Assignment 4

Continuous Field Models

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Prey-Predator Model

The requirements for the model gives us the following system of PDEs

$$\partial_t u - u(1-u) + \frac{uv}{u+\alpha} - \delta_1 \Delta u = 0 \tag{1}$$

$$\partial_t v - \gamma v - \beta \frac{uv}{u+\alpha} - \delta_2 \Delta v = 0 \tag{2}$$

$$\tag{3}$$

Where u is the population of the prey and v the predator population. The time derivatives determines the rate of growth for the populations over time. The Second terms for of respective equations 1 2 says that where there are a population of species, more of that species will be born: Reproduction. The terms involving both u and v represents the encounter between the two species. The encounter results in a decrease of the prey and an increase of the predators, at a rate determined by the parameters α and β. The diffusion term makes the populations spread out to places where populations are smaller.

To make a model out of this system of PDEs, we discretize each term

$$\frac{\partial u}{\partial t} \approx \frac{u_{t+1} - u_t}{\Delta t} \tag{4}$$

and apply an eight point stencil

$$\begin{aligned} \nabla^2 u \approx \nabla_d^2 = {} & u(x+1,y) + u(x-1,y) \\ & + u(1,y+1) + u(x,y-1) \\ & + u(x-1,y-1) + u(x-1,y+1) \\ & + u(x+1,y-1) + u(x+1,y+1). \end{aligned} \tag{5}$$

-1	-1	-1
-1	8	-1
-1	-1	-1

Figure 1: The visualized stencil in Equation 5

The discretized Laplacian stencil is easier to understand as a kernel as depicted in Figure 1 sweeping across the 2D domain.

The accuracy of the approximation increases with the kernel size and the weights can be looked up under the topic of finite differences. The same approximations goes for v. With these discretizations in mind, we can determine the state-variables for the future time step $t+1$ as a function of the states at the current time t. Because the discretized Laplacian is a rather long expression, it will be refered to as ∇_d^2, with the subscript d standing for discrete. For more details regarding our implementation, see the attached code.

$$u_{t+1} = u_t + \left(u_t(1-u_t) - \frac{u_t v_t}{u_t + \alpha} + \delta_1 \nabla_d^2 u_t \right) \Delta t \tag{6}$$

$$v_{t+1} = v_t + \left(-\gamma v_t + \beta \frac{u_t v_t}{u_t + \alpha} + \delta_2 \nabla_d^2 v_t \right) \Delta t \tag{7}$$

$$\tag{8}$$

The implementation of the model in python has the following parameters

$$\delta_1 = 1 \qquad \delta_2 = 1 \tag{9}$$

$$\alpha = 0.4 \qquad \beta = 1. \qquad \gamma = 0.5 \tag{10}$$

$$\Delta t = 0.001 \qquad \Delta k = 0.1 \tag{11}$$

uniformly random initial conditions

$$u_0(x, y) \sim 0.5 \times (1 - U(0, 1))$$
$$v_0(x, y) \sim 0.25 + 0.5 \times U(0, 1)$$

Running the simulation we observe clear oscillatory behaviour and the populations of the two species seem to stabilize as time progresses, see figure 2. The oscillatory convergence of the system towards approximately $u = 100$, $v = 120$ ca be seen more clearly in the phase space plot at the bottom of the figure 2. The simulation took a long time and therefore the simulation was not run until a convergence was close to completion. For visuals, which is always helpful, please see figure 3 with the above specified initial condition and periodic boundary conditions in x and y direction.

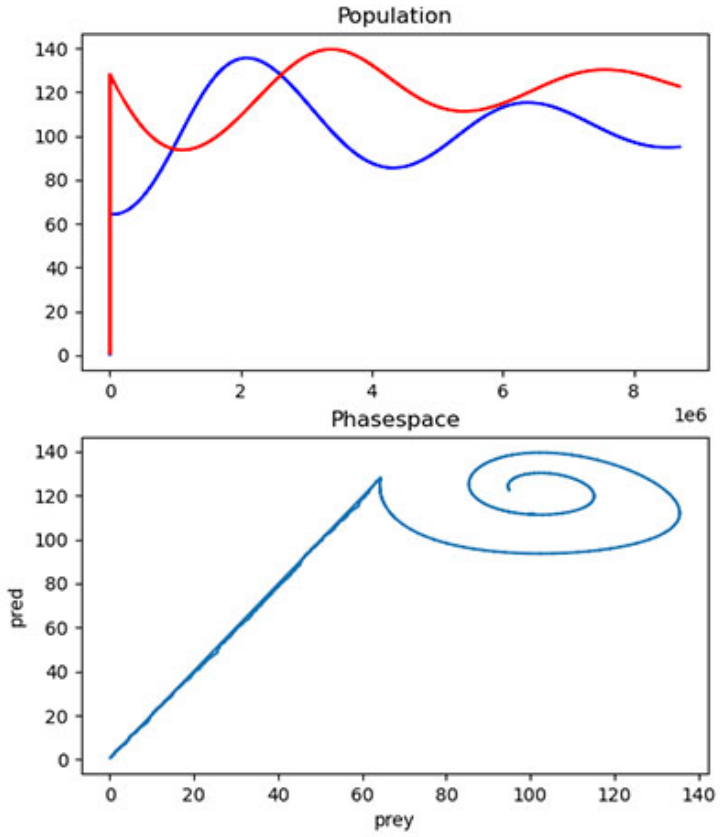

Figure 2: The total populations of the species and the corresponding phase space. Predators are represented by the variable v and its population curve is red. Prey is u and its population curve is blue

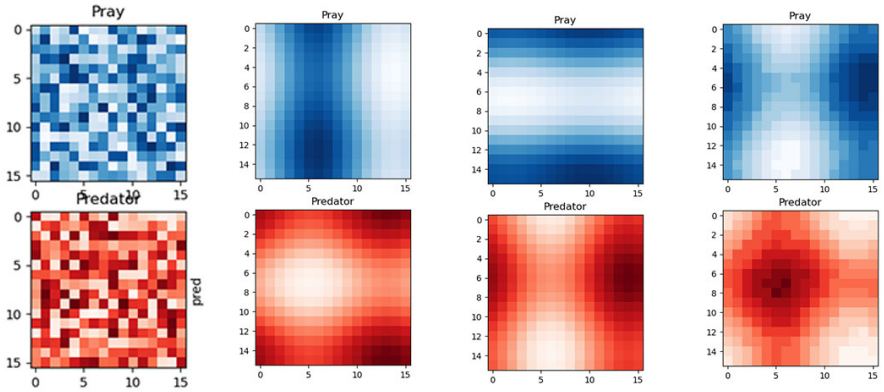

Figure 3: The 2-D spatial distribution of the simulation at 4 different time steps

Diffusive SIR model

The SIR-model is a popular model of epidemiological dynamics. It models the spread through the number of susceptible S, infected I, and the number of recovered and immune R, and the transfer rates between them. It is defined according to the system below:

$$\begin{aligned}\frac{dS}{dt} &= -aSI \\ \frac{dI}{dt} &= aSI - bI \\ \frac{dR}{dt} &= bI\end{aligned}$$

where $a,\ b,\ c \in \mathbb{R} > 0$. This standard model does not include any spatial components, but by introducing diffusion terms we can introduce a way of modeling how people move and spread the disease from one area to another. With added diffusion terms, the basic SIR-model transforms into:

$$\begin{aligned}\frac{dS}{dt} &= -aSI + \chi_S \nabla^2 S \\ \frac{dI}{dt} &= aSI - bI + \chi_I \nabla^2 I \\ \frac{dR}{dt} &= bI + \chi_R \nabla^2 R\end{aligned}$$

where once again $\chi_S,\ \chi_I,\ \chi_R \in \mathbb{R} > 0$. As in the first section, we use the stencil from equation 5 to discretize the Laplacian. For the simulation, we used values of $a = 1$, $b = 0.3$, $\chi_S = \chi_I = \chi_R = 0.3$. Results for how the disease spreads is seen in Figure 4. In this experiment, we start out with two infections as seen in the top figure, which eventually spreads to infect the entire population as time goes on, as seen in the plot for the total population dynamics shown in Figure 5. Note that the number of susceptible people at time step 0 is 1 for the whole grid, and the number of infected/recovered is 0 (except the two infection points).

For a more realistic scenario, χ_R would likely be lower than χ_S, as infected people are more likely to move around less.

Find all homogeneous equilibrium states

To find homogenous equilibrium states we replace $(S,\ I,\ R)$ with $(S_{eq},\ I_{eq},\ R_{eq})$. This means that all derivatives, both temporal and spatial, become 0. This gives us:

$$\begin{aligned} \frac{dS}{dt} &= -aSI + \chi_S \triangle S & & 0 = -aS_{eq}I_{eq} \\ \frac{dI}{dt} &= aSI - bI + \chi_I \triangle I & \Rightarrow \qquad & 0 = aS_{eq}I_{eq} - bI_{eq} \\ \frac{dR}{dt} &= bI + \chi_R \triangle R & & 0 = bI_{eq} \end{aligned}$$

For $a,\ b,\ c \neq 0$, we see that $I_{eq} = 0$ from the third equation, making all other equations 0 as well. Thus, $S_{eq},\ R_{eq}$ can take any value for homogeneous equilibrium states.

Examine the stability of the homogeneous equilibrium state without diffusion terms.

The Jacobian $\mathcal{J}$ for this system without the diffusion terms is

$$\mathcal{J}(S,I,R) = \begin{bmatrix} \frac{d}{dS}\frac{dS}{dt} & \frac{d}{dI}\frac{dS}{dt} & \frac{d}{dR}\frac{dS}{dt} \\ \frac{d}{dS}\frac{dI}{dt} & \frac{d}{dI}\frac{dI}{dt} & \frac{d}{dR}\frac{dI}{dt} \\ \frac{d}{dS}\frac{dR}{dt} & \frac{d}{dI}\frac{dR}{dt} & \frac{d}{dR}\frac{dR}{dt} \end{bmatrix} = \begin{bmatrix} -aI & -aS & 0 \\ aI & aS - b & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

Since $I = 0$ at all equilibrium points, we have

$$\mathcal{J}_{eq}(S_{eq}, I_{eq} = 0, R_{eq}) = \begin{bmatrix} 0 & -aS_{eq} & 0 \\ 0 & aS_{eq} - b & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

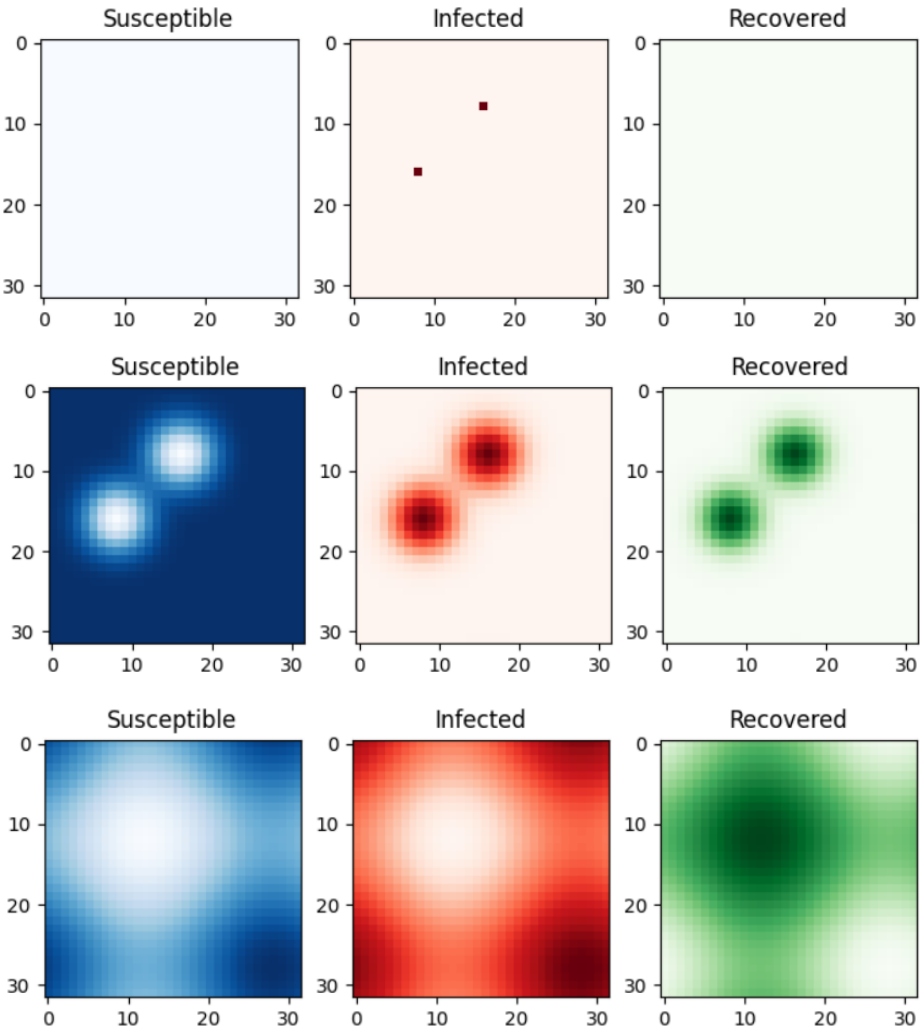

Figure 4: The spatial distributions of susceptible, infected, and recovered people at 3 different time steps.

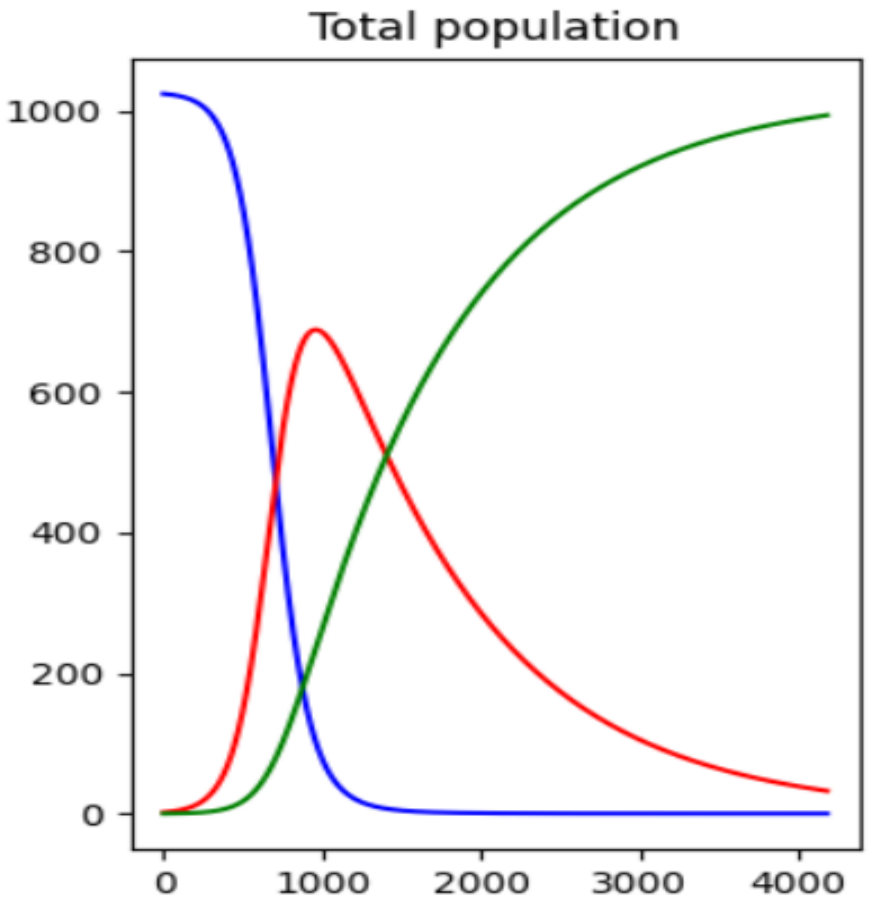

Figure 5: The rates of susceptible (blue), infected (red), and recovered (green) populations as a function of time.

Solving for the eigenvalues of this system, we get $\lambda_{1,2} = 0,\ \lambda_3 = aS_{eq} - b$. Thus, if $S_{eq} \leq \frac{b}{a}$, we may have Lyupunov stability, else its is likely an unstable saddle point. This means that if this condition if true, a large outbreak is impossible in this model since any infected people recover faster than they infect others.

Linear Stability Analysis

As per the lecture notes for linear stability analysis of Reaction-Diffusion systems, by looking at the matrix

$$\mathcal{J} - \omega^2 \vec{\chi} I = \begin{bmatrix} -aI & -aS & 0 \\ aI & aS - b & 0 \\ 0 & 0 & 0 \end{bmatrix} - \omega^2 \begin{bmatrix} \chi_S & 0 & 0 \\ 0 & \chi_I & 0 \\ 0 & 0 & \chi_R \end{bmatrix} = \begin{bmatrix} -aI - \chi_S & -aS & 0 \\ aI & aS - b - \chi_I & 0 \\ 0 & 0 & -\chi_R \end{bmatrix}$$

we can determine the stability of the equilibrium points. For stability, we need the real part of all eigenvalues to be negative for all values of ω. At any equilibrium, $I_{eq} = 0$, meaning that we can calulate eigenvalues as

$$\det \begin{bmatrix} \lambda + \omega^2 \chi_S & aS_{eq} & 0 \\ 0 & \lambda - aS_{eq} + b + \omega 2 \chi_I & 0 \\ 0 & b & \lambda + \omega^2 \chi_R \end{bmatrix} = (\lambda + \omega^2 \chi_S)(\lambda + \omega^2 \chi_R)(\lambda - aS_{eq} + b + \omega^2 \chi_I)$$

For all eigenvalues to have a negative real part for all values of ω, we thus need that $b > aS_{eq}$ or $S_{eq} < \frac{b}{a}$ for stability. For example, if we choose $a = 0.5, b = 0.3$, any equilibrium point with density $S_{eq} > 0.6$ will be unstable.

If one looks at Figure 4, we see that a single infection will diffuse to infect the whole population for when $a = 1$, $b = 0.3$, and $S = 1$, which fulfills the conditions for an unstable equilibrium. If we however reduce a to 0.2 which should constitute a stable equilibrium point, simulations show that a local outbreak does not spread much before vanishing. This suggests that this stability condition holds in simulations.

Python Code

Code files are attached with submission.