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Systematic Review

Systematic Literature Review of Models Used in the Epidemiological Analysis of Bovine Infectious Diseases

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Abstract: There are different bovine infectious diseases that show economic losses and social problems in various sectors of the economy. Most of the studies are focused on some diseases (for example, tuberculosis, salmonellosis, and brucellosis), but there are few studies on other diseases which are not officially controlled but also have an impact on the economy. This work is a systematic literature review on models (as a theoretical scheme, generally in mathematical form) used in the epidemiological analysis of bovine infectious diseases in the dairy farming sector. In this systematic literature review, criteria were defined for cattle, models, and infectious diseases to select articles on Scopus, IEEE, Xplorer, and ACM databases. The relations between the found models (model type, function and the proposed objective in each work) and the bovine infectious diseases, and the different techniques used and the works over infectious disease in humans, are presented. The outcomes obtained in this systematic literature review provide the state-of-the-art inputs for research on models for the epidemiological analysis of infectious bovine diseases. As a consequence of these outcomes, this work also presents an approach of EiBeLec, which is an adaptive and predictive system for the bovine ecosystem, combining a prediction model that uses machine-learning techniques and an adaptive model that adapts the information presented to end users.

Keywords: bovine; computer applications; epidemiology; infectious diseases; machine learning

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1. Introduction

Human health is a subject of vital importance across the world and is closely related to animal health [1,2]. Animal health has generated worldwide movements that involve both governments and organizations from different sectors. According to the Food and Agriculture Organization of the United Nations (FAO) [3], changes in livestock production increase the potential for new pathogens to emerge, grow, and spread from animals to humans globally. Healthy animals are closely related to healthy people and a healthy environment [3]. It has long been known that 60% of known infectious human diseases are of animal origin (domestic or wild animals), as well as 75% of emerging human diseases [4]. Furthermore, the regular feeding of populations with noble proteins derived from milk, egg, or meat is vital, and their lack constitutes a public health problem [3]. Experts in [3,5] indicate that 20% of global production is lost due to diseases that affect animals, suggesting that even animal diseases that are non-contagious to humans could generate serious public health problems due to the deprivation that they can cause [5]. These topics are addressed from different fields of science such as medicine, veterinary medicine, economics, informatics, statistics, and mathematics, generating new fields of research and development that seek to mitigate losses and join efforts to improve human health welfare.

For this systematic literature review, it was assumed that a 'model' is a representation of reality that is communicated through drawings, graphs, or mathematical expressions. Mathematical models are scientific models that use mathematical formalism to express relationships, variables, parameters, relationships between variables, operations, and entities to study behaviors of complex systems in situations that are difficult to observe [6].

Because of this, models play an important role in prediction, evaluation, and control of possible outbreaks of infectious diseases in humans and cattle, being developed by researchers from different areas of knowledge and who use technologies to find solutions for the various problems that are generated.

Models have been in use in health, education, and agricultural business for several years. There is a growing number of models that involve more themes, characteristics, users, etc. Each area requires the use of methodologies [7], strategies, processes, and algorithms that provide adequate support so that the models can reach their intended purpose.

Infectious diseases can be transmitted between individuals [8,9], whereas non-infectious diseases (such as arthritis) can be developed throughout an individual's life [10]. In the epidemiology of infectious diseases, the main risk factor for contracting them is the presence of infectious cases in the local population. This is reflected in the mathematical models presented in [11] for tuberculosis, in [9] for influenza, and in [12] for ebola. In the case of cattle, infectious diseases (such as bovine viral diarrhea—DVB [13], bovine leukosis [14], tuberculosis [10], and neospora [15]) can be transmitted vertically when a cow becomes pregnant and transmits the infection to the calf, or horizontally when the bovine ingests contaminated food or water, or has contact with infected animals [16,17]. The pathogens of these diseases use different means for transmission. They are endemic diseases, and diagnosis is not easy since they require laboratory tests [15] to confirm the presence of the virus, which generates costs for farmers.

As mentioned in [7], Daniel Bernoulli in [18] proposed an epidemiological model for smallpox that provided the basis for working with mathematical models in epidemiology [1,9,19]. On the other hand, Kermack and McKendrick [6], as well as MacDonald and Enko [20], show significant advances that are still in use today in epidemiologic studies. In epidemiology, models can be used to understand the dynamics of the epidemic [21] and the spread of infectious diseases by working with scattered observations [22] for individual-level knowledge of epidemiological factors, for inference about missing data, and for the incorporation of the latest information. These models can clarify how the disease is spreading and provide timely guidance to policymakers [23]. The term 'computational epidemiology' is often used when computer tools are used, such as in [24–27].

Epidemiological analysis involves applying statistical analyses, mathematical formulas, and other types of techniques to describe the epidemiological characteristics (e.g., age distribution, gender, occupation, and pathogen) of the emergence of a disease [28,29], the incidence of the disease by age and gender, and the total incidence of cases in the population during the study period, as well as for the analysis of mathematical models to describe the seasonal distribution of cases, to conduct risk factor analysis, to identify and diagnose health problems on farms, and to assist in decision-making for disease prevention and control [30].

In human health, computer tools have been developed to maintain patients' medical records, medication records, billing records, and logistics information. There are also investigations where they have used informatics for the diagnosis of diseases, the organization of treatments and decision-making (such as in the choice of medications) [30], the detection, analysis, prevention, and simulation of diseases [31], the generation of public health policies [32], and the management of diagnostic images using machine-learning algorithms [33]. In veterinary medicine, the use of computer tools also has been subject to research and advances. In [34], an expert system is used to evaluate the eradication of a disease, and in [35], machine-learning techniques are used to estimate the probability of infectious disease transmission via the movement of animals between farms.

This paper presents a systematic literature review relating the prediction models, the epidemiological analysis of infectious bovine diseases, and the set of procedures and resources (which will be called techniques) that are used to represent the epidemiological analysis. The proposal of an adaptive and predictive system for the bovine ecosystem is also briefly presented. It is worth mentioning that when performing a systematic literature review, some of the results are works on infectious diseases in humans.

Therefore, the following research questions were posed:

i. In bovine epidemiological analysis, what are the infectious diseases, the models, the techniques, and the approaches of the works found in the literature?
ii. For epidemiological analysis in animals, what are the infectious diseases, models, and techniques found in the literature?
iii. In human epidemiological analysis, what are the techniques and models found in the literature, and which of them are applicable to bovine epidemiological analysis?

To answer these questions, in the articles selected for the systematic literature review, a number of criteria have been found that are explained in the corresponding section, and based on these criteria, the main topics of this article will be explained.

This article is structured as follows. Section 2 explains the method used to select the articles that were considered for the systematic literature review carried out in this work. Section 3 presents the results of the systematic literature review and the article classification system. The contributions of the systematic literature review are presented in Section 4. In Section 5, an approach to EiBeLec is presented, which is an adaptive and predictive system for the bovine ecosystem. Finally, Section 6 presents the conclusions and implications for future work.

2. Method for Systematic Literature Review

For this systematic literature review, we consider the proposal of [36], where six steps are suggested (data recovery, pre-processing, creating and normalizing the network, creating scientific maps, analysis and visualization of the results) to analyze a field of research and to detect and visualize themes and subtopics in order to analyze and track evolution over a continuous period of time. To perform the steps discussed in this work, specialized software will be considered to help in the relation of keywords, query criteria, generation of networks, and analysis related to the query criteria and specific periods.

In [37], nine tools designed for the analysis of scientific maps were studied, evaluating five aspects: preprocessing methods, bibliometric networks, normalization measures, types of analysis allowed to be carried out, and the documentation and help available on the tool. Considering the results of this analysis, SciMAT [38] was used in this work. The objective of this tool is the analysis of scientific maps, allowing study of the evolution of the topics over periods of time, incorporating processing techniques to detect similar elements, and thus, obtaining the respective networks, the relations of the topics, and finally, reaching the most representative articles. SciMAT can organize the information by groups of authors, references, or keywords, detecting duplicates and misspelled words. In [36], the six steps to be performed when using this tool are explained. In this work, the information was organized by groups of words, making the combination of the words, their co-occurrence, and their frequency established for each word. The following subsections explain how these six steps were developed in this work.

2.1. Data Retrieval

This step starts by selecting the bibliographic databases to make the queries. In this case, Scopus, IEEE Xplorer, and ACM were considered for the period 2010–2022. Afterwards, several consultations were performed with different criteria such as “simulation”, “diseases”, “animals”, “infectious disease”, “bovine”, “Cattle”, “cow”, “mathematical model”, and “model”. Based on the results found in these searches, it was concluded that the systematic literature review process would be conducted with the search equation

'(TITLE-ABS-KEY ("infectious diseases") AND ("models") AND ("bovines" OR "cattle" OR "cow")) AND PUBYEAR > 2010'. This search was performed in each of the three databases.

2.2. Pre-Processing

From the queries made in the three bibliographic databases, the files were downloaded (in RIS format) with the following fields: title, keywords, abstract, authors, and year of publication. These files were brought into the SciMAT tool.

Data usually have errors, misspellings, and wrong author names. In some cases, it is necessary to add to or complete the information. For these reasons, the pre-processing step is necessary to clean the collected data and, in this way, improve their quality [37].

In this case three processes are considered to clean the data:

- Unification of duplicate or erroneously written elements. SciMAT allows the researcher to apply a filter by which it finds similar words and creates groups of these words.
- The temporal division of the data in different time periods. This enables analysis of the evolution of the topic.
- The reduction of data from the selection of the most cited documents and the most frequent words.

At the end of these processes, the most significant data and the relationships of the most important units of analysis remain.

2.3. Create and Normalize the Network

The objective of this step is to integrate the search criteria, the relations that were found, and the topics and subtopics so that, with this information, the search is refined. The process for making the network in SciMAT requires that the information be organized by periods. Considering that the searches covered years 2010 to 2022, the periods considered were: 2010–2012, 2013–2015, 2016–2018, and 2019–2022; the unit of analysis was 'keywords', the reduction of the data was defined by considering the elements that appear in at least three documents, and the way of constructing the network was by co-occurrence of words. SciMAT allows the user to choose between different measures of similarity (association strength, equivalence index, inclusion index, Jaccard index, and Salton's cosine) [37]. In this case, the equivalence index with a value equal to 1 was used as a measure of similarity in normalization.

2.4. Scientific Map

Two aspects must be considered to build the map:

- Reduction of the dimensionality of the data to make results more understandable. SciMAT allows data to be filtered using a minimum frequency threshold. In other words, only the element that appears in almost n documents over a certain period will be considered.
- Application of clustering algorithms, fulfilling the condition of having great internal cohesion between elements. In this case, the Simple Centers algorithm of SciMAT was used to detect the groups.

It is worth mentioning that the information obtained and the type of map may vary depending on the type of technique used to generate the scientific map. SciMAT adds the number of documents by default as a performance measure. In addition, citations from a set of documents are used to assess the quality and impact of the groups. Figure 1 shows part of the results of the scientific map generated by SciMAT.

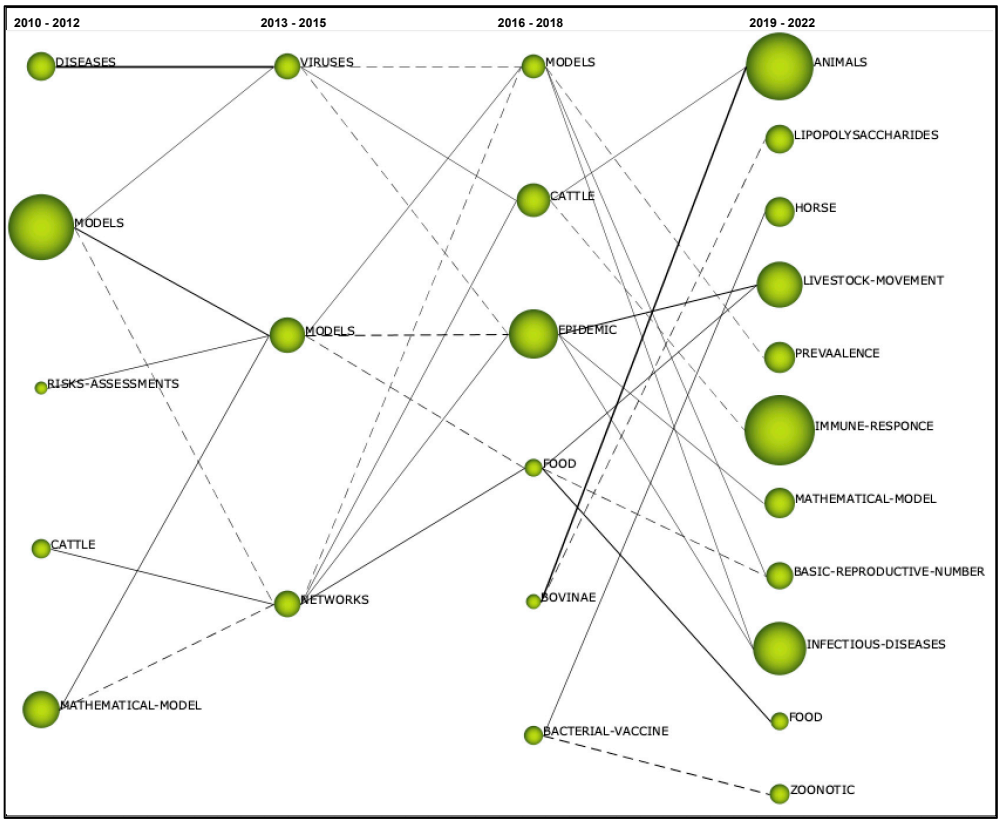

Figure 1. Thematic importance of the relation of infectious diseases and models (term 2010–2022).

2.5. Visualization

Figure 1 shows the most outstanding themes in each analysis period. The size of the sphere represents the importance of each topic. Some are repeated in different periods, but others are not. The lines that go from one period to another indicate the relation between the themes. The dashed lines show a weak relation, the solid lines show a standard relation, and the thick solid lines show a strong relation.

2.6. Analysis

Starting from the search equation in the databases using the SciMAT tool, the scientific map is formed, which is made from several graphs. Figure 1 is one of them, and in each period, the keywords are not the same. New topics appear with their associated keywords and others disappear. On the other hand, there is a subset of keywords that were kept.

These results demonstrate the importance and the relation between keyword groups and research topics. Initially, Figure 1 shows that in the different periods, the most important topics are epidemiology, diseases, mathematical models, and cattle. In the four periods considered, there is a relationship of models with different themes. However, the relation between these issues and diseases shows that there are few works on these topics.

Furthermore, it can be concluded that these results generate workspaces in which new relationships can be proposed as guides for future work with topics that are not present and topics that do not have a relation. In the studies considered, there is no evidence of the use of machine-learning algorithms to perform epidemiological analysis of infectious diseases in cattle.

3. Results of the Systematic Literature Review and Article Classification System

When searching for articles in the databases, a total of 1721 documents were obtained. Applying the criteria established in the search equation to filter in the SciMAT tool resulted in 271 articles meeting these criteria. Since the keywords used in the search may not be

totally related to the main topics of the research, a new filter is applied [29], in this case manually, as can be seen in the criteria setting, which consists of analyzing the title, the abstract, the keywords, and the conclusions, to determine which articles are directly related to the research topics. After completing this step, the selected articles were reduced to 99. Figure 2 illustrates the process followed to select the articles [39].

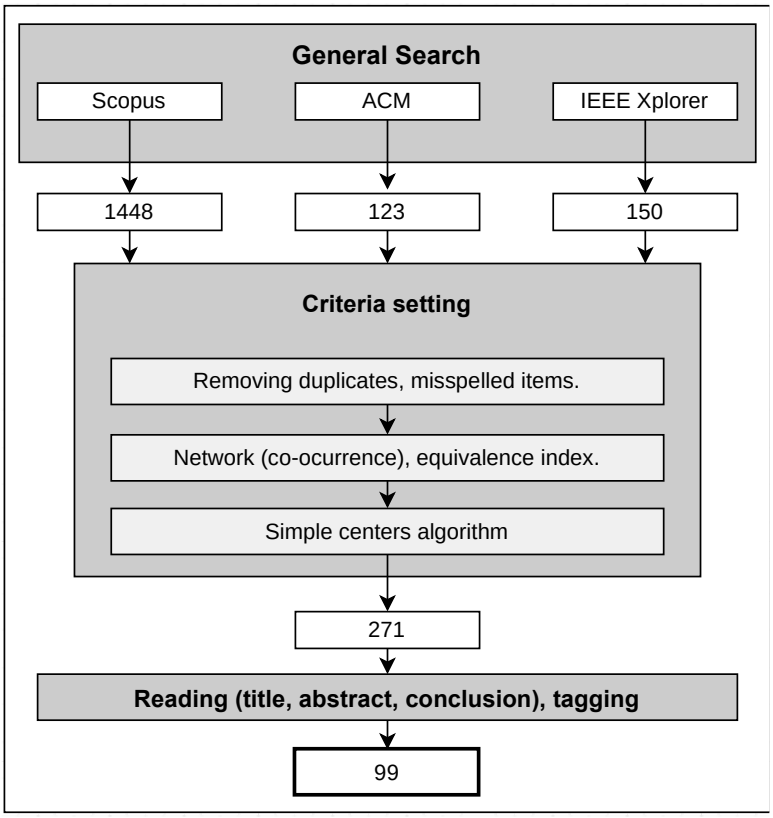

Figure 2. Flowchart.

To classify the 99 articles, 21 criteria organized into five groups (Purpose or Objective, Application Environment, Epidemiological Analysis, Techniques Used, and Software) were considered. These criteria were considered because they are mentioned in the systematic literature review of articles and are related to the research topics, organized according to whether the infectious diseases are in cattle, in other animals, or in humans. Afterwards, the groups that were considered are explained and the results of comparing the articles by criteria in each group are presented.

Purpose: Table 1 shows the result of classifying the articles according to the five criteria that help answer the question, "What is the main purpose or objective of the work?"

Table 1. Result of comparing related job–purpose or objective group.

Purpose or Objective	Bovine	Animals	Humans	Total
Behavioral analysis	[19,32,40–55]	[23,56,57]	[12,58–63]	28
Disease diagnosis	[8,14,22,41,48,49,52,64–73]	[74]	[28,31,33,59,61,62,75–87]	37
Variable analysis	[13,34,46,50,53,71,88–93]	[94–96]	[60,87,97]	18
Analysis of movement or displacement of hosts (animal where a parasite is housed) that have the disease	[11,25,45,49,52,98–102]	[35]	[12,103]	14
Disease spread	[8,19,22,23,32,34,43–47,53,54,67–70,88,98,100,104–107]	[56,57,74,95,96,108–112]	[9,12,28,59,61,76,81–83,97,113–117]	52

Application environment: It is necessary to know if the results of the analyzed works are addressed to expert users or to the public, in which scenarios the disease is studied, and if

there is any evidence that the results obtained have been applied in a real case. As all the works are not directed to the same users and scenarios, three criteria were defined; Table 2 presents the result of the classification.

Table 2. Result of comparing related job–application environment group.

Application Environment	Bovine	Animals	Humans	Total
Recipient: expert users, the public, or both	[13,14,22,32,34,45–49,64,68,88,92,93,98–100,104,106,118,119]	[23,56,57,74,94–96,108–110]	[9,12,28,31,59–63,75–81,83,97,114–117]	56
Setting (hospital, ranch, farm, city, etc.)	[11,40,41,44,47,66,67,89,90,104,118,120]	[35,56,108,111]	[28,77,97]	19
Applications in a real case	[8,22,41,53,65,70,88,105,121]	[74]	[9,33,59,61,62,81,83,85]	18

Epidemiological analysis: Epidemiological analysis is understood as the study of the distribution of diseases. In other words, epidemiology describes the distribution of the disease in terms of the agents involved, describes the places and times in which it occurs, and studies the causal or risk factors for these diseases [27]. For the epidemiological analysis of bovine infectious diseases, the five criteria shown in Table 3 are taken into account.

Table 3. Result of comparing related job–epidemiological analysis group.

Epidemiological Analysis	Bovine	Animals	Humans	Total
Demographic	[21,22,25,32,34,41,45–47,49–51,53,64,66,68,69,71,72,88,91,98,100,104,105,107,118,122,123]	[23,35,56,57,108,109,111]	[9,12,28,33,60,62,75,76,80,83–85,87,97,113,116,117]	56
Aspects related to farms, pens, and places where each host with the disease is found	[8,11,14,19,21,22,34,43–45,48,49,51,53,55,67,69,71,88–91,98–101,104,105,118,120,123]	[23,35,57,74,96,111]	[116]	41
Relationship of climate, temperature, rain and droughts	[54,93,118]	[111,112]	[33,82,84,86,115]	10
Age, gender, race, symptoms, and risk of the disease	[8,13,21,25,34,44,46,48,50,52,54,55,64,68,70,90,100,102,106,120,123,124]	[56,111]	[7,9,28,33,59–62,77,79,80,83,84,86,97,103,113,114,116]	48
Clinical data	[41,65,105,119]		[31,33,63,76,77,83,87,97,113,115]	15

Techniques used: refers to the mathematical process or algorithms used to develop the objective of the work. Table 4 shows the works according to the five techniques used:

Table 4. Result of comparing related job–techniques used group.

Techniques Used	Bovine	Animals	Humans	Total
Bayesian networks	[44,65,71,89,99,104,106,119]	[56,111]	[58]	12
Markov chains	[22,41,50,53,64,66,70]		[60,78,79,84,97,114]	13
Logistic regression	[14,19,54,67,120,123]	[108,111]	[31,75]	10
Differential equations	[19,25,32,34,43,49,52–55,68,72,88,90,105,107,118,121,125]	[23,35,57,94–96,109,110]	[12,28,61,62,117]	31
Contact networks	[8,11,21,34,45,49,52,69,91,98,100,101]	[35]	[9,76,80–82,85]	19
Machine learning	[13,40,92,93,124]	[35,74,112]	[33,59,77,80,83,84,86,103,113,115,116]	20

Software: software is used to complement the epidemiological analysis. In this group, it is considered whether the used software was specifically developed for this or if a commercial software was used (Table 5).

Table 5. Result of comparing related job–software group.

Software	Bovine	Animals	Humans	Total
Use of commercial software	[13,14,34,40,43,45,46,48,49,51,52,64,68,91–93,102,107,119]	[56,57,96]	[12,33,63,75,76,85,86,97,103,116,117]	36
Specific purpose software development	[11,21,48,100]		[9,28,31,81,84,87,97,113–115]	14

From the systematic literature review and the 21 criteria analyzed, it can be verified that no studies that consider the spread of infectious diseases in cattle using machine-learning techniques to relate aspects of the epidemiological analysis (race, gender, age, contact between animal species and clinical data) were found.

The results presented in the tables, after performing the systematic literature review and verifying the relation with the criteria, are used to answer the questions, formulated in the introduction, in the following section.

4. Contributions of the Systematic Literature Review

From the analysis of the 99 selected articles, the research questions proposed and previously mentioned will be answered.

4.1. In the Bovine Epidemiological Analysis, What Are the Infectious Diseases, the Models, the Techniques, and the Approach of the Works Found in the Literature?

In the case of bovines, the infectious diseases that were considered for the analysis (assuming that these are diseases present in many countries [42] and/or that generate social problems [105], economic losses [98], health problems in humans [48], low quality in milk and meat [13,43,120], and restrictions in livestock movement [99]) are tuberculosis [46,65,89], salmonella [69,126], brucellosis [51,55,101], bovine viral diarrhea (BVD) [13,14,32], foot and mouth disease [41,50,91], and bovine mastitis [47,90]. Of the works, 50% are aimed at personnel who are experts in bovine infectious diseases. Only four works (8%) develop software to help achieve the objective, and eighteen works (33.9%) use computer tools to analyze the information.

Table 4 shows the relation of the works according to the technique used, such as Bayesian networks [46–48,63,73,78], Markov chains [22,41,45,49,67,68,74], logistic regression [14,19,50–52,75], differential equations [19,25,31,33,43,54–56,59,60,62,65,69,76,77,79,115], contact networks [19,62,64,70], and machine learning [13,92,93]. The most-used technique is differential equations, while machine learning is presented in five jobs. In these works, these techniques were used in different ways: in some cases for disease prediction, in other cases to evaluate the vaccination behavior in herds [98,107], to evaluate the behavior of livestock when moved from one farm to another [11,45], or to detect and classify diseases with images via machine learning [40,124].

The focus of these works is diverse. For example, there is analysis of the behavior of cattle herds inside farms and the movement of livestock between farms, analysis of the effects of incomplete vaccination on cycles, simulation of the spread of a disease, and analysis of the practices carried out by farmers or breeders in selected farms. Data are based on variables related to vaccination, the study of pathogens, the spread of diseases by contact with wildlife, the number of infected animals, and the symptoms presented. Surveys [90,105], the results of previous studies [46,64], and systematic literature review [73,118] are used to collect the information, and in very few cases, studies use the information systems of government entities [69,123] or associations with updated information [118].

It is noteworthy that most of these works are focused on the prediction of diseases based on behavior and disease diagnosis [19,48,55]. These are theoretical works where the results are presented in tables and graphs that must be interpreted by experts who know about veterinary medicine.

The analysis performed helps to characterize bovine infectious diseases, identify models, and the criteria that must be considered for the selection of the model, depending on the disease. On the other hand, as can be seen in Table 3, these studies consider neither the temperatures of different geographical areas nor rain and drought. Furthermore, they do not relate the results of clinical data with other criteria of the epidemiological analysis.

One drawback in bovine infectious disease research is the lack of structured and updated information, since capturing information in animals is expensive and it is not easy to update. In many works, including [61,67,100,106], it was found that in order to perform the simulations, synthetic populations must be generated from seed data; with each simulation run, the system must continue to be fed.

One challenge for models for epidemiological analysis is the need for a proactive early warning disease detection system that can detect, identify, and contain pathogens with epidemic potential before spreading [127]. Another important factor is the weather,

particularly due to changes that have happened and will continue to happen in the future, such as rising temperatures. Changes can trigger the introduction and spread of many serious, climate-sensitive infectious diseases [126], such as mosquito-borne diseases including malaria, dengue, and viral encephalitis.

4.2. For the Epidemiological Analysis in Animals, What Are the Infectious Diseases, the Models, and the Techniques Found in the Literature?

Traditional techniques such as differential equations [23,80–82,85,86,88], logistic regression [108,111], and Bayesian networks have been identified [56], and they are still important for creating models that simulate infectious diseases and also for simulating animal behavior in their movement between farms and cities. The use of these techniques, described in the different works, shows the types of variables that must be defined, what should be considered in each case, and what is the most appropriate technique considering the objective of the work and the disease. Also, the use of artificial intelligence techniques, especially machine learning [32,85,86], is gaining strength as a means to generate data and for the capture, analysis, and processing of information.

Table 1 shows some of the different works that have generated significant contributions in the knowledge and behavior of infectious diseases and in the identification of variables that must be considered to perform simulations of a disease, such as movement and restrictions that must be taken, as well as the needs that arise in each job to achieve the stated objectives. These works are not oriented toward decision-making and do not consider end users (Table 2), but use traditional techniques and are aimed at simulating the transmission of parasites. Furthermore, the development of computer tools for the simulation of infectious diseases is deficient because there are no systems that contain updated information since it is not reported [118]; these are not used in disease surveillance and these systems are not open to the public in general. The tools developed are for expert users with knowledge of infectious diseases [56] or topics related to the consequences of the spread of infectious diseases [57].

4.3. In Human Epidemiological Analysis, What Are the Techniques and Models Found in the Literature and Which of Them Are Applicable to Bovine Epidemiological Analysis?

Study of infectious diseases in humans works from different approaches, and countries throughout the world are working to find solutions to the different problems that arise from the epidemics and pandemics of these emerging and re-emerging diseases [7]. Cases such as AIDS [7,10], H1N1 [58,93,99,100], dengue [2], malaria [49], and COVID-19 [63,117] have been studied as diseases that cause death to millions of people worldwide and that generate economic losses.

It was found that these works are addressed to experts with knowledge about the diagnosis, treatment, and risks of diseases [59]. It was also evidenced that the information is structured to cover the main criteria of the epidemiological analysis [2].

The most-used techniques in these works are Markov chains [91,92,96,97,108], differential equations [28,110,111], contact networks [9,92,93,95,98], and machine-learning algorithms [93,96,99,101,102,104,105,107,113,115]. Different studies use mathematical models that range from statistics on social media [24] to machine learning [103] and have different applications in the health field.

To support the epidemiology of infectious diseases in humans, there are computational tools that present the results of the analysis performed, as shown in Table 5. These works considered various aspects, such as the type of application, the users who use the tool, the disease, etc.

Some of these works are described below:

- A simulation tool where an infectious disease is programmed, and the tool's response is the location of the clinical facilities able to attend to it [97]. The C ++ programming language was used to develop the tool. The spread model is used to create hypothetical large-scale health events to be used by officials to plan events. To create a disease

spread and facility location simulation, the researcher can run the disease spread and clinical facility location models simultaneously and seamlessly.

- ISIS is a web browser based on a modeling and decision environment for public health epidemiologists [81]. Its components are a web user interface, databases, and models that connect to the user through middleware, the rules and models to generate the simulations, and a structured and semi-structured database management system. One aspect to highlight is the Synthetic Information Library—SIL, which contains all the information necessary to create, execute, and analyze experiments. In this case, they use machine learning methods to manage complex unstructured and semi-structured data.
- EpiSimdemics is one of the first algorithms to simulate epidemics in large, real social networks [82]. This article defines computational epidemiology as the development and use of computer models to understand the spatio-temporal spread of the disease through populations. The main design objective of EpiSimdemics is to explore the effects of complex pharmaceutical and non-pharmaceutical interventions on the spread of infectious diseases through realistic populations. In this case, they use a synthetic population that is generated from the United States census.
- Epinome is a tool that allows users to reproduce simulation scenarios, investigate a deployment outbreak using a variety of visualization tools, and direct the simulation by implementing different public health policies at predefined decision points [114]. Epinome records user actions—for example, tool selection, interactions with each tool, and policy changes—and stores them in a database for later analysis. A psychological team can use that information to study strategies that users use to search for information on diseases and possible outbreaks.
- MiTAP was developed based on natural language for the monitoring of infectious diseases [83]. It captures information from different sources such as emails, search engines, news, etc. During the processing phase, information is normalized using machine learning rules. It is a tool that helps reduce the information overload that results from staying informed from different sources.
- PopHT is a semantic web application that automates the processes of integration and extraction of massive amounts of data from different distributed sources to support the measurement and monitoring of the health system [31]. The main objective of this project is the integration of heterogeneous information: public health policies, information in health centers, and information on diseases.
- Spatiotemporal Epidemiological Modeler (STEM) is a platform developed to create spatial and temporal models of infectious diseases in humans. It uses geographic, population, demographic data, transportation information, and basic disease models. The platform is based on systems of differential equations [84]. In STEM, the researcher starts by composing a scenario and reporting information on the infected population, the city where the population is located, and the target city for evaluation. The models generated facilitate study of the spread of infectious diseases. However, there is no evidence that they consider the handling of contextual variables, and there is no user classification for the management of the application.

These works present a graphical interface to capture information and present the results of the queries. The results are presented in the form of tables and graphs. They are applications for users who are experts in the field and who have knowledge in the analysis of epidemiological data. They are oriented toward infectious diseases in humans, and the data used are from censuses that have been carried out in different years.

On the other hand, in some studies [93,104,112], it was shown that the use of tools allows description of the progress of a disease using models. These models allow clinical and expert information to be added so that researchers and decision-makers can forecast disease progression and implement control strategies.

The computer tools developed are found within the group of information systems for research on topics related to the management of the context of patients and diseases and the different users involved in the processes.

Human health research is aspiring to conduct animal health projects. It is important to mention that research conducted in human health serves as a basis for working with animals, and in different investigations, this research offers a reference for use of the models, techniques, computer tools, and strategies that were employed in the capture and analysis of information.

For these reasons, some contributions from these works can be used in bovine epidemiological analysis:

- Integration of epidemiological information with clustering techniques to determine potential areas of disease outbreaks based on daily surveillance information [2].
- Analysis of the mobility networks of people with a disease [126] allows the generation of data that can reconstruct the transmission path of the disease. Each node represents a location (for example, a farm) in space. The links between these nodes are connections between these locations. In contact networks, the nodes are individuals and the links are contacts that, therefore, represent possible transmission routes between individuals (for example, by showing how much time infected people spend together).
- The speed at which diseases travel through populations depends not only on the effective distance between locations [103], but also on how the disease is transmitted between people in those locations. This allows us to understand more about the transmission of diseases.
- The use of machine learning in human health has different approaches. For example, one study predicted the incidence of salmonellosis and its transmission from animals to humans by means of a neural network [116]. In the diagnosis of diseases such as cancer [85] and diabetes [113], the use of machine learning is more accurate because it considers the different symptoms of the patients with a greater quantity and quality of data.
- Machine-learning algorithms are used to analyze and interpret large amounts of data in an automated way, delivering accurate and actionable clinical information [95,98].

The results of these studies generate new treatments and different ways of controlling epidemics that allow us to learn techniques and algorithms and develop computer applications [81] and disease control strategies [23,113]. They can be studied and adjusted for animal diseases to make developments in line with this research area.

5. EiBeLec: Predictive and Adaptative System

In the epidemiological analysis for infectious diseases in humans, machine-learning algorithms are being used in the diagnosis of diseases, in the simulation of possible outbreaks, and to process more data and obtain better results in diagnosis. Furthermore, models related to Markov chains, Bayesian networks, and differential equations continue to be used to diagnose diseases, detect symptoms, relate diseases, and seek treatments. In relation to computer tools, these are addressed to users who are experts in epidemiological analysis.

On the other hand, in the epidemiological analysis of cattle, the models used to simulate the presence of diseases are based on differential equations, Markov chains, and Bayesian networks, while in the case of livestock movement, contact networks are used. In these cases, the development of software to complement these projects is scarce and the way of presenting results is theoretical.

This work, in performing a systematic literature review, analyzing the results, and reading the related works, presents a first approximation of an adaptive and predictive system for the bovine ecosystem, which we have called EiBeLec.

An opportunity was found to build a system that considers [16,17]: (i) the process of prediction and simulation of the spread of infectious diseases that are not subject to official control affecting the ecosystem; (ii) the use of machine-learning algorithms in the predictive model; (iii) the actors of the bovine ecosystem and their preferences; (iv) an adaptation

model that contains the profile of the disease, the context, and the user; and (v) the visualization of information considering the actors. Moreover, EiBeLec offers various services: (i) the map referencing service; (ii) the route service; and (iii) the notification service.

This will be a decision-making support system that will allow for the capture of information from the user's context for later processing. The visualization of the results will be adapted to the actor who requires them and will allow for better interpretation by easing decision-making. It is important to mention that the decision-maker is the actor, not the system.

The proposed adaptive and predictive system is made up of different components [16,17]. Figure 3 shows the general structure and the relationships between the components: (i) actors in the dairy chain in the department of Boyacá who fulfill two roles: that of users who are providing information and that of users who are using the system; (ii) information sources that supply the system with data (variables related to livestock, infectious diseases, and the actors involved in the bovine ecosystem) and relationships; (iii) the context, whose data are stored in three repositories: profiles of the bovine ecosystem, diseases, and actors; (iv) a predictive model of infectious bovine diseases that will be explained in detail later; (v) an adaptive model that takes into account the context (actors' profile, bovine ecosystem profile, and disease profile) and the results of the predictive model to adapt the information that is presented to end users through the services that the system offers; and (vi) previously mentioned services that are used by the end users of the system. Furthermore, each of these components has subdivisions and activities that complement the system.

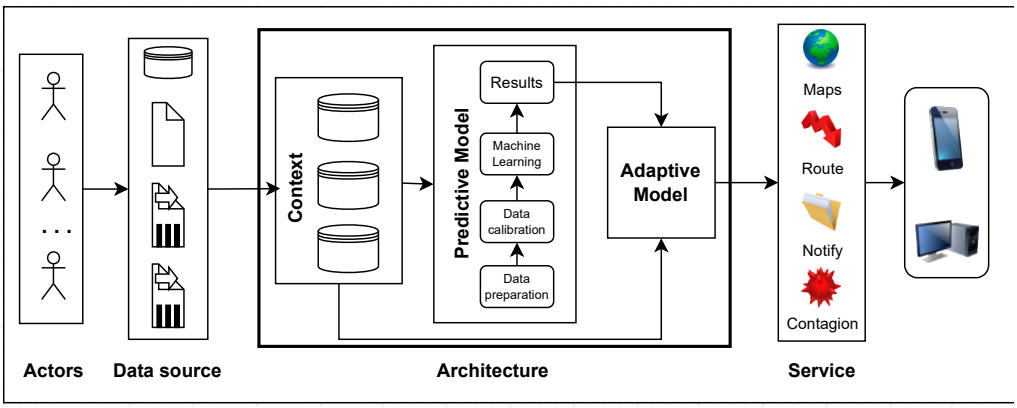

Figure 3. Adaptive and predictive system proposal: EiBeLec.

Through the main themes of the systematic literature review, the defined criteria, and the analysis that was carried out to answer the research questions, it was observed that machine-learning algorithms have different types of applications in human health, but in the case of animals, their use is not very frequent. It has also been observed that content adaptation is not widely used in the development of information systems. For these reasons, we propose the development of a predictive and adaptive system that includes:

- A predictive model. Laboratory data on a sample of bovines, among others, may be available for the prediction of infectious bovine diseases, but the relationships that may exist between these data and the risk factors of the disease are not known. This predictive model must integrate clinical laboratory data with data from risk factors (data preparation), perform a calibration of these data (data calibration), use machine-learning algorithms for the prediction process, and deliver, via said algorithms, results to the actors in the bovine ecosystem. Figure 4 shows the information to be presented to the government actor. In the upper-left part are the positive control (CP) and the negative control (CN) obtained from the clinical laboratory and the risk factors obtained through surveys and visits to farms. These are other variables to be validated in the model. In addition, the map presents the results of the predictive model. In this case, there are two possible infection outbreaks. The susceptible, exposed, and

infected values provided by the model are shown in the lower part. These values can be adjusted to see the behavior of the spread of the disease.

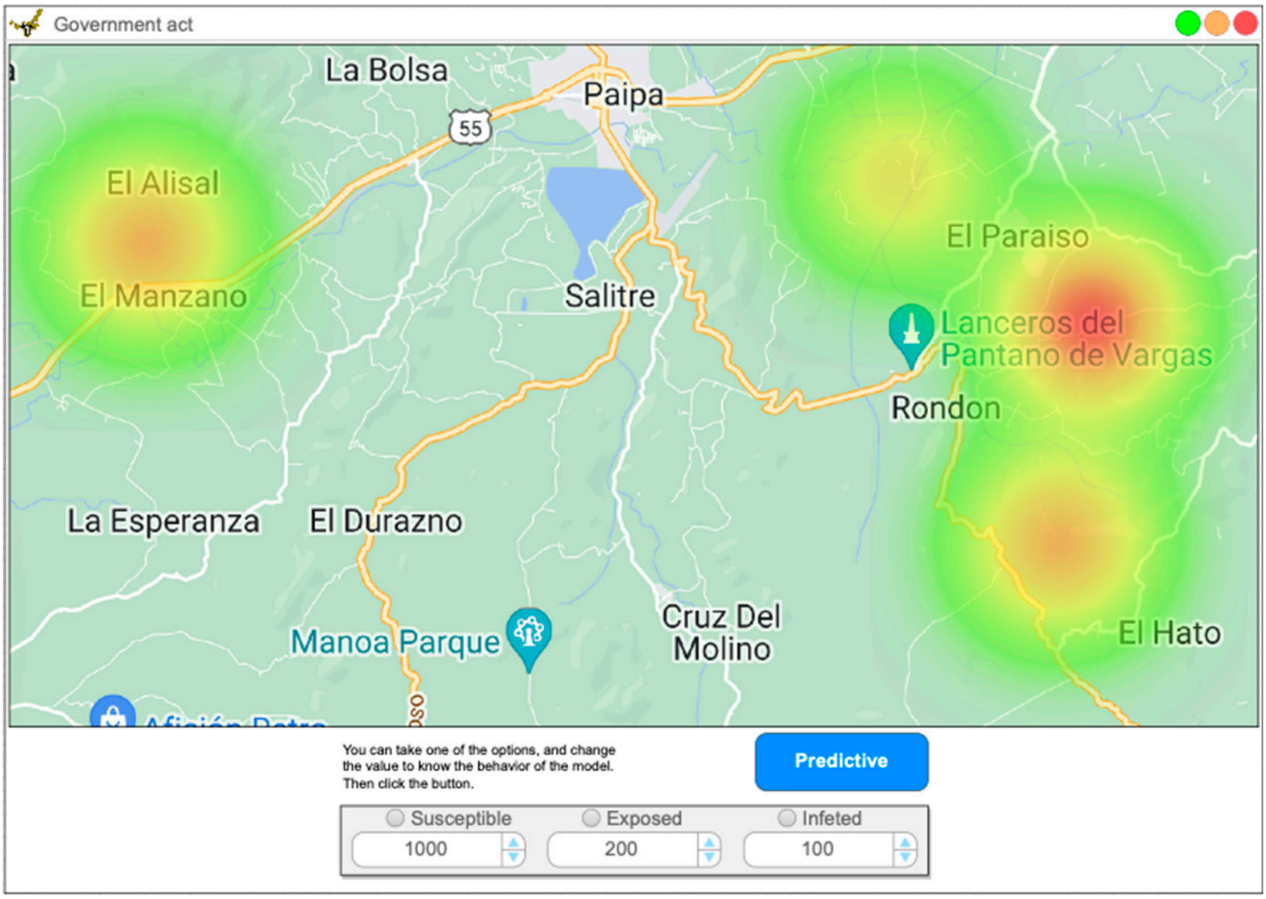

Figure 4. Government user information presentation module.

It is important to note that, after building the predictive model, it is necessary to validate the machine-learning algorithm through experiments aimed at bovine infectious diseases. The data collected on the diseases are divided into two sets: training and validation. The largest dataset is used to train the model, and a smaller dataset is used to validate the model. Finally, to calibrate the model using metrics, the results obtained are analyzed.

- An adaptive model. This takes into account the context (actor profile, bovine ecosystem profile, and disease profile) and the results of the predictive model to adapt the information that is presented to end users through the services that the system offers. In this adaptation model, the actor's profile is used in order to adapt the content and the display of the information that will be delivered to end users. For example, a user with the livestock profile through a service called notification is presented with information regarding the presence of the disease on his farm and in neighboring areas, as can be seen in Figure 5. In this case, the red dots indicate where the infected animals are. In the case of a user with the government profile, by using the service called 'contagion', the system presents the user (without the need to fill out any format) with a map of the department and the ability to select a desired area (municipality, farm, etc.) to view information on the presence of the disease and the behavior of its spread (see Figure 5).

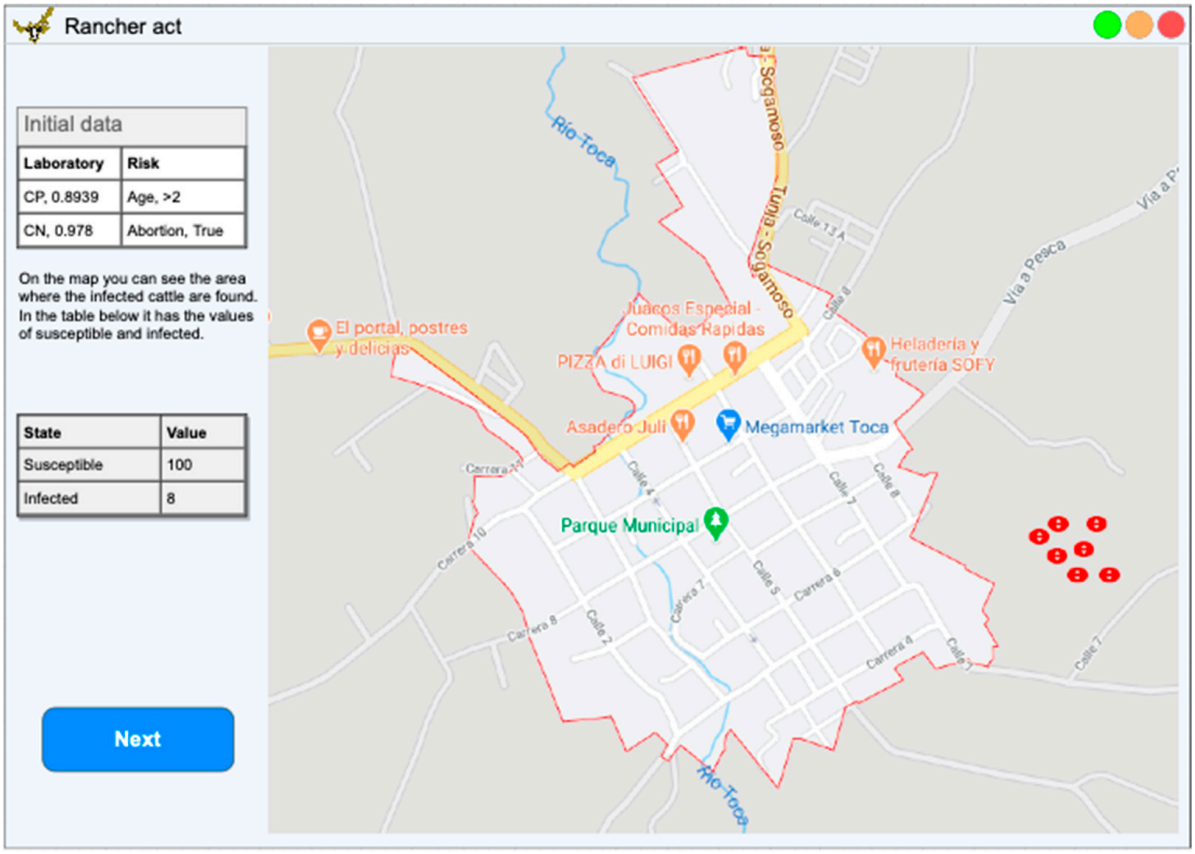

Figure 5. Presentation of the information to the livestock user.

6. Conclusions and Future Work

Based on the defined criteria and the analysis carried out in each case, it was observed that the use of models for epidemiological analysis has made many contributions to human and animal health. The systematic literature review, with the aim of answering the research questions asked, presented different results, finding works related to human health that have made advances using machine-learning techniques in the capture, analysis, and processing of information.

In addition, the use of machine learning to work with variables of diseases in humans presents proposals for the management of clinical data, relationships between variables, and models that allow diagnoses of diseases to obtain better results [13].

On the other hand, we note that the application of these studies in bovines is theoretical and that information is not updated or continuous because there are various drawbacks, such as the lack of organization in the collection of information and in the reporting of diseases, and because there is not an adequate characterization of the variables related to each disease. In this case, the most important advances are in the analysis of the movement of livestock between farms and cities, since they use contact network techniques as an innovative means to verify the relationships of livestock, disease, and how infection spreads in other individuals in the herds.

Furthermore, real-time epidemiology [27] is a rapidly developing area within public health which seeks to support policymakers in near real time as an epidemic develops. By applying these techniques in practice, researchers face the usual challenges: noisy and insufficient data, scarce resources, multiple objective functions, and little time for decision-making [104]. Solving these problems will require a multidisciplinary approach and close collaboration between computer scientists, statisticians, public health experts, and policy analysts [23,27]. Such an approach would make use of mathematical models and computer

tools to effectively and efficiently manage the information needed today [5,26], and thus propose solutions to these problems [61].

Finally, a challenge remains in the generation of machine-learning techniques, such as those used in [101,109], that would enable the design of a model that simulates the behavior of an infectious bovine disease with consideration for the geographical region, the climate, the livestock, farm, keeper, and public policymaker context.

To overcome this challenge, a first approximation of an adaptive and predictive system for the bovine ecosystem, which we have called EiBeLec, has been presented. This system includes predictive and adaptive characteristics of the proposed system. In relation to predictability, the developed tool allows integration of the data recorded by the actors with updated information, which in turn would lead to better predictions and experiments to support or reject ideas about the behavior of the disease. Adaptability is achieved by allowing the tool to be configured or adapted for the capture, processing, and analysis of information and by presentation of the results depending on the context of the user, the role they play, and the device used.

The limitations of this study include the lack of studies related to the use of the predictive models in the field of bovine infectious diseases, the small amount of raw data available, and, thus, decreased accuracy. In some cases, the entire process and development of computer tools for the analysis of infectious diseases is not reported. This research will help ranchers at all levels to quickly detect infectious diseases of cattle and receive treatment at an early stage.

For future work, the development of the predictive and adaptive model will be completed, and both the proposed system and the developed tool will be validated. To carry out these validations, it will be necessary to obtain the values of clinical tests and test the system with real users of all the profiles considered.

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