

PAPER

Measles and Rubella Surveillance in the Digital Era: A Bibliometric Analysis of Scientific Trends and Conceptual Structure

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ABSTRACT

The integration of digital technologies has profoundly transformed the surveillance of infectious diseases over recent decades. The emergence of approaches grounded in digital health, genomic surveillance, health information systems, and data analytics opens new perspectives for measles and rubella surveillance. The present study provides a systematic mapping of the scientific literature on measles and rubella surveillance in the digital era, in order to characterize its evolution, identify emerging themes, and reveal its conceptual structure. A bibliometric analysis was conducted using the Scopus database, combining terms related to measles, rubella, epidemiological surveillance, and digital technologies. Only peer-reviewed articles published in English were retained. The analyses focused on the temporal evolution of publications, the identification of trend topics, the construction of thematic maps over two successive periods, and the conceptual structure of the corpus, examined through multiple correspondence analysis (MCA). All analyses were performed using the R package Bibliometrix. A total of 154 articles published between 1990 and 2026 were included. Scientific output increased progressively, particularly from 2010 onward, reaching a peak of 27 publications in 2025. Earlier research mainly focused on conventional surveillance, vaccination, and public health, whereas recent publications place greater emphasis on digital and genomic surveillance, electronic reporting systems, and data-driven analytical approaches. The terms *machine learning*, *deep learning*, and *convolutional neural network* are positioned within the quadrant of emerging themes. The MCA explained 86.11% of the cumulative variance, indicating that the first two dimensions adequately captured the conceptual structure of the corpus. Three major thematic clusters were identified: the epidemiological surveillance of communicable diseases, vaccination strategies, and the progressive integration of digital health systems. This study provides a systematic mapping of the scientific evolution of measles and rubella surveillance in the digital era. It underscores the growing prominence of genomic surveillance and digital health systems, as well as the need to deepen the integration of artificial intelligence (AI) methods to strengthen early outbreak detection, improve real-time vaccination monitoring, and support international elimination goals.

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KEYWORDS

measles, rubella, epidemiological surveillance, digital health, bibliometric analysis, artificial intelligence (AI), genomic surveillance

1 INTRODUCTION

Measles and rubella remain among the vaccine-preventable viral diseases that continue to pose a major challenge to global public health, despite the progress achieved in immunization programs over recent decades. Measles, characterized by high transmissibility and strong epidemic potential, continues to cause recurrent outbreaks in several regions of the world, particularly in settings marked by insufficient vaccination coverage, population movements, or disruptions in health-care systems. Rubella, generally mild in children and adults, represents a major threat during pregnancy because of the risk of congenital rubella syndrome (CRS), which can lead to severe congenital abnormalities and neonatal complications. In this context, epidemiological surveillance plays a crucial role in early case detection, the monitoring of transmission chains, the evaluation of vaccination programs, and the prevention of outbreaks.

The central role of surveillance in measles and rubella control has been emphasized by the World Health Organization (WHO) in its Measles and Rubella Strategic Framework 2021–2030, which identifies high-quality case-based surveillance, laboratory confirmation, and timely data use as essential components for achieving and sustaining elimination goals. This framework further underscores the need to strengthen national surveillance capacities and adopt innovative tools and methodologies to support evidence-based public health action [1].

Historically, measles and rubella surveillance relied on clinical reporting systems, field investigations, and laboratory confirmation performed in reference laboratories. The rapid evolution of digital technologies and health information systems has profoundly transformed these approaches. The progressive integration of electronic reporting systems, digital health platforms, geographic information systems (GIS), big data analytics, genomic surveillance, and predictive analytics tools has contributed to improving the timeliness, accuracy, and effectiveness of surveillance systems. More recently, the rise of artificial intelligence (AI) and machine learning (ML) methods has opened new perspectives for epidemic modeling, outbreak prediction, automated signal detection, and decision support in public health [2–5].

The COVID-19 pandemic accelerated this digital transformation by promoting the adoption of data-driven tools, real-time disease monitoring systems, and interactive surveillance dashboards that enabled the rapid visualization and dissemination of epidemiological information. This transformation has progressively shaped measles and rubella surveillance programs, in which innovative technologies are increasingly integrated into conventional systems to optimize the collection, analysis, and interpretation of epidemiological data.

Consequently, the scientific literature dedicated to measles and rubella surveillance has experienced notable growth and now encompasses diverse disciplines such as epidemiology, medical informatics, digital public health, bioinformatics, and AI. However, despite this expansion, no comprehensive bibliometric mapping has yet systematically characterized the scientific evolution of the field, identified emerging themes related to the integration of digital technologies, or highlighted the conceptual structure underlying research in this area. This gap limits the understanding of ongoing scientific dynamics and makes it difficult to identify priority research directions.

Bibliometric analysis represents a particularly suitable approach to address this need. Based on a structured corpus of publications, it enables the quantitative examination of the evolution of a scientific field, the identification of its main research directions, the mapping of emerging themes, and the exploration of its conceptual structure.

The present study therefore aims to conduct a bibliometric analysis of the scientific literature on measles and rubella epidemiological surveillance in the era of digital technologies. More specifically, it pursues four objectives: (i) to characterize the temporal evolution of scientific production in this field; (ii) to identify the main research themes and their dynamics over time; (iii) to map the relationships among the concepts addressed in the literature; and (iv) to highlight the conceptual structure of the field and the thematic axes that organize it. By providing an integrated overview of the scientific evolution of this domain, this study offers researchers and public health decision-makers a reference framework for guiding future research and supporting the development of more effective surveillance systems.

2 MATERIALS AND METHODS

2.1 Study design and rationale

This study adopts a bibliometric approach to systematically examine the scientific production dedicated to the epidemiological surveillance of measles and rubella in the context of digital technologies. Bibliometrics was selected as the main methodological framework due to its ability to provide a rigorous quantitative analysis of a large volume of publications, enabling both the characterization of publication trends over time and the exploration of the intellectual and conceptual structure of the field. This approach offers an integrated overview of the state of research by identifying the main themes addressed as well as the relationships among concepts.

2.2 Data source and search strategy

Data were retrieved from the Scopus database, which was selected for its broad multidisciplinary coverage, the quality and consistency of its bibliographic metadata, and its reliability in indexing peer-reviewed scientific publications at the international level. Scopus is widely recognized as one of the principal sources for bibliometric research in public health and biomedical sciences, owing to its standardized indexing system and extensive coverage of high-impact journals. These characteristics facilitate the retrieval, organization, and analysis of bibliographic records and ensure the homogeneity of the corpus throughout the study. Furthermore, the use of a single database reduces potential duplication and inconsistencies that may arise when merging records from multiple sources. While this approach provides a structured and coherent corpus for bibliometric analysis, the findings are bounded by the scope of Scopus indexing and may not encompass publications indexed exclusively in other databases. Nevertheless, Scopus provides substantial coverage of the scientific production related to measles and rubella surveillance in the digital era.

The search strategy was designed to identify, as comprehensively as possible, publications related to the epidemiological surveillance of measles and rubella while incorporating dimensions associated with digital technologies and AI. The search was conducted in April 2026. As a result, the corpus includes all publications indexed in Scopus at the time of data retrieval, including early-access articles dated 2026. No time restriction was applied in order to capture the entire evolution of the field since its earliest publications. The following query was used:

TITLE-ABS-KEY ((measles OR rubella OR “congenital rubella syndrome”) AND (surveillance OR “epidemiological surveillance” OR “disease surveillance” OR “public health surveillance” OR monitoring) AND (“artificial intelligence” OR “machine learning” OR “digital health” OR “big data” OR “electronic health” OR ehealth OR mhealth OR GIS OR “predictive analytics” OR “genomic surveillance” OR informatics OR “real-time surveillance” OR “electronic reporting” OR “digital epidemiology” OR “health information systems” OR “data mining”))

This query targets publications in which terms related to measles, rubella, or congenital rubella syndrome appear in conjunction with terms associated with epidemiological surveillance and digital technologies, in the title, abstract, or author keywords.

2.3 Selection criteria and corpus constitution

The constitution of the corpus followed a systematic approach based on pre-defined selection criteria to ensure the relevance and scientific quality of the publications analyzed. The initial search in Scopus retrieved 203 documents.

Two inclusion criteria were subsequently applied. First, only peer-reviewed scientific articles (*document type: article*) were retained, leading to the exclusion of letters, notes, editorials, conference proceedings, and other document types. This choice was made to focus the analysis on complete studies that had undergone a peer-review process, thereby strengthening the reliability of the corpus. Second, only documents published in English were included, in order to ensure the linguistic homogeneity of the corpus and to allow a consistent interpretation of titles, abstracts, and keywords, particularly in the context of analyses based on term co-occurrence and thematic mapping.

After applying these criteria, the final corpus retained for analysis comprised 154 articles (see Figure 1).

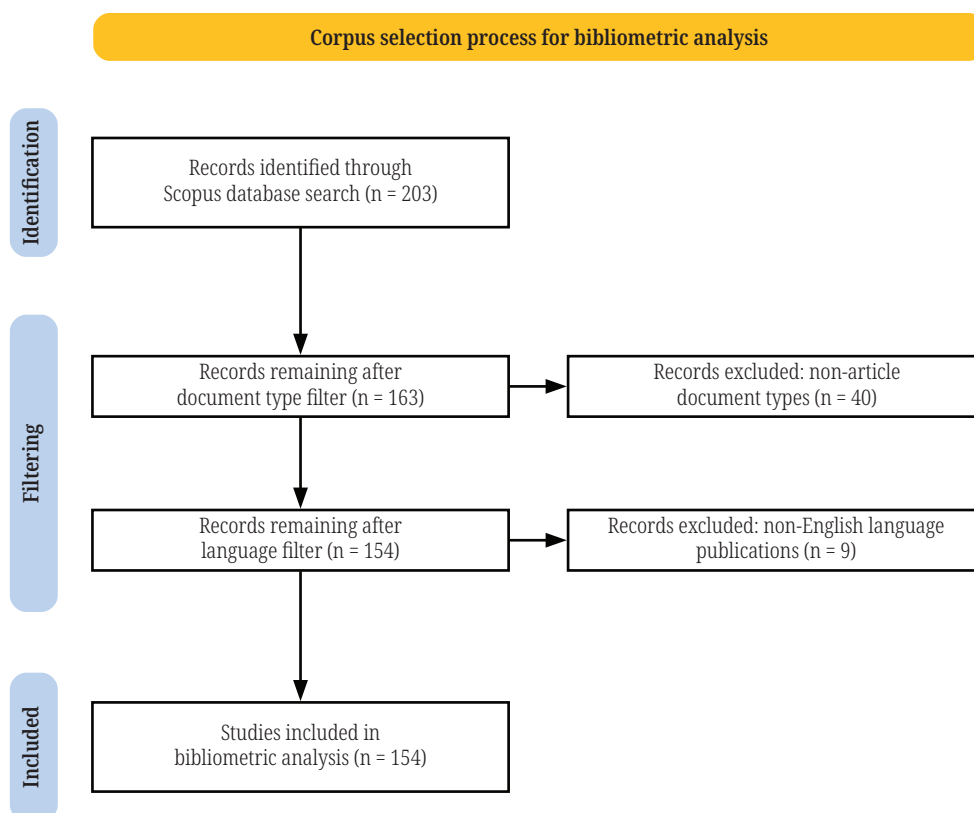


Fig. 1. Study selection flowchart for corpus constitution

2.4 Analytical framework and tools

Bibliometric analyses were conducted using the R package *Bibliometrix*, an open-source tool widely used in the scientific literature for bibliometric and scientometric studies, run in the RStudio environment (version 2023.12.1+402). The interactive interface *Biblioshiny* (version 5.0), integrated into *Bibliometrix*, was used for corpus management, the conduct of analyses, and the generation of associated graphical visualizations.

The analysis focused on four complementary dimensions. First, the annual evolution of scientific production was examined to characterize the publication dynamics of the field. Second, the identification of trend topics was used to highlight the dominant themes and their evolution over time. Third, thematic maps were generated for two successive periods (1990–2020 and 2021–2026) to compare the conceptual dynamics of the field along the axes of centrality and density. Finally, a multiple correspondence analysis (MCA) was conducted on the keywords to identify the structuring axes and thematic clusters characterizing the corpus.

To ensure methodological transparency and support reproducibility, the specific parameters applied in each of these analyses are presented as follows. The *trend topics* analysis was performed using all keywords available in the corpus, with a minimum keyword frequency threshold of five occurrences and a maximum of three words displayed per year. For the thematic evolution analysis, the maximum number of words was set to 250, the minimum cluster frequency to five per 1,000 documents, and the minimum weight index to 0.1. Theme detection and clustering were performed using the Walktrap algorithm. Finally, the conceptual structure analysis was conducted through MCA, with the number of terms set to 50 to explore the relationships among the most representative concepts and identify the main thematic clusters within the corpus.

3 RESULTS

3.1 Descriptive analysis

Temporal evolution of scientific production. Figure 2 presents the annual evolution of scientific production related to measles and rubella surveillance integrating digital technologies and data-driven approaches. The earliest publications identified in the corpus appeared in the early 1990s, followed by a limited and irregular annual output until the early 2000s. From around 2005 onward, the number of annual publications increased progressively, and this growth intensified after 2010, culminating in a peak of 27 publications in 2025. The lower number of publications observed in 2026 ($n = 9$) should be interpreted with caution, as the bibliographic data were collected in April 2026, when the indexing of 2026 publications was still in progress. Additional publications may therefore be indexed subsequently, potentially increasing the final publication count for the year.

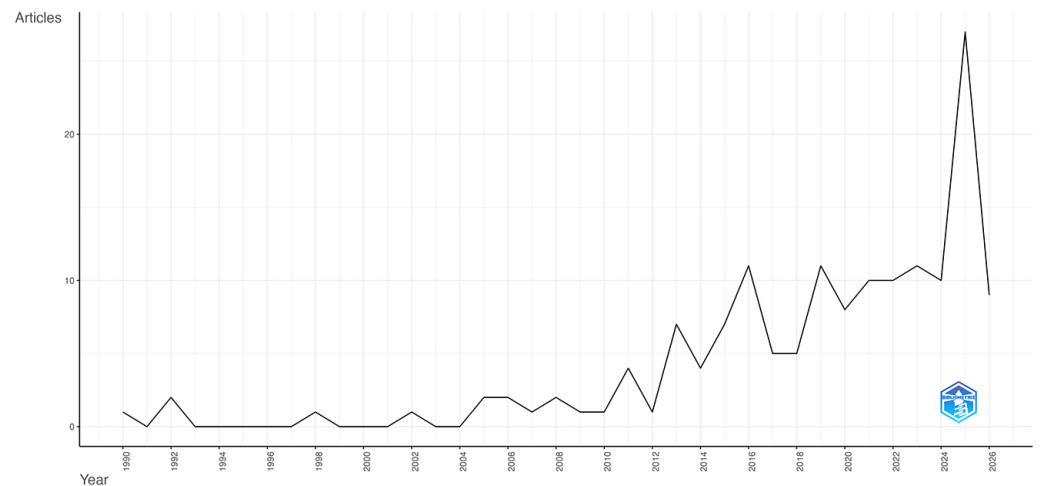


Fig. 2. Annual scientific production

Trend topics analysis. Figure 3 presents the temporal evolution of the main research themes identified in the corpus. The early years are dominated by general terms such as *information systems*, *data collection*, and *infection control*. From the 2010s onward, the terms *vaccination*, *measles*, *disease outbreaks*, *surveillance*, and *public health* become more frequent. In the most recent period, the analysis reveals the emergence of terms such as *machine learning*, *epidemiology*, *vaccination coverage*, and *SARS-CoV-2 vaccine*, as well as terms directly associated with the COVID-19 pandemic, notably *COVID-19*, *pandemic*, and *coronavirus disease 2019*.

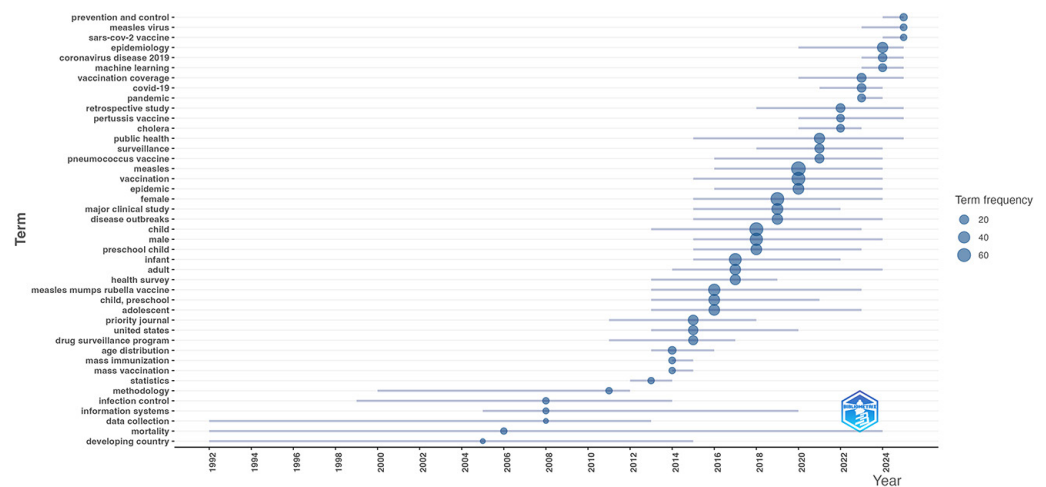


Fig. 3. Trend topics analysis

3.2 Thematic evolution

Thematic structure of the period 1990–2020. The thematic map corresponding to the period 1990–2020 (see Figure 4) reveals a predominance of themes related to vaccination, public health, and the surveillance of communicable diseases. The terms *vaccination*, *child*, and *female* occupy a central position in the field. The cluster comprising *measles*, *health survey*, and *measles vaccine* highlights the importance of health surveys and vaccination monitoring in the literature of this period. The themes *disease surveillance* and *communicable disease(s)* appear as specialized

topics, associated with conventional epidemiological surveillance systems. Overall, this first period is characterized by an orientation focused on vaccination, traditional surveillance, and public health strategies.

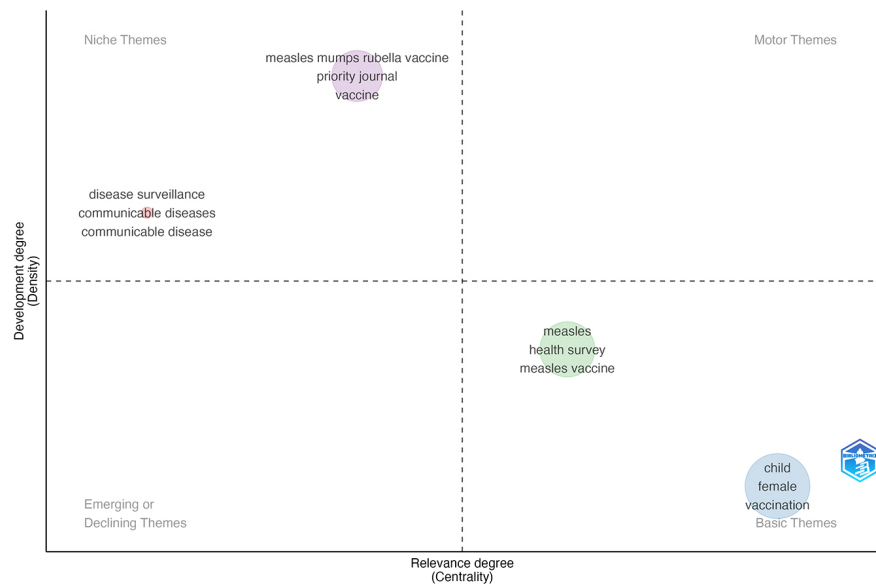


Fig. 4. Thematic map for the period 1990–2020

Thematic structure of the period 2021–2026. The thematic map for the period 2021–2026 (see Figure 5) reveals a diversification of research axes compared to the previous period. The terms *measles*, *epidemiology*, and *epidemic* emerge as motor themes of the field, while *vaccination*, *child*, and *female* remain among the central themes. The map also highlights the rise of topics related to virology and genetics, notably *measles virus*, *virology*, and *genetics*. Finally, the terms *deep learning*, *convolutional neural network*, and *infectious disease* are positioned in the quadrant of emerging or declining themes (low centrality, low density). Their recent appearance in the trend topics analysis confirms an emerging rather than declining character, reflecting a research area in its early stage of structuration.

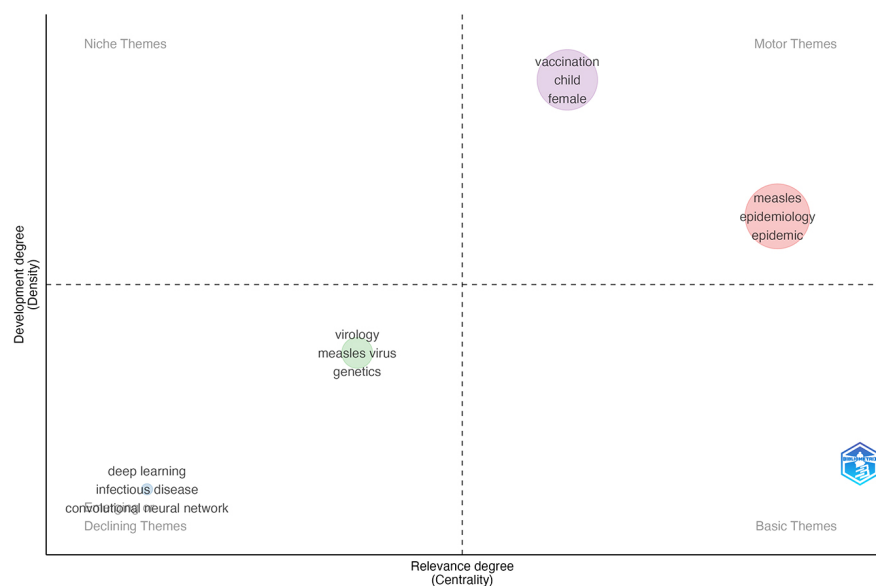


Fig. 5. Thematic map for the period 2021–2026

3.3 Conceptual structure analysis

Figure 6 presents the conceptual structure map obtained through MCA. The first two dimensions account for 64.69% and 21.42% of the variance, respectively, corresponding to a cumulative total of 86.11% of the variance.

The first dimension (Dim 1) distinguishes, on the left side of the axis, terms associated with the surveillance of communicable diseases and outbreak management (*disease surveillance, population surveillance, public health, epidemic, disease outbreaks, and COVID-19*), from terms on the right side related to vaccination and immunization (*vaccination, immunization, measles mumps rubella (MMR) vaccine, electronic health record, drug surveillance program, and several pediatric vaccines*).

The second dimension (Dim 2) distinguishes, in the upper part of the axis, terms related to vaccination programs, pharmacovigilance, and surveillance systems (*vaccines, drug safety, adverse drug reaction reporting systems, electronic health record, and surveillance*), from terms in the lower part associated with demographic and population-level characteristics (*child, infant, newborn, adolescent, female, male, and incidence*).

The joint examination of the two dimensions allows the identification of three main thematic clusters within the corpus: the epidemiological surveillance of communicable diseases, vaccination strategies, and the progressive integration of digital health systems.

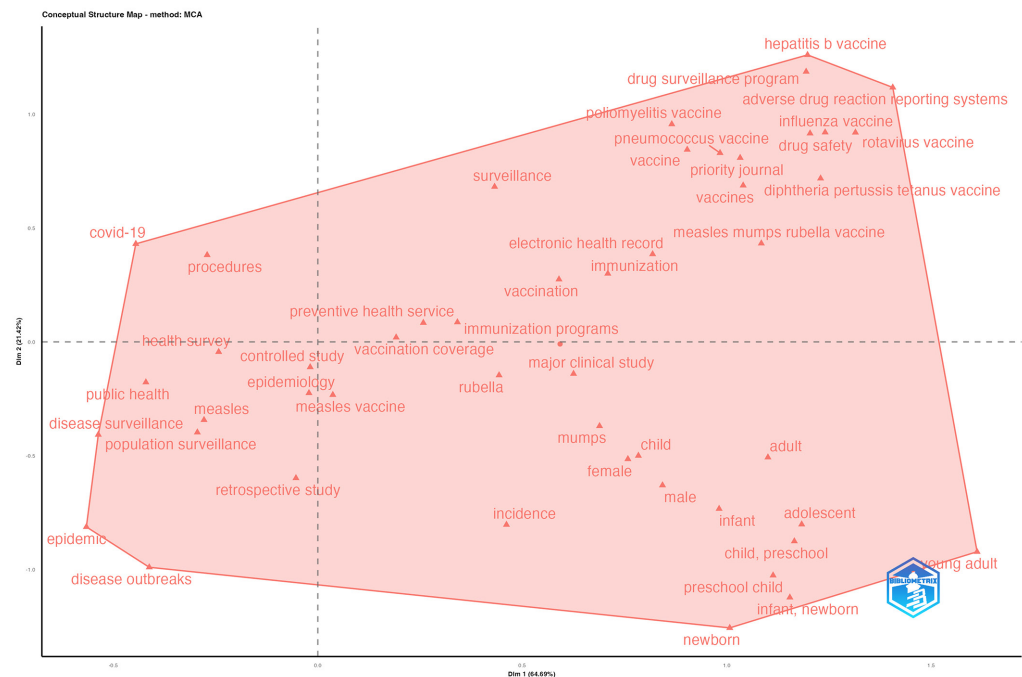


Fig. 6. Multiple correspondence analysis (MCA) of keyword relationships

4 DISCUSSION

This bibliometric analysis highlights three major findings regarding the epidemiological surveillance of measles and rubella in the era of digital technologies. First, scientific production has experienced sustained growth since the mid-2000s, with a marked acceleration over the past decade. Second, the conceptual structure of the

field is organized around three complementary axes: epidemiological surveillance of communicable diseases, vaccination strategies, and the progressive integration of digital health systems. Third, despite the overall expansion of the field, approaches explicitly grounded in AI and ML remain at an emerging stage in the literature dedicated to these two diseases.

The observed evolution reflects a growing interest in the integration of digital tools, health information systems, and advanced analytical methods into infectious disease surveillance. The presence, within the recent corpus, of terms such as *electronic health record*, *health information systems*, *electronic reporting*, and *informatics* underscores the expanding role of information technologies in the collection, management, and analysis of epidemiological data. These approaches contribute to improving the timeliness of case detection, optimizing outbreak notification, and facilitating the monitoring of vaccination programs, particularly in contexts requiring real-time surveillance.

The presence of the terms *measles virus*, *virology*, and *genetics* in the recent thematic map (see Figure 5) reflects the growing importance of genomic surveillance in understanding measles transmission dynamics. Several studies emphasize that the genetic characterization of viruses constitutes a key component of surveillance systems, enabling the tracking of strain circulation and the documentation of the interruption of endemic transmission [6–18]. These approaches notably contribute to distinguishing imported cases from local transmission and to improving the understanding of global patterns of viral spread. Methodological advances in molecular diagnostics, including RT-PCR, RT-qPCR, and LAMP [19–22], as well as the use of new biological matrices such as oral fluids or dried blood spot samples [23, 24], also represent a complementary research axis in the literature by facilitating rapid virus detection and surveillance in resource-limited settings.

The analyzed literature indicates that measles remains strongly influenced by inequalities in vaccination coverage. Several studies describe outbreaks occurring in under-vaccinated populations, particularly within certain marginalized communities and among some groups of young adults [25–30]. Nosocomial transmission also constitutes a factor contributing to disease spread, including in countries that have achieved elimination goals [31, 32]. These observations suggest that the persistence of pockets of susceptibility continues to undermine elimination efforts. Vaccination and elimination strategies appear to be broadly effective but remain dependent on homogeneous and sustained coverage. Several studies show that measles and rubella elimination is achievable, as illustrated by the experiences of the United States and other regions [33–35]. However, the persistence of imported cases and vaccination gaps highlights the fragility of these achievements and the need to maintain reinforced surveillance.

Regarding rubella, the analyzed literature highlights the central role of molecular surveillance in understanding virus circulation and preventing congenital rubella syndrome [21, 22, 34, 36, 37]. Although this disease represents a major issue in elimination strategies, its scientific visibility appears to be more limited than that of measles, which may reflect a greater research prioritization toward the latter.

Although the integration of digital technologies is progressing, the bibliometric findings show that approaches explicitly associated with AI remain relatively underdeveloped in the field of measles and rubella surveillance. The terms *machine learning*, *deep learning*, and *convolutional neural network* are mainly positioned within the quadrant of emerging themes in the thematic maps. This configuration suggests that the application of advanced AI methods in this field is still at an early stage, although their increasing presence in recent publications reflects a developing scientific interest.

The recent emergence, within the trend topics analysis (see Figure 3), of themes related to *COVID-19*, *pandemic*, and *SARS-CoV-2 vaccine* further illustrates the influence of the pandemic on the evolution of research in epidemiological surveillance. The global health crisis appears to have contributed to reinforcing the adoption of digital tools, real-time surveillance systems, and data-driven analytical approaches in infectious disease surveillance, including for measles and rubella.

The findings of this study have several implications. From a public health perspective, they highlight the need to further integrate digital surveillance systems into national immunization programs, particularly to strengthen early outbreak detection and real-time vaccination monitoring. From a research perspective, the limited representation of AI-based approaches constitutes a priority area for development: the design of predictive algorithms, automated epidemic signal detection models, and decision-support tools could contribute to improving the effectiveness of surveillance systems. Finally, the maintenance and strengthening of genomic surveillance appear essential to support the elimination goals for measles and rubella, as well as to characterize circulating strains during disease outbreaks.

Several limitations should be considered when interpreting the findings. First, the analysis was conducted exclusively using the Scopus database which, despite its broad multidisciplinary coverage, may have excluded certain relevant publications indexed only in other databases such as Web of Science or PubMed. This may have prevented the corpus from fully capturing the entirety of the scientific literature related to measles and rubella surveillance. Moreover, the journal selection, indexing practices, and document classification specific to Scopus may influence the visibility of certain research topics, geographic regions, or disciplinary perspectives. As a result, certain themes, publication trends, or conceptual relationships identified in this study may be underrepresented or overrepresented relative to the entire field. Nevertheless, Scopus offers high-quality bibliographic metadata particularly well suited for bibliometric analyses, and the final corpus of 154 peer-reviewed articles published over more than three decades provides a substantial and coherent basis for identifying the main scientific trends and conceptual structures characterizing the field.

Second, the use of a keyword-based search strategy may have introduced selection bias due to terminological variations and the use of synonyms in scientific publications. In particular, the inclusion of the term “monitoring” was intended to maximize the sensitivity of the search strategy and capture potentially relevant studies related to surveillance activities. However, as this term is broader than epidemiological surveillance, it may have led to the inclusion of some publications with a less direct focus on the field. This limitation, inherent to comprehensive bibliometric search strategies, was partially mitigated by combining the term “monitoring” with specific keywords related to measles, rubella, surveillance, and digital technologies.

Third, bibliometric methods primarily allow the exploration of quantitative structures within the literature—such as keyword frequencies, co-occurrence relationships, and thematic clustering—but do not permit the assessment of the methodological quality or scientific robustness of individual studies. Therefore, the findings should be interpreted as an overall representation of the conceptual organization and evolution of the field rather than as a qualitative evaluation of the included publications.

Finally, although this study specifically targeted dimensions related to digital technologies, the emerging status of AI approaches in this field restricts the possibility of conducting an in-depth exploration of certain technological applications. Despite these limitations, the study offers a comprehensive overview of the scientific

evolution of measles and rubella surveillance in the digital era, and provides a structured framework for understanding how digital technologies are progressively integrated into this surveillance.

5 CONCLUSION

This bibliometric analysis provides a structured overview of the evolution of scientific research on measles and rubella surveillance in the era of digital technologies. The findings highlight a sustained growth in scientific production since the mid-2000s, particularly marked over the past decade, along with a conceptual organization of the field around three complementary axes: the epidemiological surveillance of communicable diseases, vaccination strategies, and the progressive integration of digital health systems. Genomic surveillance and health information systems have gained increasing prominence in the recent literature, while approaches explicitly grounded in AI and ML remain at an emerging stage.

By providing a systematic mapping of this field, this study offers researchers and public health decision-makers a reference framework to guide future research and support the development of more effective surveillance systems. The perspectives emerging from this analysis call for deeper integration of AI methods, predictive analytics, and digital health technologies into measles and rubella surveillance, in order to strengthen early outbreak detection, improve vaccination monitoring, and support internationally defined elimination goals. In a context where the persistence of pockets of susceptibility and the cross-border circulation of viruses continue to threaten vaccination achievements, the reinforcement of digital surveillance systems represents an essential lever to preserve the progress achieved and anticipate the epidemiological challenges ahead.

To address these challenges, several research directions emerge from the present analysis. First, future studies could examine how AI and ML models can improve the early detection and prediction of measles and rubella outbreaks using real-time surveillance data. Second, further research is needed to determine how digital health platforms and electronic reporting systems can be optimized to enhance vaccination coverage monitoring and identify pockets of susceptibility. Finally, additional investigation could assess how genomic surveillance data can be integrated with epidemiological and digital health information to strengthen epidemic response and support elimination strategies. Addressing these questions may contribute to the development of more responsive, data-driven, and integrated surveillance systems.

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