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Edition 2025 – Modeling of Epidemic Propagation Phenomena
(NCMBM'2025) December 9, 2025, M'sila (Algeria).

CERTIFICATE OF PARTICIPATION

The organizing committee of the Fourth National Conference on "Mathematics, Biology and Medicine" certifies that:

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Predicting Cutaneous Leishmaniasis Dynamics Through Mathematical Modeling.

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≪ **Modeling of Epidemic Propagation Phenomena** ≫
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Predicting Cutaneous Leishmaniasis Dynamics Through Mathematical Modeling

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Abstract

This study introduces an advanced SEIAR(H)-SI(M) model designed to analyze and understand the dynamics of cutaneous leishmaniasis transmission. The model is applied to recent health data from Algeria, focusing on M'Sila province, which has recently recorded a high disease incidence. We examine the existence, uniqueness, and stability of the solutions, as well as the basic reproduction number, equilibrium points, and their stability. The results reveal that the disease-free equilibrium is stable when the basic reproduction number is less than one, indicating that the disease can be controlled through appropriate preventive measures. Simulations show a direct correlation between transmission rates and the number of susceptible and infected individuals, emphasizing the importance of timely interventions to prevent disease outbreaks. Recommended strategies include environmental control measures, awareness campaigns, and early diagnosis and treatment protocols. This study highlights the necessity of continuously monitoring health data and adjusting model parameters to ensure its effectiveness and sustainability. The findings emphasize the importance of targeted interventions to reduce the basic reproduction number below one, thereby controlling the spread of cutaneous leishmaniasis and safeguarding public health.

Key words: Mathematical modeling; cutaneous leishmaniasis; numerical simulation; estimation parameters.

2010 Mathematics Subject Classification: 34A08; 62P10; 92-10; 92B05; 93-10.

1. Introduction

Cutaneous leishmaniasis is one of the most prevalent parasitic diseases worldwide, posing a significant public health challenge in numerous countries, particularly in the Middle East, North Africa, and parts of South America. The disease is primarily transmitted through the bite of infected female Phlebotomus sandflies, which thrive in semi-arid and rural environments. Cutaneous leishmaniasis is characterized by the appearance of skin ulcers or lesions, which, although not fatal, can cause permanent scars (Figure 1). In some cases, the disease can progress to more severe forms if left untreated [1].

Cutaneous leishmaniasis represents an increasing burden, with the World Health Organization (WHO) estimating over 700 000 to 1 million new cases annually, primarily in endemic regions [1]. The disease is transmitted through the bite of infected female Phlebotomus sandflies, which inject Leishmania parasites into the host's skin. These parasites then multiply within macrophages, leading to skin ulcers or lesions (Figure 2). The spread of this disease is driven by several factors, including urbanization,

Figure 1: Symptoms of cutaneous leishmaniasis [1].

environmental changes, population displacement, and socioeconomic challenges that hinder access to healthcare. Developing effective strategies for prevention, treatment, and control of cutaneous leishmaniasis is essential to reduce its impact on affected communities [2].

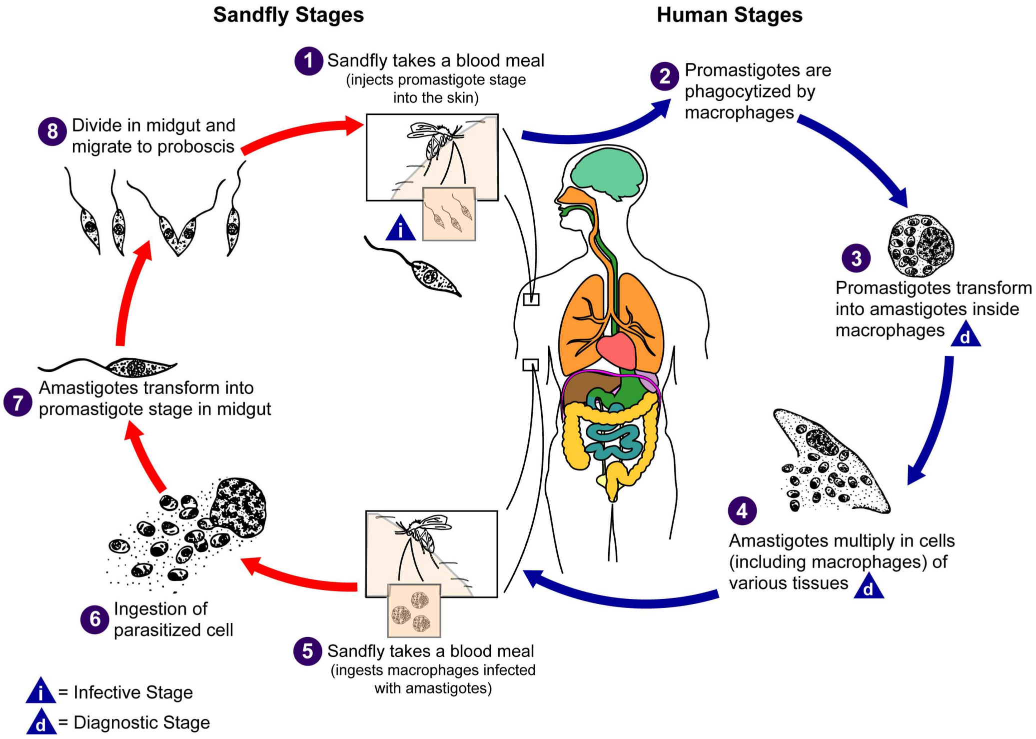

Figure 2: Life-cycle of cutaneous leishmaniasis transmission [3].

Mathematics play a crucial role in addressing the challenges posed by infectious diseases, including cutaneous leishmaniasis [4, 5, 6, 7, 8]. Mathematical models use equations to simulate the complex dynamics of disease transmission between humans and sandflies. By employing ordinary differential equations, these models provide insights into how various factors–such as environmental changes, population displacement, healthcare accessibility, and control interventions–affect the spread of the disease.

Mathematical models not only help in understanding current epidemic dynamics but also serve as predictive tools for assessing the potential outcomes of proposed control strategies before their implementation [9, 10, 11, 12]. For instance, these models can estimate the impact of public health measures such as vector control programs, improved sanitation, and increased healthcare accessibility [13, 14]. They allow for the simulation of different scenarios to evaluate the effectiveness of various interventions, aiding policymakers in designing optimal strategies to control the disease.

By incorporating real epidemiological data from affected regions, mathematical models can accurately identify the factors contributing to outbreaks and highlight critical areas for intervention to reduce disease spread.

In this study, the dynamics of the epidemic are modeled by dividing the total human population (denoted as H) into five distinct classes:

- S_H: Susceptible individuals.
- E_H: Exposed individuals.
- I_H: Symptomatic infectious individuals.
- A_H: Asymptomatic infectious individuals.
- R_H: Recovered individuals.

Additionally, the sandfly population surrounding the human population (denoted as M) is divided into:

- S_M: Susceptible sandflies.
- I_M: Infected sandflies.

The parameters of the SEIAR(H)–SI(M) model are defined as follows:

- Λ indicates the rate of increase in the susceptible individuals.
- λ represents the rate of increase in the susceptible sandflies.
- $\mu < \Lambda$ expresses the natural death rate for humans.
- $\upsilon < \lambda$ presents the natural death rate of sandflies.
- β is the probability rate of disease transmission from infected sandflies to susceptible humans.
- γ is the probability rate of disease transmission from infected humans to susceptible sandflies.
- κ represents the proportion of recovered individuals who lose temporary immunity and become susceptible again.
- $\theta < 1$ probability that an exposed human develops symptomatic cutaneous leishmaniasis infection after leaving the incubation period.
- δ is the rate at which the treated population leave the class E_H
- q and p are the recovery rates from infectious populations I_H and A_H respectively.

Our analysis of the disease transmission dynamics for cutaneous leishmaniasis relies on differential equations. By modeling the progression of the disease based on available health data, we can identify the key factors contributing to its spread.

Numerous studies explore mathematical models related to the spread of infectious diseases (e.g., [13, 14, 15, 16]). These studies offer mathematical tools for analyzing the evolution of diseases over time and examining the impact of various factors, such as transmission and treatment rates, on the dynamics of disease spread. These models provide valuable insights that can help guide control strategies and evaluate the effectiveness of different health interventions.

Motivated by the above-mentioned works, we propose the following system of ordinary differential equations for $0 \leq t \leq \ell < \infty$:

$$\left\{ \begin{array}{lll} \dfrac{dS_H(t)}{dt} & = & \Lambda H(t) + \kappa R_H(t) - \left(\dfrac{\beta I_M(t)}{M(t)} + \mu \right) S_H(t) \\ \dfrac{dE_H(t)}{dt} & = & \dfrac{\beta I_M(t)}{M(t)} S_H(t) - (\delta + \mu) E_H(t) \\ \dfrac{dI_H(t)}{dt} & = & \theta \delta E_H(t) - (p + \mu) I_H(t) \\ \dfrac{dA_H(t)}{dt} & = & (1 - \theta) \delta E_H(t) - (q + \mu) A_H(t) \\ \dfrac{dR_H(t)}{dt} & = & p I_H(t) + q A_H(t) - (\kappa + \mu) R_H(t) \\ \dfrac{dS_M(t)}{dt} & = & \lambda M(t) - \left(\dfrac{\gamma (I_H(t) + A_H(t))}{H(t)} + \upsilon \right) S_M(t) \\ \dfrac{dI_M(t)}{dt}) & = & \dfrac{\gamma (I_H(t) + A_H(t))}{H(t)} S_M(t) - \upsilon I_M(t). \end{array} \right. \tag{1}$$

In system (1), the first five equations represent the dynamics of the human population, whereas the last two equations describe the dynamics of the sandfly population.

To better understand the transmission dynamics of infectious diseases between humans and sandflies in the SEIAR(H)–SI(M) model outlined in system (1), we refer to the following chart:

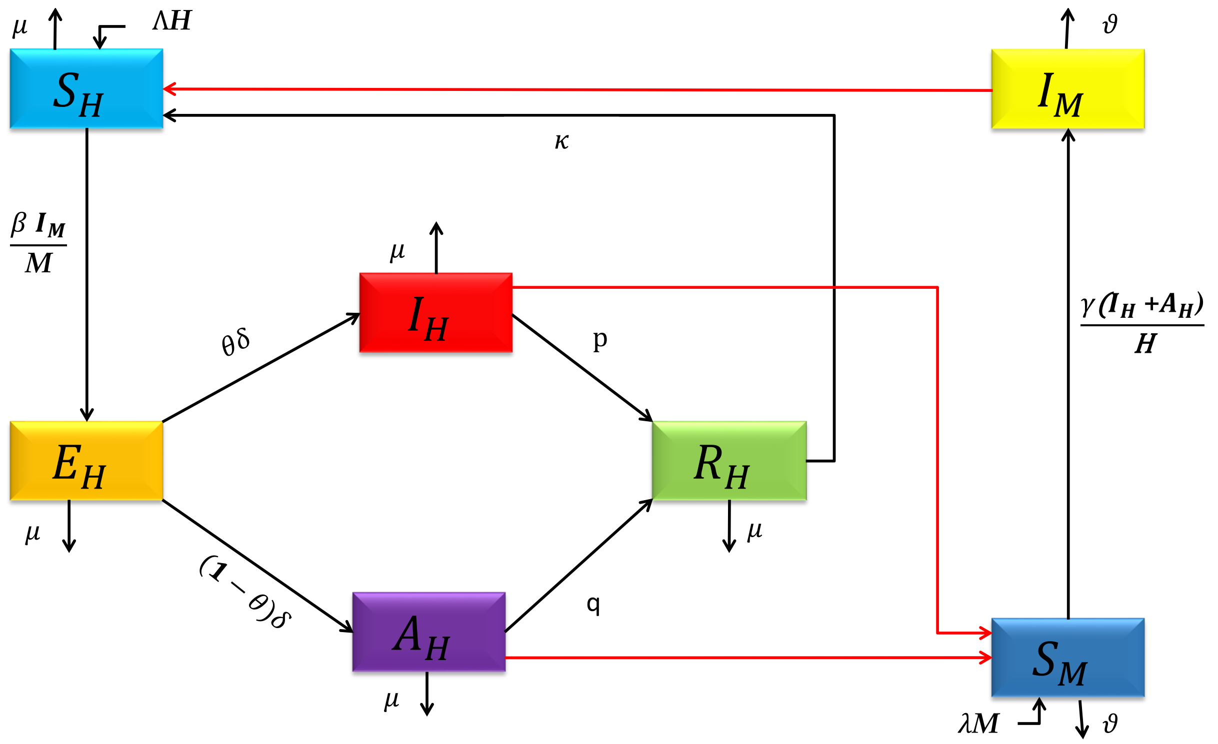

Figure 3: Flowchart of SEIAR(H)–SI(M).

This study aims to provide a comprehensive understanding of the dynamics involved in the transmission of cutaneous leishmaniasis and the factors that influence it. We begin by analyzing the behavior of the SEIAR(H)–SI(M) mathematical model, examining its solutions' existence, uniqueness, and stability, ensuring that the model's solutions are applicable and sustainable in various contexts. Additionally, we determine the basic reproduction number, explore the equilibrium points within the model, and analyze their stability to guide disease control strategies and predict future trends.

We validate the accuracy of our model using real data from Algeria, focusing on M'Sila province, because it has recently recorded a high incidence of the disease in the country. By doing so, we aim to identify local factors contributing to the spread of cutaneous leishmaniasis. This validation process enhances the model's precision and helps develop targeted and effective strategies for disease control.

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Faculty of Mathematics and Informatics
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The Fourth National Conference on "Mathematics, Biology and Medicine" Edition 2025 – Modeling of Epidemic Propagation Phenomena (NCMBM'2025) December 9, 2025, M'sila (Algeria)

NCMBM'2025

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Aims and Scope:

This edition follows the first edition organized in 2022, the second in 2023, and the third in 2024. It will be dedicated to the **Modeling of Epidemic Propagation Phenomena**.

The objective of the conference is to serve as a platform for researchers in the field of **mathematical modeling in Biology and Medicine** to exchange ideas and explore the latest advances in this area.

The conference's areas of interest include, among others, the following topics:

- **Mathematical Methods in Biology and Medicine.**
- **Epidemic Propagation Models.**

NCMBM'2025 Program

Tuesday 9th December 2025

08h 30 – 09h 00: Reception & Registration
09h 00 – 09h 30: Opening Ceremony (Library Hall, Faculty of Mathematics and Informatics - North Pole - University of M'sila).

Time	Plenary Session
09h30 – 10h 30	**Chairman**: Pr Noureddine Benhamidouche, Univ. M'sila. **Speaker**: Pr Schehrazad Selmane, Univ. STHB , **Modeling in Public Health**.
10h 30 – 11h 00	**Chairman**: Pr Abdelmouhcene Sengouga, Univ. M'sila. **Speaker**: Dr. Bilal Basti, Univ. M'sila, **Predicting Cutaneous Leishmaniasis Dynamics Through Mathematical Modeling**.
11h 00 – 11h 40	**Poster Session & Coffee break**

Time	Chairman: Pr Yacine Arioua, Univ. M'sila.
11h 40 – 12h 00	**Speaker**: Dr Bilal Lounnas, Univ. M'sila, **Dimensionality Reduction in Medical Data: A PCA-Based Approach for Disease Prediction**.
12h 00 – 12h 20	**Speaker**: Dr Somia Djiab, Univ. M'sila, **Review of SIRC epidemic models: Mathematical modeling of Influenza A infection virus.**

Time	Chairman: Dr. Bachir Gagui, Univ. M'sila.
12h 20 – 12h 40	**Speaker**: Dr Souad Bounouiga, Univ. M'sila, **Forecasting Dengue Fever Dynamics Using Simulation and Theoretical Analysis.**
12h 40 – 13h 00	**Speaker**: Dr Meroua Medjoudja, Univ. Ouargla, **Analysis of stability and Hopf bifurcation of a fractional order HBV model with time delay.**

Time	Closing
13h 00 – 13h 30	**Closing Ceremony**
13h 30	**Lunch**

NCMBM'2025 Program

Tuesday 9th December 2025

Poster Session	**Chairman: Dr. Saad Abdelkebir, Univ. M'sila.**
Fatima Benziadi Univ. Saida	Nonparametric recursive estimate for right-censored conditional mode function with ergodic functional data
Boubakr Lamouri Univ. Adrar	Global dynamics of a PDE-based nonlocal dispersal SIR epidemic model
Rabah Djemiat Ens Hydraulics, Blida	Examination of Traveling Wave Behavior for Nonlinear Evolution Models
Imane Djaidja Univ. M'sila	General Decay Of The Solution To A Linear Viscoelastic System With Delay
Kaouther Bouchama Univ. M'sila	Numerical Study Of The Space–Time Fractional Diffusion Equation With The Riesz-Caputo-Katugampola Fractional Derivative
Affaf Rezig Univ. Bouira	Existence And Stability Of A Timoshenko Beam With Memory
Brahim Benaissi Univ. M'sila	Global Solutions of Nonlinear Fractional Diffusion Equations with Applications to Epidemic Spread Modeling
Mohamed Bouguerroumi Univ. Bouira	Energy Decay of the von Kármán system
Amina Haimed Univ. M'sila	Solving Nonlinear Fredholm Integral Equations by the Newton–Kantorovich Method Combined with the Composite Repeated Trapezoidal Rule
Abderrazak Touam Univ. Saida	Analyzing a Hypothetical Hospital's Performance during Pandemics Using COVID-19 (2020) Data and SIR–M/M/c Models with the aim of improving future health preparedness

Note: *It is recommended that posters be presented in A0 format.*

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PURE AND APPLIED MATHEMATICS LABORATORY
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THE FOURTH NATIONAL CONFERENCE IN "MATHEMATICS, BIOLOGY AND MEDICINE" EDITION 2025 – « MODELING OF EPIDEMIC PROPAGATION PHENOMENA »

DECEMBER 9, 2025, M’SILA (ALGERIA)

ABOUT

This edition follows the first edition organized in 2022, the second organized in 2023 and the third organized in 2024 it will be dedicated to Modeling of epidemic propagation phenomena.

The objective of the conference is to serves as platform for researchers and scientists in field of mathematical modeling in Biology and Medicine, to exchange ideas and explore the latest advances in this field.
Our conference includes keynote speeches, and posters.

TOPICS

- **Mathematical Methods in Biology and Medicine**
- **Epidemic Propagation Models**

REGISTRATION FEES

- PhD students: 1500 DA
- Scientist (Teacher): 4000 DA

SUBMISSION

Authors are invited to submit their abstracts to the following address:

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Deadline: November 15, 2025

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