methods 17, 557–558 (2020). https://doi.org/10.1038/s41592-020-0856-2

[2] Libkind Sophie, Baas Andrew, Halter Micah, Patterson Evan and Fairbanks James P..2022 An algebraic framework for structured epidemic modelling. Phil. Trans. R. Soc. A. 380:20210309