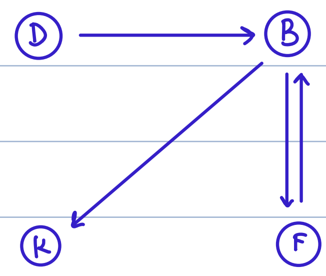
Anushka Sinha

02712 | PS4

11/09/23

1. a.



State set:

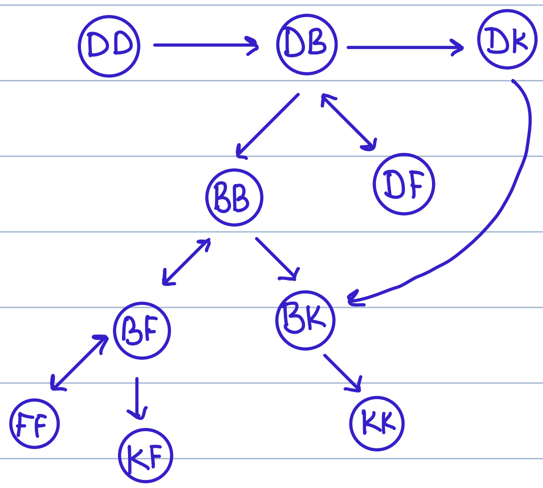
D: digestive tract

B: bloodstream

F: fat

K: kidney

b.

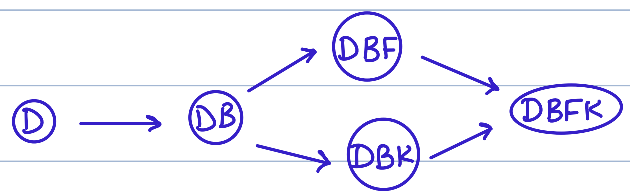


State Set:

DD, DB, DK, DF, BB, BF, BK, KK, FF, KF

Each set represents movement of molecule 1 and molecule 2.

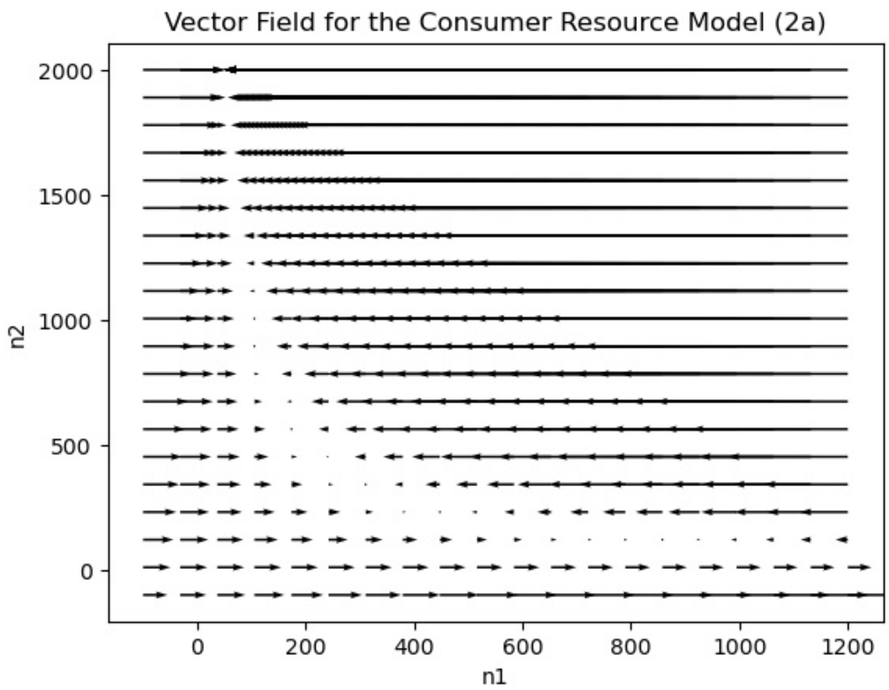
c.



State set:

D, DB, DBF, DBK, DBFK

2. a.



b.

$$\frac{dn_1}{dt} = \theta - acn_1n_2 = 0$$

$$1000 - 1 \times 0.01 \times n_1 \times n_2 = 0$$

$$1000 - 0.01 n_1 n_2 = 0$$

$$0.01 n_1 n_2 = 1000$$

$$n_1 n_2 = \frac{1000}{0.01} = 100,000$$

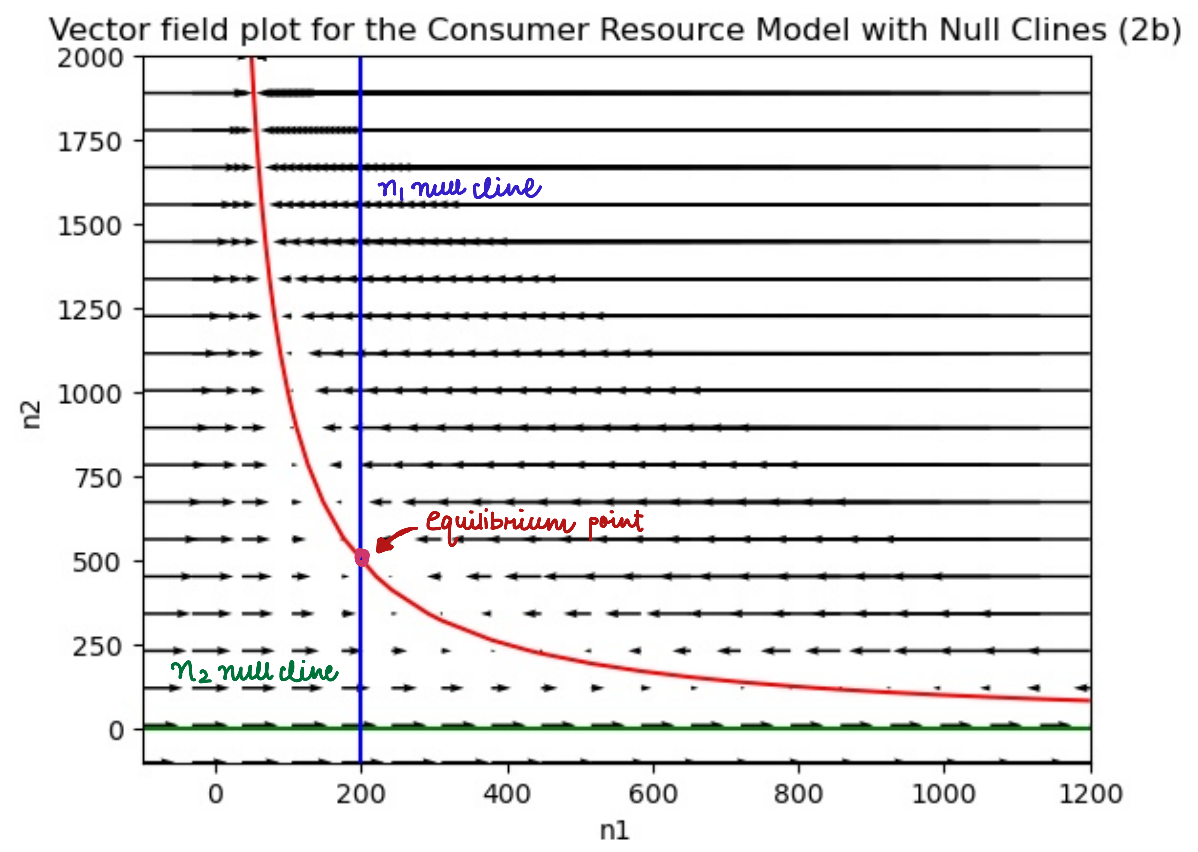
$$\frac{dn_2}{dt} = \epsilon acn_1n_2 - \gamma n_2 = 0$$

$$(0.0005)(1)(0.01) n_1 n_2 - (0.001) n_2 = 0$$

$$0.000005 n_1 n_2 - 0.001 n_2 = 0$$

$$n_2 (0.000005 n_1 - 0.001) = 0$$

$$n_2 = 0 \qquad n_1 = 0.001 / 0.000005 = 200$$

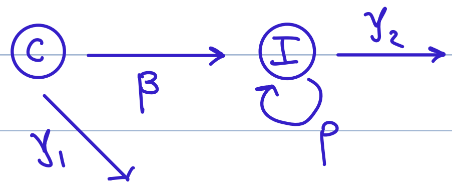


(c) Based on the plot above, we observe that the system move towards the equilibrium when the null clines (n_1 and n_2) intersect.

This implies that the resources and consumers will reach a stable point given the model parameters.

However, since vector field provides more of a qualitative analysis, we cannot make any definite conclusions about whether the system will be pushed to equilibrium or not. Additionally, vector field plots are heavily influenced by different initial states which makes it more unreliable for making such predictions.

③



Equation form:

$$\frac{dC}{dt} = (-\beta - \gamma_1)C$$

$$\frac{dI}{dt} = \beta C + pI - \gamma_2 I = \beta C + I(p - \gamma_2)$$

Vector form

$$\begin{pmatrix} \frac{dC}{dt} \\ \frac{dI}{dt} \end{pmatrix} = \begin{bmatrix} -\beta-\gamma_1 & 0 \\ \beta & p-\gamma_2 \end{bmatrix} \begin{bmatrix} C \\ I \end{bmatrix}$$

Equilibria of the system: $\frac{dC}{dt} = 0$, $\frac{dI}{dt} = 0$

$$\Rightarrow \quad 0 = (-\beta - \gamma_1)C^*$$

$$\Rightarrow \quad C^* = 0 \text{ is a solution}$$

$$\Rightarrow \quad 0 = \beta C + I^*(p - \gamma_2)$$

$$\Rightarrow \quad 0 = \beta(0) + I^*(p - \gamma_2)$$

$$\Rightarrow \quad I^* = \frac{0}{(p-\gamma_2)} = 0$$

Stability Analysis: Jacobian

$$J = \begin{bmatrix} \frac{\partial}{\partial C}((-\beta-\gamma_1)C) & \frac{\partial}{\partial I}((-\beta-\gamma_1)C) \\ \frac{\partial}{\partial C}(\beta C - \gamma_2 I + pI) & \frac{\partial}{\partial I}(\beta C - \gamma_2 I + pI) \end{bmatrix}$$

$$J = \begin{bmatrix} -\beta-\gamma_1 & 0 \\ \beta & \rho-\gamma_2 \end{bmatrix}$$

From J, $r_1 = -\beta-\gamma_1$ $\quad r_2 = \rho-\gamma_2$

Since the question says parameters are always positive, the first eigenvalue r_1 will always be negative. Therefore, only the sign of r_2 will determine the stability of the equilibrium.

When $\frac{\rho}{\gamma_2} > 1$, the equilibrium will be unstable since that will make $r_2 > 0$. Therefore, the growth rate (ρ) in the organ must be larger than the death rate (γ_2) in the organ and so the tumor will grow.

When $\frac{\rho}{\gamma_2} < 1$, the equilibrium will be stable since that will make $r_2 < 0$ as well. Therefore, the growth rate (ρ) in the organ must be smaller than the death rate (γ_2) in the organ and so the tumor will disappear.

4. a.

$$S \xrightarrow{\lambda_1 IS/N} I \xrightarrow{\lambda_2 I} R$$

States: $S \longrightarrow$ susceptible population

$I \longrightarrow$ infected population

$R \longrightarrow$ dead population

Rate equations: $$\frac{dS}{dt} = -\lambda_1 I \frac{S}{N}$$

$$\frac{dI}{dt} = \lambda_1 I \frac{S}{N} - \lambda_2 I$$

$$\frac{dR}{dt} = \lambda_2 I$$

CTMM: $$p_{ij}(t) = Pr\{q(t) = q_j \mid q(0) = q_i\}$$

$$p_{SI}(t) = Pr\{q(s+t) = I \mid q(s) = S\} \quad \forall\ s > 0$$

$$p_{IR}(t) = Pr\{q(s+t) = R \mid q(s) = I\} \quad \forall\ s > 0$$

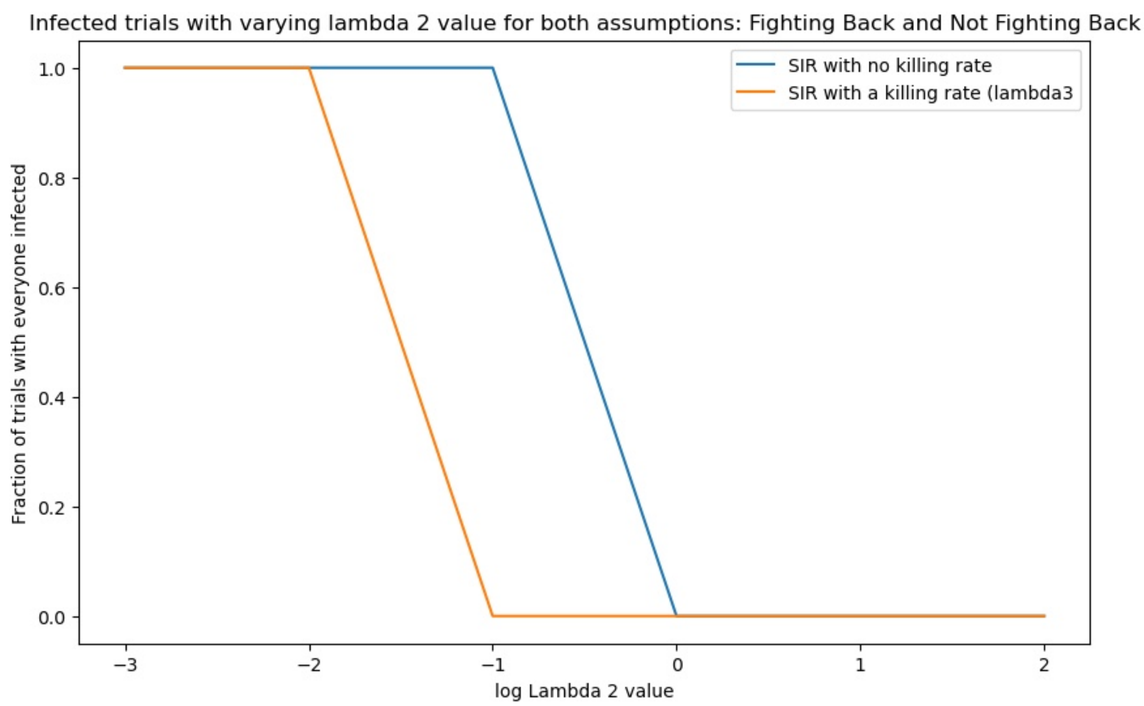
(b)

```
def function():
    while I > 0:
        infection_rate = λ1 I S/N
        death_rate = λ2 I
        t_infection = exp(infection_rate)
        t_death = exp(death_rate)
        if t_death < t_infection:
            I -= 1
            R += 1
        else:
            S -= 1
            I += 1
    return (S, I, R)
```

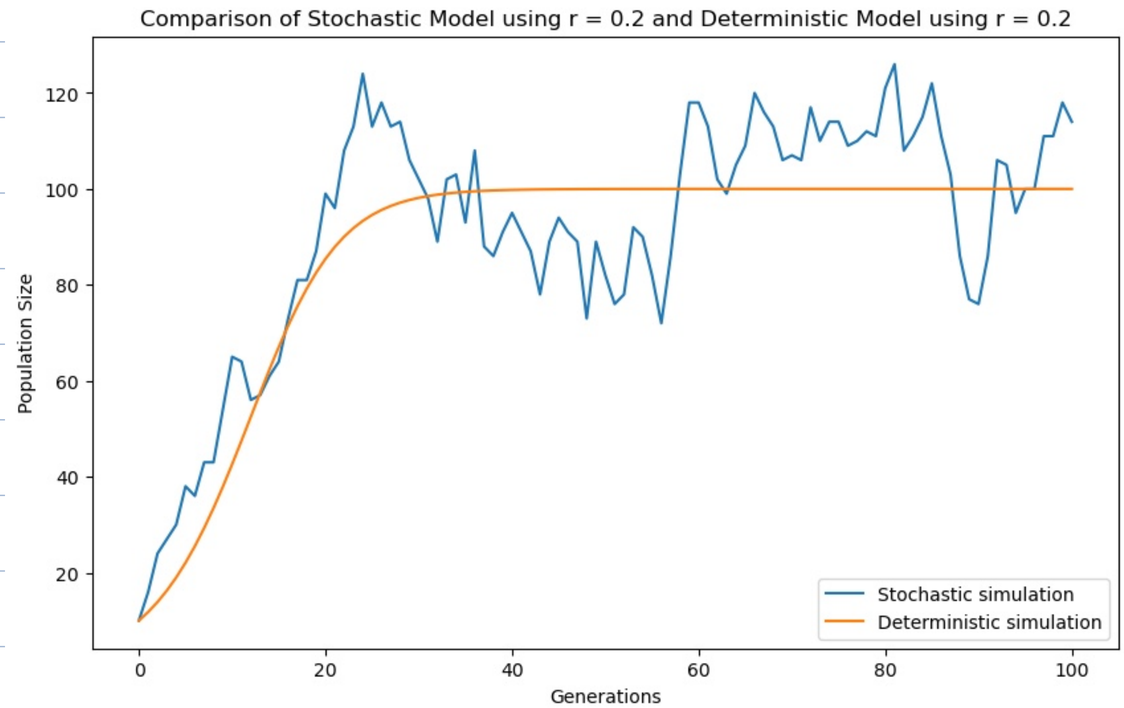
(c)

```
def function():
    while I > 0:
        infection_rate = λ1 I S/N
        death_rate = λ2 I + λ3 S/(S+I+R)
        t_infection = exp(infection_rate)
        t_death = exp(death_rate)
        if t_death < t_infection:
            I -= 1
            R += 1
        else:
            S -= 1
            I += 1
    return (S, I, R)
```

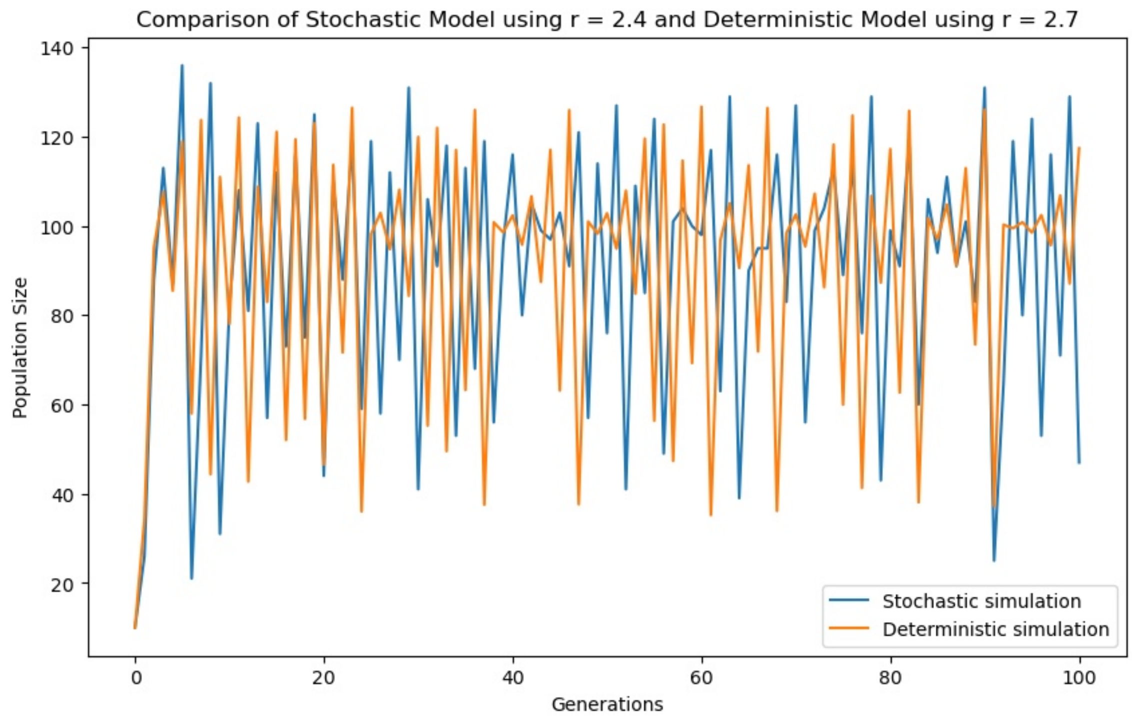
d. e. Jupyter notebook



f. I would conclude that fighting back against zombies sometimes helpful. Fighting back is sometimes helpful because the rate of fighting back gets added towards the death rate of zombies. Based on the graph, we can observe that fighting back leads to a drop in fraction of trials with everyone infected when $\lambda_2 \geq 0.1$, which is intuitive because it's causing more zombies death to occur bringing down the number of infections. When the number of zombies is increasing at a higher rate (low λ_2), the ability to fight off zombies decreases because number of humans decreases rapidly. And, when the natural death rate is already high (high λ_2), the effort of fighting back does not make a difference. Fighting back only has a significant impact when there are enough healthy people to fight and the natural death rate (λ_2) is not too high or too low.



Comparison of Stochastic Model using r = 0.2 and Deterministic Model using r = 0.2
Population Size
Generations
Stochastic simulation
Deterministic simulation



Comparison of Stochastic Model using r = 2.4 and Deterministic Model using r = 2.7
Population Size
Generations
Stochastic simulation
Deterministic simulation

In the 1st plot with $r = 0.2$, there is a significant difference between the observed trajectory of the deterministic and stochastic models of logistic growth. The deterministic logistic growth shows a smooth increase and then plateaus around the carrying capacity and therefore displays a sigmoidal curve. However, the stochastic model shows a lot of fluctuations around the deterministic curve, therefore displaying impacts of random poisson distributed births and deaths.

In the 2nd plot, both deterministic and stochastic models of logistic growth display similar fluctuations and oscillatory behavior which makes it difficult to infer which trajectory on the graph represents a deterministic or a stochastic model. From these two plots, we can infer that the value of r influences the trajectory of deterministic model. When $r = 0.2$, the deterministic model displays an expected trajectory. However, as the r increases, we observe deterministic chaos where a deterministic model displays fluctuations and oscillatory behavior like the stochastic model.