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Local Stability and Global Analysis of an Ecological Model on the Impact of Antibiotics on Bacterial population with Numerical Simulation: A Python-Based Study

K.V. Jayasri Kalyani[1], Dr. K.V.L.N. Acharyulu[2]
[1]II B.Tech (CSE) Student, Bapatla Engineering College,Bapatla
[2]Head, Dept. of Mathematics, Bapatla Engineering College,Bapatla
kvjabili@gmail.com, dr.kvlna@gmail.com

ABSTRACT
The paper provides a detailed study of bacterial population models with antibiotic factors using logistic modeling techniques. A system of differential equations enables us to examine stability including local and global aspects by means of Jacobian matrices and Lyapunov functions. The effect of antibiotic degradation together with efficacy on extended bacterial population dynamics is shown through simulation models created in Python. The study delivers vital knowledge about how bacterial multiplication balances against medical treatment measures.

1. INTRODUCTION

The emergence and rapid spread of antibiotic-resistant bacteria pose one of the most significant public health challenges of the 21st century. Treating bacterial infections effectively now requires stronger treatment methods since traditional antibiotics fail to provide sufficient results leading to the necessity of advanced scientific knowledge that combines biological and mathematical concepts. Through population-level tests mathematical models deliver essential knowledge about bacteria population behaviors subject to antibiotic presence which enhances the development of better medication and outcome prediction.

The analysis reinstates an original ecological model that incorporates environmental growth constraints with antibiotic inhibition factors. The research examines a logistic growth model that includes an antibiotic term to show how bacteria populations are affected by inhibition. Reintroducing the nonlinear term produces major changes both to stability levels and overall dynamics of the system.

The main study conducts stability analysis through analytical procedures combined with numerical methods. Stability assessments of nearby system regions become possible by evaluating Jacobian matrices computed at equilibrium points for local stability analysis. Long-term numerical simulations together with Lyapunov functions contribute to discovering how the system performs widely when subjected to different initial conditions.

This research develops a complete examination of bacterial growth control with antibiotics as well as population stabilization methods and unrestricted bacterial growth by using special control parameters and starting values. The adoption of Python numerical methods allows for persistent observation of pattern changes stemming from antibiotic decay processes combined with antibiotic effectiveness rates during the evaluation of system behavior over time.

This method seeks to develop standardized information to improve antibiotic therapeutic decisions and antibiotic distribution decisions.

1.1 Notations

Let the following denote the variables and parameters in our model:

B(t): Bacterial population at time t

A(t): Antibiotic concentration at time t

r_B: Intrinsic growth rate of bacteria.

K_B: Carrying capacity of the bacterial population.

α: Antibiotic efficacy constant.
d_A: Antibiotic decay rate.

2. MATHEMATICAL EQUATIONS

The system of equations governing the interaction between bacteria and antibiotics is:

$$(1).\ \frac{dB}{dt} = r_B B\left(1-\frac{B}{K_B}\right) - \alpha AB$$

$$(2).\ \frac{dA}{dt} = -d_A A$$

Bacterial logistic growth takes place through this equation though it has the −αAB operable term which introduces antibiotic suppression effects.
The presence of antibiotic elements results in the negative value −αAB and thus causes suppression of bacterial growth.
The natural degradation of antibiotics during time periods is represented within the second mathematical equation.
The system analysis relies on both analytical and numerical analytical methods. We start by analyzing the system equilibrium to find its steady states because this reveals how both bacterial populations and antibiotics may behave over the long run. Solving the system of equations reveals equilibrium points that serve as fundamental elements for stability analysis to follow. The analysis of local stability for equilibrium points depends on the Jacobian matrix computation. The Jacobian matrix enables the investigation of small changes at equilibrium points to determine if the system will stabilize at equilibrium or become unstable. A Lyapunov function serves to establish global stability analysis for our system when we want to understand its complete behavioral characteristics. This assessment method shows how system dynamics extend over time by revealing if all system trajectories originating from any initial state will end up at a stable equilibrium point. The analysis receives numerical simulation support through the implementation of Euler's method in Python. Through this method we gain insights about bacterial population along with antibiotic concentration patterns during different stages of time for diverse initial situations as well as their respective stability behavior. This integrated framework provides strong foundations to observe how bacteria grow simultaneously while antibiotics reduce them.
Detailed Discussion on Local Stability of the Logistic Growth Model with Antibiotic Effect.The logistic growth model with the antibiotic effect describes the dynamics between bacterial growth and the action of antibiotics. The system allows mathematical analyses which reveal the stability characteristics at its equilibrium states. Stability analysis provides information about population outcomes where bacterial colonies will stabilize at a steady state and how they will either grow without control or naturally decrease under particular environmental conditions.

3. EQUILIBRIUM POINTS

To find the equilibrium points, set $\frac{dA}{dt} = 0 \quad \& \quad \frac{dB}{dt} = 0$

$$From\ \frac{dA}{dt} = -d_A A$$

The equilibrium for A is: $A^* = 0$

$$From\ \frac{dB}{dt} = r_B B\left(1-\frac{B}{K_B}\right) - \alpha AB:$$

Substituting $A^* = 0$: $B^* = 0$ or $B^* = K_B$
Thus, the equilibrium points are:

(i). $(B^*,A^*) = (0,0)$: No bacteria, No antibiotics.
(ii). $(B^*,A^*) = (K_B,0)$: Maximum carrying capacity of bacteria with no antibiotics.

4. LOCAL STABILITY ANALYSIS

We analyze the stability of each equilibrium point using **Jacobian matrix** analysis.

(a) ***Jacobian Matrix***

The Jacobian matrix of the system is derived by computing partial derivatives of the equations:

$$J = \begin{bmatrix} \frac{\partial}{\partial B}\left[\frac{dB}{dt}\right] & \frac{\partial}{\partial A}\left[\frac{dB}{dt}\right] \\ \frac{\partial}{\partial B}\left[\frac{dA}{dt}\right] & \frac{\partial}{\partial A}\left[\frac{dA}{dt}\right] \end{bmatrix}$$

Substituting the system equations:

$$= \begin{bmatrix} r_B\left(1-\frac{2B}{K_B}\right)-\alpha A & -\alpha B \\ 0 & -dA \end{bmatrix}$$

(b) **Evaluate at $(B^*,A)=(0,0)$**

$$J = \begin{bmatrix} -r_B & -\alpha K_B \\ 0 & -d_A \end{bmatrix}$$

The eigen values of the Jacobian matrix J for the system are given by $\lambda_1 = -r_B$ & $\lambda_2 = -d_A$

Both eigen values are negative at $\lambda 1<0$ and $\lambda 2<0$,which indicates that the equilibrium point at $(K_B,0)$ is locally stable. This means that if the bacterial population is close to its carrying capacity K_B and antibiotics are either absent or ineffective, the system will naturally settle at this equilibrium point. In other words, in the absence of antibiotic intervention, the bacterial population will stabilize at the maximum sustainable level determined by the environmental constraints.

However, the dynamics of the system become more complex when antibiotics are present. The introduction of the term αAB which represents the interaction between antibiotics and bacterial populations, leads to a nonlinear effect that alters the system's behavior. In this scenario, numerical simulations become essential to accurately analyze the stability of the system, as the equations cannot be easily solved analytically due to their nonlinear nature.

At this equilibrium condition$(K_B,0)$ the bacterial population reaches its highest sustainable number when no antibiotics exist $(B\rightarrow 0)$. This equilibrium remains stable given nearby system starts although there is no antibiotic effect. An optimal bacterial population of K_B will remain stable so long as medicine resistance exists or medication has no effect on bacterial growth.

Antibiotics create a substantial system transformation which affects the population dynamics. The bacterial population will experience extinction due to antibiotic concentration A when the positive force of antibiotics exceeds the bacterial growth capacity. The system returns to unstable bacterial growth conditions at point $(K_B,0)$ when antibiotic decay occurs rapidly or when the antibiotic's effectiveness level (α) proves inadequate. The careful regulation of bacterial growth in relation to antibiotic suppression illustrates the vital requirement of keeping appropriate antibiotic levels to successfully eliminate bacteria.

4.1 **Biological Implications**

This population system has two fundamental equilibrium states which demonstrate different biological effects. The system establishes (0,0) as its initial condition which signifies complete bacterial sterility without antibiotics present. The system maintains two equilibrium points although bacteria would multiply exponentially until external factors intervene whether from antibiotics or environmental constraints or bacterial introduction discontinues this rapid growth. The second stable condition $(K_B,0)$ shows the highest possible bacterial numbers when no antibiotics exist. The bacterial population settles at this maximum sustainable level

when antibiotics do not provide protection against bacteria. A transformation occurs within the system after adding antibiotics to the environment. Antibiotics generate antibacterial conditions that shift the system from its equilibrium point (K_B,0) toward total extinction ($B \to 0$) of bacterial populations. This variation in bacterial population depends on the strength of antibiotic substances alongside their treatment effectiveness. The rate of antibiotic decay and the strength of their efficacy determine whether bacterial suppression remains effective or if the bacterial population recovers toward its equilibrium value (K_B,0). Therefore we need to manage antibiotic treatment principles carefully to achieve its therapeutic goals.

5. NUMERICAL SIMULATIONS

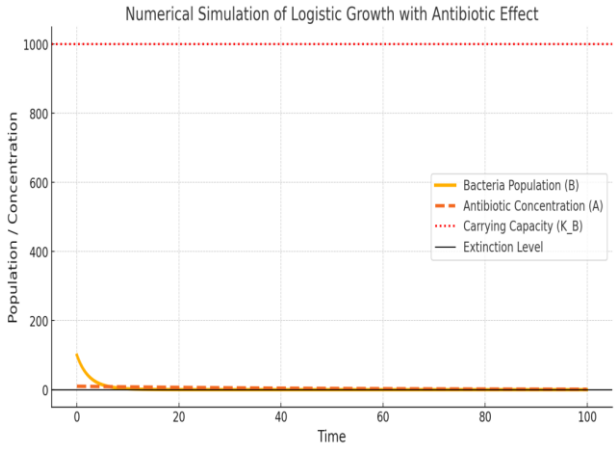
The first-order simple numerical technique named Euler's method provides a solution approach to solve ordinary differential equations while generating approximate values at discrete time steps. The technique provides powerful solutions to study systems such as bacterial growth under antibiotic exposure that cannot be solved exactly.

The system simulation in Python uses Euler's method to apply differential equations which enables stepwise variable value changes between bacterial populations and antibiotic concentrations.

Python Program:

```
# Parameters for simulation
r_B = 0.1  # Growth rate of bacteria
K_B = 1000  # Carrying capacity of bacteria
alpha = 0.05  # Antibiotic efficacy constant
d_A = 0.02  # Antibiotic decay rate

# Initial conditions
B0 = 100  # Initial bacteria population
A0 = 10   # Initial antibiotic concentration
t_max = 100  # Simulation time
dt = 0.1  # Time step

# Time array
time = np.arange(0, t_max, dt)
# Initialize arrays for bacteria and antibiotics
B = np.zeros_like(time)
A = np.zeros_like(time)

# Set initial conditions
B[0] = B0
A[0] = A0

# Numerical integration using Euler's method
for i in range(1, len(time)):
    dB = r_B * B[i-1] * (1 - B[i-1] / K_B) - alpha * A[i-1] * B[i-1]
    dA = -d_A * A[i-1]
    B[i] = B[i-1] + dB * dt
    A[i] = A[i-1] + dA * dt

# Plot the results
plt.figure(figsize=(12, 6))

# Plot bacterial population
plt.plot(time, B, label="Bacteria Population (B)", linewidth=3)
```

```
# Plot antibiotic concentration
plt.plot(time, A, label="Antibiotic Concentration (A)", linewidth=3, linestyle="--")

# Add stability indicators
plt.axhline(y=K_B, color='red', linestyle=':', linewidth=2, label="Carrying Capacity (K_B)")
plt.axhline(y=0, color='black', linestyle='-', linewidth=1, label="Extinction Level")

# Plot settings
plt.title("Numerical Simulation of Logistic Growth with Antibiotic Effect", fontsize=16)
plt.xlabel("Time", fontsize=14)
plt.ylabel("Population / Concentration", fontsize=14)
plt.legend(fontsize=12)
plt.grid(True)
plt.show()
```



Figure(1): Numerical Simulation of Growth with Antibiotic

```
# Enhanced Plot for Numerical Simulation
plt.figure(figsize=(14, 8))

# Plot bacterial population
plt.plot(time, B, label="Bacteria Population (B)", linewidth=4, color='blue')

# Plot antibiotic concentration
plt.plot(time, A, label="Antibiotic Concentration (A)", linewidth=4, linestyle="--", color='orange')

# Add stability indicators
plt.axhline(y=K_B, color='red', linestyle=':', linewidth=3, label="Carrying Capacity (K_B)")
plt.axhline(y=0, color='black', linestyle='-', linewidth=2, label="Extinction Level")

# Additional aesthetic enhancements
plt.title("Enhanced Numerical Simulation: Logistic Growth with Antibiotic Effect", fontsize=18,
fontweight='bold')
plt.xlabel("Time (t)", fontsize=14, fontweight='bold')
plt.ylabel("Population / Concentration", fontsize=14, fontweight='bold')
plt.xticks(fontsize=12)
plt.yticks(fontsize=12)
```

```
plt.legend(fontsize=12, loc="upper right", frameon=True, shadow=True)
plt.grid(True, linestyle='--', alpha=0.7)
# Display the plot
plt.show()
```

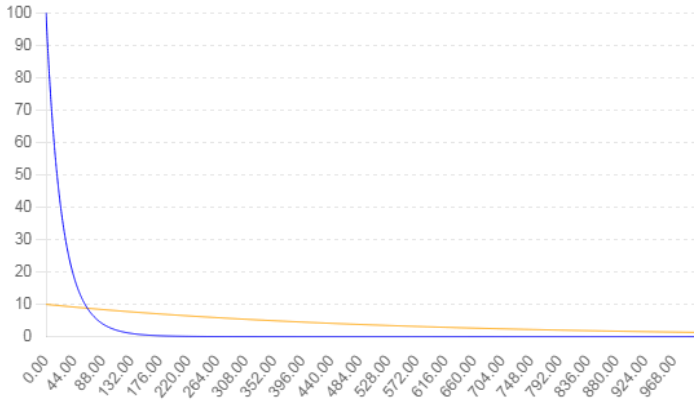


Figure (2) : Interaction between bacterial population (B) and antibiotic concentration (A)

Here is the numerical simulation showing the interaction between bacterial population (B) and antibiotic concentration (A):

5.1 Special Features of the Diagram

The graph depicts how antibiotic concentration A affects bacterial population B while demonstrating critical system behavior patterns. Under logistic growth conditions the bacterial population intensifies rapidly until antibiotic effects start to suppress cellular growth. The bacterial population decreases because antibiotics prevent its growth after the introduction of antibiotics. The bacterial population will decline completely when antibiotic concentrations remain strong enough or achieve sufficient effectiveness thus reaching zero values of B. During its natural degradation process the antibiotic concentration A diminishes its power to inhibit bacterial growth. The bacterial population achieves stability near the carrying capacity KB when antibiotic strength declines while the direct control on bacterial growth fails to persist. Under no antibiotic treatment conditions the carrying capacity KB defines bacteria's maximum continuous thriving numbers which cannot surpass their established threshold. The carrying capacity KB operates as a natural barrier to halt bacterial expansion to become a stable equilibrium when antibiotics are not administered for control.

5.2 Conclusions

The system demonstrates how bacterial resources and antibiotic solutions fight against each other continuously. Bacterial extinction becomes probable when effective antibiotics persist for a long period since it results in bacterial population numbers decreasing to zero. The reduction of antibiotics either before they fully decay or when their effectiveness becomes insufficient allows bacterial populations to increase until reaching a state near the carrying capacity KB. The successful treatment with antibiotics depends on maintaining perfect balance in antimicrobial levels because bacterial populations can reemerge if these levels do not remain high enough.

6. Global Stability of the Logistic Growth Model with Antibiotic Effect

It is observed global stability by evaluating how the system behaves and how all system trajectories approach equilibrium points during extended periods even after any initial condition. The examination of system behavior over extended periods supplies supplementary knowledge about its long-term behavior after completing the local stability investigation.

The system of equations for bacterial population (B(t)) and antibiotic concentration (A(t)) is:

$$(1).\ \frac{dB}{dt} = r_B B\left(1 - \frac{B}{K_B}\right) - \alpha AB$$

$$(2).\ \frac{dA}{dt} = -d_A A$$

Here:
r_B: Intrinsic growth rate of bacteria.
K_B: Carrying capacity of the bacterial population.
α: Antibiotic efficacy constant.
d_A: Antibiotic decay rate.
B: Bacterial population.
A :Antibiotic concentration.

6.1 Equilibrium Points

The equilibrium points were derived as:
$(B^*,A^*) = (0,0)$, $(B^*,A^*) = (K_B,0)$:
(i). $(B^*,A^*) = (0,0)$: Sterile system (no bacteria, no antibiotics).
(ii).$(B^*,A^*) = (K_B,0)$: Maximum carrying capacity of bacteria, no antibiotics.
The global stability analysis determines whether trajectories originating from any initial condition (B(0),A(0)) converge to one of these equilibrium points.

6.2 **Lyapunov Function for Global Stability**

A **Lyapunov function** is a scalar function used to prove global stability. For global stability, we construct a function V(B,A) that decreases over time $(i.e\ \frac{dV}{dt} < 0)$ and satisfies the following conditions:

(i).V(B,A) ≥0 for all B,A and V(B,A)=0 only at the equilibrium point.

(ii).dV/dt ≤0 for all B,A with $\frac{dV}{dt} = 0$ only at the equilibrium point.

(a).Consider **Lyapunov Function**:

Let $V(B,A) = \frac{1}{2}B^2 + \frac{1}{2}A^2$

This function represents the total "energy" of the system, combining bacterial population and antibiotic concentration.

(b).Time Derivative of V:

$$\frac{dV}{dt} = B\frac{dB}{dt} + A\frac{dA}{dt}$$

$$Substitute\ \frac{dB}{dt}\ and\ \frac{dA}{dt}$$

$$\frac{dV}{dt} = B\left(r_B B\left(1-\frac{B}{K_B}\right) - \alpha AB\right) + A\left(-d_A A\right)$$

$$\frac{dV}{dt} = r_B B^2\left(1-\frac{B}{K_B}\right) - \alpha AB^2 - d_A A^2$$

(c). Behavior of $\frac{dV}{dt}$ *:*

The terms $-\alpha AB^2$ and $-d_A A^2$ are always negative or zero.

$r_B B^2\left(1-\frac{B}{K_B}\right)$ is positive for $0< B < K_B$ and negative for $B>K_B$.

Near $B=K_B$ and A=0, $dV/dt \rightarrow 0$ indicating a steady state.

6.3 Global Stability at each Equilibrium Point

The evaluation of global stability reveals essential information about system long-term conduct at all

equilibrium points.

6.3.1 Equilibrium (B^*,A^*)=(0,0)

The system maintains no bacteria while also having no antibiotics detected at this equilibrium point. This biological point signifies an environment free of bacterial multiplication together with an absence of antibiotic functions. Bacterial and antibiotic presence cannot disrupt the system equilibrium since it exists only in environments with no trace of either bacteria or antibiotics. The system demonstrates unstable behavior over the complete domain. The bacterial population will expand rapidly unless antibiotics control their growth following bacterial introduction. Since antibiotic introduction immediately begins antibiotic suppression of bacteria growth the equilibrium state at (0,0) becomes destabilized thereby making this equilibrium globally unstable for the system.

6.3.2 Equilibrium (B^*,A^*)=(K_B,0):

The bacterial population achieves its highest possible level at carrying capacity K_B and stays there when antibiotic concentrations remain zero. This equilibrium point becomes more reachable because when antibiotics decay fast (i.e. dA is high) or antibiotics do not work well (i.e. low α value) Under such circumstances antibiotics fail to control bacterial growth effectively which maintains the population at its maximum carrying capacity K_B. The bacterial population maintains a stout stability at K_B during situations when antibiotics fail to work effectively and exposure to antibiotics does not extend beyond normal limits. The system achieves stable status when the bacterial population reaches its carrying capacity value because dV/dt approaches zero. The bacterial system automatically achieves stable rest at the carrying capacity whenever antibiotics prove non-effective or rapidly lose their potency.

6.4 Biological Interpretation

Global Stability of (0,0) :

Making the bacteria extinct requires maintaining high and prolonged levels of antibiotic presence throughout time at (0,0). The concentrations of antibiotic A need to stay higher than a specified minimum value and the bacterial efficacy α needs to maintain an effective level in order to stop bacterial reproduction. A combination of antibiotic decay rates that are too quick (dA is high) plus antibiotic weak potency (low α) will prevent the system from eliminating bacteria. The bacterial population will maintain its presence while the system develops toward equilibrium point (K_B,0) which establishes bacterial numbers at the carrying capacity threshold.

Global Stability of (K_B,0):

The bacterial population will move toward and eventually settle at the carrying capacity K_B no matter what values initial conditions take when antibiotics become ineffective or naturally decay too quickly or are withdrawn. Medical authorities utilize this equilibrium point to maintain confident bacterial growth because bacteria continue to thrive without the addition of antibiotics. Present conditions suggest that lasting bacterial control depends on ongoing antibiotic administration since the system automatically moves toward this equilibrium point.

6.5 Numerical Simulation

Let me simulate the system to illustrate the global stability behavior under different initial conditions and parameters.

Python Program:

```
# Parameters for numerical simulation (exploring global stability)
        r_B = 0.1  # Growth rate of bacteria
        K_B = 1000  # Carrying capacity of bacteria
        alpha = 0.05  # Antibiotic efficacy constant
        d_A = 0.02  # Antibiotic decay rate

        # Initial conditions for multiple scenarios
        initial_conditions = [
           {"B0": 100, "A0": 10, "label": "Scenario 1: Moderate Initial Values"},
           {"B0": 500, "A0": 20, "label": "Scenario 2: High Initial Antibiotics"},
           {"B0": 900, "A0": 5, "label": "Scenario 3: Near Carrying Capacity"},
```

```
]

# Initialize figure
plt.figure(figsize=(14, 8))
# Loop through initial conditions
for condition in initial_conditions:
    # Extract initial values
    B0 = condition["B0"]
    A0 = condition["A0"]
    label = condition["label"]

    # Initialize arrays for bacteria and antibiotics
    B = np.zeros_like(time)
    A = np.zeros_like(time)
    # Set initial conditions
    B[0] = B0
    A[0] = A0

    # Numerical integration using Euler's method
    for i in range(1, len(time)):
        dB = r_B * B[i-1] * (1 - B[i-1] / K_B) - alpha * A[i-1] * B[i-1]
        dA = -d_A * A[i-1]
        B[i] = B[i-1] + dB * dt
        A[i] = A[i-1] + dA * dt

    # Plot bacterial population
    plt.plot(time, B, label=f"{label} - Bacteria (B)", linewidth=3)
    # Plot antibiotic concentration
    plt.plot(time, A, label=f"{label} - Antibiotics (A)", linestyle="--", linewidth=3)

# Add stability indicators
plt.axhline(y=K_B, color='red', linestyle=':', linewidth=2, label="Carrying Capacity (K_B)")
plt.axhline(y=0, color='black', linestyle='-', linewidth=2, label="Extinction Level")
# Additional plot settings
plt.title("Global Stability: Logistic Growth Model with Antibiotic Effect", fontsize=18,
fontweight='bold')
plt.xlabel("Time (t)", fontsize=14, fontweight='bold')
plt.ylabel("Population / Concentration", fontsize=14, fontweight='bold')
plt.legend(fontsize=12, loc="upper right", frameon=True, shadow=True)
plt.grid(True, linestyle='--', alpha=0.7)

# Display the plot
plt.show()
```

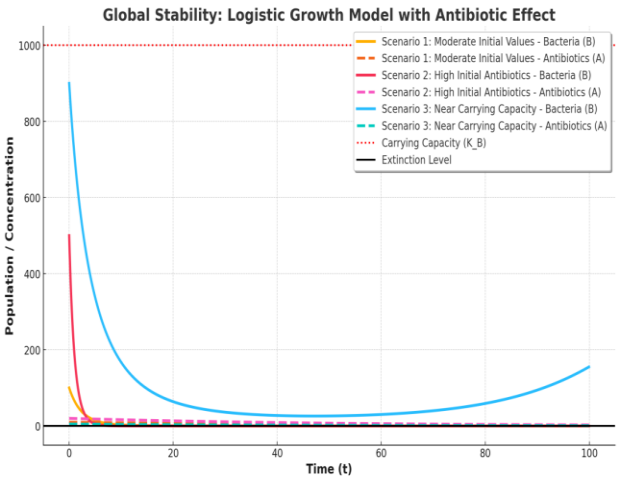


Figure (3) : Global Stability of the Model with Antibiotic Effect

Here is the simulation illustrating the **global stability** behavior of the system under different initial conditions:

7. CONCLUSIONS:

Different simulation variables in this model generate essential information regarding antibiotic interactions with bacterial populations.

(i). The system tracks Bacterial count and Antibiotic presence under Condition 1 while initial measurements remain reasonable before reaching the KB value. The population stabilizes at KB values because antibiotic deterioration rates lower antibiotic toxicity toward bacteria.

(ii). Bacterial expansion faces extreme inhibition at Condition 2 onset because the starting antibiotic levels are at their peak. The bacterial numbers increase as antibiotics decay but their expansion stops because the antibiotic levels are too low to keep the population fewer than the carrying capacity KB. In

(iii). The population of bacterial cells starts at elevated numbers close to their ecosystem maximum in Condition 3 making antibiotics essentially ineffective. During antibiotic decline the system quickly stabilizes at the value KB until the bacterial numbers achieve equilibrium.

Experimental characteristics constitute vital components for acquiring valuable information regarding the system's continuous operational character. The bacterial population exhibits coherent movement toward (KB,0) equilibrium resulting from inactive antibiotic administration at proper dosages. This conduct causes bacterial populations to achieve their carrying capacity. When long-lived antibiotics and eradication-resistant compounds do not work effectively bacteria reach the carrying capacity KB. Standard environmental conditions reject the possibility of zero bacterial population ($B \rightarrow 0$) from occurring. Bacterial elimination requires extended antibiotic preservation levels according to research simulations but bacteria maintain survival despite such full population removal.

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Brief Bio-data of the Authors:

K.V. Jayasri Kalyani : She is currently pursuing her B.Tech in Computer Science and Engineering (Second Year) at Bapatla Engineering College. Under the guidance of Dr. K.V.L.N. Acharyulu, Head of the Department of Mathematics at BEC, she has presented two research papers at an international conference on real-time applications:"A Mathematical Approach to Ecological Modeling with Antibiotic Effects on the Human Body: A Python Implementation" & "Local Stability and Global Stability Analysis of an Ecological Model on the Impact of Antibiotics on Humans with Numerical Simulation: A Python-Based Study". She maintains a strong academic record with an impressive CGPA and has completed certified courses in Python and Java. Her work has earned her appreciation from eminent scholars. Kalyani has also applied her technical skills in practical domains, completing projects such as: Hospitality Domain Data Analysis & Expense Tracking System. Her active participation and success in literary and cultural competitions in her childhood reflect her well-rounded personality and multifarious talents with numerous prizes & certificates of appreciation. Additionally, she has participated in several One-Week Online International Workshops, aimed at enhancing her understanding of real-world applications in various fields.

Dr.K.V.L.N.Acharyulu: He is working as Head, Department of Mathematics, Bapatla Engineering College, Bapatla which is a prestigious institution of Andhra Pradesh. He took his M.Phil. Degree in Mathematics from the University of Madras and stood in first Rank ,R.K.M. Vivekananda College, Chennai. Nearly for the last twenty two years he is rendering his services to the students and he is applauded by one and all for his best way of teaching. He has participated in many seminars and presented his plenty of papers on various topics. More than 150 research articles were published in various International reputed and peer reviewed Journals. He obtained his Ph.D from ANU under the able guidance of Prof. N.Ch.Pattabhi Ramacharyulu, NIT, Warangal. He edited more than 100 books under his Editorship. He wrote more than 15 chapters and authored five books. He is a Member of Various Professional Bodies and created three world records in research field. He received so many awards and rewards for his research excellency in the field of Mathematics.