# Modeling Bacterial Growth and Antibiotic Effects Using Partial Differential Equations

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## Abstract

This study proposes a mathematical model based on Partial Differential Equations (PDEs) to simulate bacterial growth, antibiotic effects, and the emergence of resistance. The model incorporates diffusion, reaction, and advection terms to describe bacterial proliferation, antibiotic action, and environmental constraints. By solving the PDEs numerically, we visualize bacterial population dynamics and resistance evolution. This approach provides a continuous and scalable framework for studying infection control and antibiotic resistance mechanisms.

## Introduction

Bacterial growth and antibiotic resistance are critical issues in public health. While discrete models like cellular automata are useful, continuous models based on PDEs offer a more mathematically rigorous framework for understanding bacterial dynamics. This study uses PDEs to model bacterial density, antibiotic concentration, and resistance development over time and space. The model is implemented in Python, leveraging numerical methods to solve the equations and visualize the results.

## Methods

The model is based on a system of Partial Differential Equations (PDEs) that describe the spatial and temporal dynamics of bacterial density (B), antibiotic concentration (A), and resistant bacteria density (RR):

1. Bacterial Growth and Diffusion:

$$\partial B/\partial t = DB \nabla 2B + rB(1 - B/K) - \mu AB$$

   - DB: Diffusion coefficient of bacteria.
   - r: Growth rate of bacteria.
   - K: Carrying capacity of the environment.
   - μ: Mortality rate due to antibiotics.

2. Antibiotic Diffusion and Decay:

$$\partial A/\partial t = DA \nabla 2A - \delta A$$

   - DA: Diffusion coefficient of antibiotics.
   - δ: Decay rate of antibiotics.

3. Resistant Bacteria Dynamics:

$$\partial R/\partial t = DB \nabla 2R + \gamma \mu AB$$

   - γ: Probability of developing resistance.

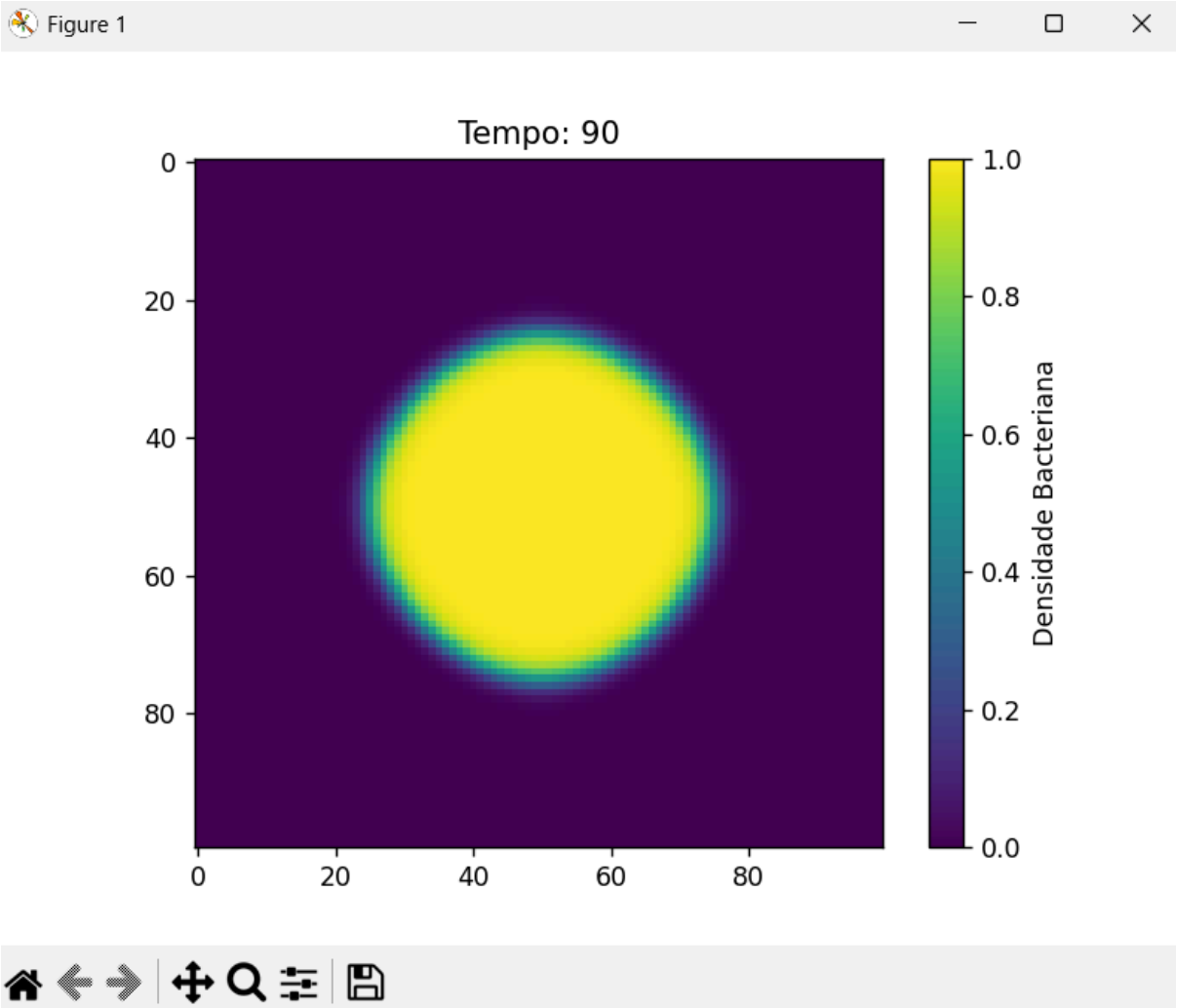
The equations are solved numerically using finite difference methods and Gaussian smoothing to ensure stability and accuracy.

## Results and Discussion

The simulation results show the following key dynamics:

1. Bacterial Growth:
    - Initially, bacteria grow and spread uniformly in the absence of antibiotics.
    - The growth follows a logistic pattern, reaching the carrying capacity of the environment.
2. Antibiotic Effects:
    - When antibiotics are introduced, bacterial density decreases significantly in regions with high antibiotic concentration.
    - The effectiveness of antibiotics depends on their diffusion rate and decay rate.
3. Resistance Development:
    - Resistant bacteria emerge in regions where antibiotics are present.
    - Over time, resistant bacteria dominate the population, highlighting the challenge of antibiotic resistance.
4. Environmental Constraints:
    - Physical barriers and nutrient limitations can restrict bacterial growth and spread.
    - The model demonstrates how environmental factors influence bacterial dynamics.

**Figure 1: Simulation of bacterial density over time. The circular pattern suggests isotropic growth without external environmental constraints. The density map indicates that bacterial proliferation follows a continuous gradient, with maximum density at the colony center.**




Source: Author's own work.

## Conclusion

This cellular automaton-based model effectively simulates bacterial growth in a homogeneous environment.

The results demonstrate continuous spatial expansion and density distribution, highlighting diffusion-like growth dynamics. Unlike PDE-based models, the cellular automaton approach provides a discrete yet visually intuitive representation of bacterial colonization. Future work could incorporate antibiotic effects, resistance development, and environmental heterogeneity to enhance the biological realism of the model.

## References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