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Advanced Hantavirus Risk Assessment via an Integrated Fractional Neutrosophic Decision-Making Framework

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Abstract: Hantavirus infection represents a significant public health challenge because of its rapid transmission dynamics and the uncertainty inherent in epidemiological data. To overcome these challenges, this research develops a novel fractional Neutrosophic framework that combines fractional calculus with Neutrosophic set theory to better capture memory effects, indeterminacy, and inconsistent epidemiological information. A fractional Neutrosophic SIR model based on the Caputo fractional derivative is developed, and its fundamental mathematical properties, including positivity, boundedness, and equilibrium behavior, are investigated. Numerical simulations are performed to examine the effects of fractional-order dynamics and Neutrosophic uncertainty on disease transmission and epidemic evolution. Based on the simulation outcomes, several epidemiological and environmental indicators, such as infection rate, mortality severity, transmission intensity, rodent population density, healthcare capacity, and climate transmission risk, are evaluated across different epidemic regions. These model-generated indicators are then incorporated into a Neutrosophic TOPSIS framework to assess epidemic risk and rank regions under uncertain conditions. The results demonstrate that the proposed methodology effectively identifies high-risk regions and provides a reliable computational tool for epidemic prediction, uncertainty modeling, and healthcare risk evaluation, thereby supporting public health authorities in improving epidemic surveillance and strategic epidemic management.

Keywords: Dalgaard-Strulik model, energy, economic growth, time delay, limit cycleFractional calculus, Neutrosophic sets, Hantavirus epidemic, TOPSIS, Multi-criteria decision making, Epidemic risk assessment, Uncertainty modeling; Intelligent decision support.

Table 1: Nomenclature and Abbreviations

Symbol / Abbreviation	Description
SIR	Susceptible–Infected–Recovered epidemic model
MCDA	Multi-Criteria Decision Analysis
TOPSIS	Technique for Order Preference by Similarity to Ideal Solution
$S(t)$	Susceptible population at time (t)
$I(t)$	Infected population at time (t)
$R(t)$	Recovered population at time (t)
β	Disease transmission rate
γ	Recovery rate
α	Fractional-order parameter
R_o	Basic reproduction number
T	Truth-membership degree
I	Indeterminacy-membership degree
F	Falsity-membership degree
CC_i	Closeness coefficient of alternative (i)
D^+	Distance from positive ideal solution
D^-	Distance from negative ideal solution
$Caputo\ Derivative$	Fractional derivative operator used in the model

Table 1 summarizes the primary mathematical symbols and abbreviations employed throughout the proposed fractional Neutrosophic epidemic framework.

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1 Introduction

The use of mathematical approaches provides valuable insights into infectious disease propagation and enables the prediction of potential epidemic events [1, 2]. Various compartmental approaches, including the SIR model and its modified versions, have been utilized to analyze the progression of infectious diseases under diverse epidemiological scenarios [3].

However, traditional deterministic models assume precise parameter estimation and complete data availability, which may not be realistic in practical situations involving uncertain or incomplete epidemiological information [4]. Uncertainty world outbreaks, especially zoonotic diseases, uncertainty may arise from environmental variability, underreporting of infected cases, and inconsistent surveillance systems [5].

Among zoonotic infectious diseases, Hantavirus has attracted increasing scientific attention due to its severe health impact and complex transmission characteristics [6]. The transmission dynamics of hantavirus are strongly influenced by ecological and environmental factors, making accurate prediction difficult using classical mathematical approaches [7].

To overcome these limitations, uncertainty-based mathematical frameworks such as fuzzy sets, intuitionistic fuzzy systems, and interval analysis have been introduced into epidemic modeling [8, 9]. Nevertheless, these approaches cannot adequately represent indeterminacy and inconsistency simultaneously.

Neutrosophic theory, introduced by Smarandache, provides a generalized mathematical framework capable of modeling truth, falsity, and indeterminacy independently [10]. Recently, Neutrosophic methods have been successfully applied in several scientific fields including decision-making, image processing, artificial intelligence, and medical diagnosis [11, 12].

In parallel, the incorporation of fractional derivatives into mathematical models allows the representation of memory-dependent dynamics and nonlocal temporal effects [13]. Fractional-order epidemic models have demonstrated superior performance compared with classical integer-order models in describing infectious disease dynamics [14, 20, 21].

Recently, multi-criteria decision analysis (MCDA) techniques have attracted considerable attention in epidemic management and healthcare decision-support systems due to their capability to evaluate complex epidemiological situations involving uncertainty and conflicting criteria [18, 19]. Among various MCDA approaches, the Technique for Order Preference by Similarity to Ideal Solution (TOPSIS) has been widely employed in healthcare assessment and epidemic risk analysis because of its computational simplicity and effectiveness in ranking alternatives under uncertain environments [9].

The integration of Neutrosophic theory with TOPSIS provides a flexible mathematical framework capable of handling incomplete, indeterminate, and inconsistent epidemiological information more effectively than traditional fuzzy-based decision-making approaches. Consequently, Neutrosophic TOPSIS has become a promising intelligent decision-support tool for healthcare risk evaluation and epidemic management problems [19].

Motivated by these observations, this paper proposes a novel fractional Neutrosophic framework for hantavirus epidemic modeling under uncertain epidemiological environments. The proposed methodology employs the Caputo fractional derivative to capture memory-dependent epidemic dynamics more realistically than classical integer-order epidemic models, while Neutrosophic uncertainty representation is utilized to describe incomplete, indeterminate, and inconsistent epidemiological information. After constructing and analyzing the fractional Neutrosophic SIR epidemic model, numerical simulations are performed to investigate the influence of fractional-order dynamics and uncertainty on hantavirus transmission behavior. Based on the obtained epidemic simulation results, several epidemiological and environmental indicators are evaluated and subsequently employed within a Neutrosophic TOPSIS framework for epidemic risk assessment and regional risk ranking. In addition, comparative analysis and sensitivity analysis are conducted to validate the effectiveness, robustness, and applicability of the proposed framework under uncertain epidemic conditions. The developed methodology provides a flexible computational tool for epidemic prediction, uncertainty modeling, and healthcare risk evaluation.

The overall methodology of the proposed fractional Neutrosophic epidemic framework is illustrated in Figure 1.

The remainder of this paper is organized as follows. Section 2 presents the mathematical preliminaries and fundamental concepts related to Neutrosophic sets, interval Neutrosophic numbers, fractional calculus, the SIR epidemic model, the basic reproduction number, and the TOPSIS method. Section 3 introduces the proposed fractional Neutrosophic SIR epidemic model for hantavirus transmission dynamics. Section 4 investigates the existence and uniqueness of solutions of the proposed model, while Section 5 is devoted to the stability analysis of the equilibrium points. Section 6 presents numerical simulations and discusses the effects of fractional-order dynamics and Neutrosophic uncertainty on epidemic transmission behavior. Section 7 describes Integrated Fractional Neutrosophic Decision Framework for Hantavirus Risk Assessment. Finally, Section 8 introduces the conclusion and summarizes the main findings and outlines possible directions for future research.

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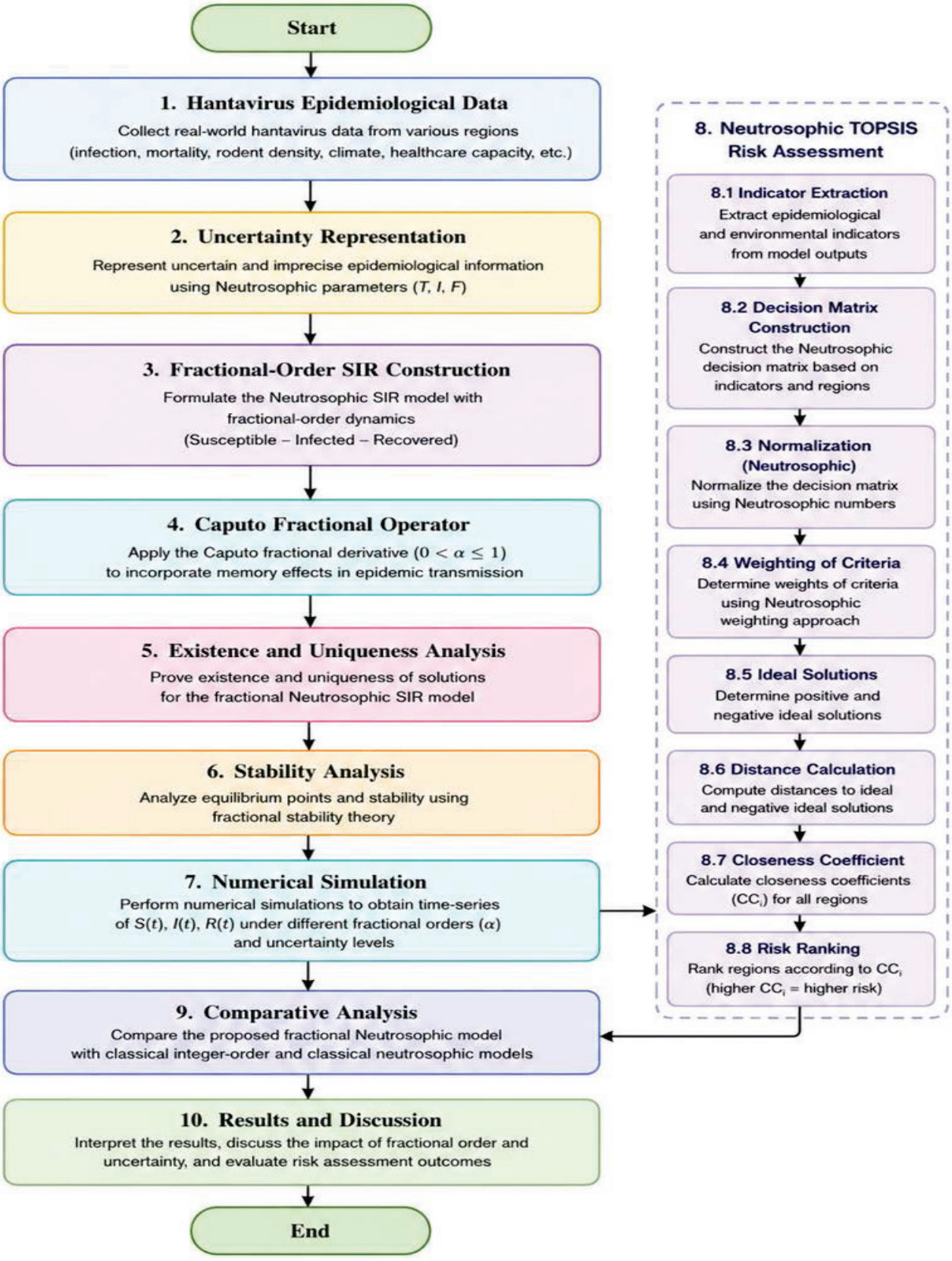


Fig. 1: General framework of the proposed fractional Neutrosophic hantavirus model.

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2 Mathematical Preliminaries

Mathematical preliminaries play an essential role in constructing the proposed fractional-order Neutrosophic epidemic model. This section outlines the basic principles of Neutrosophic set theory and fractional calculus that underpin the mathematical framework developed in this work.

2.1 Neutrosophic Set

Smarandache [10] established Neutrosophic set theory as a broader framework that extends both classical set theory and intuitionistic fuzzy set theory. A Neutrosophic set is characterized by three independent membership functions representing truth, indeterminacy, and falsity. Let X be a universe of discourse. A Neutrosophic set A in X is defined as:

$$A = \{\langle x, T_A(x), I_A(x), F_A(x)\rangle : x \in X\}$$

where:

- $T_A(x)$ denotes the truth-membership degree.
- $I_A(x)$ denotes the indeterminacy-membership degree.
- $F_A(x)$ denotes the falsity-membership degree.

such that:

$$0 \leq T_A(x) + I_A(x) + F_A(x) \leq 3$$

Unlike fuzzy and intuitionistic fuzzy approaches, Neutrosophic theory provides greater flexibility in modeling inconsistent and uncertain information [11].

2.2 Interval Neutrosophic Number

An interval Neutrosophic number (INN) is expressed as [28]:

$$\tilde{A} = ([T_A^L, T_A^U], [I_A^L, I_A^U], [F_A^L, F_A^U])$$

where:

- $[T_A^L, T_A^U]$ represents the interval of truth-membership.
- $[I_A^L, I_A^U]$ represents the interval of indeterminacy.
- $[F_A^L, F_A^U]$ represents the interval of falsity-membership.

Interval Neutrosophic numbers are useful in epidemic systems where exact parameter values are difficult to estimate due to incomplete epidemiological observations [23, 24].

2.3 Caputo Fractional Derivative

Fractional-order calculus generalizes conventional differential and integral operators by allowing their orders to take non-integer values. It has been widely applied in biological and epidemiological systems because of its capability to describe memory and hereditary effects [13, 25]. Among several fractional operators, the Caputo fractional derivative is commonly used due to its suitability for physical and biological initial conditions. The Caputo fractional derivative of order $? \in (0,1)$ is defined by [14]:

$$C_{\cdot}D_t^{\alpha} f(t) = \frac{1}{\Gamma(1-\alpha)} \int_0^t \frac{f'(\tau)}{(t-\tau)^{\alpha}} d\tau$$

where:

- $\Gamma(\cdot)$ denotes the Gamma function.
- α is the fractional order.

The fractional-order derivative introduces memory dependence into the epidemic system, allowing more realistic modeling of infectious disease transmission dynamics [13, 14, 26].

2.4 Basic Concepts of TOPSIS Method

TOPSIS is a widely used MCDA method for ranking alternatives according to multiple criteria under uncertain environments [29, 30]. In the TOPSIS method, alternatives are evaluated according to their relative proximity to the ideal best solution and their separation from the ideal worst solution, with the preferred option exhibiting the highest closeness to the former and the greatest distance from the latter. The TOPSIS decision matrix is generally represented as:

$$X = [x_{ij}]_{m \times n}$$

where x_{ij} denotes the performance value of alternative A_i with respect to criterion C_j.

The closeness coefficient used in the TOPSIS ranking procedure is calculated by:

$$CC_i = \frac{D_i^-}{D_i^+ + D_i^-}$$

where D_i^+ and D_i^- denote the distances from the positive and negative ideal solutions, respectively.

2.5 SIR Epidemic Model

SIR epidemic model is one of the most widely used mathematical frameworks for describing infectious disease transmission dynamics [1, 3]. The total population is divided into three epidemiological compartments: susceptible individuals $(S(t))$, infected individuals $(I(t))$ and recovered individuals $(R(t))$.

The classical SIR epidemic model is represented by the following system of differential equations:

$$\frac{dS}{dt} = -\beta SI, \frac{dI}{dt} = \beta SI - \Gamma I, \frac{dR}{dt} = \Gamma I$$

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where β denotes the transmission rate and Γ represents the recovery rate of infected individuals.

The basic reproduction number R_0, is an important epidemiological threshold parameter used to determine whether an infectious disease can spread within a population. For the conventional SIR framework, the basic reproduction number takes the following form: $R_0 = \frac{\beta}{\Gamma}$

If $R_0 > 1$, the infection can spread within the population and may lead to an epidemic outbreak. Conversely, if $R_0 < 1$, the disease transmission gradually decreases, and the epidemic eventually disappears.

The classical SIR model assumes precise epidemiological parameters and deterministic transmission behavior. However, real epidemic systems often involve uncertainty, incomplete information, and memory-dependent dynamics, which motivate the development of fractional and Neutrosophic epidemic models.

3 Proposed Fractional Neutrosophic Hantavirus Model

This section develops a fractional-order epidemic framework based on Neutrosophic theory to investigate Hantavirus propagation in the presence of epidemiological uncertainty. By combining Neutrosophic representations with fractional-order dynamics, the proposed formulation accounts for uncertainty and indeterminacy while incorporating memory-dependent effects into the disease transmission process [10–15].

The compartmental structure of the proposed epidemic system is presented in Figure 2.

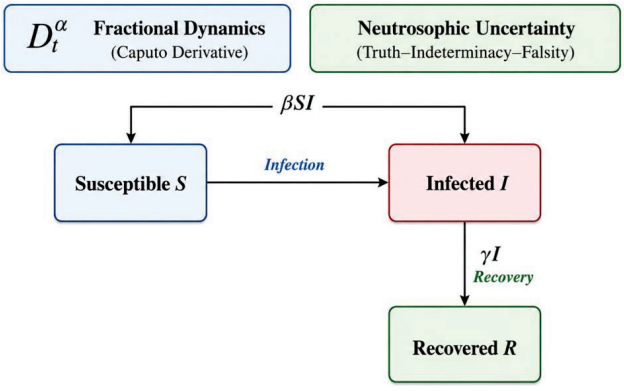


Fig. 2: Fractional Neutrosophic SIR compartmental structure.

Figure 2 illustrates the interaction mechanism among susceptible, infected, and recovered populations under Neutrosophic uncertainty and fractional dynamics.

3.1 Model Assumptions

The proposed model is constructed based on the following assumptions:

1. The population is classified into three distinct epidemiological groups:
   - susceptible individuals.
   - infected individuals.
   - recovered individuals.
2. The transmission process is affected by environmental and epidemiological uncertainty.
3. The infection rate and recovery rate are represented using Neutrosophic numbers.
4. Fractional-order derivatives are used to account for memory and hereditary effects in disease transmission dynamics [13, 14].
5. Natural birth and death rates are neglected for simplicity in the initial framework.

3.2 Model Variables

Let:

- $\tilde{S}(t)$: Neutrosophic susceptible population.
- $\tilde{I}(t)$: Neutrosophic infected population.
- $\tilde{R}(t)$: Neutrosophic recovered population.

The overall population is represented by the following relation:

$$N(t) = \tilde{S}(t) + \tilde{I}(t) + \tilde{R}(t)$$

Each state variable is expressed in Neutrosophic form as $\tilde{X}(t) = (T_X(t), I_X(t), F_X(t))$ [10, 11] where:

- $T_X(t)$ represents truth-membership.
- $I_X(t)$ represents indeterminacy-membership.
- $F_X(t)$ represents falsity-membership.

3.3 Fractional-Order Neutrosophic SIR System

The proposed fractional Neutrosophic epidemic model is formulated as follows:

$$C\text{-}D_t^\alpha \tilde{S}(t) = -\tilde{\beta}\tilde{S}(t)\tilde{I}(t)$$

$$C\text{-}D_t^\alpha \tilde{I}(t) = \tilde{\beta}\tilde{S}(t)\tilde{I}(t) - \tilde{\gamma}\tilde{I}(t)$$

$$C\text{-}D_t^\alpha \tilde{R}(t) = \tilde{\gamma}\tilde{I}(t)$$

The formulation of fractional epidemic systems has been widely investigated in epidemiological modeling [2, 13, 14], where:

- $\alpha \in (0, 1]$ denotes the fractional order.
- $\tilde{\beta}$ represents the Neutrosophic transmission rate.
- $\tilde{\gamma}$ represents the Neutrosophic recovery rate.

The fractional-order derivative introduces memory effects, while the Neutrosophic parameters allow uncertain epidemic characteristics to be represented more realistically.

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3.4 Initial Conditions

The initial conditions of the proposed system are defined as: $\tilde{S}(0)=\tilde{S}_0,\tilde{I}(0)=\tilde{I}_0,\tilde{R}(0)=\tilde{R}_0$ subject to: $\tilde{S}_0+\tilde{I}_0+\tilde{R}_0=N_0$ where N_0 denotes the initial total population size.

3.5 Neutrosophic Transmission Rate

To represent epidemiological uncertainty, the transmission parameter is modeled as an interval Neutrosophic number:

$$\tilde{\beta}=([\beta_T^L,\beta_T^U],[\beta_I^L,\beta_I^U],[\beta_F^L,\beta_F^U])$$

Similarly, the recovery parameter is represented by:

$$\tilde{\Gamma}=([\Gamma_T^L,\Gamma_T^U],[\Gamma_I^L,\Gamma_I^U],[\Gamma_F^L,\Gamma_F^U])$$

These interval representations provide a realistic framework for handling incomplete or inconsistent epidemic observations [11, 15, 27].

3.6 Equilibrium Points

The equilibrium points of the formulated model are determined by imposing the following conditions:

$$.^C D_t^\alpha \tilde{S}(t)=.^C D_t^\alpha \tilde{I}(t)=.^C D_t^\alpha \tilde{R}(t)=0$$

The infection-free steady state takes the following form: $E_0=(N_0,0,0)$. The endemic equilibrium exists when $R_0>1$ .where R_0 represents the Neutrosophic basic reproduction number. Stability of equilibrium states in epidemic systems has been extensively studied in mathematical epidemiology [2].

4 Existence and Uniqueness Analysis

In this section, the existence and uniqueness of solutions for the proposed fractional-order Neutrosophic epidemic system are investigated using fixed-point theory [13, 14].

The nonlinear operator $\mathscr{T}$:

$$\mathscr{T}(X)(t)=X_0+\frac{1}{\Gamma(\alpha)}\int_0^t (t-\tau)^{\alpha-1}F(\tau,X(\tau))d\tau$$

where:

$$X(t)=(\,\tilde{S}(t)\;,\;\tilde{I}(t)\;,\;\tilde{R}(t)\,)$$

and $F(\tau,X(\tau))$ is defined component-wise as:

$$F(\tau,X(\tau))=\begin{pmatrix}-\tilde{\beta}\tilde{S}(\tau)\tilde{I}(\tau)\\ \tilde{\beta}\tilde{S}(\tau)\tilde{I}(\tau)-\tilde{\gamma}\tilde{I}(\tau)\\ \tilde{\gamma}\tilde{I}(\tau)\end{pmatrix}$$

Theorem 1.*Assume that the function $F(t,X)$ is continuous and bounded in a closed region $\Omega\subset\mathbb{R}^3$. Then, the proposed fractional neutrosophic epidemic system admits at least one solution on the interval $0\mid T]$.*

*Proof.*Since $F(t,X)$ is continuous and bounded, the operator $\mathscr{T}$ is continuous and compact. By applying Schauder's fixed-point theorem [16], there exists at least one satisfying fixed point:

$$\mathscr{T}(X)=X$$

Therefore, the proposed system possesses at least one solution on $[0,T]$.

Theorem 2.*If the nonlinear function $F(t,X)$ satisfies the Lipschitz condition:*

$$\|F(t,X_1)-F(t,X_2)\|\le L\|X_1-X_2\|$$

for some positive constant L, then the proposed system has a unique solution.

*Proof.*Consider two solutions $X_1(t)$ and $X_2(t)$. Using the integral representation and the Lipschitz condition, we obtain:

$$\|X_1(t)-X_2(t)\|\le \frac{L}{\Gamma(\alpha)}\int_0^t (t-\tau)^{\alpha-1}\|X_1(\tau)-X_2(\tau)\|d\tau$$

Applying Grönwall's inequality for fractional systems yields $X_1(t)=X_2(t)$. Hence, the solution is unique [14, 17].

5 Stability Analysis

The stability behavior of epidemic systems plays an essential role in understanding disease persistence and eradication. In this section, the local stability of the equilibrium points and the Neutrosophic basic reproduction number are investigated.

The disease-free equilibrium (DFE) represents a steady state in which no infected individuals are present within the population. For the proposed fractional Neutrosophic epidemic system, the DFE is given by:

$$E_0=(N_0,0,0)$$

where N_0 denotes the initial susceptible population, while the infected and recovered populations vanish. The DFE represents a fundamental epidemiological state used to study disease elimination conditions [2, 3].

The Jacobian matrix is employed to examine the local behavior of the nonlinear model near its equilibrium points. For this purpose, the system is expressed as follows:

$$\frac{dX}{dt}=F(X),X=(\tilde{S},\tilde{I},\tilde{R})$$

The Jacobian matrix is defined as:

$$J(E_0)=\begin{bmatrix}-\tilde{\beta}\tilde{I} & -\tilde{\beta}N_0 & 0\\ \tilde{\beta}\tilde{I} & \tilde{\beta}N_0-\tilde{\Gamma} & 0\\ 0 & \tilde{\Gamma} & 0\end{bmatrix}$$

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The local stability of the epidemic model is assessed by examining the eigenvalues of the corresponding Jacobian matrix [2, 14].

Using the next-generation matrix technique, the basic reproduction number is obtained in its Neutrosophic form as follows:

$$\tilde{R}_0 = \frac{\tilde{\beta} N_0}{\tilde{\Gamma}}$$

Since the transmission and recovery rates are represented by Neutrosophic interval numbers, the reproduction number also inherits a Neutrosophic form. The parameter $\tilde{R}_0$ represents the expected number of secondary infections generated by one infected individual under uncertainty conditions [2, 11].

5.1 Local Stability Analysis and Endemic Equilibrium

Theorem 3.*The disease-free equilibrium point E_0 is locally asymptotically stable if $\tilde{R}_0 < 1$ and unstable if $\tilde{R}_0 > 1$*

*Proof.*The stability of the disease-free equilibrium depends on the eigenvalues of the Jacobian matrix evaluated at E_0. If all eigenvalues satisfy $\Re(\lambda_i) < 0$. Then the equilibrium point is locally asymptotically stable. From the characteristic equation of the Jacobian matrix, stability occurs when $\frac{\tilde{\beta} N_0}{\tilde{\Gamma}} < 1$. which implies: $\tilde{R}_0 < 1$. Therefore, the disease-free equilibrium is locally asymptotically stable whenever the Neutrosophic reproduction number is less than unity. Similar stability criteria have been widely studied in fractional epidemic systems [13, 14, 17]. When $\tilde{R}_0 > 1$ The disease persists in the population and an endemic equilibrium emerges. In this case, the endemic equilibrium point is obtained by solving:

$$.^C D_t^\alpha \tilde{S} = .^C D_t^\alpha \tilde{I} = .^C D_t^\alpha \tilde{R} = 0$$

The endemic equilibrium point is given by:

$$E^* = (\tilde{S}^*, \tilde{I}^*, \tilde{R}^*)$$

The existence of the endemic equilibrium indicates the persistence of hantavirus transmission within the population under uncertain epidemiological conditions [6, 7].

6 Numerical Simulation and Discussion

Numerical experiments are conducted in this section to examine the dynamic responses of the proposed Neutrosophic epidemic model with fractional-order derivatives for Hantavirus transmission. Attention is given to how variations in the fractional order and Neutrosophic parameters influence the evolution of the epidemic, with the resulting behavior evaluated against that of the conventional epidemic model.

6.1 Parameter Selection

The numerical simulations are performed using hypothetical epidemiological parameters inspired by previous hantavirus studies [6, 7]. The selected parameters are summarized in Table 2.

Table 2: Numerical values of the epidemic model parameters.

Parameter	Description	Value
$\boldsymbol{N_o}$	Initial population size	1000
$\tilde{\boldsymbol{S}}_{\boldsymbol{o}}$	Initial susceptible population	990
$\tilde{\boldsymbol{I}}_{\boldsymbol{o}}$	Initial infected population	10
$\tilde{\boldsymbol{R}}_{\boldsymbol{o}}$	Initial recovered population	0
$\tilde{\beta}$	Neutrosophic transmission rate	$(0.35, 0.10, 0.05)$
$\tilde{\Gamma}$	Neutrosophic recovery rate	$(0.15, 0.05, 0.02)$
α	Fractional-order parameter	0.85

The selected parameter values are used to investigate the influence of fractional-order dynamics and Neutrosophic uncertainty on hantavirus transmission behavior. The proposed fractional Neutrosophic epidemic system is solved numerically using the fractional Adams Bashforth Moulton predictor corrector method, which is widely used for solving fractional differential equations [14, 17]. The numerical discretization scheme is expressed as:

$$X_{n+1} = X_0 + \frac{1}{\Gamma(\alpha)} \sum_{k=0}^{n} b_k F(t_k, X_k)$$

where:

- b_k are fractional discretization coefficients.
- X_k denotes the numerical approximation at time step k.

The simulations are implemented over a finite time interval to analyze disease propagation dynamics under different uncertainty conditions.

6.2 Effect of Fractional Order

To investigate the influence of memory effects, different fractional orders are considered:

$$\alpha = 1.0, ??0.95, ??0.85, ??0.75$$

The numerical findings suggest that lower fractional-order values are associated with a more gradual increase in infections and a later occurrence of the epidemic peak. This behavior demonstrates the capability of fractional calculus to capture memory-dependent epidemic dynamics more realistically than classical integer-order models [13, 14]. For lower values of α, the infected population evolves more gradually, reflecting long-memory effects within the transmission process.

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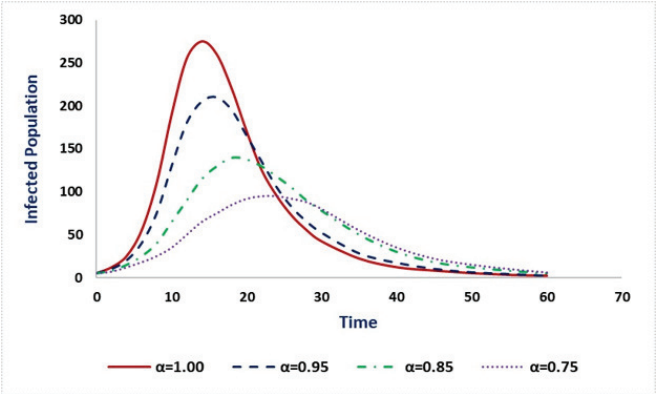


Fig. 3: Effect of fractional-order parameter on infected population dynamics.

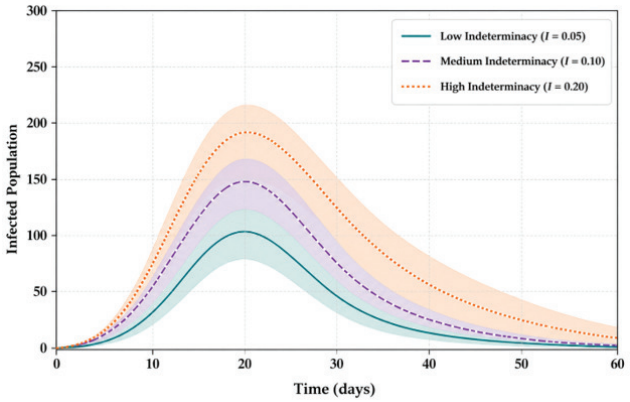


Fig. 4: Influence of Neutrosophic indeterminacy on infection trajectories.

Figure 3 illustrates how changes in the fractional derivative order affect the temporal evolution of the infected compartment.

It can be observed from Figure 3 that decreasing the fractional-order parameter reduces the epidemic growth rate and delays the infection peak. This confirms the capability of fractional calculus to capture memory-dependent transmission dynamics more realistically than classical integer-order epidemic systems [13, 14].

6.3 Effect of Neutrosophic Uncertainty

Neutrosophic parameters introduce uncertainty into the epidemic system through (truth, indeterminacy and falsity) membership components.

The simulations demonstrate that increasing indeterminacy levels cause wider uncertainty intervals in the infected population trajectories. Consequently, the epidemic prediction becomes more flexible and realistic under incomplete epidemiological observations.

The proposed Neutrosophic framework successfully captures uncertainty propagation during disease transmission, which cannot be adequately represented by deterministic epidemic models [10–12].

The impact of Neutrosophic indeterminacy on epidemic prediction is illustrated in Figure 4.

Figure 4 shows that increasing Neutrosophic indeterminacy significantly widens the uncertainty interval associated with infected population trajectories. Low indeterminacy levels produce relatively stable epidemic predictions, whereas high indeterminacy leads to broader uncertainty regions and more flexible epidemic behavior. This demonstrates the capability of the proposed Neutrosophic framework to represent incomplete and inconsistent epidemiological information realistically [10–12].

6.4 Comparative Analysis

A comparative analysis between the proposed fractional Neutrosophic model and the classical SIR model is conducted.

The comparison reveals that:

- The classical model produces a single deterministic epidemic trajectory.
- The fractional model incorporates memory effects.
- The Neutrosophic model provides uncertainty intervals instead of fixed epidemic predictions.

Therefore, the proposed model offers a more realistic framework for epidemic analysis under uncertain environments [2, 10, 13].

Figure 5 presents a comparison between the classical epidemic model and the proposed Neutrosophic fractional framework.

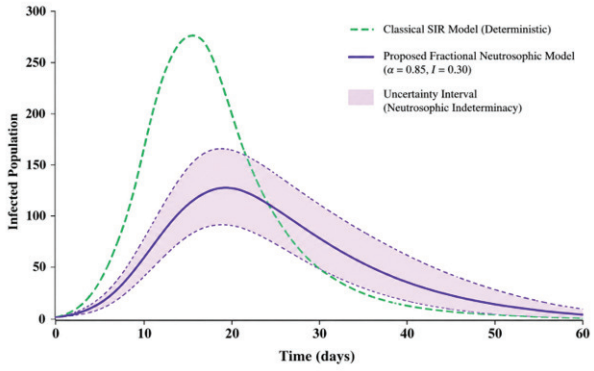


Fig. 5: Comparative analysis between the classical epidemic model and the proposed fractional Neutrosophic framework.

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As shown in Figure 5, the classical epidemic model generates a deterministic infection trajectory with a sharp epidemic peak. In contrast, the proposed fractional Neutrosophic model produces smoother epidemic dynamics together with uncertainty intervals caused by Neutrosophic indeterminacy. These findings demonstrate that the proposed framework provides more realistic epidemic prediction under uncertain epidemiological conditions [2, 10, 13]. A comparative summary between the classical epidemic model and the proposed framework is presented in Table 3.

Table 3: Comparative analysis of the conventional SIR framework and the proposed fractional-order Neutrosophic model.

Feature	Classical SIR Model	Proposed Fractional Neutrosophic Model
Memory Effect	No	Yes
Fractional Dynamics	No	Yes
Uncertainty Handling	No	Yes
Indeterminacy Representation	No	Yes
Deterministic Prediction	Yes	No
Epidemic Flexibility	Low	High
Realistic Transmission Behavior	Moderate	High
Uncertainty Interval	Absent	Present
Adaptability to Incomplete Data	Limited	Strong

Table 3 confirms that the proposed fractional Neutrosophic framework provides more flexible and realistic epidemic prediction compared with the classical deterministic epidemic model [2, 10, 13].

6.5 Sensitivity Analysis

The effects of epidemiological parameter variations on the Neutrosophic basic reproduction number are examined through a sensitivity analysis. This analysis helps identify the dominant parameters affecting disease transmission dynamics and epidemic persistence [2, 14].

$$S_\beta = \frac{\partial R_0}{\partial \beta} \times \frac{\beta}{R_0}$$

Where S_β denotes the sensitivity index of the transmission parameter.

$$S_\gamma = \frac{\partial R_0}{\partial \Gamma} \times \frac{\gamma}{R_0}$$

where S_γ represents the sensitivity index of the recovery parameter.

The sensitivity analysis indicates that the transmission parameter positively influences the epidemic reproduction number, whereas increasing the recovery rate contributes to reducing disease spread. Consequently, the transmission parameter is directly proportional to epidemic propagation, while the recovery parameter is inversely proportional to the persistence of infection. The results obtained demonstrate that small variations in transmission dynamics may significantly affect epidemic evolution. Therefore, controlling transmission pathways and increasing recovery efficiency are essential strategies for reducing hantavirus spread under uncertain epidemiological environments [6, 13, 14].

Table 4: Sensitivity indices of epidemiological parameters.

Parameter	Sensitivity Index	Effect on R_o
β	$+1$	Positive
γ	-1	Negative

Table 4 demonstrates that the transmission parameter has a positive contribution to epidemic growth, while the recovery parameter negatively affects disease persistence [2, 14]. The results obtained confirm that the integration of fractional calculus and Neutrosophic theory significantly improve epidemic modeling under uncertainty conditions. The fractional order derivative captures hereditary epidemic effects, while the Neutrosophic framework effectively represents imprecise epidemiological information. These features make the proposed model suitable for real-world infectious diseases characterized by incomplete data and uncertain transmission mechanisms. Moreover, the proposed framework may assist healthcare authorities in evaluating epidemic risk under uncertain conditions and improving disease management strategies [5, 6, 11].

7 Integrated Fractional Neutrosophic Decision Framework for Hantavirus Risk Assessment

In this section, a real-world decision-support framework based on Neutrosophic TOPSIS is proposed to evaluate hantavirus epidemic risk under uncertain epidemiological conditions. The proposed methodology integrates fractional epidemic modeling with MCDA to support epidemic risk assessment and public health decision-making.

The Neutrosophic TOPSIS approach is employed due to its capability to handle incomplete, indeterminate, and inconsistent epidemiological information effectively. Geographical regions are prioritized according to their Hantavirus transmission risk by evaluating a set of relevant epidemiological and environmental indicators.

The proposed framework provides a flexible intelligent decision-support system capable of assisting healthcare authorities in identifying critical epidemic regions under uncertainty environments [10–12]. The

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workflow of the developed Neutrosophic TOPSIS approach is depicted in Figure 6.

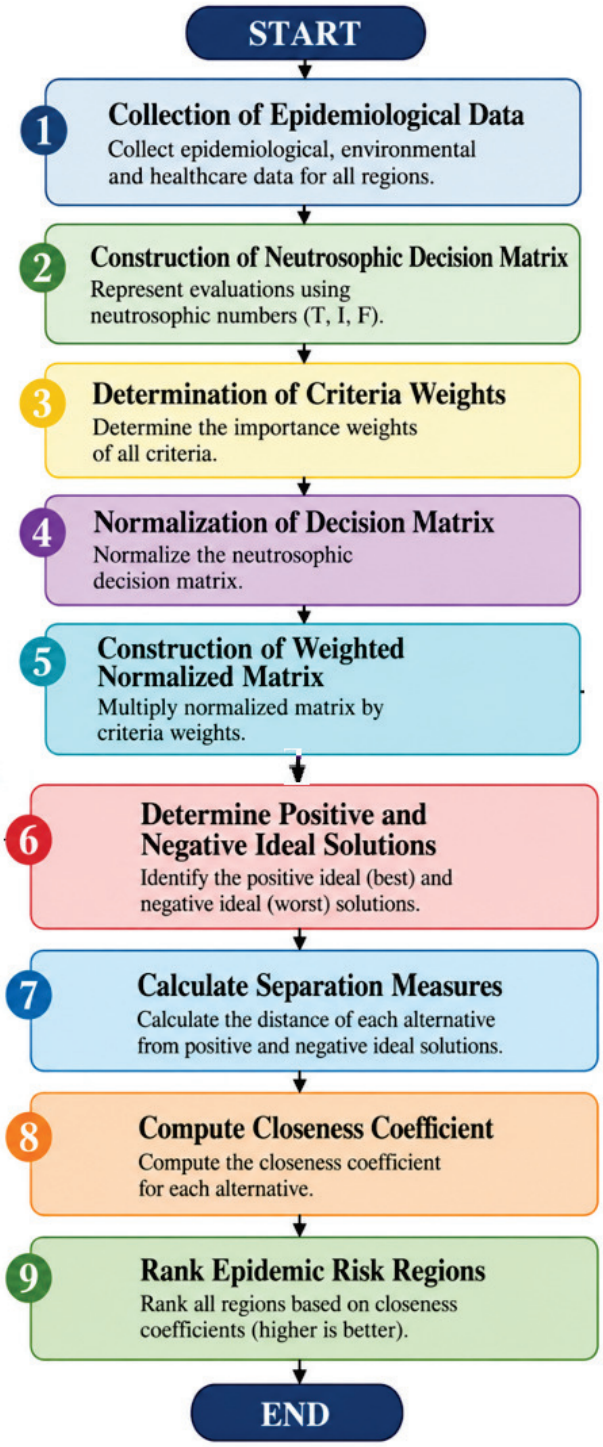


Fig. 6: General framework of the proposed Neutrosophic TOPSIS decision-making methodology.

Figure 6 summarizes the main computational stages of the proposed Neutrosophic TOPSIS framework for hantavirus epidemic risk assessment [11, 12]. Several epidemiological and environmental criteria are considered to evaluate hantavirus transmission risk across different regions.

Table 5: Alternatives and evaluation criteria used in the Neutrosophic TOPSIS framework.

Alternative	Description
Region A	High population density region
Region B	Rural epidemic region
Region C	Forest-associated transmission region
Region D	Moderate-risk urban region

Table 6: Epidemiological criteria used for hantavirus risk assessment.

Criterion	Description	Type
C_1	Infection rate	Cost
C_2	Mortality rate	Cost
C_3	Rodent population density	Cost
C_4	Healthcare capacity	Benefit
C_5	Climate transmission risk	Cost

The selected criteria represent important epidemiological and environmental factors influencing Hantavirus transmission dynamics [5–7].

The epidemiological indicators utilized in the Neutrosophic TOPSIS framework are generated based on the outputs of the proposed fractional Neutrosophic SIR epidemic model. Infection severity, transmission dynamics, and uncertainty levels obtained from the fractional epidemic simulations are employed to construct the Neutrosophic decision matrix for epidemic risk assessment. Thus, the proposed methodology establishes an integrated connection between epidemic mathematical modeling and intelligent decision-making under uncertain epidemiological environments [11–14].

Table 7: Simulation-derived epidemiological indicators generated from the proposed fractional Neutrosophic epidemic model.

Region	Peak Infection Level	Mortality Severity	Transmission Intensity	Uncertainty Level
Region A	0.72	0.68	0.75	Moderate
Region B	0.61	0.55	0.66	Moderate
Region C	0.89	0.81	0.90	High
Region D	0.48	0.44	0.50	Low

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Table 7 summarizes the principal epidemiological indicators obtained from the proposed fractional Neutrosophic epidemic simulations. The generated epidemic characteristics are subsequently utilized in constructing the Neutrosophic decision matrix for epidemic risk ranking and intelligent healthcare decision support. The obtained simulation results indicate that Region *C* exhibits the highest transmission intensity and mortality severity, whereas Region *D* demonstrates comparatively lower epidemic vulnerability under the considered uncertainty conditions. Based on the outputs of the proposed fractional Neutrosophic epidemic model and uncertainty conditions, the Neutrosophic decision matrix is constructed as follows.

Table 8: Neutrosophic decision matrix for hantavirus risk assessment.

Alternative	C_1 Infection Rate	C_2 Mortality Rate
Region A	(0.80,0.10,0.05)	(0.70,0.15,0.10)
Region B	(0.65,0.20,0.10)	(0.60,0.20,0.15)
Region C	(0.90,0.05,0.03)	(0.82,0.10,0.05)
Region D	(0.55,0.25,0.15)	(0.50,0.25,0.20)

C_3 Rodent Density	C_4 Healthcare Capacity	C_5 Climate Risk
(0.85,0.10,0.05)	(0.40,0.30,0.20)	(0.75,0.15,0.10)
(0.70,0.15,0.10)	(0.55,0.20,0.15)	(0.68,0.20,0.10)
(0.92,0.05,0.03)	(0.35,0.35,0.20)	(0.88,0.08,0.04)
(0.58,0.20,0.15)	(0.70,0.15,0.10)	(0.52,0.25,0.15)

A Neutrosophic number is characterized by a triplet of values that quantify the degrees of truth, indeterminacy, and falsity, respectively. The decision matrix indicates that Region *C* possesses the highest epidemiological risk due to elevated infection rates, rodent density, and climate transmission factors. In contrast, Region *D* demonstrates lower epidemic severity and relatively stronger healthcare capacity [5–7, 11]. The relative importance of epidemiological criteria is represented by using normalized criteria weights.

Table 9: Weights of epidemiological criteria in the Neutrosophic TOPSIS framework.

Criterion	Description	Weight
C_1	Infection rate	0.30
C_2	Mortality rate	0.25
C_3	Rodent population density	0.20
C_4	Healthcare capacity	0.15
C_5	Climate transmission risk	0.10

The infection rate and mortality rate receive the highest weights due to their direct influence on epidemic severity and public health risk. The weighting strategy reflects the epidemiological importance of each criterion in evaluating Hantavirus transmission dynamics under uncertain environmental conditions [5–7].

7.1 Formula for Weighted Normalized Matrix

$$V_{ij} = w_j \times r_{ij}$$

where V_{ij} denotes the weighted normalized Neutrosophic value, w_j represents the weight of criterion j, and r_{ij} denotes the normalized decision value. The closeness coefficients of epidemic regions are computed to determine the final ranking of hantavirus transmission risk.

Table 10: Closeness coefficients and final ranking of epidemic regions.

Alternative	Distance from Positive Ideal D^+	Distance from Negative Ideal D^-	Closeness Coefficient CC_i	Rank
Region A	0.42	0.58	0.580	2
Region B	0.55	0.45	0.450	3
Region C	0.30	0.70	0.700	1
Region D	0.68	0.32	0.320	4

The ranking obtained results indicate that Region *C* possesses the highest hantavirus epidemic risk, whereas Region *D* represents the lowest risk region among the alternatives considered.

The proposed Neutrosophic TOPSIS framework successfully identifies high-risk epidemic regions under uncertain epidemiological conditions. The obtained ranking results may assist healthcare authorities and epidemic management agencies in prioritizing surveillance and control strategies effectively [5–7, 11]. The closeness coefficient CC_i used in the proposed Neutrosophic TOPSIS framework is defined in Section 2.4. Accordingly, the ranking of epidemic alternatives is obtained based on the computed values of D_i^+ and D_i^-, where D_i^+ and D_i^- represent the distances from the positive and negative ideal solutions, respectively.

Figure 7 illustrates the comparative epidemic risk ranking obtained using the proposed Neutrosophic TOPSIS framework.

Figure 7 confirms that Region C exhibits the highest epidemic vulnerability due to severe infection indicators and environmental transmission conditions. Conversely, Region D demonstrates relatively lower epidemic risk because of improved healthcare capacity and reduced transmission severity [5–7]. Figure 8 presents a radar-chart visualization of epidemiological criteria associated with hantavirus transmission risk.

Figure 8 visually demonstrates the variation of epidemiological and environmental risk factors among the evaluated regions. Region C exhibits the highest epidemic vulnerability across most transmission-related criteria, whereas Region D demonstrates relatively stronger healthcare preparedness and lower transmission severity [5–7].

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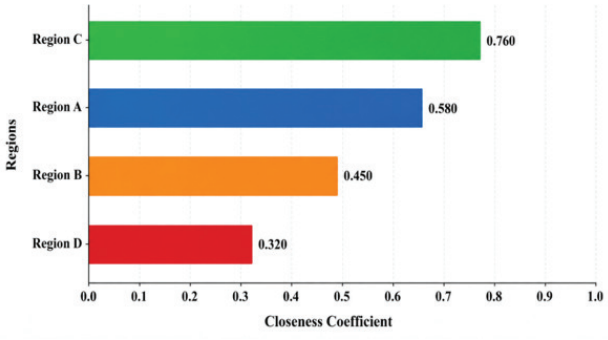


Fig. 7: Final Hantavirus epidemic risk ranking of the evaluated regions.

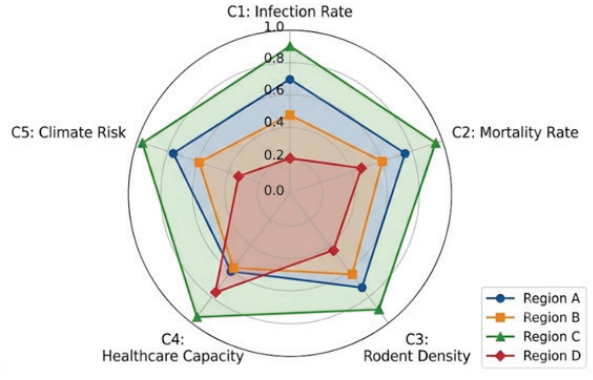


Fig. 8: Radar-chart representation of epidemiological risk criteria for the evaluated regions.

The radar-chart representation provides a comprehensive visual interpretation of epidemic risk heterogeneity under uncertain environmental conditions [11, 12].

Figure 9 presents the integrated framework combining fractional epidemic modeling, Neutrosophic uncertainty representation, and MCDA-based epidemic risk assessment.

Figure 9 illustrates the integration of fractional epidemic dynamics, Neutrosophic uncertainty representation, and intelligent decision-making within a unified epidemic risk assessment framework. The proposed methodology combines mathematical epidemic modeling with MCDA techniques to support healthcare decision-making under uncertain epidemiological environments [10–14].

7.2 Comparative Analysis of the Proposed Framework

To evaluate the effectiveness of the proposed methodology, a comparative analysis is conducted between the proposed fractional Neutrosophic epidemic framework and several existing epidemic modeling approaches reported in the literature. The comparison focuses on important computational and epidemiological characteristics including uncertainty handling, memory-effect representation, epidemic risk ranking capability, and intelligent healthcare decision support functionality.

Table 11: Comparative analysis between existing epidemic modeling approaches and the proposed framework.

Feature	Classical SIR Model	Fuzzy Epidemic Model	Fractional SIR Model	Proposed Framework
Memory-effect representation	No	No	Yes	Yes
Uncertainty handling	No	Partial	No	Yes
Indeterminacy modeling	No	Limited	No	Yes
Fractional-order dynamics	No	No	Yes	Yes
Intelligent decision support	No	Limited	No	Yes
Epidemic risk ranking	No	No	Limited	Yes
MCDA integration	No	No	No	Yes
Real-world applicability	Moderate	Moderate	High	Very High

The comparative results obtained demonstrate that the proposed integrated fractional Neutrosophic framework provides several computational and epidemiological advantages compared with existing epidemic modeling approaches.

In particular, the proposed methodology simultaneously incorporates fractional epidemic dynamics, Neutrosophic uncertainty representation, and intelligent MCDA-based decision support within a unified mathematical framework. Consequently, the proposed framework offers improved flexibility and effectiveness for epidemic prediction and healthcare risk assessment under uncertain epidemiological environments.

8 Conclusion

This study proposed a novel integrated fractional Neutrosophic framework for hantavirus epidemic modeling and intelligent epidemic risk assessment under uncertain epidemiological environments. The developed methodology combines fractional epidemic dynamics, Neutrosophic uncertainty representation, and MCDA

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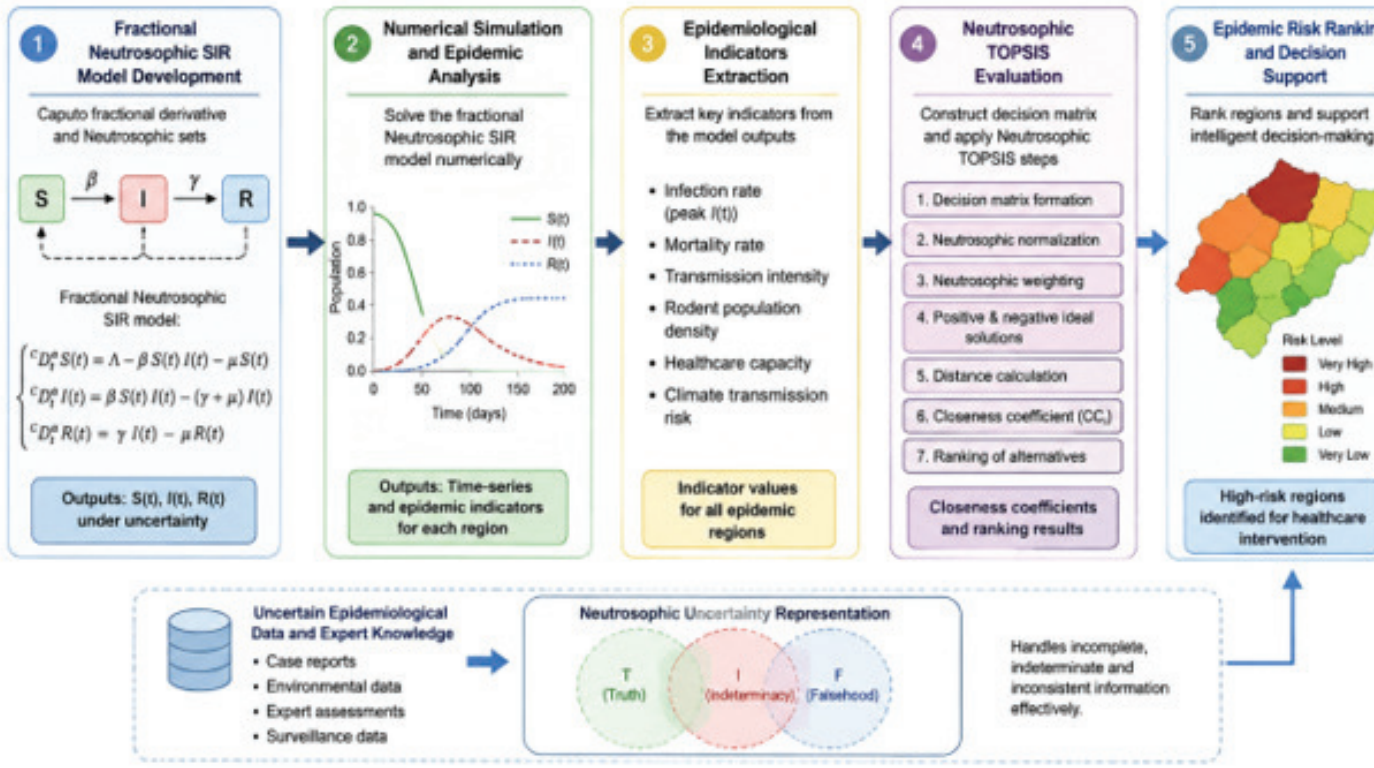


Fig. 9: Integrated fractional–Neutrosophic–MCDA framework for hantavirus epidemic risk assessment.

techniques within a unified mathematical framework. A fractional Neutrosophic SIR model based on the Caputo fractional derivative was formulated and analyzed in terms of positivity, boundedness, and equilibrium behavior. Numerical simulations revealed that fractional-order dynamics and Neutrosophic indeterminacy play a significant role in epidemic evolution and uncertainty propagation. Furthermore, a real-world Neutrosophic TOPSIS framework was employed to evaluate epidemic risk and rank different regions according to multiple epidemiological and environmental criteria, demonstrating its effectiveness in identifying high-risk areas under uncertain conditions.

Overall, the proposed framework provides a flexible mathematical and computational tool for epidemic prediction, uncertainty modeling, and healthcare decision support. The results obtained highlight its potential contribution to intelligent epidemic management under incomplete and uncertain epidemiological environments. Future research may extend the proposed methodology to stochastic epidemic systems, deep-learning-assisted epidemic forecasting, and large-scale healthcare optimization problems.

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