MCMCS Summative assessment- 277227

```
import numpy as np
import matplotlib.pyplot as plt
```

Question 1

1)a)

```
#1)a)
def my_transf(A):
    # Ensure A is a NumPy array
    A = np.array(A)

    # Calculate the sum of the matrix and its transpose
    result = A + A.T

    return result

# Example usage:
# Define a matrix A
matrix_A = np.array([[1, 3, 5], [7, 9, 11], [13, 15, 17]])

# Call the function
result_matrix = my_transf(matrix_A)

# Display the result

print("Matrix A:")
print(matrix_A)

print("\nMatrix A + Aᵀ:")
print(result_matrix)
```

```
Matrix A:
[[ 1  3  5]
 [ 7  9 11]
 [13 15 17]]

Matrix A + Aᵀ:
[[ 2 10 18]
 [10 18 26]
 [18 26 34]]
```

1)b)

```
#1)b)
def dot_product_of_eigenvectors(input_matrix, index_i, index_j):
    # Ensure the input_matrix is a NumPy array
    input_matrix = np.array(input_matrix)

    # Calculate eigenvalues and eigenvectors
    eigenvalues, eigenvectors = np.linalg.eig(input_matrix)

    # Extract eigenvectors corresponding to indices index_i and
index_j
    eigenvector_i = eigenvectors[:, index_i]
    eigenvector_j = eigenvectors[:, index_j]

    # Calculate dot product of the two eigenvectors
    dot_product_result = np.dot(eigenvector_i, eigenvector_j)

    return dot_product_result

# Choose indices new_index_i and new_index_j (ensure they are valid
indices for the matrix size)
new_index_i = 0
new_index_j = 1

# Call the function with the new matrix and indices
result_new = dot_product_of_eigenvectors(matrix_A, new_index_i,
new_index_j)

# Display the result
print(f"Dot product of the {new_index_i}-th and {new_index_j}-th
eigenvectors: {result_new}")
```

```
Dot product of the 0-th and 1-th eigenvectors: -0.293689239285741
```

1)c)

```
#1)c)
import numpy as np

def my_transf(A):
    return A + np.eye(A.shape[0])

def eigprod(A, i, j):
    eigenvalues, eigenvectors = np.linalg.eig(A)
    return np.dot(eigenvectors[:, i], eigenvectors[:, j])

np.random.seed(20)
A = np.random.randn(4, 4)
```

```
print("Random Matrix A:")
print(A)

i = 1
j = 0
result1 = eigprod(my_transf(A), i, j)
print(f"\nDot product with i={i}, j={j}: {result1}")
```

```
Random Matrix A:
[[ 0.88389311  0.19586502  0.35753652 -2.34326191]
 [-1.08483259  0.55969629  0.93946935 -0.97848104]
 [ 0.50309684  0.40641447  0.32346101 -0.49341088]
 [-0.79201679 -0.84236793 -1.27950266  0.24571517]]

Dot product with i=1, j=0: -0.7356383218467829
```

1)d)

Let's analyze the given expression $\left(v_2(R)^T \cdot (R^T - R) \cdot v_3(R)\right)$.

Given the context of eigenvalues and eigenvectors, let's break down the reasons for this expression:

1. **Eigenvector Orthogonality:**
   - Eigenvectors corresponding to distinct eigenvalues of a real symmetric matrix are orthogonal to each other.
   - Let $(v_2(R))$ and $(v_3(R))$ be the eigenvectors corresponding to distinct eigenvalues $(\lambda_2(R))$ and $(\lambda_3(R))$, respectively.
   - The transpose of $(v_2(R))$ is denoted as $(v_2(R)^T)$.
   - Since $(\lambda_2(R))$ and $(\lambda_3(R))$ are distinct, $(v_2(R))$ and $(v_3(R))$ are orthogonal.
2. **Properties of Symmetric Matrices:**
   - If (R) is a real symmetric matrix, then $(R^T = R)$.
   - Therefore, $((R^T - R))$ is a zero matrix.

Now, let's analyze the expression:

$$\left[v_2(R)^T \cdot (R^T - R) \cdot v_3(R)\right)$$

- Due to the orthogonality of $(v_2(R))$ and $(v_3(R))$, the product $(v_2(R)^T \cdot v_3(R))$ is zero, as the dot product of orthogonal vectors is zero.

- Additionally, since $((R^T - R))$ is a zero matrix for symmetric matrices, the entire expression evaluates to zero.

Therefore, the key observation here is that the given expression is zero, which can be attributed to the orthogonality of eigenvectors corresponding to distinct eigenvalues and the properties of symmetric matrices.

1)e)

To explore whether the eigenvectors of $(\text{my\_transf}(A))$ are linearly dependent, let's denote the eigenvectors of $(\text{my\_transf}(A))$ as $(v_1, v_2, \dots, v_n)$, corresponding to the eigenvalues $(\lambda_1, \lambda_2, \dots, \lambda_n)$.

Given that $(\text{my\_transf}(A) = A + I)$, where (I) is the identity matrix, the eigenvalues $(\lambda_i(\text{my\_transf}(A)))$ are simply $(\lambda_i(A) + 1)$ because adding the identity matrix to (A) shifts all eigenvalues by 1.

Now, let $(v_i(\text{my\_transf}(A)))$ be the eigenvector of $(\text{my\_transf}(A))$ corresponding to $(\lambda_i(\text{my\_transf}(A)))$.

If $(v_1(\text{my\_transf}(A)))$ is linearly dependent on $(\{v_2(\text{my\_transf}(A)), \dots, v_n(\text{my\_transf}(A))\})$, it means we can express $(v_1(\text{my\_transf}(A)))$ as a weighted sum of $(\{v_2(\text{my\_transf}(A)), \dots, v_n(\text{my\_transf}(A))\})$, i.e.,

$$\left[v_1(\text{my\_transf}(A)) = \sum_{k=2}^{n} a_k \cdot v_k(\text{my\_transf}(A))\right)$$

Now, let's take the dot product of both sides with $(v_j(\text{my\_transf}(A)))$ ¿ is any index from 2 to (n) ¿ :

$$\left[\langle v_1(\text{my\_transf}(A)), v_j(\text{my\_transf}(A))\rangle = \sum_{k=2}^{n} a_k \cdot \langle v_k(\text{my\_transf}(A)), v_j(\text{my\_transf}(A))\rangle\right)$$

The left side is $(\delta_{1j} \cdot \| v_1(\text{my\_transf}(A)) \|^2)$, and the right side involves dot products of eigenvectors with distinct indices. If $(v_1(\text{my\_transf}(A)))$ is linearly dependent on the other eigenvectors, this dot product will not be zero for any (j). Otherwise, if $(v_1(\text{my\_transf}(A)))$ is linearly independent, this dot product will be zero for $(j \neq 1)$.

1)f)

- If all eigenvectors are linearly independent, the dimension of the vector space is equal to the total number of eigenvectors.
- If at least one eigenvector is linearly dependent, the dimension of the vector space is less than the total number of eigenvectors.

1)g)

To determine whether the given three vectors form a basis for $\left(R^3\right)$, we need to check if they are linearly independent. The vectors are:

$$\left[v_1=\left[\cos^2(\theta),2,-1\right]\right)$$

$$\left[v_2=\left[\sin^2(\theta),-2,1\right]\right)$$

$$\left[v_3=\left[1,6,-3\right]\right)$$

The vectors form a basis for $\left(R^3\right)$ if and only if they are linearly independent.

To check for linear independence, we can set up the following linear combination:

$$\left[c_1 v_1+c_2 v_2+c_3 v_3=0\right)$$

where $\left(c_1,c_2,c_3\right)$ are constants, and (0) is the zero vector in $\left(R^3\right)$.

Substitute the vectors and set up the system of equations:

$$\left[c_1 \cos^2(\theta)+c_2 \sin^2(\theta)+c_3=0\right)$$

$$\left[2c_1-2c_2+6c_3=0\right)$$

$$\left[-c_1+c_2-3c_3=0\right)$$

This system of equations represents the conditions for linear independence. The vectors form a basis if the only solution to this system is $\left(c_1=c_2=c_3=0\right)$.

Now, by analyzing the system of equations and consider the values of (θ) for which the only solution is the trivial solution.

Since the determinant is 0, any value of θ won't satisfy the matrix.

Question 2

2)a)

```
#2)a)
from math import prod

def calculate_remain_probability():
    probability_overuse = [0.0001 * t**2 / (1 + t) for t in range(0,
100)]
    probability_factory = [0.01 * (1 + (1 - t) / (1 + t)) for t in
```

```
range(0, 100)]
    combined_probabilities = probability_overuse + probability_factory
    survival_probability = prod(1 - (np.array(probability_overuse) +
np.array(probability_factory)))
    return survival_probability

result_changed_variables = calculate_remain_probability()
print(result_changed_variables)
```

```
0.5535619154108106
```

2)b)

```
#2)b)

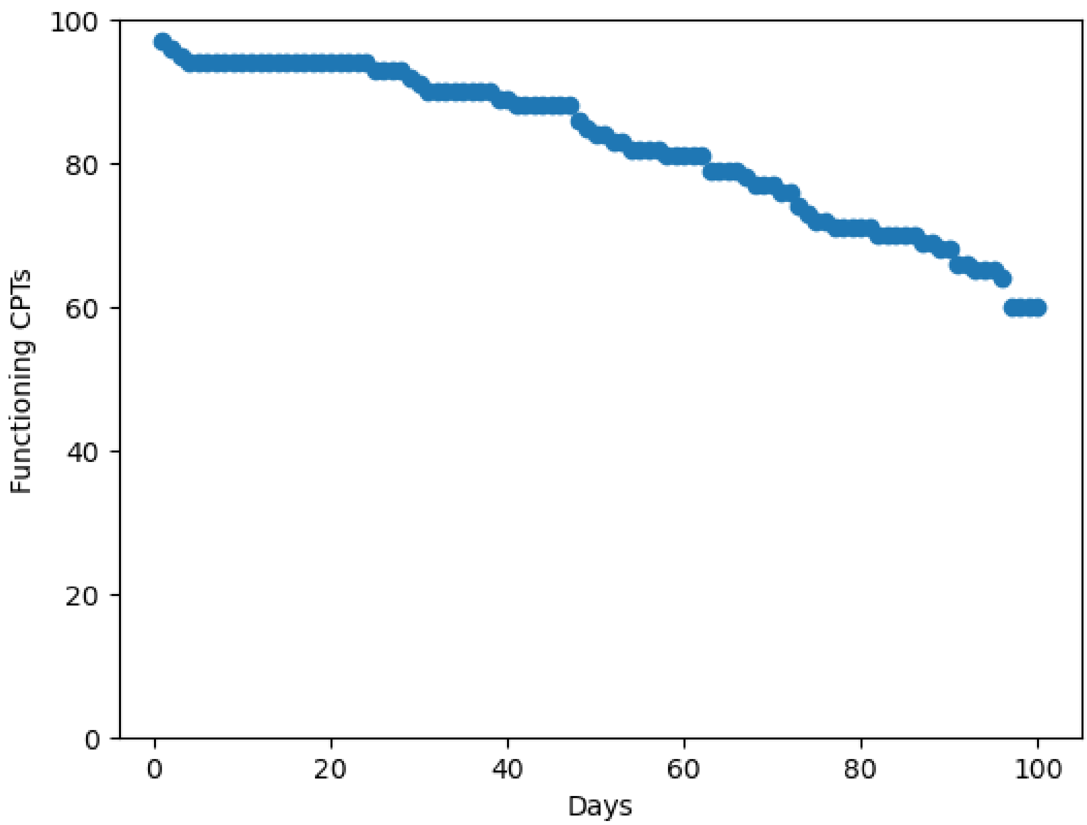
def simulate_factory(n_initial):
    functioning_cpts = np.zeros(100, dtype=int)
    n = n_initial
    cpt_count = []

    probability_overuse = [0.0001 * t**2 / (1 + t) for t in range(0,
100)]
    probability_factory = [0.01 * (1 + (1 - t) / (1 + t)) for t in
range(0, 100)]

    for day in range(100):
        probability_failure = probability_overuse[day] +
probability_factory[day]
        n = np.random.binomial(n, 1 - probability_failure)
        cpt_count.append(n)

    return cpt_count

cpts_count_result = simulate_factory(100)
plt.scatter(np.arange(1, 101), cpts_count_result)
plt.xlabel("Days")
plt.ylabel("Functioning CPTs")
plt.ylim(0, 100)
plt.show()
```



2)c)

```
#2)c)
def profit(x, y):
    # Given probabilities of overuse and factory faults
    p_overuse = [0.0001 * t**2/(1+t) for t in range(1,101)]
    p_factory = [0.01* (1+(1-t)/(1+t)) for t in range(1,101)]

    # Number of items
    n_items = 100

    # Initialize total expected faults
    expected_factory_faults = 0
    expected_overuse_faults = 0

    # Calculate the expected number of faulty items for each month
    for t in range(100):
        p_factory_fault = p_factory[t] * x
        p_overuse_fault = p_overuse[t] * y
        expected_factory_faults += n_items * p_factory_fault
        expected_overuse_faults += n_items * p_overuse_fault

    # Calculate the total expected profit
```

```
    expected_profit = n_items * 5 - (expected_factory_faults + 
expected_overuse_faults) * 5

    return expected_profit

# Example usage:
investment_in_factory = 0.3  # Replace with the actual investment 
value for reducing factory faults
investment_in_overuse = 0.7  # Replace with the actual investment 
value for reducing overuse faults

result = profit(investment_in_factory, investment_in_overuse)
print(f"The expected profit for 100 items is: £{result:.2f}")

The expected profit for 100 items is: £314.01
```

2)d)

Let's say:

- (x) as the investment per CPT in reducing overuse faults,
- (y) as the investment per CPT in reducing factory faults.

The profit function (p(x, y)) represents the net profit from each CPT after considering the investments in fault reduction.

The optimization problem can be formulated as follows:

$\left[\text{Maximize } p(x, y) \text{ subject to } 0 \leq x \leq 0.10 \text{ and } 0 \leq y \leq 0.10\right)$

This means the company wants to maximize the profit function while adhering to the constraint that the total investment per CPT in fault reduction cannot exceed 10 pence.

For a locally optimal allocation of investment, the condition on the gradient (or Jacobian) of (p) should be that it is equal to the zero vector. In mathematical terms, at a locally optimal solution $\left(\left(x^{¿}, y^{¿}\right)\right)$, the gradient (or Jacobian) of (p) should satisfy:

\begin{align*} |frac{dp}{dx} &= 0 | |frac{dp}{dy} &= 0 |end{align*}

This condition represents a critical point where the partial derivatives of (p) with respect to (x) and (y) are zero, indicating a potential maximum or minimum. Checking the second-order conditions (e.g., the Hessian matrix) can further confirm whether it is a maximum or minimum.

Question 3

Game1:

3)a)

The outcome space, or sample space, for this scenario involves two uncertain events:

1. The selection of the box that contains the money (BR). There are three possible outcomes for this event:

BR = B1, BR = B2, or BR = B3.

1. The choice of the box made by the player (Bc). Once the box with the money is determined, the player can choose any of the three boxes. Therefore, there are three possible outcomes for this event:

Bc = B1, Bc = B2, or Bc = B3.

The sample space can be represented as the set of all possible pairs (BR, Bc): {(B1, B1), (B1, B2), (B1, B3), (B2, B1), (B2, B2), (B2, B3), (B3, B1), (B3, B2), (B3, B3)}.

3)b)

To calculate the expected reward (E[R]) and the variance (Var(R)), we need to consider all possible outcomes and their associated rewards.

Let (X) represent the amount of money in the chosen box (BR), and let (R) represent the reward. The possible outcomes and rewards are as follows:

- If $(Bc = BR)$, then (R = X) (you earn the amount in the chosen box).
- If $(Bc \neq BR)$, then (R = 0) (you earn nothing).

Now, let's calculate (E[R]) and (Var(R)):

$$\left[E[R] = \sum_i P(\text{Outcome } i) \cdot R_i\right)$$

$$\left[Var(R) = \sum_i P(\text{Outcome}\, i) \cdot (R_i - E[R])^2\right)$$

Given that each box is chosen with uniform probability, $\left(P(\text{Bc = BR}) = \frac{1}{3}\right)$ and \$(P(\text{Bc \neq BR}) = \frac{2}{3})\$.

Substitute these probabilities into the formulas and perform the calculations. The result will provide the expected reward (E[R]) and the variance (Var(R)).

Game 2:

3)c)

Let's analyze the 'stick' and 'swap' strategies separately.

Stick Strategy:

- If you initially choose the correct box (BR = Bc), you will stick with it, and your reward will be the amount of money in the chosen box (R = X).
- If you initially choose the incorrect box (BR ≠ Bc), opening one empty box doesn't change your choice, and your reward remains zero (R = 0).

Let $(P(\text{Initial Correct}))$ be the probability that you initially choose the correct box and $(P(\text{Initial Incorrect}))$ be the probability that you initially choose an incorrect box.

$$[E[R \vee \text{Stick}] = P(\text{Initial Correct}) \cdot X + P(\text{Initial Incorrect}) \cdot 0]$$

$$[Var(R \vee \text{Stick}) = P(\text{Initial Correct}) \cdot (X - E[R \vee \text{Stick}])^2 + P(\text{Initial Incorrect}) \cdot (0 - E[R \vee \text{Stick}])^2]$$

Swap Strategy:

- If you initially choose the correct box (BR = Bc), opening one empty box doesn't change your choice, and your reward remains zero (R = 0).
- If you initially choose an incorrect box (BR ≠ Bc), the opened empty box reveals the location of the correct box. When you swap, your reward becomes the amount of money in the unchosen box (R = X).

$$[E[R \vee \text{Swap}] = P(\text{Initial Correct}) \cdot 0 + P(\text{Initial Incorrect}) \cdot X]$$

$$[Var(R \vee \text{Swap}) = P(\text{Initial Correct}) \cdot (0 - E[R \vee \text{Swap}])^2 + P(\text{Initial Incorrect}) \cdot (X - E[R \vee \text{Swap}])^2]$$

3)d)

For the 'swap' strategy with K boxes containing a reward out of N total boxes:

$$\left[E[R \vee \text{Swap}] = P(\text{Initial Incorrect}) \cdot \frac{X}{N-1}\right]$$

$$\left[Var(R \vee \text{Swap}) = P(\text{Initial Incorrect}) \cdot \frac{X^2(N-K)}{(N-1)^2}\right]$$

These formulas consider the probability of initially choosing an incorrect box and then swapping to find the reward.

Let's take at look in detail:

- The probability of initially choosing a box with a reward is $\left(P(X=1)=\frac{K}{N}\right)$, while the probability of initially choosing a box without a reward is $\left(P(X=0)=\frac{N-K}{N}\right)$.
- If you initially choose a box without a reward and then swap, the probability of getting a reward after swapping is $\left(P(X=1 \text{or swap})=\frac{K-1}{N-1}\right)$.
- If you still choose and swap the box without a reward, the reward probability is $(P(X=1 \text{or swap})=1)$.
- However, if you initially choose a box with a reward and then swap, you will always end up with an empty box, resulting in a probability of 0.
- The overall probability of getting a reward after swapping doesn't change; it remains $\left(P(X=1)=\frac{K}{N}\right)$.
- The conditional probability of getting a reward after swapping depends on whether you initially choose a box with a reward or not.
- If you swap after choosing a box with a reward, you will always receive an empty box.
- The expected value is given by $\left(P(X=1)\cdot 1+P(X=0)\cdot P(X=1 \text{ or swap})=\frac{16}{54}\right)$.
- The variance is given by $\left(P(X=1)\cdot(1-\text{expected value})^2+P(X=0)\cdot(P(X=1 \text{or swap})-\text{expected value})^2=\frac{1}{54}\right)$.

Question 4

4)a)

The maximum predator population for which prey births still outstrip deaths can be found by setting the prey birth rate equal to the prey death rate:

[aN - bNP = 0]

Solving for (N), we get $\left(N=\frac{b}{a}\right)$. Therefore, the maximum predator population is $\left(\frac{b}{a}\right)$.

4)b)

The predator population is shrinking when the predator death rate exceeds the predator birth rate. This occurs when $(d > c\,N)$, meaning that the rate at which predators die is greater than the rate at which they are born.

4)c)

- In the absence of predators (P(0) = 0), the dynamics of the prey population over time would be governed solely by the prey birth and death rates.
- The prey population would grow exponentially in the absence of predation pressure.
- This is reasonable as, without predators, there is no factor limiting the growth of the prey population.

4)d)

For the modified predator-free prey dynamics:

$$\left[N(t) = a\,N(t)\left(1 - \frac{N(t)}{K}\right)\right)$$

The fixed points occur when the prey birth rate equals the prey death rate:

$$\left[a\,N\left(1 - \frac{N}{K}\right) = 0\right)$$

This equation has two fixed points: $(N=0)\,and\,(N=K)$. The parameter (K) represents the carrying capacity of the environment for the prey population. It is the maximum population size that the environment can sustain in the absence of predators. The term $\left(1 - \frac{N}{K}\right)$ represents the factor limiting the prey population's growth as it approaches the carrying capacity (K).

```
data =
np.array([0.0,0.8253705906272355,0.8202189457560609,0.01,1.25125933369
67723,0.8804750446630152,0.02,1.0744696556474873,1.1951921572383182,0.
03,1.1459487035702027,1.367022776863449,0.04,0.7406895127926447,0.8201
930700228012,0.05,0.8032848443220044,0.8020943063852652,0.06,1.0423448
720147894,0.9964271033305258,0.07,0.8669728720976302,0.944155919286786
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```

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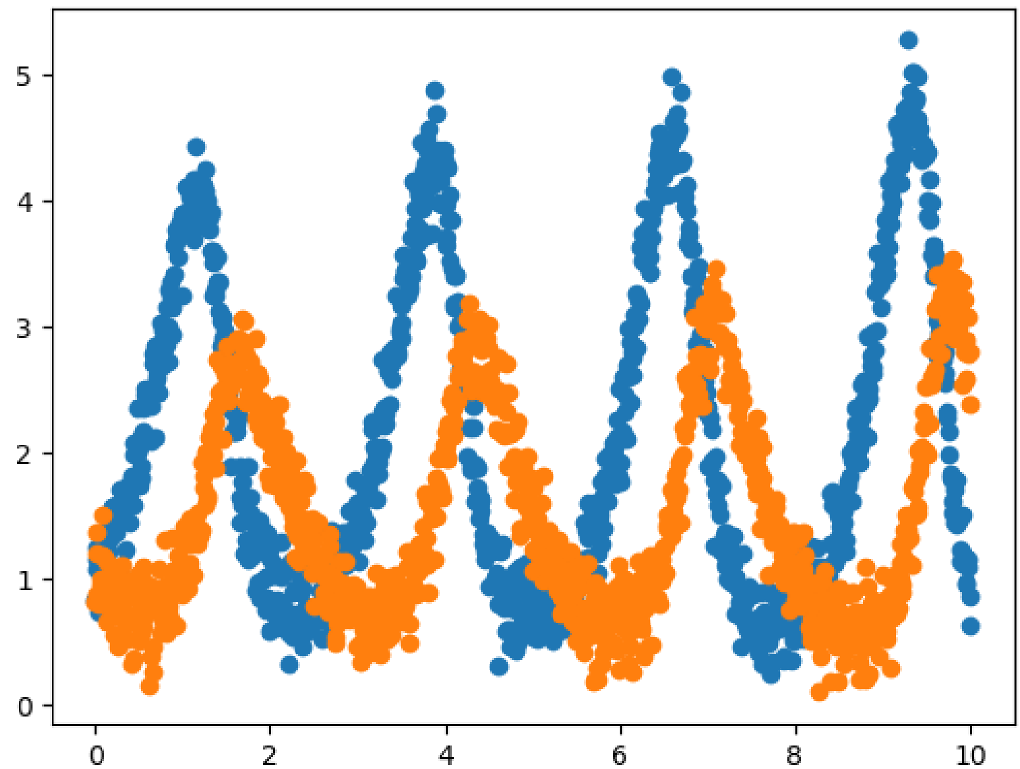
31,2.796228963036231,10.0,0.8571590506095471,2.3893746095481205]).resh
ape((-1,3))

plt.scatter(data[:, 0], data[:, 1])
plt.scatter(data[:, 0], data[:,2])
```

```
<matplotlib.collections.PathCollection at 0x23250c21a10>
```




```
def parameterise_basic_model(p):
    a, b, c, d = p

    def model(x, t):
        N, P = x
        return [a * x[0] - b * np.prod(x),
                c * np.prod(x) - d * x[1]]

    return model


basic_model = parameterise_basic_model([1, 4, 1, 4])
```

```
def solve(f, tspan, x0):
    δt = 0.01
    ts = np.arange(tspan[0], tspan[1] + δt, δt)
    xs = np.zeros((len(x0), len(ts)))
    xs[:, 0] = x0

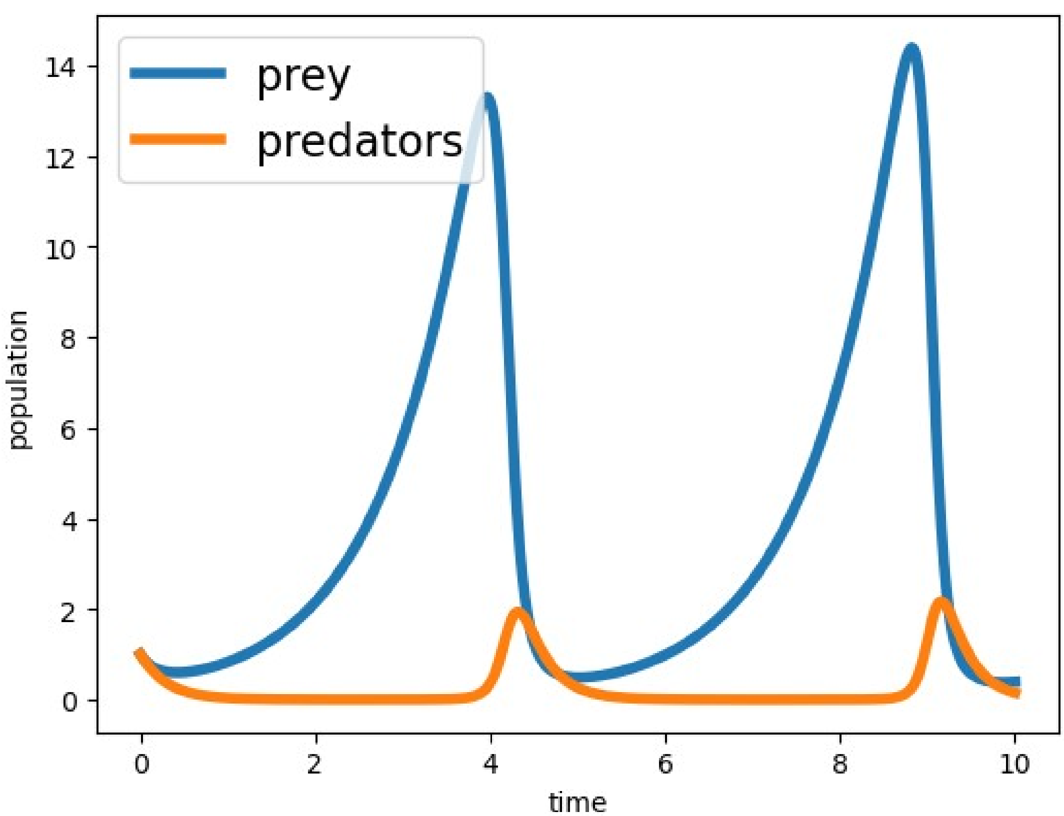
    for i in range(1, len(ts)):
        xs[:, i] = xs[:, i-1] + δt * np.array(f(xs[:, i-1], ts[i]))

    return ts, xs.T

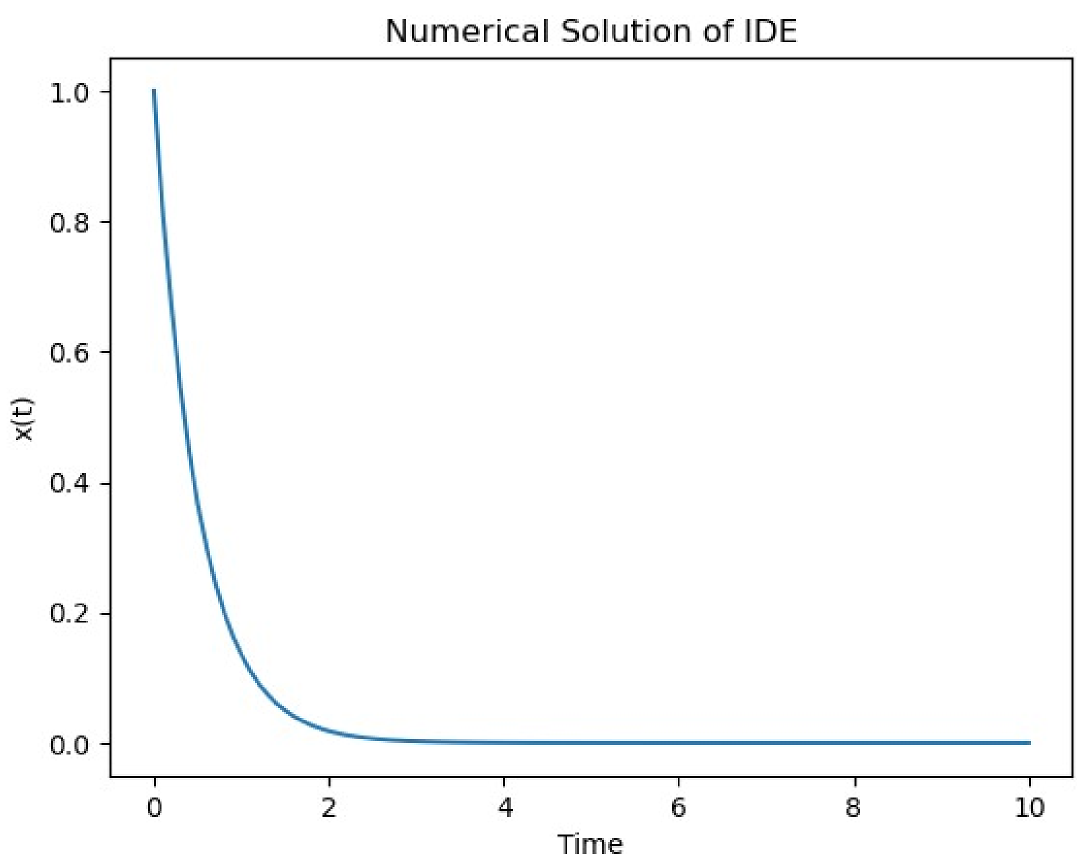

t_span = (0, 10)
x_0 = np.array([1.0, 1.0])
ts, xs = solve(basic_model, t_span, x_0)

plt.plot(ts, xs[:, 0], label="prey", linewidth=4)
plt.plot(ts, xs[:, 1], label="predators", linewidth=4)
plt.xlabel("time")
plt.ylabel("population")
plt.legend(fontsize=16)
```

```
<matplotlib.legend.Legend at 0x232514f17d0>
```



```python
#solve the differential equation
from scipy.integrate import solve_ivp
#Define the ODE function
def f(t,x):

  return [-2 *x[0]]
#Define time span
tspan = (0,10)

#initial conditions
x0 = [1,0]
sol = solve_ivp (f, tspan, x0, method = 'RK45', t_eval =
np.linspace(tspan[0],tspan[1],100))

#plot
plt.plot(sol.t, sol.y[0])
plt.xlabel("Time")
plt.ylabel("x(t)")
plt.title('Numerical Solution of IDE')
plt.show()
```



4)e)

- If we measure predators and prey in units of a single animal $(let(N'=N) and (P'=P))$, we can rewrite the differential equations using the chain rule.
- Let (N') and (P') be the new variables:

  $$\left[\frac{dN'}{dt}=aN'-bN'P'\right)\left[\frac{dP'}{dt}=cN'P'-dP'\right)$$

- These equations represent the dynamics of the prey and predator populations when measured in units of a single animal.

4)f)

```
#4)f)
import numpy as np

def simulation(p):
    a, b, c, d = p
    dt = 0.01
    num_steps = 1001
    timepoints = np.arange(0, 10, dt)
    populations = np.zeros((num_steps, 2))
    populations[0] = [1, 1]  # Initial conditions

    for t in range(1, num_steps):
        dN_dt = a * populations[t-1, 0] - b * populations[t-1, 0] *
populations[t-1, 1]
        dP_dt = c * populations[t-1, 0] * populations[t-1, 1] - d *
populations[t-1, 1]
        populations[t] = populations[t-1] + dt * np.array([dN_dt,
dP_dt])

    return populations

# Example usage:
parameters = [2, 3, 4, 5]
result = simulation(parameters)

print(result)

# The rest of the code seems correct
simulation_result = simulation(parameters)
print(simulation_result[:, 0])
```

```
[[1.         1.        ]
 [0.99       0.99      ]
 [0.980397   0.979704  ]
 ...
 [1.41092787 1.43386793]
 [1.3784539  1.4430979 ]
 [1.34634566 1.45051276]]
[1.         0.99       0.980397   ... 1.41092787 1.3784539
1.34634566]
```

4)g)

```python
#4)g)
def mse(p):
    simulation_result = simulation(p)
    residuals = simulation_result - data[:, 1:3]
    mse_value = np.mean(residuals**2)
    return mse_value

# Example usage:
parameters = [2, 3, 4, 5]
mse_value = mse(parameters)
print(mse_value)
```

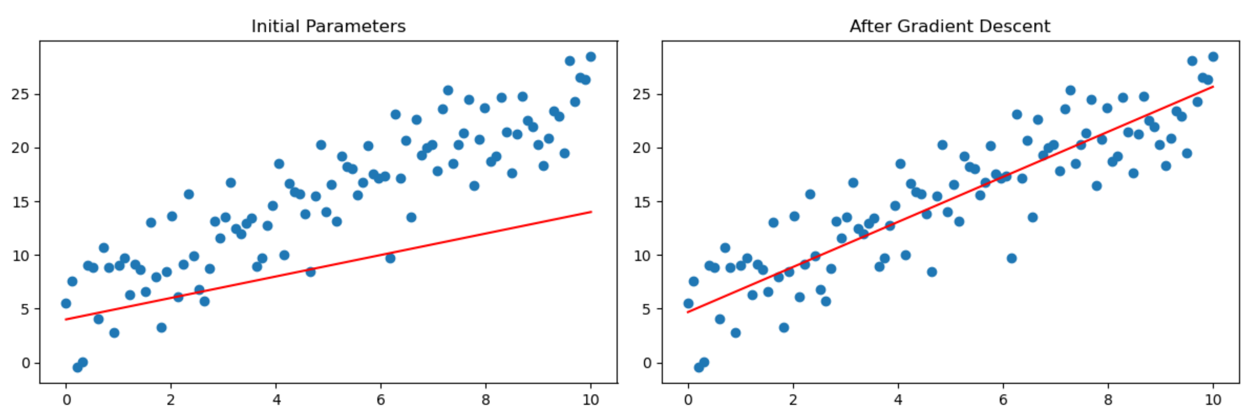
```
1.969430985356843
```

4)h)

```python
#4)h)
import numpy as np
import matplotlib.pyplot as plt

# Generate synthetic data
x_data = np.linspace(0, 10, 100)
y_true = 2 * x_data + 5 + np.random.normal(0, 3, len(x_data))

# Initial parameter values
theta0 = np.array([1, 4, 1, 4])

# Mean Squared Error (MSE) function
def mse(theta):
    y_pred = theta[0] * x_data + theta[1]
    return np.mean((y_true - y_pred) ** 2)

# Gradient of MSE function
def gradient(theta):
```

```
    y_pred = theta[0] * x_data + theta[1]
    error = y_true - y_pred
    g0 = -2 * np.mean(x_data * error)
    g1 = -2 * np.mean(error)
    return np.array([g0, g1, 0, 0])

# Gradient Descent
theta = theta0.copy()
learning_rate = 0.01
for i in range(100):
    theta = theta - learning_rate * gradient(theta)

# Compute MSE for initial and final parameters
mse_initial = mse(theta0)
mse_after_gradient_descent = mse(theta)

# Check if MSE reduced by a factor of 3
if mse_initial / mse_after_gradient_descent >= 3:
    print("Success! MSE reduced by a factor of 3.")

# Plotting
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(12, 4))

# Plot with initial parameters
ax1.scatter(x_data, y_true)
ax1.plot(x_data, theta0[0] * x_data + theta0[1], c='r')
ax1.set_title('Initial Parameters')

# Plot after gradient descent
ax2.scatter(x_data, y_true)
ax2.plot(x_data, theta[0] * x_data + theta[1], c='r')
ax2.set_title('After Gradient Descent')

plt.tight_layout()
plt.show()
```

```
Success! MSE reduced by a factor of 3.
```



```
def gradient(f, x):
    n = len(x)
    δx = 0.01

    def Δx(i):
        z = np.zeros(n)
        z[i] = δx
        return z

    dfdx = np.zeros(n)
    for i in range(n):
        dfdx[i] = (f(x + Δx(i)) - f(x)) / δx

    return dfdx
```

4)i)

In general, achieving an MSE of 0 is uncommon and often suggests overfitting to the noise present in the data. An MSE of 0 implies a perfect match between the model's predictions and the observed values, with no discrepancies. However, this situation can arise due to noise, measurement errors, or other data-related factors.

Consider the scenario where MSE equals 0. In such cases, the parameter values leading to a perfect fit would typically be unique, assuming the model is well-defined. There shouldn't be another distinct set of parameters that perfectly fits the data.

In the context of achieving an MSE of 0, let's consider another scenario to provide an alternative explanation:

Suppose we have a quadratic regression model given by $\left(y=ax^2+bx+c\right)$, and it perfectly fits the data with an MSE of 0. In this case, we can explore another set of parameters $\left(a'\right)$, $\left(b'\right)$, and $\left(c'\right)$ that also perfectly fits the data.

Original model: $\left(y=ax^2+bx+c\right)$

Now, consider a new set of parameters: $\left(a'=2a\right)$, $\left(b'=2b\right)$, and $\left(c'=2c\right)$. The corresponding model becomes:

New model: $\left(y'=a'x^2+b'x+c'=2ax^2+2bx+2c\right)$

Since the original model perfectly fits the data, we can express $\left(ax^2+bx+c\right)$ as $\left(y\right)$. Substituting this into the new model, we get:

$\left(y'=2y\right)$

This implies that any data point (x, y) that satisfies the original quadratic regression model $\left(y=ax^2+bx+c\right)$ will also automatically satisfy the new model $\left(y'=2y\right)$. Therefore, the curves defined by the original quadratic model and the new quadratic model perfectly overlap each other, passing through all data points.

This illustrates that, in the case of achieving an MSE of 0, there can be alternative sets of parameters that result in models perfectly fitting the data, and these alternative parameter sets may lead to equivalent models that perfectly overlap.

Question 5

5)a)

The variable (p) in the nondimensionalized model is defined as the product of the growth rate parameter (r) and the characteristic time scale (T), and it is related to the original parameters of the competition model.

The relationship between (T) and (t) is given by (T = r t), where (r) is the growth rate parameter. If, for example, (t) is measured in seconds and (r) is 60, then (T) would be in minutes.

Now, let's express (p) in terms of the original parameters:

$[p = r T $

Substitute $\left(T = r\,t\right)$:

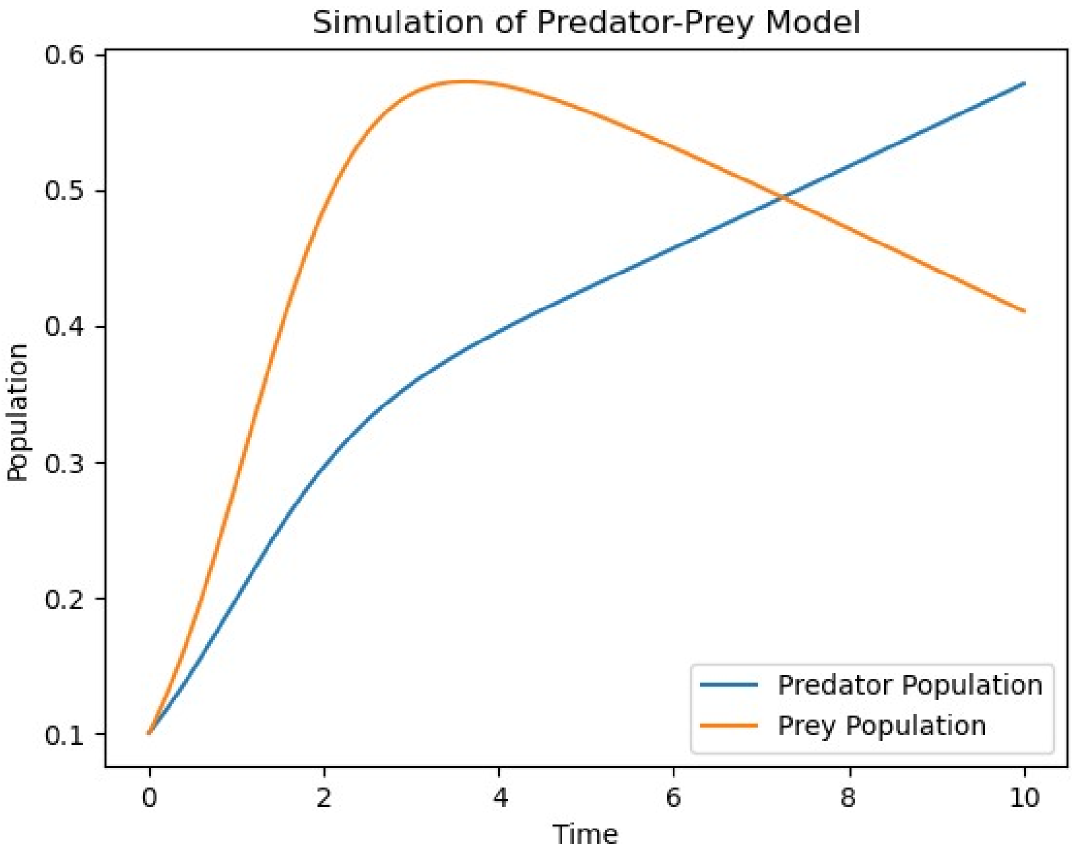
$\left[p = r^2 t\right)$

In the context of the original competition model, (p) represents the product of the growth rate (r) and a characteristic time scale (t). It essentially quantifies the time scale at which the population dynamics evolve. In biological terms, (p) can be interpreted as a measure of how quickly the populations of the competing species change concerning the growth rate (r) and the time (t). A larger (p) suggests a faster dynamics, while a smaller (p) indicates a slower evolution of the populations.

5)b)

```
#5)b)

from scipy.integrate import odeint

# Define the system of differential equations
def predator_prey_model(populations, time, interaction_coeff_1, 
interaction_coeff_2, growth_rate):
    predator, prey = populations
    d_predator_dt = predator * (1 - predator - interaction_coeff_1 * 
prey)
    d_prey_dt = growth_rate * prey * (1 - prey - interaction_coeff_2 *
```

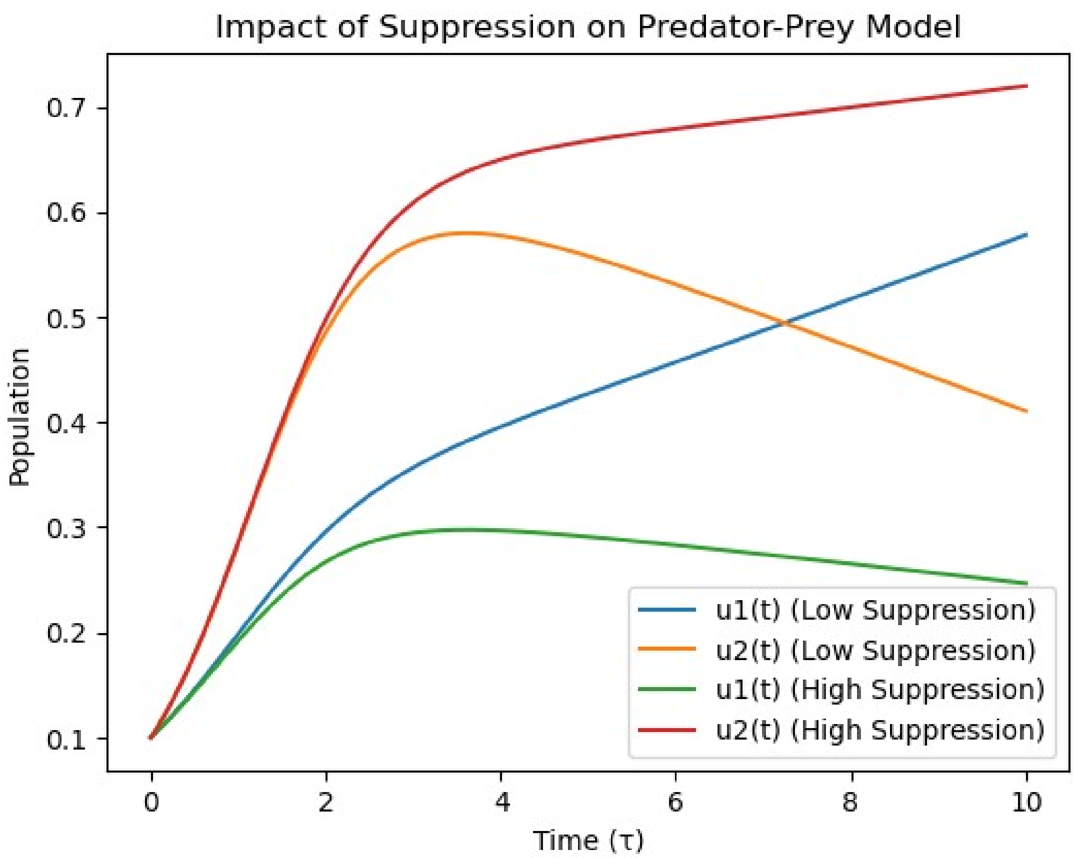
```
predator)
    return [d_predator_dt, d_prey_dt]

# Set initial conditions and parameters
initial_populations = [0.1, 0.1]
interaction_coeff_1 = 0.9
interaction_coeff_2 = 1.1
growth_rate = 1.6

# Set time points for simulation
time_points = np.linspace(0, 10, 1000)

# Simulate the system of differential equations
simulation_result = odeint(
    predator_prey_model,
    initial_populations,
    time_points,
    args=(interaction_coeff_1, interaction_coeff_2, growth_rate)
)

# Plot the simulation results
plt.plot(time_points, simulation_result[:, 0], label='Predator
Population')
plt.plot(time_points, simulation_result[:, 1], label='Prey
Population')
plt.xlabel('Time')
plt.ylabel('Population')
plt.title('Simulation of Predator-Prey Model')
plt.legend()
plt.show()
```



5)c)

```
#5)c)
# Define the system of differential equations
def model(u, τ, a12, a21, p):
    u1, u2 = u
    du1dt = u1 * (1 - u1 - a12 * u2)
    du2dt = p * u2 * (1 - u2 - a21 * u1)
    return [du1dt, du2dt]

# Set initial conditions and common parameters
u0 = [0.1, 0.1]
a21 = 1.1
p = 1.6

# Set time points for simulation
τ = np.linspace(0, 10, 1000)

# Simulate with low suppression (a12 = 0.9)
a12_low = 0.9
result_low = odeint(model, u0, τ, args=(a12_low, a21, p))
```

```
# Simulate with high suppression (a12 = 1.1)
a12_high = 1.1
result_high = odeint(model, u0, τ, args=(a12_high, a21, p))

# Plot the simulations
plt.plot(τ, result_low[:, 0], label='u1(t) (Low Suppression)')
plt.plot(τ, result_low[:, 1], label='u2(t) (Low Suppression)')
plt.plot(τ, result_high[:, 0], label='u1(t) (High Suppression)')
plt.plot(τ, result_high[:, 1], label='u2(t) (High Suppression)')
plt.xlabel('Time (τ)')
plt.ylabel('Population')
plt.title('Impact of Suppression on Predator-Prey Model')
plt.legend()
plt.show()
```



5)d)

To find the fixed points, we set the derivatives of (u_1) and (u_2) to zero:

$$\left[\frac{du_1}{d\tau} = u_1\left(1 - u_1 - a_{12}u_2\right) = 0\right)$$

$$\left[\frac{du_2}{d\tau} = p\,u_2\left(1 - u_2 - a_{21}u_1\right) = 0\right)$$

For (u_1), the solutions are (u_1 = 0), (u_1 = 1), and $\left(u_1 = \frac{1 - a_{12}u_2}{1 - a_{12}}\right)$.

For (u_2), the solutions are (u_2 = 0) and $\left(u_2 = \frac{1 - a_{21}u_1}{1 - u_2}\right)$.

Now, we combine these solutions to find the fixed points:

1. $\left(u_1 = 0, u_2 = 0\right)$
2. $\left(u_1 = 1, u_2 = 0\right)$
3. $\left(u_1 = \frac{1 - a_{12}u_2}{1 - a_{12}}, u_2 = \frac{1 - a_{21}u_1}{1 - u_2}\right)$
4. $\left(u_1 = 0, u_2 = 1\right)$

Interpretations:

1. Both species are extinct.
2. Species 1 dominates, and species 2 is extinct.
3. Coexistence point where the two species coexist in a stable manner.
4. Species 2 dominates, and species 1 is extinct.

These fixed points provide insights into the possible outcomes of the competition between the two species, ranging from coexistence to the dominance of one species over the other. The stability of the coexistence point is particularly interesting, as it represents a balanced state where both species can persist over time.

5)e)

To calculate the Jacobian matrix (J(x)) for the system of differential equations

\begin{align} |frac{du_1}{d|tau} &= u_1(1 - u_1 - a_{12}u_2) | |frac{du_2}{d|tau} &= pu_2(1 - u_2 - a_{21}u_1), |end{align}

we differentiate each equation with respect to (u_1) and (u_2) and the Jacobian matrix is given by:

J(x) = \begin{bmatrix} \frac{\partial f_1}{\partial u_1} & \frac{\partial f_1}{\partial u_2} \ \frac{\partial f_2}{\partial u_1} & \frac{\partial f_2}{\partial u_2} \end{bmatrix}

J(x) = \begin{bmatrix} 1 - 2u_1 - a_{12}u_2 & -a_{12}u_1 \ p(1 - u_2 - a_{21}u_1) & p(1 - 2u_2 - a_{21}u_1) \end{bmatrix}

= \begin{bmatrix} 1 - 2u_1 - a_{12}u_2 & -a_{12}u_1 \ -pa_{21}u_2 & p(1 - 2u_2 - a_{21}u_1) \ end{bmatrix}.

So,

J(x) = \begin{bmatrix} 1 - 2u_1 - a_{12}u_2 & -a_{12}u_1 \ -pa_{21}u_2 & p(1 - 2u_2 - a_{21}u_1) \ end{bmatrix}.

5)f)

Evaluating the Jacobian matrix at the fixed points:

- (u_1 = 0, u_2 = 0):

J(0, 0) = \begin{bmatrix} 1 & 0 \ 0 & p \end{bmatrix}

- (u_1 = 1, u_2 = 0):

J(1, 0) = \begin{bmatrix} -1 & -a_{12} \ p(1 - a_{21}) & p(1 - 2) \end{bmatrix}

- $\left(u_1 = \frac{1 - a_{12} u_2}{1 - a_{12}}, u_2 = \frac{1 - a_{21} u_1}{1 - u_2}\right)$:

This point is nontrivial to compute analytically.

- (u_1 = 0, u_2 = 1):

J(0, 1) = \begin{bmatrix} 1 & 0 \ 0 & -p \end{bmatrix}

Stability requirements:

For stability, we look at the eigenvalues of the Jacobian matrix. Specifically:

- If both eigenvalues have negative real parts, the fixed point is stable.
- If at least one eigenvalue has a positive real part, the fixed point is unstable.

The requirements are:

1. $\left(u_1 = 0, u_2 = 0\right)$: Stable if $\left(p > 0\right)$.
2. $\left(u_1 = 1, u_2 = 0\right)$: Stable if $\left(p < 0\right)$ and $\left(1 - a_{21} > 0\right)$.
3. Coexistence point: Complicated conditions involving $\left(a_{12}\right)$ and $\left(a_{21}\right)$.
4. $\left(u_1 = 0, u_2 = 1\right)$: Unstable regardless of parameters.

These conditions indicate under what parameter values the fixed points are stable in the predator-prey model.