

Review

Spatial Analysis of Mosquito-Borne Diseases in Europe: A Scoping Review

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Abstract: Mosquito-borne infections are increasing in endemic areas and previously unaffected regions. In 2020, the notification rate for Dengue was 0.5 cases per 100,000 population, and for Chikungunya <0.1/100,000. In 2019, the rate for Malaria was 1.3/100,000, and for West Nile Virus, 0.1/100,000. Spatial analysis is increasingly used in surveillance and epidemiological investigation, but reviews about their use in this research topic are scarce. We identify and describe the methodological approaches used to investigate the distribution and ecological determinants of mosquito-borne infections in Europe. Relevant literature was extracted from PubMed, Scopus, and Web of Science from inception until October 2021 and analysed according to PRISMA-ScR protocol. We identified 110 studies. Most used geographical correlation analysis ($n = 50$), mainly applying generalised linear models, and the remaining used spatial cluster detection ($n = 30$) and disease mapping ($n = 30$), mainly conducted using frequentist approaches. The most studied infections were Dengue ($n = 32$), Malaria ($n = 26$), Chikungunya ($n = 26$), and West Nile Virus ($n = 24$), and the most studied ecological determinants were temperature ($n = 39$), precipitation ($n = 24$), water bodies ($n = 14$), and vegetation ($n = 11$). Results from this review may support public health programs for mosquito-borne disease prevention and may help guide future research, as we recommended various good practices for spatial epidemiological studies.

Keywords: vector-borne diseases; spatial analysis; geographic distribution; GIS; Europe



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1. Introduction

Due to climate change, deforestation, environmental degradation, urbanisation, human mobility, globalisation, and changes in public health practices, the incidence of vector-borne infectious diseases has been increasing [1]. This upsurge is not only due to these factors but also to genetic alterations found in infectious agents and to greater resistance acquired by the vectors to insecticides [2]. In addition, some of these factors explain the emergence of vectors and vector-borne diseases in new regions, namely in areas of the northern hemisphere, and a growing incidence in endemic areas [1].

Vectors transmit parasites, viruses, and bacteria that cause human diseases which are vector-borne diseases. The pathogens of humans or animals to humans can be transmitted by mosquito vectors [2]. Mosquitos ingest disease-producing microorganisms from an infected host (human or animal) during a blood meal as they are blood-sucking insects

and transmit them to a new host after the pathogen has been replicated. When a mosquito becomes infectious, it can transmit the pathogen for the rest of its life [3].

The transmission of mosquito-borne diseases in recent decades has increased [4] due to the diversity of mosquito-borne pathogens [5] and the reduction in vector control efforts [6].

Worldwide, Malaria, Dengue, Zika, Chikungunya, and other mosquito-borne diseases infect more than one billion people, meaning more than one million deaths each year [3].

Mosquitoes are dipterous insects from the Culicidae family [7]. They are one of the most important vectors because, more than any other group of organisms, they are the biggest indirect cause of morbidity and mortality among humans [1]. Among the mosquito-borne diseases, their importance in Europe and as emerging zoonoses, a few stand out: Dengue, Chikungunya, Yellow Fever, and Zika, caused by viruses; and Malaria, caused by protozoan parasites [1]. Since the 70's, mosquito-borne pathogens have spread to previously infection-free areas and have caused an increase in the number of infections in endemic areas. Viruses transmitted by *Aedes aegypti* mosquitoes and *Aedes albopictus* pose a danger to a large percentage of the world's population and so they are becoming a greater public health issue [8].

Invasive mosquitoes are recognised by their ability to colonise new territories. Since the 1990s, it has been noticed an increase in the spread of invasive mosquitoes in Europe, being an example of this is the introduction of *Aedes aegypti* in Madeira, Portugal, in the 20th century; the presence of *Aedes albopictus* in most parts of southern Europe; the distribution of *Anopheles* mosquito from Portugal to south-eastern Sweden; and the propagation of *Culex pipiens* mosquito all over Europe [9]. Consequently, local cases of infection have been reported, namely the local autochthonous transmission of Malaria in France and Greece; localised cases of Dengue, Zika, and Chikungunya virus diseases occurred in the EU; and the West Nile virus continues to rise in Europe, reaching counties like the Netherlands and Germany [10]. In fact, in December 2021, the ECDC (European Centre for Disease Prevention and Control) stated that recently “Europe has faced changes in the epidemiological situation of vector-borne diseases” and that “to mitigate the impact of vector-borne diseases, a comprehensive approach to vector control is needed”, which involves, among other aspects “collaboration between several disciplines (. . .) for effective surveillance, adequate risk assessment, early detection, communication (. . .) and the pathogens they transmit” [10].

Spatial analysis tools and Geographic Information Systems (GIS) are increasingly used in surveillance and epidemiological investigation. Spatial modelling of invasive species has been a particularly relevant research topic recently, as the prevalence of vector-borne diseases has expanded considerably due to the intensification of human mobility and intercontinental trade [11]. However, despite the recognition of the extreme importance of geographical factors (for example, urban agglomerations, land use, fauna and flora, climatic conditions, etc.), spatial analysis has only been considered a fundamental tool for the study and investigation of invasive species since the second half of the last decade [12].

Spatial analysis allows different ways of approaching the problem, namely: mapping areas of susceptibility, vulnerability, and risk; studying habitat adaptability or dispersion patterns; crossing multi-source information and integrating it in predictive models; identifying and visualising spatio-temporal co-occurrence across multiple clusters [13–15]; and estimating the dynamics of vector-borne diseases [16], such as disease spread rate, cyclical pattern, direction, intensity and risk of spreading to new regions [15]. Ultimately, spatio-temporal analysis can facilitate surveillance of vector-borne diseases by allowing decision-makers to allocate resources to fight outbreaks [15].

With the growing number of public health research studies, new spatial analysis methods have been developed specifically to be applied in epidemiological studies [17]. However, despite this being an emergent and promising research topic, reviews summarising the studies that have applied spatial analysis on mosquito-borne diseases research are scarce and focus primarily on specific mosquito-borne diseases, more precisely on Dengue [17–20]. Therefore, the identification and systematisation of the spatial analysis methods, software,

and ecological variables employed in mosquito-borne disease investigation will be useful to geographers, epidemiologists, and biologists, among other researchers.

Under this background, the objective of the present scoping review is to identify and describe the methodological approaches used in investigations of the spatial variation of mosquito-borne diseases and its potential influencing ecological factors (e.g., environmental, socioeconomic, and healthcare-related) within the existing literature. This scoping review will focus on studies from Europe because it is a territory of completely different features than African, South American, and Asian countries (where mosquito-borne diseases are more burdensome and endemic). In addition, as previously mentioned, Europe has faced changes in the epidemiological situation of vector-borne diseases due to urbanisation [10], climate change, and human mobility, which led to a recent reintroduction of the mosquitoes and affected the dynamics of many mosquito-borne diseases.

2. Materials and Methods

The scoping review followed the methodology proposed by Arksey and O'Malley [21], which is organized into five steps: (1) identifying the research question and (2) the relevant studies; (3) selecting the studies according to inclusion criteria; (4) charting and interpreting data; (5) summarising and reporting of results. Results will be reported according to PRISMA-ScR (PRISMA extension for Scoping Reviews) [22]. The study protocol can be found at: <https://zenodo.org/record/6758947#.YrmaIXbMKUk>, accessed on 30 September 2021. The PRISMA-ScR can be found in Supplementary Table S4—Preferred Reporting Items for Systematic reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) Checklist.

2.1. Identifying the Research Question

This review is centred around the following main research question: 'which spatial analysis methods are used to investigate the spatiotemporal variation of mosquito-borne diseases in Europe and the biotic and abiotic factors that may relate to its presence?'

2.2. Identifying the Relevant Studies

Searches were conducted using PubMed (<http://www.ncbi.nlm.nih.gov/pubmed>, accessed on 30 September 2021), Scopus (<https://www.scopus.com/>, accessed on 30 September 2021), and Web of Science (<https://www.webofknowledge.com/>, accessed on 30 September 2021) from inception until October 2021.

We used the following set of keywords related with the methodological approach—"Spatial analysis", "mapping", "space-time", "geographic information system", "spatial cluster*", "spatio-temporal", "spatiotemporal", "geographic distribution"—a second set of keywords related with the disease, infection and/or vector—"encephalitis", "malaria", "dengue", "yellow fever", "West Nile", "Chikungunya", "Zika", "filariasis", "Sindbis", "Pogosta disease", "Karelian fever", "Ockelbo disease", "tularemia", "Mosquito"—and a last set of keywords to restrict the search to studies that included European countries (ECDC (European Centre for Disease Prevention and Control) definition)—"Europe", "Austria", "Belgium", "Bulgaria", "Croatia", "Cyprus", "Czechia", "Denmark", "Estonia", "Finland", "France", "Germany", "Greece", "Hungary", "Iceland", "Ireland", "Italy", "Latvia", "Liechtenstein", "Lithuania", "Luxembourg", "Malta", "Netherlands", "Norway", "Poland", "Portugal", "Romania", "Slovakia", "Slovenia", "Spain", "Sweden", "UK", "United Kingdom". The entire search strategy was adapted to the syntax of the individual database from the following conceptual structure and is provided in the supplementary material (Table S1).

A reference management software (EndNote 20, Clarivate Analytics (Philadelphia, PA, USA)) was used to import and organise the references and remove duplicates [23].

2.3. Selecting the Studies According to Inclusion Criteria

We selected studies that focused on mosquito-borne diseases and used spatial analysis methods. Studies were excluded hierarchically based on the following exclusion criteria: (1) study type (reviews, reports, abstracts, editorials, comments); (2) not written in Portuguese, Spanish, Italian, French, German, or English; (3) not about mosquito-borne diseases/infections or their vectors; (4) no spatial analysis was conducted. No temporal restrictions were imposed.

Two examiners (SM and AIR) analysed titles and abstracts to detect studies that did not meet the inclusion criteria or that did not have full texts. Then, full texts were read and those that did not meet the inclusion criteria were removed. When the two reviewers disagree, the final decision was made by a third examiner (JR). Forward and backward citation tracking of articles included in the review was performed to identify additional papers.

The study selection process is represented in the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) flowchart [24] from Figure 1. Out of 1755 eligible studies, after reading the abstracts and keywords, 156 were selected in the second step and finally, 110 studies were selected in the last stage after a thorough reading and analysis of the full paper.

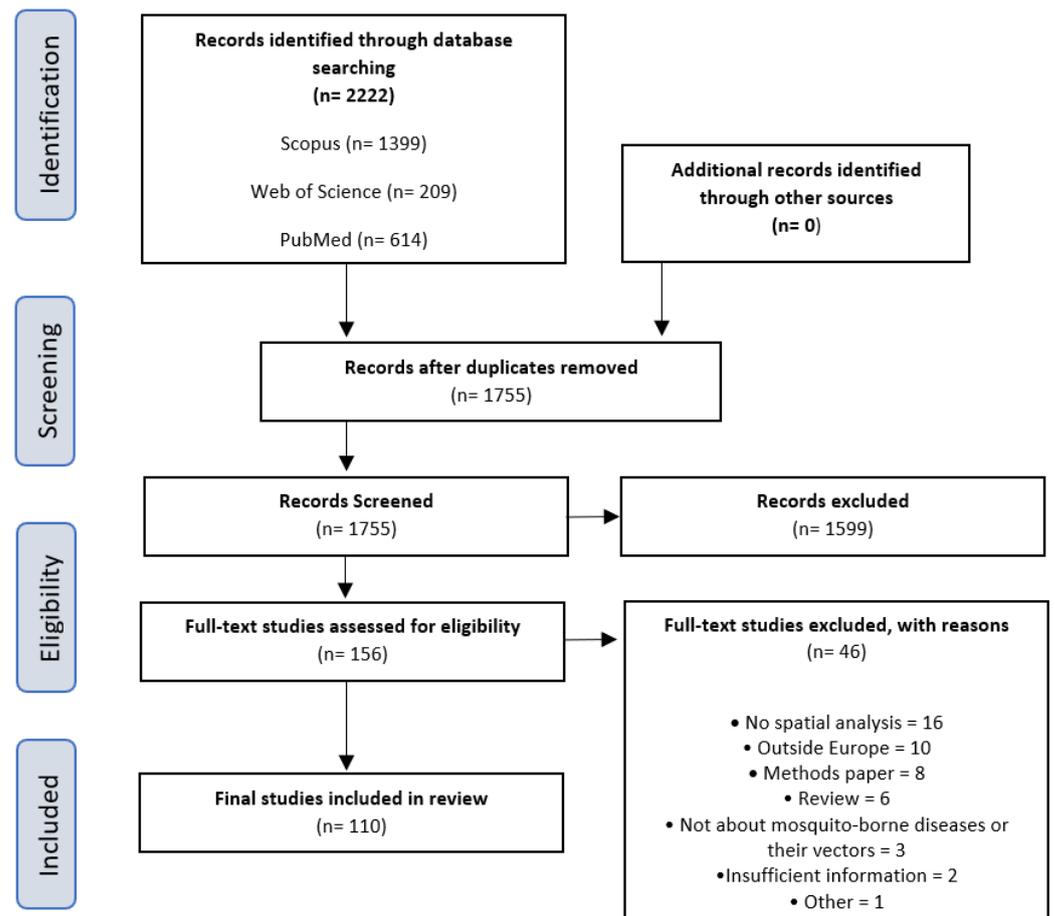


Figure 1. Flow of information through the different phases of the scoping review.

2.4. Charting and Interpreting Data

The results were structured by general characteristics (e.g., country/region, year of publication); by themes according to the diseases and/or mosquitoes studied; by the scale of analysis (size of the spatial units) and geographic extent (global, continental, regional or local); type of outcome data used (notification or survey); the methodology used for spatial analysis; studied ecological determinants.

Regarding the type of outcome data used, notifications correspond to data on diseases/infections that, by statutory requirements, must be reported to the public health authority whenever a case is detected, while surveys are typically sample-based and designed for research purposes or to assess the prevalence of infection/disease within a particular territory [25]. The spatial analysis methodology was divided into three main groups proposed by Elliot and Wartenberg—disease mapping, geographic correlation studies, and disease clusters and clustering [26]. Disease mapping studies commonly measure morbidity or mortality for small geographic areas through smoothed or unsmoothed maps (e.g., graduated colour maps, graduated symbol maps, heatmaps, etc.). Geographic correlation studies investigate geographic variations across population groups in exposure to ecological factors relating them to health outcomes measured on a particular geographic scale. Finally, disease clusters and clustering studies consist of the investigation of excess events above a background rate either in time and/or in space.

Regarding the determinants, these were grouped into two categories: biotic and abiotic. Biotic factors are related to, or caused by living organisms, and abiotic factors are related to or caused by the non-living part of an ecosystem that shapes its environment. To name a few, as biotic factors, we have vector abundance, host abundance, and population density; and as abiotic factors, we have climatic and socioeconomic factors.

2.5. Collating, Summarising, and Reporting Results

We synthesised the information from the papers using the previously described research question and scope of the investigation. Tables and figures were created to systematise and summarise the information. Counts and proportions were used to summarise study findings and characteristics.

The main software used was EndNote for reading, organizing, and selecting studies. In addition, Excel 365 and ArcGIS software were also used to create tables and graphs and to map the geographic distribution of the studies.

3. Results

3.1. General Characteristics

A total of 110 studies were included in the present review. More details on the characteristics of the included studies can be found in the Supplementary Material (Table S2). The years 2020, 2017, and 2014 concentrated the highest number of studies, with 14, 13, and 11 publications, respectively. The timeline from Figure 2 shows that the number of studies on the topic has grown over time.

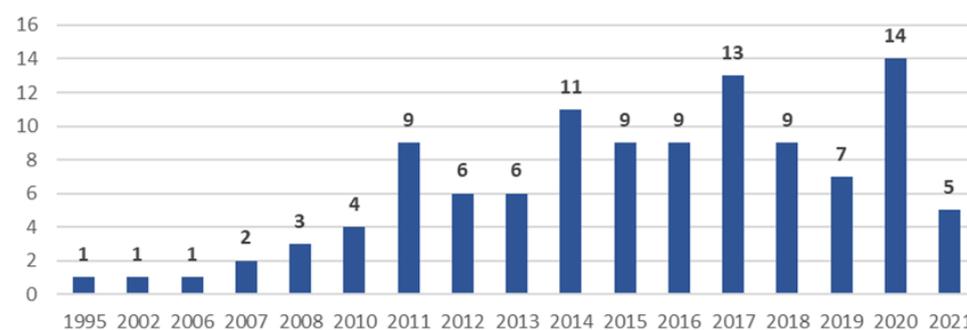


Figure 2. Number of studies by year of publication (1995–2021).

Examining the map of the geographic distribution of the studies, a total of 16 European countries have studied at supranational, national, regional, or local levels. Italy is the country with the most scientific studies ($n = 18$), followed by Germany ($n = 10$) and Spain ($n = 9$) (Figure 3).

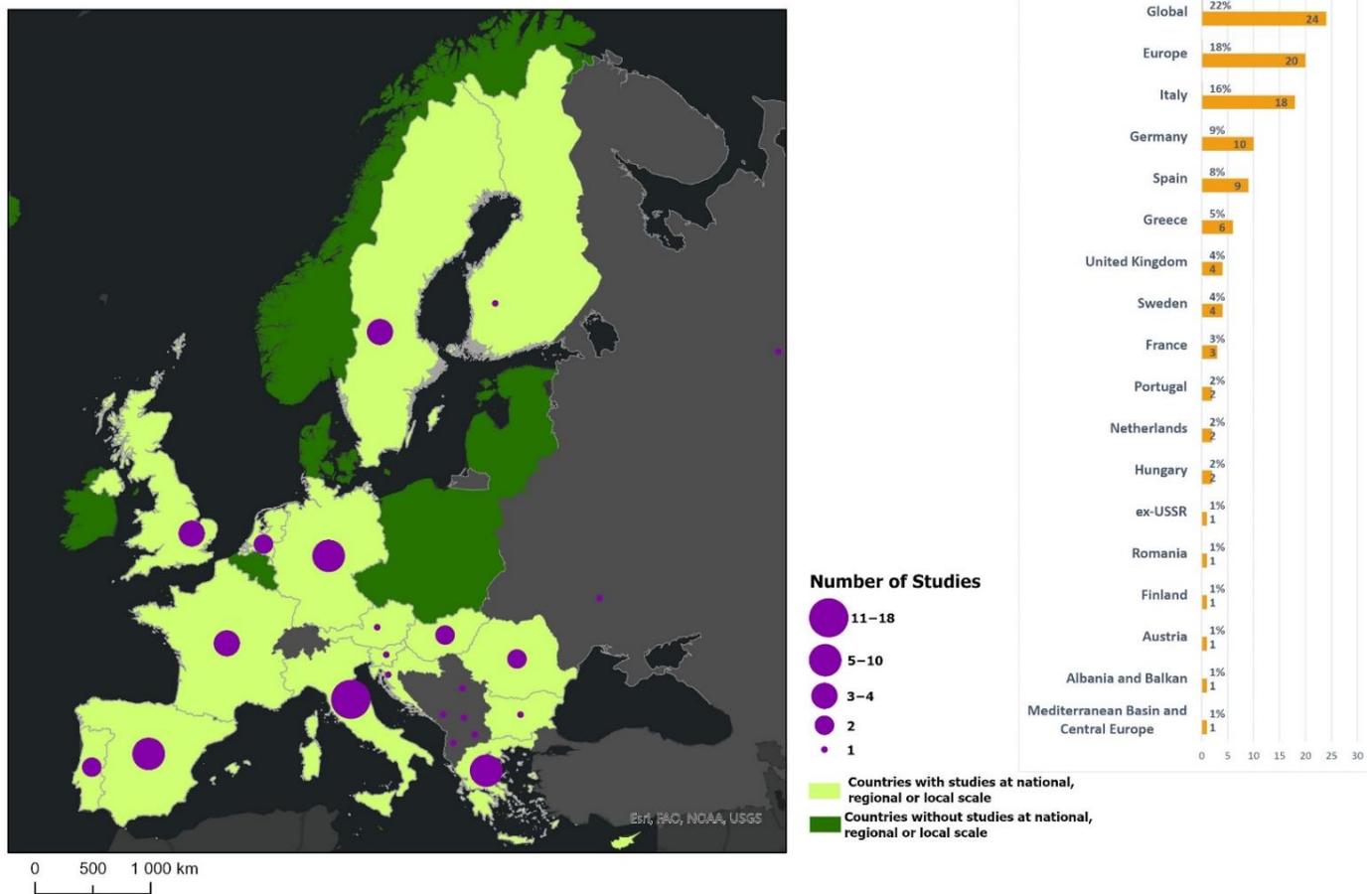


Figure 3. Geographic distribution of the studies according to the countries of origin in Europe.

3.2. Studied Vectors and Infections/Diseases

The most investigated vectors are those of Dengue, Malaria, Chikungunya, and West Nile Virus, with 32 (24%), 26 (19%), 26 (19%), and 24 (18%) studies, respectively. With a smaller number of studies, 6% of studies focused on Zika, and the remaining studies analysed all mosquito communities, Rift Valley fever virus, Tularemia, Encephalitis, and others (*Dirofilaria/dirofilariosis*; *Xylella fastidiosa* and Hemoparasites and ectoparasites (acari and dipterans)) with 5%, 3%, 2%, 2%, and 2% of studies respectively (Figure 4). Italy is the European country where the most studies have been carried out, where eight studies focused on Chikungunya, another eight on West Nile Virus, and five on Dengue. Germany is the country where Malaria is most frequently studied with six studies. In the UK and in Spain the most commonly studied infections were Tularemia ($n = 2$) and Zika ($n = 1$), respectively (Figure 4).

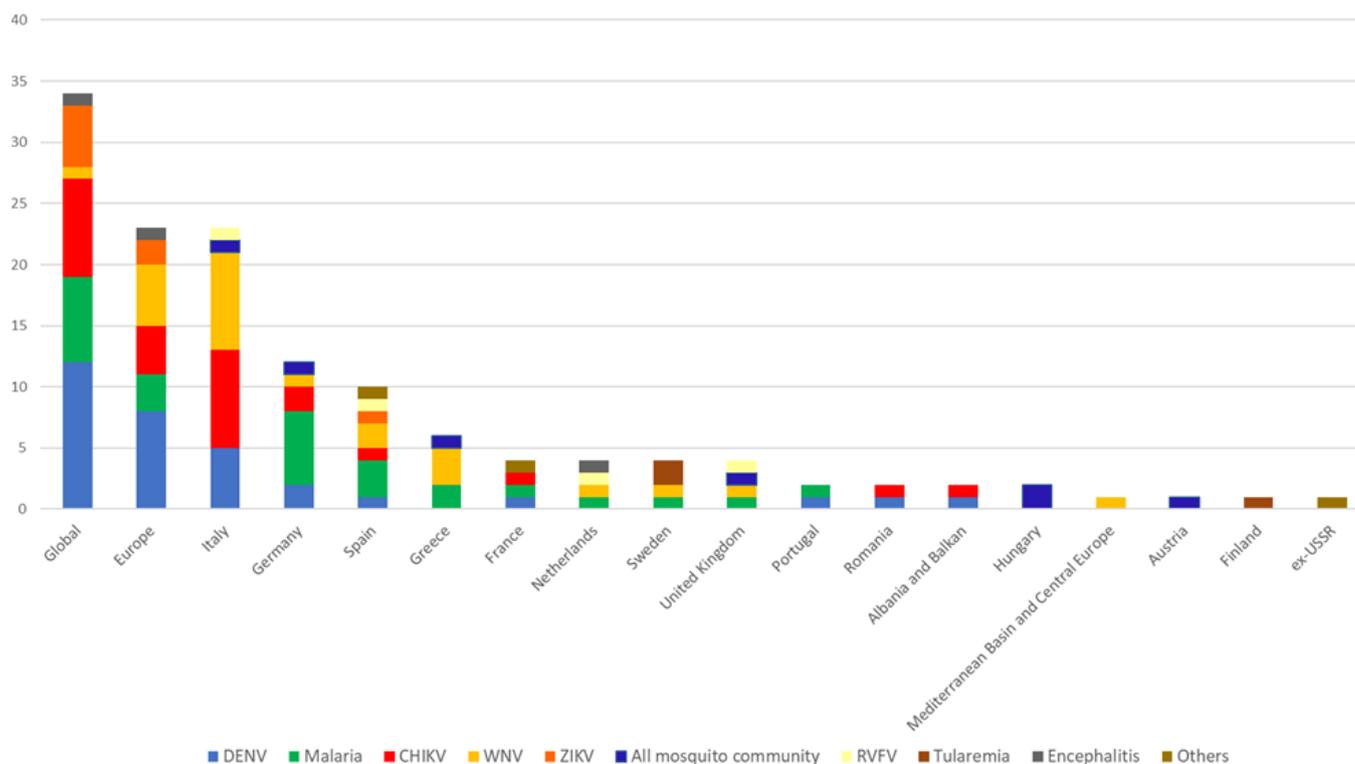


Figure 4. Number of studies by vectors caused by mosquitoes (DENV = Dengue, CHIKV = Chikungunya, WNV = West Nile Virus, ZIKV = Zika, RRVFV = Rift Valley fever virus).

3.3. Data Used, Type of Data, Geographical Extent, and Spatial Scale

Studies were conducted at different scales, with the study unit size ranging from 0.0005 km² to 400 km² (median 4 km², IQR 8 km²) and the mean population per area ranging from 1738 inhabitants to 60,000,000 inhabitants (median 28,048 inhabitants, IQR 662,501 inhabitants).

Studies have very different geographical extents: 42 (38%) were carried out at the national level, 24 (22%) at the global level (i.e., covering the entire world), 21 (19%) at the continental level, 19 (17%) at the regional level, and four (4%) at the local level. Regarding the type of data, 47 studies obtained data from notifications and 63 studies collected data using surveys.

3.4. Studied Biotic and Abiotic Factors

The abiotic variables most used to analyse the relationship with infections and to estimate probability and risk were temperature in first place, in 35% of the studies, followed by precipitation in 22% and water bodies in 13% (Figure 5). Regarding the biotic factors, the most studied variables were the human population data or ratio (5%), population density (3%), and animals in farms (3%) (Figure 6).

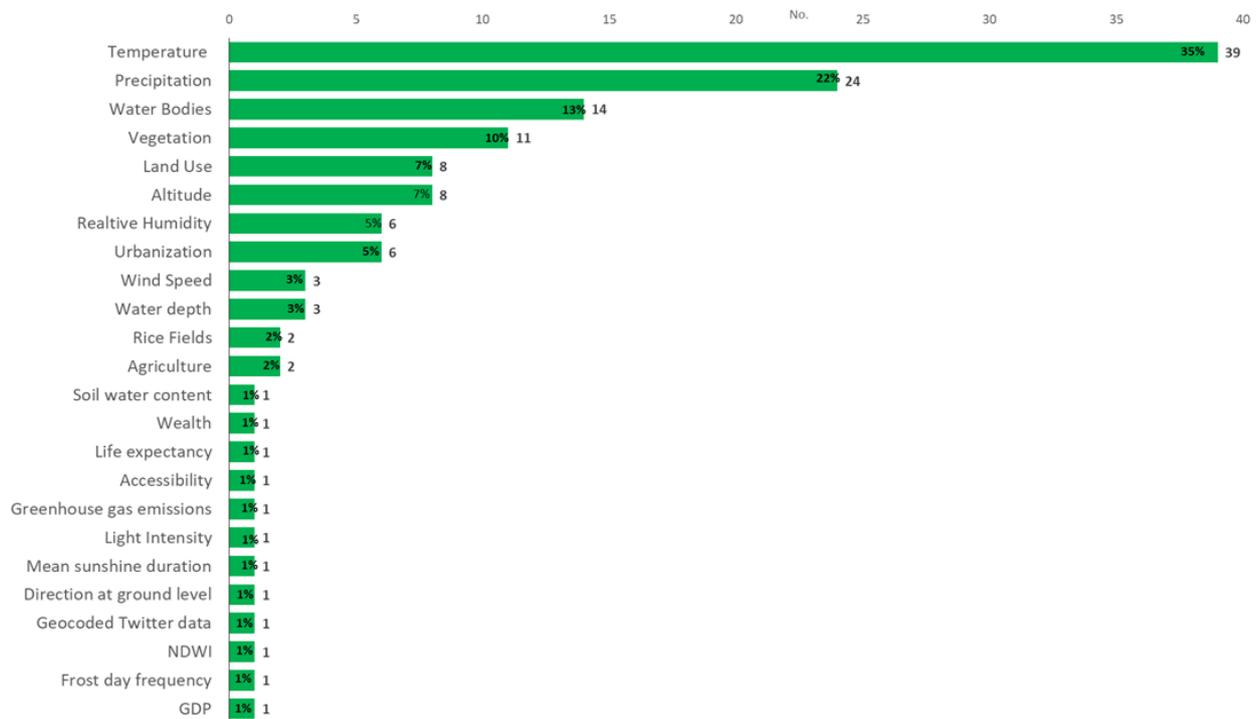


Figure 5. Number and percentage of studies by abiotic variables.

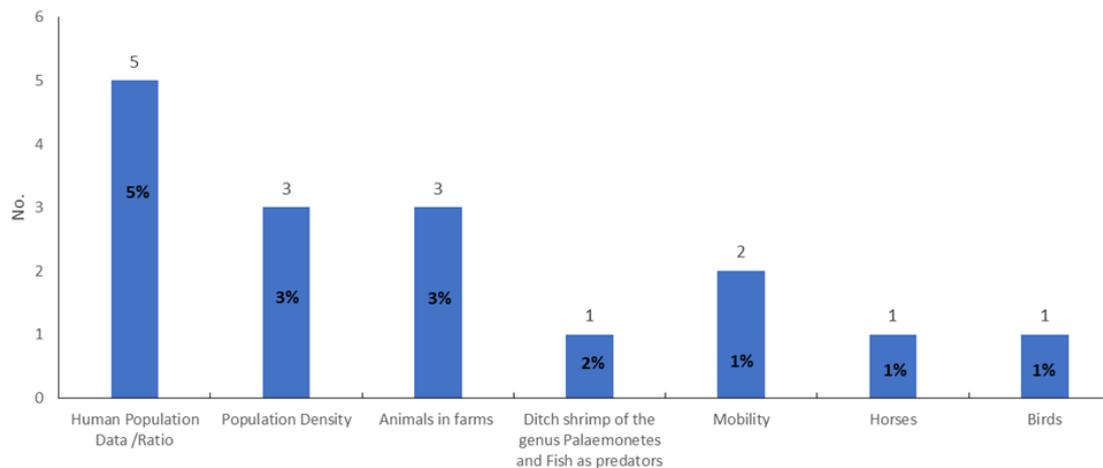


Figure 6. Number and percentage of studies by biotic variables.

3.5. Spatial Analysis Methods

Nearly half (46%) of the studies used geographic correlation analyses, and in the rest, in equal parts, clustering and surveillance analyses (27%), and disease mapping (27%) were used (Table S1). The three most widely used software for the analyses were: R Core Team software (37%), ArcGIS Desktop: Release 10. Environmental Systems Research Institute (ESRI), Redlands, CA (33%) and QuantumGis (QGIS) (9%) (the complete list can be found in Supplementary Table S3).

3.6. Disease Mapping

Disease mapping studies reported and mapped the geographic distribution of the occurrences of the diseases under investigation and analyse the geographic distribution of different mosquito species. They represented the incidence or abundance of mosquito-borne infections and mosquitoes using statistical or descriptive mapping techniques. Many created suitability maps or maps with the predicted distribution of individual species

or species complexes. They also used predictive analysis methods based on ecological variables to identify and map risk areas suitable for transmission.

The most used methods in this spatial analysis group were the risk maps ($n = 32$), rate maps ($n = 31$), and case count maps ($n = 14$).

3.7. Clusters, Clustering, and Surveillance

The studies that applied clusters, clustering, and disease surveillance performed a geographic analysis of the location of cases to detect high-risk areas, such as outbreaks, and conducted a statistical analysis of spatiotemporal patterns through point density and modelling to study the dynamics of mosquitoes.

The most used methods were Kernel Density Estimation ($n = 6$), Mahalanobis Distance Analysis ($n = 3$), GetisOrd statistic (hotspot analysis) ($n = 3$) and Autocorrelation I Moran's ($n = 2$).

Most studies using cluster analysis focused on single infections and/or vectors, while a few explored co-clusters of more than one infection/vector [27]. To cite a few examples: in Italy, Dengue clusters tended to be located in coastal and urban areas [28–30]; in Greece, central Greece emerged as an important hotspot of Malaria, especially in districts with more water bodies [31]; in Sweden, hotspots of Malaria were concentrated around big inland lakes and in southernmost Sweden [31,32]; at a more global extent, France and the UK constitute critical Malaria hotspots with the highest number of cases, more than 4000 imported cases per year on average [33].

3.8. Geographic Correlation Studies

The geographic correlation studies analysed the correlation between ecological variables and the breeding and propagation of mosquito vectors. Investigations under this category produced maps that described the spatial patterns of ecological and sociodemographic determinants and the effects of environmental changes and investigated the spatial and temporal structure of disease transmission caused by those determinants, mainly by temperature. Additionally, they fitted simulation models that incorporated the principal mechanisms of the vector transmission cycle and combined them with fine spatial and temporal resolution data to study the time-series of factor suitability for transmission throughout time [34]. These studies found significant relationships between the habitat pattern and the pattern of mosquito clusters and biotic and abiotic factors [35]. A considerable amount also examined the potential global distributions of vectors in relation to global climate variation.

The most used methods were generalized linear models (GLM) ($n = 20$), spatial prediction ($n = 16$), ecological niche model of occurrence ($n = 12$), conventional logistic ($n = 10$), regression models with spatial terms ($n = 9$), Bayesian models ($n = 8$), generalized additive models (GAM) ($n = 7$), Pearson's correlation ($n = 5$) and kriging estimation ($n = 4$) (Table 1).

Table 1. Spatial methods used in spatial analysis of Mosquito-Borne Diseases in Europe ($n = 110$).

Method Category	Method	Number	References
Disease mapping	Risk map	32	[31,34,36–65]
	Rate map	31	[31,32,34,38–40,42,44–47,50,53,54,56,58–61,64,66–76]
	Case counts maps	14	[28,42,68,75,77–85]
	Temporal trend map	10	[32,34,43,45,59,60,66,75,86,87]
	Distance map	10	[43,50,54,64,66,78,81,82,88,89]
	Predictive map	9	[31,37,43,45,55,57,62,64,90]
	Travel/time map	8	[81,82,85,91–95]
	Suitability map	6	[37,43,51,56,57,96]
	Dot map	3	[88,97,98]

Table 1. Cont.

Method Category	Method	Number	References
Clusters, clustering, and surveillance	Kernel density map	6	[31,32,49,96–98]
	GetisOrd statistic (Hotspot analysis)	3	[29,31,32]
	Mahalanobis Distance Analysis	3	[43,54,77]
	Autocorrelation I Moran's	2	[94,99]
	Kulldorff's spatial scan statistic	1	[88]
	Mann-Kendall Test	1	[89]
	Ripley's K Function	1	[66]
Geographic correlation			
	Generalized linear models (GLM)	20	[30,38,41,48,56,61,66,88,93–95,100–108]
	Spatial prediction	16	[31,43,49,50,54,55,57,61,65,73,75,96,109–112]
	Ecological niche models of occurrence	12	[49,50,52,53,55,70,73,87,96,111–113]
	Conventional logistic	10	[44,46,50,57,65,80,104,114–116]
	Regression models with spatial terms	9	[47,57,62,64,65,81,88,95,108]
	Bayesian models	8	[41,66,75,99,110,111,117,118]
	Generalized Additive Models (GAM)	7	[29,30,41,50,74,100,103]
	Pearson's Correlation	5	[32,35,38,106,115]
	Kriging estimation	4	[36,46,47,58]

Table 2 summarises the results from the correlation studies for each of the studied ecological factors.

The factors that were more frequently significantly associated with the studied outcomes were temperature ($n = 39$), precipitation ($n = 22$), water bodies ($n = 14$), vegetation ($n = 11$), land use ($n = 8$), and altitude ($n = 8$).

On the other hand, some studies found non-significant associations with precipitation ($n = 2$), urbanisation, and relative humidity ($n = 1$).

Table 2. Predictors of the presence of vector-borne mosquito species.

Variable	Non-Significant Association	Positive Association	Negative Association
Abiotic factors			
Precipitation	[80,115]	[38,46,56,87,89,98,102,103,107,119–124]	[30,32,86,96,102,104,107,125,126]
Temperature		[30,32,34,38,46,47,56,58–61,71,80,86,89,96,98,99,101–107,115,116,119–123,125–129]	[68,96,102,103,124]
Wind speed		[103]	[116,126]
Altitude		[56,61,101,102,130]	[80,96,105]
Land Use		[30,38,46,64,80,105,107,125]	
Water bodies		[30,35,38,46,56,64,89,99,105,107,126,130,131]	[80]
Water depth		[99,125]	[125]
NDWI (Normalized difference water index)			[107]
Vegetation		[30,35,38,61,80,86,105,107,119,131]	[30,124]
Rice fields		[64,86]	
Soil water content			[116]
Frost day frequency		[124]	
Urbanization	[96]	[30,61,105,107]	[124]
Wealth			[124]
Life expectancy			[124]

Table 2. Cont.

Variable	Non-Significant Association	Positive Association	Negative Association
Accessibility		[119]	
Relative Humidity	[102]	[119,120,125]	[115,116]
Greenhouse gas emissions			[71]
Light Intensity		[103]	
Mean sunshine duration		[125]	
Direction at ground level		[103]	
Geocoded Twitter data-Geolocated activity data and computed mobility patterns of users		[127]	
GDP-Gross domestic product			[124]
Agriculture		[80]	[61]
Biotic factors			
Population Density		[107,119]	[46]
Mobility		[81,94]	[94]
Human Population Data/Ratio		[30,71,104,106,126]	
Ditch shrimp of the genus Palaemonetes and Fish as predators			[99]
Birds			[80]
Horses		[80]	
Animals in farms		[56,61,63]	

To cite a few examples, in Europe as a whole, geographical accessibility, absolute humidity, and annual minimum temperatures were the strongest predictors for the presence of *Aedes* vectors [119]. In addition, the best environmental predictors of West Nile Fever outbreaks in Europe were climatic (maximum temperature of the warmest month and annual temperature range), human-related (rain-fed agriculture, density of poultry and horses), and topo-hydrographic variables (presence of rivers and altitude) [80]. In the Netherlands, higher elevation, precipitation, day and night temperature, and vegetation indices were important predictors of the occurrence of *An. plumbeus* [48]. In Hungary, wetlands were important target areas for mosquito control [132]. In Italy, *Ae. albopictus* was mostly found near areas with a human presence and urban landscape [38], while *Culex pipiens* had a more scattered distribution and could be found in wilder and less urbanised areas [100]. Finally, in Spain, unsuitable areas for *Culex pipiens* were located at higher altitudes and in colder regions [96].

4. Discussion

This scoping review has demonstrated that investigations apply various spatial analysis techniques to studying mosquito-borne infections in Europe. Most studies used geographical correlation analysis with a wide range of spatial modelling techniques implemented in specialised statistical software. The remaining studies used spatial cluster detection methods and disease mapping, mostly done using frequentist approaches in GIS software such as the ArcGis (ESRI), GRASS GIS, R software, QuantumGis, and GeoDa [27,29,36,45,49,66,76,88]. The most frequently studied infections were Dengue, Malaria, Chikungunya, and West Nile Virus, and the most widely studied ecological determinants were temperature and precipitation, as well as water bodies and vegetation. Studies were predominantly conducted at a global or a continental level and in particular countries such as Italy, Germany, and Spain.

Overall, spatial analysis studies applied to mosquito-borne infections and vectors in Europe have increased over the last two decades. While most approaches are based on classical frequentist statistical methods, such as generalised linear models, recent advances

in computing, statistical methodology, and the availability of high-resolution, geographically referenced databases led to the use of new techniques such as Bayesian Models, geostatistical methods such as Kriging estimation and ecological niche models. These methods should be used to the detriment of the previous ones because they account for spatial dependency and other analytic challenges, such as spatial confounding and small number problems [26]. Innovative analytical and pioneering skills and tools in spatial statistics should be employed to analyse existing data allowing to inform policymakers and other stakeholders better. For that, and to overcome the complexity of spatial analysis and spatial data management, it is important to invest in the development of intuitive and ready-to-use software for spatial epidemiological analysis. In fact, in the last years, many examples have emerged. For instance, many sophisticated analytical tools suitable for Big Data (e.g., Mann-Kendall space-time trend analysis, convolutional neural network approaches [133,134], image classification) are now implemented in commercial software like ArcGIS Pro, while at the same time many researchers and developers have created and updated open-source apps and software to facilitate spatial analyses (SaTScan, GeoDA, Crimestat, among others).

According to the studies included in this review, the threat of viruses to Europe is low but uncertain, justifying the need to keep monitoring from areas of greatest predicted environmental suitability of mosquito-borne infections, especially in the Mediterranean and central Europe. The results of some studies have verified where there is a risk of introducing and spreading the infectious diseases under study and also showed that the temporal variation in the number of publications over the years is driven by the fluctuating topicality of mosquito-borne diseases in the medium and large-scale climate conditions [126]. Air temperature and, to a lesser degree, relative humidity, soil water content and wind speed seem to significantly affect the epidemiology of mosquito vectors in Europe [116]. Many studies identify clusters of infections and vectors covering specific localities and regions within certain European countries [36,66,83,97,98,114]. In these areas, the risk of disease transmission should be reduced by reducing mosquito-human contact by reducing mosquito populations and eliminating breeding sites.

Spatial analysis, through the use of innovative tools like the ones referred above, has the potential to help identify target areas, biotic and abiotic ecological determinants, and assess the risk of emergence or re-emergence of vectors and mosquito-borne infections, as demonstrated by various studies [27,64]. In fact, the implementation of the spatial analysis techniques substantially helped to improve the results of the mosquito abatement programs [131]. In addition, the results of these analyses provide relevant information for surveillance activities aiming to identify where the local transmission is higher and where is the potential for the vector-borne introduction [66].

4.1. Strengths and Limitations

This is the first review to provide the range and depth of published studies using spatial analysis techniques to analyse the geographical distribution of mosquito and mosquito-borne diseases in Europe and associated biotic and abiotic determinants. Our search strategy was exhaustive and transparent, in accordance with the scoping reviews' methodological guidelines, covered a period of circa 25 years, and provided an evidence base for future spatial epidemiology studies on the topic. This scoping study began at the end of July 2021 and the selected studies were retrieved in October 2021 for analysis, as defined in the study protocol found at: <https://zenodo.org/record/6758947#.YrlkAnbMKUk> (accessed on 9 August 2021).

However, some limitations of this scoping review must be discussed. Firstly, the studies that were not indexed in the searched databases or (if they were) not available in the included languages were omitted. Secondly, the scoping review methodology has some inconveniences despite being the most suitable for the purpose of our study. For example, no restrictions were placed on the included studies to guarantee homogeneity because it does not allow for the meta-analysis of the associations between ecological factors and

outcomes. Even so, the meta-analysis would not be feasible due to the fact that research on this topic is recent, heterogeneous, and sparse. In addition, our literature review, like others, is subject to publication bias; it is recognised that the studies most likely to be published are those with significant associations.

4.2. Evidence Gaps and Recommendations

The present scoping review allowed us to identify evidence gaps that should be addressed in future studies on the topic. One of the weaknesses in this scoping review is the lack of investigations carried out at the finer scales using local geographical extents. It is fundamental in precision public health (PPH) and in the efficient allocation of resources, using finer scales to identify clusters of cases/vectors and inequalities to monitor disease variation. Additionally, few studies explored the issue of the Modifiable Areal Unit Problem (MAUP) in spatial analyses which affects the study conclusions due to the number and the size of the scale used to define the same areas [89,135]. As part of sensitivity analysis, we recommend that studies consider using multiple geography levels to assess how robust the results are to the chosen geographies. We also found that there are no studies in some countries located in northern Europe due to the lower influx of vectors. However, it is essential to highlight that with climate change, it is advisable to monitor changes in biodiversity and climate in these areas to anticipate a future introduction of vectors. Thus, more studies should be conducted in northern European regions. The results also highlight the difficulties in modelling climate and viruses. It is difficult to predict the incidence of infectious diseases, despite the predicted changes that result in the distribution of the vector. The local temperature adaptation, vector-pathogen interactions, and human-derived landscape changes are distinctive processes that may have important roles in creating future dynamics of pathogen transmission. Therefore, more complex study designs (e.g., system approach, agent-based models) should be used to capture such dynamics. Despite the growing recognition of One Health, few studies explicitly addressed the entire triad of animals-humans-environment in their analysis [136]. Finally, while the included studies addressed a wide range of biotic and abiotic factors, the role of socioeconomic factors has been insufficiently addressed. However, they are well-established determinants of communicable and non-communicable human and animal diseases [137–139]. Since, to prevent and control the dissemination of infection in both humans and animals, sanitation and enhancement of hygiene practices are very important, socioeconomic factors may constitute major determinants of mosquito-borne disease [137]. However, as demonstrated by a recent literature review [140], focused on endemic countries, the association between socioeconomic conditions and vector-borne diseases is unclear and may be highly situationally dependent. Thus, by adding to the current body of literature other continents, namely Europe—where socioeconomic conditions are better but socioeconomic inequalities in health and pockets of poverty persist—may help to better understand the directionality of the associations between mosquito-borne infections and socioeconomic factors and design tailored interventions according to the socio-economic profile of the communities. Hence, future studies should explore the direct and indirect associations between socioeconomic factors (e.g., area level deprivation, population literacy, education, housing conditions) and mosquito-borne infections.

5. Conclusions

In the contemporary context of globalisation and climate change, the spatial analysis of mosquito-borne infections and their vectors constitutes an essential component for understanding the present and future burden of these emerging diseases in Europe. Our review described the spatial analysis approaches and potential predictors used in mapping mosquito-borne infection risk. Results from this review may help guide researchers aiming to conduct spatial epidemiological studies of mosquito-borne infections and may support public health and territorial planning policies and programs towards vector control and mosquito-borne disease prevention in Europe.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/su14158975/s1>, Table S1: Full search strategy; Table S2: Detailed information from all the studies; Table S3: Software used in the studies of the Scoping Review: Total and frequency (%), Table S4: Preferred Reporting Items for Systematic reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) Checklist.

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