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Analyzing Disease Detection Dynamics with Nano Biosensors: an Analytical Approach Using the Homotopy Perturbation Method

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ABSTRACT

This study is necessary for early and accurate detection of infectious diseases including tuberculosis, cholera, and COVID-19 using nano biosensors. The paper primarily models and analyzes the detection dynamics among the circulating human population divided into susceptible, exposed, infected, detected, and recovered compartments. The detection dynamics are ruled by a system of nonlinear differential equations that will be solved analytically using the HPM to obtain the numerical solution. Graphical representations are used to explain the detection process and show how nano biosensors play a role in identifying and mitigating disease spread. The import of this work lies in the advancement of understanding the detection mechanisms of disease and providing a framework for improving performance in biosensors. The outcome reveals that applying HPM is feasible for modeling diseases, and discussions have identified some of the advantages of this method compared to other mathematical ones, which could be further used in simulation-based comparisons towards validation and optimization.

Keywords: Nano biosensors; Disease detection; Differential equations; HPM.

1. INTRODUCTION

Infectious diseases have become more complex in diagnosis and management because of high transmission rates and the hurdle in early detection. Nano biosensors open a new horizon in detecting diseases at the molecular level, allowing for real-time analysis and enhanced response to outbreaks. Nano-scaled biosensors, which combine nanomaterials and nanostructures, have been installed for biomedical applications such as pathogenic bacteria monitoring, virus recognition, and disease biomarker detection (Wang *et al.* 2013). Nano-biosensors offer several advantages and are ideally suited to biomedical applications, which could be made as extremely flexible devices that allow biomedical analysis with speediness, excellent selectivity, and high sensitivity (Kulkarni *et al.* 2022).

Nano biosensors detect biological markers of several diseases, providing an important tool for early intervention. In most cases, nanomaterials will be used to improve the sensitivity and specificity of a detection system to allow diagnoses at earlier stages and with greater accuracy. This paper provides a model of disease detection using nano biosensors based on compartmental dynamics and derives an analytical solution using the Homotopy Perturbation Method (HPM) (Kerry *et al.* 2021). Nano biosensors came into existence from two disciplines namely Nanotechnology and Biosensors. Usually, these are the types of sensors that come from nanomaterials, and the interesting thing is that they have not been mentioned here. Still, these are not the dedicated sensors that can catch such nano-range measures/activities. Nanomaterials with profound physiochemical properties that may differ intensely from the nanostructures generated at a macroscale belong exclusively to humanity from nanotechnology (Ramesh *et al.* 2023).

The global spread of infectious diseases has a significant negative impact with even large outbreaks such as COVID-19, tuberculosis and cholera emphasising the need for improved detection and control measures. There is no need to emphasize that the early and accurate identification of pathogens is a valuable tool for disease management, as it can allow timely interventions to halt widespread transmission and ultimately save lives (Mishra *et al.* 2019). Herein, nano biosensors have been developed as a potential approach in disease diagnosis with their reliable high sensitivity and specificity and real-time monitoring ability. These high-level devices use nanomaterial characteristics to identify the biomarkers at the milli-molecular level; hence, they effectively identify any disease in its initial stages (Ma *et al.* 2024).

Nanobiosensors, when used appropriately, can find an important place in modern disease detection by identifying and confirming infections early and accurately-as in the case of the disease-causing agents which manifest as tuberculosis, cholera, and COVID-19.

These biosensing devices can detect the biomarkers at extremely low concentrations through the incorporation of nanomaterials and biosensing technologies, paving the way for real-time monitoring for rapid intervention against outbreaks of infectious diseases. In this study, the dynamics of infectious disease detection are modeled using a SEIRD compartmental framework (Susceptible, Exposed, Infected, Detected, Recovered); while solving the mathematical modeling problem via Homotopy Perturbation Method (HPM) to analyze the improvement in disease detection rates attributed to nanobiosensors and the reduction in the spread of diseases. Nano biosensors have the potential to improve disease diagnosis early and rapidly with great accuracy. Such early diagnosis will facilitate timely medical intervention and better treatment outcomes for patients. Earlier diagnosis greatly improves the chances of containing disease outbreaks and will limit further propagation within communities through early diagnosis of diseases that are usually asymptomatic. Their integration within the public health strategies can boost global surveillance capability-a help in monitoring, predicting, and control of infectious diseases more efficiently. Furthermore, technological developments in nanomaterial-based biosensors would provide the selectivity, stability, and sensitivity plus cost-effectiveness that are key factors that make them a proposed solution for large-scale implementation in healthcare systems around the globe. Real-time monitoring capability allows for better outbreak management and reduced mortality along with enhanced preparedness for pandemic response, particularly in resource-limited settings. The integration of mathematical programming and biosensor technology in this study gives the necessary background for identification and intervention strategies for a more impactful global public health response.

Mathematical modeling can help us more comprehensively understand disease detection/dynamics and the impact of early intervention using nano biosensors. Compartmental model-based dynamics predict the disease transduction within a host population and the efficacies of various strategies, such as nano-biosensors, which detect these pathogens and curtail their spread (Govindan *et al.* 2024). PDE modeling of disease detection dynamics uses nonlinear differential equations describing the flow between compartments in susceptible, exposed, infected, detected, and recovered populations.Nanoparticles are integrated during fabrication, and the resulting biosensors are called nano-biosensors. Nanomaterials are always the most investigated and examined because of the wide range of bioanalytical activities they provide in fields such as bio-imaging, diagnostics, medication administration, and the treatment they enable (Ranjani *et al.* 2024).

These nonlinear systems are solved best using analytical methods, such as HPM. HPM is a semi-analytical method that can be effectively used to approximate solutions for nonlinear equations by reducing a complicated problem into a relatively simple problem with the help of a homotopy parameter (Saranya *et al.* 2020). It applies exceptionally effectively when traditional numerical approaches are too involved or time-consuming. Applying HPM helps introduce valuable information regarding how nano biosensors affect disease discovery and re-collection rates, hence improving detection strategies and ultimately reducing infections (Suganya *et al.* 2022).

This work finds an analytical solution to the disease detection dynamics using nano biosensors. Such a project, however, will comprise a mathematical model that exposes the ability of nano biosensors to alter the disease dynamics and solve the potential deployment systems for optimizing biosensor work in disease control. Despite the immense potential, the current application of nanotechnology in medicines and medical devices faces substantial technical challenges within the complex regulatory policies (Sreejith *et al.* 2024).

2. MATHEMATICAL MODEL FORMULATION

A mathematical model in disease detection by nano biosensors can be built by dividing the population into five compartments representing different disease progression stages. The population is divided into five compartments (Maugeri *et al.* 2020; Jung *et al.* 2023).

- **Susceptible (S):** Individuals who are vulnerable to contracting the disease.
- **Exposed (E):** Individuals exposed to the disease are not yet symptomatic.
- **Infected (I):** Infected but asymptomatic persons who have not yet been detected.
- **Detected (D):** Infected persons who nano biosensors have detected.
- **Recovered (R):** Persons who have recovered from the disease after either being detected or infected.

The total population N(t),at any time t, is the sum of these compartments:

$$N(t) = S(t) + E(t) + I(t) + D(t) + R(t) \quad \dots (1)$$

The dynamics between these compartments are governed by a nonlinear ordinary differential equations (ODEs) system. The susceptible population decreases as they get exposed to the disease, and exposed individuals progress to the infected stage at a rate σ. Infected individuals are either detected by nano biosensors at a rate α or remain undetected. Detected individuals can then recover at a rate μ, while the overall system may experience natural or disease-related death rates (Sabariah *et al.* 2023; Ahmad *et al.* 2020).

The following set of differential equations governs the dynamics of disease transmission and detection using nano biosensors:

2.1 Susceptible Population

The susceptible population refers to the individuals who have not encountered the disease but are likely to be infected. The group has no immunity and can be easily infected if exposed to an infected person. In a disease detection model, the susceptible group is the most important because the disease spread rate mainly depends on the interactions of the susceptible and infected populations. Preventive measures like vaccination or preventive behavior can reduce susceptible individuals and significantly mitigate the spread of the disease.

$$\frac{dS(t)}{dt} = -\beta S(t)I(t) \quad \ldots (2)$$

where β is the infection rate.

2.2 Exposed Population

The exposed population is those who have already been infected but are either not symptomatic or cannot be picked up by conventional methods or nano biosensors. This is the incubation period where the disease is present but not yet contagious or symptomatic in the individual. The exposed population is crucial in the model. It plays a vital role in disease dynamics since it will eventually move into the infected category and contribute to the spread of the disease once its infection becomes active (Heng *et al.* 2020).

$$\frac{dE(t)}{dt} = \beta S(t)I(t) - \sigma E(t) \quad \ldots (3)$$

where σ is the rate at which exposed individuals become infected.

2.3 Infected Population

This population consists of those infected; it is therefore represented by individuals who have begun developing symptoms or are within the infectious phase of the disease. These individuals can spread the disease amongst others and thus tend to be the center of treatment or detection efforts. In this model, the infected population, being critical for spreading the disease, shares it with the susceptible population. One main focus on controlling the outbreak is to reduce the number of infected individuals through detection and isolation (Dixit *et al.* 2021).

$$\frac{dI(t)}{dt} = \sigma E(t) - (\alpha + \delta)I(t) \quad \ldots (4)$$

where α is the rate at which nano biosensors detect infected individuals, andδ is the disease-induced death rate.

2.4 Detected Population

It is the population that has been detected to be infected through nano biosensors or any other type of diagnostic tool. The ability to detect earlier makes it possible to intervene early and initiate treatment on time to prevent further transmission. Recovering or further isolating detected patients would reduce the impression of the disease on the population. This compartment emphasizes the role of technology in managing and controlling the spread of disease by ensuring timely intervention (Chunyan *et al.* 2014).

$$\frac{dD(t)}{dt} = \alpha I(t) - \mu D(t) \quad \ldots (5)$$

where μ is the recovery rate for detected individuals.

2.5 Recovered Population

Recovered are those who have recovered from the infection and are no longer at risk for transmitting it, usually due to treatment or induction of natural immunity. In many models, recovery is associated with inducing immunity, such that recovered individuals are reinfected. The recovered population increases as individuals who are infected and detected recover from the treatment. This group determines the long-term consequences of a disease outbreak; many recoveries tend to contribute to herd immunity and reduce disease spread within the entire population (Akbari *et al.* 2024).

$$\frac{dR(t)}{dt} = \tau I(t) + \mu D(t) \quad \ldots (6)$$

where τ is the recovery rate

2.6 Initial Conditions

We assume the following initial conditions for the system:

$$S(0)=S_0, E(0)=E_0, I(0)=I_0, D(0)=D_0, R(0)=R_0 \quad \ldots (7)$$

These represent the initial population sizes in each compartment at time t=0.

2.7 Advantages of HPM

The following are the advantages posed in the modeling of disease detection dynamics using nano biosensors via nonlinear differential equations solution using Modified Homotopy Perturbation Method (MHPM). This approximation reduces the long computational time in comparison with classical numerical methods like the Runge-Kutta method. Another point of advantage comes from the fact that no small perturbation parameter is required, as is done in the classical perturbation technique, which makes HPM more flexible in treating highly nonlinear problems. It is

quite simple, and its implementation is straightforward; it reduces a complex nonlinear equation to a series of simpler solvable equations while retaining accuracy. The method gives more insight into parameter dependencies, which help epidemiologists in analysing effects of detection rate, infection rate, and recovery rate in developing disease models. HPM is truly remarkable in being widespread across several scientific fields-that includes epidemiology, nanotechnology, and biosensor optimization-representing the real versatility the method offers. Combining an accurate solution with computational efficiency and cope creates a unique proposition for using that type of method. Thus, a powerful method for improving mathematical modeling for disease detection and biosensor technology development exists in homotopy perturbation method.

3. SOLVING THE SYSTEM OF EQUATIONS

The system of differential equations can be solved numerically using methods such as the Runge-Kutta method for ordinary differential equations. We can, however, find approximate solutions using the Homotopy Perturbation Method (HPM) (Shanthi *et al.* 2014).

3.1 Homotopy Perturbation Method (HPM)

The Homotopy Perturbation Method (HPM) is a semi-analytical technique for solving linear and nonlinear differential equations. It combines the classical perturbation techniques with the homotopy concept in topology (Selvamani *et al.* 2024; Swaminathan *et al.* 2019; Anitha *et al.* 2024). One starts by deforming a complex problem into a simpler one, easily solved as a power series expansion. The steps to be followed are the following:

3.1.1 Define the Problem (Nonlinear System of Equations)

The compartments of the disease detection model are represented by the following set of nonlinear ordinary differential equations (ODEs) that we are working with:

$$\frac{dS(t)}{dt} = -\beta S(t)I(t) \quad \dots (8)$$

$$\frac{dE(t)}{dt} = \beta S(t)I(t) - \sigma E(t) \quad \dots (9)$$

$$\frac{dI(t)}{dt} = \sigma E(t) - (\alpha + \delta)I(t) \quad \dots (10)$$

$$\frac{dD(t)}{dt} = \alpha I(t) - \mu D(t) \quad \dots (11)$$

$$\frac{dR(t)}{dt} = \tau I(t) + \mu D(t) \quad \dots (12)$$

These equations model the interactions between the Susceptible (S), Exposed (E), Infected (I), Detected (D), and Recovered (R) populations, along with parameters like infection rate (β), detection rate (α), and recovery rate (μ).

3.1.2 Construct the Homotopy

The key idea of HPM is to construct a homotopy that continuously deforms a complex problem into an easy one. We introduce a homotopy parameter $p \in [0,1]$, such that when p=0, the problem is reduced to a simple, solvable form, and when p=1, the original problem is retrieved.

We define the homotopy H(ν,p)as:

$$H(\nu, p) = (1 - p)L(\nu) + pN(\nu) \quad \dots (13)$$

L(ν) represents a simplified version of the problem, typically a linear approximation and N(ν) represents the nonlinear system of equations.

For each differential equation, we introduce the homotopy as:

$$H(\nu, p) = (1 - p)[\text{ Linear operator}] + p[\text{ Nonlinear operator}]$$

$$\dots (14)$$

At p=0, the solution is easy to find; at p=1, it corresponds to the solution of the complete nonlinear problem.

3.1.3 Expand the Solution as a Power Series

We assume that the solution can be expanded in a power series in p:

$$S(t) = S_0(t) + pS_1(t) + p^2S_2(t) + \cdots \quad \dots (15)$$

$$E(t) = E_0(t) + pE_1(t) + p^2E_2(t) + \cdots \quad \dots (16)$$

$$I(t) = I_0(t) + pI_1(t) + p^2I_1(t) + \cdots \quad \dots (17)$$

$$D(t) = D_0(t) + pD_1(t) + p^2D_2(t) + \cdots \quad \dots (18)$$

$$R(t) = R_0(t) + pR_1(t) + p^2R_2(t) + \cdots \quad \dots (19)$$

3.1.4 Substitute the Series into the Homotopy Equation

Substitute the power series expansion for each differential equation into the homotopy equation. This will give a series of equations in terms of powers of p.

For example, for the Susceptible equation:

$$\frac{dS(t)}{dt} = -\beta S(t)I(t) \quad \dots (20)$$

Substituting the series expansion for S(t) and I(t), we get:

$\frac{d}{dt}(S_0(t)+pS_1(t)+p^2S_2(t)+\ldots) = -\beta(S_0(t)+pS_1(t)+\ldots)(I_0(t)+pI_1(t))$ … (21)

3.1.5 Equating Powers of p

By equating the coefficients of like powers of p, we get a system of equations to solve for each $S_0(t)$,$S_1(t)$, …

For example, at p^0:

$$\frac{dS_0(t)}{dt} = -\beta S_0(t) I_0(t) \quad \ldots (22)$$

At p^0:

$$\frac{dS_1(t)}{dt} = -\beta\left(S_0(t)I_1(t) + S_1(t)I_0(t)\right) \quad \ldots (23)$$

Solve each equation iteratively, starting from the most straightforward equation.

3.1.6 Iterative Solution

Start with the initial approximation S_0, E_0, I_0, D_0, R_0. These are typically chosen based on the initial conditions of the problem. Then, solve for higher-order terms $S_1(t), S_2(t)$, …

3.1.7 Summing the Series

Once the terms$S_0(t), S_1(t), S_2(t),$ ... are found, the solution for S(t) is:$S(t) = S_0(t) + S_1(t) + S_2(t) + \cdots$

Similarly, for other compartments:

$$E(t) = E_0(t) + E_1(t) + \cdots; I(t) = I_0(t) + I_1(t) + \cdots \quad \ldots (24)$$

$$D(t) = D_0(t) + D_1(t) + \cdots; \quad R(t) = R_0(t) + R_1(t) + \cdots \quad \ldots (25)$$

3.1.8 Solution for Our Model

Given the complexity of solving this system, we can rely on symbolic or numerical computation software (e.g., MATLAB, Mathematica) to calculate the solution.

3.2 Approximate Solution for Susceptible S(t)

Let us consider, S(0)=S_0 , I(0)=I_0. At time S(t) approximate to:

$$S(t) \approx S_0 e^{-\beta I_0 t} \quad \ldots (26)$$

This indicates that the population of the susceptible drops down as the infection continues. Although these solutions for S(t) may be applied, other approximate solutions will still need to be made for E(t), I(t), D(t), and R(t).

4. RESULT AND DISCUSSION

Hereafter, for the solution form, a schematic profile of S(t), E(t), I(t), D(t), and R(t) with time will be sketched to show the actual disease spreading by the role of nano biosensors in recognizing infections. The analytically expressed solutions for the different compartments are given below. Such solutions will provide a fascinating insight into how different parameters, such as detection rate (α) and infection rate (β), affect the disease detection process through nano biosensors. Simulating these solutions will help optimize detection techniques and early diagnosis and treatment responses.

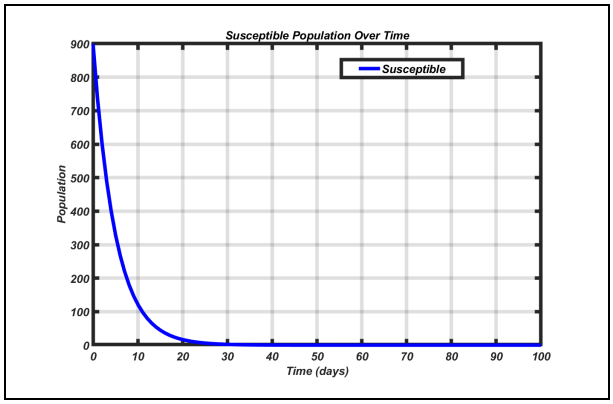

Fig. 1: Shows the dynamics of the susceptible compartment over time

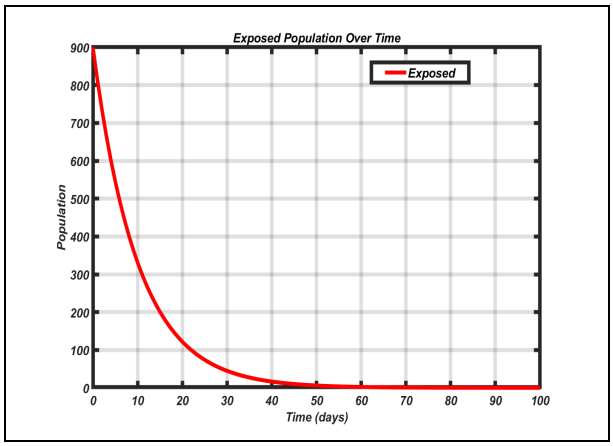

Fig. 2: Displays the dynamics of the exposed compartment over time

Figure 1 shows the change in the susceptible population over time as disease spreads. The x-axis represents time in days, while the y-axis indicates the total amount of susceptible individuals. The blue curve rapidly drops down, indicating a high rate of transmission, where the individual quickly moves into either the infected or detected state. Rapid decline, especially during the first 30 days, indicates the disease

operates aggressively, decreasing the count of the uninfected cohort in short time trajectories. Over time, the shape of the curve approaches zero, meaning that almost all individuals are sick, recovered, or detected. This follows the structure of epidemic models like SEIRD (Susceptible-Exposed-Infected-Recovered-Detected), meaning that effective surveillance systems, such as nano-biosensors, are important for early detection and containment of further cases. The figure emphasizes the importance of early intervention strategies in the successful outbreak control and improvement of public health.

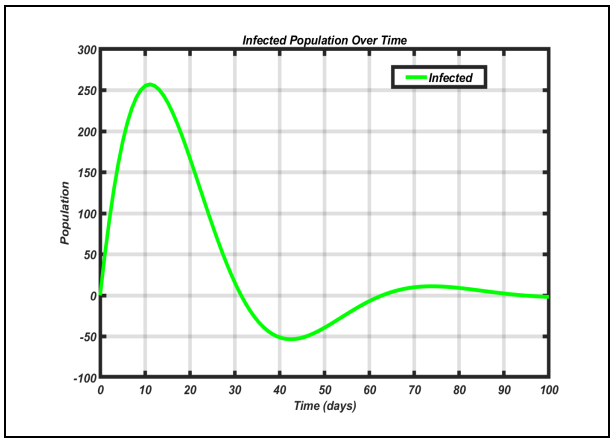

Fig. 3: Shows the dynamics of the infected compartment over time

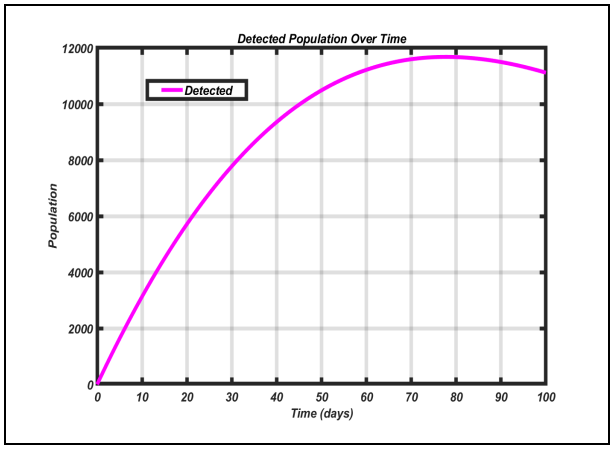

Fig. 4: Displays the dynamics of the detected compartment over time

Figure 2 trails the decline of the exposed population in some period, presumably within such an epidemiological frame as the SEIR model (Susceptible-Exposed-Infectious-Recovered). The x-axis means time, in days, the y-axis refers to the number of individuals in the exposed category. Initially, the exposed population was at around 900 but exponentially decreased in time to very close to zero. This is indicative that people were exiting the exposed category, by either becoming infectious or due to recovery mechanisms like quarantine or immunity. The red curve, labeled "Exposed," illustrates this process-a rapid decline in the beginning followed by slower change. The general behavior of the curve suggests that disease transmission and intervention measures cause a drastic change in the number of exposed people over time.

Figure 3 shows the dynamics of infected individuals over time in the epidemiological model. The x-axis represents time in days, and the y-axis denotes the number of infected population. Infected population increases sharply and reaches a maximum of about 250 in the first 10 days. This implies early rapid infectiousness around the onset of the outbreak. After this peak, infected individuals drop significantly, which could be interpreted as victims either recovering, becoming immune, or being placed under some sort of intervention regimes. By day 40, the curve dips below zero, indicating artifacts in the model (numeric inaccuracies) or even overestimation of transitions in the total population. Oscillations/re-emergence may be observed around day 60. Here the infected population is stabilizing around zero. The green curve labeled as "Infected" captures these dynamics, thereby indicating that there is a potential cyclic nature of disease transmission possibly dictated by factors such as reinfection, waning immunity, or other external interventions.

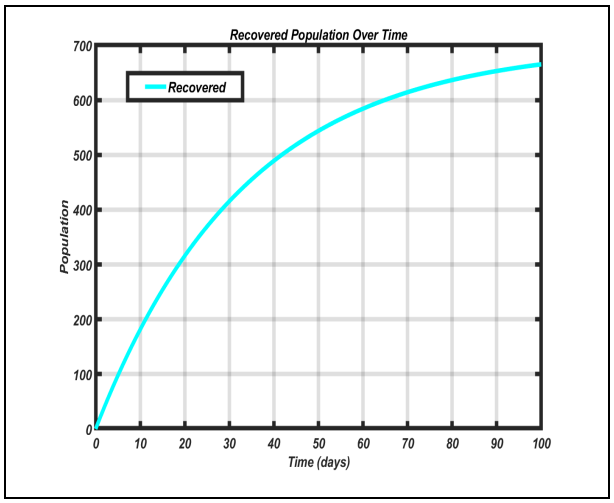

Fig. 5: Displays the dynamics of the recovered compartment over time

Figure 4 delineates the detected population over time within the context of an epidemiological model. The x-axis reflects days while the y-axis indicates the number of detected cases. The magenta curve denoted with "Detected" illustrates a continuous upwards motion in detected cases, from zero to around 12,000 by roughly day 80. This shows that as time passes, it is expected that more members of the population will become detected, quite possibly from an increase in testing, surveillance, or just the natural course of the outbreak. Toward the end, a small decline appears in the detected population,

possibly resulting from recovery, the diminished existence of the infected population in the community, or modification in detection tactics, etc. The shape of the curve shows that it is cumulative, where the percentage detection in early days rises at an exponential pace and then flattens once the outbreak stabilizes.

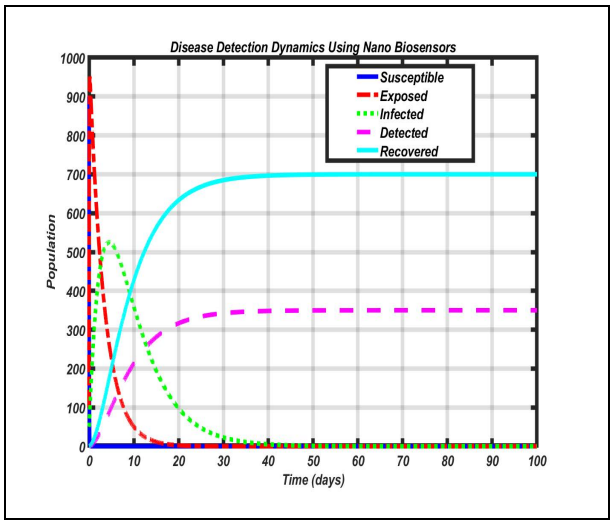

Fig. 6: Displays the SEIRD model with nano biosensor integration

Figure 5 represents the recovered population rises within time during an epidemic that is likely to have been modeled using an SIR (Susceptible-Infected-Recovered) framework. In the x-axis, time in days, ranging from 0 to 100, is represented. In the y-direction, the number of recovered goes from 0 up to about 700. Starting at zero, the curve in cyan illustrates the S-shaped growth where rapid growth is followed by leveling off. Hence, the rate of recovery is increasing with an increase in the number of people infected and recovering; rate of recovery will slow down as the outbreak is controlled and fewer members of society become infected. The initial leveling suggests that most of the population has gained immunity or that the spread of the infection is drastically reduced.

In Figure 6, SEIRD diagram shows the 100-day dynamics of the disease: close to "Detected" in the SEIRD model, probably showing the impact of nano biosensors in outbreak management. The susceptible population (blue) drops rapidly as the exposure (red, dashed) spikes early on, before being transitioned to the infected state (green, dotted), which, later, would reduce as recovery or detection takes place. The detected population (magenta, dashed) raises steadily, as nano biosensors play a role in spotting infections, eventually plateauing when the detecting levelled off. In parallel, there is the slow increase and stabilization of the recovered population (cyan) which indicates control over the outbreak or herd immunity. This underscores the influence of early detection on the epidemic's rate and resolution.

4.1 Limitations and Challenges of Using HPM

Although the Homotopy Perturbation Method (HPM) is efficient and computationally feasible for solving nonlinear differential equations in disease detection modeling, it has many limitations and challenges. An important one is that HPM yields an approximate analytical solution, rather than the exact solution, meaning that its accuracy depends on the number of terms kept in the perturbation series. The greater the number of terms, the more complex the mathematics of the higher-order approximations, which requires higher computational resources. HPM is for deterministic models, thus making it less suited for stochastic variations in disease spread, for instance, random variations of transmission rates or external environmental influences driving the process. The convergence of HPM strongly reposes on a somewhat well-selected starting approximation, which might hinder if roots are not guessed appropriately. Further, while HPM can effectively model disease detection dynamics, the practical implementation requires further validation via numerical simulations and real-world epidemiological data. These will be very important in addressing their challenges of hybrid modeling, enhanced numerical statistics, and advanced computational technologies toward optimizing the use of HPM for disease detection and biosensor applications.

4.2 Role of Simulations in Refining the Model and Validation Criteria

The incorporation of simulations is the key for refining the mathematical model, as it enables research to test a variety of combinations of different parameter values, detect detection efficiency, and maximize biosensor deployment strategies. By simulating the dynamics of different disease under different circumstances, adjustments to the model could be made for it to be able to adequately represent the real-world patterns of disease detection. Through computation simulation, an investigation will be made into the influence of various detection rates (α), infection rates (β), and recovery rates (μ) on disease spread and containment, thereby improving model prediction capabilities.

To examine the accuracy and reliability of the predictions made by the model, several validity tests will be used. First, the comparative analysis with real-world epidemiologic data from previous outbreaks of infectious diseases (such as COVID-19, tuberculosis, and cholera) will assess how well the model replicates real disease trends. In addition to this, error analysis and convergence testing will evaluate how far away the numerical simulations' analytical solutions are via the Homotopy Perturbation Method (HPM), thereby allowing consistency in the obtained results. The model must furnish evidence of reproducibility, that is, producing

similar predictions in the simulation when put under comparable input conditions. And lastly, critical metrics such as time to detection, height of the infection peak, and recovery trends will be assessed to show that the model would distinctively handle the impact of nano biosensors on disease detection. This series of validation will embolden confidence in the model's use to advance disease surveillance and optimize biosensor-based detection strategies.

5. APPLICATION OF THE HOMOTOPY PERTURBATION METHOD

Homotopy perturbation approach HPM is a potent analytical method geared towards solving nonlinear equations that may be experienced in different applications, such as nanotechnology. Let us look at the problem in nanotechnology.

5.1 Application of HPM in Nano-biosensors

The Homotopy Perturbation Method presents a modeling technique for analysing the dynamics of disease detection using nano biosensors. This technique provides complete approximate analytical solutions with very low computational costs than fully numerical methods. The Homotopy Perturbation Method generally reduces complexity while maintaining efficiency and accuracy as compared with traditional numerical techniques such as the Runge-Kutta method, which demands a considerable number of computational resources to solve nonlinear differential equations. In such cases, HPM is highly suitable for real-time disease monitoring and the integration of biosensors as faster and reasonably correct solutions are produced. However, while HPM is efficient in computational terms, it has limitations when it comes to being used for highly complex and mathematical large-scale epidemiological models. The precision of HPM is an equation that deviates with the number of terms in the perturbation series, so extremely nonlinear systems can become very arduous to generate a higher-order approximation. Furthermore, whereas HPM is probably more amenable for deterministic models, it might very likely require some modification for incorporating stochastic elements inherent in real-world detection of diseases. Nevertheless, HPM has always remained a potent application in optimizing disease detection models. With HPM, simulation runs much faster and allows one to fine-tune the performance of nano biosensors and deployment strategies. By combining the real-time data from biosensors with machine learning algorithms and HPM-based models, its computational feasibility can be further improved. This makes it a viable and scalable option to enhancing global disease surveillance and outbreak management.

5.2 Inferring the Diffusion of Nanoparticles in a Biologic Medium

5.2.1 Problem Statement

Let us look at the biological medium diffusion of nanoparticles. This process is also described using the nonlinear diffusion equation. Targeted delivery of drugs using nanoparticles to specific cells or tissues deserves such importance. The diffusion equation can be expressed as.

$$\frac{\partial C}{\partial t} = D\frac{\partial^2 C}{\partial x^2} + \alpha C^2$$

Where

- C(x,t) represents the concentration of nanoparticles at position x and time t.
- D stands for the diffusion constant.
- α repose a reaction rate constant, generally assumed to represent the interaction of nanoparticles with the biological milieu.

The boundary conditions of the problem could be:

- $C(0,t)=C_0$, where C_0 is the initial concentration of nanoparticles at x=0,
- $\frac{\partial C}{\partial x}(L,t) = 0$ at x=L, indicating no flux at the boundary.

5.2.2 Step-by-Step Solution Using HPM

Step 1: Construct the Homotopy

The HPM introduces a homotopy parameter $p\in[0,1]$ and constructs a homotopy that continuously deforms from an initial approximation to the exact solution. We rewrite the original equation as follows:

$$\frac{\partial C}{\partial t} = D\frac{\partial^2 C}{\partial x^2} + \alpha C^2$$

We introduce a homotopy function:

$$H(C,p) = (1-p)\left(\frac{\partial C}{\partial t} - D\frac{\partial^2 C}{\partial x^2}\right) + p\left(\frac{\partial C}{\partial t} - D\frac{\partial^2 C}{\partial x^2} - \alpha C^2\right) = 0$$

For p=0, we have the linear problem:

$$\frac{\partial C}{\partial t} = D\frac{\partial^2 C}{\partial x^2}$$

For p=1, we recover the original nonlinear problem.

Step 2: Express C as a Power Series in p

We assume the solution C(x,t) can be expressed as a power series in p:

$$C(x,t) = C_0(x,t) + pC_1(x,t) + p^2C_2(x,t) + \cdots$$

When p=1, this series gives the exact solution.

Step 3: Substitute the Series into the Homotopy Equation

Substituting the series expansion into the homotopy equationH(C,p)=0, we get:

$$\frac{\partial(C_0 + pC_1 + p^2C_2)}{\partial t} = D\frac{\partial^2(C_0 + pC_1 + p^2C_2)}{\partial x^2} + p\alpha(C_0 + pC_1 + \cdots)^2$$

Matching terms with the same power of p:

For p^0:

$$\frac{\partial C_0}{\partial t} = D\frac{\partial^2 C_0}{\partial x^2}$$

This is a linear diffusion equation.

For p^1:

$$\frac{\partial C_1}{\partial t} = D\frac{\partial^2 C_1}{\partial x^2} + \alpha {C_0}^2$$

Step 4: Solve the Resulting Equations Sequentially

Solving for $C_0(x,t)$

The linear equation for C_0:

$$\frac{\partial C_0}{\partial t} = D\frac{\partial^2 C_0}{\partial x^2}$$

Assume an initial condition $C_0(x,0) = C_0 \exp(-\lambda x^2)$, a typical form for diffusion processes.

The solution is:

$$C_0(x,0) = C_0 \exp(-\lambda x^2) \exp(-D\lambda t)$$

Solving for C_1 (x,t)

Substituting C_0(x,t) into the equation for C_1:

$$\frac{\partial C_1}{\partial t} = D\frac{\partial^2 C_1}{\partial x^2} + \alpha {C_0}^2$$

This partial differential equation can be solved using standard techniques like the separation of variables, and the result is a more complex solution, which also includes the effect of the nonlinear interaction term $\alpha {C_0}^2$.

Step 5: Construct the Final Solution

The final solution for C(x,t) will be the initial terms' sum.

$$C(x,t) = C_0(x,t) + C_1(x,t) + C_2(x,t) + \cdots$$

Interpretation of the Solution:

The HPM provides an approximative analytical solution to the nonlinear diffusion equation that describes nanoparticle transport in biological tissue. The first term C_0 is a linear solution, and all terms beyond the first are in principle nonlinear.

5.3 Heat Transfer in Nanofluids Application

Nanofluids are fluids that have small, suspended nanoparticles. This implies improved thermal properties and greater applicability in heat transfer systems such as electronic cooling or heat exchangers. A typical problem involves determining the temperature distribution in a nanofluid flowing through a channel.

5.3.1 Problem Statement

A 1D heat transfer model for a nanofluid is given by the following nonlinear partial differential equation:

$$\frac{\partial T}{\partial t} = k\frac{\partial^2 T}{\partial x^2} + \alpha T^n$$

Where:

T(x,t) - is the temperature distribution,
k - is the thermal conductivity,
α - is a coefficient representing the heat generation due to nanoparticles,
n - is a constant representing the degree of nonlinearity.

5.3.2 Solution Procedure using HPM

Now predict T by constructing the homotopy:

Let the homotopy equation be:

$$H(T,p) = (1-p)\left(\frac{\partial T}{\partial t} - k\frac{\partial^2 T}{\partial x^2}\right) + p\left(\frac{\partial T}{\partial t} - k\frac{\partial^2 T}{\partial x^2} - \alpha T^n\right) = 0$$

Let p∈[0,1] denote the parameter embedding.

Step 1: Expand T(x,t) as a power series in p.

$$T(x,t) = T_0(x,t) + pT_1(x,t) + p^2T_2(x,t) + \cdots$$

Substituting in a homotopy equation: Subsequently, we can collect the coefficient for each power of p and solve them sequentially:

p^0term gives:

$$\frac{\partial T_0}{\partial t} = k\frac{\partial^2 T_0}{\partial x^2}$$

The solution is of the form:

$$T_0(x,t) = A\exp(-k\lambda^2 t)\cos(\lambda x)$$

Where initial and boundary conditions determine A and λ.

p^1 term gives:

$$\frac{\partial T_1}{\partial t} = k\frac{\partial^2 T_1}{\partial x^2} + \alpha {T_0}^n$$

Substituting $T_0(x,t)$ into this equation:

$$\frac{\partial T_1}{\partial t} = k\frac{\partial^2 T_1}{\partial x^2} + \alpha(A\exp(-k\lambda^2 t)\cos(\lambda x))^n$$

Assuming$T_1 = B\exp(-k\lambda^2 t)\cos(\lambda x)$, substituting back, we can solve for B.

The final solution combining both terms up to the first order in p is approximately:

$$T(x,t) \approx A\exp(-k\lambda^2 t)\cos(\lambda x) + \frac{\alpha A^n}{(k\lambda^2)n}(1 - \exp(-nk\lambda^2 t))\cos(\lambda x)$$

The complete solution provides insight into how nanoparticles influence heat transfer, aiding in optimizing nanofluid-based cooling systems.

5.4 Reaction Kinetics of Nanocatalysts Application

Nanocatalysts enhance reaction rates due to their large surface area, playing a significant role in chemical processes like hydrogen production or pollutant degradation. Understanding their kinetics can involve solving nonlinear rate equations.

5.4.1 Problem Statement

Consider a chemical reaction catalyzed by nanoparticles with the following nonlinear ordinary differential equation representing the concentration C(t) of a reactant:

$$\frac{\partial C}{\partial t} = -kC^m$$

Where:

C(t) - is the concentration of the reactant over time,
k - is the reaction rate constant,
m - is an order of reaction that might be non-integer due to nanoscale effects.

5.4.2 Step-by-Step Solution Using HPM

Step 1: Construct the homotopy:

Create a homotopy equation:

$$H(C,p) = (1-p)\left(\frac{\partial C}{\partial t} + kC\right) + p\left(\frac{\partial C}{\partial t} + kC^m\right) = 0$$

Step 2: Expand C(t) as a power series in p:

$$C(t) = C_0(t) + pC_1(t) + p^2C_2(t) + \cdots$$

Step 3: Substitute into the homotopyequation:Collecting terms of the same power in p, solve sequentially:

p^0term gives:

$$\frac{\partial C_0}{\partial t} = -kC_0$$

The solution is of the form:

$$C_0(t) = C(0)e^{-kt}$$

p^1 term gives:

$$\frac{\partial C_1}{\partial t} = -kC_1 + k{C_0}^m$$

Substituting $C_0(t) = C(0)e^{-kt}$ into this equation:

$$\frac{\partial C_1}{\partial t} = -kC_1 + k\left(C(0)e^{-kt}\right)^m$$

To solve this, use an integrating factor$(t) = e^{kt}$

$$e^{kt}\frac{\partial C_1}{\partial t} + ke^{kt}C_1 = kC(0)^m e^{-k(m-1)t}$$

Integrating both sides gives:

$$C_1(t) = \frac{C(0)^m}{1-m}\left(e^{-k(m-1)t} - e^{-kt}\right)$$

The final solution for C(t) combining$C_0(t) + C_1(t)$ is

$$C(t) \approx C_0(t)e^{-kt} + \frac{C(0)^m}{1-m}\left(e^{-k(m-1)t} - e^{-kt}\right)$$

These solutions give insight into the behavior of nanofluid heat transfer and nanocatalyst reaction kinetics using the Homotopy Perturbation Method (HPM). These solutions help understand the enhanced catalytic activity

of nanoparticles and optimize conditions for industrial chemical processes.

6. CONCLUSION

This study explicitly demonstrates the potential of nano biosensors as a disruptive technology for the early and accurate detection of infectious diseases like tuberculosis, cholera, and COVID-19. The dynamics of disease detection by incorporating a compartmental model governed by nonlinear differential equations proved very effective. The HPM provided a good and efficient method of solving these equations, offering an apparent analytic and numerical understanding of the detection process. Graphical results focus on how nano biosensors can affect the spread of diseases by producing and identifying infections promptly. Moreover, the work lays a solid foundation that could lead to the optimization of biosensor performance in real life and contributes to more advanced insight regarding mechanisms of disease detection. Results are described with the benefits of HPM during the disease modeling, accompanied in the simulation-based validations and refinements for ensuing implementations of biosensors into global health applications.

Future Directions and Enhancements in Nano-biosensor Modeling

The next phase of this research will focus on enhancing the mathematical model to improve the precision and functionality of nano biosensor-based disease detection systems. One of the main improvements will consist in the incorporation of stochastic elements, meaning that these new components will allow for a much better representation of the real-world variability in terms of disease transmission and existing rates of detection. Furthermore, the inclusion of real-time epidemiological data in the models will be prioritized, as it allows predictions made by the model to correlate with real-world disease events. To then further optimize nano biosensor technologies, we will focus on hybrid modeling approaches, combining the Homotopy Perturbation Method with advanced numerical techniques for improved computational accuracy and efficiency. This helps guide the adaptation of disease conditions within the model and reinforce the predictive abilities of biosensor-based surveillance systems.

Another crucial step is model validation with larger scale simulation and live biosensor data, which provides the insight into how different detection rates (α) and intervention strategies affect the disease spread and containment. Other efforts may include integration of the model with machine learning algorithms to allow automated optimization of biosensor performance with dynamism in disease spreads. In the end, these initiatives will lead to the development of a more powerful, scalable, and more globally relevant nano biosensor system which can find application in early disease detection, preventing outbreak and better decision-making by public health managers.

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