(IJACSA) International Journal of Advanced Computer Science and Applications,
Vol. 16, No. 9, 2025

An Analytical Review of Environmental and Machine Learning Approaches in Dengue Prediction

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Abstract—**In recent years, dengue has gained prominence as a priority public health challenge due to increasing incidences of spread. The main objective of this systematic literature review (SLR) is to explore the use of environmental factors and machine learning (ML) techniques to combat dengue, based on studies published between 2020 and 2024. For this purpose, 56 studies were selected from a balanced distribution of PubMed, Web of Science, Scopus and Springer Link, under the Preferred Reporting Items for Systematic Reviews and meta-analyses (PRISMA) method. The results obtained made it possible to determine that the climatological variables, such as temperature difference, humidity concentration and rainfall volume, are conditioning factors in the spread of the dengue virus. As for ML models, Random Forest and Support Vector Machines proved to be more accurate than traditional methods in detecting risk areas. The highest scientific production corresponded to the year 2024, with 25% of the studies, while India, with 14.29%, and the United States, with 12.50%, stood out as the countries with the highest contribution. In conclusion, ML techniques have enormous potential for strengthening early detection systems and optimizing resources in high-risk areas, but further research is needed in this field due to the lack of data availability and replicability of models.**

Keywords*—*Public health analytics; machine learning models; disease prediction; environmental risk factors; dengue surveillance; health data analysis

I. INTRODUCTION

In recent decades, dengue, a viral disease transmitted by bites from mosquitoes, such as Aedes albopictus and Aedes aegypti, has gained prominence as a major public health threat, affecting both tropical and subtropical regions. The increasing prevalence of the disease, together with the challenges associated with its control in areas of high population density, underscores the need to address this problem on a global scale, a concern supported by the United Nations (UN), which has pointed out the effects of climate change on the geographical spread of dengue [1]. In this regard, the World Health Organization (WHO) has identified dengue as a global priority, promoting various strategies and policies for its control and prevention in endemic areas [2]. The scenario is conditioned by various factors that create conditions conducive to spread in the environment.

The proliferation of mosquito vectors is directly linked to climate, especially variations in temperature, rainfall and humidity, which facilitate the spread of dengue [3]. Abnormal climatic factors and rainfall create favorable conditions for the transmission of the virus, which increases the risk in both urban and rural areas, raising the incidence of the disease [4], [5]. Climate change has altered the natural habitats of these mosquitoes, favoring their expansion into new regions. In Spain, the presence of Aedes albopictus since 2014 has raised the risk of autochthonous transmission in Mediterranean areas [6]. In February 2023, two cases of dengue were reported in Ibiza, Spain, related to the presence of the transmitting mosquito, detected in the region since 2014. This fact highlights the importance of monitoring non-endemic areas where the vector has been introduced [7]. In 2018, an outbreak of dengue hemorrhagic fever in Vietnam underlined the importance of early detection by real-time reverse transcription (RT-PCR), a technique that made it possible to identify the serotypes responsible and prevent new outbreaks [8]. Pharmacological investigations have identified compounds such as CHEMBL376820, which exhibit inhibitory properties against dengue serotype 2, representing a significant advance in treatment strategies [9]. The use of ML artificial intelligence technique has shown a significant impact on the optimization of dengue prevention and control strategies, allowing foreseeing outbreaks and improving interventions in at-risk areas. In Espírito Santo, Brazil, Aedes albopictus was identified as a transmitter of DENV-1 and ZIKV, complicating control efforts in both urban and rural areas [3]. Regarding diagnostic techniques, triplex polymerase chain reaction with reverse transcription and real-time quantification (Triplex RT-qPCR) has been widely recognized for its high sensitivity and specificity in detecting serotypes in endemic areas [10]. ML-based predictive models, such as Gradient Boosting Machines (GBM) and Artificial Neural Networks (ANN), achieved an accuracy of 80.6% in identifying key factors, which improves dengue control decisions [11]. Furthermore, ANNs, within these models, have demonstrated high performance, with receiver operating characteristics of 0.8324 and an accuracy of 0.7523. The main risk factors identified include age, antigenemia on-structural protein 1 of the dengue virus (NS1) and the coexistence of Immunoglobulin M (IgM) and Immunoglobulin G (IgG). This approach could facilitate rapid prognoses during outbreaks, interpreting immunological dynamics and contributing to vaccine development [12].

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In terms of immunization, the Dengvaxia vaccine has been shown to be effective in children between 9 and 16 years of age who have previously experienced the disease, significantly reducing the number of severe cases and patients requiring hospitalization. However, before administering the vaccine, it is essential to perform blood tests to determine whether the individual has previously contracted dengue, as there is an increased risk of serious complications if the disease has not been experienced [13]. Similarly, the tetravalent mRNA vaccine has demonstrated promising immune responses, positioning itself as a viable alternative in the prevention of dengue virus [14].

The present study is justified by the growing global concern about the impact of dengue on public health, particularly in those regions where environmental factors facilitate its spread. Despite advances in control, the disease continues to represent a global challenge. This paper aims to review the literature to identify the main environmental factors that contribute to dengue transmission and to evaluate the potential of ML techniques to improve outbreak prediction, prevention and control strategies, to contribute to the implementation of more effective interventions.

II. LITERATURE REVIEW

Previous research on dengue has highlighted technological advances that have contributed to improved diagnostic accuracy and accessibility. The study [15] developed a microfluidic device (Cygnus) used for rapid detection and serotyping of NS1 protein in plasma samples using multiplex immunoassays, resulting in 82% sensitivity and 86% specificity, with potential for epidemiological surveillance. Similarly, the study [16] identified immunoreactive peptides corresponding to E and NS1 proteins to discover dengue-specific IgM and IgG antibodies, using peptide synthesis tests and ELISA, obtaining results with sensitivity levels of (73.33-96.66%) and specificity levels of (82.14-100%), offering an economically cost-effective solution for diagnosis by serology.

The work of [17] implemented a machine learning model to predict Aedes albopictus suitability on a global scale based on climatic and environmental data, which revealed that suitable habitats will expand markedly in the northern hemisphere, exposing an additional billion people by the mid-21st century. On the other hand, research by [18] examined the prevalence of DENV-1 and DENV-2 serotypes in Karachi, Pakistan, using immunochromatographic and PCR detection techniques, identifying that 80% of cases corresponded to DENV-2, associating its spread to favorable climatic conditions and disorganized urbanization. Finally, the analysis of [19] explored the impact of climate change on the distribution of Aedes albopictus in China, using data observed between 1970 and 2021 along with classification tree models, which allowed projecting that the risk of dengue will cover almost all of China by 2050 and 2080, affecting 1.2 billion people, with winter temperatures and summer precipitation as key factors in its spread.

The study by [20] developed and validated a triplex RT-qPCR protocol to detect chikungunya, dengue and zika viruses in mosquitoes simultaneously, employing specific primers and probes, demonstrating low detection thresholds (1.32x10^0 for CHIKV, 3.79x10^0 for DENV1-4 and 2.06x10^0 for ZIKV), so there was no cross-reactivity with homogenates of Aedes aegypti mosquitoes, evidencing its suitability for vector surveillance in endemic areas. In turn, the research of [21] evaluated the VECTRACK system, which combines optical sensors and machine learning, for automatic counting and classification of Aedes albopictus and Culex pipiens in field conditions. The results showed a high correlation between visual and automatic identification (Spearman: 0.97 for females and 0.89 for males), with an efficiency comparable to conventional traps, which supported its potential for continuous monitoring with minimal human intervention.

In [22], they addressed the prediction of dengue outbreaks in Bangladesh by means of climate data analysis and the application of machine learning algorithms, such as Support Vector Machine (SVM), Decision Tree and Random Forest, achieving an accuracy of 96.73% with the SVM model, confirming that temperature, humidity and rainfall are fundamental predictive factors. In the research by [23], they developed a methodology to predict dengue incidences in 20 Brazilian cities, integrating climatological data, Internet searches and autoregressive terms, where the Random Forest and LASSO regression models proved to be robust, with global search data as strong predictors. In addition, the study by [24] applied ensemble machine learning techniques to identify factors associated with dengue transmission, analyzing variables such as vapor pressure and precipitation, which improved the accuracy of the predictive models and highlighted the usefulness of ML in mosquito-borne disease surveillance.

It should be noted that numerous studies on the subject highlight the importance of adopting modeling and computational engineering techniques for the analysis of this type of disease. For example, the study [25] made use of ML practices known as logistic regression, ANN and bagging assembly, aimed at predicting the inherent risk of shock in patients carrying dengue virus, using clinical and physiological data collected at a university-level medical facility, highlighting that the bagging assembly method achieved a 14.5% increase in accuracy compared to other approaches, identifying hemoglobin as a key indicator for predicting severe complications. Also, in [26], they proposed a fractional mathematical derivation to analyze the dynamics of Zika and dengue co-infection, validating the model with epidemiological data from Brazil and sensitivity analysis. The results showed that the rate of human transmission of Zika and vector mortality are determining factors in controlling both diseases. Table I presents a summary of the main findings and limitations of the literature review.

TABLE I. SYNTHESIS OF FINDINGS AND LIMITATIONS IN DENGUE LITERATURE

References	**Main Resulted**	**Limitations**
[15]	Cygnus device detects NS1 with 82% sensitivity in 40 minutes in multiplex.	Requires enhancement of antibodies to DENV-1. Do not test in rural areas.
[16]	E/NS1 protein peptides identify IgM/IgG (73.33-96.66%) in sensitivity.	Cross-reactivity with other Flaviviruses. Cost not evaluated.
[17]	ML model predicts global expansion of A. albopictus in the northern hemisphere.	Omits vector control policies in projections.
[18]	DENV-2 predominant (80%) in Karachi, associated with disorganized urbanization.	Limited to one Pakistani city. Does not analyze future climate.
[19]	Winter temperature key to A. albopictus distribution in China between 93.0% to 98.8% accuracy.	Does not validate with socioeconomic data.
[20]	Triplex RT-qPCR detects CHIKV/DENV/ZIKV in mosquitoes, with no cross-reactivity.	Detection thresholds are not compared to other methods.
[21]	VECTRACK system identifies Aedes/Culex with 97% correlation in females and 89% correlation in males with visual-ML.	Only tested in Italy. Does not evaluate cost-effectiveness.
[22]	SVM predicts dengue outbreaks with 96.73% accuracy in temperature and rainfall climates.	Data limited to Bangladesh.
[23]	Random Forest and LASSO predict incidence in 20 Brazilian cities.	Requires real-time internet search data.
[24]	Ensemble models improve accuracy in dengue prediction with vapor pressure and precipitation.	Does not specify omitted climatic variables.
[25]	Bagging algorithm predicts dengue shock with 14.5% more accuracy than hemoglobin indication.	Data from a single medical center.
[26]	Fractional mathematical model validates Zika-Dengue co-dynamics in Brazil.	Does not include public health interventions.

III. METHODOLOGY

This section will describe the procedures used to carry out the systematic study on models of ML and environmental variability applicable to the prediction of dengue outbreaks, in accordance with PRISMA 2020 regulations.

A. Purpose and Research Questions

The study comprehensively analyzed scientific literature on the integration of environmental variables such as climatic, ecological and urban variables with ML models for dengue outbreak forecasting. By means of the PRISMA 2020 method, the latest trends, challenges and opportunities for improvement in predictive models were identified, with the purpose of guiding future research towards solutions of greater precision and relevance in the field of public health. In this sense, the following central question arises as the main objective of the analysis:

Question 1: What are the advances and limitations identified in the scientific literature on the use of environmental factors and ML techniques in dengue prediction?

B. Sources of Information and Search Strategy

The methodical search for the studies was carried out on February 7, 2025; for this purpose, four renowned databases in the field of health sciences and cutting-edge technologies were consulted: PubMed, Web of Science, Scopus, and Springer Link. The criteria for selecting these sources were their capacity for exhaustive indexing of peer-reviewed literature, as well as their editorial impact factor and their thematic relevance according to the objectives of the study.

In the development of the search strategy, standardized descriptors combined with Boolean operators were used. The unified conceptual structure was as follows: ("Public Health Analytics" OR "Health Data Analysis") AND ("Machine Learning Models" OR "Deep Learning Algorithms") AND ("Disease Prediction" OR "Epidemic Forecasting") AND ("Environmental Risk Factors" OR "Climatic Determinants" OR "Urban Health Indicators") AND ("Dengue Surveillance" OR "Arbovirus Monitoring").

The search code was adapted to the syntactic and functional characteristics of each database. Despite the structural adaptations, the integrity of the search was preserved in all cases.

In addition, temporal filters were performed to restrict the search exclusively to documents published between 2020 and 2024, as well as language filters, so that only documents written entirely in English were included. Furthermore, using databases that allowed this, including PubMed, an additional restriction was introduced to limit the availability of text (abstract, full text) and species (human).

As a result of the systematic search process, a total of 1593 documents were obtained. Fig. 1 shows their distribution by database source and provides a quantitative view of the coverage and retrieval efficiency.

C. Inclusion and Exclusion Criteria

Research was selected by prioritizing climatic conditions, epidemiological patterns and predictive approaches. Inclusion and exclusion criteria applicable in this review of the scientific literature are detailed below.

1) Inclusion criteria

a) Research was published between 2020 and 2024, to ensure that the evidence collected reflects the most recent advances in the field.

b) Studies that provide primary data on the use of ML techniques or the impact of environmental factors on dengue prediction and control.

c) Documentation available in English only, to maintain consistency and facilitate interpretation of results.

d) Papers that explore aspects such as predictive models, climatic variables, vector ecology or dengue transmission dynamics related to the focus of study relevant to the research question

2) Exclusion criteria

a) Publications outside the 2020–2024-time range, since they would not reflect the current state of knowledge.

b) Articles that do not provide empirical evidence, such as reviews, meta-analyses, commentaries or theoretical studies without original data.

c) Papers in languages other than English, to avoid inconsistencies in interpretation and analysis.

d) Research that is not directly related to dengue, its environmental factors or ML-based prediction methods.

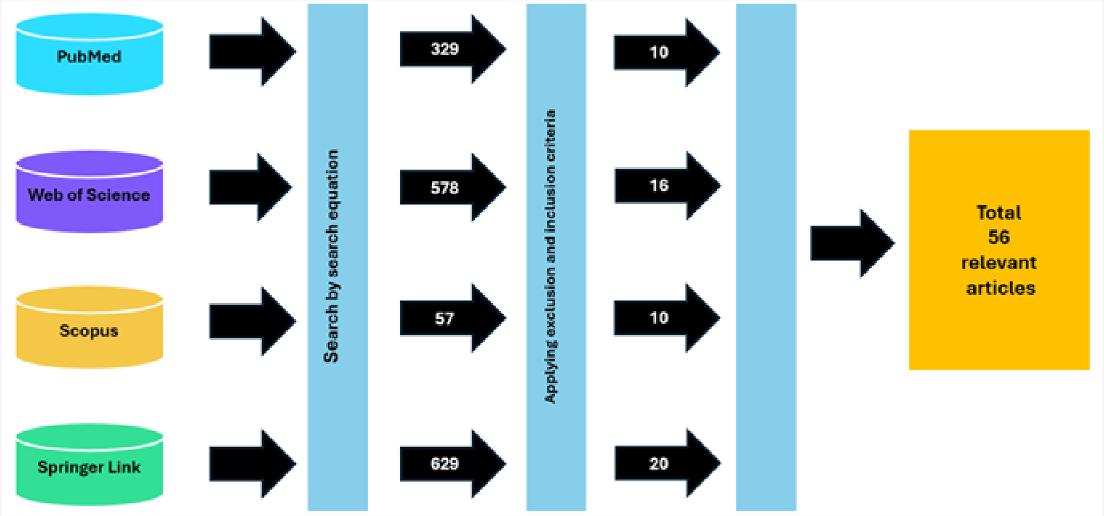


Fig. 1. Distribution of studies by database.

D. Study and Data Selection Process

The records were managed using the Mendeley® reference manager, where specific collections were created for each database. Subsequently, the records were exported and imported in ".RIS" format to Rayyan®, a tool specialized in systematic reviews, allowing efficient detection and categorization of duplicates.

After the screening phase, the system automatically detected and eliminated 222 duplicate papers. In addition, 32 other secondary literature articles, including systematic reviews and meta-analyses, were excluded according to pre-established eligibility criteria.

The completeness of the selection process was carried out jointly by three reviewers who worked in consensus from the beginning in rigorous analysis procedures to minimize bias in each case; however, if difficulties or disagreements arose regarding the inclusion of certain literary studies, a fourth reviewer, a specialist in methodology, intervened to resolve those discrepancies to ensure methodological consistency. In this way, we were able to select only the studies most relevant to the focus of the study, guaranteeing the rigor and transparency of the review. Table II shows the number of duplicates and systematic reviews eliminated by database source.

After the selection phase in the Rayyan environment, we proceeded to work with the eligible studies to organize them in a data matrix established in Microsoft Excel spreadsheets designed specifically for the systematized analysis. The matrix included previously defined categorization fields to disaggregate the information, such as the database of origin, the title of the article, the year of publication, the type of publication, the country of origin, the methodological approach (qualitative, quantitative or mixed), and the results directly related to the research objective.

TABLE II. DISTRIBUTION OF DUPLICATES AND SYSTEMATIC REVIEWS BY DATABASE

Database	Duplicates	Systematic Reviews
PubMed	16	13
Web of Science	123	0
Scopus	3	2
Springer Link	80	17
Total	**222**	**32**

The import of data grouped by bibliographic source of origin was carried out by two reviewers of the team, who worked closely together to ensure accuracy and completeness. A third member of the team inspected and verified the existence of inconsistencies or possible misinterpretations within the data. At this stage, it was not necessary to contact the original authors of the studies, since the information contained in the articles allowed the analysis to be carried out.

The work methodology, characterized by its structure and collaborative access developed by the group, made it possible to identify thematic patterns and methodological trends, particularly in the integration of environmental variables in dengue transmission prediction models. Fig. 2 shows the distribution of the documents, showing the number of items collected, discarded and finally selected using the PRISMA 2020 Shiny tool.

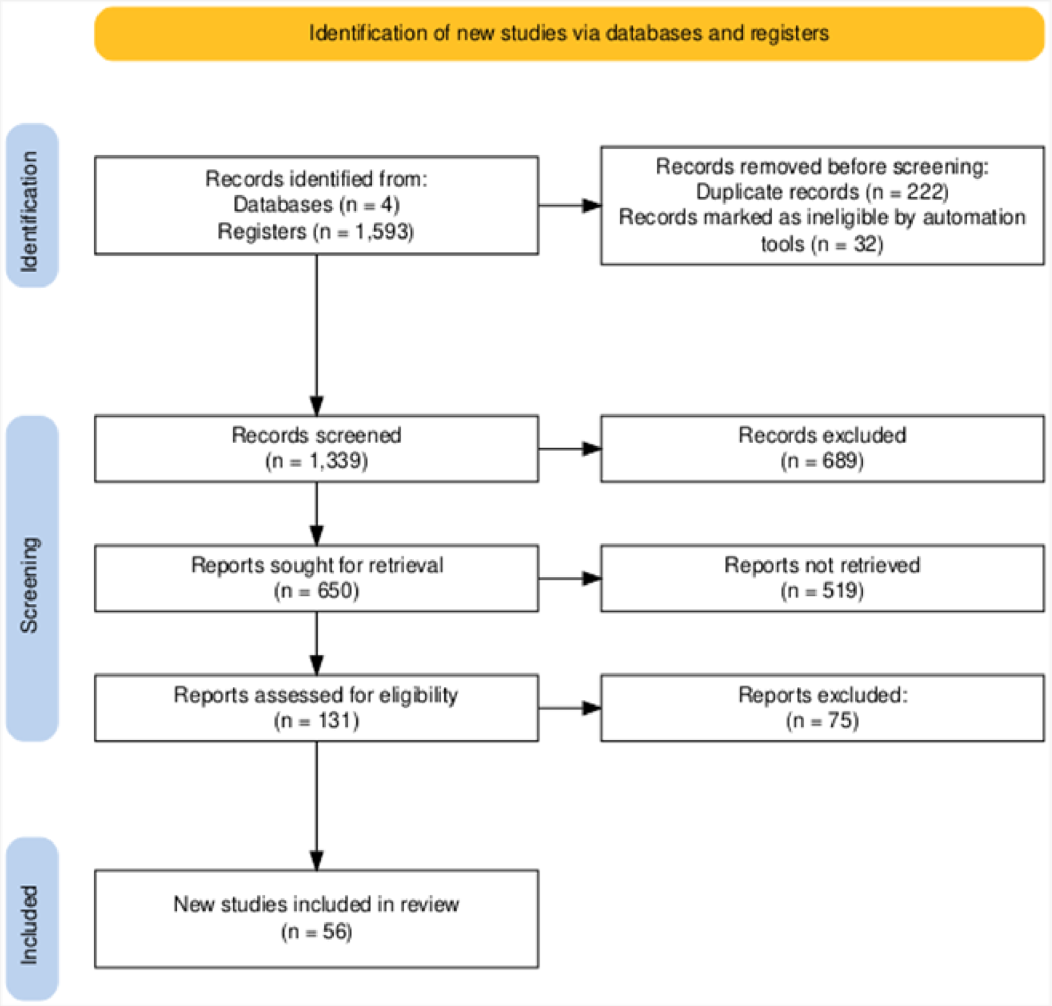


Fig. 2. PRISMA method.

E. *Type of Study*

The PRISMA methodology was implemented in this study according to the guidelines up to version 2020, to ensure systematic rigor [27]. Regarding the elaboration of the PRISMA flowchart, an R package with the specific application Shiny was used, which enhanced transparency through the graphical representation of the selection phases [28]. A strict application of eligibility criteria and detailed documentation contributed to strengthening validity and replicability.

F. *Risk of Bias Assessment*

This review did not use standardized instruments to assess the risk of bias in the primary studies. This decision responds to the descriptive and exploratory nature of the analysis, which did not include quantitative syntheses or meta-analyses that required weighing individual methodological quality. However, as an alternative measure of rigor, we applied rigorous inclusion criteria that excluded secondary literature, duplicate studies, and publications without direct empirical evidence. This ensured that only primary research relevant to the qualitative analysis was incorporated into the discussion, while critically examining the methodological limitations of the studies included in the review. PRISMA checklist 2020 is given in Appendix (Table IX).

IV. RESULTS

The results of this SLR were structured under the methodological standard defined by PRISMA. Initially, a total of 1593 articles were identified from the PubMed, Web of Science, Scopus and Springer Link databases. Achieving this initial compilation was the result of using the predefined keywords and their combinations in search strings in a rigorous manner. Table III details the distribution of the articles collected in this phase, including the number and percentage corresponding to each database.

TABLE III. DISTRIBUTION OF STUDIES INITIALLY

Database	Quantity	Percentage
PubMed	329	20.65%
Web of Science	578	36.28%
Scopus	57	3.58%
Springer Link	629	39.49%

After numerically counting, the collected documents, a preliminary analysis was performed, which led to the creation and application of initial filters in Rayyan, including the elimination of duplicates and the exclusion of non-relevant documents. This process was critical, as it allowed the exclusion of non-primary documents, which ensured the quality of the documents. The Rayyan system detected duplicates, and after manually evaluating the articles placed under observation, 254 articles were excluded (222 duplicates and 32 systematic reviews), thus reducing the set of studies to 1339. This distribution by origin, quantity, and percentage value is shown in Table IV.

TABLE IV. Distribution of Studies in Phase 1

Database	Quantity	Percentage
PubMed	300	22.40%
Web of Science	455	33.98%
Scopus	52	3.88%
Springer Link	532	39.73%

Subsequently, in "Phase 1", relevant filters were applied to visually analyze the titles and specific keywords related to dengue and its vectors, such as Aedes albopictus, Aedes aegypti, Dengue virus and Mosquito Vectors. Performing this filtering allowed discarding 689 studies, since they were not aligned with what the research seeks, due to that the set was reduced to 650 studies. Table V shows the distribution of the studies selected in this phase, evidencing the rigorous application of the thematic relevance criteria.

TABLE V. Distribution of Items in Phase 1

Database	Quantity	Percentage
PubMed	183	28.15%
Web of Science	209	32.15%
Scopus	27	4.15%
Springer	231	35.54%

In Phase 2, a hybrid process combining automated filters and manual review of the abstracts of the remaining 650 articles was carried out. This approach made it possible to assess the relevance of each study in terms of its objective, methodology and results, applying predefined inclusion and exclusion criteria. For the process, we used words more focused on what we sought to analyze in the abstracts of each study, the inclusion words used were "Aedes albopictus", "Dengue virus", "Public Health Analytics", "Disease Prediction", "Machine Learning Models" and "Environmental Risk Factors". Likewise, we sought to exclude studies that included topics such as "cells", "prevalence", "in vitro", "animal models" and "mice", since they were not aligned with the objectives of the review. A total of 519 studies were excluded, and the selection set was reduced to 131, as shown in Table VI.

TABLE VI. Distribution of Articles in Phase 2 After Review of Abstracts

Database	Quantity	Percentage
PubMed	41	31.30%
Web of Science	22	16.79%
Scopus	12	9.16%
Springer Link	56	42.75%

Finally, for the last process called "Phase 3", the 131 studies selected up to the previous phase were reviewed in full text. This process involved the exhaustive and detailed evaluation of each study to determine whether its content information responded to the research question and met the established quality and relevance criteria. As a result, 75 additional articles were excluded, resulting in a final set of "56" studies of which 55 corresponded to journal articles and 1 to conference proceedings. Table VII presents the final distribution of the included studies that fully complied with the SLR requirements, showing their origin, quantity and percentage value of the total.

TABLE VII. Final Distribution of Items in Phase 3

Database	Quantity	Percentage
PubMed	10	17.86%
Web of Science	16	28.57%
Scopus	10	17.86%
Springer Link	20	35.71%

As mentioned above, the completeness of the study selection process, from the initial count to the final phase 3, was carried out entirely in Rayyan software, supported by data in Microsoft Excel, guaranteeing transparency and thoroughness at each stage. Fig. 3 shows the final distribution of the 56 selected studies, classified according to the databases used for this SLR, while the length is reflected in the bar graph corresponding to the exact number of studies included by each source, highlighting the contribution of each one to the final set.

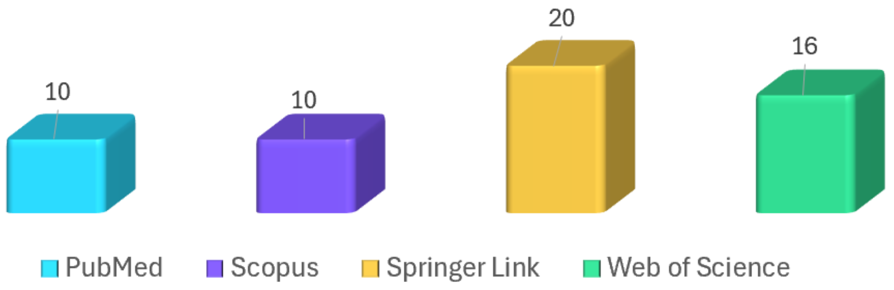


Fig. 3. Distribution of studies by databases.

The analysis of the temporal distribution by number of studies pertaining to the years between 2020 and 2024 reveals significant concentrations of impact. The year 2024 stood out as the year with the highest production, representing 25% of the total number of publications, with 14 documents. This was followed by the year 2021, which contributed 13 with a value of 23.21%, while 2020 contributed 12 documents at 21.43%. For their part, 2023 and 2022 presented a lower contribution, with 11 in 19.64% and 6 in 10.71%, respectively. The trend suggests that the topic has been addressed by researchers over time, highlighting the increase in ML techniques, which in turn consider environmental factors to be important in combating dengue in recent years. Fig. 4 illustrates this temporal distribution, highlighting the relevance of the studies published in the most recent period.

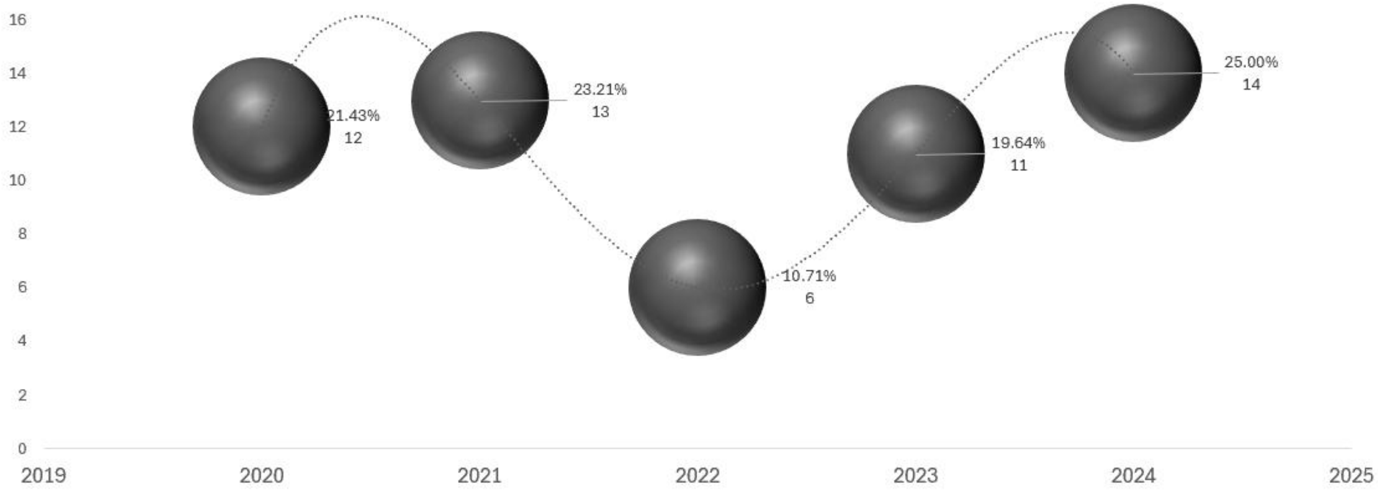
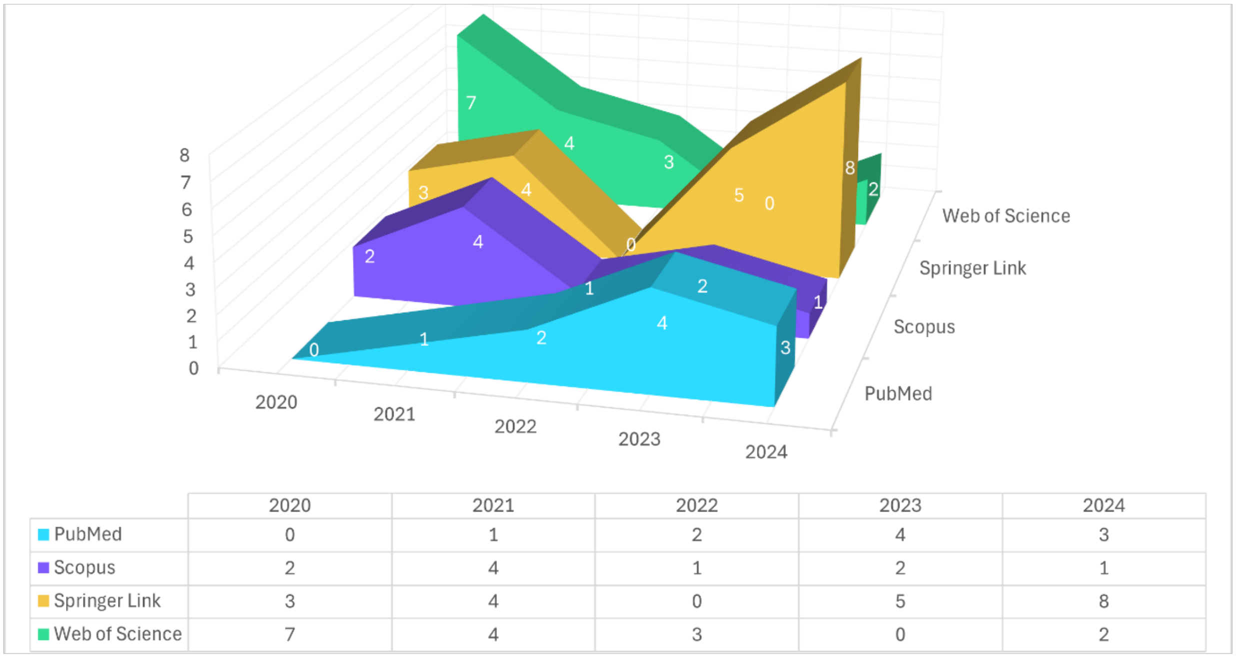


Fig. 4. Number of studies by year of publication.

When the origin of the studies was broken down according to the databases and their annual distribution, interesting patterns were observed. In 2020, most studies came from Web of Science with a value of 7, followed by Springer Link with 3 and Scopus at 2, while PubMed recorded no contributions. Regarding 2021, contributions were more evenly distributed, where Scopus, Springer Link and Web of Science had several 4 each respectively, and only PubMed had 1. For 2022, Web of Science again stood out with 3, while PubMed contributed 2 and Scopus 1, with no contributions from Springer Link. In 2023, Springer Link registered the highest contribution with 5 articles, followed by PubMed with 4 and Scopus with 2, with no studies coming from Web of Science. Finally, in 2024, Springer Link led again with 8 studies being the one with the highest impact by contribution, followed by PubMed with 3, Scopus with 1 and Web of Science with 2. Fig. 5 visually presents evolutionary distribution, highlighting the periods analyzed.



	2020	2021	2022	2023	2024
🟦 PubMed	0	1	2	4	3
🟪 Scopus	2	4	1	2	1
🟨 Springer Link	3	4	0	5	8
🟩 Web of Science	7	4	3	0	2

Fig. 5. Number of studies per year and databases.

The geographical distribution of the 56 studies included reflects the participation of several countries among which the most relevant belong to the continental regions of Asia and North America. In this sense, India was the main contributor, with 8 articles worth 14.29% of the total, followed by China with 6 articles worth 10.71% and the United States with 7 articles worth 12.50%. On the other hand, in Europe, Italy stood out with 4 studies at 7.14%, while countries such as France, Spain and Switzerland made more modest contributions. In other regions, Malaysia with 5 at 8.93% and Bangladesh with 4 at 7.14% also showed significant participation. On the other hand, countries such as Ghana, Pakistan, Tanzania and Mexico, among others, contributed 1 to 3 studies each, representing smaller percentages. This geographical distribution is evidence of the globalization of research on the subject, although with a notable concentration in countries with greater scientific and technological development. It should be noted that all the papers were published in English, which reinforces its role as the predominant language in global scientific dissemination. Fig. 6 presents this geographical distribution on a global scale in detail.

Fig. 6. Geographical distribution of publications.

The studies included were classified according to their type of methodological approach, obtaining results where the quantitative approach was the most representative with a value of 98.21%, while it was identified that there was only one study with the mixed approach that composed a qualitative and quantitative analysis and therefore obtained its mixed label in 1.79%. Regarding the membership of Springer Link databases, it contributed the most quantitative studies represented in 19 with 33.93%, followed by Web of Science in 16 with 28.57%, Scopus and PubMed with 10 in 17.86% respectively. The only study with a mixed approach came from Springer Link. This methodological distribution reflects the preference for quantitative approaches in dengue-related research, possibly due to the nature of the data and the ML techniques applied.

As for the type of research, all 56 included studies correspond to completely different distributions due to the quantities, where there are original articles with 98.21% and conference proceedings with 1.79%. The predominance of original articles highlights the relevance of this format in the generation of knowledge on the application of ML techniques and environmental factors in dengue control.

To deepen the thematic analysis of the selected studies, the VOSviewer tool was used to construct a network of co-occurrences of keywords. It was possible to observe how research on dengue and its vectors is organized into thematic clusters clearly differentiated by color. The classification by clusters allows an understanding of the direct relationships between keywords, establishing specific themes, where the red cluster represents the attraction and repellency of mosquitoes by certain stimuli colored odors or CO2, whose definition is associated with terms such as "Aedes aegypti", "repellent" and "carbon-dioxide". On the other hand, the green cluster, constituted by connections such as "larvicidal", "Culicidae" and "plant-extracts", exposes the strategies of larval control and the understanding of their interaction with ecology. In the blue cluster, such as "prevalence", "dengue fever" and "optimal control" for efforts to understand how the disease spreads and how to control it effectively. Meanwhile, the purple cluster in "public health" and "citizen science", which emphasizes the importance of community involvement and public health policies in preventing outbreaks.

Finally, it is highlighted that the strongest connections in the co-occurrence network is that between "Aedes albopictus" belonging to the pink cluster and "dengue" to the purple cluster, visually it can be seen that both words have a considerable size with respect to the others, since their size represents the highest number of mentions in research, confirming the relevance of this mosquito in the transmission of the disease. Fig. 7 visually illustrates these relationships, offering a clear and proportional overview of the most researched topics and their connections.

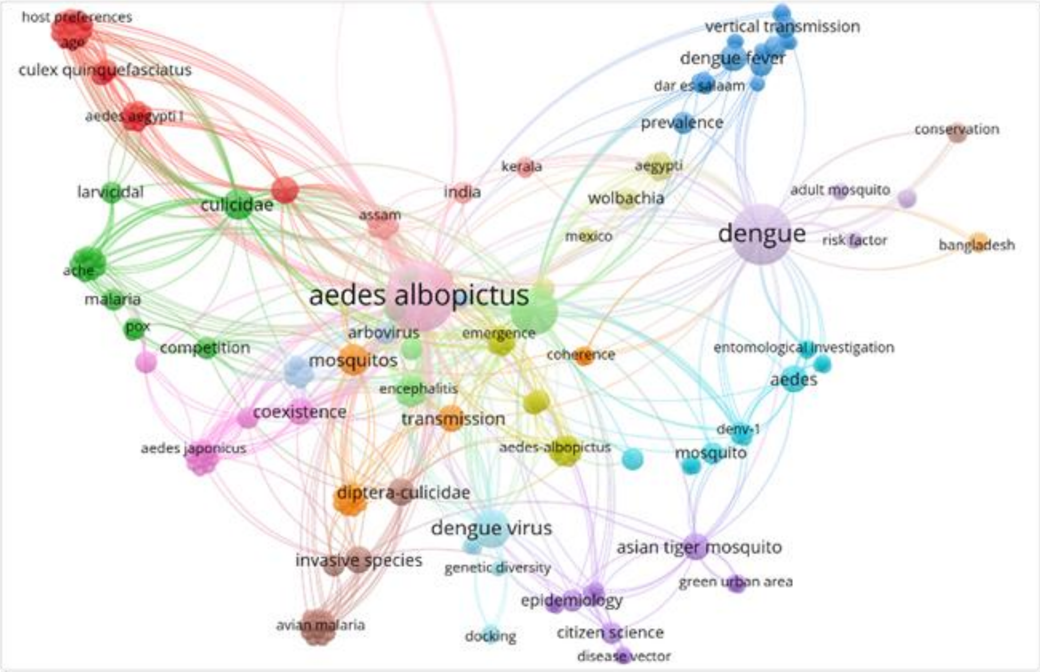


Fig. 7. Bibliometric scan of literature.

V. DISCUSSION

A. *What are the Advances and Limitations Identified in the Scientific Literature on the Use of Environmental Factors and ML Techniques in Dengue Prediction?*

The possibilities of predicting the occurrence of dengue through environmental factors and ML techniques constitute a field of opportunities to address public health challenges. Recent studies in scientific literature highlight the disruptive potential of technology to achieve substantial progress in short periods of time. In this line, the application of ANNs stands out because they provide a high degree of accuracy when analyzing climatological variables such as temperature, humidity and precipitation. The combination of these techniques with the Mosquito Oviposition Index makes it possible to identify areas at risk with greater accuracy. However, there are limitations such as accessibility to historical data and overfitting of local value sets, which compromises the effectiveness of the predictions.

The work done by [22] used machine learning algorithms, such as SVM, Decision Tree and Random Forest, from which climate parameters observed in Bangladesh were analyzed, achieving an accuracy of 96.73%. This method scientifically demonstrated that climatic variables are a decisive indicator of the occurrence of epidemic outbreaks. On the other hand, in [23] a methodological framework was devised to forecast the occurrence of dengue cases in 20 Brazilian cities, by integrating climatic data, Internet queries and autoregressive terms. The robustness of the Random Forest and LASSO regression models was demonstrated, highlighting the potential of Internet browsing data as powerful predictive indicators.

In the domain of environmental factors, the study of [17] implemented machine learning models with the objective of predicting the global-scale suitability of natural habitats for Aedes albopictus as a direct function of climate and environmental data, showing results that indicate that mosquito-friendly habitats will expand markedly in the northern hemisphere, exposing a billion people by the middle of the 21st century. Similarly, research [19] analyzed the impact of global warming on the distribution region of Aedes albopictus in China, using data observed during the period from 1970 to 2021 combined with classification tree models, the result of which projected that the risk of dengue would cover China in its entirety in future years between 2050 and 2080, reaching 1.2 billion people affected, due to winter temperatures and summer precipitation as the main factors in its propagation.

In [25], they developed a ML-based predictive model for the statistical calculation of the risk of shock in patients with dengue, using clinical and physiological data collected in a university medical center, being combined models such as logistic regression and ANN, achieving that the bag assembly method obtained a 14.5% increase in accuracy compared to other approaches, identifying hemoglobin as a fundamental predictor of the severity of complications. In this regard, the study [26] provided a fractional derivative mathematical model for the analysis of Zika and dengue codynamics. The model was subjected to validation tests based on epidemiological data from Brazil and sensitization analyses, the results of which showed that the speed of human transmission and vector mortality are conditioning factors for the control of both diseases, suggesting strategies aimed at attenuating human-to-human transmission.

Among the limitations identified, overfitting to local data, noted in [22], reduces the ability of the models to generalize to other regions. In addition, the lack of complete historical climate data, mentioned in [17], limits the accuracy of predictions based on environmental factors. Furthermore, another considerable challenge is the high cost of implementing advanced technologies, such as the VECTRACK system evaluated in [21], whose effectiveness requires considerable investments in infrastructure and training. Progress in this area is presented in Table VIII, where the advances and limitations found in literature are grouped as follows.

TABLE VIII. ADVANCES AND LIMITATIONS IN DENGUE PREDICTION WITH ENVIRONMENTAL FACTORS AND ML

#	Advances	Limitations	Quantity	References
1	Outbreak prediction using temperature and Mosquito Oviposition Index (MOI)	Incomplete climate data; low spatial and temporal resolution	6	[29], [30], [31], [32], [33], [34]
2	ANN to predict incidence	Overfitting local data; limited generalizability; low interpretability	8	[35], [36], [37], [38], [39], [40], [41], [42]
3	Satellite data for mapping risk zones	High cost; coverage and cloudiness issues; high computational demand	5	[43], [44], [45], [46], [47]
4	Vertical transmission in mosquitoes	Poor generalization; limited epidemiological evidence	4	[48], [49], [50], [51]
5	Identification of antivirals with molecular docking	Limited experimental validation; absence of clinical trials	3	[52], [53], [54]
6	Network analysis to identify vectors	Dependence on quality data; risk of bias in incomplete data	4	[55], [56], [57], [58]
7	One Health" approach to surveillance	Complexity in interdisciplinary coordination; insufficient infrastructure	3	[59], [60], [61]
8	Vaccine development with immunogenic peptides	Low stability; limited immunogenicity; production barriers	4	[62], [63], [64], [65]
9	Vector control with Wolbachia	Difficulty of large-scale implementation; uncertainty regarding social acceptance	3	[66], [67], [68]
10	Prediction with socioeconomic factors	Incomplete socioeconomic data; regional heterogeneity	4	[69], [70], [71], [72]
11	Autoregressive Integrated Moving Average (ARIMA) models for time series	Limitations in long-term forecasts; low robustness to abrupt changes	3	[73], [74], [75]
12	Human mobility analysis	Restricted access to data; representativeness biases	3	[76], [77], [78]
13	Vector susceptibility by serotype	High variability between species and serotypes; lack of longitudinal data	4	[79], [80], [81], [82]
14	Deep Learning (DL) for outbreak prediction	Requires large volumes of data; risk of overfitting; low interpretability	2	[83], [84]

The results presented in Table VII show the various advances and limitations that exist in the development of environmental factors and ML techniques for dengue prediction. In this regard, the use of satellite data for mapping risk zones is relevant, allowing the delimitation of vulnerable areas with high precision. On the other hand, the focus on vertical transmission in mosquitoes offers valuable knowledge on the conservation of the vector in different populations. Regarding antiviral identification initiatives, certain techniques, such as molecular docking, show promising results, while network analysis has emerged as an innovative way to detect transmission patterns of the disease and its vectors. In terms of integrated surveillance systems for dengue viruses, the "One Health" approach brings together human health, animal health and the environment.

Despite these advances, many limitations remain. Among them, the high cost of implementing technologies such as satellite data and Wolbachia vector control makes them difficult to adopt in resource-poor regions. In addition, the limited experimental validation of antiviral compounds and the reliance on quality data in network analysis represent major challenges. At the same time, the complexity of interdisciplinary coordination of the "One Health" approach and limitations in large-scale production of peptide-based immunogenic vaccines highlight the need for improved cooperation and more infrastructure. Finally, the lack of accurate socioeconomic data and the difficulties in obtaining data on human mobility diminish the effectiveness of predictive models.

Likewise, a critical aspect identified in this review is the validation of ML models. Although it is true that several studies report significant metrics, it is important to exercise caution.

For example, the problem of overfitting in ANN and DL models can be observed, where local patterns are adjusted excessively. This limits their ability to generalize in contexts where geography is changing. Similarly, the problem of data leakage can also be observed, which occurs when the validation set is leaked into the training, and this can artificially inflate performance indicators.

Another important and well-known challenge is class imbalance. In many contexts, dengue outbreaks are a small fraction of the data compared to non-outbreak periods.

Consequently, it is recommended that future work address the following issues:

- Cross-validation that captures the sequential nature of outbreaks.
- Strategies to mitigate class imbalance.
- External generalization evaluations, testing models on data from different regions.

VI. CONCLUSIONS

This study addressed the relationship between environmental factors and the application of ML techniques in the prediction and control of dengue spread. For this purpose, an SLR was performed that analyzed 56 studies selected from various databases such as Springer Link which contributed 35.71% of the studies, followed by Web of Science with 28.57%, PubMed with 17.86% and Scopus with 17.86%, reflecting a representative and balanced distribution of the available scientific knowledge related to the subject during the period between 2020 and 2024.

Thanks to this research, it has been possible to discover essential trends linked to environmental factors that affect the spread of dengue, specifically the variation in temperature, humidity rate and precipitation regime. The effectiveness of various ML applications was also tested, highlighting the superiority of models based on supervised learning, such as Random Forest and SVM, for the classification and estimation of outbreaks compared to traditional approaches. On the other hand, it was found that the integration of geospatial and epidemiological data in the analyzed models is becoming more and more frequent, thus contributing to strengthening the accuracy in the identification of risk areas and planning of interventions.

This work will make a major contribution to public health research expertise by laying a strong foundation for the development of more potent anti-dengue measures. In particular, the findings emphasize the potential of forecasting methods to optimize early warning systems and focus resources on high-risk sectors. But there are also considerable limitations, such as the heterogeneity in the quality of the available data, which affects the comparability of the studies; the non-standardization of methodological approaches, which hinders the replicability of the models. These limitations are an opportunity for future research to optimize the integration of environmental data, improve the robustness of predictive models in real scenarios and explore innovative approaches, such as the use of unsupervised learning techniques to identify incipient patterns in the spread of dengue. In this way, it will be feasible to progress towards approaches that are more functional, durable and oriented to the specific needs of the territorial entities concerned by the disease.

AUTHORS' CONTRIBUTIONS

Conceptualization, O.I-V.; methodology, J.C-P, E.F-I and L.C-H; validation, J.C-P; formal analysis, J.C-P, E.F-I and L.C-H.; investigation, O.I.-V and J.C-P; data curation, E.F-I; writing—original draft preparation, O.I-V, J.C-P, E.F-I and L.C-H; writing—review and editing, O.I.-V; visualization, O.I-V, J.C-P, E.F-I and L.C-H. All authors have read and agreed to the published version of the manuscript.

FUNDING

This research received no external funding.

Institutional Review Board Statement: Not applicable

Informed Consent Statement: Not applicable.

DATA AVAILABILITY STATEMENT

The data used in this systematic review were collected from publicly accessible sources cited in the references. No primary data was generated.

CONFLICTS OF INTEREST

The authors declare no conflict of interest.

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APPENDIX

TABLE IX. PRISMA CHECKLIST 2020

Section/Topic	**Item**	**Checklist item**	**Location where item is reported**
TITLE			
Title	1	Identify the report as a systematic review.	Page 1
ABSTRACT			
Structured abstract	2	Refer to the PRISMA 2020 checklist for abstracts.	Page 1
INTRODUCTION			
Justification	3	Describe the rationale for the review in the context of existing knowledge.	Page 2
Objectives	4	Provide an explicit statement of the objectives or questions addressed by the review.	Page 2
METHODS			
Eligibility Criteria	5	Specify the inclusion and exclusion criteria for the review and how studies were grouped for synthesis.	Page 6
Sources of information	6	Specify all databases, registries, websites, organizations, reference lists, and other sources searched or queried to identify studies. Specify the date of the last search or query of each source.	Page 5
Search strategy	7	Present the complete search strategies for all databases, records, and websites, including the filters and limits used.	Page 5
Study selection process	8	Specify the methods used to decide whether a study met the review's inclusion criteria, including how many reviewers examined each record and each retrieved report, whether they worked independently, and, if applicable, the details of the automation tools used in the process are collected.	Page 6 and 7
Data extraction process	9	Specify the methods used to collect data from the reports, including how many reviewers collected data from each report, whether they worked independently, any process for obtaining or confirming data from study investigators, and, if applicable, details of automation tools used in the process.	Page 7
List of data	10a	List and define all the results for which data was searched. Specify whether all results that were compatible with each outcome domain in each study were searched (e.g., for all measures, time points, analyses) and, if not, the methods used to decide which results to collect.	Page 7
	10b	List and define all other variables for which data were sought (e.g., participant and intervention characteristics, sources of funding). Describe the assumptions made about any missing or unclear information.	Not applicable
Assessment of the record of bias of the individual studies	11	Specify the methods used to assess risk of bias in the included studies, including details of the tools used, how many review authors assessed each study and whether they worked independently and, if applicable, details of the automation tools used in the process.	Page 8
Measures of effect	12	Specify for each outcome the effect measure(s) (e.g., risk ratio, mean difference) used in the synthesis or presentation of the results.	Not applicable
Synthesis method	13a	Describe the processes used to decide which studies were eligible for each synthesis (e.g., tabulating the characteristics of the study intervention and comparing them to the groups planned for each synthesis (item #5)).	Page 7
	13b	Describe the methods required to prepare data for presentation or synthesis, such as handling missing summary statistics or data conversions.	Page 7
	13c	Describe any methods used to tabulate or visually display the results of individual studies and syntheses.	Page 7 and 8
	13d	Describe any methods used to synthesize the results and provide a rationale for the options. If a meta-analysis was performed, describe the models, methods for identifying the presence and degree of statistical heterogeneity, and the software packages used.	Not applicable
	13e	Describe any methods used to explore possible causes of heterogeneity among study results (e.g., subgroup analysis, meta-regression).	Not applicable
	13f	Describe any sensitivity analyses performed to assess the robustness of the synthesized results.	Not applicable