Application of interactive modeling in epidemiology education

Maftuxa Sayfullayeva [a], Odila Islamova, Zoya Chay, Ozoda Abduganiyeva, Shaxzadaxan Tadjibayeva

Tashkent University of Information Technologies named after Muhammad al-Khwarizmi, Tashkent, Uzbekistan

[a] *Corresponding author: maftuha87@mail.ru*

Abstract. Epidemiological modeling is a vital tool for understanding, forecasting, and controlling the spread of diseases. Given the complexity of these models, innovative approaches are required for their effective teaching and study. Interactive simulations serve as a powerful pedagogical tool for mastering epidemiological concepts within computer science education. This article explores the benefits of using interactive simulations in the educational process for researchers studying epidemiological models, the role of programming languages such as Matlab and Python, and provides an example of graphical visualization in Matlab.

INTRODUCTION

Epidemiological models (e.g., SIR, SEIR, etc.) are often based on systems of differential equations, and understanding their dynamics can be complex [1]. Interactive simulations provide the following advantages: Users can change model parameters (e.g., infection rate, recovery rate) and observe their impact on the spread of the disease in real time. Instead of passively listening to lectures, students and young researchers actively participate in the process, absorbing knowledge through practical experience. Depicting complex data and trends using graphs and charts facilitates understanding. Realistic epidemic conditions can be modeled in a safe environment.

For researchers, such simulations can become a valuable tool not only in developing and testing new models but also in explaining these complex topics to their students [2].

There are several programming languages and tools for creating interactive simulations of epidemiological models. Thanks to its powerful matrix calculations, an extensive library of mathematical functions, and graphical visualization tools (for example, creating interactive interfaces via App Designer), it is widely used in scientific and engineering fields, including epidemiological modeling. Its specialized toolboxes are of great importance to researchers. It is developing rapidly thanks to its simple syntax, many libraries (NumPy, SciPy, Matplotlib, Plotly, Bokeh), and open source code. Tools such as Jupyter Notebooks allow for interactive code writing and easy presentation of results [3].

Both languages are strong in their own way, and the choice may depend on the specific requirements of the project, available resources, and the personal preferences of the researcher. Users can change model parameters (e.g., infection rate, recovery rate) and observe their impact on the spread of the disease in real time. Depicting complex data and trends using graphs and charts facilitates understanding. Realistic epidemic conditions can be modeled in a safe environment.

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Let's consider the following parabolic problem in non-divergent form:

$$\frac{\partial u}{\partial t} = u^{n}\ \nabla(u^{m-1}\nabla u) - bu(1-u^{n-1}) \tag{1}$$

$$(t > 0,\ x \in R^N),\ u(0,x) = u_0(x),\ x \in R^N \tag{2}$$

Here $b > 0,\ m \geq 1,\ n > 1$. In [4], this problem is proposed as a mathematical model for the process of virus spread, and the properties of the solutions to this problem are obtained. In [5], the author considers the Cauchy problem for a degenerate parabolic equation in non-divergent form, representing a diffusion approximation of an epidemic spread model in a closed population without remission. The author proves the existence and uniqueness of a weakly defined solution, as well as some qualitative properties. We have proven that the solution to this problem possesses the properties of finite velocity of virus propagation and spatial localization of virus spread.

In fact, the substitution

$$u(t,x) = \exp(-bt)w(\tau(t),x) \tag{3}$$

in equation (1) leads it to the form

$$\frac{\partial w}{\partial \tau} = w^n \nabla (w^{m-1} \nabla w) + b \exp(b(n+m)\tau(t) w^n)$$

where

$$\tau(t) = \frac{1}{b(n+m)}(1 - \exp(b(n+m)t)) < \frac{1}{b(n+m)}$$

is since $\exp(b(n+m)t) = (b(m+n)\tau(t) - 1)^{-1}$.

Then, transforming to the variable $\tau(t)$, it is easy to see that the last equation is converted to the following form:

$$\frac{\partial w}{\partial \tau} = w^n \nabla (w^{m-1} \nabla w) + \frac{1}{b(n+m)\tau(t) - 1} w^n \tag{4}$$

Let us move to the self-similar equation by setting:

$$w(\tau(t),x) = f(\xi),\ \xi = |x| / [b(n+m)\tau(t) - 1]^{1/2}$$

Then we obtain the following self-similar equation:

$$L(f) \equiv f^n \xi^{1-N} \frac{d}{d\xi}(\xi^{1-N} f^{m-1} \frac{df}{d\xi}) + \frac{1}{2}\xi \frac{df}{d\xi} + f^n = 0 \tag{5}$$

Consider the function $\bar{f}(\xi) = (a - (m+n-1)\frac{\xi^2}{4})_+ 1^{1/(n+m-1)}$, $a > 0$, where the notation $(m)_+ = \max(0,m)$ is used. It is easy to calculate that $L(\bar{f}(\xi)) = -(N/2)\bar{f} + \bar{f}^n \leq 0$.

Since $\bar{f}^n \xi^{1-N} \frac{d}{d\xi}(\xi^{1-N} \bar{f}^{m-1} \frac{d\bar{f}}{d\xi}) + \frac{1}{2}\xi \frac{d\bar{f}}{d\xi}^n = (-N/2)\bar{f}$ the function $u_+(t,x) = \exp(-bt)\bar{f}(\xi)$ possesses the property $u_+(t,x) \equiv 0$ at $|x| \geq 2(a/(n-1))^{1/2}\tau(t) < \infty, n > 1$. Since $\max \tau(t) = \frac{1}{b(n+m)}$ the solution to problem (1) possesses the property of spatial localization. Viruses are concentrated in the region $|x| \leq [b(n+m)\tau(t) - 1]^{1/2}$.

This equation is a degenerate parabolic equation, commonly used to model complex physical or biological processes, such as the spread of a virus. Due to its nonlinear properties and the complexity of the analytical solution, numerical methods such as the finite difference method are applied.

Consider the application of the finite difference method to solve the equation in the one-dimensional case ($x \in \square^1$). We discretize the temporal and spatial variables:

Time step: $t_k = k\Delta t$, where $k = 0,1,2,\ldots$. Spatial step: $x_j = j\Delta x$, where $j = \ldots,-1,0,1,\ldots$.

Let the value of the function u at these points be denoted as $u_j^k = u(x_j, t_k)$.

Using the finite difference method, we approximate the derivatives:

Time derivative: Using the forward (explicit) difference:

$$\frac{\partial u}{\partial t} \approx \frac{u_j^{k+1} - u_j^k}{\Delta t}$$

Spatial derivative: The term $\nabla^T(v(u)\nabla u)$ is approximated using central differences:

$$\frac{\partial}{\partial x}\left(v(u)\frac{\partial u}{\partial x}\right) \approx \frac{1}{\Delta x}\left[v(u_{j+1/2})\frac{u_{j+1}^k - u_j^k}{\Delta x} - v(u_{j-1/2})\frac{u_j^k - u_{j-1}^k}{\Delta x}\right] \tag{6}$$

Where the values $u_{j\pm1/2}$ can be taken as average values, for example:

$$v(u_{j+1/2}) \approx v\left(\frac{u_{j+1}^k + u_j^k}{2}\right).$$

Substituting these approximations into the original equation, we obtain the following calculation formula for each point (j,k):

$$\frac{u_j^{k+1} - u_j^k}{\Delta t} = \frac{1}{(\Delta x)^2}\left[v_{j+1/2}(u_{j+1}^k - u_j^k) - v_{j-1/2}(u_j^k - u_{j-1}^k)\right] - bu_j^k(u_j^k)^{m-1} \tag{7}$$

From here, we can express the value u_j^{k+1} at the next time step:

$$u_j^{k+1} = u_j^k + \frac{\Delta t}{(\Delta x)^2}\left[v_{j+1/2}(u_{j+1}^k - u_j^k) - v_{j-1/2}(u_j^k - u_{j-1}^k)\right] - \Delta t \cdot b(u_j^k)^m \tag{8}$$

Based on this formula, the following algorithm is constructed:

Set initial conditions: $u_j^0 = u_0(x_j)$ for all j. Set boundary conditions: If the problem is considered on a bounded domain, boundary conditions are taken into account (e.g., $u(0,t) = u(L,t) = 0$).

Execute time loop: For each step $k = 0,1,2,\ldots$, the value u_j^{k+1} is calculated for each interior point j according to the specified formula.

This method is called an explicit scheme. For its stability, the time step Δt and the spatial step Δx must satisfy a certain condition.

RESEARCH RESULTS

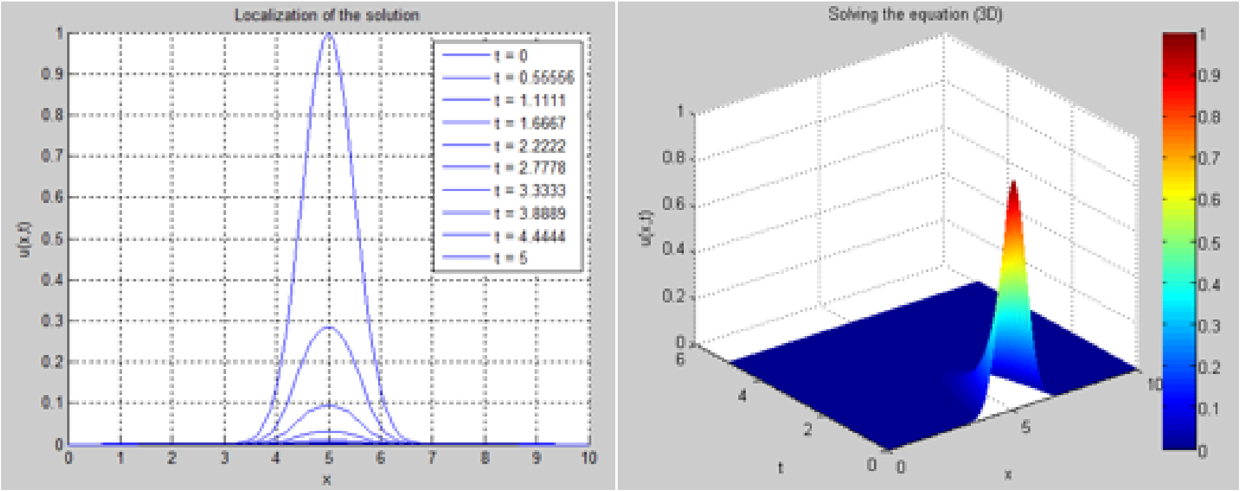

FIGURE 1. Graphs illustrating the virus spread with the property of spatial localization are presented.

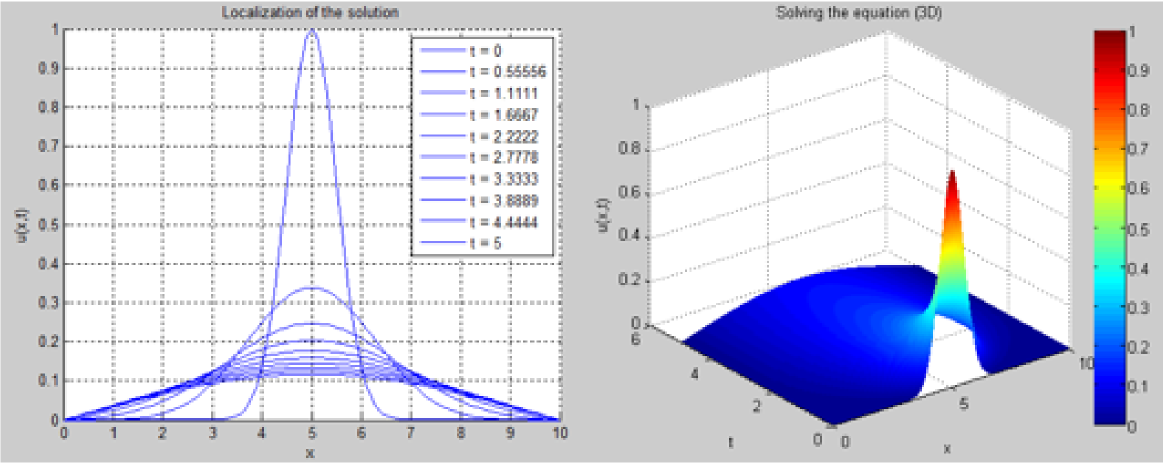

FIGURE 2. Evolution of virus distribution in the case of linear diffusion (n=1, m=1). The localization effect vanishes, resulting in the rapid expansion of the virus throughout the entire spatial domain without a sharp boundary.

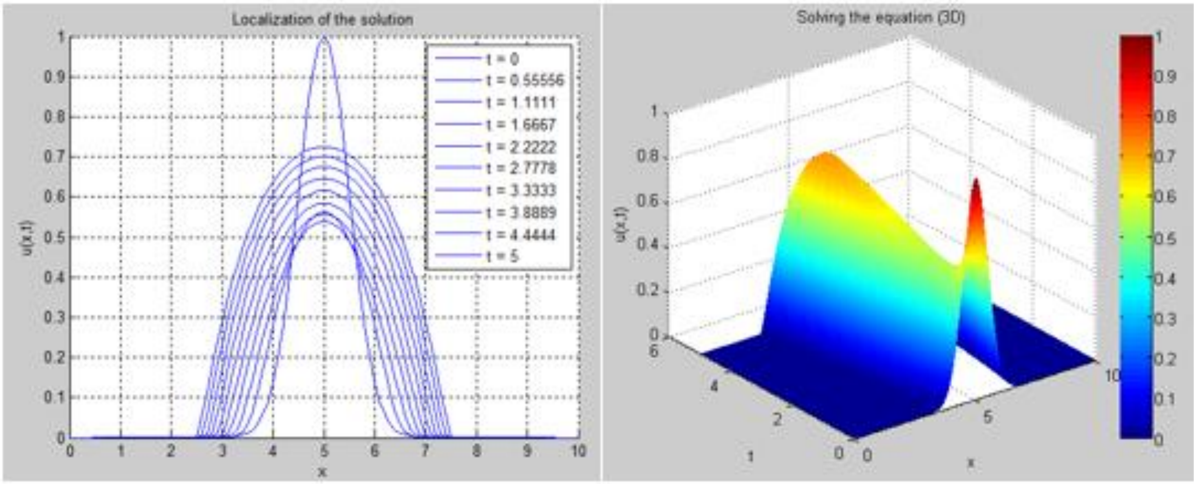

FIGURE 3. When the parameter b takes a negative value ($b < 0$), the reaction term acts as a source of growth rather than decay. In this case, the virus concentration does not stabilize or decrease; instead, it undergoes rapid exponential growth. Even if nonlinear diffusion ($n, m > 1$) is present, the intense multiplication of the virus can eventually overcome the localization effect, leading to an uncontrolled epidemic outbreak across the entire domain.

The spatial localization property in a virus model is of great significance. It suggests scenarios where an epidemic can be naturally contained or its spread inherently limited, in contrast to models predicting unlimited propagation [6, 7]. If the parameter b is negative ($b < 0$), the reaction term represents an intense proliferation source. This leads to an exponential growth in virus concentration, where the peak density increases rapidly over time. Under these conditions, the virus eventually overcomes the spatial constraints of the nonlinear diffusion, resulting in an uncontrolled and aggressive spread across the entire domain [8-9].

For interactive modeling using Matlab App Designer or GUIDE, sliders and input fields can be added to change parameters (n, m, initial conditions), with the graph updating automatically.

There are certain challenges in implementing interactive epidemiological simulations in education. Models that approximate real-life situations can be computationally complex. Developing high-quality simulations requires programming expertise. It is also crucial to effectively integrate these simulations into the educational curriculum.

Future developments are expected in areas such as the use of virtual and augmented reality (VR/AR) technologies, the application of machine learning algorithms for model parameter calibration, and the creation of more user-friendly interfaces. This will help make the study of epidemiological modeling more engaging and effective.

CONCLUSIONS

The integration of interactive simulations into the study of epidemiological dynamics represents a significant advancement in computer science education and mathematical modeling. This study demonstrates that utilizing high-level programming environments, such as MATLAB and Python, allows for a comprehensive exploration of complex biological processes through numerical analysis.

The developed numerical models effectively illustrate the property of spatial localization and the finite speed of virus propagation. By analyzing degenerate parabolic equations, students can observe the transition from a localized infection to an uncontrolled spread, providing deep insights into the stability of biological systems.

Through interactive dashboards (MATLAB App Designer), learners can perform real-time sensitivity analysis. Manipulating the reaction coefficient b and nonlinearity parameters n and m showcases the dual nature of epidemic scenarios: from natural containment ($b > 0$) to aggressive exponential growth ($b < 0$), fostering a sophisticated understanding of model behavior. The application of the finite difference bridges the gap between theoretical calculus and practical algorithmic implementation. This reinforces essential skills in discretization, convergence analysis, and the assessment of CFL (Courant–Fredric's–Loewy) stability conditions.

Interactive simulations transform the educational landscape by replacing static formulas with dynamic, observable experiments. This approach not only enhances the mastery of complex mathematical concepts but also cultivates the analytical mindset required for modern research. Looking forward, the evolution of this field lies in the integration of Virtual and Augmented Reality (VR/AR) and Machine Learning algorithms for automated parameter calibration. These technologies will further enhance the fidelity of educational resources, preparing the next generation of researchers to tackle global health challenges with advanced computational tools.

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