

RESEARCH ARTICLE

Epidemiology of hand, foot, and mouth disease on networks using neutrosophic algebraic structures

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Abstract - Hand, Foot, and Mouth Disease (HFMD) is a viral disease common among children and spreads rapidly through close-contact networks. Various studies have been conducted on neutrosophic, most recently in the field of infectious disease epidemics. Traditional epidemiological models, such as Susceptible-Exposed-Infected-Recovered (SEIR), often fail to account for uncertainties and indeterminate relationships inherent in real-world disease transmission. This study introduces a modelling approach that integrates neutrosophic algebraic structures and neutrosophic graphs, providing a framework that captures both deterministic and indeterminate aspects of HFMD dynamics. The population is represented by the group of integers modulo 9, denoted as $\mathbb{Z}_9$, which is transformed into a neutrosophic group to incorporate degrees of truth, indeterminacy, and falsehood in transmission processes. Neutrosophic graphs are constructed to illustrate the interactions between epidemiological states. By combining algebraic structures and neutrosophic, this approach offers a novel perspective on epidemic modelling and offers more adaptable and useful information into HFMD spread, particularly in environments characterized by incomplete or uncertain data.

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1. Introduction

Hand, Foot, and Mouth Disease (HFMD) is a viral infection primarily affecting infants and young children, especially those under five years of age [1]. It is characterized by fever, oral ulcers, and rashes on the hands and feet, and remains a persistent public health concern, especially in regions with high population density like childcare centres and schools [2]. There is uncertainty regarding the progress and treatment of HFMD due to the complicated transmission dynamics, which can be affected by carriers with no symptoms, indirect contact, and various levels of immunity and personal hygiene. First identified in New Zealand in 1957 [3], HFMD has since become endemic in many parts of the world. It has high prevalence in Southeast Asia, including Malaysia, Singapore, Mongolia, and Vietnam [4]. For instance, an outbreak in Sarawak, Malaysia, in 1997 resulted in 2626 cases and 31 deaths [5]. Mathematical modelling for HFMD is relatively short history compared to other common infectious diseases like measles or malaria, but it has developed rapidly in the past two decades [4]. Previous studies primarily used deterministic models. For example, Wang and Sung [6] applied a seasonally forced Susceptible - Infectious - Recovered - Susceptible (SIRS) model to evaluate the impact of weather on enterovirus infections in Taiwan, while Zhang et al. [4] used a SIRS model that consists of natural birth, death, and disease-caused death to predict the number of infectives and the duration of the outbreak in Sarawak. Recently, Zhao et al. [7] developed a stage-structured Susceptible - Exposed - Infected - Recovered - Susceptible (SEIRS) model with temperature-dependent latent periods, revealing that time-averaged systems may underestimate infection risks. Despite these advancements, such models do not fully capture the uncertainties inherent in real-world transmission, such as unreported cases or variable immunity levels.

Uncertainty in epidemic models arises from factors such as varying levels of confusion, transmission, and recovery among individuals. Zadeh [8] addressed these issues in 1965 through the development of fuzzy set theory, which provides methods to manage the ambiguity and indeterminacy present in mathematical models. This theory has been applied in various fields, such as in [9], where the authors considered the dynamics of HFMD using the SEIR epidemic model and then presented the results based on the simulation using Takagi-Sugeno Fuzzy system method. In 2023, model of HFMD is examined with fuzzy parameters [10]. The model is then solved by Non-Standard Finite Difference (NSFD) scheme. Arif et al. [11] proposed a novel Fuzzy Computational Scheme for the SIR epidemic model aimed at improving the understanding of infectious disease dynamics and providing stronger basis for public health decision-making. This approach integrates the classical SIR framework with fuzzy technique to address the uncertainties and complexities inherent in disease transmission. Epidemic modelling has more commonly employed fuzzy technique to address uncertainties in diseases such as malaria [12], HIV [13], measles [14] and other infectious outbreaks.

Neutrosophic theory, an extension of fuzzy set introduced by Smarandache [15], provides a mathematical framework for handling uncertainty, indeterminacy, and inconsistency simultaneously. Although this theory has been applied in various fields, its use in epidemic modelling, particularly through neutrosophic algebraic structures, remains underexplored. Prior research has introduced neutrosophic algebraic structures, including neutrosophic groups, fields, and

matrices [16-19] and neutrosophic graphs [20]. Zubairu and Ibrahim [21] laid early groundwork by using neutrosophic algebra to simulate disease spread, yet comprehensive models incorporating both algebraic and network structures remain underexplored. New neutrosophic groupoid and subgroupoid are introduced by Al-Hamido [22] in a new way which is more natural than the previous versions. In the study, the authors discussed and proved some results on the relationship between new and classical neutrosophic algebraic structures. This study integrates neutrosophic algebraic structures with network theory to model HFMD transmission. Both certain and uncertain interactions between epidemiological states, including susceptibility, infection, transmission, quarantine, and recovery, can be represented using this approach. By modelling these states as vertices within neutrosophic viral graphs and applying the integer modulo n , $\square_n$, the way disease spreads through both direct and indeterminate ways are examined. By bridging the gap between epidemiological modelling and algebraic concept, the proposed model helps more effective public health interventions and provides deeper insights into disease behaviour in uncertain environments.

2. Methodology

In this section, the nine state variables are defined and justified. Their selection is based on the epidemiological characteristics of HFMD, including transmission, incubation, asymptomatic infection, and intervention measures such as quarantine and hospitalization. This structure ensures a comprehensive yet mathematically tractable representation of HFMD dynamics within the proposed neutrosophic network framework.

2.1 The Set of Generators of Neutrosophic Group for $\square_9$

For the purpose of model formulation and analysis, the following assumptions are adopted. The total population is constant over the time horizon considered, and children under five years of age constitute the most susceptible group. Asymptomatic individuals can transmit the virus and acquired immunity may be serotype-specific and only temporary. Environmental fomites (e.g., toys and surfaces) are assumed to play a significant role in transmission. Deceased and recovered individuals are treated as removed from the chain of transmission and, for modeling convenience, grouped into a single removed class. Finally, demographic characteristics such as sex, gender, and race are assumed not to affect infection rates. The definitions of the state variables and their associated epidemiological categories in the proposed HFMD network model are presented in Table 1.

Table 1. Some variable declarations related to the HFMD model

Variable	Epidemiological categories
U	Insusceptible individuals (lower risk)
S	Susceptible individuals (mainly children under 5)
E	Exposed individuals (infected but not yet infectious)
M	Symptomatic infected individuals
A	Asymptomatic infected individuals
Q	Quarantined individuals
R	Recovered individuals
H	Hospitalized individuals (if model considers severity)
D	Deceased individuals (rare in HFMD, but may be included in severe cases)
G	Total population

There are nine epidemiological categories involved in this study, which are Insusceptible U , Susceptible S , Exposed E , Asymptomatic infected A , Symptomatic infected M , Quarantined Q , Recovered R , Hospitalized H , and Deceased D . In such a case, $U, S, E, M, A, Q, R, H, D$ are subset of a group G , that is $(U, S, E, M, A, Q, R, H, D) \subset G$. The integer modulo n , $\square_n$ is utilized to represent the subsets of G . In this case, each element of $\square_9$ maps to one of these compartments, ensuring a one-to-one correspondence between algebraic elements and disease states. This makes $\square_9$ a natural algebraic structure for modelling HFMD dynamics. However, the methodology is not limited to nine states. More generally, the framework can be constructed over $\square_n$, where n represents the number of compartments relevant to the disease being modeled. This generalization enhances the adaptability of the neutrosophic algebraic approach, making it applicable not only to HFMD but also to other infectious diseases with different transmission structures.

Definition 2.1 [18]: Neutrosophic group

The neutrosophic group generated by indeterminacy I for any group G under $*$ is defined by $N(G) = \{ \langle G \cup I \rangle, * \} = \{ a + bI \mid a, b \in G \}$, where I is the neutrosophic element with the property $I^2 = I$. Let $U = 0, S = 1, E = 2, M = 3, A = 4, Q = 5, R = 6, H = 7, D = 8$. Hence, $G = \square_9 = \{0, 1, 2, 3, 4, 5, 6, 7, 8\}$ where G to be the group of integer modulo 9. Now, let a neutrosophic group $N(\square_9) = \{ \langle \square_9 \cup I \rangle, +_9 \} = \{ a + bI \mid a, b \in \square_9 \}$ is a group under addition modulo 9 and I denotes indeterminacy. The symbol I does not serve as the group identity element (which remains 0); instead, it models uncertainty in epidemiological transitions. Generators are determined and used to construct

neutrosophic graphs representing state transitions. Thus, the neutrosophic group can also be regarded as a group. Thus, the elements of $N(\square_9)$ are as follows:

$$N(\square_9) = \left\{ \begin{array}{l} 0, 1, 2, 3, 4, 5, 6, 7, 8, I, 2I, 3I, 4I, 5I, 6I, 7I, 8I, \\ 1+I, 2+I, 3+I, 4+I, 5+I, 6+I, 7+I, 8+I, \\ 1+2I, 2+2I, 3+2I, 4+2I, 5+2I, 6+2I, 7+2I, 8+2I, \\ 1+3I, 2+3I, 3+3I, 4+3I, 5+3I, 6+3I, 7+3I, 8+3I, \\ 1+4I, 2+4I, 3+4I, 4+4I, 5+4I, 6+4I, 7+4I, 8+4I, \\ 1+5I, 2+5I, 3+5I, 4+5I, 5+5I, 6+5I, 7+5I, 8+5I, \\ 1+6I, 2+6I, 3+6I, 4+6I, 5+6I, 6+6I, 7+6I, 8+6I, \\ 1+7I, 2+7I, 3+7I, 4+7I, 5+7I, 6+7I, 7+7I, 8+7I, \\ 1+8I, 2+8I, 3+8I, 4+8I, 5+8I, 6+8I, 7+8I, 8+8I \end{array} \right\}.$$

The generators are obtained from the union of generator classes that partition $N(G)$. Therefore, the set of generators of $\square_9$ is $\{1, 2, 4, 5, 7, 8\}$.

2.2 The Neutrosophic Graph Related to Disease Propagation on the Network

Source In this study, vertices correspond to neutrosophic elements representing epidemiological states. Edges represent possible transitions between states:

- Solid edges indicate confirmed transitions (e.g., Infected $\rightarrow$ Recovered).
- Dashed edges indicate indeterminate or uncertain transitions (e.g., Asymptomatic $\rightarrow$ Quarantined).

Each element of $\square_9$ was carefully assigned to the different phases of viral transmission and the edge derives from $\{\langle \square_9 \cup I \rangle, +_9\}$. The kind of graph is presented in Figure 2.

Definition 2.2 [17]: A neutrosophic graph is a graph in which at least one edge is an indeterminacy denoted by dotted lines.

3. Results and Discussion

The construction of the neutrosophic group over $\square_9$ leads to a partitioned structure where each element of the form $a + bI$ represents a state in the HFMD progression, and subsets containing the identity $0 + 0I$ form cyclic structures under addition modulo 9. Each generator thus initiates a deterministic or indeterminate sequence of transitions between epidemiological states.

Proposition 3.1: If $\{\langle \square_9 \cup I \rangle, +_9\}$ is a cyclic neutrosophic group generated by a , then this group generates $n - 4$ elements.

Proof: Although $N(G)$ itself is not strictly a group, it always contains a subgroup that preserves group properties. Let $\square_n$ denote the cyclic group within $N(G)$, and set $G = \langle \square_n \rangle$, an n -th finite cyclic group. The generators of G are of the form ra , where $\gcd(r, n) = 1$. For the case $n = 9$, take $r \in \square_9 = \{0, 1, 2, 3, 4, 5, 6, 7, 8\}$. Clearly, $\gcd(0, 9) \neq 1$, while $\gcd(1, 9) = 1$ holds. Consequently, only certain values of r qualify as valid generators, and each such generator yields exactly $n - 4$ distinct elements in $N(G)$. $\square$

The generators of $N(G)$ are as follows:

$$\begin{aligned}
\langle 1+4I \rangle &= \langle 2+8I, 4+7I, 5+2I, 7+I, 8+5I \rangle, \langle 1+5I \rangle = \langle 2+I, 4+2I, 5+7I, 7+8I, 8+4I \rangle, \\
\langle 1+7I \rangle &= \langle 2+5I, 4+I, 5+8I, 7+4I, 8+2I \rangle, \langle 1+8I \rangle = \langle 2+7I, 4+5I, 5+4I, 7+2I, 8+I \rangle, \\
\langle 2+I \rangle &= \langle 4+2I, 8+4I, 1+5I, 5+7I, 7+8I \rangle, \langle 2+2I \rangle = \langle 4+4I, 8+8I, 1+I, 5+5I, 7+7I \rangle, \\
\langle 2+4I \rangle &= \langle 4+8I, 8+7I, 1+2I, 5+I, 7+5I \rangle, \langle 2+5I \rangle = \langle 4+I, 8+2I, 1+7I, 5+8I, 7+4I \rangle, \\
\langle 2+7I \rangle &= \langle 4+5I, 8+I, 1+8I, 5+4I, 7+2I \rangle, \langle 2+8I \rangle = \langle 4+7I, 8+5I, 1+4I, 5+2I, 7+I \rangle, \\
\langle 4+I \rangle &= \langle 8+2I, 7+4I, 2+5I, 1+7I, 5+8I \rangle, \langle 4+2I \rangle = \langle 8+4I, 7+8I, 2+I, 1+5I, 5+7I \rangle, \\
\langle 4+4I \rangle &= \langle 8+8I, 7+7I, 2+2I, 1+I, 5+5I \rangle, \langle 4+5I \rangle = \langle 8+I, 7+2I, 2+7I, 1+8I, 5+4I \rangle, \\
\langle 4+7I \rangle &= \langle 8+5I, 7+I, 2+8I, 1+4I, 5+2I \rangle, \langle 4+8I \rangle = \langle 8+7I, 7+5I, 2+4I, 1+2I, 5+I \rangle, \\
\langle 5+I \rangle &= \langle 1+2I, 2+4I, 7+5I, 8+7I, 4+8I \rangle, \langle 5+2I \rangle = \langle 1+4I, 2+8I, 7+I, 8+5I, 4+7I \rangle, \\
\langle 5+4I \rangle &= \langle 1+8I, 2+7I, 7+2I, 8+I, 4+5I \rangle, \langle 5+5I \rangle = \langle 1+I, 2+2I, 7+7I, 8+8I, 4+4I \rangle, \\
\langle 5+7I \rangle &= \langle 1+5I, 2+I, 7+8I, 8+4I, 4+2I \rangle, \langle 5+8I \rangle = \langle 1+7I, 2+5I, 7+4I, 8+2I, 4+I \rangle, \\
\langle 7+I \rangle &= \langle 5+2I, 1+4I, 8+5I, 4+7I, 2+8I \rangle, \langle 7+2I \rangle = \langle 5+4I, 1+8I, 8+I, 4+5I, 2+7I \rangle, \\
\langle 7+4I \rangle &= \langle 5+8I, 1+7I, 8+2I, 4+I, 2+5I \rangle, \langle 7+5I \rangle = \langle 5+I, 1+2I, 8+7I, 4+8I, 2+4I \rangle, \\
\langle 7+7I \rangle &= \langle 5+5I, 1+I, 8+8I, 4+4I, 2+2I \rangle, \langle 7+8I \rangle = \langle 5+7I, 1+5I, 8+4I, 4+2I, 2+I \rangle, \\
\langle 8+I \rangle &= \langle 7+2I, 5+4I, 4+5I, 2+7I, 1+8I \rangle, \langle 8+2I \rangle = \langle 7+4I, 5+8I, 4+I, 2+5I, 1+7I \rangle, \\
\langle 8+4I \rangle &= \langle 7+8I, 5+7I, 4+2I, 2+I, 1+5I \rangle, \langle 8+5I \rangle = \langle 7+I, 5+2I, 4+7I, 2+8I, 1+4I \rangle, \\
\langle 8+7I \rangle &= \langle 7+5I, 5+I, 4+8I, 2+4I, 1+2I \rangle \text{ and } \langle 8+8I \rangle = \langle 7+7I, 5+5I, 4+4I, 3+2I, 2+I \rangle.
\end{aligned}$$

The neutrosophic cyclic additive structure over $\square_9 \cup I$ is presented as below.

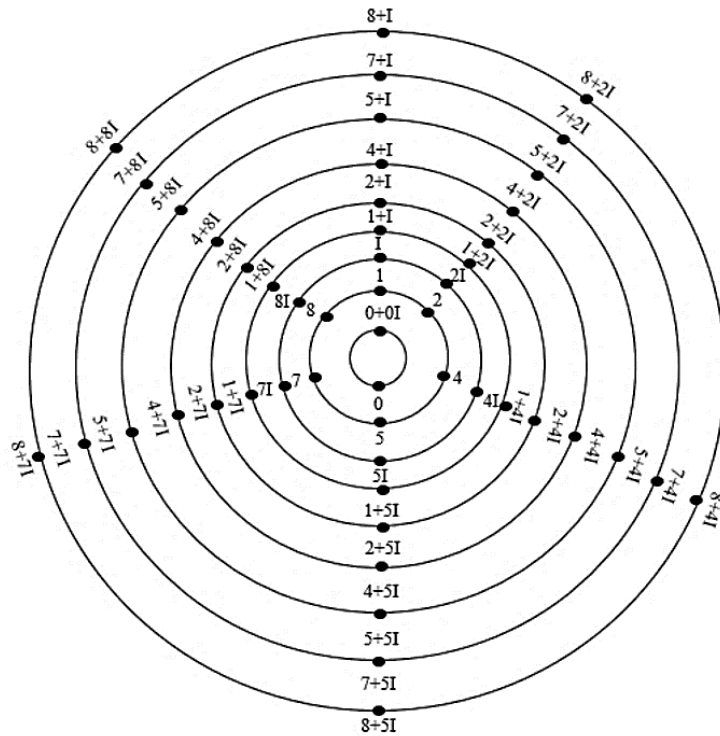


Figure 1. Neutrosophic cyclic graph of $\square_9 \cup I$

Figure 1 illustrates the neutrosophic cyclic graph of $\square_9 \cup I$, where each vertex represents a neutrosophic element of the form $a+bI$, with $a, b \in \square_9$ and I is the indeterminacy component. The graph consists of 81 elements arranged in concentric circular layers, each corresponding to a fixed indeterminate coefficient bI , increasing radially from the origin $0+0I$ to $8+8I$. Vertices closer to the origin represent states with lower uncertainty (e.g., symptomatic, confirmed cases), while outer layers represent more uncertain states (e.g., asymptomatic or untraced contacts). This visual layout suggests that disease transmission within groups of similar uncertainty levels may be more frequent or immediate than across them. In the context of infectious disease modelling, particularly for illnesses such as HFMD, each element can represent a distinct epidemiological state, combining known clinical factors with indeterminate or uncertain conditions.

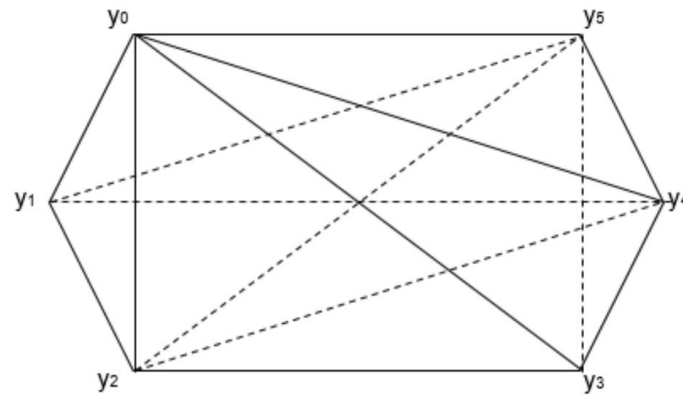


Figure 2. Neutrosophic viral transmission graph of HFMD

In the neutrosophic transmission graph, the vertex y_0 acts as the generator of the system, initiating connects with all other vertices within its generating set. This position represents its role as the primary source of infection, characterized by a strong tendency to spread rapidly to other states. The solid edges from y_0 indicate confirmed transmission pathways. Figure 2 shows the viral transmission graph, which incorporates both confirmed transmission pathways (solid edges) and uncertain ones (dashed edges). In contrast, the dashed edges between vertices such as y_1 and y_4 , y_2 and y_5 , y_3 and y_5 , and y_4 and y_5 signify vague relationships. These uncertain connections reflect real-world ambiguities, such as incomplete contact tracing, asymptomatic transmission, or delays in detection, which are inherently accommodated within the neutrosophic framework.

The variables y_1, y_2, y_3, y_4 , and y_5 represent different compartments in an HFMD transmission model over time t . Specifically, y_1 denotes the number of susceptible individuals, primarily children under the age of five who are at higher risk of contracting the infection due to lower immunity and close-contact environments. The variable y_2 represents the infected population, referring to individuals who have contracted HFMD and may exhibit symptoms. Meanwhile, y_3 corresponds to active transmitters, that is, infected individuals who can spread the disease to others, whether symptomatic or asymptomatic. The compartment y_4 denotes individuals who have been quarantined or isolated to prevent further transmission, reflecting control measures taken during outbreaks. Finally, y_5 represents the recovered population, consisting of individuals who have overcome the infection and are assumed to have gained some level of immunity. Together, these variables describe the dynamic progression of HFMD within a population.

Susceptible individuals y_1 are connected to quarantine y_4 and recovery y_5 , reflecting the typical pathway from exposure to containment and eventual recovery. Infected individuals y_2 also relate to quarantine and recovery, as per standard disease management protocols. Transmitters y_3 are connected to recovery y_5 , as they may recover after transmitting the virus. Quarantined individuals y_4 connect back to both susceptible and infected states, acknowledging that those under quarantine could have originated from either category and the recovered population y_5 connects to susceptible, infected, and transmitter nodes, encapsulating the full spectrum of disease progression.

4. Conclusions

The neutrosophic viral transmission graph provides a comprehensive framework to model the progression of HFMD by both deterministic and indeterminate relationships between epidemiological states. By representing individuals as vertices and categorizing edges into confirmed (solid) and uncertain (dashed) interactions, the model captures the complex, real-world uncertainties inherent in disease transmission, such as asymptomatic cases, delayed diagnoses, and incomplete contact tracing. Notably, the role of the generator, vertex y_0 illustrates the immediate and impact of a primary case, while the structured transitions among susceptible (y_1), infected (y_2), transmitter (y_3), quarantined (y_4), and recovered (y_5) states reflect realistic pathways of HFMD spread. The graph also reveals that while certain transitions (e.g., from infected to recovered) are expected, others remain uncertain due to behavioural or clinical variability. Overall, this neutrosophic approach enhances the constancy of disease modelling by accommodating ambiguity and partial knowledge by providing the potential to support public health strategy and decision-making in uncertain environments, but further empirical validation is required. Future work should include numerical simulations and empirical validation using real HFMD data to demonstrate practical applicability.

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have influenced the work reported in this study.

CRedit Authorship Contribution Statement

Norarida Abd Rhani (Conceptualization; Formal analysis; Validation; Supervision)

Nor Fariyah Azman (Literature review; Methodology; Writing – original draft)

Nurul Fatimah Erman (Literature review; Methodology)

Nadia Ahmad Satmi (Literature review; Methodology)

Suriana Alias (Review and editing; Validation)

Firdawati Mohamed (Review and editing; Validation)

All authors reviewed and approved the final version of the manuscript.

Availability of the Data and Materials

The data used to support the findings of this study are included within the article.

Ethical Declarations

No artificial intelligence tools were used in the preparation of this manuscript. All content was developed manually by the authors. This study did not involve human participants or animals. Ethical approval was therefore not required.

Generative Artificial Intelligence Declarations

The authors claim that artificially intelligent-assisted technologies, such as generative AI, were not used to generate content, ideas, or theories. We have just utilised AI to enhance readability and refine the language. This was used with extreme human control and oversight. The authors take full responsibility for reviewing and approving the content.

References

- [1] Wang Y, Zhao H, Ou R et al. Epidemiological and clinical characteristics of severe hand-foot-and-mouth disease (HFMD) among children: A 6-year population-based study. *BMC Public Health*. 2020 May 27;20(1):801. <https://doi.org/10.1186/s12889-020-08961-6>
- [2] Li XW, Ni X, Qian SY et al. Chinese guidelines for the diagnosis and treatment of hand, foot and mouth disease (2018 edition). *World Journal of Paediatrics*. 2018 Oct;14(5):437-47. <https://doi.org/10.1007/s12519-018-0189-8>
- [3] Robinson CR, Doane FW, Rhodes AJ. Report of an outbreak of febrile illness with pharyngeal lesions and exanthem: Toronto, summer 1957 - isolation of group A coxsackie virus. *Canadian Medical Association Journal*. 1958 Oct 15;79(8):615. <https://pubmed.ncbi.nlm.nih.gov/13585281/>
- [4] Zhang T, Zhang Z, Yu Z, Huang Q, Gao D. Effects of behavior change on HFMD transmission. *Journal of Biological Dynamics*. 2023 Dec 31;17(1):2244968. <https://doi.org/10.1080/17513758.2023.2244968>
- [5] Chuo F, Tiing S, Labadin J. A simple deterministic model for the spread of hand, foot and mouth disease (HFMD) in Sarawak. In 2008 Second Asia International Conference on Modelling & Simulation (AMS). 2008 May 13; 947-952. <https://doi.org/10.1109/AMS.2008.139>
- [6] Wang YC, Sung FC. Modelling the infections for Enteroviruses in Taiwan. Institute of Environmental Health, China Medical University College of Public Health, Taipei. 2004. https://doi.org/10.1093/aje/163.suppl_11.S192-c
- [7] Zhao H, Shi L, Wang J, Wang K. A stage structure HFMD model with temperature-dependent latent period. *Applied Mathematical Modelling*. 2021 May 1;93:745-61. <https://doi.org/10.1016/j.apm.2021.01.010>
- [8] Zadeh LA. Fuzzy sets. *Information and control*. 1965 Jun 1;8(3):338-53. [https://doi.org/10.1016/S0019-9958\(65\)90241-X](https://doi.org/10.1016/S0019-9958(65)90241-X)
- [9] Putri AY, Handayani D, Saragih R. The dynamic of hand-foot-mouth disease model using Takagi-Sugeno fuzzy system. In: *AIP Conference Proceedings* 2020 Sep 22; 2264(1):020004. <https://doi.org/10.1063/5.0024050>
- [10] Baleanu D, Dayan F, Ahmed N, Rafiq M, Raza A, Ahmad MO. Computational investigation of hand foot mouth disease dynamics with fuzziness. *Computers, Materials & Continua*. 2023 May 1;75(2). <https://doi.org/10.32604/cmc.2023.034868>
- [11] Arif MS, Abodayeh K, Nawaz Y. A hybrid SIR-fuzzy model for epidemic dynamics: A numerical study. *CMES-Computer Modeling in Engineering and Sciences*. 2024 Mar 11;139(3):3417-34. <https://doi.org/10.32604/cmes.2024.046944>
- [12] Mangongo YT, Bukweli JD, Kampempe JD. Fuzzy global stability analysis of the dynamics of malaria with fuzzy transmission and recovery rates. *American Journal of Operations Research*. 2021 Oct 13;11(6):257-82. <https://doi.org/10.4236/ajor.2021.116017>
- [13] Lefevr N, Kanavos A, Gerogiannis VC, Iliadis L, Pintelas P. Employing Fuzzy Logic to Analyze the Structure of Complex Biological and Epidemic Spreading Models. *Mathematics* 2021, 9, 977. Applications of Fuzzy Optimization and Fuzzy Decision Making. 2021:37. <https://doi.org/10.3390/math9090977>
- [14] Dayan F, Ahmed N, Rafiq M, Raza A, Khan I, Eldin EM. A reliable numerical investigation of an SEIR model of measles disease dynamics with fuzzy criteria. *Scientific Reports*. 2023 Sep 22;13(1):15840. <https://doi.org/10.1038/s41598-023-42953-x>
- [15] Smarandache, F. Neutrosophic theory and its applications. 2014.

- [16] Smarandache F. A unifying field in logics: Neutrosophic logic. *Philosophy*. 1999;1-141.
- [17] Kandasamy WBV, Smarandache F. Basic neutrosophic algebraic structures and their application to fuzzy and neutrosophic models. 2004;4:5-12. <https://doi.org/10.6084/M9.FIGSHARE.1015531>
- [18] Kandasamy WBV, Smarandache F. Some neutrosophic algebraic structures and neutrosophic N -algebraic structures. 2006. <https://arxiv.org/pdf/math/0603581>
- [19] Agboola AA, Akwu AD, Oyebo YT. Neutrosophic groups and subgroups. *International journal of mathematical combinatorics*. 2012 Sep 1;3:1-9. <https://mathcombin.com/upload/file/20150127/1422320633982016018.pdf#page=6>
- [20] Kandasamy WBV, Ilanthenral K, Smarandache F. Neutrosophic graphs: A new dimension to graph theory. 2015.
- [21] Zubairu A, Ibrahim AA. The spread of infectious disease on network using neutrosophic algebraic structure. *Open Journal of Discrete Mathematics*. 2017 Apr 24;7:77–86. <https://doi.org/10.4236/ojdm.2017.72009>
- [22] Al-Hamido RK. A new neutrosophic algebraic structures. *Journal of Computational and Cognitive Engineering*. 2023;2(2):150-4. <https://doi.org/10.47852/bonviewJCCE2202213>

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