What do we have learned about mastitis spatial analysis during the last 30 years?

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SUMMARY

Mastitis is the main disease in dairy farms worldwide. However, even after decades of research, mastitis is still a difficult disease to control, because multiple environmental, management and pathogen factors are involved. This review aims to analyze the most influential research works, in order to systematize the knowledge body on spatial analysis of mastitis. Our results indicate that the main techniques found for spatial data analysis of mastitis using udder health indicators like somatic cell count (SCC) and somatic cell score (SCS), are clustering, spatial correlation, and interpolation. We finally perceived that the lack of national databases of dairy production for each country may be a limiting factor for conducting spatial epidemiology research at both the national and local levels.

KEY WORDS

Milk, somatic cell count, geographic information systems, cluster, review.

INTRODUCTION

Mastitis continues to be one of the most prevalent and challenging diseases in dairies. It consists of an inflammation of udder tissues due to various causes, including physical damage, chemical irritation, or infection caused by several pathogens. Nowadays, mastitis control in dairy farms is still difficult, although studies go back more than hundreds of years. This is caused by the multifactorial nature of the disease and complex etiology[1]. The typical outcome of mastitis is a reduction of milk yield and quality. Mastitis, since a common disease, causes a significant cost increase, mainly in terms of decreased production[2]. This disease is a worldwide issue because of the economic losses, which augmented more than 100 times in the last 40 years[3].

The somatic cell count (SCC) per milliliter of milk, is a measure of both udder health and milk quality. It can be measured for individual cows or in bulk milk from a herd. SCC data provide a more objective measure of udder health than veterinary records of Clinical Mastitis (CM)[4]. SCC and bacterial count are commonly known indicators for raw milk quality, the last reflecting the milking and storing conditions[5,6]. The log-transformed SCC—Somatic Cell Score [$SCS = \log_2 (SCC/100,000) + 3$]—follows a normal distribution, and has been broadly used to diagnose udder inflammation and examine milk quality[7].

Several risk and protective factors associated with SCS have been widely investigated in observational studies. Such factors include the influence of cow characteristics (breed, parity); management factors (milking, udder hygiene, housing system, calving conditions); environmental factors (climate), and relations among these different aspects on the SCS level[7]. Others researchers have suggested dividing them into cow, herd, management, and ecological level factors. Cow-level factors include breed, age, days in lactation, body condition score, and hygiene of the cows. Herd-level factors comprise the type of housing/bedding and herd size. Management factors involve dry-cow treatment, farmer characteristics, SCC data collection, milking equipment maintenance, buying-in and quarantine of replacements, duration of the milking process, fore-milking, milking mastitic cows first, and pre- and post-milking teat-dipping. Ecological factors encompass the time of year and geographical region[8].

Several studies dealing with animal epidemiology, surveillance, and contagious diseases monitoring have used spatial analysis, being less common the application of these techniques to production diseases like mastitis[4]. Near 200 microorganisms that cause bovine mastitis have been identified. The list includes bacteria, yeast and fungi; initial emphasis was focused at contagious bacteria, but a variety of opportunistic pathogens are frequently identified in modern dairy herds[9]. Therefore is complicated to spatially follow the disease, since different niche and ways of transmission. The main pathogens are classified as contagious (*Staphylococcus aureus*, *Streptococcus agalactiae*, and *Mycoplasma bovis*), environmental (*Escherichia coli*, *Streptococcus spp.*) and opportunistic (Non aureus staphylococci NAS like: *Staphylococcus chromogenes* and *Staphylococcus haemolyticus*)[10,11].

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Spatial distribution of herds associated to environmental factors may play a role on mastitis development. Certain climate conditions may trigger pathogen proliferation leading to an increase on mastitis burden in dairy herds[12]. Spatial variation of dairy equipment sharing may also foster the spreading of contagious pathogens between farms[13]. Mastitis spatial effects could also be explained by management practices in neighbouring farms[14].

Therefore, information of space-time patterns of herd-level mastitis may be useful for designing surveillance programs against contagious pathogens[15]. And, spatial epidemiological studies could meaningfully assist to defining strategies for dairy herd health improvement at regional or national level[16]. Thus, the purpose of this work is to present a timely review, in order to, define a benchmark on spatial analysis of mastitis, and to promote further research on it.

SPATIAL ANALYSIS

Veterinary spatial and temporal epidemiology emerged in the late 1990s, after becoming very popular in the field of human disease epidemiology. The advances accomplished in this area of knowledge have facilitated not only the identification and adjustment of thresholds of explaining variables but also the development of new hypotheses regarding disease transmission[17].

During the last 30 years, Geographic Information Systems (GIS) have provided researchers new tools for exploring and analyzing health data[18]. Spatial analysis in a Geographic Information System (GIS) environment can be divided into three broad categories: visualization, exploration, and modeling. Frequently, over a recurrent investigation method, these groups tend to superpose[19]. They can be used to visualize the distribution of infectious disease morbidity or mortality, identify hotspots or clusters, and uncover relationships between spatiotemporal infectious disease patterns and host or environmental characteristics[20].

Spatial analysis is a useful analytical technique that helps identify the environmental risk for disease, detecting anomalies in reporting and, monitoring spatiotemporal changes of disease[4]. Spatial analysis can be applied to conduct four fundamental tasks in epidemiology, 1) to improve the understanding of geographical patterns of morbidity and production, 2) to facilitate optimal allocation of resources for disease control, 3) to determine the potential effectiveness of disease interventions, and 4) to carry out studies of aetiological factors[8].

Table 1 shows the main studies about spatial analyses of udder health and milk quality parameters. Herds can be georeferenced and included in a database with descriptive variables such as spatial location, health concerns, and milk quality indicators. All these variables can be considered to define areas with similar spatial characteristics, and variables of interest can be further explored to figure out hidden relationships between them[16,21]. Such spatial epidemiological studies at country level can contribute to the development of regional policies, support strategies definition for improving dairy health[16], and to be a tool for directing the actions of industry and milk producers[6].

Spatial epidemiology is attracting the interest of researchers in veterinary preventive medicine. Regional dissimilarities such as population heterogeneity, weather and terrain character-istics, agricultural activities, health strategy, and the existence of events (cattle fairs) could have a significant impact on disease transmission and control, whether for emerging or endemic disease[22]. Nowadays, data on spatial location of herds or even individual animals is routinely recorded in many countries, providing an opportunity to conduct spatial analyses to better understand the distribution and determinants of endemic diseases[4].

A wide range of techniques are available to examine spatial patterns of mastitis, from geostatistics to point process methods[22]. Disease mapping, clustering, and ecological analysis are included in spatial epidemiology, their use depend on specific requirements when evaluating ill-health etiology. There is usually a close relationship between these branches[18].

Spatial modeling lets explore spatial patterns, quantify the effects of known disease risk factors, and then focus on unexplained spatial clustering[23]. Until last decade, the methods available dealt only with binary variables, and cluster detection for diseases measured by continuous variables remained an unexplored field. Nevertheless, several diseases can be better approached through continuous biological indicators[22]. To optimize spatial analysis, data should be analyzed using more than one technique[24].

Spatial analysis can be split into three different components: visualization, exploration, and modeling[19]. Others divided spatial epidemiology into disease mapping, geographic correlation/regression studies, and clustering- disease clusters- surveillance[25,26], although it can be noted that such grouping may be considered artificial or synthetic, since all these methods can be applied on a interrelated-way on specific cases. Nevertheless, any classification may be useful for a better comprehension of existing methodologies and approaches. Our proposal for arranging spatial data analysis approaches can be found in Figure 1. The next sections describe both the importance of access to proper data and, the main studies according to predominant types of spatial analysis used for mastitis and milk-related indicators.

SPATIAL ANALYSIS OF MILK QUALITY AND MASTITIS

A small number of studies have been carried out aiming at spatial analysis of milk quality indicators or mastitis. There are few reported investigations of the spatial distribution of dairy production indices[8]. Dragovich[27] explored the spatial association between rainfall, milk quotas, and quantity of milk collected in Australia. Wood[28] studied differences in milk production between geographical regions. Others analyzed geographical region as a variable in a number of large-scale studies using mastitis survey data[29-31]. One large-scale report from the United Kingdom presented a visual analysis of dairy production at the national level, including the number and location of herds, milk production by geographic area and location of milk collection and processing plants[32].

Most of them found that differences in natural resources, dairy farm structures, and market features cause country regions to apply diverse dairy management systems, which may be reflected in various levels of technical performance[33].

Thus, the spatial analysis gives an opportunity to identify poor udder health areas as targets for further, more in-depth, studies to identify reasons[4].

Table 1 - Main research papers related to spatial analysis of milk and mastitis indicators.

| Year	Authors	Journal	Title and Country	Spatial Analysis	Methods
2004	Sæbø & Frigessi	Genet. Sel. Evol.	A genetic and spatial Bayesian analysis of mastitis resistance. Norway	Mapping Modeling (Bayesian)	36 178 first lactation cows. Bayesian proportional hazards model is used for modeling the time to first veterinary treatment of clinical mastitis, including both genetic and environmental covariates. Markov chain Monte Carlo methods (MCMC) were used for inference.
2005	Clements *et al.*	Prev. Vet. Med	Bayesian spatio-temporal modelling of national milk-recording data of seasonal-calving New Zealand herds	Mapping Modeling (Bayesian)	June 2001-May 2002. 10 448 herds. Bayesian spatio-temporal modeling approach. Linear regression models were developed with spatially structured and unstructured random effects, a linear temporal trend random effect and spatial-temporal interactions.
2006	Gay *et al.*	J. Dairy Sci.	Spatial and temporal patterns of herd somatic cell score in France	Mapping Clustering (Space-Time)	1996-2000. 5 210 herds. Linear regression model for each year allowed adjustment for risk factors (breed, mean parity, amount of calvings per season, herd size, and farm altitude). Cluster detection based on Hellinger distance between spatial distributions. Temporal ASCS patterns were explored using a computation of correlations and comparisons between spatial structures of different years.
2007	Gay *et al.*	Vet. Res.	A spatial hazard model for cluster detection on continuous indicators of disease: application to SCS. France	Mapping Clustering (Space)	2000, 34 142 dairy herds. The model allowed the simultaneous estimation of the effects of known risk factors and potential spatial clusters on SCS, and the mapping of the estimated clusters and their range.
2011	Wolff *et al.*	Geospat. Health	Spatial patterns of recorded mastitis incidence and SCC in Swedish dairy cows: implications for surveillance	Mapping	September 2008-August 2009. 3 851 herds. Spatial distribution of CM odds was estimated from available records and compared with udder health based on measurements of SCC derived from official milk recording.
2014	Mweu *et al.*	Prev. Vet. Med	Spatiotemporal patterns, annual baseline and movement-related incidence of *S. agalactiae* infection in Danish dairy herds: 2000-2009	Mapping Clustering (Space)	1999-2009. To describe the spatiotemporal patterns of infection with *S. agalactiae* in the population of Danish dairy herds and to estimate the annual herd-level baseline and movement-related incidence risks of *S. agalactiae* infection over the 10-year period.
2016	Arede *et al.*	Acta Vet. Scand.	A space-time analysis of *Mycoplasma bovis*: Bulk tank milk antibody screening results from all Danish dairy herds in 2013-2014	Clustering (Space)	June 2013-July 2014. Aproximately 3 500 herds measured. The objective was to investigate the evolution of spatial distribution of *M. bovis* in dairy herd population. Repeated bulk tank milk samples were used as a proxy for the herd-level diagnosis. Descriptive and spatial analyses were performed for the 4 screening rounds. Spatial globalclustering was evaluated through a modified K-function method, and local clusters by scan statistics.
2017	Läpple *et al.*	Eur. Rev. Agric. Econ.	Sustainable technology adoption: a spatial analysis of the Irish Dairy Sector	Modeling	The paper explored spatial effects in the adoption of sustainable technologies using Bayesian spatial probit models.
2019	Giannak-opoulos *et al.*	Vet. Microbiol.	Use of geographical information system and ecological niche modelling for predicting potential space distribution of subclinical mastitis in ewes. Greece	Ecological Niche Modeling	2 198 clinically healthy ewes, 111 farms. To recognize areas potentially of high risk for increased frequency of subclinical mastitis in ewes. Analyzed by an Ecological Niche Model. 2 analyses: one for subclinical mastitis & one for subclinical mastitis caused by slime-producing staphylococci. A model was constructed; sheep farms were divided into 2 clusters, according to prevalence of subclinical mastitis: farms in the upper three quartiles were used as occurrence points ('infected farms'); farms in the lower quartile were (pseudo)negative points.
2020	Dias *et al.*	Semin. Cienc. Agrar.	Spatial characterization of hygienic-sanitary indicators of refrigerated raw milk from Rondônia state. Brazil	Mapping Clustering (Space)	2015. 566 milk cooling tanks, 6 792 data subsets from 2 209 farmers. To identify SPC and SCC clusters in milk samples. Spatial distribution maps of the quality indicators. Spatial dependence was evaluated by geostatistics, using the ordinary kriging method for data interpolation.
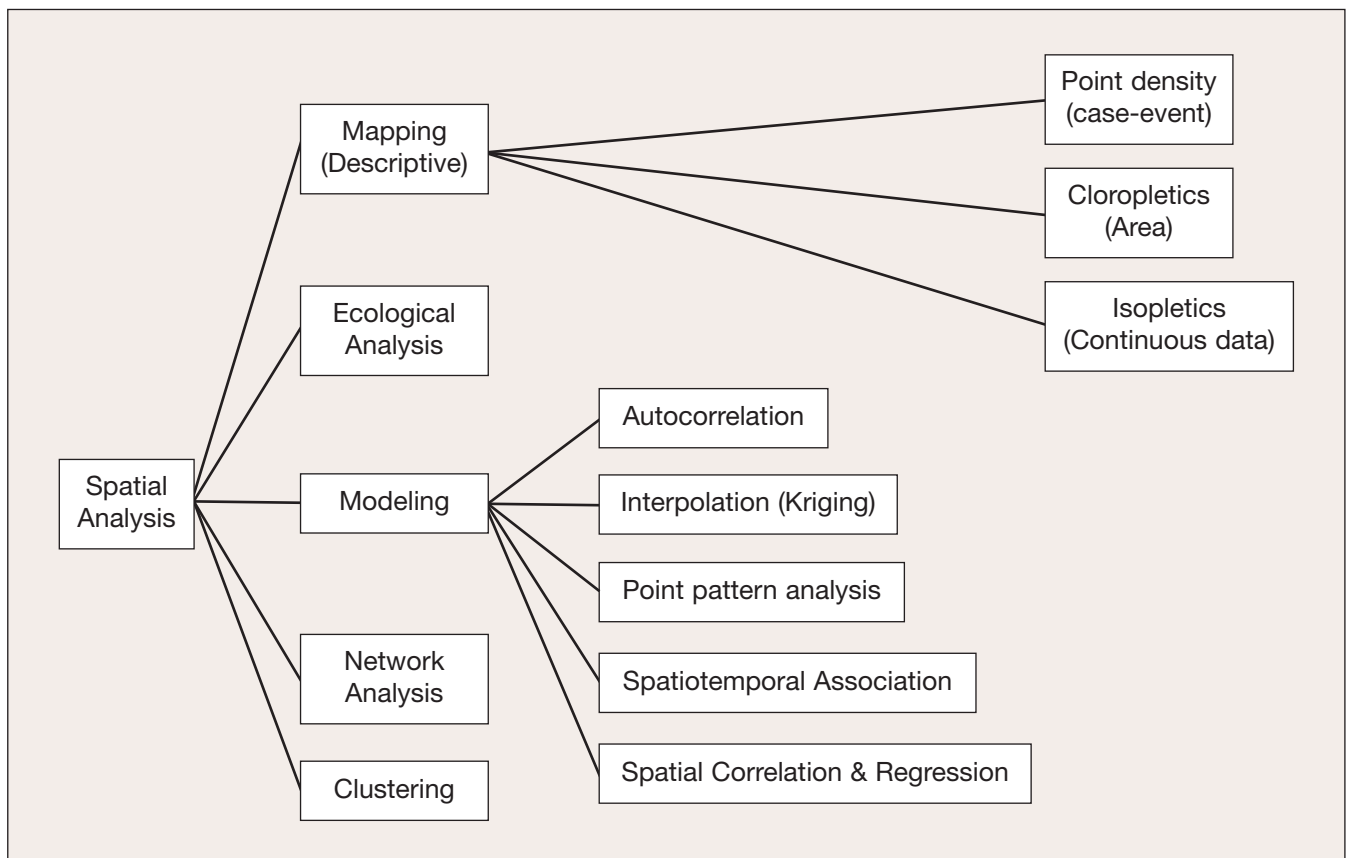
Figure 1 - Classification of spatial analysis.

Data sources for analyzing milk quality and mastitis

The first historic information about structured organization of milk recording date back to France in 1907. Milk recording spread to many countries as follows: USA 1883, Denmark 1895, Germany 1897, France 1905, Australia 1909, Argentina 1911, Canada 1911, South Africa 1917 and Spain 1933. A publication of 1935 titled "Dairy Cow Recording in Different Countries", listed 34 countries practicing milk recording[1]. Mastitis studies are concentrated in places with a national and well-established milk recording system, such as Nordic countries[2,4,13,15], New Zealand[8], France[7,22], and Brazil[6,34].

As examples of the extent of these data record systems, the Livestock Improvement Corporation (LIC, Hamilton, New Zealand) manages an extensive herd production-recording database known as MINDA, containing information from approximately 98% of New Zealand's 14,500 dairy farms, including milk-recording data from approximately 85%[8].

All Swedish veterinarians are required to report data, within one week, on diseases to the national disease recording system (NADRS). The report should include identification at the herd or individual animal level, diagnosis, date, treatment's detail, recommended withdrawal period and veterinarian's unique identifier.

The Swedish official milk recording system (SOMRS) was developed in the 70's and combines production data for cattle with a recording scheme that includes disease data based on records made by veterinarians and also, to a lesser extent, directly by the farmers. For herds participating in the SOMRS, veterinary data are regularly transferred from NADRS to SOMRS and used by farmers, herd advisors, and researchers[4].

The Irish Farm Accountancy Data Network (FADN) data are collected through the Irish National Farm Survey (NFS) data collection team, established in 1972. A statistically representative random sample of 1,100 farms (population of approximately 110,000 farms) is surveyed yearly. Farms are classified into six farming systems. There are about 300 dairy farms in the NFS each year from an approximate population of 17,000 dairy farms[14].

The Danish Cattle Database contains information on bacteriological culture of bulk tank milk (BTM) samples collected from the mandatory *S. agalactiae* surveillance scheme. Herd-specific geo-coordinates and test date are specified. Cattle daily movement data is recorded on the Central Herd Register (Danish Veterinary and Food Administration). Detailing animal identification, movement date, identity and type (beef, dairy, breeder, dealer, market, animal show, communal pasture, and animal hospital) of source and destination locations[13]. Danish Cattle Database comprises other pathogens like *M. bovis*, but the information available about herd locations lacks spatial aggregation. Other countries data are from passive disease surveillance plans and only have information about cases. Denmark's information contained the entire target population. However, the data presented few downsides in sampling with an irregular time- frame and duration for each screening round[15].

A well-functioning system for recording cattle diseases can be useful not only for herd management and breeding programs, but also for improving food traceability, facilitating surveillance of emerging diseases and improving food safety[4].

Descriptive analysis

Maps are one of the most powerful tools to visually communicate data[25]. Data visualization is the first step in disclosing the complex structure in data, not only to create interest and attract the attention of the viewer but also to provide a way of discovering the unexpected. Although plots of data and other graphical displays are among the fundamental tools for analysts in general, for a spatial analyst, visualizing spatial data usually means using a map[18].

The majority of spatial analysis related to milk indicators and mastitis are only descriptive, showing a visual analysis of dairy production and/or its quality indicators[21,32,35,36]. However, it is sometimes necessary to optimally estimate exposures in places where there is not enough data, based on known exposure values from nearby geographic points; this is achieved through the use of exposure models[25]. Gay et al.[7,22] used a kernel smoothing technique when mapped representations to explore spatial and temporal patterns that required a spatial interpolation to represent local farm density and annual milk somatic cell score (ASCS) intensity. Clements et al.[8] revealed the density of the selected farms by a kernel smoothing technique using a Gaussian function; the farm density was geographically non-homogeneous.

Aiming to visualize the spatial distribution of dairy cows in Sweden, Wolf et al.[4] produced a map using a Gaussian kernel smoothed density algorithm (30 km fixed bandwidth); choice of appropriate kernel function is less significant than size of the bandwidth, larger bandwidths yielding smoother surfaces[37]. To describe the distribution of clinical mastitis and udder health (UD) score throughout Sweden, two surfaces were constructed using Gaussian-kernel smoothing. The first based in all herds CM-positive (case) over all herds CM-negative (control). The second was based on number of cows with a poor UD score on at least one test milking (numerator) above the total number of cattle in each herd (denominator). The geographical distribution of Sweden's dairy cows was strongly heterogeneous. Small areas contain high proportions of the country's dairy cows. Areas identified with poor udder health could be targets for further studies to find the causes. Authors mentioned the lack of qualified cattle practitioners in such areas as one possible reason. Therefore, the spatial distribution of cattle practitioners in Sweden could be an interesting subject to study[4].

Another Nordic study[13] applied kernel smoothing technique to the yearly location of tank cases and non-cases of *S. agalactiae*. Risk maps for each year were created by dividing the kernel density surfaces for cases and the population summing case and non-case densities.

Clustering

A cluster could be defined as a geographically and temporally bound group of close values that is unlikely to have occurred at random[38]. There are different types of clustering, including general and specific[18]. Due to their contagious or point-source nature, ill-health and diseases often cluster in time and/or space; overlooking this characteristic can lead to a delay in controlling or eradicating the health problem[17]. Therefore, the issue of cluster detection is of major interest, since targeting possible causes for high disease concentration can assist in control and prevention.

The main techniques used in cluster detection rely on scan statistics. The principle is to compare the observed number of cases inside a moving window to the expected number of cases under some distribution assumptions (e.g., Poisson, Bernoulli)[22].

Clustering studies on milk quality already allowed the identification of regional differences that can assist in the management of herds[6]. In addition to potentially expediting control efforts, cluster identification techniques enable the researcher or healthcare official to identify and adjust for confounding factors and to generate new hypotheses regarding disease transmission[17].

There are few spatial cluster detection methods dealing with diseases quantified by continuous variables, like dairy cow subclinical mastitis[22]. The identification of SCS spatial clusters could display focused variation factors (e.g., climate accidents, emerging strains or pathogens, or wide local use of deleterious bulls) that are too infrequent, with respect to the general population, to be cleared up through large-scale spatial studies. The detection of SCS spatiotemporal clusters could help local technicians supervise mastitis risk by detecting areas with improved or worsened udder health. Controls and interventions could be spatially and temporally targeted, from focused epidemiological studies to the follow-up of management or environmental conditions. Performing a regression model before the cluster detection would be a recommended procedure to focus on unexplained clustering and to try to identify new risk factors that are relevant on broader spatial scales[7].

Cluster analyses are undoubtedly the most used for spatial assessment of mastitis, milk and related data. Arede et al.[15] studied four Danish dairy herd population cross-sectional screenings of *M. bovis* in BTM (3700 herds) between June 2013-July 2014. They mapped spatial distribution evolution of *M. bovis* in herds. Gay et al.[7] studied a cohort of 15% of French dairy herds (at least 20 cows) from 1996 to 2000 (5,210 herds) and used an original cluster detection approach adapted to continuous variables to analyze the spatial and temporal patterns of SCS in France.

Both approaches could be useful for locals to manage mastitis risk more accurately and could be an efficient way to dynamically improve milk quality at the national level. Gay et al.[22] also clustered herd SCS data through a method based on a spatial hazard model. They employed a 2000-year dataset of SCS for 34,142 French dairy herds and important SCS risk factors. It included mean parity, percentage of winter and spring calvings, and herd size.

Dias et al.[6] carried out a study on 566 milk cooling tanks of three microregions of Rondônia state, Brazil. Data used were official monthly analyses of Standard Plate Count (SPC) and SCC. Geographical location, type (individual or collective), and the number of producers who delivered milk to the collective tank were also obtained. Their objectives were to identify clusters of Bacterial Count and CCS and to evaluate the influence of time of year and tank type on the hygienic-sanitary quality indicators of milk.

The degree of dependence (DD) was calculated and categorized into: weak ≤ 25%, moderate from 26% to 75%, and strong > 75%. Spatial analysis demonstrated weak spatial dependence for SCC (DD = 22.02; r^2 = 0.73) and moderate for SPC (DD = 25.93; r^2 = 0.17), at up to 100 and 15 km respectively, indicating low accuracy in the identification of areas with common characteristics for SCC and greater precision for SPC. Carvalho and Souza[36] observed moderate spatial dependence for SCC in herds of this microregion.

Spatial modeling

Spatial modeling combines both visualization and exploration techniques with statistical analysis for disentangling what spatial pattern is presented in the data i.e. clustered, dispersed, or random[19]. Tobler's often-cited first law of geography captures the essence of spatial autocorrelation: "Everything is related to everything else, but near things are more related than distant things". It means that spatial autocorrelation decreases as a function of the distance between the target observation and the remaining ones[19].

Interpolating point samples of a continuous variable that distributes across space is another type of spatial modeling[39]. A case of optimal interpolation is known as kriging, which can be used to predict values and their standard errors indicating where the interpolation is less reliable. Small population studies are more susceptible to errors or local variations than studies conducted over larger areas[26]. Kriging models take advantage of spatial dependence in the data to develop smooth surfaces[19]. Mweu et al.[13] employed ordinary kriging for interpolating herd hygienic indicators, obtained from risk values. These were estimated using a logistic regression model for herds locations, extracted from the year-specific mixed-effects logistic regression models. These authors developed continuous risk surfaces, specific for each year. Dias et al.[6] estimated, using the same method (ordinary kriging) the values of milk sanitary indicators for the locations not sampled, without bias and with minimal variance.

Spatial correlation and regression

Predicting health while exploring for other known risk factors leads to suggestive evidence of statistical (and potentially causal) associations. Regarding spatial analyses on mastitis and dairy indicators, spatial correlation and regression analyses have frequently been employed before clustering. For example, ASCS was directly correlated to mean parity and spring calvings but negatively correlated with the number of calvings in summer and autumn, and also altitude. The breed factor was also highly significant[7]. While the spatial correlation showed positive and significant at 150 km distance with an approximated exponential form.

Sæbø & Frigessi[2] investigated the spatial patterns of mastitis in Norway at district level and considered climatic, environmental, herd features, and management factors. Adjacent veterinary districts were assumed to be similar regarding environmental conditions. They found a significant effect of environmental conditions to mastitis. The lowest risk of disease was detected to the southern part of the country.

In New Zealand, dairy farms were plotted on a map by using their geographic coordinates in order to explore mean individual cow somatic cell count (MICSCC), milk constituents and mean milk yield with data spanning from June 2001 to May 2002 for 11,045 herds. A second phase of the study included the analysis of sales questionnaires for 10,448 herds, gathering herd-level variables such as number of cows, heifers and calves, land area, number of sets of milking cups in the dairy, date of onset of calving, calving pattern (seasonal or year-round). Although they found some spatial dependence for SCC, spatiotemporal interactions were still small[8].

In order to investigate the distribution of veterinary registered cases of CM in Sweden, a cross-sectional study, covering a full year (September 2008 - August 2009) of herd level annual production data from SOMRS database was carried out. Data used were udder disease score (geometric mean of individual cow's SCCs of last three months tests), the incidence rate of CM (cases/100 by cow-years), CM cumulative incidence (number of cows), average herd-size (in cow-years), and geometric mean bulk milk SCC (BMSCC; cells/ml). Herd geographical location was retrieved from the Swedish Board of Agriculture, 83% of the herds (3,851) met the inclusion criterion. The study revealed two scenarios 1) areas with significantly lower odds for CM but with a high proportion of cows with a poor udder health score, suggesting an under-reporting of CM; and 2) areas with significantly higher odds for CM despite a low proportion of cows with a poor udder health score, suggesting mastitis over-treatment[4].

One of the most used models to predict the spatial distribution of living organisms is the so-called maximum entropy approach, or simply MaxEnt, which works with only presence data and environmental variables datasets in order to characterize spatial distribution of a certain species. Pixels with occurrence records constitute the sample points and the features are environmental parameters. MaxEnt methodology utilizes both continuous and categorical data[40]. An Ecological Niche Modelling was used for studying ruminant mastitis and proved to be effective in locating potentially increased risk areas for an infection, as well as to identify environmental/ecological conditions under which it would most likely develop[12].

Aiming to detect potential areas of high risk for increased frequency of subclinical mastitis, a maximum entropy modeling using data obtained from 2198 ewes with clinically normal udders living in 111 sheep farms (with 35,925 ewes) across 13 administrative regions of Greece was carried out. In each farm, 20 clinically healthy ewes were examined with conventional microbiological trials: California Mastitis Test (CMT) and Microscopic cell counting method. Staphylococcal strains were tested for *in-vitro* slime production. Subclinical mastitis was considered positive when a bacteriologically positive milk sample with concurrently increased CMT score (≥ 'l') plus neutrophil and lymphocyte proportion (≥ 65% of all leukocytes) were detected. Subclinical mastitis was analyzed against several explaining climatic and topographic variables at 1 km spatial resolution. Distance between sheep farms was the most contributing factor to the response variable, following altitude, maximum temperature of warmest month and the total precipitation of driest month. Validation of results showed that more than 76% of infected farms were located in areas predicted as high risk for prevalence for clinical mastitis[12].

CONCLUSIONS

The primary objective of this work is to discuss about mastitis as a topic for spatial research. Mastitis determination is closely related to milk quality indicators. Depending upon the scale or level of the study, the existence of local or national records on dairy production will be mandatory to be able to explore spatial patterns or causal relationships between explanatory variables against mastitis as a response variable, using proxies such as SCC or SCS. Despite mastitis has been studied during several years around the world, only few studies considering the spatial variability are reported until now, ranging from environmental, proximity, herd characteristics and management studies, intrinsically linked to their spatial location. This disease must be analyzed at different spatiotemporal scales in or-

der to find out hidden patterns and/or relationships that help design herd management plans at the national, regional and local levels. A number of reasons explain the scarcity of mastitis studies: 1) complex etiology and multifactorial behavior of mastitis, 2) lack of official databases, especially in developing countries. Main techniques reported for mastitis spatial data analysis include clustering, spatial correlation, interpolation, and correlation. A national database system on dairy production, for each country, will pave the way to be able to start doing exploratory analyses regarding mastitis not only for improving understanding of underlying factors of mastitis, but for designing control measures applicable directly in herds.

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