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Bibliometric Analysis

# Global research trends in mathematical modeling for epidemiology: A bibliometric analysis

**Williams Chiari**[1*] **and Voltisa Thartori**[2]

[1]Division of Mathematical and Physical Sciences, Graduate School of Natural Science and Technology, Kanazawa University, Kanazawa, Japan; [2]Health Sciences Department, Curtin University, Miri, Malaysia

*Corresponding author: williamschiari@stu.kanazawa-u.ac.jp

## Abstract

Mathematical modeling has become an indispensable tool in epidemiology, particularly in infectious disease transmission dynamics and public health decisions. Over the past decades, modeling methods have evolved from traditional approaches to AI-driven methods to offer better predictive measures and capability to process large, complex data. The coronavirus 19 (COVID-19) pandemic made a pivotal turn in the field, where almost half of the papers published in the study were written since the beginning of the COVID-19 (2019–2025). The aim of this study was to explore mathematical modeling in epidemiology using bibliometric analysis. Metadata were retrieved from Scopus database and processed using VosViewer for network visualization analysis. A total of 11,032 papers were retrieved, where eight research clusters were found, covering topics from basic reproduction models, disease control covering tuberculosis & human immunodeficiency virus (HIV), vaccination, and most recently being the COVID-19 pandemic. Studies on mathematical modeling in epidemiology were most reported by authors from the United States (documents: 3689, citations: 181054), United Kingdom (documents: 1785, citations: 93842), and China (documents: 1089, citations: 29379). This study provides insight into current progress in epidemiological modeling and identifies less-explored topics that warrant further investigation to meet future global health challenges, including the development of robust, adaptive models that integrate artificial intelligence and deep learning for data-deficient settings.

**Keywords**: Mathematical modeling, epidemiology, infectious disease, COVID-19, global health

## Introduction

Mathematical modeling has been a crucial tool in understanding the dynamics of epidemiology, particularly infectious disease transmission, an important aspect in public health decisions and disease control strategies. A review article published in 2004 emphasized the critical importance of mathematical modeling in tracking the emergence and re-emergence of infectious diseases, highlighting how these models managed to respond to evolving microbial threats, for instance, HIV/AIDS, SARS, and influenza [1]. Early mathematical models were developed, as mentioned in previous study [2], establishing one of the foundational concepts of modeling, such as basic reproduction number, which helped determine whether a disease would spread or die out within a population. Over the years the models evolved, incorporating other parameters such as contact rates, vaccination coverage, and population mobility [3,4,5], all of which affect the disease transmission. Utilizations of mathematical modeling in epidemiology also involved the detailed frameworks to analyze these dynamics, using differential equations to model the existing changes in population compartments [6]. These early models were pivotal in managing infectious diseases

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over the years, including influenza and HIV [7,8], leading to their importance in the context of emerging global health threats.

Years after the development of the aforementioned early models, the advent of network-based models brought a new level of sophistication and insight to predict the spread of diseases among populations. Pastor-Satorras & Vespignani became one of the first to introduce the concept of epidemic spreading in scale-free networks, indicating how disease transmission might accelerate through highly connected individuals in a population—a "hub" [9], and it was proven to be crucially relevant during the coronavirus 19 (COVID-19) pandemic, where a research article published on Science journal in 2020, demonstrated how undocumented infections and asymptomatic carriers facilitated the rapid spread of the virus on a global scale [10]. Mathematical models became an important aspect for policymakers, where they may offer important strategies for containment, testing, and vaccination [11]. The COVID-19 pandemic marked a massive shift in the increase of research in this field, where efforts were dedicated to further understanding and mitigating the spread of the SARS-CoV-2 virus.

Recent years have also been an important step to further the technology in mathematical modeling, particularly for infectious disease transmission, where advancements in artificial intelligence, machine learning, and big data analysis have managed to greatly develop the model by refining predictions and improving real-time data analysis. The integration of AI-driven approaches managed to enable the rapid adaptation to different models to account for new variants or changing disease transmission patterns. Chae et al. in 2018 [12] discussed how deep learning models like deep neural network (DNN) and long-short term memory (LSTM) managed to outperform traditional models such as the autoregressive integrated moving average (ARIMA) in predicting infectious diseases, utilizing vast amounts of social media and environmental data to improve disease transmission forecasting [12].

Despite having major development in recent years, the utilization of mathematical modeling in epidemiology requires further reviews in illustrating the current progress of this research field, therefore, this review paper exists to inform the readers on the research trend and landscape to help related researchers in designing future research. To achieve this, bibliometric approaches are employed to study the emerging topics of mathematical modeling in epidemiology. For instance, this study analyzes the research trend of COVID-19 pandemics, which was a relatively new and rapidly evolving topic by the year it was published, as well as other samples in essential oils and polymeric materials research trend [13,14]. Similar bibliometric approaches have also been applied to wastewater treatment microplastics, revealing key patterns and research trends within these specialized areas [15,16]. As the field continues to evolve, this study answer the following research questions: (1) How has the use of mathematical models in epidemiology evolved, particularly in response to its widespread application during the COVID-19 pandemic? (2) What are the key areas of focus for researchers using mathematical models to study infectious diseases? Are there any less explored subfields within the research theme that warrant further investigation in the future?

## Methods

This study utilized Scopus database to retrieve relevant papers of mathematical modeling in epidemiology (**Figure 1**). The keywords inputted to the Scopus database search are as follows: ("Mathematical Model" OR "Mathematical Modeling" OR "Math Model" OR "Math Modeling" OR "Mathematic Model" OR "Mathematics Model") AND ("Infectious Disease" OR "Epidemic Model" OR "Disease Spread" OR "Epidemiology" OR "Compartmental Model")", which were then filtered based on their publication status, document types (original article, conference paper, review, short survey). Several irrelevant subject areas retrieved from the Scopus database were also filtered out such as Arts and Humanities, Earth and Planetary Science, Dentistry and others including undefined subjects. No year published restriction was applied for the data retrieval (1962–2025), with further observation conducted to compare the publications written before and after the COVID-19 pandemic. The exported data was carefully cross-checked to eliminate potential paper duplicates and titles irrelevant to the study. The retrieved database was finally exported as CSV (.csv) file and inputted on VosViewer 1.6.20 for visualization analysis purposes.

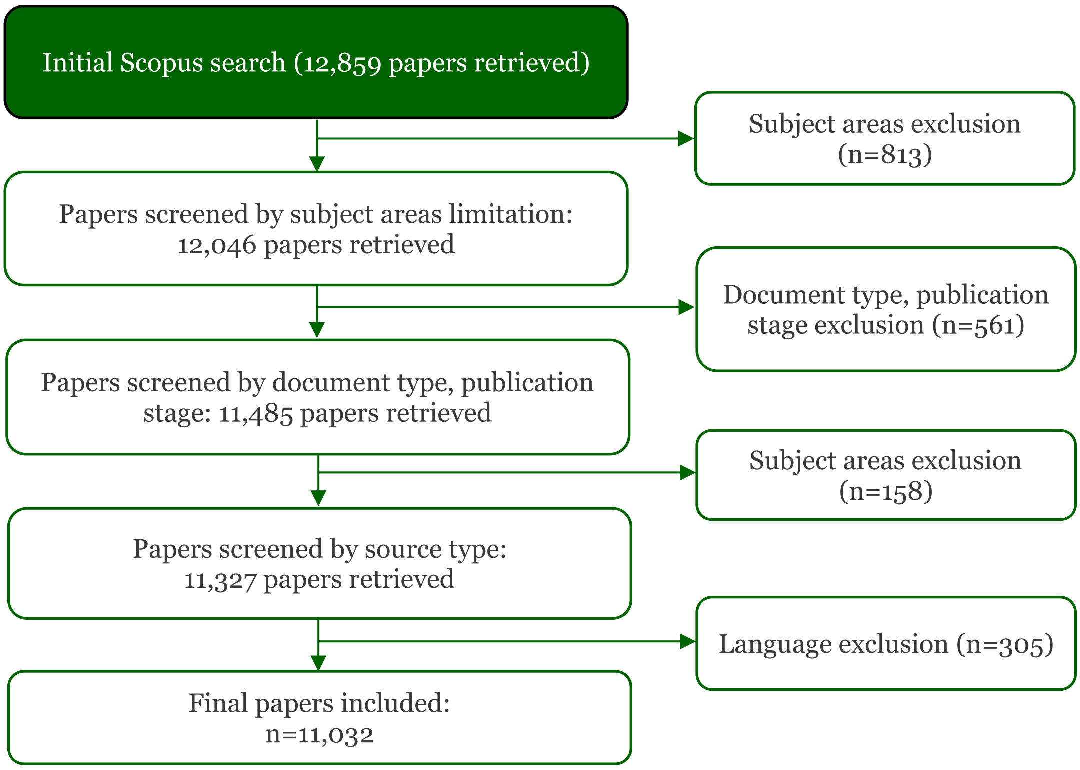

Figure 1. Flowchart of mathematical modeling in infectious diseases literature search and filtering process.

## Results

### Characteristics of identified papers on mathematical modeling in epidemiology

A total of 11,032 papers consisted of original articles (n=9524; 86.3%), conference papers (n=761; 6.9%), review papers (n=713; 6.5%), and other documents (n=34; 0.3%) studying mathematical modeling in epidemiology were retrieved on the Scopus database (**Figure 2**). There was a sharp increase in papers published since 2019, notably due to the beginning of COVID-19 pandemic, accumulating a total of 46.6% of the total papers published in the study as retrieved from the database.

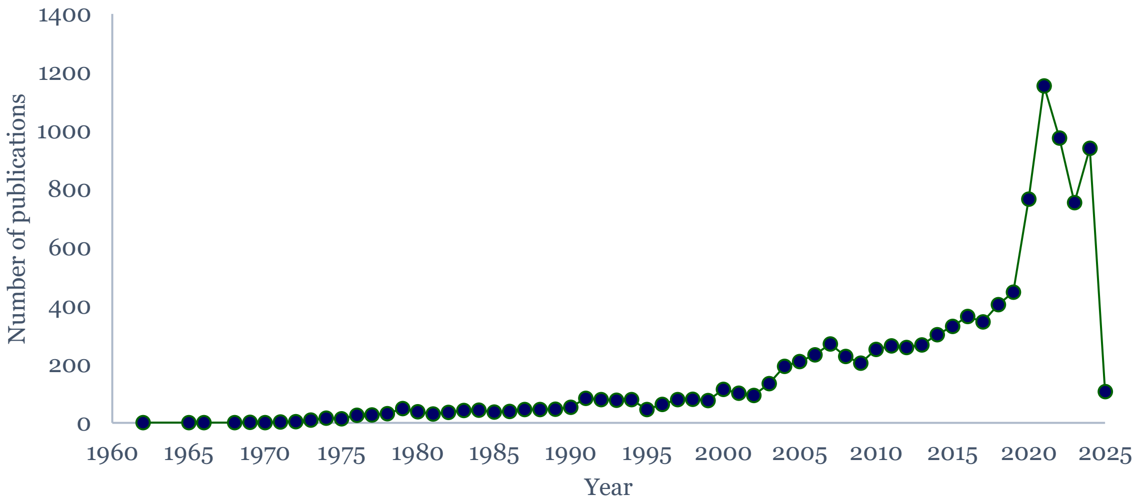

Figure 2. Publication trend of mathematical modeling in epidemiology studies.

Medicine (n=4419; 40.05%), Mathematics (n=3797; 34.41%), Biochemistry, Genetics, and Molecular Biology (n=2282; 20.68%), and Agricultural and Biological Sciences (n=2027; 18.37%) were the most studied subject areas in relation to mathematical models and epidemiology

(**Table 1**). Out of 11032 retrieved papers, only 14 out of 159 journals published more than 100 papers of related study.

Table 1. Top ten subject areas related to mathematical modeling in epidemiology

| No | Subject area | Number of papers |
|---|---|---|
| 1 | Medicine | 4,419 |
| 2 | Mathematics | 3,797 |
| 3 | Biochemistry, genetics, and molecular biology | 2,282 |
| 4 | Agricultural and biological sciences | 2,027 |
| 5 | Immunology and microbiology | 1,934 |
| 6 | Computer science | 1,293 |
| 7 | Environmental science | 1,115 |
| 8 | Engineering | 1,058 |
| 9 | Multidisciplinary | 841 |
| 10 | Physics and astronomy | 755 |

## Top authors, organizations, countries, and funding sources

The most prolific author, as per the data retrieved, was Anderson RM (n=64; 0.58%), followed by Nishiura H (n=60; 0.54%), Ferguson NM, and Abu-Raddad LJ (n=46, 0.42%). In regard to the most productive funding sources supporting the study, the National Institutes of Health ranked first (n=865; 7.84%), followed by the U.S. Department of Health and Human Services (n=661; 5.99%), being the only two organizations to support more than 500 publications (**Table 2**).

Table 2. Top ten funding sources for mathematical modeling in epidemiology study

| No | Funding source | Status | Number of papers |
|---|---|---|---|
| 1 | National institutes of health | Government | 865 |
| 2 | US department of health and human services | Government | 662 |
| 3 | National science foundation | Government | 466 |
| 4 | National natural science foundation of China | Government | 445 |
| 5 | European commission | European union | 314 |
| 6 | National institute of allergy and infectious diseases | Government | 298 |
| 7 | UK research and innovation | Government | 293 |
| 8 | Medical research council | Government | 286 |
| 9 | National institute of general medical sciences | Government | 248 |
| 10 | Ministry of science and technology of the people's Republic of China | Government | 209 |

## Top mathematical modeling in epidemiology articles based on citation

There was a total of 389,090 citations for 11,032 papers, averaged 35.27 citations per paper and 6079.53 citations per year (1962–2025). The most cited paper was written by Van Den Driessche P & Watmough J (2002) (**Table 3**) on the reproduction numbers in compartmental disease transmission models. The aforementioned paper was cited almost twice as many as the secondly cited paper written by Hethcote, H.W in 2000, reviewing the evolution and application of mathematical models in epidemiology. Seven papers exceeded 2000 citations, with only one originating before 2000.

Table 3. Top ten most cited published articles on mathematical modeling in epidemiology

| Rank | Title | Author(s) | Year of publication | Times of citations | Ref. |
|---|---|---|---|---|---|
| 1 | Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission | Van Den Driessche, P. & Watmough, J. | 2002 | 7,232 | [2] |
| 2 | Mathematics of infectious diseases | Hethcote, H.W. | 2000 | 4,845 | [6] |
| 3 | Epidemic spreading in scale-free networks | Pastor-Satorras, R. & Vespignani, A. | 2001 | 4,750 | [9] |
| 4 | Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV-2) | Li, R. et al. | 2020 | 2,399 | [10] |

| Rank | Title | Author(s) | Year of publication | Times of citations | Ref. |
|---|---|---|---|---|---|
| 5 | Gut metagenome in European women with normal, impaired and diabetic glucose control | Karlsson, F.H. et al. | 2013 | 2,358 | [17] |
| 6 | Global epidemiology of hepatitis C virus infection | Shepard, C.W. et al. | 2005 | 2,327 | [18] |
| 7 | Population biology of infectious diseases: Part I | Anderson, R.M. & May, R.M. | 1979 | 2,201 | [19] |
| 8 | Social contacts and mixing patterns relevant to the spread of infectious diseases | Mossong, J. et al. | 2008 | 1,993 | [20] |
| 9 | From epidemiological synergy to public health policy and practice: The contribution of other sexually transmitted diseases to sexual transmission of HIV infection | Fleming, D. T., & Wasserheit, J. N. | 1999 | 1,882 | [21] |
| 10 | Modeling and variable selection in epidemiologic analysis | Greenland, S. | 1989 | 1,841 | [22] |

## Results from co-authorship networking analysis

The relationship between authors, including their affiliated institutions and countries, can be examined through network analysis of co-authored papers. This analysis can reveal collaboration patterns and identify key authors, institutions, and countries actively contributing to research on mathematical modeling of infectious diseases. The analysis can reveal collaboration trends and highlight key authors, institutions, and countries contributing to research on mathematical modeling of infectious diseases. Visualization maps were generated using VOSviewer, where nodes of varying sizes and colors represent authors, institutions, or countries within their respective clusters. These nodes are connected by lines indicating Link Strength (LS), which reflects the number of co-authored papers and the intensity of collaboration between two entities. Total Link Strength (TLS) is calculated by summing all links connected to a node, providing an overall measure of the strength of relationships among authors, institutions, or countries.

The authors' co-citation analysis was conducted with the following thresholds—minimum number of documents per author set at 10 and minimum number of citations per author set at 5. Of 34,478 detected authors from the retrieved data, 203 met the thresholds. The author with the highest number of citations was van den Driessche (citations: 8420; TLS: 405), followed closely by Anderson RM (citations: 8,167; TLS: 124). TLS did not correlate with citation counts, for instance, May RM (citations: 7,606; TLS: 5) was co-cited only in five papers. The density visualization of authors' co-citation highlights key researchers in the field, with Hiroshi N, Roy MA, and Neil MF, among the most frequently cited (**Figure 3**). The red and yellow regions of the visualization indicated stronger co-citation networks among authors, indicating influential clusters of authors working on the study, with the authors in red regions being the most influential.

Organization-based co-authorship analysis was conducted on 29,173 organizations or funding sources, also restricted with the same thresholds of a minimum five papers per organization and ten minimum citations requirements, in which 51 met the thresholds (**Figure 4**). The network visualization indicates how key organizations are involved in collaboration on the study, where the London School of Hygiene (Documents: 28; citations: 1057) and Tropical Medicine and Fogarty International Center (Documents: 11; citations: 1991) appear as central nodes, indicating how influential their published papers were.

Lastly, country-based co-authorship analysis was carried out on 107 detected countries from the database, in which after being restricted to the same thresholds as previously applied, 95 countries met the thresholds (**Figure 5**). The United States (documents: 3,689; citations: 18,1054; TLS: 2,727), United Kingdom (documents: 1,785; citations: 93,842; TLS: 2,149), and China (documents: 1,089; citations: 29,379; TLS: 891) emerge as central nodes, which indicate their dominant roles in global research collaborations. Different colors of nodes also highlighted how often certain countries conducted research collaborations on the study, highlighting a localized research effort on continental aspect.

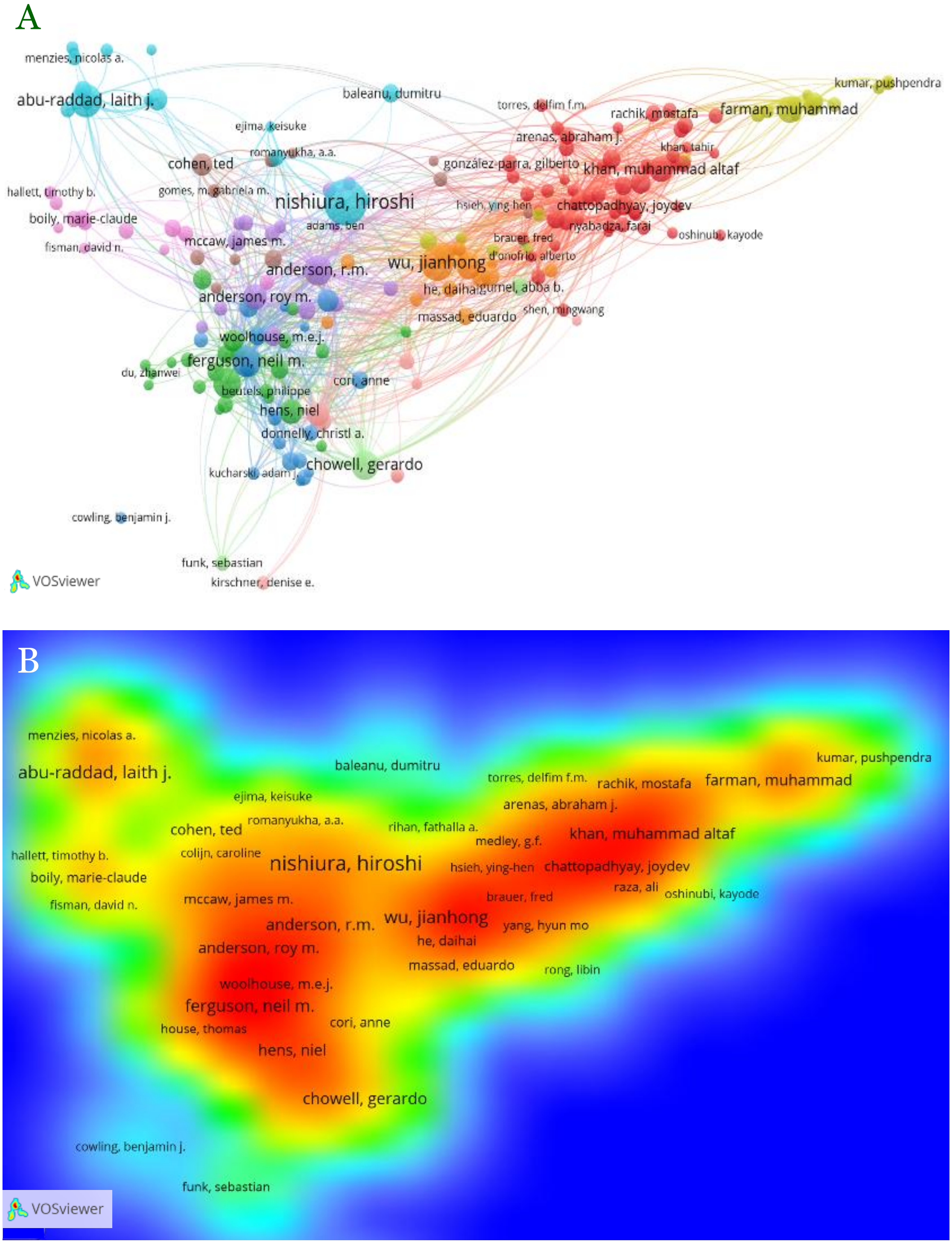

Figure 3. (A) Network visualization of authors' co-citation (weights: documents). (B) Density visualization of authors' co-citation (weights: documents).

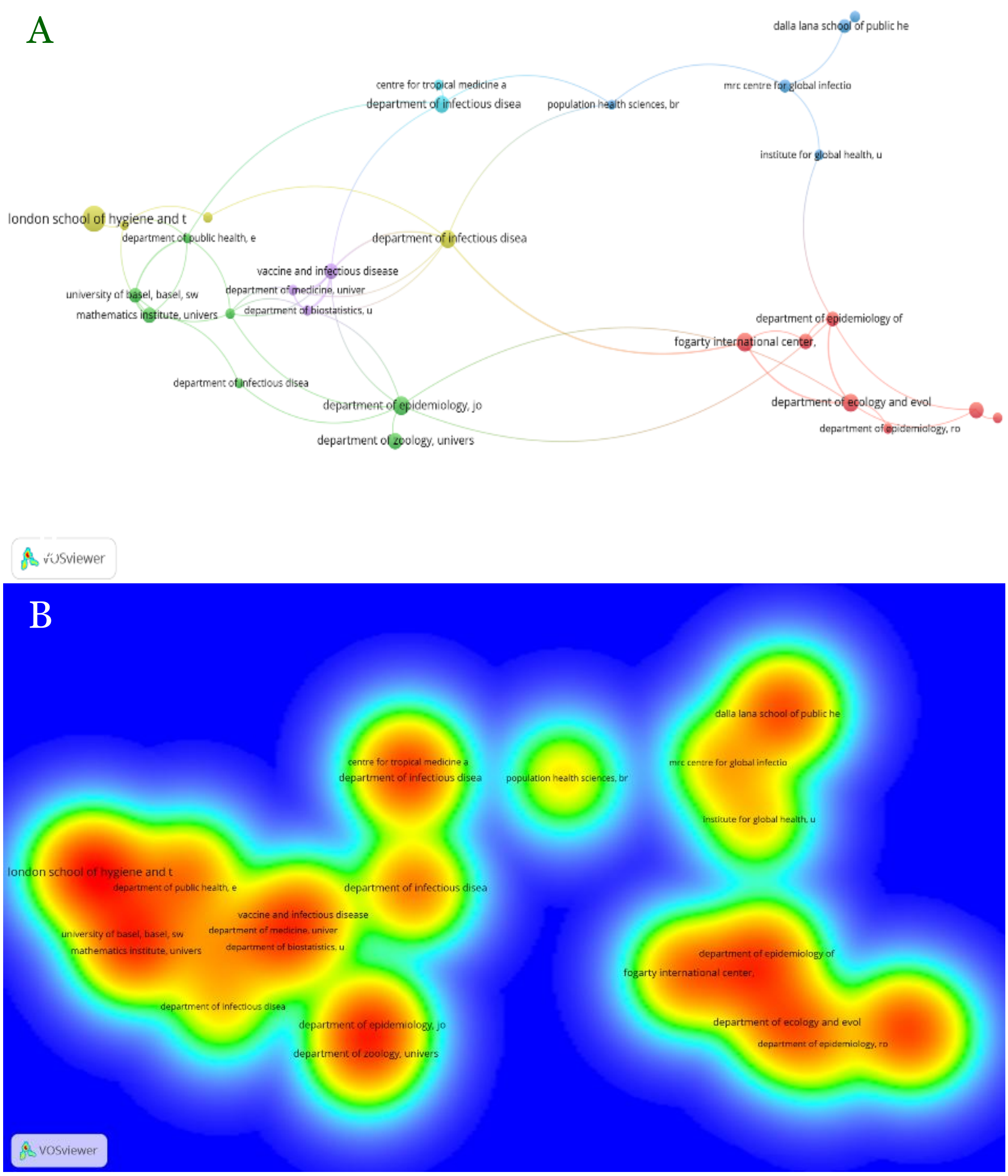

Figure 4. (A) Network visualization of organizations' co-authorship (weights: documents). (B) Density visualization of organizations' co-authorship (weights: documents).

## Keyword co-occurrence analysis

A keyword co-occurrence analysis was conducted to determine the frequency of connected terms among papers and to identify emerging trends within the research field. The network and density visualization maps represented each keyword as a node, where links between nodes indicated their co-occurrence in research publications. The size of each node and link varies, reflecting the one keyword's popularity and the strength of its association with other terms, generally a group of nodes of the same link would create clusters of research subthemes.

A total of 17,173 keywords were identified, a minimum occurrence threshold of nine was applied (**Figure 6**). A total of 106 keywords met the threshold, with the most used keywords in the study on mathematical modeling in epidemiology were COVID-19 (occurrences: 1,043; TLS: 2,188), Epidemiology (occurrences: 1,089; TLS: 1,908), and Mathematical Model (occurrences: 1,089; TLS: 1,668). The network visualization presented in **Figure 6** indicated how these three keywords were the most influential keywords in the study. Notably, COVID-19 emerged as the dominant keyword, consistent with the publication surge post-2019.

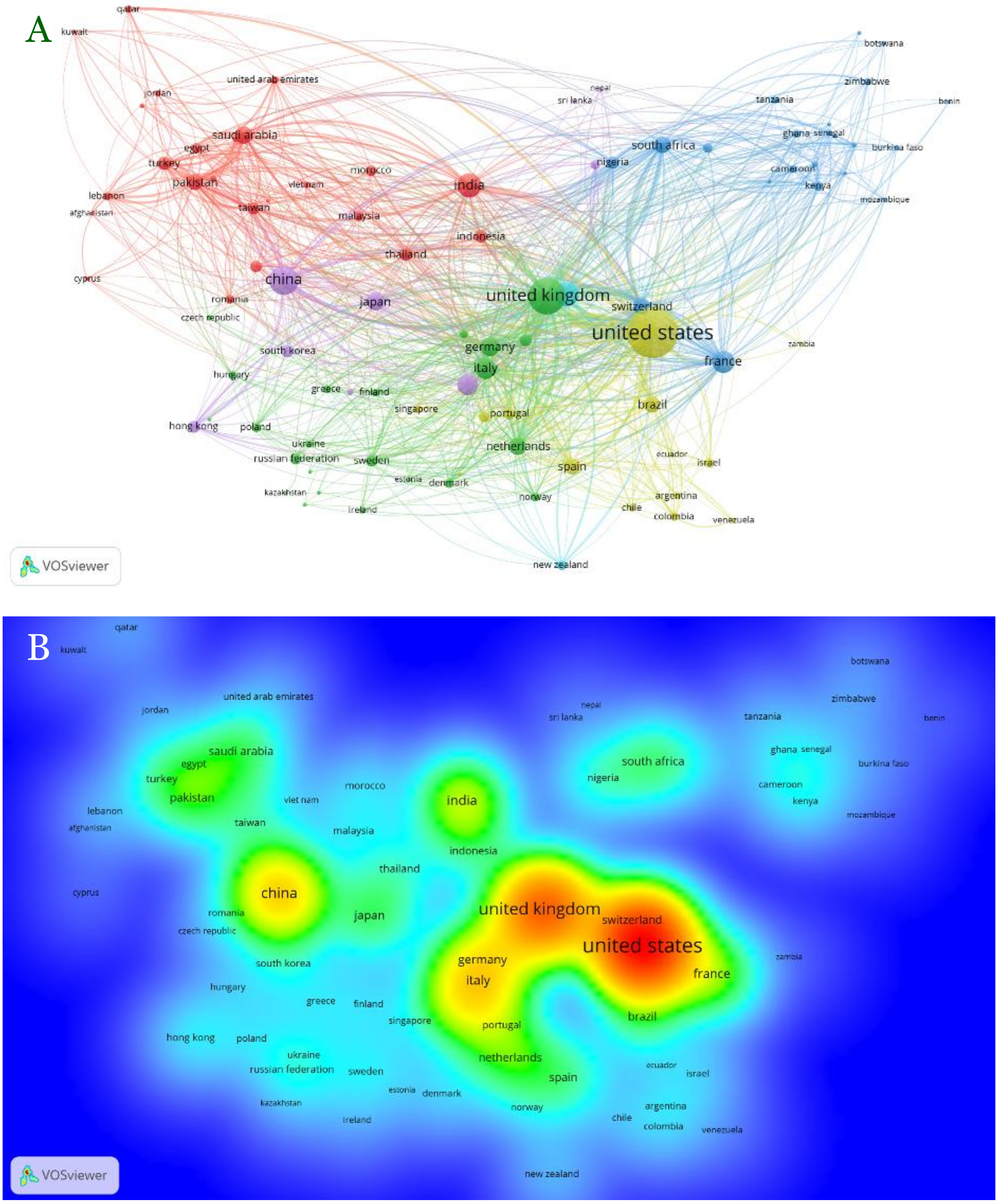

Figure 5. (A) Network visualization of countries' co-authorship (weights: documents). (B) Density visualization of countries' co-authorship (weights: documents).

Research clusters were also formed among the keywords used in research study, with different colors as the difference. Each nodes' color grouped these keywords based on the keywords' closeness to a certain research subtheme of the study. The research clusters, according to the visualization, was presented in **Table 4**, with each cluster generally being close to a research trend. Density visualization of the keywords indicated how certain keywords played an important role in becoming the central figures of the research study, with the ones in red region being the most influential.

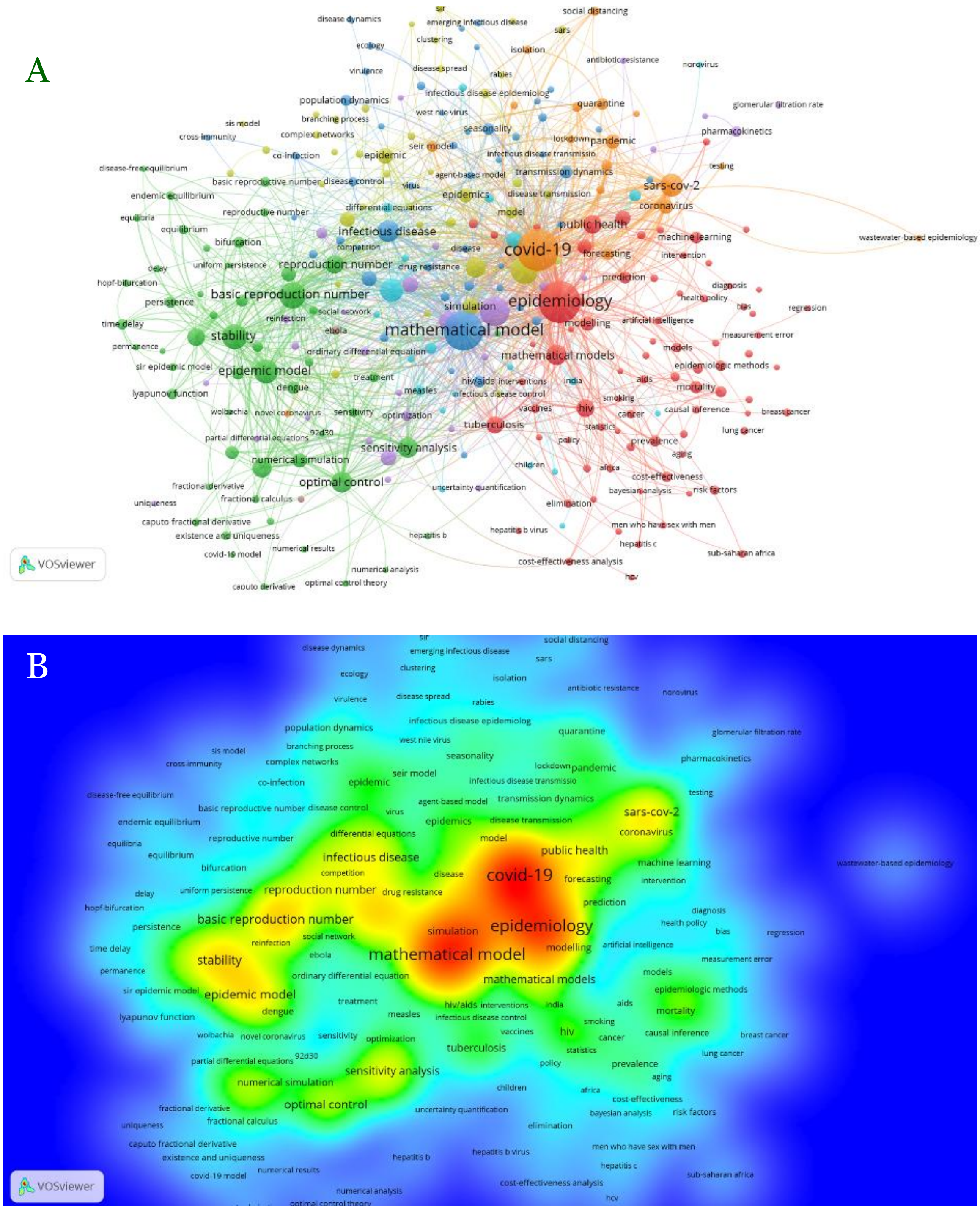

Figure 6. (A) Network Visualization of keywords' co-occurrences (weights: occurrences). (B) Density visualization of keywords' co-occurrences (weights: occurrences).

Table 4. Clusters of trending microalgal-bacterial research sub-topics

| Cluster (color) | Keywords of interest | Research trend |
|---|---|---|
| Red (I) | Epidemiology, public health, tuberculosis, HIV | Mathematical modeling for disease control, public health surveillance |
| Green (II) | Basic reproduction number, stability analysis, optimal control | Stability and control in epidemic models, optimization of public health strategies |
| Mustard (III) | SIR model, simulation, disease transmission | Simulation and analysis of disease spread using SIR models |
| Orange (IV) | COVID-19, contact tracing, forecasting | Real-time modeling for COVID-19 spread, contact tracing, and forecasting outbreaks |

| Cluster (color) | Keywords of interest | Research trend |
|---|---|---|
| Blue (V) | Disease ecology, population dynamics, transmission dynamics | Mathematical approaches to disease dynamics, ecological modeling of disease spread |
| Purple (VI) | Parameter estimation, compartmental models, pharmacokinetics & pharmacodynamics | Parameter estimation in epidemiological models, incorporation of pharmacokinetics in epidemic modeling |
| Cyan (VII) | Vaccination, immunology, hospitalization | Modeling vaccination strategies, immunological responses, and hospitalization dynamics |
| Brown (VIII) | Ebola, Dynamical System | Dynamical system approaches to Ebola virus spread, complex modeling of disease outbreaks |

## Discussion

The COVID-19 pandemic significantly reshaped the mathematical modeling study in epidemiology research, accelerating the study on the spread and control of infectious diseases. Mathematical models also evolved in adapting to technological advancement changes, such as the use of machine learning and artificial intelligence, demonstrating their significance over future potential rapid adaptation in times of crisis.

Trends and shifts in the landscape of mathematical modeling in epidemiology studies were particularly rising following the onset of the COVID-19 pandemic. Out of 11,032 papers retrieved from the Scopus database, over 40% of the total papers were published from COVID-19 pandemic onwards (2019–2025). This dramatic increase emphasized the central role of mathematical modeling in addressing rising global health challenges, particularly in understanding the spread and control of infectious diseases.

Advancements in technology also caused the emergence of machine learning and artificial intelligence (AI), particularly over the spread of infectious disease tracking. The incorporation of AI, machine learning and big data analytics managed to incorporate the traditional mathematical models, where these technologies were used to refine the accuracy of disease spread predictions. Studies integrating AI-driven methods such as deep neural networks (DNNs) and long short-term memory (LSTM) networks were found to outperform traditional mathematical methods, one of which being the autoregressive integrated moving average (ARIMA). With that regard, AI-driven methods managed to showcase the potential of modern technologies to help enhancing the speed and adaptability of disease models, particularly potential future global health outbreak like COVID-19.

Geographic and institutional patterns also emerged. Among 107 countries, the United States, United Kingdom, and China were the only nations each publishing more than 1,000 papers. Institutionally, the London School of Hygiene & Tropical Medicine and the Fogarty International Center played central roles. Network visualizations indicated extensive collaboration across organizations to confront infectious-disease challenges using mathematical modeling.

Keyword analysis confirmed the prominence of COVID-19 (the most frequent keyword) and revealed multiple research clusters. These clusters emphasize the need for real-time modeling to inform contact tracing, vaccination, and outbreak forecasting. Prior to COVID-19, models frequently focused on HIV and tuberculosis [23,24], emphasizing transmission dynamics and control strategies. As the field expanded during the pandemic, clusters around real-time modeling, contact tracing, and outbreak forecasting became prominent [25-27]. Susceptible–infected–recovered (SIR) models remained a staple, with refinements that improved the prediction of infectious-disease trajectories [28].

Before the pandemic, mathematical modeling in epidemiology concentrated on foundational topics such as the basic reproduction number, vaccination strategies, and general transmission dynamics [2,29,30]—areas that remain essential for guiding control and mitigation. COVID-19 further accelerated progress and raised questions about model choice (e.g., uncertainty around exit strategies requires more accurate prediction capability [31]). The incorporation of AI and machine learning has been crucial, given their ability to handle large, complex, high-dimensional data in real time [32,33]. However, model performance depends on data that are accurate and timely [34]; effectiveness is compromised when data are scarce, inaccurate, delayed, or unreliable

[35–38]. This reveals a critical gap: improved data-integration techniques that maintain model performance in data-deficient settings. Addressing this gap will require advances in data collection and fusion to enhance adaptability and deliver reliable predictions despite imperfect inputs.

Finally, evidence in this bibliometric analysis necessarily reflects published research at the time of assessment; relevant studies may not yet be available. Moreover, our coverage is limited to Scopus-indexed publications. Nonetheless, bibliometric analysis remains a robust approach to characterize the current research landscape and to highlight directions for future work.

# Conclusion

Mathematical modeling in epidemiology has expanded rapidly, especially since COVID-19, shaping infectious-disease management and public-health strategy. As the field evolves, traditional approaches must adapt to advances in AI and deep learning to enhance precision and predictive flexibility. Going forward, progress will depend on robust, adaptive models that perform reliably in data-deficient settings.

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## Competing interests

The authors declare no conflicts of interest.

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## Underlying data

Derived data supporting the findings of this study are available from the corresponding author on request.

## Declaration of artificial intelligence use

We hereby confirm that no artificial intelligence (AI) tools or methodologies were utilized at any stage of this study, including during data collection, analysis, visualization, or manuscript. All work presented in this study was conducted manually by the authors without the assistance of AI-based tools or systems.

# How to cite

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