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Simulation Of Bacterial Population Distribution Using Reaction-Diffusion Equation

Syahrul Mubarak^{1,a)}, Muhammad Yusri Ansyah Alam^{1,b)},
Muhammad Habibul Gustian^{1,c)}, Jonatan Arialdo Manurung^{1,d)},
Ikhsan Rasyidin^{1,e)}, Mutoharoh^{2,f)}

¹*Department of Physics, Universitas Negeri Jakarta, Jl R. Mangun Muka No. 1 Jakarta Timur
13220, Indonesia*

²*Industry Engineering Study Program, Universitas Krisnadwipayana, Bekasi, Jatiwaringin 13077,
Indonesia*

Email: ^{a)}syahrul_1306622074@mhs.unj.ac.id, ^{b)}yusri_1306622027@mhs.unj.ac.id,
^{c)}muhammad_1306622048@mhs.unj.ac.id, ^{d)}jonatan_1306622044@mhs.unj.ac.id,
^{e)}ikhsan_1306622040@mhs.unj.ac.id, ^{f)}mutoharoh@unkris.ac.id

Abstract

The distribution of bacterial populations in an environment is influenced by various factors, including the use of antibiotics and environmental conditions that affect the diffusion process. Diffusion is the movement of particles from a high-concentration environment to a low-concentration environment. The diffusion process is essential in the human body system, such as the diffusion of oxygen and carbon dioxide in the respiratory system and the diffusion of Ca in the synapse. This research uses a research method in the form of a simulation method. This method is carried out by designing a simulation program for spreading bacteria in a container with the Python programming language with the application of Partial Differential Equations. The PDE used in this research and observation is from the diffusion reaction function. This mathematical equation is used to predict the movement of bacteria in the available containers in this simulation method research. The animation of the distribution of bacteria in a container shows how fast the bacteria experience a diffusion reaction. The purple color on the screen shows the empty container and the yellow color is the bacteria starting from the highest to the lowest concentration. then there is the anti-bacterial soap factor, which is one drop denoted by a red line. From that, we can conclude that the larger the space, the faster the spread of bacteria. This study successfully developed a bacterial population distribution model using the reaction-diffusion equation and visualized the results with

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Matplotlib in Python. The application of this method allows us to solve the reaction-diffusion equation numerically and understand the pattern of bacterial spread under various environmental conditions. This study presents an educational simulation designed to enhance understanding of bacterial population dynamics through reaction-diffusion equations. The simulation effectively demonstrates key concepts in bacterial population distribution, providing valuable insights for educators. Visualization of the simulation results shows that Matplotlib effectively provides a clear and informative graphical representation of complex biological phenomena.

Keywords: bacterial populations, diffusion, differential equations

INTRODUCTION

The distribution of bacterial populations in an environment is influenced by various factors, including the use of antibiotics and environmental conditions that affect the diffusion process. Diffusion is the movement of particles from a high-concentration environment to a low-concentration environment. The diffusion process is essential in human body systems, such as the diffusion of oxygen and carbon dioxide in the respiratory system, the diffusion of Ca at the synapse in the nervous system, the diffusion of some molecules that occur in the kidneys to maintain blood homeostasis in the urinary system, and the diffusion of substances (drugs) in various human body systems. The diffusion process is fundamental in various biological and chemical systems, including the human body and microbiological environment. In this case, it is essential to understand how bacteria can spread and develop in an environment through diffusion processes and chemical reactions (Ignacio & Maldonado, 2024).

One of the causes of infectious diseases is bacteria (Casanova & Abel, 2024). In this world, there has been an evolution of bacterial resistance caused by the extensive use of antibiotics. This evolution has become one of the main challenges in treating infections. According to a report from the European Center for Disease Prevention and Control (ECDC), inappropriate use of antibiotics can accelerate the development of antibiotic resistance in bacterial communities. This suggests the need for a deep understanding of the interactions between antibiotics and bacterial populations and how changing environmental conditions can affect the spread of bacteria (David et al., 2019).

Infections are one of the leading causes of death in the world, with 15 million people dying in 2010. Bacteria and viruses were behind two-thirds of these deaths. In recent years, various applications and models have been developed to simulate the effects of antibiotic therapy on bacterial population dynamics. These simulations aim to better understand how various factors influence the spread and resistance of bacteria and support the development of more effective control strategies. One approach is modeling using reaction-diffusion equations, which allow a more detailed analysis of how interactions between diffusion and chemical reactions can affect the distribution of bacteria in a system (Lou & Salako, 2023).

Diffusion reactions are also relevant in studying microorganisms' growth and antibacterial activity. In this study, we took a microbiological subject, namely bacteria that experience diffusion in a container. Bacteria are microbiological and always experience movement by spreading when placed in a container with certain conditions. This characteristic encourages us to choose bacteria as the subject of this research (Han et al., 2021).

The reaction-diffusion model has been widely used to understand the characteristics and dynamics of the spread and growth of bacterial populations in an environment. In this study, our main focus is the spread of bacteria in a two-dimensional container, which describes the dynamics of the bacterial population in a container that is influenced by diffusion and logistic reactions for bacterial growth. This study uses independent variables, including diffusion coefficient and bacterial growth rate, and uses variables in the form of antimicrobial substances (soap). This soap or antimicrobial substance can inhibit bacterial growth and even eliminate bacteria, depending on the concentration. This research aims to study how the diffusion reaction is applied to the spread of bacteria and how bacteria can spread in a container by considering the factor of antimicrobial substances (soap). This model is also expected to predict how bacteria will spread and grow in various conditions and how the results of interventions with the addition of antimicrobial substances can affect their population.

Understanding bacterial population dynamics is crucial in educational settings. Simulations offer an interactive approach to grasping these complex concepts, providing students with a visual and practical tool to understand bacterial spread and resistance. Previous studies have explored simulations in various biological contexts, but few focus on integrating reaction-diffusion equations specifically for educational purposes. This study aims to address this gap by offering a simulation that enhances students' understanding of bacterial dynamics through reaction-diffusion equations. The simulation not only provides a detailed view of bacterial spread but also serves as an educational resource to improve comprehension of microbial community dynamics in various environments.

Therefore, this study, which focuses on simulating the spread of bacterial populations using reaction-diffusion equations, has the potential to significantly impact the field of infection control. By providing deeper insights into the mechanisms underlying bacterial spread and resistance, our approach is expected to lead to the development of more effective and sustainable infection control strategies. Additionally, it will improve our understanding of microbial community dynamics in various environments.

METHOD

This research uses a research method in the form of a simulation method. This method is carried out by designing a simulation program for the spread of bacteria in a container with the Python programming language with the application of Partial Differential Equations. The PDE used in this research and observation is from the diffusion reaction function, according to the mathematical equations, namely $\partial u / \partial t = D_b \nabla^2 u + ru(1 - u) - su$ and $\frac{\partial s}{\partial t} = D_s \nabla^2 s$. These mathematical

equations are not just theoretical but are used to predict the movement of bacteria in the container, demonstrating the practical application of our research.

The simulation was developed with interactive features to facilitate classroom use. It includes pre-defined scenarios and guided instructions for educators. Students interact with a user-friendly interface to adjust variables such as diffusion coefficients and bacterial growth rates, observing real-time visualizations of bacterial spread.

In this simulation method, we use several libraries in Python, such as numpy, scipy, and matplotlib. The creation of the simulation program begins by initializing the required coefficients, such as the diffusion coefficient and the start and end time of the simulation of the spread of bacteria and soap. Then, programming is done to display the visualization of the results in the form of a 2-dimensional depiction of the spread of bacteria in the container. In addition, a simulation of soap droplets at a particular time is also made to see the effect on the spread of bacteria in the container.

To support educators, we provide detailed user guides and interactive tutorials. These resources offer setup instructions, lesson integration tips, and troubleshooting support to maximize the simulation's educational effectiveness.

This simulation will visualize the results in the form of an animation of the spread of bacteria in the container. It will also show an animation when soap or antibacterial substances are dripped into one point in the container and the effect of the soap on existing bacteria.

RESULTS AND DISCUSSION

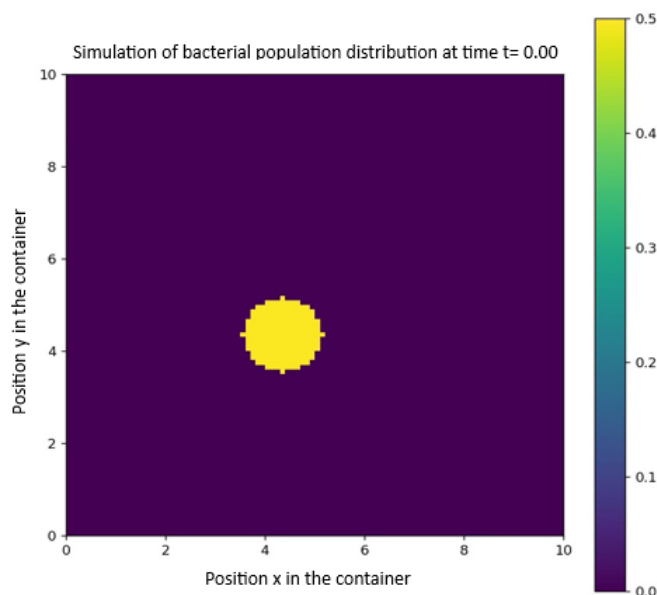


Figure 1. Simulation of bacterial population distributin at time $t=0.00$

This simulation starts from the distribution of bacteria at time = 0. In this condition, the bacteria are depicted as a full circle without any fading at all. This shows that the bacteria are still gathered in one container and have not experienced a diffusion reaction caused by the room in the container.

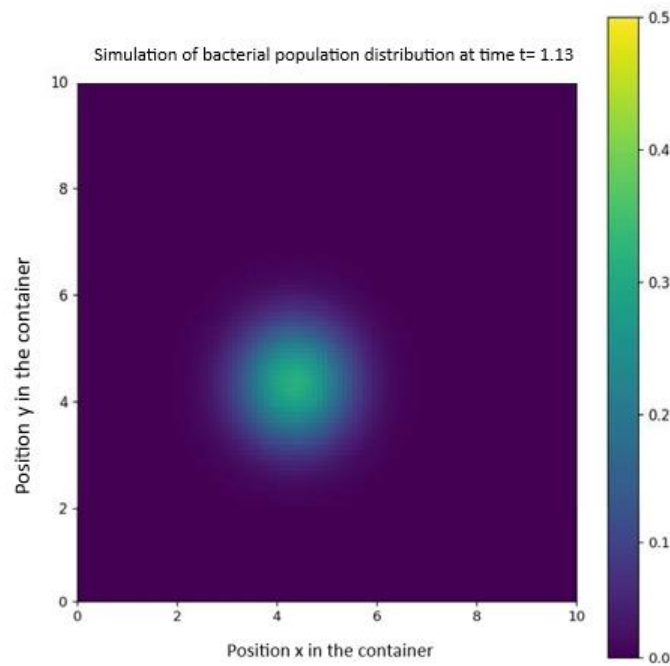


Figure 2. Simulation of bacterial population distributin at time $t=1.13$

Continuing from the previous simulation, the spread of bacteria has entered 1 second or precisely 1.13 seconds. In this condition, the bacteria are depicted with a circle shape, but they have started to fade. This is because the bacteria have begun to experience a diffusion reaction due to the influence of empty space in the container.

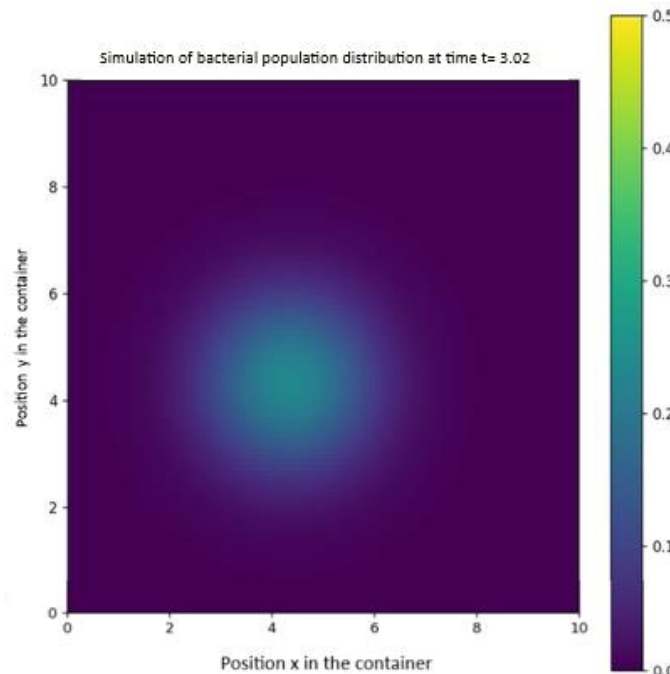


Figure 3. Simulation of bacterial population distributin at time $t=3.02$

Continuing from the previous simulation, this time, the distribution of bacteria has entered the 3rd second or precisely at 3.02 seconds. In this condition, the bacteria are depicted with a circle, but the shape of the circle is not well formed, and the bacteria are fading. This is because bacteria with

space in the container experience a diffusion reaction where the concentration of bacteria, starting from the highest concentration, slowly begins to decrease in terms of bacterial concentration.

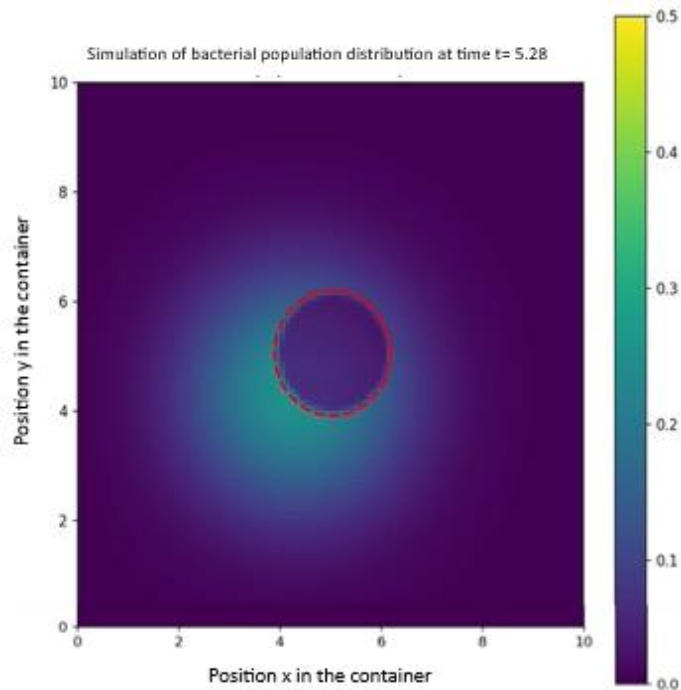


Figure 4. Simulation of bacterial population distributin at time $t=5.28$

Continuing from the previous simulation, this time, the distribution of bacteria has entered the 5th second, or precisely at 5.28 seconds. In this condition, something new is added, namely antibacterial soap. At this moment, the soap is only dripped one drop as an experimental material. The result is striking: the bacteria, though maintaining their shape, immediately disappear in the part that is dripped with antibacterial soap. This dramatic disappearance is due to the potent antibacterial factor contained in the soap, demonstrating its power to eliminate bacteria.

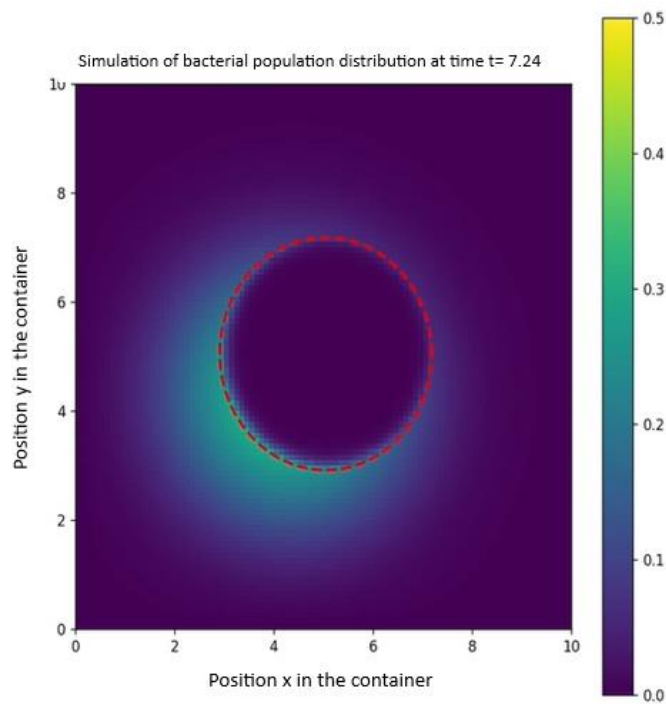


Figure 5. Simulation of bacterial population distributin at time t=7.24

Continuing from the previous simulation, this time, the distribution of bacteria has entered the 7th second, or to be precise, 7.24 seconds. The bacteria's shape remains in its previous form, but after being dripped with antibacterial soap, the bacteria that initially only disappeared in the part that was dripped by the bacteria began to affect the entire bacteria. This progressive disappearance is due to the increasing efficiency of the antibacterial factor contained in the soap, demonstrating its ability to eliminate bacteria over time.

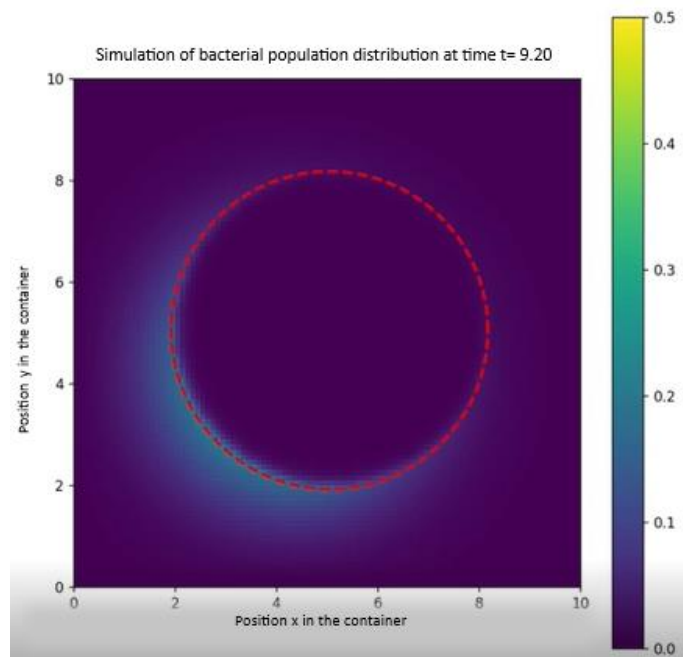


Figure 6. Simulation of bacterial population distributin at time t=9.20

Based on the previous simulation, this time, the distribution of bacteria has entered the 9th second or precisely at 9.20 seconds. In this condition, the bacteria began to disappear as a whole. The shape of the bacteria remains in its previous form, but after being dripped with antibacterial soap, the bacteria that initially only disappeared in the part that was dripped by the bacteria began to affect the entire bacteria. This is due to the antibacterial factor contained in the soap so that the bacteria in the container increasingly disappear.

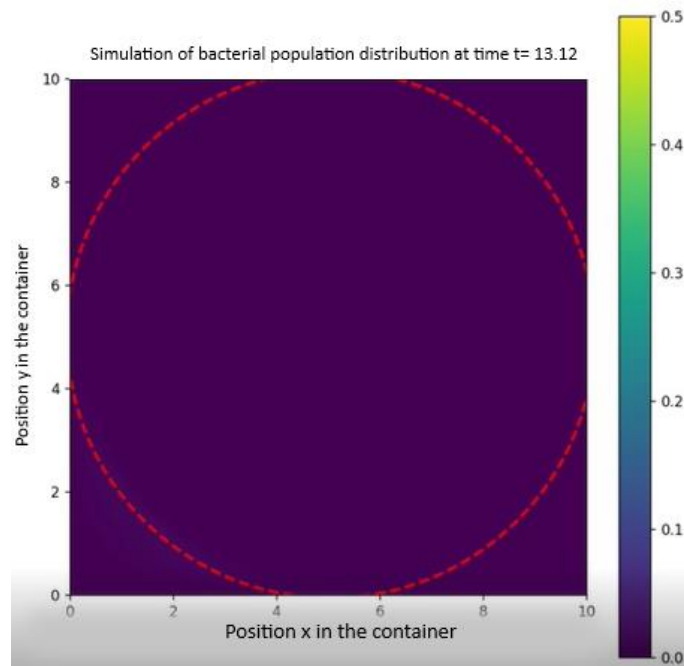


Figure 7. Simulation of bacterial population distributin at time t=13.12

When the simulation has entered its final period, this time, the distribution of bacteria has entered the 13th second or precisely at 13.12 seconds. In this condition, the bacteria have disappeared completely. The shape of the bacteria has wholly disappeared. This is due to the antibacterial factor contained in the soap so that the bacteria in the container disappear. This also proves that antibacterial soap can eliminate bacteria efficiently.

Moreover, finally, the distribution of bacteria has entered the 15th second. In this condition, the bacteria have entirely disappeared due to the influence of antibacterial soap.

The animation of the distribution of bacteria in a container shows how fast the bacteria undergo a diffusion reaction. The purple on the screen shows an empty container, and the yellow color shows bacteria starting from the highest to the lowest concentration. Then, there is the antibacterial soap factor, in which a red line denotes one drop. From there, we can conclude that the greater the space, the faster the spread of bacteria.

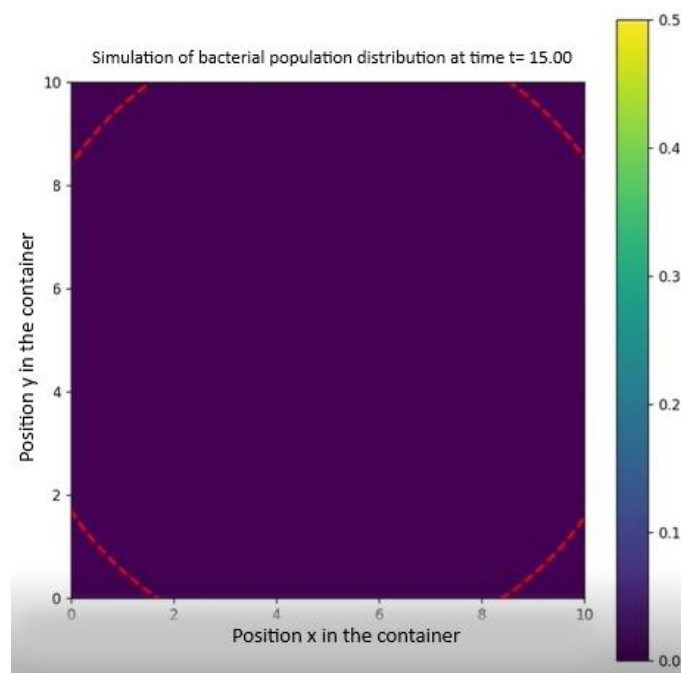


Figure 8. Simulation of bacterial population distributin at time t=15.00

Feedback from educators indicates that this interactive visualization enhances student understanding of bacterial population dynamics by offering a more engaging and dynamic approach compared to traditional teaching methods. Through this simulation, students can visually grasp how bacterial spread is influenced by factors such as space and the presence of antibacterial substances, thereby reinforcing their learning experience.

CONCLUSION

This research successfully developed a bacterial population distribution model using the reaction-diffusion equation and visualized the results with Matplotlib in Python. Applying this method allows us to solve the reaction-diffusion equation numerically and understand the pattern of bacterial distribution under various environmental conditions.

Visualization of simulation results shows that Matplotlib effectively provides clear and informative graphical representations of complex biological phenomena. These findings can help develop more effective bacterial control strategies and optimize industrial processes involving the growth of microorganisms.

This research, with its robust foundation, has the potential to significantly impact various fields such as microbiology, environmental engineering, and biotechnology. It paves the way for further studies and practical applications, including the extension of this model to different types of bacteria or the utilization of more advanced visualization techniques.

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