

SIR Model: Puffer's Disease

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Why'd we choose the SIR Model (ODE Edition)

- Keep it simple stupid!
 - Leaves room for creativity
 - Plenty of background knowledge on SIR model
 - Allows us to change more parameters and experiment more
 - Make a simple model more complicated (not fun, but cool to mess around with)
 - Can work the hardest on a topic well known
- Interesting topic
 - Studying effects of steepness of negative feedback loops
 - Too much ecology in LS 7B, gotta switch things up



How'd we come up with Puffer's Disease?

- 1) Met up together and chose the SIR model (reasons discussed previously)
- 2) Added a new state variable (infectious but not symptomatic)
- 3) Came up with a cool name for the disease
- 4) Wanted to incorporate other aspects real life diseases into our model
 - a) Incorporated a vaccine
 - b) Used parameters that have values according to real life
 - i) Susceptible people have a 2% chance more of becoming infected from symptomatic individuals than asymptomatic individuals
 - ii) Individuals will always be asymptomatic before they become symptomatic
- 5) Made the flow diagram, model assumptions, and parameters accordingly



Puffer's Disease Model

In epidemiology, a common way to model the spread of an infectious disease called Puffers Disease is to track the number of susceptible individuals (S), the number of individuals of those who are infectious but not yet symptomatic (N), the number of currently infected and symptomatic individuals (I), and the number of individuals who have recovered from the disease with immunity (M). (All rates listed below are per day rates)

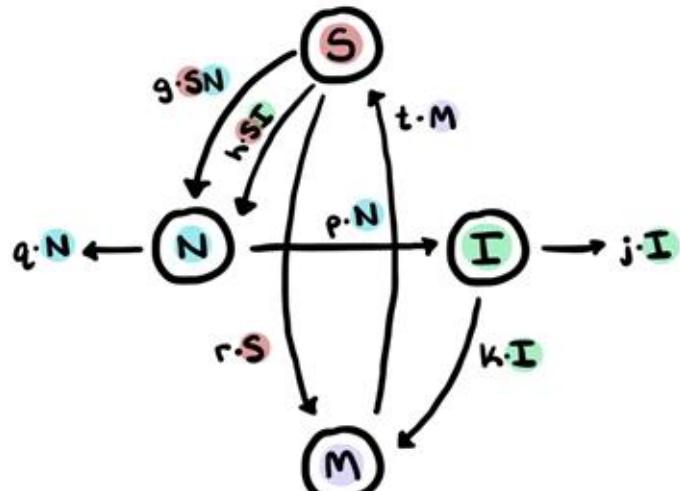


Puffer's Disease Parameters and Assumptions

- Susceptible people become infected in 3% of encounters with asymptomatic individuals.
 - Parameter g: Per capita rate at which susceptible people become infected with encounters with asymptomatic individuals
- 7% of encounters between susceptible and infected and symptomatic individuals result in new infections.
 - Parameter h: per capita rate at which susceptible and infected+symptomatic individuals result in people becoming infected
- Infected and symptomatic people die at a per capita rate of 0.0005.
 - Parameter j: per capita death rate of infected and symptomatic individuals
- Infected and symptomatic people recover at a per capita rate of 0.5
 - Parameter k: per capita recovery rate of infected and symptomatic people
- When people recover they become immune to the disease
- Newly infected individuals do not immediately exhibit symptoms and are initially asymptomatic. (meaning: All susceptible individuals that become infected will become infectious but not symptomatic before passing away or becoming infectious and symptomatic)
- Asymptomatic infected individuals begin to exhibit symptoms after a 4 day period. In other words, 25% of the asymptomatic individuals become symptomatic each day.
 - Parameter p: rate at which asymptomatic individuals become symptomatic
- Newly infected asymptomatic individuals die at a per capita rate of .0001
 - Parameter q: per capita death rate of newly infected asymptomatic individuals
- Susceptible people can gain immunity by getting vaccinated. The per capita rate at which susceptible people choose to get vaccinated occurs at 0.07
 - Parameter r: per capita rate of susceptible individuals getting vaccinated
- People immune to the disease through vaccination or exposure both gradually lose their immunity over the course of 6 months; in other words, the per capita rate of immune (M) individuals becoming susceptible again is about .006
 - Parameter t: per capita rate of immune individuals becoming susceptible again



Flow Diagram



$$\begin{aligned}S' &= tM - gSN - hSI - rS \\N' &= gSN + hSI - qN - \rho N \\M' &= rS + kI - tM \\I' &= \rho N - kI - jI\end{aligned}$$

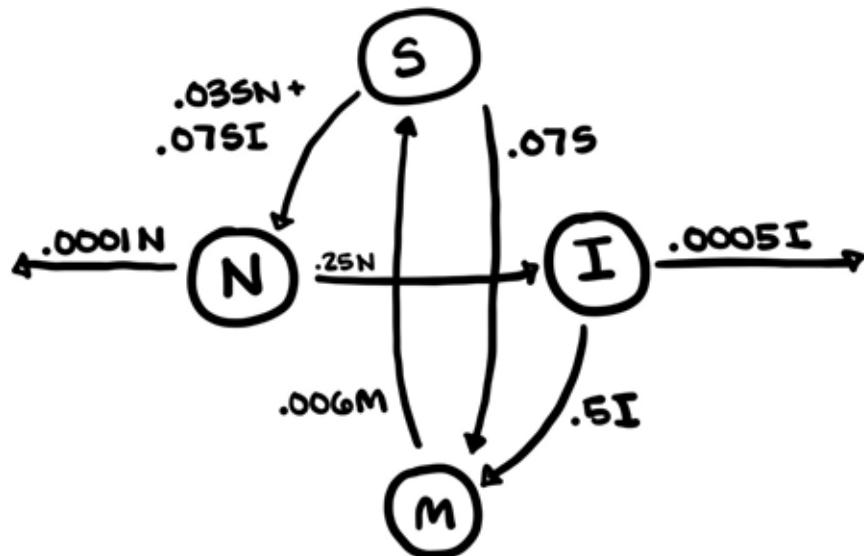
ODE equations with specified numbers:

$$S' = 0.006M - .03SN - .07SI - 0.7S$$

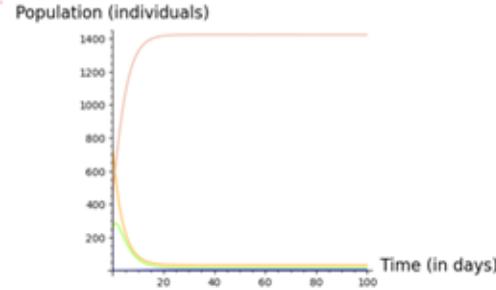
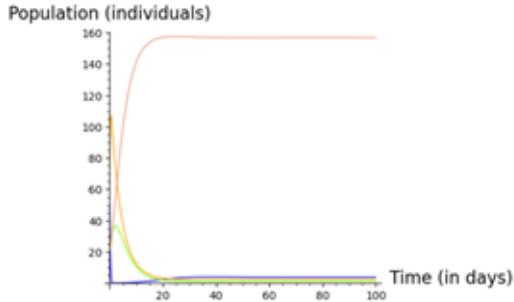
$$N' = .03SN + .07SI - .25N - 0.001N$$

$$I' = .25N - 0.0005I - .5I$$

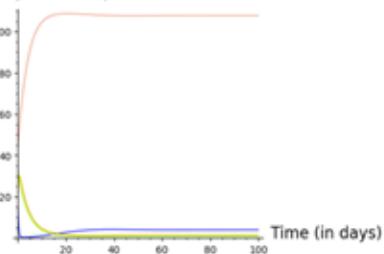
$$M' = .07S + .5I - .006M$$



Simulations: Differing initial conditions



- Dark Salmon: Immune
 - Orange: Infected but not symptomatic
 - Chartreuse: Infected and symptomatic
 - Blue: Susceptible



Simulations: Differing Parameter Values





Simulation Observations

- Changing parameter values changes the relative proportions of each group in the model but the end behavior remains a constant value (all populations approach a constant value over time).
- Changing initial conditions changes the population values of each group in the model but the graph remains the same otherwise. In the long run, the immune group represents the majority of the population.
- No oscillations because our system of equations does not have steep enough negative feedback loop that would add oscillations to our graphs



Stability Analysis: Equilibria

```
In [4]: var("S","N","I","M")
S_prime= 0.006*M-.03*S*N-.07*S*I-.7*S
N_prime=.03*S*N+.07*S*I-.25*N-.001*N
I_prime=0.25*N-.0005*I-.5*I
M_prime=.07*S+.5*I-.006*M
sol = solve([S_prime==0,N_prime==0,I_prime==0,M_prime==0],(S,N,I,M))
show(sol)
```

Out[4]:

$$\left[[S = 0, N = 0, I = 0, M = 0], \left[S = \left(\frac{35893}{9290} \right), N = \left(-\frac{251502251}{129131} \right), I = \left(-\frac{125625500}{129131} \right), M = \left(-\frac{20925942037}{258262} \right) \right] \right]$$

Note: Only the equilibrium point (0,0,0,0) is viable when taking into account biological significance as the other equilibrium point requires negative population values.



Stability Analysis: Finding Eigenvalues



In [28]:

```
e = jp.eigenvalues()[0].n()
f = jp.eigenvalues()[1].n()
g = jp.eigenvalues()[2].n()
h = jp.eigenvalues()[3].n()
print(e)
print(f)
print(g)
print(h)
```

Out[28]:

```
-0.700604660498101
-0.00539533950189902
-0.5005000000000000
-0.2510000000000000
```

```
a = jw.eigenvalues()[0].n()
b = jw.eigenvalues()[1].n()
c = jw.eigenvalues()[2].n()
d = jw.eigenvalues()[3].n()
print(a)
print(b)
print(c)
print(d)

-0.493690658233948 - 2.47237963497601e-13*I
-0.264732791921670 + 2.45423245827562e-13*I
-0.0000288484236889985 + 1.36221592172362e-15*I
125.946141377886 + 4.52501748315739e-16*I
```



Stability Analysis: Eigenvalues continued

Each of the eigenvalues associated with the point (0,0,0,0) are less than 0, indicating that the equilibrium point of the model at (0,0,0,0) is stable.

In the case of the eigenvalues for the point

$$\left[S = \begin{pmatrix} 35893 \\ 9290 \end{pmatrix}, N = \begin{pmatrix} -251502251 \\ 129131 \end{pmatrix}, I = \begin{pmatrix} -125625500 \\ 129131 \end{pmatrix}, M = \begin{pmatrix} -20925942037 \\ 258262 \end{pmatrix} \right]$$

3 of the eigenvalues contain a positive real part of the complex eigenvalue while 1 of the eigenvalues has a negative real part of the complex eigenvalue. This implies that the equilibrium point has a stability most similar to that of an unstable spiral.