Enhancing syndromic surveillance for fallen dairy cattle: modelling and detecting mortality peaks at different administrative levels

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Keywords: fallen; dairy cattle; syndromic surveillance; hierarchical time series; ARIMA models; Spain

Resumé

La collection automatisée de données non-spécifiques chez le bétail combinée avec les techniques actuelles d'exploration de données et les analyses de séries temporelles facilitent le développement de la surveillance syndromique vétérinaire. Ces approches peuvent améliorer la surveillance traditionnelle des maladies des animaux. Un exemple est l'analyse continue de données sur les bovins morts qui sont enregistrées au niveau de la ferme. Pourtant, il faut mener des recherches additionnelles pour mettre en place ce processus comme système de signes d'alertes. L'objet de l'étude est 1) créer un méthode pour déterminer automatiquement les paramètres des modèles de Moyenne Mouvants et Intégrés Autorégressifs classiques (ARIMA) en incluant la tendance et saisonnalité agrégés à différents niveaux spatiaux, en prédisant 2) la mortalité à venir au cours d'une période n; et 3) détecter des pics de mortalité. L'application de ce travail est illustrée en utilisant des ensembles de données de bétail laitier morts dans deux régions d'Espagne. La mortalité hebdomadaire enregistrée est modélisée à niveau du comté, de la province et de la région entre 2006 et 2013. En utilisant ces modèles, la mortalité est prédite entre janvier 2014 et juin 2015. Les comptes de mortalité qui sont hors des limites de confiance prédites sont identifiés comme des pics de mortalité. Les causes de tels pics de mortalité dans quelques fermes affectées sont évaluées en utilisant des données des rapports d'expert détenus par les compagnies d'assurance. Ce travail permet de comparer les patrons temporels du bétail laitier mort entre les différentes populations illustrant une approche originale pour obtenir des informations à partir des données de mortalité à différents niveaux administratifs.

Abstract

The automated collection of non-specific data from livestock combined with current techniques of data mining and time series analyses facilitate the development of veterinary syndromic surveillance. This type of approach may enhance traditional surveillance of animal diseases. An example involves the continuous analysis of fallen cattle data, which are registered at farm level. However, further research is needed to incorporate such monitoring processes within an early warning system. This study presents a process aimed at 1) fitting automatically the parameters of the classical AutoRegressive Integrated Moving Average models (ARIMA) including patterns of trend and seasonality aggregated at different spatial levels, 2) predicting the mortality at n-ahead period; and 3) detecting mortality peaks. The application of this work is illustrated in the context of fallen dairy cattle data sets from two regions of Spain. The mortality levels registered by week are modelled at county, province and region levels between 2006 and 2013. Using these models the mortality is predicted between January 2014 and June 2015. Values of mortality that are out of the predicted confidence limits are identified as mortality peaks. The causes of such mortality peaks in some affected farms are assessed using data from expert's reports held by associated insurance companies This work compares patterns of fallen dairy cattle in populations with disparate management and environmental conditions with the aim of illustrating a novel approach to obtain information from mortality data at different administrative levels.

Introduction

The current enhancement of data mining tools and other advanced spatial-temporal analysis allow us to obtain information on the health status of the animal population from diverse automated data of non-specific nature in near real time (Dórea *et al.,* 2013, Dupuy *et al.,* 2013). This can provide an important complementary approach to enhance traditional animal surveillance systems which are intended to identify sub-populations at high risk, assess the impact of intervention measures or passed events, substantiate freedom of diseases and serve as a source of early warning (Dórea *et al.,*2011).

Previous studies have demonstrated the potential of the cattle mortality data registered at farm level for syndromic surveillance (Alba *et al.,* 2015a, 2015b, Perrin *et al.,* 2010). In the Alba's study the baseline patterns of fallen bovine were assessed for the main production types in Catalonia (Spain) using retrospective data collected between 2006 and 2013. The mortality was modelled at region level using AutoRegressive Integrated and Moving Average models (ARIMA) with adjustments for trend and seasonality. At province and county level the patterns were visually explored using hierarchical time series structures. The current study builds on this work in that it aims to dynamically model the mortality registered at different administrative levels. This system integrated data and fitted automatically the parameters of ARIMA models for series at different administrative levels. Assuming that the mortality may be predicted based on retrospective data, the selected ARIMA models are used to predict the mortality of n-ahead periods for the levels studied. This paper illustrates the system's functionality for dairy cattle mortality in two Spanish regions, forecasting the mortality and identifying unusual events of high mortality.

Materials and methods

The system involved the monitoring the weekly counts of mortalities recorded between 2006 and 2015 on dairy cattle farms located in two regions of Spain; R1 (Asturias) and R2 (Catalonia) (see Fig 1). The cattle mortality was assessed at county, province and region levels.

Populations of study

Data set and sources

Mortality registered at farm level and cattle population data were provided by the Subdirección General de Sanidad e Higiene Animal y Trazabilidad del Ministerio de Agricultura y Pesca, Alimentación y Medio Ambiente (MAPAMA), in collaboration with the Entidad Estatal de Seguros Agrarios (ENESA) and the Agrupación Española de Entidades Aseguradoras de los Seguros Agrarios Combinados S.A. (AGROSEGUROS).

Descriptive analysis and selection of target sub-populations

Initially the annual populations of dairy cattle between 2006 and 2015 were described for R1 and R2. For every region basic statistics on the number of herds and animals under surveillance were computed. The mortality registered by week at different administrative levels was described using hierarchical time series structures (Hyndman *et al.* 2011, Hyndman *et al.* 2014). This method allowed for the observation and selection of those series at county, province and region level that could be modelled using an ARIMA model. Provinces and counties with the highest number of farms and highest figures for cattle mortality registered at farm level were selected.

Modelling

Retrospective data of the studied administrative levels were divided into training and testing data sets. Part of the data collected between 2006 and 2013 were used as a training data set to fit an ARIMA model. These parametric models were broadly used in classical time series analysis applied to different problems related to veterinary and public health disciplines (Lee *et al.,* 2010, Neumann *et al.* 2014). In general, the ARIMA(p,d,q) model is defined by the equation:

$$X_t = \alpha + \rho_1 X_{t-1} + \rho_2 X_{t-2} + \cdots + \rho_p X_{t-p} + Z_t + \theta_1 Z_{t-1} + \theta_2 Z_{t-2} + \cdots + \theta_q Z_{t-q}, \quad (1)$$

where X_t correspond to the series at time t, α the intercept of the model, $\rho_1, \rho_2, \ldots, \rho_p$ the coefficients of the autoregressive part, $\theta_1, \theta_2, \ldots, \theta_q$ the coefficients of the moving average part and $Z_t, Z_{t-1}, \dots, Z_{t-q}$ the error terms of the model. Trend and seasonality were considered as covariates in the ARIMA(p,d,q) model by using the following equation:

$$Y_t = \gamma_0 + \gamma_1 t + \gamma_2 \sin\left(\frac{2\pi t}{52}\right) + \gamma_3 \cos\left(\frac{2\pi t}{52}\right) + \gamma_4 \sin\left(\frac{2\pi t}{26}\right) + \gamma_5 \cos\left(\frac{2\pi t}{26}\right) + X_t\,, \qquad (2)$$

where Y_t was the observed series and X_t was the ARIMA(p,d,q) model expressed in the equation (1). The parameter γ_1 captured the possible linear trend of the series, γ_2 and γ_3 the annual seasonality, and γ_4 and γ_5 the biannual seasonality. Here the trigonometric part corresponded to the first and the second order Fourier terms commonly used in the analysis of time series (Brockwell *et al.* 2002). To determine the most appropriate values for p, d and q and trend and/or seasonal coefficients for each series (in eq. 1 and 2), an automated routine was developed. This routine allowed the selection of the model based on the following criteria: lowest value for Bayesian Information Criterion (BIC) proposed by Schwarz (Schwarz, 1978), statistical significance of the parameters of the model at a reasonable significance level (i.e. 5%), and lack of autocorrelation of residuals assessed through the Auto-Correlation Function (ACF) and the Partial Auto-Correlation function (PACF). Consequently, the best ARIMA model was that one in which the lack of autocorrelation was completely satisfied and showed appropriate results for BIC and statistical significance of the parameters (Lee *et al*. 2013, Neumann *et al.*, 2014, Brockwell *et al.*, 2002, Schwarz, 1978).

This process combined different values of p, d and q for the ARIMA(p,d,q) models. In fact, p and q could take values from 0 to 5, and d could take 0 or 1. It should be noted that when d=1, the series was differentiated avoiding the possible linear trend. These models were used to predict the weekly patterns of mortality for 2014 and 2015 and detect unexpected mortality peaks. These predictions were generated at once for the entire period. The data collected during the period 2014 and 2015 were used as testing data set. Mortality peaks were identified by comparing real observations with upper predicted 95%confidence limits computed for each fitted model, using the observations recorded during the previous two weeks for comparison. Once a peak was detected, investigation should be conducted at farm level to determine the specific causes of mortality. With this aim, if an unusual mortality was detected by the system during a week at a specific administrative level, all the farms from which carcasses had been collected were listed. Since in some regions the number of farms involved was very high and it was difficult to recover all relevant documentation, the researchers decided to prioritize investigations in those farms which had unusual high levels of mortality. With this objective, the counts of mortality recorded during the previous two weeks were assessed in all the listed farms. Those farms in which the mortality peak exceeded in 3 counts the mortality recorded over the previous two weeks were considered as suspicious. The possible causes of death in some of these herds were explored based on information gathered from experts' reports of the insurance companies.

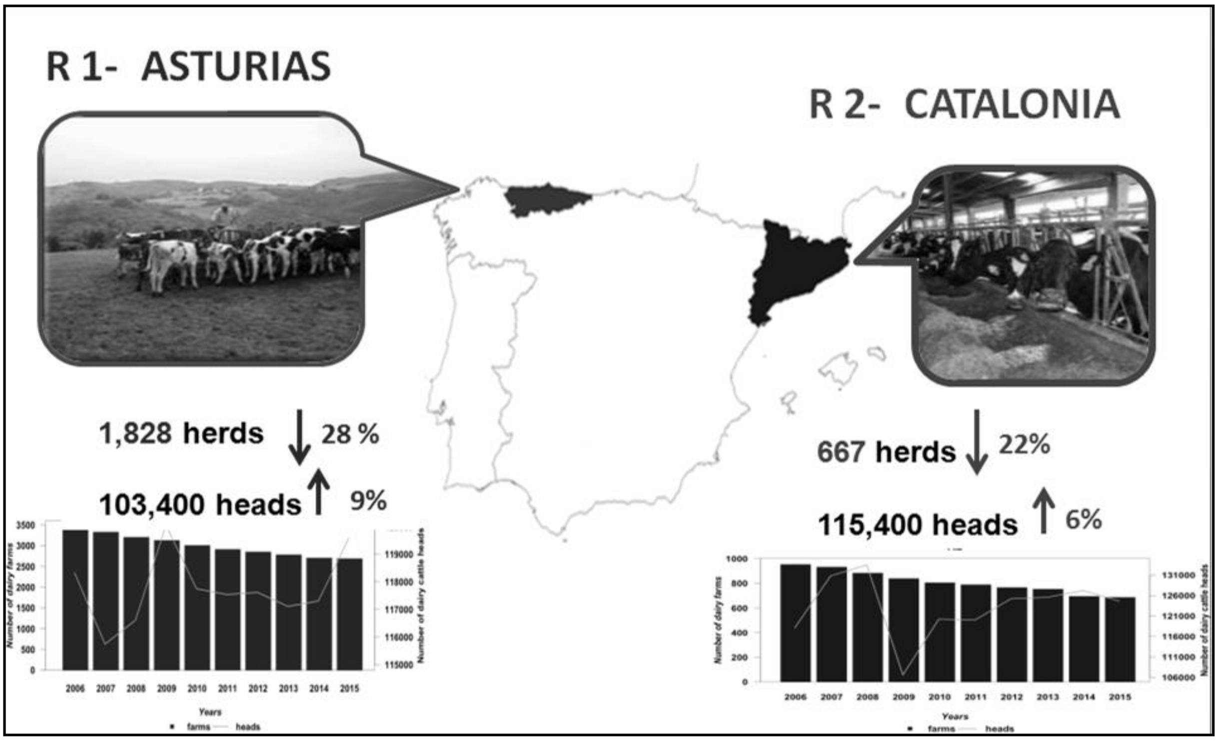
Results

Annual evolution of dairy cattle in Asturias (R1) and Catalonia (R2)

Between 2006 and 2015 a median of 1,828 farms with 103,400 heads in R1 and 667 farms with 115,400 heads in R2 were monitored. Over this period the number of dairy farms decreased in both regions (R1 -28% and R2 -21.7% respectively). However, the overall number of dairy cattle heads increased by 9.3% in R1 and 5.6% in R2. Figure 1 shows the evolution of the number of farms and heads per year, suggesting that the dairy farms constantly decreased over time in both regions; while the number of heads varied with a different pattern between regions. It is interesting to mention that in 2009 in the region R1 the number of dairy cattle increased substantially, while during the same year in the region R2 the number of dairy cattle decreased.

Table 1 provides a descriptive summary of the dairy cattle population by region (R1 and R2), province (P1-P3) and county (C1-C14).

Figure 1. Evolution year-by-year of the dairy cattle population between 2006 and 2015



(A) Evolution of dairy cattle population between 2006 and 2015 in the region R1. (B) Evolution of fallen dairy cattle population between 2006 and 2015 in the region R2.

Table 1. Description of dairy farms and cattle by region, province and county between 2006 and 2015.

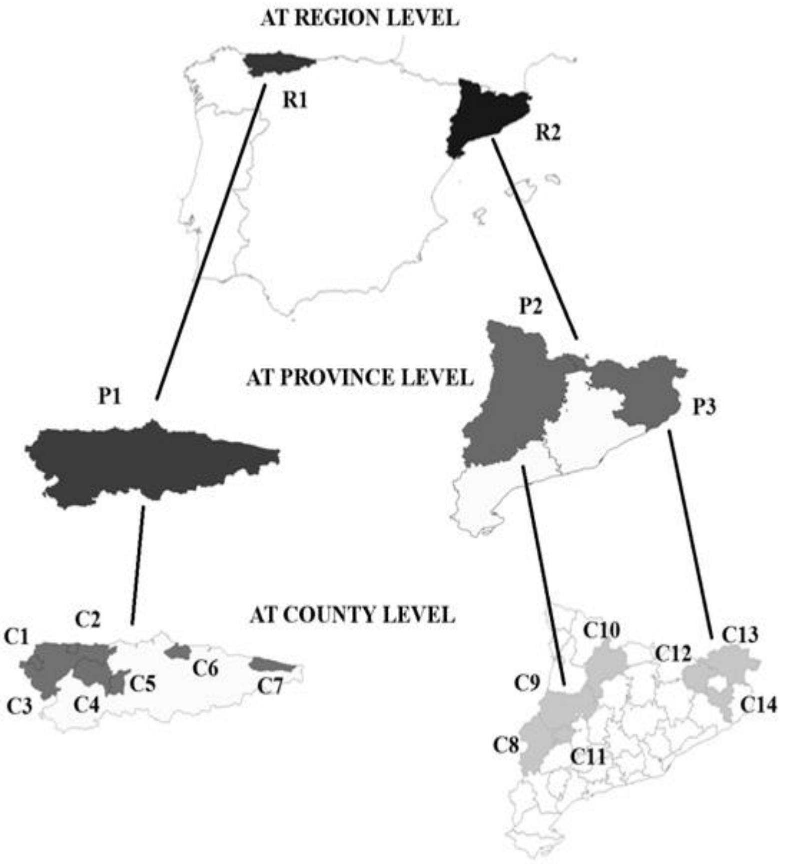
Zones of study	Number of farms	Size of farms. *Median (range)*	Number of carcass disposal visits	Number of carcasses	Number of carcasses collected by week *Median (range)*
R1(and P1)	2,681	74 (1-561)	90,086	109,744	221 (151-326)
C1	343	77 (1-369)	13,400	16,114	32 (13-61)
C2	302	71 (1-407)	12,860	15,440	31 (10-58)
C3	400	63 (1-561)	12,561	15,145	30 (14-58)
C4	425	75 (1-430)	14,547	17,205	34 (12-68)
C5	143	84 (2-240)	4,779	5,924	12 (3-25)
C6	314	82 (1-487)	11,514	14,850	29 (13-62)
C7	71	88 (5-218)	3,404	4,350	8 (0-20)
R2	799	198 (1-3,639)	85,295	153,520	308 (144-502)
P2	212	220 (1-3,639)	23,427	49,557	104 (40-197)
P3	308	191 (6-1,933)	32,896	56,274	106 (54-200)
C8	22	297 (3-3,369)	3,783	9,331	17 (2-52)
C9	21	526 (14-2,005)	3,709	10,022	19 (3-55)
C10	98	192 (1-1,556)	10,309	18,107	36 (9-75)
C11	25	206 (17-1,403)	3,418	9,055	17 (4-58)
C12	41	197 (6-559)	4,705	7,701	15 (2-37)
C13	61	231 (7-905)	8,247	14,265	28 (11-73)
C14	54	228 (6-1,933)	6,695	14,778	29 (10-70)

Region R1 is made up of only one province (P1) and from these seven counties were considered (C1 to C7); while two provinces (P2 and P3) were considered from region R2 together with an additional seven counties (C1 to C14) from these provinces.

Our system analysed data at region level of a total of 9,018,970 carcasses across 2,681 farms of R1 and 34,995,990 carcasses in 799 farms of R2. The system covered approximately 77% and 81% of the dairy farms in R1 and R2, respectively. The region R1 had 3.4 times more dairy farms than R2, although R1 had a median herd size 2.75 times smaller than in R2. The total number of visits performed by the carcass disposal services was quite similar in both regions (i.e. 90,086 in R1 versus 85,295 in R2). Therefore, the number of carcasses collected per visit was slightly higher in R2 than in R1, i.e. ~1.8 in R2 versus ~1.2 in R1.

In addition, our study considered the mortality data from three provinces in R1 and R2, including the most important counties within these provinces in terms of the number of dairy cattle (Figure 2).

Figure 2. Map of regions, provinces and counties included in the study.



ARIMA models selected for each series

The parameters of the ARIMA models selected for each series with their corresponding covariates are shown in Table 2 and in Figures 3 and 4. At region level, for both regions R1 and R2, the fallen dairy cattle figures followed an annual and biannual seasonality pattern with an increasing trend over time. The number of collected carcasses increased substantially during January and February in both regions. However, the increase in mortality seen in R2 was more evident during July and August. Of note is the fact that in R2 at the county level it can be seen that the trend and seasonality are more pronounced than in R1 (Table 2). Whereas the mortality patterns among counties were more homogeneous in R2 than in R1.

Peaks detected in region R1/P2 and counties C1-C7, highlighting those peaks detected both at region/province and county levels.

Peaks detected in region R2, provinces P2-P3 and counties C8-C14, highlighting those peaks detected both at province and county levels.

Table 2. Summary of the basic traits of the ARIMA(p,d,q) models provided by the automatic monitoring system for series at region, province and county levels

Zone of study	ARIMA(p,d,q)	Trend (direction)	Seasonality	
			Annual	Biannual
R1-P1	1,0,1	yes (+)	yes	yes
C1	0,1,1	yes (+)	yes	yes
C2	0,1,1	no	yes	yes
C3	1,0,1	yes (+)	no	yes
C4	0,1,1	yes (+)	no	yes
C5	1,0,1	yes (+)	yes	no
C6	0,1,1	yes (+)	yes	yes
C7	1,0,1	yes (-)	yes	no
R2	0,1,1	yes (+)	yes	yes
P2	0,1,1	yes (+)	yes	yes
P3	1,0,1	yes (+)	yes	yes
C8	0,1,1	yes (+)	yes	yes
C9	2,1,2	yes (+)	yes	yes
C10	0,1,1	yes (+)	yes	yes
C11	4,1,2	yes (+)	yes	yes
C12	1,0,1	yes (+)	yes	yes
C13	0,1,1	yes (+)	yes	yes
C14	3,1,1	yes (+)	yes	yes

Figure 3. Mortality peaks associated with region R1

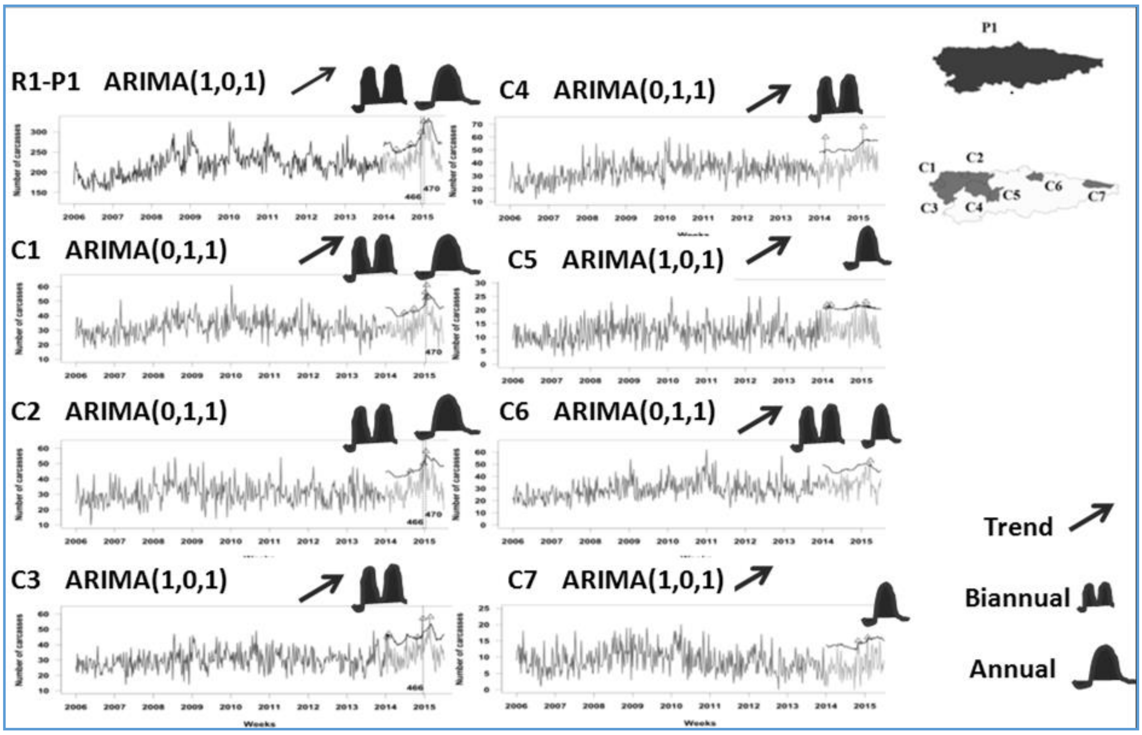
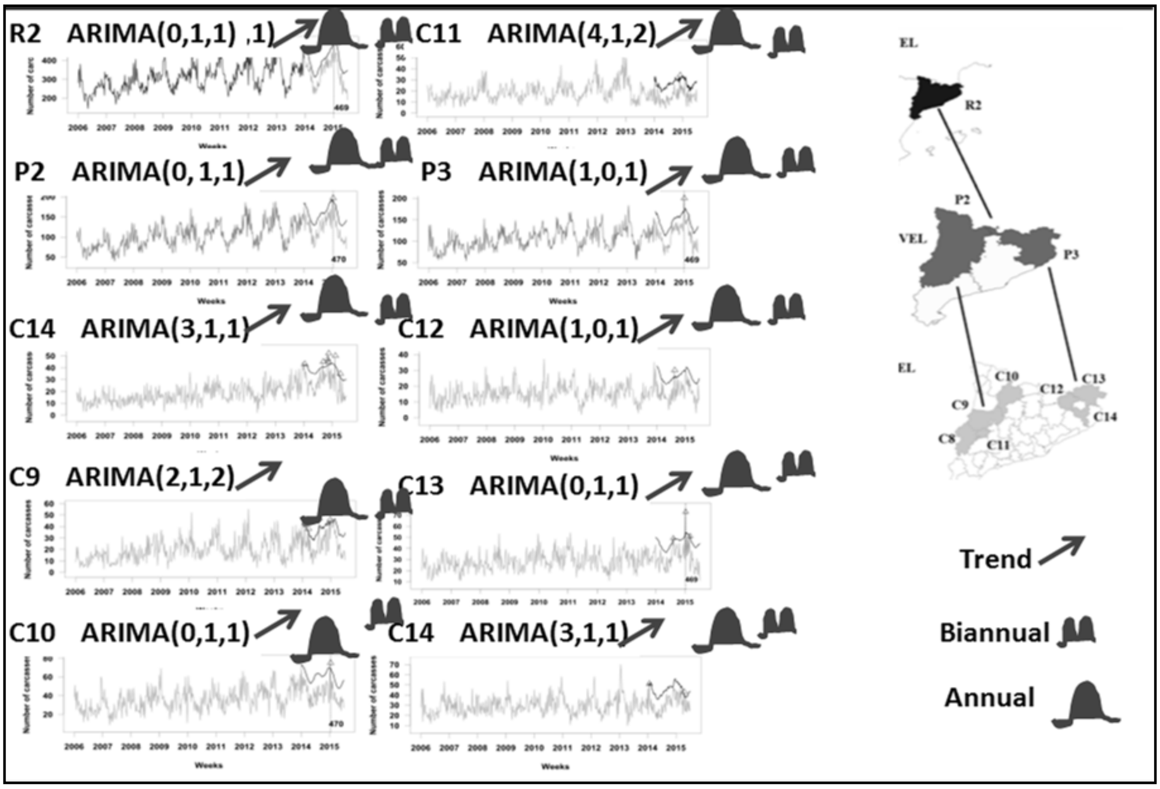


Figure 4. Mortality peaks associated with region R2



Prediction of abnormal peaks of mortality between 2014 and 2015

At province level six mortality peaks were detected (four peaks in R1 and two in R2). At county level 44 mortality peaks were detected. It is worth mentioning that in R1, two of the four peaks detected at province level were also detected at county level; while in R2 both peaks detected at the province level were also detected at county level (see Figures 3 and 4).

Common causes of death detected in dairy cattle at herd level

Using information gathered from the experts' reports of insurance companies the cause of death was explored in a total of 171 out of 1,312 fallen heads (13%). The vast majority of causes of deaths (87%) could not be assessed due to difficulties in collecting data. The preliminary exploration of the more usual causes registered by the insurance companies are listed in Table 3.

The explained mortality was mainly associated with calving, and also with trauma and nutritional disorders. Reproductive disorders in adults, including mastitis, were also a significant cause of mortality. It is worthy to mention that in the region R2 many of these deaths were related to nutritional disorders. At a county level results were obtained for 13 out of 25 (52%) of the detected peaks in R1 and for 7 out of 19 (36.8%) in R2. At this geographical level, the causes of mortality of approximately 80%-85% of the cases were unknown. However, for the rest of the cases, the causes of mortality were basically associated to reproductive, trauma and nutritional disorders in adults.

Table 3. Relative frequencies of some causes of mortality related to the mortality peaks detected at region, province and county levels between 2014 and 2015

Causes of dairy mortality	R1-P1	C1-C7	R2-P2-P3	C8-C15
Unknown	81.39%	83.09%	78.03%	84.07%
Degenerative disorders				
Locomotor disorders	0.66%	0.64%	1.52%	0.29%
Nutritional disorders	2.99%	3.86%	13.26%	1.29%
Respiratory disorders	0.33%	0.00%	0.76%	0.72%
Reproductive disorders (calves)	6.31%	4.83%	4.17%	9.61%
Reproductive disorders (adults)	1.33%	1.69%	0.00%	0.72%
Trauma	4.98%	4.59%	1.52%	2.30%
Mastitis	1.99%	0.89%	0.76%	0.29%
Parasitism	0.00%	0.16%	0.00%	0.43%
Enterotoxaemia	0.00%	0.24%	0.00%	0.29%

Discussion

This study presents an approach to the model mortality patterns at diverse administrative levels with disparate sub-populations. The work builds a routine to identify automatically the parameters of classical ARIMA models considering trend and seasonality, enhancing the implementation of a monitoring and alert system for mortality in dairy cattle. This work shows the application of this system for two dissimilar cattle populations in Spain, R1 and R2. R2 included a lower number of farms than R1, most of the herds were intensive production systems with larger herd size. In R1 the vast majority of farms were extensive production systems with smaller herd size (see Table 1).

Different ARIMA models were identified for the provinces and counties included in the study, even in the same region (Table 2). In R1 the baseline patterns were more heterogeneous, irregular and also more farms were involved in each mortality peak compared to R2. In R1 an overall good picture of the possible causes of death was more complex to get than in R2. The number of recorded carcasses increased over time in all regions, provinces and counties, except for the county C7 in which a linear negative trend was detected and for the county C2 in which there was no significant linear trend. At county level in the region R2, the ARIMA models were quite similar presenting patterns of increasing linear trend, and annual and biannual seasonality, although the selected models for counties C9, C11 and C14 departed from the others. This last region (and its provinces and counties) presented a more homogeneous profile of mortality than the region R1, the corresponding series being easier to model. However, in region R2 the selected ARIMA models at county level indicated differences among them, some showing patterns of seasonality while others did not.

Most of the mortality peaks detected at province level were also detected at the county levels in both regions (Figures 3 and 4). Some of those that were detected in different provinces and counties temporally agree, indicating the magnitude of the event.

The use of ARIMA models had some limitations, since only those sub-populations that showed regular patterns of mortality without events that indicated no mortality were suitable for modelling. For this reason it was necessary to previously describe and visualize all the series and, based on this initial assessment, select those series that were adequate to be determined by this classical model. When counts are very low, other methods such as Integer-Valued AutoRegressive models (INAR) (Fernández-Fontelo *et al.,* 2017) and Hermite Integer-Valued AutoRegressive models (HINAR) (Alba *et al.,* 2015b, Moriña *et al.* 2011) can be used, also in addition to non-parametric approaches based on P-splines (Eilers *et al.* 2015).

Moreover, the use of the number of recorded carcasses per week between 2006 and 2013 as a response variable regardless of any type of restriction had other relevant limitations. Between 2006 and 2013 some changes in the population and mortality events could have occurred, but these were not considered in the model. In this sense, if information to identify hidden events in the basal series (2006-2013) were available, it should be included in the corresponding model(s) in order to increase the sensitivity of this system. In addition, the use of counts of fallen cattle aggregated at county, province or region levels as proxy measures without considering the specific herd size at each farm, could cause an over-expression of the larger farms, and mask unusual mortality events in small farms. The response variable currently used could sometimes be non-specific since the farm census neither the ages of the bovines were taken into account. Accordingly, in an updated system this information should be included, encouraging the researcher to consider these factors when mortality data are recorded. We believe that to enhance the accuracy of the system and identify unusual events of mortality in different sub-populations, it would be important to include the herd size, age and/or sex as covariates and also monitor the mortality rate as a proxy measure taking into account the census of the population. The predictions explored here involved look one and a half years ahead. In this sense it would be necessary to extract signals that we wanted to detect in the long term and thus to remove these aberrations that we aim to be detected in the future.

Another important operational constraint found in this study was the difficulty in determining the specific aetiology of mortality peaks from retrospective data collected more than three years in the past. It is likely that insurance companies will introduce some biases when documenting possible causes, since the companies only record those causes that receive compensation, and have no motivation to include an accurate diagnosis. These findings indicate the need investigate peaks of mortality in the short term by addressing specific causes of mortality through investigations conducted in the field with clinical practitioners and farmers. In spite of these limitations, the exploratory analysis indicated that the causes of mortality in these populations were associated with calving problems as well as nutritional disorders trauma and other reproductive problems.

Despite the stated limitations, this work illustrates a useful approach to monitoring mortality at regional and more detailed levels, to identify unusual events of mortality and the magnitude of these events. Moreover, this system may provide essential information to identify spatio-temporal sub-populations at high risk so that resources can be effectively allocated to prevent and/or control disease outbreaks.

Acknowledgement

We want to thank the valuable contribution of the technicians of ENESA, AGROSEGUROS and REGA for their contribution and also for supplying the data. We also want to thank to the technical staff of Los Servicios Oficiales del MAPAMA, to the researchers of CReSA-IRTA and, a special thanks to Dr. Joaquim Segalés (CReSA-IRTA), Dr. Jordi Casal (CReSA-IRTA) and Dr. Andrés Pérez (University of Minnesota) for their support during the elaboration of this work.

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