Effects of control measures on the spread of LA-MRSA among Danish pig herds between 2006 and 2015 – a simulation study

There has been a rapid increase in Danish pig herds testing positive for livestock-associated Methicillin-resistant Staphylococcus aureus (LA-MRSA) since the first screening in 2008. Despite a national action plan to control LA-MRSA in the Danish pig population, 88% of pig herds tested positive in a 2016 cross-sectional study of 57 herds. The national action plan was initiated in April 2015 and aimed to reduce the spread of LA-MRSA among pig herds. However, its success is uncertain. We used a simulation model mimicking the spread of LA-MRSA among pig herds between 2006 and 2015 to evaluate the impact of control strategies if these had been implemented in 2007 or 2010. The strategies were combinations of the following control measures: (1) a reduced number of herds using high-risk antibiotics, (2) a reduced probability of indirect transmission among herds via humans, (3) movement restrictions, and (4) voluntary eradication in 5–7.5% of the herds. Almost all tested control strategies simulated a reduction in the spread of LA-MRSA. The combination of two, three or four intervention strategies showed additive effects and led to larger reductions in the predicted herd prevalence. In addition, the prevalence of LA-MRSA-positive herds at the time when control measures were initiated influenced the effects of the control strategies. Combining the simulated control measures can be considered in future action plans to control LA-MRSA.
Continuing occurrence of vancomycin resistance determinants in Danish pig farms 20 years after removing exposure to avoparcin
Vancomycin-resistant Enterococcus spp. is a major health problem worldwide and livestock have been implicated in constituting a reservoir for the transmission of vancomycin resistance to zoonotic pathogens. Vancomycin resistance determinants can be situated on mobile genetic elements and transferred between bacterial species. The livestock reservoir must therefore be included in a risk assessment of the vancomycin resistance burden. Avoparcin, a vancomycin analogue, has not been used in Danish pig production for over 20 years and vancomycin has never been used. The objective of this study was to screen faecal samples from Danish pig farms for nine selected vancomycin resistance determinants. We found at least four different vancomycin resistance determinants in all screened Danish pig farms (665 finisher farms and 78 sow farms). The vancomycin resistance determinants present in vanB or vanG clusters were found at significantly different levels in sow and finisher farms. However, vanA was not detected in any of the farms. In conclusion, vancomycin resistance determinants are still present in Danish pig production 25 years after the ban on avoparcin use.

Low accuracy of Bayesian latent class analysis for estimation of herd-level true prevalence under certain disease characteristics—An analysis using simulated data
Estimation of the true prevalence of infected individuals involves the application of a diagnostic test to a population and adjusting according to test performance, sensitivity and specificity. Bayesian latent class analysis for the estimation of herd and animal-level true prevalence, has become increasingly used in veterinary epidemiology and is particularly useful in incorporating uncertainty and variability into analyses in a flexible framework. However, the approach has not yet been evaluated using simulated data where the true prevalence is known. Furthermore, using this approach, the within-herd true prevalence is often assumed to follow a beta distribution, the parameters of which may be modelled using hyperpriors to incorporate both uncertainty and variability associated with this parameter. Recently however, the authors of the current study highlighted a potential issue with this approach, in particular, with fitting the distributions and a tendency for the resulting distribution to invert and become clustered at zero. Therefore, the objective of the present study was to evaluate commonly specified models using simulated datasets where the herd-level true prevalence was known. The specific purpose was to compare findings from models using hyperpriors to those using a simple beta distribution to model within-herd prevalence. A second objective was to investigate sources of error by varying characteristics of the simulated dataset. Mycobacterium avium subspecies paratuberculosis infection was used as an example for the baseline dataset. Data were simulated for 1000 herds across a range of herd-level true prevalence scenarios, and models were fitted using priors from recently published studies. The results demonstrated poor performance of these latent class models for diseases characterised by poor diagnostic test sensitivity and low within-herd true prevalence. All variations of the model appeared to be sensitive to the prior and tended to overestimate herd-level true prevalence. Estimates were substantially improved in different infection scenarios by increasing test sensitivity and within-herd true prevalence. The results of this
study raise questions about the accuracy of published estimates for the herd-level true prevalence of paratuberculosis based on serological testing, using latent class analysis. This study highlights the importance of conducting more rigorous sensitivity analyses than have been carried out in previous analyses published to date.

**Outcomes From Using Mortality, Antimicrobial Consumption, and Vaccine Use Data for Monitoring Endemic Diseases in Danish Swine Herds**

The aim of this study was to assess the potential of using multiple data sources currently available in Denmark for monitoring swine diseases. The study included farms that, based on serology, changed from “negative” to “positive” status for Porcine Reproductive and Respiratory Syndrome (PRRS), enzootic pneumonia (Mycoplasma hyopneumonia), and porcine pleuropneumonia (Actinobacillus pleuropneumoniae) between January 2014 and September 2017. These corresponded to 45 swine farms working as individual operation units (i.e., their disease status is independent from other farms) and 81 farms that were part of joint operation units (i.e., 2 or more farms considered to be an epidemiological unit, having swine and personnel are transferred among them, that have the same disease status). Additionally, a total of 95 farms with a negative status for these three diseases during the study period were also included in the study. Changes in mortality data, antimicrobial consumption, and vaccine use at herd level were monitored using Shewhart control charts prior to, during, and after these farms were found positive for the three diseases. The analysis was run separately for the different age groups–weaners (up to 30 kg), sows and finishers herds–within each farm. Briefly, the highest percentage of herds generating alarms was generated up to 3 months before they changed their disease status based on mortality (30%) and 1 month after based on antimicrobial use for respiratory diseases (100%). Porcine pleuropneumonia showed to be the disease with the highest impact on these data at herd level; alarms based on the three data streams were generated in the same month that herds changed their status to porcine pleuropneumonia-positive, as well as the following months. Alarms based on vaccine use generally occurred within the same month or after changes in disease status. False alarms were found in 2% (median value) of the herds for the different age groups based on mortality and antimicrobial use for respiratory diseases in healthy farms. Monitoring changes in mortality data, antimicrobial consumption, and vaccine use showed changes (i.e., warnings) at herd level prior to confirmation from diagnostic tests.
Analysis of the dynamics of Staphylococcus aureus in two Danish dairy cattle herds

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Building the foundation for veterinary register-based epidemiology: A systematic approach to data quality assessment and validation

Epidemiological studies often use data from registers. Data quality is of vital importance for the quality of the research. The aim of this study was to suggest a structured workflow to assess the quality of veterinary national registers. As an example of how to use the workflow, the quality of the following three registers was assessed: the Central Husbandry Register (CHR), the database for movement of pigs (DMP) and the national Danish register of drugs for veterinary use (VetStat). A systematic quantitative assessment was performed, with calculation the proportion of farms and observations with “poor quality” of data. “Poor” quality was defined for each measure (variable) either as a mismatch between and/or within registers, registrations of numbers outside the expected range, or unbalanced in- and outgoing movements. Interviews were conducted to make a complementary qualitative assessment. The proportion of farms and observations within each quality measure varied. This study highlights the importance of systematic quality assessment of register data and suggests a systematic approach for such assessments and validations without the use of primary data.

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Can we detect outbreaks at herd-level earlier when combining multiple data sources? The aim of this study was to explore the potential of using multiple data sources for monitoring swine diseases.

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Diagnostiske undersøgelser af luftvejsinfektioner og antibiotikabehandling af kalve

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Drivers for Livestock-Associated Methicillin-Resistant Staphylococcus Aureus Spread Among Danish Pig Herds - A Simulation Study
To gain insight into the rapid increase in the number of livestock-associated Methicillin-resistant Staphylococcus aureus (LA-MRSA)-positive herds in Denmark, we developed an individual-based Monte Carlo simulation model. We aimed to assess whether transmission of LA-MRSA via pig movements could explain the observed increase in the number of positive herds in Denmark, and to evaluate the effect of other between-herd transmission mechanisms. Pig movements alone were not sufficient to mimic the observed increase in LA-MRSA-positive herds in Denmark in any of the modelled scenarios. The model identified three factors that played important roles in the between-herd spread of LA-MRSA: (1) the within-herd dynamics, (2) the frequency and effectiveness of indirect transmissions, and (3) unexplainable introduction of LA-MRSA to swine herds. These factors can act as starting points for the development of LA-MRSA control programs in pig herds in order to limit the risk of its transmission to humans.

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Evaluation of a multiplex immunoassay for bovine respiratory syncytial virus and bovine coronavirus antibodies in bulk tank milk against two indirect ELISAs using latent class analysis
Bovine respiratory syncytial virus (BRSV) and bovine coronavirus (BCV) are responsible for respiratory disease and diarrhea in cattle worldwide. The Norwegian control program against these infections is based on herd-level diagnosis using a new multiplex immunoassay. The objective of this study was to estimate sensitivity and specificity across different cut-off values for the MVD-Enferplex BCV/BR SV multiplex, by comparing them to a commercially available ELISA, the SVANOVIR® BCV-Ab and SVANOVIR® BRSV-Ab, respectively. We analyzed bulk tank milk samples from 360 herds in a low- and 360 herds in a high-prevalence area. As none of the tests were considered perfect, estimation of test characteristics was performed using Bayesian latent class models. At the manufacturers' recommended cut-off values, the median sensitivity for the BRSV multiplex and the BRSV ELISA was 94.4 [89.8–98.7 95% Posterior Credibility Interval (PCI)] and 99.8 [98.7–100 95% PCI], respectively. The median specificity for the BRSV multiplex was 90.6 [85.5–94.4 95% PCI], but only 57.4 [50.5–64.4 95% PCI] for the BRSV ELISA. However, increasing the cut-off of the BRSV ELISA increased specificity without compromising sensitivity. For the BCV multiplex we found that by using only one of the three antigens included in the test, the specificity increased, without concurrent loss in sensitivity. At the recommended cut-off this resulted in a sensitivity of 99.9 [99.3–100 95% PCI] and specificity of 93.7 [88.8–97.8 95% PCI] for the multiplex and a sensitivity of 99.5 [98.1–100 95% PCI] and a specificity of 99.6 [97.6–100 95% PCI] for the BCV ELISA.

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Latent class analysis of real time qPCR and bacteriological culturing for the diagnosis of Streptococcus agalactiae in cow composite milk samples

Streptococcus agalactiae (S. agalactiae) has re-emerged as a mastitis pathogen among Norwegian dairy cows. The Norwegian cattle health services recommend that infected herds implement measures to eradicate S. agalactiae, this includes a screening of milk samples from all lactating cows. The performance of the qPCR-test currently in use for this purpose has not been evaluated under field conditions. The objective of this study was to estimate the sensitivity and specificity of the real-time qPCR assay in use in Norway (Mastitis 4 qPCR, DNA Diagnostics A/S, Risskov, Denmark) and compare it to conventional bacteriological culturing for detection of S. agalactiae in milk samples. Because none of these tests are considered a perfect reference test, the evaluation was performed using latent class models in a Bayesian analysis. Aseptically collected cow-composite milk samples from 578 cows belonging to 6 herds were cultured and tested by qPCR. While 37 (6.4%) samples were positive for S. agalactiae by bacteriological culture, 66 (11.4%) samples were positive by qPCR. The within-herd prevalence in the six herds, as estimated by the latent class models ranged from 7.7 to 50.8%. At the recommended cut-off (cycle threshold 37), the sensitivity of the qPCR was significantly higher at 95.3 (95% posterior probability interval [PPI] [84.2; 99.6]) than that of bacteriological culture at 58.2 (95% PPI [43.8; 74.4]). However, bacterial culture had a higher specificity of 99.7 (95% PPI [98.5; 100.0]) compared to the qPCR at 98.5 (95% PPI [94.6; 99.9]). The median estimated negative predictive values of qPCR was consistently higher than those of the BC at all estimated prevalences, and the superiority of the qPCR increased with increasing within-herd prevalence. The median positive predictive values of BC was in general higher than the estimates for the qPCR, however, at the highest prevalence the predictive ability of both tests were similar.
Modeling the cost of eradicating livestock-associated methicillin-resistant staphylococcus aureus in countries with a high proportion of positive herds

Due to an increased incidence of human infections, livestock-associated methicillin-resistant Staphylococcus Aureus (LA-MRSA) in pigs and its spread into the human population has been a major public and political issue in Denmark. Similar concerns are also being raised about LA-MRSA in other Western European countries. At a time when the proportion of LA-MRSA-positive pig farms was low, Norway adopted a 'trace and destroy' strategy aimed at keeping LA-MRSA out of the pig population. However, to date, no country with a high proportion of LAMRSA-positive pig herds has chosen to use an eradication strategy. This study analyses the cost and complexities of conducting an LA-MRSA eradication program in a situation where a large proportion of herds are positive. The total cost of the eradication program was estimated based on the following components: 1) planning, 2) monitoring and testing, 3) cleaning and disinfection, 4) production gains and losses, 5) net reduction in breeding exports, and 6) loss of genetic progress, including the costs of a mitigating caesarean section strategy in breeding herds. Costs were related to the depopulation of 1 million sows, to gilt supply (as this was an important limiting factor during an eradication program in Denmark), and to aggregated losses linked to a temporary halt on breeding progress. Using conservative assumptions, the total eradication costs were estimated at €1.8 billion, broken down into: planning costs (3%), monitoring and testing (6%), cleaning and disinfection (19%), production gains and losses (33%), net loss from breeding exports (19%) and loss of genetic progress (20%). The long-term effects of an LA-MRSA eradication program for Danish pig production were uncertain and were therefore not taken into account in the analysis.
Persistence of antimicrobial resistance genes from sows to finisher pigs

Antimicrobial resistance in pigs has been under scrutiny for many years. However, many questions remain unanswered, including whether the initial antimicrobial resistance level of a pig will influence the antimicrobial resistance found at slaughter. Faecal samples from finishers pigs from 681 farms and from sows from 82 farms were collected, and levels of seven antimicrobial resistance genes, ermB, ermF, sulI, sulII, tet(M), tet(O), and tet(W), were quantified by high-capacity qPCR. There were 40 pairs of observations where the finishers were born in the farms of the sows. The objective of this study was to evaluate whether the levels of AMR genes found in finisher pigs at slaughter were associated with the levels in the farm where the finishers were born, and whether the levels of the AMR genes were equal in the sow and finisher pig populations. We found a significant positive correlation between the levels of AMR genes in finishers and the sows in the farms where the pigs were born for some of the genes (ermB (ρ = 0.47, p-value = 0.002), ermF (ρ = 0.41, p-value = 0.03), and tet(O) (ρ = 0.33, p-value = 0.04)). Furthermore, there were significant differences between AMR gene levels for the sow and finisher populations for ermB, ermF, sulI, sulII, tet(O), and tet(W), though not for tet(M).

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Risk factors for the occurrence of livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) in Danish pig herds

Livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) is widespread in many European countries including Denmark, where 88% of randomly selected production herds tested positive in 2016. In the present study, we investigated herd-level risk factors for farms being classified as LA-MRSA positive (study 1), in addition to herd-level risk factors for farms changing status from LA-MRSA negative to LA-MRSA positive during a 2-year period (study 2). Risk factors previously identified in other studies were confirmed in study 1: large herd size, herd type (lower risk in herds with sows) and number of pig suppliers. Due to the effect of herd type, data from sow herds (N = 41) and herds without sows (N = 166) were analysed separately. A univariable analysis found that the variables significantly associated with LA-MRSA status for sow herds were: use of wet feed in the sow units; higher weights of piglets at weaning; availability of a delivery room on the farm; cleaning of aisles after pigs were moved; number of pigs per weaner section; number of pigs purchased in the past year, and factors related to rodent control and human traffic in the herd. In herds without sows, the univariable analysis showed that the presence of other species of animal on the farm; negative pressure ventilation; full sectioning; frequent visits from the veterinarian; peroral use of tetracyclines for weaners; number of pigs purchased in the past year, and factors related to rodent control and human traffic in the herd were significantly associated with LA-MRSA status. For herds that changed from LA-MRSA negative to positive (study 2), having a company contract for mouse control, having more than one pig supplier and using group medication in the drinking water were the variables associated with LA-MRSA status in the univariable analysis. We did not succeed in building a biologically meaningful multivariable model based on any of the datasets and, as observed in similar studies, many of the risk factors identified in the univariable analysis were related to herd size. It was therefore not possible to determine whether it was the size of the herd or related factors that were the causal risk factors for being LA-MRSA positive.

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Send more data: a systematic review of mathematical models of antimicrobial resistance

Antimicrobial resistance is a global health problem that demands all possible means to control it. Mathematical modelling is a valuable tool for understanding the mechanisms of AMR development and spread, and can help us to investigate and propose novel control strategies. However, it is of vital importance that mathematical models have a broad utility, which can be assured if good modelling practice is followed. The objective of this study was to provide a comprehensive systematic review of published models of AMR development and spread. Furthermore, the study aimed to identify gaps in the knowledge required to develop useful models. The review comprised a comprehensive literature search with 38 selected studies. Information was extracted from the selected papers using an adaptation of previously published frameworks, and was evaluated using the TRACE good modelling practice guidelines. None of the selected papers fulfilled the TRACE guidelines. We recommend that future mathematical models should: a) model the biological processes mechanistically, b) incorporate uncertainty and variability in the system using stochastic modelling, c) include a sensitivity analysis and model external and internal validation. Many mathematical models of AMR development and spread exist. There is still a lack of knowledge about antimicrobial resistance, which restricts the development of useful mathematical models.

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A Cow- and Herd-specific Bio-Economic Model of Intramammary Infections in Dairy Cows

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A cross-sectional study of oral antibacterial treatment patterns in relation to specific diarrhoeal pathogens in weaner pigs

According to international guidelines, the use of antibacterials should be evidence based and prudent. This register-based, cross-sectional study investigates the potential effect of laboratory findings on the patterns of antibacterial oral (batch) medication of weaner pigs, and the level of compliance with national guidelines for antibacterial use. The study population includes 1,736 weaner herds (=65% of all Danish weaner pigs) that were subject to laboratory analysis from the National Veterinary Institute on Brachyspira pilosicoli, Lawsonia intracellularis, and E.coli (F4 and F18) in 2014. Antibacterial prescription data were obtained from the national database, VetStat. These showed that antibacterial prescriptions for use in weaner pigs was 8.6% lower in spring 2015 compared to spring 2014. The antibacterial use per pig tended (p = 0.08) to decrease more in herds with negative laboratory results compared to herds with a moderate or massive occurrence of either of the pathogens. Irrespective of the laboratory findings on diarrhoeal pathogens, tetracyclines were the most frequently used antibacterials by a substantial margin, both 3 months prior to and 2-5 months after laboratory analysis. According to the national guidelines, tetracyclines are the second or third-choice antibacterial for treatment of diarrhoeal pathogens, due to resistance and co-resistance patterns. Compliance with the guidelines increased in 14% of the herds, mostly following identification of B. pilosicoli within the herd. Between 10% and 20% of the herds did not use batch treatment, despite the presence of moderate–massive amounts of the pathogens.
A mechanistic model for spread of livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) within a pig herd

Before an efficient control strategy for livestock-associated methicillin resistant *Staphylococcus aureus* (LA-MRSA) in pigs can be decided upon, it is necessary to obtain a better understanding of how LA-MRSA spreads and persists within a pig herd, once it is introduced. We here present a mechanistic stochastic discrete-event simulation model for the spread of LA-MRSA within a farrow-to-finish sow herd to aid in this. The model was individual-based and included three different disease compartments: susceptible, intermittent or persistent shedder of MRSA. The model was used for studying transmission dynamics and within-farm prevalence after different introductions of LA-MRSA into a farm. The spread of LA-MRSA throughout the farm mainly followed the movement of pigs. After spread of LA-MRSA had reached equilibrium, the prevalence of LA-MRSA shedders was predicted to be highest in the farrowing unit, independent of how LA-MRSA was introduced. LA-MRSA took longer to spread to the whole herd if introduced in the finisher stable, rather than by gilts in the mating stable. The more LA-MRSA positive animals introduced, the shorter time before the prevalence in the herd stabilised. Introduction of a low number of intermittently shedding pigs was predicted to frequently result in LA-MRSA fading out. The model is a potential decision support tool for assessments of short and long term consequences of proposed intervention strategies or surveillance options for LA-MRSA within pig herds.
A multivariate dynamic linear model for early warnings of diarrhea and pen fouling in slaughter pigs

We present a method for providing early, but indiscriminant, predictions of diarrhea and pen fouling in grower/finisher pigs. We collected data on dispensed feed amount, water flow, drinking bouts frequency, temperature at two positions per pen, and section level humidity from 12 pens (6 double pens) over three full growth periods. The separate data series were co-modeled at pen level with time steps of one hour, using a multivariate dynamic linear model. The step-wise forecast errors of the model were unified using Cholesky decomposition. An alarm was raised if the unified error exceeded a set threshold a sufficient number of times, consecutively. Using this method with a 7 day prediction window, we achieved an area under the receiver operating characteristics curve of 0.84. Shorter prediction windows yielded lower performances, but longer prediction windows did not affect the performance.

A prospective observational longitudinal study of new-onset seizures and newly diagnosed epilepsy in dogs

Seizures are common in dogs and can be caused by non-epileptic conditions or epilepsy. The clinical course of newly diagnosed epilepsy is sparsely documented. The objective of this study was to prospectively investigate causes for seizures (epileptic and non-epileptic) in a cohort of dogs with new-onset untreated seizures, and for those dogs with newly diagnosed epilepsy to investigate epilepsy type, seizure type and the course of disease over time, including the risk of seizure recurrence. Untreated client-owned dogs experiencing new-onset seizures were prospectively enrolled in a longitudinal observational study including clinical investigations and long-term monitoring at the Copenhagen University Hospital for Companion Animals. A baseline clinical assessment was followed by investigator/owner contact every eight weeks from inclusion to death or end of study. Inclusion of dogs was conducted from November 2010 to September 2012, and the study terminated in June 2014. One hundred and six dogs were included in the study. Seventy-nine dogs (74.5%) were diagnosed with epilepsy: 61 dogs (77.2%) with idiopathic epilepsy, 13 dogs (16.5%) with structural epilepsy and five dogs (6.3%) with suspected structural epilepsy. A non-epileptic cause for seizures was identified in 13 dogs and suspected in 10 dogs. Four dogs in which no cause for seizures was identified experienced only one seizure during the study. In dogs with idiopathic epilepsy 60% had their second epileptic seizure within three months of seizure onset. Untreated client-owned dogs experiencing new-onset seizures were prospectively enrolled in a longitudinal observational study including clinical investigations and long-term monitoring at the Copenhagen University Hospital for Companion Animals. A baseline clinical assessment was followed by investigator/owner contact every eight weeks from inclusion to death or end of study. Inclusion of dogs was conducted from November 2010 to September 2012, and the study terminated in June 2014. One hundred and six dogs were included in the study. Seventy-nine dogs (74.5%) were diagnosed with epilepsy: 61 dogs (77.2%) with idiopathic epilepsy, 13 dogs (16.5%) with structural epilepsy and five dogs (6.3%) with suspected structural epilepsy. A non-epileptic cause for seizures was identified in 13 dogs and suspected in 10 dogs. Four dogs in which no cause for seizures was identified experienced only one seizure during the study. In dogs with idiopathic epilepsy 60% had their second epileptic seizure within three months of seizure onset. Twenty-six dogs with idiopathic epilepsy (43%) completed the study without receiving antiepileptic treatment. The natural course of idiopathic epilepsy (uninfluenced by drugs) was illustrated by highly individual and fluctuating seizure patterns, including long periods of remission. Cluster seizures motivated early treatment. In a few dogs with a high seizure frequency owners declined treatment against the investigators advice. Epilepsy is the most likely diagnosis in dogs presenting with new-onset seizures. The course of idiopathic epilepsy is highly individual and might not necessarily require long-term treatment. This must be considered when advising owners about what to expect with regard to treatment and prognosis.
A Robust Statistical Model to Predict the Future Value of the Milk Production of Dairy Cows Using Herd Recording Data

The future value of an individual dairy cow depends greatly on its projected milk yield. In developed countries with developed dairy industry infrastructures, facilities exist to record individual cow production and reproduction outcomes consistently and accurately. Accurate prediction of the future value of a dairy cow requires further detailed knowledge of the costs associated with feed, management practices, production systems, and disease. Here, we present a method to predict the future value of the milk production of a dairy cow based on herd recording data only. The method consists of several steps to evaluate lifetime milk production and individual cow somatic cell counts and to finally predict the average production for each day that the cow is alive. Herd recording data from 610 Danish Holstein herds were used to train and test a model predicting milk production (including factors associated with milk yield, somatic cell count, and the survival of individual cows). All estimated parameters were either herd- or cow-specific. The model prediction deviated, on average, less than 0.5 kg from the future average milk production of dairy cows in multiple herds after adjusting for the effect of somatic cell count. We conclude that estimates of future average production can be used on a day-to-day basis to rank cows for culling, or can be implemented in simulation models of within-herd disease spread to make operational decisions, such as culling versus treatment. An advantage of the approach presented in this paper is that it requires no specific knowledge of disease status or any other information beyond herd recorded milk yields, somatic cell counts, and reproductive status.
A simulation study to evaluate the performance of five statistical monitoring methods when applied to different time-series components in the context of control programs for endemic diseases

Disease monitoring and surveillance play a crucial role in control and eradication programs, as it is important to track implemented strategies in order to reduce and/or eliminate a specific disease. The objectives of this study were to assess the performance of different statistical monitoring methods for endemic disease control program scenarios, and to explore what impact of variation (noise) in the data had on the performance of these monitoring methods. We simulated 16 different scenarios of changes in weekly sero-prevalence. The changes included different combinations of increases, decreases and constant sero-prevalence levels (referred as events). Two space-state models were used to model the time series, and different statistical monitoring methods (such as univariate process control algorithms–Shewhart Control Chart, Tabular Cumulative Sums, and the V-mask- and monitoring of the trend component–based on 99% confidence intervals and the trend sign) were tested. Performance was evaluated based on the number of iterations in which an alarm was raised for a given week after the changes were introduced. Results revealed that the Shewhart Control Chart was better at detecting increases over decreases in sero-prevalence, whereas the opposite was observed for the Tabular Cumulative Sums. The trend-based methods detected the first event well, but performance was poorer when adapting to several consecutive events. The V-Mask method seemed to perform most consistently, and the impact of noise in the baseline was greater for the Shewhart Control Chart and Tabular Cumulative Sums than for the V-Mask and trend-based methods. The performance of the different statistical monitoring methods varied when monitoring increases and decreases in disease sero-prevalence. Combining two or more methods might improve the potential scope of surveillance systems, allowing them to fulfill different objectives due to their complementary advantages.
antimicrobial classes had both negative and positive correlations with the AMR genes. From 10-42% of the variation in AMR gene levels could be explained in the final regression models, indicating that antimicrobial exposure is not the only important determinant of the AMR gene levels.

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Computational algorithm for lifetime exposure to antimicrobials in pigs using register data – the LEA algorithm
Accurate and detailed data on antimicrobial exposure in pig production are essential when studying the association between antimicrobial exposure and antimicrobial resistance. Due to difficulties in obtaining primary data on antimicrobial exposure in a large number of farms, there is a need for a robust and valid method to estimate the exposure using register data. An approach that estimates the antimicrobial exposure in every rearing period during the lifetime of a pig using register data was developed into a computational algorithm. In this approach data from national registers on antimicrobial purchases, movements of pigs and farm demographics registered at farm level are used. The algorithm traces batches of pigs retrospectively from slaughter to the farm(s) that housed the pigs during their finisher, weaner, and piglet period. Subsequently, the algorithm estimates the antimicrobial exposure as the number of Animal Defined Daily Doses for treatment of one kg pig in each of the rearing periods. Thus, the antimicrobial purchase data at farm level are translated into antimicrobial exposure estimates at batch level. A batch of pigs is defined here as pigs sent to slaughter at the same day from the same farm. In this study we present, validate, and optimise a computational algorithm that calculate the lifetime exposure of antimicrobials for slaughter pigs. The algorithm was evaluated by comparing the computed estimates to data on antimicrobial usage from farm records in 15 farm units. We found a good positive correlation between the two estimates. The algorithm was run for Danish slaughter pigs sent to slaughter in January to March 2015 from farms with more than 200 finishers to estimate the proportion of farms that it was applicable for. In the final process, the algorithm was successfully run for batches of pigs originating from 3,026 farms with finisher units (77% of the initial population). This number can be increased if more accurate register data can be obtained. The algorithm provides a systematic and repeatable approach to estimating the antimicrobial exposure throughout the rearing period, independent of rearing site for finisher batches, as a lifetime exposure measurement.

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Publication information
Determinants for Treatments in Relation to Udder Health in Danish Dairy Cattle Farms

Regular cow level registrations in the Danish Cattle Database include registrations about e.g. milk yield, SCC and calvings, but also about diseases and antibiotic treatments of cows. These data could potentially be a useful source of information for the development of herd-specific udder health management programs tailored to the farmer’s preference. With tailored programs farmers may be more motivated to adopt effective management programs that can also enhance a prudent use of antibiotics.

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Determinants of antimicrobial treatment for udder health in Danish dairy cattle herds

Societal pressure to limit the use of antibiotics in livestock production systems, including dairy cattle systems, is consistently increasing. To motivate farmers to reduce antibiotic usage, it is important to understand the factors that determine whether a cow will be treated with antibiotics or not. If farmers’ usual practices regarding antibiotic treatments are taken into account, they may be motivated to adopt control measures that can facilitate prudent use of antibiotics and are at the same time cost-effective. In this study, we analyzed database recordings of milk yield and somatic cell count from the routine milk recording scheme, clinical registrations of mastitis and PCR results, and cow factors such as days in milk and parity in relation to antibiotic treatments for 518 dairy herds in Denmark. Farm-wise logistic regressions were used to predict antimicrobial treatment based on these factors. The resulting regression coefficients of 422 herds were further analyzed by principal component analysis and clustering to determine the driving predictors for treatment in different groups of farms. The results showed that determinants that were most important for predicting antibiotic treatments vary from one farm to another. Health indicators such as PCR or somatic cell count were most indicative for treatment on some farms, whereas other groups seemed to depend more on production factors (milk yield) or later culling of the cows. This shows that farmers behave differently and differences can be identified in register data. This information can be considered when developing cost-effective herd-specific control measures of mastitis to promote prudent use of antibiotics in Danish dairy cattle farms.

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Contributors: Gussmann, M. K., Græsbøll, K., Toft, N., Nielsen, S. S., Farre, M., Kirkeby, C. T., Halasa, T.
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Epidemiological and economic consequences of purchasing livestock infected with Mycobacterium avium subsp. paratuberculosis

Paratuberculosis (PTB) is a chronic disease which may lead to reduced milk yield, lower animal welfare and death in cattle. The causative agent is Mycobacterium avium subsp. paratuberculosis (MAP). The economic consequences are particularly important incentives in the control and eradication of the infection. One strategy to control PTB in a herd is to purchase animals from farms with a low risk of MAP infection. We wanted to investigate the epidemiological and economic consequences of buying livestock from different supplier farms of low, medium or high risk, as well as farms with unknown status. We also wanted to estimate the probability of spontaneous fadeout if the farmer of an initially MAP-free herd bought a specified number of infected animals in a single year, or continually bought infected animals. This was achieved through simulation modeling, and the effects of consistently introducing one, five or ten infected animals annually into an initially infection-free herd was also modeled. Our findings show that once infected, a farm can relatively safely purchase animals from other low and medium-risk farms without experiencing an increase in the prevalence, highlighting the importance of certification programmes. Furthermore, farms free of MAP are highly susceptible and cannot purchase more than a small number of animals per year without having a high risk of being infected. The probability of spontaneous fadeout after 10 years was 82% when introducing a single infected animal into an initially MAP-free herd. When purchasing ten infected animals, this probability was 46%. The continual purchase of infected animals resulted in very low probabilities of spontaneous fadeout. We demonstrated that MAP-free farms can purchase a small number of animals, preferably from certified farms, each year and still remain free of MAP. Already infected farms have little risk of increasing the prevalence on a farm when purchasing animals from other farms.

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Methods for estimating disease transmission rates: Evaluating the precision of Poisson regression and two novel methods

Precise estimates of disease transmission rates are critical for epidemiological simulation models. Most often these rates must be estimated from longitudinal field data, which are costly and time-consuming to conduct. Consequently, measures to reduce cost like increased sampling intervals or subsampling of the population are implemented. To assess the impact of such measures we implement two different SIS models to simulate disease transmission: A simple closed population model and a realistic dairy herd including population dynamics. We analyze the accuracy of different methods for estimating the transmission rate. We use data from the two simulation models and vary the sampling intervals and the size of the population sampled. We devise two new methods to determine transmission rate, and compare these to the frequently used Poisson regression method in both epidemic and endemic situations. For most tested scenarios these new methods perform similar or better than Poisson regression, especially in the case of long sampling intervals. We conclude that transmission rate estimates are easily biased, which is important to take into account when using these rates in simulation models.

Modelling spread of MRSA within a pig herd

Modelling spread of MRSA within a pig herd

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Contributors: Sørensen, A. I. V., Toft, N., Espinosa-Gongora, C., Græsbøll, K., Boklund, A., Larsen, J., Hisham Beshara Halasa, T.
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Mortality in Danish Swine herds: Spatio-temporal clusters and risk factors

The aim of this study was to explore spatio-temporal mortality patterns in Danish swine herds from December 2013 to October 2015, and to discuss the use of mortality data for syndromic surveillance in Denmark. Although it has previously been assessed within the context of syndromic surveillance, the value of mortality data generated on a regular and mandatory basis from all swine herds remains unexplored in terms of swine surveillance in Denmark.

A total of 5010 farms were included in the analysis, corresponding to 1896 weaner herds, 1490 sow herds and 3839 finisher herds. The spatio-temporal analysis included data description for spatial, temporal, and spatio-temporal cluster analysis for three age groups: weaners (up to 30 kg), sows and finishers. Logistic regression models were used to assess the potential factors associated with finisher and weaner herds being included within multiple-herd clusters.

The spatio-temporal distribution of mortality changed over time, and suggested a general increase in mortality for the months of January and July for the three age groups. A large number of single-herd clusters (i.e. clusters with only one herd), and fewer multiple-herd clusters (i.e. clusters with at least two herds) were found. The herd size affected whether weaner herds were within multiple-herd clusters, and factors such farm type, SPF status and presence of atrophic rhinitis had an impact on finisher herds being inside vs. outside multiple-herd clusters in the univariable analysis. However, due to a strong correlation between variables, only farm type remained in the multivariable analysis for the finisher herds.

The higher mortality observed for the months of January and July could be linked to infrequent updates of the data used to calculate mortality. The presence of single-herd clusters might indicate welfare and disease issues, while multiple-herd clusters could suggest the presence of infectious diseases within the cluster area. The impact of farm type is linked to the fact that larger farms specialize in only one age group, with high biosecurity and more specialized personnel, and subsequently a lower mortality.

Mortality data have a potential use in disease surveillance. However, detected clusters might not be due to disease, but the result of changes such as herd management practices. Further analysis to explore other spatio-temporal monitoring methods is needed before mortality data can be incorporated into a Danish disease monitoring system.

Network analysis of pig movements: Loyalty patterns and contact chains of different holding types in Denmark

Understanding animal movements is an important factor for the development of meaningful surveillance and control programs, but also for the development of disease spread models. We analysed the Danish pig movement network using static and temporal network analysis tools to provide deeper insight in the connection between holdings dealing with pigs, such as breeding and multiplier herds, production herds, slaughterhouses or traders. Pig movements, which occurred between 1st January 2006 and 31st December 2015 in Denmark, were summarized to investigate temporal trends such as the number of active holdings, the number of registered movements and the number of pigs moved. To identify holdings and holding types with potentially higher risk for introduction or spread of diseases via pig movements, we
determined loyalty patterns, annual network components and contact chains for the 24 registered holding types. The total number of active holdings as well as the number of pig movements decreased during the study period while the holding sizes increased. Around 60-90% of connections between two pig holdings were present in two consecutive years and around one third of the connections persisted within the considered time period. Weaner herds showed the highest level of in-loyalty, whereas we observed an intermediate level of in-loyalty for all breeding sites and for production herds. Boar stations, production herds and trade herds showed a high level of out-loyalty. Production herds constituted the highest proportion of holdings in the largest strongly connected component. All production sites showed low levels of in-going contact chains and we observed a high level of out-going contact chain for breeding and multiplier herds. Except for livestock auctions, all transit sites also showed low levels of out-going contact chains. Our results reflect the pyramidal structure of the underlying network. Based on the considered disease, the time frame for the calculation of network measurements needs to be adapted. Using these adapted values for loyalty and contact chains might help to identify holdings with high potential of spreading diseases and thus limit the outbreak size or support control or eradication of the considered pathogen.

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Opportunities and challenges when pooling milk samples using ELISA
Testing large quantities of samples in order to detect one or more test-positive sample(s) is expensive and time-consuming. It is possible to optimize this process by pooling samples. Two frameworks to produce different hierarchical and non-hierarchical pooling schemes were tested and compared to standard pooling. Their efficiency and the potential savings were determined as a function of prevalence and the number of pooled samples.

The potential benefit of pooling samples is dependent upon the changes in the analytical sensitivity and specificity of the test used when diluting test-positive samples by pooling. To illustrate this, the sensitivity of antibody ELISA on pooled samples of bovine milk for Salmonella Dublin, Mycobacterium avium spp. paratuberculosis, and bovine virus diarrhea was tested. For these milk assays, the analytical sensitivity decreased rapidly with increasing pool sizes.

The efficiency of pooling is usually only measured by the number of tests performed, yet real savings depend on all the costs involved in the pooling process. These may differ between laboratories depending on the available equipment and the salaries of the technicians, among other factors. Therefore, several cost parameters were introduced to describe the total cost and thereby calculate the total savings. In terms of overall savings, both tested schemes were potentially optimal depending on the prevalence, possible pool size, and the cost of retesting. For the pool sizes of interest in this study, the three-stage hierarchical pooling scheme was often marginally more efficient in terms of the total number of tests. However, if the price of re-pooling was high, the two-stage scheme performed better in terms of total savings. In addition, for low prevalences and the possibility of pooling a large number of samples, the two-stage non-hierarchical test may be more efficient, both in terms of number of tests and overall cost. In order to apply these results in different laboratory settings, a free Shiny WebApp was developed, to compare several pooling schemes with different cost parameters.
Reporting guidelines for diagnostic accuracy studies that use Bayesian latent class models (STARD-BLCM)

Evaluation of medical tests is usually based on comparing their results to those from a perfect reference (gold standard) procedure. The Standards for Reporting of Diagnostic Accuracy (STARD) initiative (http://www.equator-network.org/reporting-guidelines/stard/) developed reporting guidelines for studies designed to estimate the accuracy of tests when disease status is known. The original STARD statement was initially published in seven journals, while an updated version — STARD2015 — has been recently released. More than 200 biomedical journals encourage its use in their instructions to authors. An affordable, reliable, and noninvasive reference standard does not always exist as is the case for infectious diseases with a long latent period (e.g., in chronic infections such as tuberculosis). In such situations test accuracy can be estimated using latent class models that do not require knowledge of disease status (i.e., disease status is a latent variable). Statistical methods were introduced in this context by Hui and Walter and have been successfully applied since then, with the majority of the work being carried out in a Bayesian framework. While STARD provides useful reporting guidelines for diagnostic accuracy studies when a reference standard is available, it required modification and extension to address crucial aspects that are unique to latent class analysis:In the absence of a perfect reference test, the target condition must be explicitly described when performing a latent class analysis to estimate test accuracy. Latent class models, in conjunction with what the tests under evaluation actually detect (e.g., organisms or immune responses to organisms), define the latent status. Thus, a definition/interpretation of the latent disease or infection under consideration from a biological perspective is critical to communicate effectively the contextual meaning of the sensitivity and specificity estimates.A detailed description of the latent class model and its assumptions is required. A meta-analysis found that 28% of the studies that used latent class models to estimate diagnostic test accuracy failed to report any evidence that assumptions were verified or that the underlying models were of adequate fit to the data at hand. Bayesian latent class analysis requires reporting the details and justification of the prior distributions used in the primary and sensitivity analysis. This task takes on increased importance when using non-identifiable latent class models. We adapted the STARD checklist in order to fulfill the reporting requirements for diagnostic test accuracy studies that use Bayesian latent class models. The new guidelines, termed Standards for the Reporting of Diagnostic accuracy studies that use Bayesian Latent Class Models, have been recently published and are available online (https://www.equator-network.org/reporting-guidelines/stard-blcms/). Further, a mailing list has been created and those interested can freely subscribe (http://lists.uth.gr/mailman/listinfo/lcmate). Standards for the Reporting of Diagnostic accuracy studies that use Bayesian Latent Class Models is relevant to both Bayesian and frequentist estimation methods but the focus is on the former. It should prove to be a useful tool for the sound application of latent class models in the evaluation of diagnostic tests and promote optimal reporting practices for studies that use such models.
Risk factors associated with spatio-temporal clusters of high mortality in Danish swine herds

What were our motivation and objective? Mortality data are recorded to fulfill the European Commission requirements which ensures a continuous data flow for a surveillance system. Before using these data as part of a syndromic surveillance system, it is necessary to understand why increasing changes in mortality happen. The aim of this study was to identify spatio-temporal clusters of high mortality in Danish swine herds and associated risk factors.

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Sampling pig farms at the abattoir in a cross-sectional study – Evaluation of a sampling method

A cross-sectional study design is relatively inexpensive, fast and easy to conduct when compared to other study designs. Careful planning is essential to obtaining a representative sample of the population, and the recommended approach is to use simple random sampling from an exhaustive list of units in the target population. This approach is rarely feasible in practice, and other sampling procedures must often be adopted. For example, when slaughter pigs are the target population, sampling the pigs on the slaughter line may be an alternative to on-site sampling at a list of farms. However, it is difficult to sample a large number of farms from an exact predefined list, due to the logistics and workflow of an abattoir. Therefore, it is necessary to have a systematic sampling procedure and to evaluate the obtained sample with respect to
the study objective. We propose a method for 1) planning, 2) conducting, and 3) evaluating the representativeness and reproducibility of a cross-sectional study when simple random sampling is not possible. We used an example of a cross-sectional study with the aim of quantifying the association of antimicrobial resistance and antimicrobial consumption in Danish slaughter pigs. It was not possible to visit farms within the designated timeframe. Therefore, it was decided to use convenience sampling at the abattoir. Our approach was carried out in three steps: 1) planning: using data from meat inspection to plan at which abattoirs and how many farms to sample; 2) conducting: sampling was carried out at five abattoirs; 3) evaluation: representativeness was evaluated by comparing sampled and non-sampled farms, and the reproducibility of the study was assessed through simulated sampling based on meat inspection data from the period where the actual data collection was carried out. In the cross-sectional study samples were taken from 681 Danish pig farms, during five weeks from February to March 2015. The evaluation showed that the sampling procedure was reproducible with results comparable to the collected sample. However, the sampling procedure favoured sampling of large farms. Furthermore, both under-sampled and over-sampled areas were found using scan statistics. In conclusion, sampling conducted at abattoirs can provide a spatially representative sample. Hence it is a possible cost-effective alternative to simple random sampling. However, it is important to assess the properties of the resulting sample so that any potential selection bias can be addressed when reporting the findings.

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Simulating control of paratuberculosis in Danish dairy herds

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Spatial patterns of antimicrobial resistance genes in a cross-sectional sample of pig farms with indoor non-organic production of finishers

Antimicrobial resistance (AMR) in pig populations is a public health concern. There is a lack of information of spatial distributions of AMR genes in pig populations at large scales. The objective of the study was to describe the spatial pattern of AMR genes in faecal samples from pig farms and to test if the AMR genes were spatially randomly distributed with respect to the geographic distribution of the pig farm population at risk. Faecal samples from 687 Danish pig farms were collected in February and March 2015. DNA was extracted and the levels of seven AMR genes (ermB, ermF, sulI, sulII,
tet(M), tet(O) and tet(W)) were quantified on a high-throughput real-time PCR array. Spatial differences for the levels of the AMR genes measured as relative quantities were evaluated by spatial cluster analysis and creating of risk maps using kriging analysis and kernel density estimation. Significant spatial clusters were identified for ermB, ermF, sull and tet(W). The broad spatial trends in AMR resistance evident in the risk maps were in agreement with the results of the cluster analysis. However, they also showed that there were only small scale spatial differences in the gene levels. We conclude that the geographical location of a pig farm is not a major determinant of the presence or high levels of AMR genes assessed in this study.

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STARD-BLCM: Standards for the Reporting of Diagnostic accuracy studies that use Bayesian Latent Class Models
The Standards for the Reporting of Diagnostic Accuracy (STARD) statement, which was recently updated to the STARD2015 statement, was developed to encourage complete and transparent reporting of test accuracy studies. Although STARD principles apply broadly, the checklist is limited to studies designed to evaluate the accuracy of tests when the disease status is determined from a perfect reference procedure or an imperfect one with known measures of test accuracy. However, a reference standard does not always exist, especially in the case of infectious diseases with a long latent period. In such cases, a valid alternative to classical test evaluation involves the use of latent class models that do not require a priori knowledge of disease status. Latent class models have been successfully implemented in a Bayesian framework for over 20 years. The objective of this work was to identify the STARD items that require modification and develop a modified version of STARD for studies that use Bayesian latent class analysis to estimate diagnostic test accuracy in the absence of a reference standard. Examples and elaborations for each of the modified items are provided. The new guidelines, termed STARD-BLCM (Standards for Reporting of Diagnostic accuracy studies that use Bayesian Latent Class Models), will facilitate improved quality of reporting on the design, conduct and results of diagnostic accuracy studies that use Bayesian latent class models.

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Publication information
Treatment Patterns for Mastitis in Danish Dairy Cattle Farms

General information
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Organisations: National Veterinary Institute, Epidemiology, Seges Knowledge Centre for Agriculture, University of Copenhagen
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Research output: Contribution to conference › Poster – Annual report year: 2017 › Research › peer-review

What tools are useful for monitoring endemic diseases? A simulation study based on different time-series components.

Control and eradication programs play an important role in disease monitoring and surveillance. It is important to follow up on implemented strategies to reduce and/or eliminate a specific disease. The objectives of this study were to investigate the performance of different detection methods, including methods commonly used in biosurveillance as well as state space models, for monitoring the effect of endemic disease control and eradication programs. We simulated 16 different scenarios of changes in disease sero-prevalence, inspired by real-world data from the Danish PRRS (Porcine Reproductive and Respiratory Syndrome) monitoring program. The changes included increases, decreases and/or constant sero-prevalence levels in different combinations. Two state space models were used to model the simulated data and different monitoring methods, such as univariate process control algorithms (UPCA) and monitoring of the trend component were tested. The performance was evaluated as the proportion of iterations with an alarm for a given week. Results revealed that the different UPCA performed differently with respect to detecting increasing and decreasing changes in sero-prevalence. The trend-based methods performed well for detecting the first event but its performance was poorer in adapting to several consecutive events. The different monitoring methods had different performances in monitoring increasing and decreasing changes in disease sero-prevalence, showing that the objectives of the monitoring program should be taken into account when choosing which methods to use. The principles used in this study can also be applied in disease surveillance of (re-)emerging diseases.

General information
Publication status: Published
Organisations: National Veterinary Institute, Epidemiology, University of Copenhagen
Contributors: Lopes Antunes, A. C., Jensen, D., Hisham Beshara Halasa, T., Toft, N.
Pages: 5-8
Publication date: 2017

Host publication information
Title of host publication: Proceedings of the 3rd International Conference on Animal Health Surveillance - beyond animal health surveillance
Place of publication: Wellington
Publisher: New Zealand Veterinary Association
Adaptive Test Schemes for Control of Paratuberculosis in Dairy Cows

Paratuberculosis is a chronic infection that in dairy cattle causes reduced milk yield, weight loss, and ultimately fatal diarrhea. Subclinical animals can excrete bacteria (Mycobacterium avium ssp. paratuberculosis, MAP) in feces and infect other animals. Farmers identify the infectious animals through a variety of test-strategies, but are challenged by the lack of perfect tests. Frequent testing increases the sensitivity but the costs of testing are a cause of concern for farmers. Here, we used a herd simulation model using milk ELISA tests to evaluate the epidemiological and economic consequences of continuously adapting the sampling interval in response to the estimated true prevalence in the herd. The key results were that the true prevalence was greatly affected by the hygiene level and to some extent by the test-frequency. Furthermore, the choice of prevalence that will be tolerated in a control scenario had a major impact on the true prevalence in the normal hygiene setting, but less so when the hygiene was poor. The net revenue is not greatly affected by the test-strategy, because of the general variation in net revenues between farms. An exception to this is the low hygiene herd, where frequent testing results in lower revenue. When we look at the probability of eradication, then it is correlated with the testing frequency and the target prevalence during the control phase. The probability of eradication is low in the low hygiene herd, and a test-and-cull strategy should probably not be the primary strategy in this herd. Based on this study we suggest that, in order to control MAP, the standard Danish dairy farm should use an adaptive strategy where a short sampling interval of three months is used when the estimated true prevalence is above 1%, and otherwise use a long sampling interval of one year.

General information
Publication status: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Dynamical Systems, University of Copenhagen
Contributors: Kirkeby, C. T., Græsbøll, K., Nielsen, S. S., Christiansen, L. E., Toft, N., Hisham Beshara Halasa, T.
Number of pages: 13
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URLs:
http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0167219
Source: PublicationPreSubmission
Source-ID: 127519447
Research output: Contribution to journal › Journal article – Annual report year: 2016 › Research › peer-review
A register-based study of the antimicrobial usage in Danish veal calves and young bulls

High antimicrobial usage and multidrug resistance have been reported in veal calves in Europe. This may be attributed to a high risk of disease as veal calves are often purchased from numerous dairy herds, exposed to stress related to the transport and commingling of new animals, and fed a new ration. In this study, we used national register data to characterize the use of antimicrobials registered for large Danish veal calf and young bull producing herds in 2014. A total of 325 herds with veal calf and potentially young bull production were identified from the Danish Cattle database.

According to the national Danish database on drugs for veterinary use (VetStat), a total of 537,399 Animal Daily Doses (ADD200) were registered for these 325 herds during 2014. The amount of antimicrobials registered in 2014 varied throughout the year, with the highest amounts registered in autumn and winter. Antimicrobials were registered for respiratory disorders (79%), joints/limbs/CNS disorders (17%), gastrointestinal disorders (3.7%) and other disorders (0.3%). Of the registered antimicrobials, 15% were for oral and 85% for parenteral administration. Long-acting formulations with a therapeutic effect of more than 48h covered 58% of the drugs for parenteral use. Standardized at the herd-level, as ADD200/100 calves/day, antimicrobial use distributed as median [CI95%] for starter herds (n=22): 2.14 [0.19;7.58], finisher herds (n=24): 0.48 [0.00;1.48], full-line herds (n=183): 0.78 [0.05;2.20] and herds with an inconsistent pattern of movements (n=96): 0.62 [0.00;2.24]. Full-line herds are herds, which purchase calves directly from a dairy herd and raise them to slaughter. Furthermore, we performed a risk factor analysis on the 183 herds with a full-line production. Here, we investigated, whether the number of suppliers, the number of calves purchased, the frequency of purchase, the average age at introduction, the average time in the herd and vaccination influenced the amount of antimicrobials used in the herds. The final multivariable regression analysis revealed that the number of calves introduced was positively associated with the antimicrobial use in the herd.

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Organisations: National Veterinary Institute, Section for Epidemiology, SEGES Økologi
Contributors: Fertner, M. E., Toft, N., Martin, H. L., Boklund, A.
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Web of Science (2016): Impact factor 1.987
Web of Science (2016): Indexed yes
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Keywords: Antibacterials, Antibiotics, Herd size, Multivariable regression, Supplier, Veal calves
DOI: 10.1016/j.prevetmed.2016.07.004
Source: FindIt
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A simulation model for the spread of LA-MRSA within a pig herd

General information
Publication status: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Statens Serum Institut
Contributors: Sørensen, A. I. V., Boklund, A., Toft, N., Larsen, J., Hisham Beshara Halasa, T.
Number of pages: 1
Publication date: 2016
A single-blinded phenobarbital-controlled trial of levetiracetam as mono-therapy in dogs with newly diagnosed epilepsy

Treatment of canine epilepsy is problematic. Few antiepileptic drugs have proven efficacy in dogs and undesirable adverse effects and pharmacoresistance are not uncommon. Consequently, the need for investigation of alternative treatment options is ongoing. The objective of this study was to investigate the efficacy and tolerability of levetiracetam as mono-therapy in dogs with idiopathic epilepsy. The study used a prospective single-blinded parallel group design. Twelve client-owned dogs were included and were randomised to treatment with levetiracetam (30 mg/kg/day or 60 mg/kg/day divided into three daily dosages) or phenobarbital (4 mg/kg/day divided twice daily). Control visits were at days 30, 60 and then every 3 months for up to 1 year. Two or more seizures within 3 months led to an increase in drug dosage (levetiracetam: 10 mg/kg/day, phenobarbital: 1 mg/kg/day). Five of six levetiracetam treated dogs and one of six phenobarbital treated dogs withdrew from the study within 2-5 months due to insufficient seizure control. In the levetiracetam treated dogs there was no significant difference in the monthly number of seizures before and after treatment, whereas in the phenobarbital treated dogs there were significantly (P = 0.013) fewer seizures after treatment. Five phenobarbital treated dogs were classified as true responders (>= 50% reduction in seizures/month) whereas none of the levetiracetam treated dogs fulfilled this criterion. Adverse effects were reported in both groups but were more frequent in the phenobarbital group. In this study levetiracetam was well tolerated but was not effective at the given doses as mono therapy in dogs with idiopathic epilepsy. (C) 2015 Elsevier Ltd. All rights reserved.

A space-time analysis of Mycoplasma bovis: bulk tank milk antibody screening results from all Danish dairy herds in 2013-2014

Mycoplasma bovis is an important pathogen causing severe disease outbreaks in cattle farms. Since 2011, there has been an apparent increase in M. bovis outbreaks among Danish dairy cattle herds. The dairy cattle industry performed cross-sectional antibody screening for M. bovis on four occasions, using the indirect BIO K 302 M. bovis enzyme-linked immunosorbent assay (ELISA) (Bio-X, Belgium) in bulk tank milk from all dairy herds between June 2013 and July 2014. The objective of this study was to investigate the evolution of the spatial distribution of M. bovis in the Danish dairy herd population throughout the study period. Repeated bulk tank milk samples were used as a proxy for the herd-level diagnosis. Descriptive and spatial analyses were performed for the four screening rounds. Based on a previous diagnostic test evaluation study, the M. bovis status for each herd was determined as test-positive or test-negative using a cut-off of 50 optical density coefficient %. The spatial global clustering was evaluated through a modified K-function method, and local clusters were identified by scan statistics. The results showed that M. bovis test-positive herds had a dynamic pattern
in space. The global clustering analysis showed that M. bovis test-positive herds were spatially correlated in rounds one, three and four. These findings were supported to some extent by the local clustering analysis, which found significant high- and low-risk spatial clusters in rounds one and three in the north and south of the mainland. The clusters with a high risk of observing test-positive herds did not remain between sampling rounds, indicating that M. bovis did not tend to persist upon emergence in dairy herds. In contrast, the clusters with a low risk of observing test-positive herds persisted in the same area throughout the study period.

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Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
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Web of Science (2016): Impact factor 1.472
Web of Science (2016): Indexed yes
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DOIs:
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Source-ID: 2292483853
Research output: Contribution to journal › Journal article – Annual report year: 2016 › Research › peer-review

Changes in group treatment procedures of Danish finishers and its influence on the amount of administered antimicrobials
When treating groups of pigs orally, antimicrobials can be administered through either feed or water. During the last decade, the group treatment procedure for finishers has shifted from feed to water administration. We hypothesized that farms implementing this change in treatment procedure would increase their total amount of administered antimicrobials. Based on Danish national register data, we performed a retrospective cohort study with three groups. The cohort of primary interest (Cohort Change) consisted of 50 finisher farms which changed their group treatment procedure from feed administration to water administration between 2008 and 2009. In addition, we identified 221 farms where treatment was administered through feed (Cohort Feed), and another 553 farms where treatment was administered through water (Cohort Water). Both of these groups retained their original treatment procedure throughout the study period. Cohort Change experienced a significant increase in the total amount of prescribed antimicrobials between the years. This increase might be caused by the treatment of more pigs, since antimicrobials administered through the feed are mainly administered at the pen level, while antimicrobials administered in water are mainly administered at the section level. However, we cannot exclude that a change in clinical disease has influenced the amount of prescribed antimicrobials. No change was observed in the other two cohorts. Furthermore, the difference in the amount of prescribed antimicrobials between the years was significantly different in Cohort Change when compared to both Cohort Water and Cohort Feed. Results from this study demonstrate that farms changing their procedure of group treatment from feed administration to water administration may increase their overall use of antimicrobials.

General information
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Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Contributors: Fertner, M. E., Boklund, A., Dupont, N. H., Toft, N.
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Publication information
Comparing algorithms performance for monitoring endemic disease: a simulation study based on the Danish PRRSV monitoring program

General information
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Organisations: National Veterinary Institute, Section for Epidemiology, National Veterinary Institute
Contributors: Lopes Antunes, A. C., Dorea, F., Hisham Beshara Halasa, T., Toft, N.
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Electronic versions:
IPVS_abstract.pdf
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Control of African swine fever epidemics in industrialized swine populations

African swine fever (ASF) is a notifiable infectious disease with a high impact on swine health. The disease is endemic in certain regions in the Baltic countries and has spread to Poland constituting a risk of ASF spread toward Western Europe. Therefore, as part of contingency planning, it is important to explore strategies that can effectively control an epidemic of ASF. In this study, the epidemiological and economic effects of strategies to control the spread of ASF between domestic swine herds were examined using a published model (DTU-DADS-ASF). The control strategies were the basic EU and national strategy (Basic), the basic strategy plus pre-emptive depopulation of neighboring swine herds, and intensive
surveillance of herds in the control zones, including testing live or dead animals. Virus spread via wild boar was not modelled.

Under the basic control strategy, the median epidemic duration was predicted to be 21 days (5th and 95th percentiles; 1-55 days), the median number of infected herds was predicted to be 3 herds (1-8), and the total costs were predicted to be €326 million (€256–€442 million). Adding pre-emptive depopulation or intensive surveillance by testing live animals resulted in marginal improvements to the control of the epidemics. However, adding testing of dead animals in the protection and surveillance zones was predicted to be the optimal control scenario for an ASF epidemic in industrialized swine populations without contact to wild boar. This optimal scenario reduced the epidemic duration to 9 days (1–38) and the total costs to €294 million (€257–€392 million). Export losses were the driving force of the total costs of the epidemics.

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Contributors: Hisham Beshara Halasa, T., Bøtner, A., Mortensen, S., Christensen, H., Toft, N., Boklund, A.
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Determining the optimal number of individual samples to pool for quantification of average herd levels of antimicrobial resistance genes in Danish pig herds using high-throughput qPCR

The primary objective of this study was to determine the minimum number of individual fecal samples to pool together in order to obtain a representative sample for herd level quantification of antimicrobial resistance (AMR) genes in a Danish pig herd, using a novel high-throughput qPCR assay. The secondary objective was to assess the agreement between different methods of sample pooling. Quantification of AMR was achieved using a high-throughput qPCR method to quantify the levels of seven AMR genes (ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W)). A large variation in the levels of AMR genes was found between individual samples. As the number of samples in a pool increased, a decrease in sample variation was observed. It was concluded that the optimal pooling size is five samples, as an almost steady state in the variation was observed when pooling this number of samples. Good agreement between different pooling methods was found and the least time-consuming method of pooling, by transferring feces from each individual sample to a tube using a 10 μl inoculation loop and adding 3.5 ml of PBS, approximating a 10% solution, can therefore be used in future studies.

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Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Epidemiology, Statens Serum Institut
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Dynamic generalized linear models for monitoring endemic diseases: moving beyond univariate process monitoring control algorithms

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Contributors: Lopes Antunes, A. C., Jensen, D., Hisham Beshara Halasa, T., Toft, N.
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Early warning of diarrhea and pen fouling in growing pigs using sensor-based monitoring

General information
Publication status: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Contributors: Jensen, D. B., Toft, N., Kristensen, A. R.
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Improving productivity in growing pigs by combining specific and non-specific monitoring

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Improving productivity in growing pigs by combining specific and non-specific monitoring

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Livestock-associated MRSA in the Danish cattle production

General information
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Contributors: Hansen, J. E., Pedersen, K., Fertner, M. E., Læssøe Martin, H., Rhod Larsen, A., Toft, N.
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Peer-reviewed: Yes
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Microclimate temperature play a vital role for vector borne disease transmission in the cool scandinavian climate

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Organisations: National Veterinary Institute, Section for Epidemiology, Technical University of Denmark
Contributors: Haider, N., Kristensen, B., Kirkeby, C. T., Toft, N., Bedker, R.
Pages: 70-71
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Place of publication: ZARAGOZA
Publisher: European Science Foundation
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abstractszaragoza.pdf
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Microclimatic temperature play a vital role for vector borne disease transmission in the cool Scandinavian climates

General information
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Contributors: Haider, N., Kristensen, B., Kirkeby, C., Toft, N., Bødker, R.
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Abstract_book_Zaragoza_Najmul_Haider_May2016.pdf
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Research output: Chapter in Book/Report/Conference proceeding › Conference abstract in proceedings – Annual report year: 2016 › Research › peer-review

Modeling the growth dynamics of multiple Escherichia coli strains in the pig intestine following intramuscular ampicillin treatment

Background: This study evaluated how dosing regimen for intramuscularly-administered ampicillin, composition of Escherichia coli strains with regard to ampicillin susceptibility, and excretion of bacteria from the intestine affected the level of resistance among Escherichia coli strains in the intestine of nursery pigs. It also examined the dynamics of the composition of bacterial strains during and after the treatment. The growth responses of strains to ampicillin concentrations were determined using in vitro growth curves. Using these results as input data, growth predictions were generated using a mathematical model to simulate the competitive growth of E. coli strains in a pig intestine under specified plasma concentration profiles of ampicillin.

Results: In vitro growth results demonstrated that the resistant strains did not carry a fitness cost for their resistance, and that the most susceptible strains were more affected by increasing concentrations of antibiotics that the rest of the strains. The modeling revealed that short treatment duration resulted in lower levels of resistance and that dosing frequency did not substantially influence the growth of resistant strains. Resistance levels were found to be sensitive to the number of competing strains, and this effect was enhanced by longer duration of treatment. High excretion of bacteria from the intestine favored resistant strains over sensitive strains, but at the same time it resulted in a faster return to pre-treatment levels after the treatment ended. When the duration of high excretion was set to be limited to the treatment time (i.e. the treatment was assumed to result in a cure of diarrhea) resistant strains required longer time to reach the previous level.

Conclusion: No fitness cost was found to be associated with ampicillin resistance in E. coli. Besides dosing factors, epidemiological factors (such as number of competing strains and bacterial excretion) influenced resistance development and need to be considered further in relation to optimal treatment strategies. The modeling approach used in the study is generic, and could be used for prediction of the effect of treatment with other drugs and other administration routes for effect on resistance development in the intestine of pigs.

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Organisations: Department of Applied Mathematics and Computer Science, Dynamical Systems, National Veterinary Institute, Section for Epidemiology, University of Copenhagen, University of Glasgow
Contributors: Ahmad, A., Zachariasen, C., Christiansen, L. E., Grasbøll, K., Toft, N., Matthews, L., Nielsen, S. S., Olsen, J. E.
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Models to Estimate Lactation Curves of Milk Yield and Somatic Cell Count in Dairy Cows at the Herd Level for the Use in Simulations and Predictive Models

Typically, central milk recording data from dairy herds are recorded less than monthly. Over-fitting early in lactation periods is a challenge, which we explored in different ways by reducing the number of parameters needed to describe the milk yield and somatic cell count of individual cows. Furthermore, we investigated how the parameters of lactation models correlate between parities and from dam to offspring. The aim of the study was to provide simple and robust models for cow level milk yield and somatic cell count for fitting to sparse data to parameterize herd- and cow-specific simulation of dairy herds. Data from 610 Danish Holstein herds were used to determine parity traits in milk production regarding milk yield and somatic cell count of individual cows. Parity was stratified in first, second, and third and higher for milk, and first to sixth and higher for somatic cell count. Fitting of herd level parameters allowed for cow level lactation curves with three, two, or one parameters per lactation. Correlations of milk yield and somatic cell count were estimated between lactations and between dam and offspring. The shape of the lactation curves varied markedly between farms. The correlation between lactations for milk yield and somatic cell count was 0.2–0.6 and significant on more than 95% of farms. The variation in the daily milk yield was observed to be a source of variation to the somatic cell count, and the total somatic cell count was less correlated with the milk production than somatic cells per milliliter. A positive correlation was found between relative levels of the total somatic cell count and the milk yield. The variation of lactation and somatic cell count curves between farms highlights the importance of a herd level approach. The one-parameter per cow model using a herd level curve allows for estimating the cow production level from first the recording in the parity, while a two-parameter model requires more recordings for a credible estimate, but may more precisely predict persistence, and given the independence of parameters, these can be easily drawn for use in simulation models. We also conclude that using total somatic cell count may stabilize models, and therefore, the dilution factor is of importance in Danish Holstein.

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Organisations: Department of Applied Mathematics and Computer Science, National Veterinary Institute, Section for Epidemiology, Dynamical Systems, University of Copenhagen
Contributors: Græsbøll, K., Kirkeby, C. T., Nielsen, S. S., Hisham Beshara Halasa, T., Toft, N., Christiansen, L. E.
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Monitoring endemic livestock diseases using laboratory diagnostic data: A simulation study to evaluate the performance of univariate process monitoring control algorithms

Surveillance systems are critical for accurate, timely monitoring and effective disease control. In this study, we investigated the performance of univariate process monitoring control algorithms in detecting changes in seroprevalence for endemic diseases. We also assessed the effect of sample size (number of sentinel herds tested in the surveillance system) on the performance of the algorithms.

Three univariate process monitoring control algorithms were compared: Shewart p Chart 1 (PSHEW), Cumulative Sum2 (CUSUM) and Exponentially Weighted Moving Average3 (EWMA). Increases in seroprevalence were simulated from 0.10 to 0.15 and 0.20 over 4, 8, 24, 52 and 104 weeks. Each epidemic scenario was run with 2000 iterations. The cumulative sensitivity4 (CumSe) and timeliness were used to evaluate the algorithms’ performance with a 1% false alarm rate. Using these performance evaluation criteria, it was possible to assess the accuracy and timeliness of the surveillance system working in real-time.

The results showed that EWMA and PSHEW had higher CumSe (when compared with the CUSUM) from week 1 until the end of the period for all simulated scenarios. Changes in seroprevalence from 0.10 to 0.20 were more easily detected (higher CumSe) than changes from 0.10 to 0.15 for all three algorithms. Similar results were found with EWMA and PSHEW, based on the median time to detection. Changes in the seroprevalence were detected later with CUSUM, compared to EWMA and PSHEW for the different scenarios. Increasing the sample size 10 fold halved the time to detection (CumSe = 1), whereas increasing the sample size 100 fold reduced the time to detection by a factor of 6.

This study investigated the performance of three univariate process monitoring control algorithms in monitoring endemic diseases. It was shown that automated systems based on these detection methods identified changes in seroprevalence at different times. Increasing the number of tested herds would lead to faster detection. However, the practical implications of increasing the sample size (such as the costs associated with the disease) should also be taken into account.

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Contributors: Lopes Antunes, A. C., Dorea, F., Hisham Beshara Halasa, T., Toft, N.
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Research output: Contribution to journal › Journal article – Annual report year: 2016 › Research › peer-review

Multistrain models predict sequential multidrug treatment strategies to result in less antimicrobial resistance than combination treatment

Background: Combination treatment is increasingly used to fight infections caused by bacteria resistant to two or more antimicrobials. While multiple studies have evaluated treatment strategies to minimize the emergence of resistant strains for single antimicrobial treatment, fewer studies have considered combination treatments. The current study modeled bacterial growth in the intestine of pigs after intramuscular combination treatment (i.e. using two antibiotics simultaneously) and sequential treatments (i.e. alternating between two antibiotics) in order to identify the factors that favor the sensitive fraction of the commensal flora. Growth parameters for competing bacterial strains were estimated from the combined in vitro pharmacodynamic effect of two antimicrobials using the relationship between concentration and net bacterial growth rate. Predictions of in vivo bacterial growth were generated by a mathematical model of the competitive growth of multiple
strains of Escherichia coli. Results: Simulation studies showed that sequential use of tetracycline and ampicillin reduced the level of double resistance, when compared to the combination treatment. The effect of the cycling frequency (how frequently antibiotics are alternated in a sequential treatment) of the two drugs was dependent upon the order in which the two drugs were used. Conclusion: Sequential treatment was more effective in preventing the growth of resistant strains when compared to the combination treatment. The cycling frequency did not play a role in suppressing the growth of resistant strains, but the specific order of the two antimicrobials did. Predictions made from the study could be used to redesign multidrug treatment strategies not only for intramuscular treatment in pigs, but also for other dosing routes.

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Organisations: Department of Applied Mathematics and Computer Science, Dynamical Systems, National Veterinary Institute, Section for Epidemiology, University of Copenhagen, University of Glasgow
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Optimised surveillance for paratuberculosis

General information
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Organisations: National Veterinary Institute, Section for Epidemiology, Section for Immunology and Vaccinology, University of Copenhagen
Contributors: Kirkeby, C. T., Græsbøll, K., Nielsen, S. S., Hisham Beshara Halasa, T., Toft, N., Jungersen, G.
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Research output: Contribution to conference › Poster – Annual report year: 2016 › Research › peer-review

Prevalence of paratuberculosis in the dairy goat and dairy sheep industries in Ontario, Canada
A cross-sectional study was undertaken (October 2010 to August 2011) to estimate the prevalence of paratuberculosis in the small ruminant dairy industries in Ontario, Canada. Blood and feces were sampled from 580 goats and 397 sheep (lactating and 2 y of age or older) that were randomly selected from 29 randomly selected dairy goat herds and 21
convenience -selected dairy sheep flocks. Fecal samples were analyzed using bacterial culture (BD BACTEC MGIT 960) and polymerase chain reaction (Tetracore); serum samples were tested with the Prionics Parachek enzyme-linked immunosorbent assay (ELISA). Using 3-test latent class Bayesian models, true farm-level prevalence was estimated to be 83.0% [95% probability interval (PI): 62.6% to 98.1%] for dairy goats and 66.8% (95% PI: 41.6% to 91.4%) for dairy sheep. The within-farm true prevalence for dairy goats was 35.2% (95% PI: 23.0% to 49.8%) and for dairy sheep was 48.3% (95% PI: 27.6% to 74.3%). These data indicate that a paratuberculosis control program for small ruminants is needed in Ontario.

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Reporting the national antimicrobial consumption in Danish pigs: influence of assigned daily dosage values and population measurement
Transparent calculation methods are crucial when investigating trends in antimicrobial consumption over time and between populations. Until 2011, one single standardized method was applied when quantifying the Danish pig antimicrobial consumption with the unit “Animal Daily Dose” (ADD). However, two new methods for assigning values for ADDs have recently emerged, one implemented by DANMAP, responsible for publishing annual reports on antimicrobial consumption, and one by the Danish Veterinary and Food Administration (DVFA), responsible for the Yellow Card initiative. In addition to new ADD assignment methods, Denmark has also experienced a shift in the production pattern, towards a larger export of live pigs. The aims of this paper were to (1) describe previous and current ADD assignment methods used by the major Danish institutions and (2) to illustrate how ADD assignment method and choice of population and population measurement affect the calculated national antimicrobial consumption in pigs (2007-2013). The old VetStat ADD-values were based on SPCs in contrast to the new ADD-values, which were based on active compound, concentration and administration route. The new ADD-values stated by both DANMAP and DVFA were only identical for 48 % of antimicrobial products approved for use in pigs. From 2007 to 2013, the total number of ADDs per year increased by 9 % when using the new DVFA ADD-values, but decreased by 2 and 7 % when using the new DANMAP ADD-values or the old VetStat ADD-values, respectively. Through 2007 to 2013, the production of pigs increased from 26.1 million pigs per year with 18 % exported live to 28.7 million with 34 % exported live. In the same time span, the annual pig antimicrobial consumption increased by 22.2 %, when calculated using the new DVFA ADD-values and pigs slaughtered per year as population measurement (13.0 ADDs/pig/year to 15.9 ADDs/pig/year). However, when based on the old VetStat ADD values and pigs produced per year (including live export), a 10.9 % decrease was seen (10.6 ADDs/pig/year to 9.4 ADDs/pig/year). The findings of this paper clearly highlight that calculated national antimicrobial consumption is highly affected by chosen population measurement and the applied ADD-values.
Simulating the epidemiological and economic effects of an African swine fever epidemic in industrialized swine populations

African swine fever (ASF) is a notifiable infectious disease with a considerable impact on animal health and is currently one of the most important emerging diseases of domestic pigs. ASF was introduced into Georgia in 2007 and subsequently spread to the Russian Federation and several Eastern European countries. Consequently, there is a non-negligible risk of ASF spread towards Western Europe. Therefore it is important to develop tools to improve our understanding of the spread and control of ASF for contingency planning. A stochastic and dynamic spatial spread model (DTU-DADS) was adjusted to simulate the spread of ASF virus between domestic swine herds exemplified by the Danish swine population. ASF was simulated to spread via animal movement, low- or medium-risk contacts and local spread. Each epidemic was initiated in a randomly selected herd – either in a nucleus herd, a sow herd, a randomly selected herd or in multiple herds simultaneously. A sensitivity analysis was conducted on input parameters. Given the inputs and assumptions of the model, epidemics of ASF in Denmark are predicted to be small, affecting about 14 herds in the worst-case scenario. The duration of an epidemic is predicted to vary from 1 to 76 days. Substantial economic damages are predicted, with median direct costs and export losses of €12 and €349 million, respectively, when epidemics were initiated in multiple herds. Each infectious herd resulted in 0 to 2 new infected herds varying from 0 to 5 new infected herds, depending on the index herd type.
Simulating the Epidemiological and Economic Impact of Paratuberculosis Control Actions in Dairy Cattle

We describe a new mechanistic bioeconomic model for simulating the spread of Mycobacterium avium subsp. paratuberculosis (MAP) within a dairy cattle herd. The model includes age-dependent susceptibility for infection; age-dependent sensitivity for detection; environmental MAP build up in five separate areas of the farm; in utero infection; infection via colostrum and waste milk, and it allows for realistic culling (i.e., due to other diseases) by including a ranking system. We calibrated the model using a unique dataset from Denmark, including 102 random farms with no control actions against spread of MAP. Likewise, four control actions recommended in the Danish MAP control program were implemented in the model based on reported management strategies in Danish dairy herds in a MAP control scheme. We tested the model parameterization in a sensitivity analysis. We show that a test-and-cull strategy is on average the most cost-effective solution to decrease the prevalence and increase the total net revenue on a farm with low hygiene, but not more profitable than no control strategy on a farm with average hygiene. Although it is possible to eradicate MAP from the farm by implementing all four control actions recommended in the Danish MAP control program, it was not economically attractive since the expenses for the control actions outweigh the benefits. Furthermore, the three most popular control actions against the spread of MAP on the farm were found to be costly and inefficient in lowering the prevalence when used independently.
Simulation of Spread of African Swine Fever, Including the Effects of Residues from Dead Animals
To study the spread of African swine fever (ASF) within a pig unit and the impact of unit size on ASF spread, a simulation model was created. In the model, an animal can be in one of the following stages: susceptible, latent, subclinical, clinical, or recovered. Animals can be infectious during the subclinical stage and are fully infectious during the clinical stage. ASF virus (ASFV) infection through residues of dead animals in the slurries was also modeled in an exponentially fading-out pattern. Low and high transmission rates for ASFV were tested in the model. Robustness analysis was carried out in order to study the impact of uncertain parameters on model predictions. The results showed that the disease may fade out within the pig unit without a major outbreak. Furthermore, they showed that spread of ASFV is dependent on the infectiousness of subclinical animals and the residues of dead animals, the transmission rate of the virus, and importantly the unit size. Moreover, increasing the duration of the latent or the subclinical stages resulted in longer time to disease fade out. The proposed model is a simple and robust tool simulating the spread of ASFV within a pig house taking into account dynamics of ASFV spread and the unit size. The tool can be implemented in simulation models of ASFV spread between herds.

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Spatial patterns of Antimicrobial Resistance Genes in Danish Pig Farms
Samples from 687 Danish pig farms were collected at five finisher slaughterhouses in February and March 2015. Faecal samples from five pigs per farm were collected randomly at the slaughter line and pooled into one sample per farm. DNA was extracted from the pooled samples and the level of seven antimicrobial resistance genes, ermB, ermF, sul1, sulII, tet(M), tet(O) and tet(W), was quantified by a high-throughput qPCR. It was evaluated whether the sample method resulted in a study population representative of Danish pig farms with finishers where it was found that the study population was biased towards farms having more finisher and a higher productivity. Spatial cluster analyses were performed in SaTScan®. The results showed significant spatial clusters for ermF, ermB, sulII and tet(W) whereas no significant clusters were found for sul1, tet(M) and tet(O).

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Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, National Food Institute, Research group for Genomic Epidemiology, University of Copenhagen
Contributors: Birkegård, A. C., Ersbøll, A. K., Hisham Beshara Halasa, T., Clasen, J., Folkesson, A., Vigre, H., Toft, N.
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The impact of microclimatic temperature on vector-borne disease transmission in Denmark

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Organisations: National Veterinary Institute, Section for Epidemiology
Contributors: Haider, N., Kristensen, B., Kirkeby, C., Toft, N., Bødker, R.
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The role of cattle movement in determining the incidence risk of Mycoplasma bovis in Danish dairy herds between 2013-2014

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Organisations: National Veterinary Institute, Section for Epidemiology, Technical University of Denmark, University of Copenhagen
Contributors: Arede, M., Nielsen, L. R., Halasa, T., Toft, N., Nielsen, P. K.
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Towards control of LA-MRSA - Simulation modeling of LA-MRSA spread between pig farms

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What to look for when monitoring animal diseases?

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Contributors: Lopes Antunes, A. C., Jensen, D., Hisham Beshara Halasa, T., Toft, N.
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A Bayesian herd-level diagnostic test evaluation - Mycoplasma bovis

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Contributors: Nielsen, P. K., Petersen, M. B., Nielsen, L. R., Hisham Beshara Halasa, T., Toft, N.
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Research output: Contribution to conference › Poster – Annual report year: 2015 › Research › peer-review

A comparison of 2 screening questionnaires for clinical assessment of canine cognitive dysfunction
Canine cognitive dysfunction (CCD) is a neurobehavioral syndrome occurring in some senior dogs. The diagnosis is currently primarily dependent on owner-based questionnaires addressing changes in behavior and daily routines and the exclusion of other conditions which may display clinical signs mimicking CCD. A number of CCD screening questionnaires have been published, but whether the choice of questionnaire might influence the diagnosis of CCD or not, is unclear. The objective of the present study was to correlate the total scores from 2 CCD screening questionnaires which were developed on the basis of very different strategies. The study population consisted of 50 dogs more than 8 years of age. The dogs were evaluated clinically, and the 2 questionnaires were given in a face-to-face interview with the owners. The study found a significant correlation (r = 0.83, P < 0.0001) between the 2 questionnaires. The ability to identify dogs with multiple and severe signs of CCD were equally good. This is of importance for research studying CCD case definitions and for comparisons between studies using different questionnaires. If evaluation for longitudinal changes is needed, the canine cognitive rating scale may prove more useful for assessing disease progression.

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Contributors: Schütt, T., Toft, N., Berendt, M.
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A multi-dimensional dynamic linear model for monitoring slaughter pig production
Scientists and farmers still lack an efficient way to unify the large number of different types of data series, which are increasingly being generated in relation to automatic herd monitoring. Such a unifying model should be able to account for
the correlations between the various types of data, resulting in a model which could potentially yield more information than can be gained from the individual components separately. Here we present such a model for monitoring slaughter pig production, in the form of a multivariate dynamic linear model. This model unifies three types of data (live weight, feed-and water consumption), measured at different levels of detail (individual pig and double-pen level) and with different observational frequencies (weekly and daily), using series collected for the Danish PigIT project. The presented three-dimensional model serves as a proof of concept, and it should be straightforward to expand it with additional data types.

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Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Contributors: Jensen, D. B., Cornou, C., Toft, N., Kristensen, A.
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A space-time analysis of Mycoplasma bovis in Denmark

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Big Data fra jord til bord
Danske landmænd og virksomhederne i fødevaresektoren har gode forudsætninger for at drage nytte af den rivende udvikling inden for indsamling og bearbejdning af data:
• Danmark har en stærk fødevaresektor. Det skyldes bl.a., at alle dele af værdikæden arbejder tæt sammen. Fra primærproducererne, over forarbejdningsindustrien, agroindustrien til videns- og forskningsmiljøerne. Effektiv ressourceudnyttelse og fokus på optimering i hele værdikæden gør sektoren i stand til at konkurrere på verdensmarkedet.
• Danske fødevarevirksomheder har altid været gode til at opdyrke nye forretningsmodeller og finde nye innovative veje til øget værdiskabelse. For eksempel gennem smartere måder at producere på, levere produkterne på eller at indarbejde større værdi i produkterne, så de kan sælges med større forretning.
• Dansk landbrug og hele værdikæden i fødevaresektoren producerer store mængder af data. Det skyldes bl.a. et højt automationsniveau og myndighedernes krav til dokumentation af fødevarekvaliteten, når de danske producenter leverer fødevarer til forbrugerne verden over. Der er imidlertid et stort spring fra at råde over store mængder af data til at bruge dem aktivt i forretningsudviklingen. Denne rapport viser, hvordan Big Data kan være ét af omdrejningspunkter

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Changing medication method influences total amount of administered antimicrobials

Cognitive Function, Progression of Age-related Behavioral Changes, Biomarkers, and Survival in Dogs More Than 8 Years Old

Background Canine cognitive dysfunction (CCD) is an age-dependent neurodegenerative condition dominated by changes in behavioral patterns. Cohort studies investigating cognitive status in dogs are lacking. Objectives To investigate cognitive function, progression of age-related behavioral changes, survival, and possible biomarkers of CCD in aged dogs.

Animals Fifty-one dogs >8 years old; 21 with no cognitive deficits, 17 with mild cognitive impairments (MCI) and 13 with CCD. Methods Longitudinal study. Recruitment period of 12 months and an observational period of 24 months including a baseline and 3 planned subsequent assessments. Cognitive status was determined using validated questionnaires. Plasma A-peptides were quantified using commercial ELISA assays and cytokines by a validated immunoassay.

Results Signs characterizing dogs with CCD were aimless wandering, staring into space, avoid getting patted, difficulty finding dropped food and anxiety. Thirty-three percent of dogs with a normal cognitive status progressed to MCI and 22% classified as MCI progressed to CCD during the study period. For 6 dogs diagnosed with CCD, signs of cognitive dysfunction increased with time. A diagnosis of CCD did not affect survival. The level of plasma A(42) was significantly increased (P < .05) in the CCD group (92.8 ± 24.0 pg/mL) compared to the MCI (77.0 ± 12.3 pg/mL) and normal group (74.9 ± 10.0 pg/mL), but no significant differences in concentrations of systemic inflammatory markers were detected.

Conclusions Canine cognitive dysfunction is a progressive disorder with an individual variability in the rate of cognitive decline and clinical signs. Plasma A(42) seems to be an interesting plasma biomarker of CCD.
Comparison of individual and pooled samples for quantification of antimicrobial resistance genes in swine feces by high-throughput qPCR

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There is a considerable societal interest in the careful monitoring of antimicrobial resistance (AMR) levels in human and animal populations. Sampling and data analysis can be both costly and time consuming. Optimization of sample pooling procedures is therefore important to reduce costs and analysis times. The objective of this study was to estimate how many individual fecal samples are needed to pool to get a representative sample for quantification of AMR-genes in a Danish pig herd. 20 individual fecal samples were collected from one section in a Danish pig herd. One to five rectal fecal samples were taken from each pen with respect to the number of pigs in the pen. A total of 48 pools were made of increasing number of individual samples. The levels of 9 different AMR-genes were quantified using dynamic qPCR arrays on the BioMark HD system(Fluidigm®). DNA was extracted using the Maxwell® 16 Blood DNA Purification Kit (Promega). DNA concentrations were diluted to 40 ng/μl. The efficiency of the primers was determined using standard curves. Obtained results were normalized with 16S ribosomal DNA. There were large variations in the levels of AMR-genes between individual samples. As the number of samples in a pool increased a decrease in sample variation was observed. A steady state in the sample variation was seen when pooling five or more samples. No significant difference was found between pools of five samples and pools of more. There were a significant difference between pools of five or more samples and pools of less (p < 0.0001). In order to quantify the level of AMR-genes pools of five individual samples will give a result representative of the pig herd. The findings of this study could be used in planning of observational studies.
iCull – A bioeconomic model for herd management and disease control

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Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Dynamical Systems, University of Copenhagen
Contributors: Kirkeby, C., Græsbøll, K., Nielsen, S. S., Christiansen, L. E., Toft, N., Hisham Beshara Halasa, T.
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Improving the Effect and Efficiency of FMD Control by Enlarging Protection or Surveillance Zones

An epidemic of foot-and-mouth disease (FMD) in a FMD-free country with large exports of livestock and livestock products would result in profound economic damage. This could be reduced by rapid and efficient control of the disease spread. The objectives of this study were to estimate the economic impact of a hypothetical FMD outbreak in Denmark based on changes to the economic assumptions of the model, and to investigate whether the control of an FMD epidemic can be improved by combining the enlargement of protection or surveillance zones with pre-emptive depopulation or emergency vaccination. The stochastic spatial simulation model DTU-DADS was used to simulate the spread of FMD in Denmark. The control strategies were the basic EU and Danish strategy, pre-emptive depopulation, suppressive or protective vaccination, enlarging protection or surveillance zones, and a combination of pre-emptive depopulation or emergency vaccination with enlarged protection or surveillance zones. Herds are detected either based on basic detection through the appearance of clinical signs, or as a result of surveillance in the control zones. The economic analyses consisted of direct costs and export losses. Sensitivity analysis was performed on uncertain and potentially influential input parameters. Enlarging the surveillance zones from 10 to 15 km, combined with pre-emptive depopulation over a 1-km radius around detected herds resulted in the lowest total costs. This was still the case even when the different input parameters were changed in the sensitivity analysis. Changing the resources for clinical surveillance did not affect the epidemic consequences. In conclusion, an FMD epidemic in Denmark would have a larger economic impact on the agricultural sector than previously anticipated. Furthermore, the control of a potential FMD outbreak in Denmark may be improved by combining pre-emptive depopulation with an enlarged protection or surveillance zone.

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Latent class analysis of bulk tank milk PCR and ELISA testing for herd level diagnosis of Mycoplasma bovis

The bacterium Mycoplasma bovis causes disease in cattle of all ages. An apparent increase in the occurrence of M. bovis associated outbreaks among Danish dairy cattle herds since 2011 has prompted a need for knowledge regarding herd-level diagnostic performance. Therefore, the objective of this study was to evaluate the herd-level diagnostic performance of an indirect ELISA test by comparison to a real-time PCR test when diagnosing M. bovis in cattle herds of bulk tank milk. Bulk tank milk samples from Danish dairy herds (N=3437) were analysed with both the antibody detecting BIO K 302 M. bovis ELISA kit and the antigen detecting PathoProof Mastitis Major-3 kit. As none of these are considered a gold standard test for herd-level diagnostics we applied a series of Bayesian latent class analyses for a range of ELISA cut-off values. The negative and positive predictive values were calculated for hypothetical true national prevalences (1, 5, 10, 15 and 20%) of infected herds. We estimated that the ELISA test had a median sensitivity and specificity of 60.4 [37.5-96.2 95% Posterior Credibility Interval] and 97.3 [94.0-99.8 95% PCI] at the currently recommended cut-off (37% Optical density Coefficient). These changed to 43.5 [21.1-92.5 95% PCI] and 99.6 [98.8-100 95% PCI] if the cut-off was increased to 50 ODC%. In addition, herd-level diagnosis by ELISA would result in fewer false positives at a cut-off value of 50 ODC% compared to 37 ODC% without compromising the negative predictive value.

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Mean effective sensitivity for Mycobacterium avium subsp paratuberculosis infection in cattle herds

Background: Mycobacterium avium subsp. paratuberculosis (MAP) infections in cattle are generally challenging to detect and cost-effective test strategies are consequently difficult to identify. MAP-specific antibody ELISAs for milk and serum are relatively inexpensive, but their utility is influenced by a number of factors such as herd size, herd composition and diagnostic sensitivity. The sensitivity of the test increases with the age of the tested animal, and therefore the general, or "mean effective sensitivity" (defined as the mean of the sensitivities for all animals within a population, MES), for detecting MAP within a herd is dependent upon the age distribution of the herd. For this study we used a dataset of cattle from 4,259 dairy herds and 4,078 non-dairy herds. The aim was to investigate the MES for groups of cattle considered to be reasonable entities for MAP surveillance and control, in order to assist the decision-makers in planning and optimizing these programs economically. We compared six different groups of cattle (three dairy and three non-dairy) in Denmark by calculating the MES for each herd in each group.

Results: The distribution of MES showed a large variation within and between groups, and in some groups we found a bimodal distribution of MES. Dairy herds generally showed higher MES than non-dairy herds. Dairy herds in a control programme for paratuberculosis showed a MES similar to all other dairy herds from which animals >2.0 years were tested (both groups had a median MES = 0.60). For the non-dairy groups, the sensitivity became much higher when animals <2.0 years and herds with less than 25 cattle were excluded, resulting in a median MES of 0.65.

Conclusion: The results showed that MES could indicate the effectiveness of testing different cattle groups for MAP, given that the data used are unbiased.

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Monitoring PRRS sero-prevalence in Danish breeding herds: Evaluation of algorithms performance

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Persistent Spatial Clusters of Prescribed Antimicrobials among Danish Pig Farms - A Register-Based Study
The emergence of pathogens resistant to antimicrobials has prompted political initiatives targeting a reduction in the use of veterinary antimicrobials in Denmark, especially for pigs. This study elucidates the tendency of pig farms with a significantly higher antimicrobial use to remain in clusters in certain geographical regions of Denmark. Animal Daily Doses/100 pigs/day were calculated for all three age groups of pigs (weaners, finishers and sows) for each quarter during 2012-13 in 6,143 commercial indoor pig producing farms. The data were split into four time periods of six months. Repeated spatial cluster analyses were performed to identify persistent clusters, i.e. areas included in a significant cluster throughout all four time periods. Antimicrobials prescribed for weaners did not result in any persistent clusters. In contrast, antimicrobial use in finishers clustered persistently in two areas (157 farms), while those issued for sows clustered in one area (51 farms). A multivariate analysis including data on antimicrobial use for weaners, finishers and sows as three separate outcomes resulted in three persistent clusters (551 farms). Compared to farms outside the clusters during this period, weaners, finishers and sows on farms within these clusters had 19%, 104% and 4% higher use of antimicrobials, respectively. Production type, farm type and farm size seemed to have some bearing on the clustering effect. Adding these factors as categorical covariates one at a time in the multivariate analysis reduced the persistent clusters by 24.3%, 30.5% and 34.1%, respectively.

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Pharmacodynamic modelling of in vitro activity of tetracycline against a representative, naturally occurring population of porcine Escherichia coli

The complex relationship between drug concentrations and bacterial growth rates require not only the minimum inhibitory concentration but also other parameters to capture the dynamic nature of the relationship. To analyse this relationship between tetracycline concentration and growth of Escherichia coli representative of those found in the Danish pig population, we compared the growth of 50 randomly selected strains. The observed net growth rates were used to describe the in vitro pharmacodynamic relationship between drug concentration and net growth rate based on E max model with three parameters: maximum net growth rate (α max ); concentration for a half-maximal response (E max ); and the Hill coefficient (γ). The net growth rate in the absence of antibiotic did not differ between susceptible and resistant isolates (P = 0.97). The net growth rate decreased with increasing tetracycline concentrations, and this decline was greater in susceptible strains than resistant strains. The lag phase, defined as the time needed for the strain to reach an OD600 value of 0.01, increased exponentially with increasing tetracycline concentration. The pharmacodynamic parameters confirmed that the [Formula: see text] between susceptible and resistant strains in the absence of a drug was not different. EC 50 increased linearly with MIC on a log-log scale, and γ was different between susceptible and resistant strains. The in vitro model parameters described the inhibition effect of tetracycline on E. coli when strains were exposed to a wide range of tetracycline concentrations. These parameters, along with in vivo pharmacokinetic data, may be useful in mathematical models to predict in vivo competitive growth of many different strains and for development of optimal dosing regimens for preventing selection of resistance.

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Pharmacokinetic-Pharmacodynamic Model To Evaluate Intramuscular Tetracycline Treatment Protocols To Prevent Antimicrobial Resistance in Pigs

High instances of antimicrobial resistance are linked to both routine and excessive antimicrobial use, but excessive or inappropriate use represents an unnecessary risk. The competitive growth advantages of resistant bacteria may be amplified by the strain dynamics; in particular, the extent to which resistant strains outcompete susceptible strains under antimicrobial pressure may depend not only on the antimicrobial treatment strategies but also on the epidemiological parameters, such as the composition of the bacterial strains in a pig. This study evaluated how variation in the dosing protocol for intramuscular administration of tetracycline and the composition of bacterial strains in a pig affect the level of
resistance in the intestine of a pig. Predictions were generated by a mathematical model of competitive growth of Escherichia coli strains in pigs under specified plasma concentration profiles of tetracycline. All dosing regimens result in a clear growth advantage for resistant strains. Short treatment duration was found to be preferable, since it allowed less time for resistant strains to outcompete the susceptible ones. Dosing frequency appeared to be ineffective at reducing the resistance levels. The number of competing strains had no apparent effect on the resistance level during treatment, but possession of fewer strains reduced the time to reach equilibrium after the end of treatment. To sum up, epidemiological parameters may have more profound influence on growth dynamics than dosing regimens and should be considered when designing improved treatment protocols.
Pre-test habituation improves the reliability of a handheld test of mechanical nociceptive threshold in dairy cows
Mechanical nociceptive threshold (MNT) testing has been used to investigate aspects of painful states in bovine claws. We investigated a handheld tool, where the applied stimulation force was monitored continuously relative to a pre-encoded based target force. The effect on MNT of two pre-testing habituation procedures was performed in two different experiments comprising a total of 88 sound Holsteins dairy cows kept either inside or outside their home environment. MNT testing was performed using five consecutive mechanical nociceptive stimulations per cow per test at a fixed pre-encoded target rate of 2.1 N/s. The habituation procedure performed in dairy cows kept in their home environment led to lowered intra-individual coefficient of variation of MNT (P < 0.001), increased MNT (P < 0.001) and decreased the discrepancy between applied and target force during stimulations (P < 0.001). Pre-test habituation improved the reliability of the handheld tool when used in dairy cows kept in their home environment.

Prevalence, risk factors and spatial analysis of infections with liver flukes in Danish cattle herds
Liver fluke infection, also known as fasciolosis, is a world-wide prevalent zoonotic parasitic disease infecting a wide range of host species and is caused by Fasciola hepatica. Despite of the substantial economic and animal welfare effects of the disease, knowledge on its prevalence and the factors related to its occurrence and distribution are scarce in Denmark. A retrospective study was performed using liver inspection data of approximately 1.5 million cattle for the period 2011 to 2013. Spatial analysis was carried out to explore whether the data on F. hepatica infection was clustered in space as this could help understand whether or not the infection was driven by local environmental factors. Both global and local spatial autocorrelation techniques were used. Herd level and environmental risk factors were evaluated for their association with prevalence of F. hepatica infection using Generalized Estimating Equations.
Prevalence, risk factors and spatial analysis of liver fluke infections in Danish cattle herds

Background: Fasciola hepatica, a trematode parasite (liver fluke), infects a wide range of host species causing fasciolosis. The disease is prevalent world-wide and causes considerable economic losses to the livestock industry. Fasciolosis is regarded as an emerging food-borne zoonosis. To promote awareness among farmers and to implement strategies to control the infection, this study examined the prevalence, spatial distribution and risk factors for Fasciola hepatica infection in Danish cattle herds. Methods: A retrospective population based study was performed using meat inspection data of approximately 1.5 million cattle slaughtered in the period 2011 to 2013. Annual cumulative prevalence of recorded liver fluke findings was calculated for each year. Global and local spatial cluster analysis was used to identify and map spatial patterns of Fasciola hepatica positive and negative herds to explore environmental indicators of infection. Herd level, trade and environmental risk factors were evaluated for association with infection using logistic regression. Herd infection status as predicted from the final risk factor model was compared with the observed status using heat maps to assess how well the model fitted the observed spatial pattern. Results: During the investigated period (2011-2013), an increase in annual herd prevalence was noted (2011-25.6%; 2012-28.4%; 2013-29.3%). The spatial analysis suggested significant clustering of positive and negative herds. Presence of streams, wetlands and pastures on farms showed a significant association with the presence of infection in cattle herds. Buying animals from positive herds was a risk factor on conventional farms. Additionally, risk of being infected with Fasciola hepatica was higher in non-dairy herds of medium size (>= 30 and <100) when compared to dairy and large (>=100) cattle herds. The observed spatial pattern could be reproduced by predictions of the risk factor model. Conclusions: This study showed an increase in annual herd level prevalence (2011 to 2013) indicating that an increasing proportion of herds are infected with Fasciola hepatica infection every year in Denmark. Fasciolosis was found to be associated with both herd and environmental factors where the infection was influenced by local factors that clustered geographically.
Preventing foot and mouth disease - how are the costs divided between the public authorities and the pig and cattle industries in Denmark?

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Simulating Spread of Antimicrobial Resistant Bacteria in the Pig Pen: try our online tool

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Spatial analysis and temporal trends of porcine reproductive and respiratory syndrome in Denmark from 2007 to 2010 based on laboratory submission data

Porcine reproductive and respiratory syndrome (PRRS) has been a cause for great concern to the Danish pig industry since it was first diagnosed in 1992. The causative agent of PRRS is an RNA virus which is divided into different genotypes. The clinical signs, as well as its morbidity and mortality, is highly variable between herds and regions. Two
different genotypes of PRRS virus (PRRSV) are found in Denmark: type 1 and type 2. Approximately 40% of Danish swine herds are seropositive for one or both PRRSV types. The objective of this study was to describe the temporal trend and spatial distribution of PRRSV in Danish swine herds from 2007 to 2010, based on type-specific serological tests from the PRRS surveillance and control program in Denmark using the results stored in the information management system at the National Veterinary Institute, Technical University of Denmark (DTU Vet). The average monthly seroprevalence of PRRSV type 1 was 9% (minimum of 5%; maximum of 13%) in breeding herds, and 20% (minimum of 14%; maximum of 26%) in production herds; PRRSV type 2 had an average seroprevalence of 3% (minimum of 1%; maximum of 9%) in breeding herds and of 9% (minimum of 5%; maximum of 13%) within production herds. The seroconversion rate followed a similar and consistent pattern, being higher for type 1 than for type 2 for both PRRSV types. Regarding the spatiotemporal results, the relative risk distribution maps changed over time as a consequence of the changes in PRRSV seroprevalence, suggesting a general decline in the extent of areas with higher relative risk for both type 1 and 2. Local spatial analysis results demonstrated the existence of statistically significant clusters in areas where the relative risk was higher for both herds. PRRSV type 1 seroprevalence was constantly higher than for PRRSV type 2 in both herd types. Significant spatial clusters were consistently found in Denmark, suggesting that PRRSV is endemic in these areas. Furthermore, relative risk distribution maps revealed different patterns over time as a consequence of the changes in seroprevalence.

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Temperature as a predictor of fouling and diarrhea in Slaughter pigs
The PigIT Project aims at improving welfare and production of slaughter pigs by integration of various sensor systems for alarm purposes. Here we present an exploratory analysis to assess the predictive value of temperature sensor data with respect to pen fouling and diarrhea. We recorded the temperature at four locations in two double-pens (by the drinking nipples and by the corridor) between November 2013 and December 2014. Logistic regression models were made to express the probability of fouling and diarrhea per day, and were reduced via backwards elimination. Furthermore, fitting the models was attempted with the raw temperature data as well as data averaged over 10, 15, 30 and 60 minutes. The predictive performances were evaluated with Matthews Correlation Coefficient (MCC). For diarrhea, the minimal and maximal temperatures at the water nipple and the corridor, as well as the maximal rate of temperature decrease, were found to be either significant or borderline significant. The same factors, with the addition of maximum rate in temperature increase, were found to be significant or borderline significant predictors for pen fouling. Both conditions were consistently detected at better than randomly (MCC between 0.422 and 0.557 for diarrhea, and between 0.386 and 0.560 for fouling). Thus, temperature information seems to contain predictive value in relation to fouling and diarrhea, but not enough to stand alone. It would thus be meaningful to combine this information with other available data to achieve an optimal predictive power.

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Temperature as a predictor of fouling and diarrhea in Slaughter pigs

Understanding the underlying pleiotropic relationships among quantitative traits is integral to predict correlated responses to artificial selection. The availability of large-scale next-generation sequence data in cattle has provided an opportunity to examine whether pleiotropy is responsible for overlapping QTLs in multiple economic traits. In the present study, we examined QTLs effecting cattle stillbirth, calf size, and adult stature located in the same genomic region. A genome scan with whole sequence variants revealed one QTL with large effects on the service sire calving index (SCI), and body conformation index (BCI) at the same location (~39 Mb) on chromosome 6 in Nordic Red cattle. The targeted region was analyzed for SCI and BCI component traits. The QTL peak included LCORL/NCAPG genes, which were earlier reported to influence fetal growth, and adult stature in several species. The QTL exhibited large effects on calf size and stature in Nordic Red cattle. Two deviant haplotypes (HAP1 and HAP2) were resolved, which increased calf size at birth, and affected adult body conformation. However, the haplotypes also resulted in increased calving difficulties and calf mortality due to increased calf size at birth. Haplotype locations overlapped, however linkage disequilibrium (LD) between the sites was low, suggesting two independent mutations responsible for similar effects. The difference in prevalence between the two haplotypes in Nordic Red subpopulations suggested independent origins in different populations. Results of our study identified QTLs with large effects on body conformation, and service sire calving traits on chromosome 6 in cattle. We present robust evidence that variation at the LCORL/NCAPG locus effects calf size at birth and adult stature. We suggest the two deviant haplotypes within the QTL were due to two independent mutations.

The SimSpay—Student Perceptions of a Low-Cost Build-It-Yourself Model for Novice Training of Surgical Skills in Canine Ovariohysterectomy

Practical and ethical considerations have led to an increased use of artificial substitutes for live animals in veterinary surgical skills training. However, commercially produced models are expensive and homemade models often require full-time staff to produce enough models for training large groups of students. In the Department of Veterinary Clinical and Animal Sciences of the University of Copenhagen, a low-cost build-it-yourself model, the SimSpay, was developed for novice training of surgical skills in canine ovariohysterectomy. The model did not require the use of trained technical staff or costly, hard-to-source supplies. The SimSpay was developed and implemented in the clinical veterinary curriculum in 2013. In 2014, 54 students participated in a questionnaire study to investigate their perception of the usefulness of the SimSpay as a learning tool. On a five-point Likert-type scale, students were asked to rate their perceived levels of competence, confidence, and anatomic knowledge before and after SimSpay training. Results demonstrate a strongly significant (p < .0001) increase in all three areas after training on the SimSpay. By increasing students' perceived levels of competence, confidence, and anatomic knowledge, the low-fidelity Sim Spay is a useful, low-cost learning tool for teaching...
Weaner production with low antimicrobial usage: a descriptive study

Background: Health, productivity and antimicrobial use in the production of pigs are expected to be interrelated to some extent. Previous studies on register-based data have investigated these correlations with a subsequent large variation residing at the farm level. In order to study such farm factors in more detail we designed an elaborate interview-guide. By in-depth interviews of farmers with well-managed 7-30 kg (weaner) productions we sought to describe a set of common key-factors characterizing their management practices. Identification of such common practices could be used in follow-up projects, investigating whether identified factors really are characteristic for good-practicing farmers.

Results: Eleven farms were selected for a farm visit and in-depth interview. Participating farms used less antimicrobials than the national median (8.2 animal daily doses/100 weaners/day), had a mortality below the national average (2.9%) and an average daily weight gain above the national average (443 g/day). Similarities were observed among participating farms, including the sectioning of farms, use of all-in-all-out procedures with subsequent cleaning, purchasing 7 kg weaners from only one source, as well as active participation in management by a committed farm owner. Most farmers had a specific point of focus in their management, and were convinced that this was the reason for their success. This included; feeding, treatment strategy, refurbishment of facilities and presence in the shed.

Conclusion: According to register data, participating farms were alike; in the good league regarding use of antimicrobials, mortality and daily growth. However, on-farm interviews elucidated more heterogeneity among farmers than expected. Most of the farmers had a specific point of focus, which they considered to be crucial for their good results. These results indicate the importance of non-registerable factors, highlighting the value of qualitative study techniques in the understanding of human actions. Further studies on the effect of various farmer types are recommended.
Within- and between-herd prevalence variation of Mycobacterium avium subsp. paratuberculosis infection among control programme herds in Denmark (2011-2013)

This study aimed to estimate the between- (HTP) and within- (TP) herd true prevalence distribution of Mycobacterium avium subsp. paratuberculosis (MAP) infection in dairy cattle herds participating in the Danish MAP control programme. All herds enrolled in the programme between 2011 and 2013 were included in the analysis, and one annual milk-ELISA test of all lactating cows present in such herds was considered. A Bayesian latent class model was used to obtain HTP and TP posterior distributions for each year. The model adjusts for uncertainty in age-specific test sensitivity and prior prevalence estimates. Bayesian posterior probabilities were computed in order to compare prevalence between the years. A total of 665,700 samples were included in the study, from 221,914, 224,040, and 220,466 cows sourced from 1138, 1112, and 1059 herds in years 2011, 2012, and 2013, respectively. In that period, HTP estimates of 0.92 (95% posterior probability interval (PPI), 0.87-0.96), 0.78 (95% PPI, 0.74-0.83), and 0.75 (95% PPI, 0.71-0.78) were recorded, respectively. Low TP were observed, with population mean estimates of 0.08 (95% PPI, 0.07-0.08), 0.07 (95% PPI, 0.07-0.08), and 0.07 (95% PPI, 0.06-0.07) for the three consecutive years. Statistically-important differences were recorded for HTP and population mean TP estimates between years, indicating a trend for a decreasing level of MAP infection at both herd and animal level. Model results showed that MAP infection was widespread among the Dairy cattle herds participating in the Danish control programme, though in general it was kept at very low levels.
herds enrolled in 2008-2010 started at approximately 6% and by January 2014 was reduced to about 3%. In addition to these data, a “sampling error” in August 2011 resulted in the availability of a sample of 99 herds that were not enrolled in the programme. They had a median test-prevalence of 5.5% compared to 3.1% in 268 herds from the 2006-2007 cohort tested in the same month. This sample and associated estimates were used to validate that a test prevalence reduction was due to the programme. The decline in test-prevalence has been statistically associated to herd-level factors such as low level of livestock purchases and culling of cows deemed to be infectious, but not really to other management factors. On national level, the first initiatives included training of herd health advisors, information campaigns including various sources of information material and farmer’s meetings. In the last approximately 5 years, the programme has run routinely with few specific extraordinary activities, except for a “continuous” flow of diagnostic test information four times annually in each herd. This information can be used for detection and management of infectious animals and for prevalence monitoring.

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Association of MAP specific ELISA-responses and productive parameters in 314 Danish dairy farms

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Association of map specific ELISA-responses and productive parameters in 367 danish dairy farms

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Bulk tank milk ELISA for detection of antibodies to Mycobacterium avium subsp paratuberculosis: Correlation between repeated tests and within-herd antibody-prevalence

Detection of bulk tank milk (BTM) antibodies using ELISA (BTM-ELISA) may constitute an inexpensive test for surveillance of Mycobacterium avium subsp. paratuberculosis (MAP) infection in dairy cattle herds provided that the test is accurate and consistent. The objectives of this study were to determine: (a) the correlation between repeated BTM reactions; and (b) the association between the BTM antibody ELISA-level and the within-herd prevalence of antibody-positive cows. Eight BTM samples per herd and approximately four milk samples per lactating cow per herd were collected from each of 108 Danish Holstein herds over a period of one year. All samples were tested using a commercial indirect ELISA for detection of MAP specific antibodies. The individual cow's results were dichotomised and used to estimate the within-herd antibody prevalence at each test-date. These prevalences were then combined with the ELISA reading on the BTM test-date closest to the cow-level test-date. A mixed-effect analysis of covariance with autoregressive type 1 correlation structure was carried out using the log-transformed BTM-ELISA results as outcome. This model was used to assess the correlation between repeated tests with and without correction for within-herd antibody prevalence. The repeated BTM-recordings were highly correlated with a correlation of 0.80 between samples collected 1.5 months apart. The within-herd antibody prevalence significantly influenced this estimate (p <0.0001), which dropped to 0.60 when corrected for the within-herd antibody prevalence. Although the test-results were relatively consistent and correlated with the within-herd prevalence, the magnitude of the test-values makes it difficult to use the BTM-ELISA for surveillance of MAP infections in practice.

Dynamic monitoring of weight data at the pen vs at the individual level

The PigIT project, led by the University of Copenhagen, aims at improving welfare and productivity in growing pigs using ICT methods. Automatically and manually recorded data are currently being collected in a production herd. One of the first steps of the project is to make use of the manually recorded weight data from finisher pigs. Data are collected at insertion and at the exit of the first pigs in the pen, and in few pens, the weight is recorded weekly. Dynamic linear models are fitted on the weight data, at the pig level (univariate), at the double pen level using averaged weight (univariate) and using individual pig values as parameters in a hierarchical (multivariate) model including section, double pen, and individual level. Variance components of the different models are estimated using the Expectation Maximization algorithm. The difference of information obtained at the individual vs pen level is thereafter assessed. Whereas weight data is usually monitored after a batch is being sent to the slaughter house, this method provides weekly updating of the data. Perspectives of application include dynamic monitoring of weight data in relation to events such as diarrhoea, tail biting and fouling in order to assess whether it is possible to detect deviations of patterns before or during the occurrence of these events.
Erratum: Apparent prevalence of beef carcasses contaminated with mycobacterium avium subsp. paratuberculosis sampled from danish slaughter cattle (Veterinary Medicine International)

A tabulation error appeared in Table 1. The fecal contamination data for Age <2 years and >2 years were incorrectly recorded into the table. Whereas the numbers in the table were transposed incorrectly, the actual statistical analyses remain correct. The revised table is reproduced below.

Handheld mechanical nociceptive threshold testing in dairy cows - intra-individual variation, inter-observer agreement and variation over time

All methods showed a high degree of intra-individual variation, and no combination of device and stimulation site showed superior precision. Mean difference between observers was low, and MNT was not consistent over time. Further development of the methods is required before they can be used in research to investigate possible relations between claw lesions and hyperalgesia.
iCull - a herd-specific tool for financial evaluation of the impact of paratuberculosis

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Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Dynamical Systems, University of Copenhagen
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Opportunities and challenges of using diagnostic databases for monitoring livestock diseases in Denmark
Several databases are being used in Denmark to record information at all stages and levels of modern livestock production. These databases are all developed for different purposes and gather large volumes of routinely collected data. Examples of existing databases for livestock are the Central Husbandry Register (CHR), Meat inspection database for cattle and swine, mortality database and movement database. These databases are owned by the Ministry of Food, Agriculture and Fisheries. Other databases, such as the Danish Cattle Database, are owned by the agricultural sector. In addition to the technical and political bottlenecks of gathering and combining data from the different databases, the questions remain on the sensitivity and timeliness of data for detecting unexpected animal health events. Thus, it is important to explore changes in data records over time from different databases in order to detect potential patterns. This includes describing trends, seasonality and the potential impact of covariates on the baseline patterns. The potential of these data as monitoring tools can be evaluated using performance indicators such as residuals, predictive positive values, sensitivity and specificity, and by comparing the predictions of models with previous diseases events in Denmark. A further challenge is to identify the most adequate surveillance timescale (i.e. daily, weekly or monthly basis) as well as suitable spatial distances, in order to identify outlier events when the features of the alarm (e.g. shape and amplitude) are unknown. Using rule-based anomaly detection will allow developing a spatio-temporal monitoring framework based on time-series analysis and statistical process control in order to optimize methods for detection of anomalies in data patterns and methods for early warning. It is expected that the use of such information in space and time, might provide information which can be used either directly as a syndromic surveillance tool or to aid in a more targeted or directed disease surveillance program. This will enable a timely and appropriate response to a disease outbreak, minimizing economic impacts through timely implementation of disease prevention and control measures.

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Organisations: National Veterinary Institute, Section for Epidemiology
Contributors: Lopes Antunes, A. C., Hisham Beshara Halasa, T., Toft, N.
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Event: Abstract from 8th Annual Meeting of Epizone, Copenhagen, Denmark.
Opportunities and challenges of using diagnostic databases for monitoring livestock diseases in Denmark

Several databases are being used in Denmark to record information at different stages and levels of modern livestock production gathering large volumes of routinely collected data. This poster describes an ongoing PhD project at the National Veterinary Institute of the Technical University of Denmark with the objective of developing a monitoring framework based on spatiotemporal analysis to optimize methods for detection of anomalies in submission patterns and methods for early warning.

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Persistent spatial clusters of prescribed porcine antimicrobials

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Rapportering af danske svins antibiotikaforbrug - hvor stor betydning har beregningsmetoden?

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Regional disturbances in blood flow and metabolism in equine limb wound healing with formation of exuberant granulation tissue

As in other fibroproliferative disorders, hypoxia has been suggested to play a key role in the pathogenesis of exuberant granulation tissue (EGT). The purpose of this study was to investigate metabolism and blood flow locally in full-thickness wounds healing with (limb wounds) and without (body wounds) formation of EGT. Microdialysis was used to recover endogenous metabolites from the wounds, and laser Doppler flowmetry was used to measure blood flow. Measurements were performed before wounding and 1-28 days after wounding. Blood flow was consistently lower in limb wounds than in body wounds throughout the study period with no change over time. After wounding and throughout the study period, the glucose concentration was significantly lower in limb wounds than in body wounds, whereas the lactate level showed a significantly higher concentration in limb wounds. The lactate/glucose ratio displayed a significant difference between body and limb wounds. In conclusion, the metabolic disturbances may suggest an inadequate oxygen supply during the wound healing process in equine limb wounds healing with EGT. This may be related to the inherently decreased perfusion in the wound bed of limb wounds.

Risk factors and epidemiological characteristics of new neonatal porcine diarrhoea syndrome in four Danish herds

Background: The epidemiology of New Neonatal Porcine Diarrhoea Syndrome (NNPDS) was studied in four selected herds. A total of 941 new born piglets in 86 litters were evaluated for five consecutive days. NNPDS is a newly emerged syndrome, characterized by diarrhoea within the first week of life, which is un-responsive to antibiotics and not associated with known pathogens. The aetiology behind the syndrome is unknown, and specific risk factors predisposing piglets to develop NNPDS also remain to be determined. The study evaluated sow and piglet-level risk factors for developing NNPDS and described the epidemiologic characteristics within four herds previously diagnosed with the syndrome.

NNPDS was defined as diarrhoea at any time-point during the second to fifth day of life. Results: NNPDS was observed in a total of 60% (range: 39%-89%) of first parity piglets and 36% (range: 19-65%) of piglets born by mature sows. In total of 26% of piglets had liquid faeces on the day of birth. Approximately half of these piglets developed NNPDS also remain to be determined. The study evaluated sow and piglet-level risk factors for developing NNPDS and described the epidemiologic characteristics within four herds previously diagnosed with the syndrome. NNPDS was defined as diarrhoea at any time-point during the second to fifth day of life. Results: NNPDS was observed in a total of 60% (range: 39%-89%) of first parity piglets and 36% (range: 19-65%) of piglets born by mature sows. In total of 26% of piglets had liquid faeces on the day of birth. Approximately half of these piglets developed NNPDS. In the majority of cases (50-70% of cases within herds) symptoms started on the second or third day of life. Piglets in Herd 1 had 12.8 times higher probability of developing NNPDS than piglets in Herd 4. First parity piglets had a 4.1 higher probability of developing NNPDS than piglets born by mature sows. Birth weight and faecal consistency on the day of birth were minor risk factors, each significant within one herd. Conclusions: The most important factors associated with NNPDS were herd of origin and sow-parity. The reason for one of the herds experiencing a considerably more severe outbreak than the others was not explained by factors addressed in this study. The epidemiological pattern of diarrhoea varied a lot between herds; however, in all herds first parity piglets seemed predisposed. This association may be explained by an infectious background of the syndrome, but further studies are needed to explain this association.
Risk Factors for Survival in a University Hospital Population of Dogs with Epilepsy

Background: Although a common neurological disorder in dogs, long-term outcome of epilepsy is sparsely documented.

Objectives: To investigate risk factors for survival and duration of survival in a population of dogs with idiopathic epilepsy or epilepsy associated with a known intracranial cause. Animals: One hundred and two client owned dogs; 78 dogs with idiopathic epilepsy and 24 dogs with epilepsy associated with a known intracranial cause. Methods: A retrospective hospital based study with follow-up. Dogs diagnosed with epilepsy between 2002 and 2008 were enrolled in the study. Owners were interviewed by telephone using a structured questionnaire addressing epilepsy status, treatment, death/alive, and cause of death. Results: Median life span was 7.6 years, 9.2 years, and 5.8 years for all dogs, and dogs with idiopathic epilepsy or dogs with epilepsy associated with a known intracranial cause.
Spatiotemporal analysis of the Porcine Reproductive and Respiratory Syndrome epidemic in Denmark using laboratory submission data

Porcine reproductive and respiratory syndrome (PRRS) virus infects domestic swine populations causing production losses in many European countries. The virus has two different strains designated as European (EU) and American (US) strain. It has been assumed that 30% of Danish swine herds are sero-positive with one or both PRRS strains. The PRRS surveillance program is based on serology tests performed in a monthly or annual basis for the breeding and intensive production herds respectively. The objective of this study was to characterize the PRRS epidemic in Denmark from 2007 to 2010 using retrospective spatiotemporal analysis of serological tests. Records of PRRS serology submissions made from January 2007 to December 2010 stored in the DIANOVA Information Management System at the National Veterinary Institute (DTU Vet) were used in the analysis. Each submission consists in individual blood samples collected for surveillance purposes and its frequency depends on the herd type. The herds were classified as PRRS positive or negative based on the individual serology test results for both virus strains. The prevalence of both PRRS strains was calculated on a monthly basis for the breeding and intensive production herds. The herd numbers registered in the laboratory submissions were merged with the Danish Herd Identification System database, in order to obtain the geo-coordinates of the herds. Spatiotemporal analysis was performed, in order to characterize PRRS-EU and PRRS-US distributions for both control levels.

The analyses indicated a seasonal pattern in the between-herd prevalences of PRRS-EU and PRRS-US for both herds type. The prevalence of both PRRS strains was higher in the intensive production herds (mean=37%) when compared with the breeding herds (mean=17%). The spatiotemporal analysis detected a number of clusters of PRRS-EU and PRRS-US in both herd types. This suggests that PRRS still disperse between herds and that additional control efforts should be considered.

Spatiotemporal patterns, annual baseline and movement-related incidence of Streptococcus agalactiae infection in Danish dairy herds: 2000–2009

Several decades after the inception of the five-point plan for the control of contagious mastitis pathogens, Streptococcus agalactiae (S. agalactiae) persists as a fundamental threat to the dairy industry in many countries. A better understanding of the relative importance of within- and between-herd sources of new herd infections coupled with the spatiotemporal distribution of the infection, may aid in effective targeting of control efforts. Thus, the objectives of this study were: (1) to describe the spatiotemporal patterns of infection with S. agalactiae in the population of Danish dairy herds from 2000 to 2009 and (2) to estimate the annual herd-level baseline and movement-related incidence risks of S. agalactiae infection over the 10-year period. The analysis involved registry data on bacteriological culture of all bulk tank milk samples collected as part of the mandatory Danish S. agalactiae surveillance scheme as well as live cattle movements into dairy herds during the specified 10-year period. The results indicated that the predicted risk of a herd becoming infected with S.
agalactiae varied spatiotemporally; the risk being more homogeneous and higher in the period after 2005. Additionally, the annual baseline risks yielded significant yet distinctive patterns before and after 2005 – the risk of infection being higher in the latter phase. On the contrary, the annual movement-related risks revealed a non-significant pattern over the 10-year period. There was neither evidence for spatial clustering of cases relative to the population of herds at risk nor spatial dependency between herds. Nevertheless, the results signal a need to beef up within-herd biosecurity in order to reduce the risk of new herd infections.

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**Success factors in weaner production - with limited antimicrobials, high health and productivity. Case studies from Denmark**

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**Success factors in weaner production - with limited antimicrobials, high health and productivity. Case studies from Denmark**

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Success factors in weaner production - with limited antimicrobials, high health and productivity. Case studies from Denmark

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The effect of New Neonatal Porcine Diarrhoea Syndrome (NNPDS) on average daily gain and mortality in 4 Danish pig herds

Background: The study evaluated the effect of New Neonatal Porcine Diarrhoea Syndrome (NNPDS) on average daily gain (ADG) and mortality and described the clinical manifestations in four herds suffering from the syndrome. NNPDS is a diarrhoeic syndrome affecting piglets within the first week of life, which is not caused by enterotoxigenic Escherichia coli (ETEC), Clostridium perfringens (C. perfringens) type A/C, Clostridium difficile (C. difficile), rotavirus A, coronavirus, Cystoisospora suis, Strongyloides ransomi, Giardia spp or Cryptosporidium spp. Results: Piglets were estimated to have a negative ADG of 9 and 14 g when diarrhoeic for 1 day and >1 day respectively. However, if only diarrhoeic on the day of birth, no negative effect on ADG was seen. Piglets originating from severely affected litters were estimated to have a reduced ADG of 38 g. The study did not show an overall effect of diarrhoea on mortality, but herd of origin, sow parity, birth weight, and gender were significantly associated with mortality. In one of the herds, approximately 25% of the diarrhoeic piglets vs. 6% of the non-diarrhoeic piglets died, and 74% of necropsied piglets were diagnosed with enteritis. These findings indicate that the high mortality seen in this herd was due to diarrhoea. Conclusions: NNPDS negatively affected ADG in piglets, and even piglets that were diarrhoeic for one day only experienced a reduction in ADG. However, the study showed that diarrhoea restricted to the day of birth did not affect ADG and suggested this phenomenon to be unrelated to the syndrome. Since the diarrhoeal status of the litter had important effects on ADG, future research on NNPDS probably ought to focus on piglets from severely affected litters. The study showed important dissimilarities in the course of diarrhoea between the herds, and one herd was considerably more affected than the others. Within this herd, NNPDS seemed to be associated with a higher mortality, whereas in general the study did not show lethal effects of NNPDS.

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The effect of wind shielding and pen position on the average daily weight gain and feed conversion rate of grower/finisher pigs

Pigs are known to be particularly sensitive to heat and cold. If the temperature becomes too low, the pigs will grow less efficiently and be more susceptible to diseases such as pneumonia. If the temperature is too high, the pigs will tend to foul the pen, leading to additional risks of infection. Furthermore, unpublished data show that the temperature within a single section of grower/finisher pigs can vary considerably from pen to pen, and previous studies have shown that pigs can be significantly affected by wind, even when not directly exposed to it. To address this latter concern, some pig producers and research stations have implemented a shielding to prevent winds from blowing between separate sections of the pig housing buildings. However, according to our search of the literature, no published studies have ever investigated the effectiveness of such shielding. To determine the significance of the effects of wind shielding, linear mixed models were fitted to describe the average daily weight gain and feed conversion rate of 1271 groups (14 individuals per group) of purebred Duroc, Yorkshire and Danish Landrace boars, as a function of shielding (yes/no), insert season (winter, spring, summer, autumn), start weight and interaction effects between shielding and start weight and shielding and insert season. Such a model was fitted separately to the data collected for each breed. Shielding was found to have significant interaction effects with season (p=0.007) and start weight (p=0.0002) for Duroc pigs, but no effect could be shown for Yorkshire or Danish landrace. To determine the effect of a group’s placement relative to the central corridor of a grower/finisher station, a similar model was fitted to the data for Duroc pigs, replacing shielding with distance from the corridor (1st, 2nd, 3rd or 4th pen). The effect could not be tested for Yorkshire and Danish Landrace due to lack of data on these breeds. For groups of pigs above the average start weight, a clear tendency of higher growth rates at greater distances from the central corridor was observed, with the most significant differences being between groups placed in the 1st and 4th pen (p=0.0001). A similar effect was not seen on smaller pigs. Pen placement appears to have no effect on feed conversion rate. No interaction effects between shielding and distance to the corridor could be demonstrated. Furthermore, in models including both factors, the effect of distance to corridor completely dominated over the effect of shielding, suggesting that shielding should at most be considered of secondary importance.
An Observational Study with Long-Term Follow-Up of Canine Cognitive Dysfunction: Clinical Characteristics, Survival, and Risk Factors

Background
Canine cognitive dysfunction (CCD) is a neurodegenerative condition affecting geriatric dogs and sharing several characteristics with human Alzheimer's disease (AD). CCD manifests as alterations of behavioral patterns and daily routines. Clinical signs are associated with neurodegenerative changes (eg, cortical atrophy and amyloid-beta deposits).

Objectives
To investigate clinical characteristics, survival, and risk factors with CCD. Vitamin E was investigated as a potential marker of CCD.

Methods
Ninety-four dogs >8 years of age were investigated with a validated CCD questionnaire and allocated to CCD, borderline CCD (b-CCD) and non-CCD groups. The dogs were included in 2008–2009 and followed up in an observational study until follow-up in 2012.

Results
Four key clinical signs dominated in dogs with CCD: sleeping during the day and restless at night, decreased interaction, disorientation at home, and anxiety. A number of borderline CCD cases developed into CCD over time indicating that a prodromal stage of CCD may exist. CCD did not influence survival negatively. Small breeds did not show better survival than large breeds (P = .055) and there was no difference between sexes (P = .99).

Conclusions and Clinical Importance
A few key questions addressing sleep-wake cycle, interaction, and signs of confusion and anxiety can be used as a clinical marker of CCD. Special attention should be paid to anxiety in dogs with CCD because it may be especially stressful to both dog and owner. Dogs with CCD seem to have a good chance of living a full lifespan if supported by the veterinarian and the owner.
Bayesian estimation of sensitivity and specificity of Coxiella burnetii antibody ELISA tests in bovine blood and milk

Serological tests for Coxiella burnetii (the causative agent of Q fever) antibodies are usually based on enzyme linked immunosorbent assay (ELISA) although this method is not thoroughly evaluated. The objective of this study was to determine the sensitivity and specificity of an ELISA for detection of C. burnetii antibodies in milk and blood samples, using latent class models in a Bayesian analysis. Blood and milk samples of 568 lactating cows from 17 Danish dairy cattle herds collected in 2008 were used. The best combination of sensitivity and specificity estimates was revealed at a sample to positive (S/P) cut-off of 40 for both blood and milk ELISAs. At this cut-off, sensitivity of milk ELISA was 0.86 (95% posterior credibility interval [PCI] [0.76; 0.96]). This was slightly but insignificantly higher than sensitivity of blood ELISA (0.84; 95% PCI [0.75; 0.93]). The specificity estimates of the ELISA methods on milk and blood were equal at 0.99. No conditional dependence was observed between the specificity estimates of the two test methods. However, the sensitivity estimates of both tests were significantly reduced when conditional covariances ≥40 were used. Collection of milk samples from lactating cows is relatively easy, non-invasive and inexpensive and hence milk ELISA may be a better option for screening lactating cows. But, blood ELISA is an option for screening non-lactating cattle.

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Dynamics of specific anti-Mycobacterium avium subsp. paratuberculosis antibody response through age

Mycobacterium avium subsp. paratuberculosis (MAP) causes a chronic infection in cattle. MAP infected cattle with humoral immune (HI) reactions with IgG antibodies are usually those where latency of infection has ceased and their infection is progressing towards reduced milk yield, weight loss and significant bacterial excretion in feces. The proportion of detectable infections among all infected animals that will develop disease is often referred to as ‘the tip of the iceberg’. The purpose of this study was to estimate this proportion. Test-records from 18,972 Danish dairy cows with MAP specific IgG antibodies on their final test-record were used to estimate age-specific sensitivities (Se). These cows were the infected ones considered to develop disease in a population with a representative age-distribution and were defined as cases. The specificity (Sp) of the test was estimated based on test-results from 166,905 cows, which had no MAP IgG antibodies in their final four test-records. The Sp, age-specific Se and maximum Se were used to estimate the probability of having HI at a given age resulting in the proportion of infected cows with HI at a given age. For cows 2 years of age, the proportion of detectable cases was 0.33, while it was 0.94 for cows 5 years of age. Thus, there was a significant shift in the tip of the iceberg with aging. This study provided a model for estimating the proportion of latent chronic infections that would progress to disease, and the results can be used to model infection dynamics.

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Effect of Pre-sampling Procedures on Real-time PCR used for diagnosis of intramammary infections with Staphylococcus aureus in dairy cows at routine milk recordings

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Estimation of test characteristics of real-time PCR and bacterial culture for diagnosis of subclinical intramammary infections with Streptococcus agalactiae in Danish dairy cattle in 2012 using latent class analysis

The misdiagnosis of intramammary infections (IMI) with Streptococcus agalactiae (S. agalactiae) could lead farmers to treat or cull animals unnecessarily. The objective of this field study was to estimate the sensitivity (Se) and specificity (Sp) of real-time PCR at different cut-offs for cycle threshold (Ct) values against bacterial culture (BC) for diagnosis of S. agalactiae IMI using latent class analysis to avoid the assumption of a perfect reference test. A total of 614 dairy cows were randomly selected from 6 herds with bulk tank PCR Ct value <= 39 for S. agalactiae and S. aureus. At milk recording, 2456 quarter milk samples were taken aseptically for BC and the routinely taken cow level milk samples were analyzed by PCR. Results showed that 53 cows (8.6%) were positive for S. agalactiae IMI by BC. Sensitivity of PCR at cut-offs; <= 39, <= 37, <= 34, and <= 32, was 96.2%, 91.9%, 87.2% and 73.9%, while Se of BC was 25.7%, 29.9%, 59.9% and 72.1%. Specificity of PCR at cut-offs; <= 39, <= 37, <= 34, and <= 32, was 96.8%, 96.9%, 96.7% and 97.22%, while Sp of BC was 99.7%, 99.5%, 99.2%, and 98.9%. The estimated prevalence of S. agalactiae IMI by PCR was higher than the apparent prevalence at the tested cut-offs, indicating under estimation of S. agalactiae IMI in the examined dairy cows. In conclusion, Se of PCR is always higher than Se of BC at all tested cut-offs. The lower cut-off, the more comparable becomes Se of PCR and Se of BC. The changes in Se in both PCR and BC at different Ct-value cut-offs may indicate a change in the definition of the latent infection. The similar Se of both tests at cut-off <= 32 may indicate high concentrations of S. agalactiae viable cells, representing a cow truly/heavily infected with S. agalactiae and thus easier to detect with BC. At cut-off <= 39 the latent definition of infection may reflect a more general condition of cows being positive for S. agalactiae. Our findings indicate that PCR Ct-value cut-offs should be chosen according to the underlying latent infection definition of interest. Latent class analysis proposes a useful alternative to classic test evaluation of diagnostic tests used for detection of S. agalactiae IMI in milk. (C) 2012 Elsevier B.V. All rights reserved.
Evaluation of tests for porcine endocarditis by latent class analysis

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Inter-observer agreement, diagnostic sensitivity and specificity of animal-based indicators of young lamb welfare

A scientific literature review and consensus of expert opinion used the welfare definitions provided by the Farm Animal Welfare Council (FAWC) Five Freedoms as the framework for selecting a set of animal-based indicators that were sensitive to the current on-farm welfare issues of young lambs (aged ≤6 weeks). Ten animal-based indicators assessed by observation – demeanour, response to stimulation, shivering, standing ability, posture, abdominal fill, body condition, lameness, eye condition and salivation were tested as part of the objective of developing valid, reliable and feasible animal-based measures of lamb welfare. The indicators were independently tested on 966 young lambs from 17 sheep flocks across Northwest England and Wales during December 2008 to April 2009 by four trained observers. Inter-observer reliability was assessed using Fleiss's kappa (κ), and the pair-wise agreement with an experienced, observer designated as the ‘test standard observer’ (TSO) was examined using Cohen's κ. Latent class analysis (LCA) estimated the sensitivity (Se) and specificity (Sp) of each observer without assuming a gold standard and predicted the Se and Sp of randomly selected observers who may apply the indicators in the future. Overall, good levels of inter-observer reliability, and high levels of Sp were identified for demeanour (κ = 0.54, Se ≥ 0.70, Sp ≥ 0.98), stimulation (κ = 0.57, Se = 0.30 to 0.77, Sp ≥ 0.98), shivering (κ = 0.55, Se = 0.37 to 0.85, Sp ≥ 0.99), standing ability (0.54, Se ≥ 0.80, Sp ≥ 0.99), posture (κ = 0.45, Se ≥ 0.56, Sp = 0.99), abdominal fill (κ = 0.44, Se = 0.39 to 0.98, Sp = 0.99), body condition (κ = 0.72, Se ≥ 0.38 to 0.90, Sp = 0.99), lameness (κ = 0.68, Se > 0.73, Sp = 1.00), and eye condition (κ = 0.72, Se ≥ 0.86, Sp = 0.99). LCA predicted that randomly selected observers had Se > 0.77 (acceptable), and Sp ≥ 0.98 (high) for assessments of demeanour, lameness, abdominal fill posture, body condition and eye condition. The diagnostic performance of some indicators was influenced by the composition of the study population, and it would be useful to test the indicators on lambs with a greater level of outcomes associated with poor welfare. The findings presented in this paper could be applied in the selection of valid, reliable and feasible indicators used for the purposes of on-farm assessments of lamb welfare.

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Latent class analysis of histology and bacteriology in spontaneous porcine endocarditis.

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Modeling the effect of direct and indirect contamination of on-farm bulk tank milk with Mycobacterium avium subsp. paratuberculosis

Mycobacterium avium subsp. paratuberculosis (MAP) in milk of bovine origin is suspected of being implicated in Crohn's disease in humans. Milk can be contaminated via direct excretion of MAP in milk or indirectly via fecal contamination of the milk. This study aimed at estimating the level of MAP in farm bulk tank milk and simulating the effect of direct and indirect contamination with MAP. The effect of discarding milk from test-positive cows at different prevalences was assessed. The concentration of MAP in milk was estimated using a simulation model, while taking direct and indirect contamination with MAP into account. Direct MAP contamination of milk was related to infection stages, while indirect contamination was associated with within-herd prevalence and distribution of cows in different stages of infection. Discarding of milk based on diagnostic test results was included as a control option. Median MAP load in farm bulk tank milk at within-herd infection prevalences from 7.5% to 60% were estimated to be 0.54-7.53 CFU/mL milk. Maximum concentration at the prevalence of 60% could be 1186 CFU/mL caused by shedding of high amounts of MAP in feces. At the prevalence of 15%, discarding milk from test positive cows would result in discarding 11% of milk and reduce the MAP level by 80%. Due to poor sensitivity of the diagnostic test, removing test-positive cows would not further reduce the already low concentration of MAP and it would not guarantee the milk as MAP-free. The model was relatively simple yet capable of capturing true infection status and associated contributions from milk and feces. Further knowledge on distribution of fecal excretion from infected cows is required because very few “super-shedders” might play a major role.

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Risk factors for subclinical intramammary infection in dairy goats in two longitudinal field studies evaluated by Bayesian logistic regression

Identification of risk factors for subclinical intramammary infections (IMI) in dairy goats should contribute to improved udder health. Intramammary infection may be diagnosed by bacteriological culture or by somatic cell count (SCC) of a milk sample. Both bacteriological culture and SCC are imperfect tests, particularly lacking sensitivity, which leads to misclassification and thus to biased estimates of odds ratios in risk factor studies. The objective of this study was to evaluate risk factors for the true (latent) IMI status of major pathogens in dairy goats. We used Bayesian logistic regression models that accounted for imperfect measurement of IMI by both culture and SCC.

Udder half milk samples were collected from 530 Dutch and 438 California dairy goats in 10 herds on 3 occasions during lactation. Udder halves were classified as positive or negative for isolation of a major pathogen (mostly Staphylococcus aureus) on bacteriological culture and as positive or negative for SCC (cut-off of 2000 x 10^3 cells/mL). Potentially controllable risk factors (udder conformation, teat size, teat shape, teat placement, teat-end shape, teat-end callosity thickness, teat-end callosity roughness, caprine arthritis encephalitis-virus infection status, and kidding season), and uncontrollable risk factors (parity, lactation stage, milk yield, pregnancy status, and breed) were measured in the Dutch study, the Californian study or in both studies. Bayesian logistic regression models were constructed in which the true (but latent) infection status was linked to the joint test results, as functions of test sensitivity and specificity. The latent IMI status was the dependent variable in the logistic regression model with risk factors as independent variables and with random herd and goat effects.

For the combined data from both studies, the culture-based estimate of apparent prevalence of major pathogens in udder halves was 2.6% (137/5220) and the estimate of the apparent prevalence of high SCC was 11.0% (581/5294). The model was able to estimate the performance characteristics of bacteriological culture and SCC together with the effect of risk factors on the true IMI status. Higher parity, late lactation and low milk yield were significantly related to higher odds of the latent IMI status. The only significant controllable risk factor was an udder base below the hocks.

Lack of a perfect reference test is a common problem in veterinary epidemiology and may lead to biased estimates of odds ratios or other measures of association in risk factor studies. The approach described herein can be used to address these problems. (C) 2012 Elsevier B.V. All rights reserved.
Serological diagnosis of avian influenza in poultry: is the haemagglutination inhibition test really the 'gold standard'?

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Survival and clinical outcome of dogs with ischaemic stroke
The objectives of the present study were to investigate survival time, possible predictors of survival and clinical outcome in dogs with ischaemic stroke. A retrospective study of dogs with a previous diagnosis of ischaemic stroke diagnosed by magnetic resonance imaging (MRI) was performed. The association between survival and the hypothesised risk factors was examined using univariable exact logistic regression. Survival was examined using Kaplan-Meier and Cox regression.

Twenty-two dogs were identified. Five dogs (23%) died within the first 30 days of the stroke event. Median survival in 30-day survivors was 505 days. Four dogs (18%) were still alive by the end of the study. Right-sided lesions posed a significantly increased risk of mortality with a median survival time in dogs with right-sided lesions of 24 days vs. 602 days in dogs with left sided lesions (P = 0.006). Clinical outcome was considered excellent in seven of 17(41%) 30-day survivors. Another seven 30-day survivors experienced new acute neurological signs within 6-17 months of the initial stroke event; in two of those cases a new ischaemic stroke was confirmed by MRI. In conclusion, dogs with ischaemic stroke have a fair to good prognosis in terms of survival and clinical outcome. However, owners should be informed of the risk of acute death within 30 days and of the possibility of new neurological events in survivors. Mortality was increased in dogs with right-sided lesions in this study. (C) 2012 Elsevier Ltd. All rights reserved.

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**SvSXP: a Strongylus vulgaris antigen with potential for prepatent diagnosis**

**Background**
Strongyle parasites are ubiquitous in grazing horses. Strongylus vulgaris, the most pathogenic of the large strongyles, is known for its extensive migration in the mesenteric arterial system. The lifecycle of S. vulgaris is characterised by a long prepatent period where the migrating larvae are virtually undetectable as there currently is no test available for diagnosing prepatent S. vulgaris infection. Presence of S. vulgaris larvae in the arterial system causes endarteritis and thrombosis with a risk of non-strangulating intestinal infarctions. Emergence of anthelmintic resistance among cyathostomins has led to recommendations of reduced treatment intensity by targeting horses that exceed a predetermined strongyle faecal egg count threshold. One study suggests an apparent increase in prevalence of S. vulgaris on farms where reduced anthelmintic treatment intensity has been implemented. These issues highlight the need for an accurate and reliable assay for diagnosing prepatent S. vulgaris infection.

**Methods**
Immunoscreening of a larval S. vulgaris cDNA library using hyperimmune serum raised against S. vulgaris excretory/secretory antigens was performed to identify potential diagnostic antigens. Immunoreactive clones were sequenced, one potential antigen was characterised, expressed as a recombinant protein, initially evaluated by western blot (WB) analysis, the diagnostic potential of the IgG subclasses was evaluated by ELISA, and the diagnostic accuracy evaluated using serum from 102 horses with known S. vulgaris infection status.

**Results**
The clone expressing the potential antigen encoded a S. vulgaris SXP/RAL2 homologue. The recombinant protein, rSvSXP, was shown to be a potential diagnostic antigen by WB analysis, and a target of serum IgGa, IgG(T) and total IgG in naturally infected horses, with IgG(T) antibodies being the most reliable indicator of S. vulgaris infection in horses. Evaluation of diagnostic accuracy of the ELISA resulted in a sensitivity of 73.3%, a specificity of 81.0%, a diagnostic odds ratio of 11.69; a positive likelihood ratio (LR) of 3.85 and a negative LR was 0.33. The area under the ROC curve was 0.820.

**Conclusion**
IgG(T) antibodies to recombinant SvSXP show potential for use as an antigen for prepatent diagnosis of migrating stages of S. vulgaris with moderate to good diagnostic accuracy.

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Temporal changes and risk factors for foot-pad dermatitis in Danish broilers

Foot-pad dermatitis is a major welfare concern of broilers caused by ammonia irritation from the bedding material. In Denmark, an action plan to control the condition was implemented in 2002 with monitoring through a foot scoring system at slaughter and with predefined limits that trigger sanctions. The objective of the present study was to study time trends and to identify predisposing factors on the flock lesion scores. The analysis was carried out on a database created by merging abattoir lesion data with antemortem evaluation data, and the flock productivity database managed by the farmers’ association. The database had a record for each flock and variables containing information on both flock foot-pad scores and a range of management factors. We observed a dramatic decline in flock lesion scores between the years 2002 and 2005 followed by a minimal decline hereafter. Mean flock lesion scores differed between abattoirs, and subsequent analysis was performed in a mixed effect model where abattoir was considered a random effect. The analysis showed that flock lesion scores increased when the litter quality was evaluated as poor during the on-site antemortem evaluation. Other significant risk factors were winter season as opposed to summer, low daily weight gain, straw as bedding material in contrast to wood shavings and sphagnum peat, and high age at slaughter. Stocking density was only weakly associated with flock lesion scores.


Social network analysis provides a valuable framework for understanding the dynamics of diseases on networks as well as a means for defining effective control measures. An understanding of the underlying contact pattern for a susceptible population is advisable before embarking on any strategy for disease control. The objective of this study was to characterise the network of Danish cattle movements over a 10-year period from 2000 to 2009 with a view to understanding: (1) cohesiveness of the network, (2) influential holdings and (3) structural vulnerability of the network. Network analyses of data involving all cattle movements in Denmark registered during the period of interest were performed. A total of 50,494 premises participated in 4,204,895 individual movements during the 10-year period. The results pointed to a predominantly scale-free structure of the network; though marked by small-world properties in March–April 2001 as well as in 24 other months during the period October 2006 to December 2009. The network was sparsely connected with markets being the key influential holdings. Its vulnerability to removal of markets suggests that targeting highly connected holdings during epidemics should be the focus of control efforts.
Background
Belgian Shepherds have focal genetic epilepsy. The prevalence of epilepsy has been estimated as 9.5% in the breed and as 33% in the family investigated. Dogs with epilepsy might have an increased risk of premature death.

Objective/Hypothesis
To investigate survival and selected risk factors for premature death in a Belgian Shepherd family with genetic epilepsy.

Animals
One hundred ninety-nine related Belgian Shepherds.

Methods
Longitudinal observational study, 2009–2011. Follow-up telephone interviews were all conducted using a structured questionnaire addressing epilepsy, including seizure history and phenomenology, possible remission, possible death, and cause of death.

Results
The life span of epileptic dogs was not significantly shortened by the presence of epilepsy (P = .87). Epilepsy was the predominant cause of death in the population (19/75 = 25%) and epilepsy-related deaths accounted for 70% (19/27) of all deaths in the group of dogs with epilepsy. Two probable sudden unexpected deaths related to epilepsy occurred in dogs with generalized seizures. Cluster seizures occurred in 33% (17/51) but did not significantly influence the life span of epileptic dogs. Dogs with epilepsy had an epilepsy remission proportion of 13.7%.

Conclusion and Clinical Importance
The Belgian Shepherds investigated in the present study display a focal genetic epilepsy with an overall benign course. The life span was not significantly affected by the presence of epilepsy.
Annual incidence, prevalence and transmission characteristics of *Streptococcus agalactiae* in Danish dairy herds

Contagious mastitis pathogens continue to pose an economic threat to the dairy industry. An understanding of their frequency and transmission dynamics is central to evaluating the effectiveness of control programmes. The objectives of this study were twofold: (1) to estimate the annual herd-level incidence rates and apparent prevalences of *Streptococcus agalactiae* (*S. agalactiae*) in the population of Danish dairy cattle herds over a 10-year period from 2000 to 2009 inclusive and (2) to estimate the herd-level entry and exit rates (demographic parameters), the transmission parameter, β, and recovery rate for *S. agalactiae* infection.

Data covering the specified period, on bacteriological culture of all bulk tank milk samples collected annually as part of the mandatory Danish *S. agalactiae* surveillance scheme, were extracted from the Danish Cattle Database and subsequently analysed. There was an increasing trend in both the incidence and prevalence of *S. agalactiae* over the study period. Per 100 herd-years the value of β was 54.1 (95% confidence interval [CI] 46.0–63.7); entry rate 0.3 (95% CI 0.2–0.4); infection-related exit rate 7.1 (95% CI 5.6–8.9); non-infection related exit rate 9.2 (95% CI 7.4–11.5) and recovery rate 40.0 (95% CI 36.8–43.5). This study demonstrates a need to tighten the current controls against *S. agalactiae* in order to lower its incidence.
Anxiety in veterinary surgical students: a quantitative study
The surgical educational environment is potentially stressful and this can negatively affect students' learning. The aim of this study was to investigate whether veterinary students' level of anxiety is higher in a surgical course than in a nonsurgical course and if pre-surgical training in a Surgical Skills Lab (SSL) has an anxiety reducing effect. Investigations were carried out as a comparative study and a parallel group study. Potential participants were fourth-year veterinary students who attended a surgical course (Basic Surgical Skills) and a non-surgical course (Clinical Examination Skills); both courses were offered in multiple classes (with a total of 171 students in 2009 and 156 students in 2010). All classes in 2009 participated in the SSL stage of the Basic Surgical Skills course before performing live-animal surgery, and one class (28 students) in 2010 did not. Two validated anxiety questionnaires (Spielberger's state-trait anxiety inventory and Cox and Kenardy's performance anxiety questionnaire) were used. Anxiety levels were measured before the non-surgical course (111 students from 2009) and before live-animal surgery during the surgical course (153 students from 2009 and 28 students from 2010). Our results show that anxiety levels in veterinary students are significantly higher in a surgical course than in a non-surgical course (p<.001), and that practicing in a SSL helps reduce anxiety before live-animal surgery (p<.005).

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Databases in Denmark: opportunities and constraints for welfare assessments

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Ecological determinants of highly pathogenic avian influenza (H5N1) outbreaks in Bangladesh

Background

The agro-ecology and poultry husbandry of the south Asian and south-east Asian countries share common features, however, with noticeable differences. Hence, the ecological determinants associated with risk of highly pathogenic avian influenza (HPAI-H5N1) outbreaks are expected to differ between Bangladesh and e.g., Thailand and Vietnam. The primary aim of the current study was to establish ecological determinants associated with the risk of HPAI-H5N1 outbreaks at subdistrict level in Bangladesh. The secondary aim was to explore the performance of two different statistical modeling approaches for unmeasured spatially correlated variation.

Methodology/Principal Findings

An ecological study at subdistrict level in Bangladesh was performed with 138 subdistricts with HPAI-H5N1 outbreaks during 2007–2008, and 326 subdistricts with no outbreaks. The association between ecological determinants and HPAI-H5N1 outbreaks was examined using a generalized linear mixed model. Spatial clustering of the ecological data was modeled using 1) an intrinsic conditional autoregressive (ICAR) model at subdistrict level considering their first order neighbors, and 2) a multilevel (ML) model with subdistricts nested within districts. Ecological determinants significantly associated with risk of HPAI-H5N1 outbreaks at subdistrict level were migratory birds' staging areas, river network, household density, literacy rate, poultry density, live bird markets, and highway network. Predictive risk maps were derived based on the resulting models. The resulting models indicate that the ML model absorbed some of the covariate effect of the ICAR model because of the neighbor structure implied in the two different models.

Conclusions/Significance

The study identified a new set of ecological determinants related to river networks, migratory birds' staging areas and literacy rate in addition to already known risk factors, and clarified that the generalized concept of free grazing duck and duck-rice cultivation interacted ecology are not significant determinants for Bangladesh. These findings will refine current understanding of the HPAI-H5N1 epidemiology in Bangladesh.

Effect of days in milk and milk yield on testing positive in milk antibody ELISA to Mycobacterium avium subsp. paratuberculosis in dairy cattle

Milk samples are becoming more used as a diagnostic specimen for assessment of occurrence of antibodies to Mycobacterium avium subsp. paratuberculosis (MAP). This study assessed the effect of days in milk (DIM) and milk yield on testing positive in a commercial MAP specific milk antibody ELISA among 222,774 Danish Holstein cows. Results showed that odds of testing positive on 1–2 DIM were 9–27 times higher than the rest of lactation, where the chance of testing positive varied less. The reason is most likely a high concentration of non-specific antibodies in colostrum. Consequently, samples from the first couple of DIM should be excluded from MAP testing until further information on their significance is established. Milk yield also had a significant effect on odds of testing positive due to its diluting effect. Inclusion of milk yield in the interpretation of test results could improve the diagnostic value, resulting in more predictable patterns corresponding to progression of infection.
Estimation the diagnostic performance of PathProof Mastitis PCR and bacterial culturing for the detection of Streptococcus agalactiae in milk of Danish dairy cows using latent class analysis

Evaluation of lameness prevalence in grazing and non-grazing herds Danish dairy herds - apparent vs. true prevalence

Evaluation of the antibacterial residue surveillance programme in Danish pigs using Bayesian methods
from 2005 to 2009 and limited knowledge about true prevalence and test sensitivity and specificity were included in the model.

According to the model, the true antibacterial residue prevalence in Danish pigs is very low in both sows (~0.20%) and slaughter pigs (~0.01%). Despite data constraints, the results suggest that the current screening test used in Denmark presents high sensitivity (85–99%) and very high specificity (>99%) for the most relevant antibacterial classes used in Danish pigs.

If high-risk slaughter pigs could be identified by taking into account antibacterial use or meat inspection risk factors, a potential risk-based sampling approach to antibacterial residue surveillance in slaughter pigs would allow reducing the sample size substantially, while increasing or maintaining the probability of detection. Hence, the antibacterial residue surveillance programme in Danish pigs would be more cost-effective than today.

Evaluation of two herd-level diagnostic tests for Streptococcus agalactiae using a latent class approach

Streptococcus agalactiae mastitis persists as a significant economic problem for the dairy industry in many countries. In Denmark, the annual surveillance programme for this mastitis pathogen initially based only on bacteriological culture of bulk tank milk (BTM) samples, has recently incorporated the use of the real-time PathoProof Mastitis PCR assay with the goal of improving detection of infected herds. The objective of our study was to estimate the herd sensitivity (Se) and specificity (Sp) of both tests of BTM samples using latent class models in a Bayesian analysis while evaluating the effect of herd-level covariates on the Se and Sp of the tests. BTM samples were collected from all 4258 Danish dairy herds in 2009 and screened for the presence of S. agalactiae using both tests.

The highest Se of PCR was realized at a cycle threshold (Ct) cut-off value of 40. At this cut-off, the Se of the PCR was
significantly higher (95.2; 95% posterior credibility interval [PCI] [88.2; 99.8]) than that of bacteriological culture (68.0; 95% PCI [55.1; 90.0]). However, culture had higher Sp (99.7; 95% PCI [99.3; 100.0]) compared to PCR (98.8; 95% PCI [97.2; 99.9]). The accuracy of the tests was unaffected by the herd-level covariates. We propose that screenings of BTM samples for S. agalactiae be based on the PCR assay with Ct readings of <40 considered as positive. However, for higher Ct values, confirmation of PCR test positive herds by bacteriological culture is advisable especially when the between-herd prevalence of S. agalactiae is low.

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Herd and sow-related risk factors for mortality in sows in group-housed systems
Mortality of sows is a major problem for pig production worldwide. In this study, we used hierarchical multivariable logistic analyses to investigate different risk factors for mortality at the sow and herd level in herds with group-housed pregnant sows. Data included 3652 pregnant and 1266 lactating sows from 34 sow herds. A clinical examination for 16 clinical signs was carried out for each sow, and information about 16 herd related factors was obtained by interviews. Farm records were used to obtain information about whether or not sows died suddenly or were euthanized within 3 months after the clinical examination. Factors increasing the risk of sow mortality in the gestation unit were solid pen floors (OR = 1.87), presence of vulva bites (OR = 1.73) and unwillingness to stand when approached (OR = 1.62). Factors increasing the risk of sow mortality in the lactation unit were pale vulva color (OR = 12.69), body leanness (OR = 4.11), and presence of shoulder ulcers (OR = 2.89). The estimated between herd variation was small. Thus, the findings for the sow level variables may be generally applicable for sows in herds with group housed systems.

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Latent class analysis of the diagnostic characteristics of PCR and conventional bacteriological culture in diagnosing intramammary infections caused by Staphylococcus aureus in dairy cows at dry off

Background
Staphylococcus aureus is one of the most common causes of intramammary infections in dairy cows at dry off. Reliable identification is important for disease management on herd level and for antimicrobial treatment of infected animals. Our objective was to evaluate the test characteristics of PathoProof™ Mastitis PCR Assay and bacteriological culture (BC) in diagnosing bovine intramammary infections caused by S. aureus at dry off at different PCR cycle threshold (Ct)-value cut-offs.

Methods
Sterile quarter samples and non-sterile composite samples from 140 animals in seven herds were collected in connection with the dairy herd improvement (DHI) milk recording. All quarter samples were analyzed using BC whereas all composite samples were analyzed with PathoProof™ Mastitis PCR Assay. Latent class analysis was used to estimate test properties for PCR and BC in the absence of a perfect reference test. The population was divided into two geographically divided subpopulations and the Hui-Walter 2-test 2-populations model applied to estimate Se, Sp for the two tests, and prevalence for the two subpopulations.

Results
The Se for PCR increased with increasing Ct-value cut-off, accompanied by a small decrease in Sp. For BC the Se decreased and Sp increased with increasing Ct-value cut-off. Most optimal test estimates for the real-time PCR assay were at a Ct-value cut-off of 37; 0.93 [95% posterior probability interval (PPI) 0.60-0.99] for Se and 0.95 [95% PPI 0.95-0.99] for Sp. At the same Ct-value cut-off, Se and Sp for BC were 0.83 [95% PPI 0.66-0.99] and 0.97 [95% PPI 0.91-0.99] respectively. Depending on the chosen PCR Ct-value cut-off, the prevalence in the subpopulations varied; the prevalence increased with increasing PCR Ct-value cut-offs.

Conclusion
Neither BC nor real-time PCR is a perfect test in detecting IMI in dairy cows at dry off. The changes in sensitivity and prevalence at different Ct-value cut-offs for both PCR and BC may indicate a change in the underlying disease definition. At low PCR Ct-value cut-offs the underlying disease definition may be a truly/heavily infected cow, whereas at higher PCR Ct-value cut-offs the disease definition may be a S. aureus positive cow.

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Modeling of Mycobacterium avium subsp. paratuberculosis in farm bulk tank milk

Mycobacterium avium subsp. paratuberculosis (MAP) in milk of bovine origin is suspected of being implicated in Crohn's disease in humans. Pasteurization is considered to reduce the concentration of MAP by at least 4 to 5 log10. This study aimed at estimating the level of MAP in milk at farm level and simulating the effect of different control options at different infection prevalences. The concentration of MAP in milk was estimated using a hierarchical simulation model representing individual cows in a herd while taking both direct and indirect contamination with MAP into account. Parameters included true within-herd infection prevalences with cows in different infection stages, which were used to estimate prevalences of milk and fecal shedders, and subsequently MAP concentrations in milk and feces. Cows in different infection stages were considered with different risks of excreting MAP testing positive. Furthermore, direct MAP contamination of milk was related to infection stages while indirect contamination was associated to within-herd prevalence and distribution of infection stages. Control options implemented included discarding of milk based on diagnostic test results. Median MAP load in farm bulk tank milk at within-herd infection prevalences from 7.5 to 60% were estimated to 0.74-6.81 cfu/ml, of which the contribution of direct contamination was less than 1%. Maximum concentration at the prevalence of 60% could be 1186 cfu/ml caused by shedding of high amounts of MAP in feces from super-shedders. At the prevalence of 15%, discarding milk from test positive cows would result in discarding 11% of milk and reduce the MAP level by 80%. The model was relatively simple yet capable of capturing true infection status and associated contributions from milk and feces. Further knowledge on distribution of fecal excretion from infected cows is required because very few ‘super-shedders’ might play a major role. The results can be used for a formal risk assessment including effects such as pasteurization.

Molecular epidemiology of circulating highly pathogenic avian influenza (H5N1) virus in chickens, in Bangladesh, 2007-2010
Bangladesh has been severely hit by highly pathogenic avian influenza H5N1 (HPAI-H5N1). However, little is known about the genetic diversity and the evolution of the circulating viruses in Bangladesh. In the present study, we analyzed the hemagglutinin gene of 30 Bangladeshi chicken isolates from 2007 through 2010. We analyzed the polybasic amino acid sequence motif of the cleavage site and amino acid substitution pattern. Phylogenetic history was reconstructed using neighbor-joining and Bayesian time-scaled methods. In addition, we used Mantel correlation tests to analyze the relation between genetic relatedness and spatial and temporal distances. Neighbor-joining phylogeography revealed that virus circulating in Bangladesh from 2007 through 2010 belonged to clade 2.2. The results suggest that clade 2.2 viruses are firmly entrenched and have probably become endemic in Bangladesh. We detected several amino acid substitutions, but they are not indicative of adaptation toward human infection. The Mantel correlation test confirmed significant correlation between genetic distances and temporal distances between the viruses. The Bayesian tree shows that isolates from waves 3 and 4 derived from a subgroup of isolates from the previous waves grouping with a high posterior probability (pp = 1.0). This indicates the possibility of formation of local subclades. One surprising finding of spatio-temporal analysis was that genetically identical virus caused independent outbreaks over a distance of more than 200 km and within 14 days of each other. This might indicate long distance dispersal through vectors such as migratory birds and vehicles, and challenges the effectiveness of movement restriction around 10 km radius of an outbreak. The study indicates possible endemicity of the clade 2.2 HPAI-H5N1 virus in Bangladesh. Furthermore, the formation of a subclade capable of transmission to humans cannot be ruled out. The findings of this study might provide valuable information for future surveillance, prevention and control programme.
Presence of Mycobacterium avium subsp. paratuberculosis (MAP) in milk for human consumption is a concern due to its possible relationship with Crohn's disease in humans. Pasteurization effectively reduces the MAP load by four to five logs, but the efficacy depends on the MAP concentration, which depends on the prevalence among contributing herds and individuals. Considerable variation of MAP in bulk tank milk (BTM) and individual cow's milk (IM) is reported, but factors associated with MAP occurrence in milk at farm level have not been described. This study systematically reviewed published studies aiming at estimating the occurrence of MAP in on-farm BTM and IM by meta-analysis. A total of 692 articles were identified through electronic databases and initially screened using title and abstract. The quality of the 61 potentially relevant articles was assessed using full text and 31 articles were eventually included in the meta-analysis. The apparent prevalence (AP) of MAP in BTM and IM on farm were summarized in relation to strata defined by the test used to identify MAP and the infection status of the herds/animals. There was considerable inconsistency in the reporting, resulting in missing information potentially explaining the dispersion in the estimated AP. The overall AP and 95% confidence intervals based on PCR and culture of MAP were summarized to 0.10 (0.04–0.22) in BTM and 0.20 (0.12–0.32) in IM. Quantifying the MAP load in test-positive milk samples was not possible because very few articles provided quantitative information on individual samples.
Prevalence of respiratory signs and identification of risk factors for respiratory morbidity in Swedish Yorkshire terriers

Yorkshire terriers may be prone to respiratory disease; however, limited epidemiological information is available. A cross-sectional study design was used to compare the prevalence of respiratory signs in Yorkshire terriers with the prevalence in a population of dogs in general and to identify risk factors for respiratory clinical signs within the Swedish population of Yorkshire terriers. Data on clinical signs and risk factors were obtained from a questionnaire. The prevalence of respiratory signs in general (RS) was significantly higher among Yorkshire terriers compared with control dogs (RS 56.3 per cent and 23.0 per cent), and likewise more frequent respiratory signs (FRS) (26.0 per cent and 5.0 per cent). Age, sex and breed were shown to be significant risk factors, and an interaction between age and sex was discovered. The study indicated a sex ratio reversal in the prevalence of RS – the probability of females having RS increased with advancing age, while the probability for males was fairly constant.

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Quantifying the impact of lameness on welfare and profitability of finisher pigs using expert opinions

Lameness in finisher pigs affects both animal welfare and farmers' profitability. However, information about the severity of pain and profit losses associated with individual causes of lameness is lacking. This study quantified and compared the pain and economic impact of nine different causes of lameness (e.g., infectious arthritis, claw lesions and osteochondrosis) using expert opinion. Six researchers working on animal behaviour and welfare and eight Danish pig veterinarians answered questionnaires regarding animal welfare and production, respectively. The probability of euthanasia, treatment with antibiotics and anaesthetics, and the changes in daily weight gain and feed conversion ratio were used to calculate the resulting profit loss for a pig suffering from each of the nine causes. To accommodate the uncertainty associated with the expert assessments, simulations were performed using probability distributions based on the minimum, median and maximum values. According to the experts, bone fractures caused the highest severity of pain and the largest reduction in profitability. Lesions to the claw wall and lesions to the volar area of the foot caused the lowest severity of pain. Arthritis due to Mycoplasma hyosynoviae and lesions to the volar area of the feet caused the smallest reduction in profitability. Considering the consequences of animal welfare and profitability concomitantly provides a transparent evaluation of the overall impact of lameness in finisher pigs.

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Size of the iceberg: proportion of Mycobacterium avium subsp. paratuberculosis infected cattle with and without specific antibodies

Diagnosis of chronic infections such as infections with Mycobacterium avium subsp. paratuberculosis (MAP) may be hampered by low sensitivity of diagnostic tests, because the infection remains latent. However, sensitivity increases with age because few infections remain latent. The proportion of detectable infections among all infected is often referred to as ‘the tip of the iceberg’. For MAP infections, infected cattle may be divided into those with cell-mediated immune reactions (CMI) during latent infection, and those with humoral immune reactions (HI) characterized by IgG1 antibodies. The purpose of this study was to estimate the proportion of cows having HI among all cows infected with MAP by assuming an infected cow had either CMI or HI. Prior test-records from 12,174 Danish dairy cows, which were ultimately deemed to have MAP specific IgG1 antibodies, were used to estimate age-specific sensitivities (Se). The specificity (Sp) of the test was estimated based on prior test-results among 96,138 cows, which ultimately had no MAP IgG1 antibodies. The Sp, age-specific Se and maximum Se were used to estimate the probability of having CMI and HI at a given age supplying the proportion of infected cows with HI at a given age. The Se was estimated to 0.985. Se ranged from 0.22 at 2 years of age to 0.58 at 3 years of age, 0.74 at 4 years of age to a maximum of 0.83 at 10 years of age. The resulting proportions of infected cows with HI were 0.24 at 2 years of age and 0.96 at 5 years of age, i.e. a significant shift in the size of the iceberg. Although the ‘iceberg’ concept is well-known among paratuberculosis researchers, the size of the iceberg has not previously been characterized. Results can be used for inclusion of the distribution of cows in different infection stages at different ages in mathematical modeling of infection dynamics. In practice, positive and negative predictive values can be calculated for cows at different ages and in populations with different prevalences.
Spatial differences in occurrence of paratuberculosis in Danish dairy herds and in control programme participation

Paratuberculosis is a chronic infection of economic importance to the cattle industry and a voluntary control programme is offered to Danish dairy farmers. Our objective was to evaluate spatial differences in both control programme participation and paratuberculosis prevalence in Denmark.

The study included 4414 dairy herds: 1249 were participating in the control programme, and 1503 were tested for antibodies to Mycobacterium avium subsp. paratuberculosis (MAP). Spatial differences were evaluated by kernel smoothing, kriging, and cluster analysis. Participation was lowest among herds on the island Zealand (≤23%). The risk of a herd being infected with MAP was found to be high on most of Zealand, but the uncertainty of this result was large due to a limited number of tested herds. In the rest of the country, the south western part of the peninsula Jutland had the highest risk of MAP (≥91%). The risk of MAP was also high (86–91%) in the northern part of both Jutland and Funen. The predicted apparent within-herd prevalence was highest (5–8.5%) in some local areas across Jutland, in the north western part of the island Funen, and in the south and western part of Zealand. Scan statistics located the primary cluster of herds with high apparent within-herd prevalence in the western part of Funen. Furthermore, a number of significant clusters were found in Jutland and a single significant cluster in Zealand. Consistency was found between kriging and scan statistics results with respect to location of areas with high apparent within-herd prevalence of MAP.

Potential explanations for differences in participation include herd size and local herd health advisers, whereas for example soil characteristics might influence prevalence. Further studies are needed to evaluate these and other risk factors.

Temporal development of antibodies in Mycobacterium avium subsp. paratuberculosis infected cattle

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True prevalence estimation in an on-farm welfare assessment scheme - How to deal with misclassification

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Visual outcome after corneal transplantation for corneal perforation and iris prolapse in 37 horses: 1998-2010

Reasons for performing study
We wanted to investigate the visual outcome of horses presented with iris prolapse and treated with corneal transplantation.

Objective
To evaluate the visual outcome of horses with iris prolapse treated with penetrating keratoplasty alone and penetrating keratoplasty in combination with overlying conjunctival or amniotic membrane grafting.

Methods
A retrospective medical records study of horses presented to the University of Florida Veterinary Medical Center for iris prolapse and treated with penetrating keratoplasty in the period of 1998-2010. Data collected from the medical records included signalment, clinical descriptions of ocular lesions, treatments, and therapeutic outcome.

Results
Iris prolapses in this study were caused by corneal ulcers with keratomalacia (n = 37). All horses were treated medically for infection, hyperproteinase activity and iridocyclitis, and then surgically treated with either penetrating keratoplasty alone (n = 9) or penetrating keratoplasty with either a conjunctival pedicle flap (n = 22), amniotic membrane transplant (n = 5) or amnion membrane and conjunctival pedicle flap (n = 1). The eyes were visual postoperatively in a majority of the cases (n = 24; 64.9%). Limited vision was noted in 6 eyes (16.2%), 3 eyes became phthisical (8.1%) and 4 globes were enucleated (10.8%). Graft rejection manifested as some degree of donor corneal graft opacification in all cases. Anterior synechiae were present in 48.6% of the eyes. Wound dehiscence and aqueous humour leakage were also common as post operative problems.

Conclusion
Penetrating keratoplasty alone or in combination with an overlying graft of conjunctiva or amniotic membrane can achieve a successful visual outcome in a high percentage of horses with iris prolapse.
Milk recordings and meat inspection data as a diagnostic tool for identifying dairy herds with welfare problems

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A meta-analysis comparing the effect of PCV2 vaccines on average daily weight gain and mortality rate in pigs from weaning to slaughter

The aim of this investigation was, through a meta-analysis, to review the published literature concerning the effect of PCV2 vaccination on the average daily weight gain (ADG) and on the mortality rate in pigs from weaning to slaughter.

The review was restricted to studies investigating the effect of vaccines against PCV2 published from 2006 to 2008, identified using computerised literature databases. Only studies that met the following criteria were included: commercial vaccines were used, pigs or pens were assigned randomly to vaccination versus control groups in herds naturally infected with PCV2, and vaccinated and non-vaccinated pigs were housed together. Furthermore, it was a requirement that sample size, age at vaccination, and production period were stated. The levels of ADG and mortality rate had to be comparable to those seen in modern intensive swine production.

In total, 107 studies were identified; 70 were excluded because they did not fulfill the inclusion criteria and 13 were identical to results published elsewhere.

A significant effect of PCV2 vaccination on ADG was found for pigs in all production phases. The largest increase in ADG was found for finishing pigs (41.5 g) and nursery-finishing pigs (33.6 g) with only 10.6 g increase in the nursery pigs. Mortality rate was significantly reduced for finishing pigs (4.4%) and nursery-finishing pigs (5.4%), but not for nursery pigs (0.25%). Herds negative for PRRS had a significantly larger increase in ADG compared to herds positive for PRRS. The PRRS status had no effect on mortality rate.

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Apparent Prevalence of Beef Carcasses Contaminated with Mycobacterium avium subsp. paratuberculosis Sampled from Danish Slaughter Cattle

Presence of Mycobacterium avium subsp. paratuberculosis (MAP) in beef has been reported as a public health concern because asymptotically infected cattle may contain MAP in tissues that are used for human consumption. Associations between MAP carcasses contamination and animal characteristics such as age, breed, production type, and carcass classification were assessed. Cheek muscles from 501 carcasses were sampled cross-sectionally at a Danish abattoir and tested for presence of viable MAP and MAP DNA by bacterial culture and IS900 realtime PCR, respectively. Cheek muscle tissues from carcasses of two dairy cows were positive by culture whereas 4% of the animals were estimated with ≥10 CFU/gram muscle based on realtime PCR. Age was found to be associated with carcass contamination with MAP. The observed viable MAP prevalence in beef carcasses was low. However, detection of MAP and MAP DNA in muscle tissues suggested that bacteremia occurred in slaughtered cattle.

Associations between the time of conception and the shape of the lactation curve in early lactation in Norwegian dairy cattle

Background
This study was carried out to determine if an association exists between the shape of the lactation curve before it is influenced by the event of conception and the time from calving to conception in Norwegian dairy cattle. Lactation curves of Norwegian Red cows during 5 to 42 days in milk (DIM) were compared between cows conceiving between 43 and 93 DIM and cows conceiving after 93 DIM.

Methods
Data from 23,049 cows, represented by one lactation each, with 219,538 monthly test days were extracted from the
Norwegian Dairy Herd Recording System, which represents 97% of all Norwegian dairy cows. Besides veterinary treatments, these records also included information on daily milk yield at monthly test days. The data were stratified by parity groups (1, 2, and 3 and higher) and time to conception periods (43-93 DIM and >93 DIM). The sample was selected using the following selection criteria: conception later than 42 DIM, calving season July to September, no records of veterinary treatment and the level of energy fed as concentrates between 8.69 and 12.83 MJ. The shape of the lactation curves were parameterized using a modified Wilmink-model in a mixed model analysis. Differences in the parameters of the lactation curves with different conception times were evaluated using confidence intervals.

Results
Lactation curves characterized by a low intercept and a steep ascending slope and a steep descending slope were associated with early conception across all parities. The peak milk yield was not associated with time of conception.

Conclusions
A practical application of the study results is the use of the shape of the lactation curve in future herd management. Groups of cows with impaired reproductive performance may be identified due to an unfavorable shape of the lactation curve. Monitoring lactation curves and adjusting the feeding strategy to adjust yield therefore may be useful for the improvement of reproductive performance at herd level.

Bayesian estimation of true between-herd and within-herd prevalence of Salmonella in Danish veal calves
Specialised veal producers that purchase and raise calves from several dairy herds are potentially at high risk of delivering Salmonella-infected animals to slaughter. However, the true prevalence of Salmonella infected veal producing herds and the prevalence of infected calves delivered to slaughter from infected herds are unknown in Denmark. Due to uncertainties about test sensitivity and specificity, these prevalences are not straightforward to assess. The objective of this study was to estimate the within-herd- and between-herd prevalence of Salmonella in veal calves delivered to slaughter from abattoirs in Denmark. Furthermore, it was investigated to which extent the estimates differed between a setup using both serological tests and faecal culture, compared to just serological tests, and whether the applied sampling scheme in the national surveillance programme in Denmark was sufficient to establish high posterior estimates of freedom from infection in individual herds. We used Bayesian analysis to avoid bias as a result of fixed test validity estimates. Serological test results from 753 animals and faecal culture from 1233 animals from 68 randomly selected Danish veal producing herds that delivered more than 100 calves to slaughter per year were used to estimate the prevalences and estimates of freedom from Salmonella. Serological test results of 7726 animals from 185 herds were used to compare the difference in prevalence estimates between serology alone vs. faecal culture combined with serology. We estimated that 34–57% of specialised veal producing herds were infected with Salmonella. Within the infected herds, 21–49% of the animals were infected. Few herds obtained high posterior estimates for the probability of freedom from infection given the collected data, with only six of 68 herds obtaining posterior probability of being infected less than 10%. Furthermore, this study indicated that serology is sufficiently sensitive and specific to be used for estimating the prevalence of Salmonella-infected specialised veal producing herds.
Effect of management practices on paratuberculosis prevalence in Danish dairy herds

A voluntary risk-based control program on paratuberculosis in dairy cattle was initiated in Denmark in 2006. Cows were categorized as high-risk (antibody-positive at least once within the last 3 tests) or low-risk animals based on the results of 3 to 4 annual milk ELISA detecting Mycobacterium avium ssp. paratuberculosis (MAP)-specific antibodies. High-risk animals require management practices aimed at decreasing calf exposure to MAP-contaminated colostrum and milk, and feces originating from these cows. Moreover, repeated test-positive cows are recommended for slaughter before next calving. The objective was to assess the effect of different management practices on the prevalence of MAP-specific antibodies. A questionnaire on management practices was distributed to 1,261 participating herds in December 2008. A total of 1,092 (87%) herd managers returned the questionnaire. Repeated prevalence data from 1,081 herds were available for a period up to 4.25 yr after the first test round. The changes in the prevalence of MAP-specific antibodies from the start of interventions were assessed using a hierarchical logistic model, where different management practices were assessed: a) culling of repeated test-positive cows, b) separation of high-risk from low-risk cows in calving areas, c) cleaning of calving areas after high-risk cows calved, d) removal of calves born to high-risk dams within 2 h after calving, e) use of colostrum for feeding of heifer calves from low-risk cows only, f) use of waste milk for feeding of heifer calves from low-risk cows only, g) herd size, and h) proportion of purchased animals. Multivariable analyses suggested that only the proportion of purchased animals (>15% purchased animals as well as 0 to 15% purchased animals compared with no purchased animals in the herd), culling of repeated test-positive animals, and use of waste milk from specific cow groups influenced the decrease in prevalence of MAP-specific antibodies. The control program has been running for just 4.25 yr, and it is assumed that the full effect of the risk-based management practices will only be observed after 4 to 8 yr. Therefore, lack of association between some practices and decrease in prevalence may be a reflection of a short study period. Furthermore, decreases in the prevalence of MAP-specific antibodies may not reflect discontinued transmission of MAP in all age groups.
Epilepsy in the Petit Basset Griffon Vendeen: Prevalence, Semiology, and Clinical Phenotype

Background

Epilepsy with a genetic background is increasingly being identified. In certain dog breeds, epilepsy occurs with a higher prevalence than the estimate of 1–2% reported in the general dog population.

Hypothesis

The Petit Basset Griffon Vendeen (PBGV) experiences an increased occurrence of epilepsy compared to the general dog population.

Animals

The target population consisted of all 876 PBGV dogs registered in the Danish Kennel Club from January 1, 1999 to December 31, 2008. The study population included 820 dogs that met the inclusion criteria.

Methods

A population study was conducted to estimate the prevalence of epilepsy in the Danish PBGV population. A mailed questionnaire was used to detect possible signs of epilepsy. The information was subsequently validated by telephone interviews of positive and possible positive responders and a negative responder control group, using an extensive questionnaire developed to detect epilepsy. Dogs evaluated as epilepsy positive after the telephone interview were offered a clinical investigation.

Results

The prevalence of epilepsy was estimated to be 8.9% (42/471) in the PBGV population. Average age of onset was 26.3 months. Sex and mode of response did not affect the prevalence, but a strong litter effect was seen. Among euthanized dogs, epilepsy was the predominant cause (6/45 = 13.3%).

Conclusion and Clinical Importance

Petit Basset Griffon Vendeen dogs experience an increased risk of epilepsy characterized by a relatively early onset and dominated by focal seizures with and without secondary generalization. With an estimated prevalence of 8.9% and substantial clustering within litters, a genetic factor associated with epilepsy is suspected.
Estimating test characteristics of somatic cell count to detect Staphylococcus aureus-infected dairy goats using latent class analysis

The aim of this study was to estimate test properties of composite somatic cell count (cSCC) to detect subclinically Staphylococcus aureus-infected dairy goats. Staphylococcus aureus is the most prevalent major pathogen in goats, and responsible for the majority of clinical mastitis cases. Therefore, a diagnostic tool that detects subclinical Staph. aureus infections may be useful in decreasing the number of clinical cases. We collected samples from 384 animals in 4 herds for bacteriological culture and cSCC on 3 occasions in lactation: once in early lactation, once around peak lactation, and once in late lactation. Latent class models were used to estimate test properties of cSCC and bacteriological culture in the absence of a gold standard reference test under the assumption that both tests detect Staph. aureus intramammary infection. Estimates for test properties of cSCC in early lactation at a cut-off value of 1,500 × 10³ cells/mL were 0.90 for sensitivity and 0.95 for specificity, making cSCC a useful screening tool for detection of Staph. aureus. An effect of lactation stage was observed, causing an increased sensitivity and decreased specificity in late lactation. The sensitivity of bacteriological culture was estimated to be very low in the latent class models and the models suggested that the true prevalence of Staph. aureus in dairy goat herds is much higher than what is commonly reported based on bacteriological culture. This implies that intramammary infection by Staph. aureus may be an underestimated problem in dairy goat herds, and that cSCC can be used to diagnose infected animals.

Evaluation of sensitivity and specificity of RBT, c-ELISA and fluorescence polarisation assay for diagnosis of brucellosis in cattle using latent class analysis

The sensitivity (Se) and specificity (Sp) of the Rose Bengal test (RBT), competitive ELISA (c-ELISA), serum (sFPA) and blood (bFPA) fluorescence polarisation assay for brucellosis were evaluated using latent class analysis using sera and whole blood collected from infected cattle reared in smallholder dairy farms of Zimbabwe. The latent class model allowed estimation of Se and Sp in the absence of a gold standard test. The c-ELISA had the highest Se (99.0%; 95% credible posterior interval (CPI): 94.8; 100%), while the RBT and sFPA had the highest Sp (99.0%; 95% CPI: 98.0; 99.6%). The bFPA had the lowest Se (71.3%; 95% CPI: 56.2, 83.5%), while its Sp (96.3%; CPI: 93.9; 98.0%) was marginally higher than that of the c-ELISA (95.4% CPI: 93.7; 96.8%). Therefore based on these data, test regimen using the RBT and c-ELISA could be suitable for diagnosis of brucellosis in smallholder dairies in Zimbabwe. Based on cost and ease of performance, the sFPA may be adopted as a confirmatory test, but its performance may be optimised by altering cut-off points to suit the Zimbabwean conditions. Thus, latent class models provide an alternative method for evaluating Se and Sp of diagnostic tests, which could be used to optimise test performance in different cattle populations.
Intra- and inter-observer agreement when using a descriptive classification scale for clinical assessment of faecal consistency in growing pigs

The objective of the current study was to evaluate intra- and inter-observer agreement using a descriptive classification scale with four categories, descriptive text and pictures for assessment of consistency in faecal samples from pigs post weaning. The four consistency categories were score one = firm and shaped, score two = soft and shaped, score three = loose and score four = watery.

Five observers from the same veterinary practice examined 100 faecal samples using the scale with four categories. Four of the observers examined the 100 faecal samples twice within the same day.

Within observers the difference in proportions for the individual consistency categories between two examinations was on average 0.04 (range: 0–0.10). The mean intra-observer agreement was 0.82 (range: 0.72–0.91) with a mean kappa value of 0.76 (range: 0.61–0.88).

For inter-observer agreement overall kappa was 0.64. For the 10 pair-wise comparisons the mean inter-observer agreement was 0.73 (range: 0.61–0.90) with a mean kappa value of 0.64 (range: 0.48–0.87). The difference in proportions for the individual consistency categories was on average 0.08 (range: 0–0.17).

In conclusion, the agreement observed for the descriptive classification scale with four categories, descriptive text and pictures may be categorized as a substantial to almost perfect intra-observer agreement and a moderate to almost perfect inter-observer agreement.

However, more objective measures than clinical scales may still be needed to improve intra- and inter-observer agreement in research studies.
Latent class evaluation of a milk test, a urine test, and the fat-to-protein percentage ratio in milk to diagnose ketosis in dairy cows

In this study, 3 commonly used tests to diagnose ketosis were evaluated with a latent class model to avoid the assumption of an available perfect test. The 3 tests were the KetoLac BHB (Sanwa Kagaku Kenkyusho Co. Ltd., Nagoya, Japan) test strip that tests milk for β-hydroxybutyrate, the KetoStix (Bayer Diagnostics Europe Ltd., Dublin, Ireland) test strip that tests urine for acetoacetate, and the fat-to-protein percentage ratio (FPR) in milk. A total of 8,902 cows were included in the analysis. The cows were considered to be a random sample from the population of Danish dairy cattle under intensive management, thus representing a natural spectrum of ketosis as a disease. All cows had a recorded FPR between 7 and 21 d postpartum. The KetoLac BHB recordings were available from 2,257 cows and 6,645 cows had a KetoStix recording. The recordings were analyzed with a modified Hui-Walter model, in a Bayesian framework. The specificity of the KetoLac BHB test and the KetoStix test were both high [0.99 (0.97-0.99)], whereas the specificity of FPR was somewhat lower [0.79 (0.77-0.81)]. The best sensitivity was for the KetoStix test [0.78 (0.55-0.98)], followed by the FPR [0.63 (0.58-0.71)] and KetoLac BHB test [0.58 (0.35-0.93)]. © 2011 American Dairy Science Association.

Prevalence of paratuberculosis infection in dairy cattle in Northern Italy

Paratuberculosis is a chronic granulomatous infection caused by Mycobacterium avium subsp. paratuberculosis (MAP) that affects multiple ruminant species causing important economic losses. Therefore, control programmes at herd and regional levels have been established worldwide and prevalence estimates are needed for their implementation. Although different herd-level prevalence estimations for paratuberculosis have been reported in Europe, very few studies provided comparable and interpretable values, due to poor study designs and lack of knowledge about the accuracy of the diagnostic tests used. To overcome these problems we applied a latent class analysis to the results of two prevalence studies carried out in two neighbouring Northern Italian regions (Lombardy and Veneto) that account for over 50% of the Italian dairy cattle population. Serum samples from a randomly selected number of farms in the two regions were analyzed by different ELISA tests. The herd-level Apparent Prevalences (AP) were 48% (190/391) for Lombardy and 65% (272/419) for Veneto. Median within-herd APs were 2.6% and 4.0% for Lombardy and Veneto, respectively. Posterior estimates for the herd-level True Prevalences (TP) based on a Bayesian model were very similar between the two regions (70% for Lombardy and 71% for Veneto) and close to previous estimates of infected herds in Europe. The two 95% credibility
intervals overlap each other, virtually showing only one distribution of the herd-level true prevalence for both regions. On the contrary, estimates of the within-herd TP distributions differed between the two regions (mean values: 6.7% for Lombardy and 14.3% for Veneto), possibly due to the different age distribution within the herds from the two regions.

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Register data as an identification tool for dairy herds with potential welfare problems

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Spatio-temporal magnitude and direction of highly pathogenic avian influenza (H5N1) outbreaks in Bangladesh

Background
The number of outbreaks of HPAI-H5N1 reported by Bangladesh from 2007 through 2011 placed the country among the highest reported numbers worldwide. However, so far, the understanding of the epidemic progression, direction, intensity, persistence and risk variation of HPAI-H5N1 outbreaks over space and time in Bangladesh remains limited.

Methodology/Principal Findings
To determine the magnitude and spatial pattern of the highly pathogenic avian influenza A subtype H5N1 virus outbreaks over space and time in poultry from 2007 to 2009 in Bangladesh, we applied descriptive and analytical spatial statistics. Temporal distribution of the outbreaks revealed three independent waves of outbreaks that were clustered during winter and spring. The descriptive analyses revealed that the magnitude of the second wave was the highest as compared to the first and third waves. Exploratory mapping of the infected flocks revealed that the highest intensity and magnitude of the outbreaks was systematic and persistent in an oblique line that connects south-east to north-west through the central part of the country. The line follows the Brahmaputra-Meghna river system, the junction between Central Asian and East Asian flyways, and the major poultry trading route in Bangladesh. Moreover, several important migratory bird areas were
Geostatistical analysis revealed significant latitudinal directions of outbreak progressions that have similarity to the detected line of intensity and magnitude.

Conclusion/Significance

The line of magnitude and direction indicate the necessity of mobilizing maximum resources on this line to strengthen the existing surveillance.

Stochastic models to simulate paratuberculosis in dairy herds

Stochastic simulation models are widely accepted as a means of assessing the impact of changes in daily management and the control of different diseases, such as paratuberculosis, in dairy herds. This paper summarises and discusses the assumptions of four stochastic simulation models and their use in the design of certification, surveillance, and control strategies for paratuberculosis in cattle herds. A detailed comparison is made between the Dutch JohneSSim and the Danish PTB-Simherd, using the same context of a set of control strategies in a typical Dutch/Danish herd. The conclusion is that while the models are somewhat different in their underlying principles and do put slightly different values on the different strategies, their overall findings are similar. Therefore, simulation models may be useful in planning paratuberculosis strategies in dairy herds, although as with all models caution is warranted when interpreting and generalising the results.
Structured approach to design of diagnostic test evaluation studies for chronic progressive infections in animals
Diagnostic test evaluations (DTEs) for chronic infections are challenging because a protracted incubation period has to be considered in the design of the DTE, and the adverse effects of infection may be widespread and progressive over an animal's entire life. Frequently, the specific purpose of the test is not formally considered when a test is evaluated. Therefore, the result is often a DTE where test sensitivity and specificity estimates are biased, either because of problems with establishing the true infection status or because the test detects another aspect of the infection (and analyte) than originally intended.

The objective of this paper is to outline a structured approach to the design and conduct of a DTE for diagnostic tests used for chronic infections in animals, and intended for different purposes. We describe the process from reflections about test purpose and the underlying target condition through considerations of the pathogenesis, and specification of a practical case definition, which can subsequently be used in the DTE for the specific purpose.

The process is illustrated by two examples of Mycobacterium avium subsp. paratuberculosis (MAP) infections in cattle. MAP infections are chronic and can result in different adverse effects at different time points during the incubation period. The description provides input on the process and deductive reasoning which are integral parts to develop a high-quality design of a DTE for chronic infectious diseases.
Using latent class analysis to estimate the test characteristics of the γ-interferon test, the single intradermal comparative tuberculin test and a multiplex immunoassay under Irish conditions

Considerable effort has been devoted to improving the existing diagnostic tests for bovine tuberculosis (single intradermal comparative tuberculin test [SICTT] and γ-interferon assay [γ-IFN]) and to develop new tests. Previously, the diagnostic characteristics (sensitivity, specificity) have been estimated in populations with defined infection status. However, these approaches can be problematic as there may be few herds in Ireland where freedom from infection is guaranteed. We used latent class models to estimate the diagnostic characteristics of existing (SICTT and γ-IFN) and new (multiplex immunoassay [Enferplex-TB]) diagnostic tests under Irish field conditions where true disease status was unknown. The study population consisted of herds recruited in areas with no known TB problems (2197 animals) and herds experiencing a confirmed TB breakdown (2740 animals). A Bayesian model was developed, allowing for dependence between SICTT and γ-IFN, while assuming independence from the Enferplex-TB test. Different test interpretations were used for the analysis: SICTT (standard and severe interpretation), γ-IFN (a single interpretation), and a range of interpretations for the Enferplex-TB (level-1 [high sensitivity interpretation] to level-5 [high specificity interpretation]). The sensitivity and specificity (95% posterior credibility intervals; 95% PCI) of SICTT[standard] relative to Enferplex-TB[level-1] and γ-IFN were 52.9–60.8% and 99.2–99.8%, respectively. Equivalent estimates for γ-IFN relative to Enferplex-TB[level-1] and SICTT were 63.1–70.1% and 86.8–89.4%, respectively. Sensitivity of Enferplex-TB[level-1] (95% PCI: 64.8–71.9%) was superior to the SICTT[standard], and specificity of the Enferplex-TB[level-5] was superior to γ-IFN (95% PCI: 99.6–100.0%). These results provide robust measures of sensitivity and specificity under field conditions in Ireland and suggest that the Enferplex-TB test has the potential to improve on current diagnostics for TB infection in cattle. The extent of that potential will be assessed in further studies.

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Validering samt kvalitets- og fremtidssikring af velfærdsregistreringer i svinebesætninger

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Fald i forekomsten af paratuberkulose

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Lavere forekomst af paratuberkulose i ikke-mælkeleverende besætninger

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Association between bulk-tank milk Salmonella antibody level and high calf mortality in Danish dairy herds
Salmonella enterica ssp. enterica Dublin is the most common Salmonella serotype found in the dairy sector in Denmark. Salmonella antibody level in bulk-tank milk (BTM), indicative of Salmonella Dublin infection in the herd, has been recorded regularly in all Danish dairy herds through a surveillance program since 2002. The objective of this study was to investigate whether high BTM Salmonella antibody level was associated with high calf mortality at herd level. Other risk factors for high calf mortality were also investigated: breed, production type (organic vs. conventional), number of animals...
purchased, herd size, and number of neighbor herds within a 4.9-km radius. Data from the Danish Cattle Database including the Salmonella surveillance program from September 2007 through August 2008 were used. Dairy herds with more than 20 cows were included (n = 4,337). Because of a highly right-skewed distribution of calf mortality with many zero values, calf mortality had to be dichotomized for the analysis. Therefore, in this study, high calf mortality was defined as calf mortality of more than 6.5% for calves aged 1 to 180 d. A logistic analysis was performed to identify risk factors associated with the probability of a herd having high calf mortality. The following factors were significantly associated with high calf mortality: high BTM Salmonella antibody level, odds ratio (OR) = 2.0 (95% confidence interval = 1.6–2.4), organic production OR = 1.4 (95% confidence interval = 1.1–1.7) for organic versus conventional production, and breed. Purchase of 8 or more animals increased the OR of high calf mortality more than purchase of 1 to 7 animals, which again had a higher OR compared with purchase of 0 animals. Because only 14.3% of the population consisted of herds with high BTM Salmonella status, the estimated proportion of herds with high calf mortality could only be reduced from 38.7 to 36.5% by eradicating Salmonella from the Danish cattle population (i.e., a population attributable risk of 2.2%). This showed that although there is a strong association between BTM Salmonella status and calf mortality, the problem with high calf mortality will not be solved by eradicating Salmonella. All other things equal, a population with more Salmonella-infected herds would gain a larger reduction in calf mortality from a Salmonella control campaign. Nevertheless, individual herds with a high within-herd prevalence of Salmonella are likely to benefit, both economically and regarding animal welfare, from controlling pathogenic Salmonella types in cattle.

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Data from the Danish veterinary cancer registry on the occurrence and distribution of neoplasms in dogs in Denmark
From May 15, 2005 to April 15, 2008, 1878 cases of neoplasms in dogs were reported to the web-based Danish Veterinary Cancer Registry. The proportions of malignant (38 per cent) and benign (45 per cent) tumours were similar. The most common malignant neoplasms were adenocarcinomas (21 per cent), mast cell tumours (19 per cent) and lymphomas (17 per cent). The benign neoplasms most commonly encountered were lipomas (24 per cent), adenomas (22 per cent) and histiocytomas (14 per cent). Skin (43 per cent) and the female reproductive system including mammary tissue (28 per cent) were the most common locations of neoplasia. There was a distinct breed predisposition for tumour development, with a high standard morbidity ratio (indicating a higher risk of cancer) for boxers and Bernese mountain dogs. A standard morbidity ratio below 1 was observed in German shepherd dogs and Danish/Swedish farm dogs, suggesting a lower risk of cancer in these breeds.

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Evaluation of histopathology, real-time PCR and virus isolation for diagnosis of infectious salmon anaemia in Norwegian salmon using latent class analysis

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Organisations: Addis Ababa University, Norwegian School of Veterinary Science, National Veterinary Institute, University of Copenhagen
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Evaluation of sensitivity and specificity of routine meat inspection of Danish slaughter pigs using Latent Class Analysis
Two groups of observers, regular meat inspectors and two veterinary researchers, respectively, conducted independent veterinary meat inspection of organs of slaughter pigs from organic or conventional production systems slaughtered at one abattoir in April 2005. A total of 3054 pigs (899 organic and 2155 conventional) were examined. The observed pathological disorders were grouped in four categories; respiratory disorders (RESP), parasitic disorders (PAR), intestinal disorders (INT) and heart disorders (HEART). Using a latent class model, the sensitivity (Se) and specificity (Sp) of meat inspectors and researchers were estimated without the assumption of an available gold standard. The Se for the regular meat inspection was found to be 0.92, 0.16, 0.24 and 0.49 for RESP, PAR, INT and HEART, respectively. The Se for the researchers was found to be 0.81, 0.96, 0.91 and 0.68 for RESP, PAR, INT and HEART, respectively. The Sp for the regular meat inspection was found to be between 0.98 and 1.00 for the four categories. The Sp for the researchers was found to be 0.83, 0.94, 0.76 and 0.99 for RESP, PAR, INT and HEART, respectively. The low Se of ordinary meat inspection for parasitic, intestinal and heart disorders will cause a significant underestimation of the prevalence of diseases reported to the pig producers. Based on our results the true prevalence of diseases (conventional vs. organic slaughter pigs) was (in %): 42 vs. 16, 5 vs. 51, 5 vs. 12 and 9 vs. 5 for RESP, PAR, INT and HEART, respectively.

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Prevalence of Mycobacterium avium subsp. paratuberculosis infection in adult Danish non-dairy cattle sampled at slaughter

A voluntary, risk-based control program for paratuberculosis in dairy herds was started in 2006 in Denmark. The program does not include non-dairy herds, and the occurrence of Mycobacterium avium subsp. paratuberculosis (MAP) in these herds is unknown. The objective of this study was to establish the prevalence of MAP infected adult non-dairy cattle in Denmark.

Serum samples were collected between October, 2008 and January, 2009 from every 6th animal over 24 months of age, sent to slaughter to Danish slaughterhouses from non-dairy herds. The final sample included 2345 cattle of 13 different breeds, with the largest breed group being crossbreds (of unknown breeds) (30%) and three dairy breeds (Danish Holstein, Danish Jersey and Danish Red Cattle) comprising 27% of the samples. The serum samples were tested using a MAP specific antibody ELISA (IDScreen®) and positives were defined as the sample-to-positive ratio greater than 0.60.

Estimation of the breed-specific apparent prevalences, true prevalences (TP), and true prevalences with a random effect of breed was done in a Bayesian analysis. Information about test sensitivity and specificity were based on literature data and expert information.

Regardless of the method of analysis, the estimated prevalences showed similar differences between breeds. The dairy breeds Danish Jersey, Danish Holstein and Danish Red Cattle were ranked highest (i.e. with highest prevalence) (TP medians: 13, 10, and 6, respectively). Combined, the dairy breeds had a significantly higher prevalence than the other breeds, median TP (dairy) = 15.7% vs. median TP (non-dairy) = 0.8%. For the individual non-dairy breeds, the median estimates were generally higher, illustrating the problems of ranking groups based on relatively small sample sizes.
Register data as a identification tool for dairy herds with potential welfare problems

The interrelationships between clinical signs and their effect on involuntary culling among pregnant sows in group-housing systems

Sows suffering from clinical signs of disease (e.g. lameness, wounds and shoulder ulcers) are often involuntarily culled, affecting the farmer’s economy and the welfare of the animals. In order to investigate the interrelationships between clinical signs of individual pregnant group-housed sows, we performed an explanatory factor analysis to identify factors describing the patterns of variation of clinical signs. Moreover, we investigated how these emerging factors affected the probability of a sow to be either (i) euthanized, (ii) suddenly dead, (iii) sent to slaughter due to clinical signs of disease such as claw lesions or wounds or (iv) involuntarily culled (representing a pool of sows that were either euthanized, dead or sent to slaughter due to disease). Data from 2,989 pregnant sows in group-housing systems from 33 sow herds were included in the study. A thorough clinical examination was performed for each sow by using a protocol including 16 different clinical signs. Farmers recorded all cullings and deaths and the reasons for these actions in a 3-month period after the clinical examination. Among the observed sows, 4.2% were involuntarily culled during the 3-month period. From the explanatory factor analysis, we identified three factors describing the underlying structure of the 16 clinical variables. We interpreted the factors as ‘pressure marks’, ‘wounds’ and ‘lameness’. Logistic analyses were performed to investigate the effect of the three factors and the parity number of each sow on the four outcomes: (i) euthanized, (ii) suddenly dead, (iii) sent to slaughter due to clinical signs of disease and (iv) involuntarily culled. The analyses showed that ‘lameness’ significantly increased the risk of sows to be involuntarily culled (P = 0.016) or sent to slaughter due to clinical signs of disease (P = 0.026). Lameness is generally considered to be an important welfare problem in sows, which could explain the increased risk seen in this study. By contrast, ‘pressure marks’ and ‘wounds’ did not have any significant effect on the four outcomes (P > 0.05).
An object-oriented Bayesian network modeling the causes of leg disorders in finisher herds

The implementation of an effective control strategy against disease in a finisher herd requires knowledge regarding the disease level in the herd. A Bayesian network was constructed that can estimate risk indexes for three cause-categories of leg disorders in a finisher herd. The cause-categories of leg disorders were divided into infectious causes (arthritis caused by infectious pathogens), physical causes (e.g. fracture and claw lesions), and inherited causes (osteochondrosis). Information about the herd (e.g. the herd size, floor type and number of suppliers) and information about individual pigs (e.g. results from diagnostic tests) were used to estimate the most likely cause of leg disorders at herd level. As information to the model originated from two different levels, we used an object-oriented structure in order to ease the specification of the Bayesian network. Hence, a Herd class and a Pig class comprised the basic components of the object-oriented structure. The causal structure of the model was based on evidence from published literature. The conditional probabilities used in the model were elicited from experts within the field and from the published literature. To illustrate the behaviour of the model, we investigated the value of different levels of evidence in two fictitious herds with different herd characteristics related to the risk of leg disorders (e.g. purchase policy, production type and the stocking density in pens). The model enabled us to demonstrate the value of performing systematic collection of additional information (i.e. clinical, pathological and bacteriological examination) when identifying causes of leg disorders at herd level.

A review of prevalences of paratuberculosis in farmed animals in Europe

Prevalence estimates are used by decision makers such as policy makers and risk assessors to make choices related to certain diseases and infections. Paratuberculosis, caused by Mycobacterium avium subsp. paratuberculosis (MAP), is a chronic infection particularly resulting in economic losses among farmed ruminants. Therefore, this infection is of concern for many farming industry decision makers. As a result, multiple studies have been carried out to determine the within-herd and between-herd prevalence of MAP infections. The objective of the present study was to conduct a review and, if possible, compare animal and herd level prevalences of MAP among farmed animals in Europe.

European data on prevalences of MAP in all farmed animal species were included from a review of literature. Information on target population and study design, tests used and apparent prevalences were recorded, and subsequently true prevalences were calculated when possible. A critical review of the included studies indicated that although a wide range of studies have been conducted, likely and comparable true prevalence estimates could rarely be calculated. Based on a few studies where the prevalences appeared to be plausible, it was concluded that prevalences of MAP would have to be guesstimates based on available data. The true prevalence among cattle appeared to be approximately 20% and was at least 3–5% in several countries. Between-herd prevalence guesstimates appeared to be >50%. No countries had
published sufficient information to claim freedom from MAP or just a near-zero prevalence of MAP infections. No within-flock prevalence estimates were available for goats and sheep. The between-flock prevalence guesstimates were >20%, based only on estimates from Switzerland and Spain.

Major critical issues were identified in the majority of the studies, primarily due to lack of knowledge of the test accuracy of the diagnostic test used, or due to studies where the study population did not reflect the target population. Because most of the reported studies did not yield prevalence estimates which were comparable to other studies, there is a continuing need for well-designed studies of the prevalence of MAP infections.

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Association between Salmonella and high calf mortality in Danish dairy herds

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Association between Salmonella Dublin antibodies in bulk tank milk and calf mortality in Danish dairy herds

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Comparing the epidemiological and economic effects of control strategies against classical swine fever in Denmark

In 2006, total Danish pork exports were valued at (sic)3.8 billion, corresponding to approximately 5% of the total Danish exports, and an outbreak of a notifiable disease would have dramatic consequences for the agricultural sector in Denmark. Several outbreaks of classical swine fever (CSF) have occurred in Europe within the last decade, and different control strategies have been suggested. The objective of this study was to simulate the epidemiological and economic consequences of such control strategies in a CSF epidemic under Danish conditions with respect to herd demographics and geography and to investigate the effect of extra biosecurity measures on farms. We used InterSpread Plus to model the effect of nine different control strategies: the minimum measures required by the EU plus depopulation of contact herds (EUplus), extra depopulation of neighbouring herds, extra surveillance within the protection and surveillance zones, extra biosecurity in SPF herds-or in all herds, vaccination of all pigs in the 1 or 2 km zones using live vaccine as a protective measure (vaccination-to-kill), vaccination of all weaners and finishers in the 1 or 2 km zones using an E2 marker vaccine as a suppressive measure (vaccination-to-live). Each epidemic was simulated to start in four different index herds: production herds located in low, medium and high pig density areas, respectively; and a nucleus herd in an area of high pig density. For each control strategy and index case, we calculated the size and duration of the epidemic, the number of depopulated and/or vaccinated herds and animals, the control costs borne by the public and the pig industry, respectively, as well as the loss of exports associated with the epidemic. The simulations showed that the EUplus strategy is the most effective of the evaluated strategies with respect to limiting the size, duration and cost of the epidemic, regardless of the index case. However, regarding the number of slaughtered animals, the vaccination-to-live strategies appeared to be more effective. Epidemics become larger and last longer if the index case is a nucleus herd. This implies that biosecurity in nucleus herds is extremely important to avoid transmission of CSF to these herds. Simulations showed that a Danish CSF epidemic will be moderate in most cases and will include fewer than 10 cases and last less than 2 weeks on average. However, for some iterations, long-lasting and large epidemics were observed. Irrespective of the size and duration, an epidemic is expected to be very costly due to the export losses.

 Causes of and predisposing risk factors for leg disorders in growing-finishing pigs

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Pododermatitis in Danish broiler farms 2002 - 2008

Hyperkeratosis and ulcers on foot-pads is a major welfare problem in broiler production. The problem is associated with ammonia irritation due to poor and wet litter quality. Since 2002 Danish producers have been subject to the Act on Welfare in Broilers and Parent Stock. After slaughter the veterinary inspection scores a random sample of 100 birds from each flock with regard to foot-pad lesions. The individual scores are: no lesions=0, superficial lesions=1, deeper lesions=2. These scores are summed for the flock leading to a flock lesion score between 0 and 200. A flock lesion score below 40 is considered acceptable. If the score is between 40 and 80 the farmer and his veterinarian are notified and if the total lesion score is above 80 the veterinary authorities are informed as well.

The introduction of the program has led to several initiatives among the producers to improve litter quality. Focus is on heating of the houses after cleaning, type of bedding material, ventilation and control of water spillage.

We merged data from the ante-mortem inspection, meat inspection data and the farms' efficacy monitoring on basis of farm-id, house-number and the yearly rotation number resulting in a total of 28400 observations. By plotting these data, a curvilinear development in the flocks lesion scores was observed: In the period 2002-2005 there was a rapid declined in flock lesion scores (the mean and standard deviation of the flock score was 89.0 +- 47.6 in 2002 and 46.6+- 35.1 in 2005) whereas the development was less pronounced in the period 2005 - 2008 (the mean flock score was 41.3+-35.1 in 2008).

The statistical analysis was carried out on the data from 2004 to 2008 as some variables were included only from 2004. A mixed-effect variance model was formulated with the square-root-transformed flock lesions scores as the response variable. The farm-id was set as a random effect. Statistically significant explanatory variables included: bedding material (lower scores on wood shavings than on straw), season (lower scores in summer than in winter) and growth rate (higher growth rates were associated with lower scores). Higher stocking densities led to slightly higher lesion scores in summer but to slightly lower scores in winter. The reason could be a beneficial effect of higher heat production on the bedding quality in the winter months. In the period from 2004 there was a strong shift in bedding material from 'straw' to 'wood shavings'. The flock lesion scores were stable in the 'wood shavings' flocks, whereas the scores declined for other bedding materials (mostly straw) whereby they approached the levels for wood shavings.

In conclusion, the efforts have led to an impressive decline in flock lesion scores in the years 2002 - 2005, followed by more stable levels in the period 2005 - 2008. Higher lesion scores were statistically associated with straw as bedding material, low growth rates and winter season.
Summary receiver operating characteristics (SROC) and hierarchical SROC models for analysis of diagnostic test evaluations of antibody ELISAs for paratuberculosis

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The Weak Sow Index: A new method for optimal use of clinical information in sow herds

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Validation of data collected in the Danish Veterinary Cancer Registry
The Danish Veterinary Cancer Registry (DVCR) was established in 2005 and prospectively collects information about neoplasms in Danish dogs and cats.

The present study evaluated the agreement between veterinary practice records and electronic submissions made to the DVCR from May 2005 through June 2008. The variables compared were gender, breed, diagnosis, date of birth, death and diagnosis, localization and biological behaviour of the neoplasms.

Agreement of 95% between DVCR and the original data were considered acceptable with regard to use of data in studies. Recorded proportions of agreement were: (1) breed: 97.4%; (2) diagnosis: 95.6%; (3) location: 95.6%; (4) biological behaviour: 93.0%; (5) gender: 92.5%; (6) date of death: 91.5%; (7) date of diagnosis: 80.1%; (8) date of birth: 76.7%.

All variables except date of death, birth, and diagnosis met the required 95% agreement limit. Data on dates of birth, death
Ante mortem diagnosis of paratuberculosis: A review of accuracies of ELISA, interferon-γ assay and faecal culture techniques

Infections with Mycobacterium avium subsp. paratuberculosis (MAP) can be latent for years without affecting the animal, but the animal may become infectious or clinical at some point. Diagnosis of paratuberculosis can be a challenge primarily in latent stages of the infection, and different diagnosis interpretations are usually required by the variety of decision makers. The objective of this paper was to provide a critical review of reported accuracies of ELISA tests, interferon-γ assays (IFN-γ) and faecal culture (FC) techniques used for diagnosis of three defined target conditions: MAP infected, MAP infectious and MAP affected animals.

For each animal species, target condition and diagnostic test-type, sensitivities (Se) and specificities (Sp) were summarised based on a systematic, critical review of information in literature databases. The diagnostic test information often varied substantially for tests of the same type and make, particularly ELISA, which was the most frequently reported test-type. Comparison of the various tests accuracies was generally not possible, but stratification of test-evaluations by target condition improved the interpretation of the test accuracies. Infectious and affected animals can often be detected, but Se for infected animals is generally low. A main conclusion of the review was that the quality of design, implementation and reporting of evaluations of tests for paratuberculosis is generally poor. Particularly, there is a need for better correspondence between the study population and target population, i.e. the subjects chosen for test evaluation should reflect the distribution of animals in the population where the test is intended to be used.
Assessing the prevalence of paratuberculosis in Europe

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Association between the presence of antibodies to Mycobacterium avium subspecies paratuberculosis and somatic cell count
Somatic cell counts (SCC) in bulk tank milk delivered for human consumption are one of the indicators of milk quality and are used for milk pricing. Consequently, milk from cows with high SCC is frequently used by farmers for feeding of calves to lower the SCC in bulk tank milk. Young calves are more susceptible to Mycobacterium avium ssp. paratuberculosis (MAP) and may acquire the infection early in life through ingestion of MAP-contaminated milk. The occurrence of MAP antibodies can be an indicator of MAP shedding. Because MAP can be shed in milk from infected cows, and antibodies to MAP can be an indicator of the infectious status, an association between antibodies to MAP and high SCC can result in high-SCC milk being at risk of containing MAP. Feeding milk containing high SCC to susceptible calves may result in MAP infections. Somatic cell counts and MAP antibodies in milk were measured repeatedly in 7,251 cows from 26 Danish dairy herds to investigate the association between the occurrence of MAP antibodies and high SCC. The results of robust regression showed a log-linear relationship between the age at first positive ELISA and the age at first high SCC sample (R² = 0.51). Of the 1,733 cows positive for MAP antibodies and with high SCC, high SCC was detected prior to MAP antibodies in 46% of the cows. Still, in 40% of the cows, MAP antibodies were detected before a high SCC. Therefore, the findings do not point to a causal relationship between high SCC and antibodies to MAP, but suggest a strong association and highlight a potentially increased risk of MAP transmission when milk with high SCC is fed to calves.

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Colostrum and milk as risk factors for infection with Mycobacterium avium subspecies paratuberculosis in dairy cattle

Mycobacterium avium ssp. paratuberculosis (MAP) infections cause major losses to the dairy industry. Transmission of MAP occurs primarily via feces and in utero, but MAP can also be excreted in colostrum and milk. The objective of this study was to determine whether colostrum and milk fed to calves are important risk factors for infection with MAP. A questionnaire was sent to 1,050 farms participating in the Danish control program on paratuberculosis in early 2007. Details on practices regarding colostrum and milk feeding between 1999 and 2006 were obtained from 808 (77%) herds. Nine vaccinated herds were excluded. Information on MAP antibody-ELISA results, date of birth, and herd of birth of 93,994 animals was obtained from the Danish Cattle Database. A 2-level logistic regression model was fitted with a dichotomized ELISA response, with outcome, age, source of colostrum, and milk as fixed effects, and herd as a random effect. Animals fed colostrum from multiple cows had an odds ratio of 1.24 of being ELISA positive compared with animals fed colostrum from their own dam only. Calves suckling with foster cows had an odds ratio of 2.01 of being ELISA positive compared with calves fed milk replacer. Feeding bulk tank milk and pooled milk from cows with high somatic cell counts did not increase the risk of being ELISA positive. Overall, the results of the study suggested that source of milk was not of great importance for the transmission of MAP, but colostrum should be fed only from the dam of that calf.

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Evaluation of test-strategies for estimating probability of low prevalence of paratuberculosis in Danish dairy herds

Paratuberculosis is a chronic infection affecting cattle and other ruminants. In the dairy industry, losses due to paratuberculosis can be substantial in infected herds and several countries have implemented national programmes based on herd-classification to manage the disease. The aim of this study was to develop a method to estimate the probability of low within-herd prevalence of paratuberculosis for Danish dairy herds. A stochastic simulation model was developed using the R(R) programming environment. Features of this model included: use of age-specific estimates of test-sensitivity and specificity; use of a distribution of observed values (rather than a fixed, low value) for design prevalence; and estimates of the probability of low prevalence (Pr-Low) based on a specific number of test-positive animals, rather than for a result less than or equal to a specified cut-point number of reactors. Using this model, five herd-testing strategies were evaluated: (1) milk-ELISA on all lactating cows; (2) milk-ELISA on lactating cows 4 years old; (4) faecal culture on all lactating cows; and (5) milk-ELISA plus faecal culture in series on all lactating cows. The five testing strategies were evaluated using observed milk-ELISA results from 19 Danish dairy herds as well as for simulated results from the same herds assuming that they were uninfected. Whole-herd milk-ELISA was the preferred strategy, and considered the most cost-effective strategy of the five alternatives. The five strategies were all efficient in detecting infection, i.e. estimating a low Pr-Low in infected herds, however, Pr-Low estimates for milk-ELISA on age-cohorts were too low in simulated uninfected herds and the strategies involving faecal culture were too expensive to be of practical interest. For simulated uninfected herds, whole-herd milk-ELISA resulted in median Pr-Low values >0.9 for most herds, depending on herd size and age-structure. None of the strategies provided enough power to establish a high Pr-Low in smaller herds, or herds with a younger age-structure. Despite this, it appears as if the method is a useful approach for herd-classification for most herds in the Danish dairy industry.

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The association between disease and profitability in individual finishing boars at a test station

Endemic diseases in finisher herds are considered to be costly for the pig producer. We investigated the effect of diseases on the profit margin using data from a Danish boar test station (n = 5777) collected from July 2002 to December 2004. Boars reaching a target slaughter weight of at least 80 kg were included in the study. Oral and parenteral treatments were used as indicator of disease in the finishing period and, pathological lesions were used as indicator of disease at slaughter. Profit margin was calculated individually for each boar as the difference between the total revenue and the variable costs. A multivariable hierarchical model was constructed to investigate the association between the risk factors: oral treatment (yes/no), parenteral treatment (yes/no), pathological findings (yes/no), breed (Duroc, Hampshire, Landrace, Yorkshire) and weight at 4 weeks with the outcome variable: profit margin. The results showed that treatment in the finishing period had a negative effect on the profit margin. According to the least square means estimates, boars that were treated parenterally had a reduction in the profit margin of 2.24 €. This corresponded to a reduction in the profit margin of 17%. Boars treated orally had a reduction of 0.88 €, which corresponded to a reduction in the profit margin of 7%. Pathological findings, breed and weight at 4 weeks were also significantly associated with the profit margin. The effect of pathological findings was influenced by breed and caused a reduction in the range from 0.54 to 2.41 € (corresponding to a reduction in the profit margin ranging from 4 to 20%). The results were robust to changes in price of a 30 kilogram piglet and, relatively robust in regard to changes in the feed price. However, price per kilogram carcass weight appeared to influence the economic effect of oral and parenteral treatment and pathological findings on the profit margin. The effect of oral and parenteral treatments was also sensitive to changes in medicine prices.

The distribution of the pathogenic nematode Nematodirus battus in lambs is zero-inflated

Understanding the frequency distribution of parasites and parasite stages among hosts is essential for efficient experimental design and statistical analysis, and is also required for the development of sustainable methods of controlling infection. Nematodirus battus is one of the most important organisms that infect sheep but the distribution of parasites among hosts is unknown. An initial analysis indicated a high frequency of animals without N. battus and with zero egg counts, suggesting the possibility of a zero-inflated distribution. We developed a Bayesian analysis using Markov chain Monte Carlo methods to estimate the parameters of the zero-inflated negative binomial distribution. The analysis of 3000 simulated data sets indicated that this method out-performed the maximum likelihood procedure. Application of this
technique to faecal egg counts from lambs in a commercial upland flock indicated that N. battus counts were indeed zero-inflated. Estimating the extent of zero-inflation is important for effective statistical analysis and for the accurate identification of genetically resistant animals. Copyright © 2008 Cambridge University Press.

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The use of critical reviews and meta-analysis of diagnostic test evaluations - illustrated by diagnostic tests for paratuberculosis

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A review of diagnostic accuracies of ELISA and faecal culture in cattle

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Assessing the convergence of Markov Chain Monte Carlo methods: An example from evaluation of diagnostic tests in absence of a gold standard

The accessibility of Markov Chain Monte Carlo (MCMC) methods for statistical inference have improved with the advent of general purpose software. This enables researchers with limited statistical skills to perform Bayesian analysis. Using MCMC sampling to do statistical inference requires convergence of the MCMC chain to its stationary distribution. There is no certain way to prove convergence; it is only possible to ascertain when convergence definitely has not been achieved. These methods are rather subjective and not implemented as automatic safeguards in general MCMC software. This paper considers a pragmatic approach towards assessing the convergence of MCMC methods illustrated by a Bayesian analysis of the Hui–Walter model for evaluating diagnostic tests in the absence of a gold standard. The Hui–Walter model has two optimal solutions, a property which causes problems with convergence when the solutions are sufficiently close in the parameter space. Using simulated data we demonstrate tools to assess the convergence and mixing of MCMC chains using examples with and without convergence. Suggestions to remedy the situation when the MCMC sampler fails to converge are given. The epidemiological implications of the two solutions of the Hui–Walter model are discussed.

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Assessment of management-related risk factors for paratuberculosis in Danish dairy herds using Bayesian mixture models

Transmission of Mycobacterium avium subsp. paratuberculosis (Map) to susceptible animals is primarily considered to occur via faeces and milk originating from infectious cows. However, studies of factors resulting in increased transmission of Map are difficult to perform due to a long and unpredictable incubation period and inaccurate diagnostic tests. A multi-level Bayesian mixture model has been shown to predict the infection status of an individual cow more precisely than traditional cut-off based methods used for interpretation of diagnostic test-information, thereby increasing the precision of the diagnostic information.

The objective of our study was to assess management-related risk factors for within-herd transmission of Map. Management-related risk factors were recorded in 97 Danish dairy herds. Twenty-six months following that recording, the antibody status of all lactating cows (n = 7410) in the same herds was measured by the use of an ELISA. A multi-level Bayesian mixture model was used to assess the association between the probability of infection of individual cows and 41 herd-level management-related risk factors using univariable analyses. In this model, the continuous OD value was used to estimate the probability of infection, corrected for known animal covariates and laboratory factors. The statistical significance of the potential risk factors was assessed by calculating odds ratios and their 95% credibility posterior intervals.

Four significant risk factors were identified: housing of cows in bed stalls compared to housing in tie stalls; low level of hygiene in the feeding area of calving areas; low amounts of straw in the bedding of the calving area; high animal density among young stock >12 months of age. Surprisingly, the hygiene level in the calving area was not found to affect the odds of infection.

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Contributors: Nielsen, S. S., Toft, N.
Bayesian mixture models for within-herd prevalence estimates of bovine paratuberculosis based on a continuous ELISA response

Diagnostic inference by use of assays such as ELISA is usually done by dichotomizing the optical density (OD)-values based on a predetermined cut-off. For paratuberculosis, a slowly developing infection in cattle and other ruminants, it is known that laboratory factors as well as animal specific covariates influence the OD-value, but while laboratory factors are adjusted for, the animal specific covariates are seldom utilized when establishing cut-offs. Furthermore, when dichotomizing an OD-value, information is lost. Considering the poor diagnostic performance of ELISAs for diagnosis of paratuberculosis, a framework for utilizing the continuous OD-values as well as known coavariates could be useful in addition to the traditional approaches, e.g. for estimating within-herd prevalences.

The objective of this study was to develop a Bayesian mixture model with two components describing the continuous OD response of infected and non-infected cows, while adjusting for known covariates. Based on this model, four different within-herd prevalence indicators were considered: the mean prevalence in the herd; the age adjusted prevalence of the herd for better between-herd comparisons; the rank of the age adjusted prevalence to better compare across time; and a threshold-based prevalence to describe differences between herds. For comparison, the within-herd prevalence and associated rank using a traditional dichotomization approach based on a single cut-off for an OD corrected for laboratory variation was estimated in a Bayesian model with priors for sensitivity and specificity.

The models were applied to the OD-values of a milk ELISA using samples from all lactating cows in 100 Danish dairy herds in three sampling rounds 13 months apart. The results of the comparison showed that including covariates in the mixture model reduced the uncertainty of the prevalence estimates compared to the cut-off based estimates. This allowed a more informative ranking of the herds where low ranking and high ranking herds were easier to identify.
Evaluation of three serological tests for brucellosis in naturally infected cattle using latent class analysis

Seralogical methods are traditionally used in diagnosis of brucellosis. However, the comparative performance of these tests and their accuracy under the local environment in Zambia has not been assessed. Thus, the objective of our study was to evaluate the diagnostic performance of three serological tests for brucellosis; Rose Bengal Test (RBT), competitive ELISA (c-ELISA) and Fluorescence Polarisation Assay (FPA) in naturally infected cattle in Zambia without an appropriate reference test to classify animals into truly infected and non-infected.

Seralogical test results from a study to determine sero-prevalence were used to compare the performance of RBT, c-ELISA and FPA in diagnosing brucellosis in traditional cattle. Since none of the tests can be seen as a perfect reference test or gold standard, their performance in a population of naturally infected cattle was evaluated using latent class analysis which allows the sensitivity (Se) and specificity (Sp) to be estimated in the absence of a gold standard. The highest Se was achieved by the c-ELISA (97%; Credible Posterior Interval (CPI) = 93–100%) and the highest Sp by the FPA (93%; CPI = 85–99%), conversely these tests also had the lowest Sp and Se, respectively, with the RBT performing well in both the Se (93%; CPI = 84–98%) and Sp (81%; CPI = 61–97).

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Evaluation of three serological tests for diagnosis of Maedi-Visna virus infection using latent class analysis

Maedi-Visna virus (MVV) infection in sheep is present in several European countries, including Norway. The current Norwegian surveillance and control programme for MVV infection uses three serological tests: an agar gel immunodiffusion test (AGID) and two commercially available indirect ELISAs (Institut Pourquier, P-ELISA and HYPHEN BioMed, H-ELISA). From 18 flocks with suspected or confirmed MVV infection, sera from naturally infected sheep were obtained, and sensitivity (Se) and specificity (Sp) of the three tests were estimated in absence of a perfect reference test using latent class models in a Bayesian analysis. The AGID had higher Sp (95% posterior credibility interval (PCI) [98.4; 99.9]) than either ELISA (95% PCI: P-ELISA, [95.1; 99.0]; H-ELISA, [91.4; 96.6]), but much lower Se (95% PCI: AGID, [41.4; 59.8]; P-ELISA, [92.7; 100.0]; H-ELISA, [90.9; 99.4]). Currently the P-ELISA is used for screening and positive samples are subsequently confirmed by a setup using all three tests in a serial reading. The Se and Sp of the serial interpretations with and without the H-ELISA were estimated. The results suggested that the H-ELISA could be dropped as a confirmatory test as the Se of the three test serial reading was reduced significantly without adding a significant improvement of the Sp compared to the serial reading of the P-ELISA and AGID alone. However, the perceived cost of false positives versus false negatives will influence this decision. Estimates of the predictive values for the tests and combinations suggested that the P-ELISA is a good choice of screening, but confirmatory tests are needed to achieve acceptable levels of positive predictive values.

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Geographic risk factors for inter-river dispersal of Gyrodactylus salaris in fjord systems in Norway

Gyrodactylus salaris has been recorded in 46 Norwegian rivers since 1975 and is considered a threat to Atlantic salmon stocks. The primary introductions of G. salaris (primary infected rivers) have been accounted for by specific events, as reported in the literature. The parasite has subsequently dispersed to adjacent localities (secondary infected rivers). The objective of this paper is to address the occurrence of secondary infections by examining the hypothesis of inter-river dispersal of G. salaris. A dispersal model for the secondary river infections via migrating infected fish is proposed. Due to the limited tolerance of G. salaris to salinity, both freshwater inflow to dispersal pathways and dispersal distance were expected to influence the probability of inter-river dispersal. Eighteen rivers were categorised as primary infected rivers, 28 as secondary infected rivers, and 54 as rivers at risk. Four risk factors: the log10 freshwater inflow; the dispersal distance; the time at risk; and the salmon harvest were combined in a multi-variable logistic regression model of the probability of secondary infection. The final multi-variable model included log10 freshwater inflow (Wald chi-square = 9.93) and dispersal distance (Wald chi-square = 6.48). Receiver operating characteristic analyses of the final model supported freshwater inflow as a strong predictor of G. salaris infection status. The strong influence of the freshwater inflow on the probability of secondary infection adds further support to the hypothesis of inter-river dispersal of G. salaris through fjords.

Modeling the causes of leg disorders in finisher herds

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Review of prevalences of paratuberculosis in farmed animals in Europe

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Serum C-reactive protein concentration as an indicator of remission status in dogs with multicentric lymphoma

Background: The acute-phase protein C-reactive protein (CRP) is used as a diagnostic and prognostic marker in humans with various neoplasias, including non-Hodgkin's lymphoma.

Objective: To evaluate if CRP could be used to detect different remission states in dogs with lymphoma.

Animals: Twenty-two dogs with untreated multicentric lymphoma.

Methods: Prospective observational study. Blood samples were collected at the time of diagnosis, before each chemotherapy session, and at follow-up visits, resulting in 287 serum samples.

Results: Before therapy, a statistically significant majority of the dogs (P = .0019) had CRP concentrations above the reference range (68%, 15/22). After achieving complete remission 90% (18/20) of the dogs had CRP concentrations within the reference range, and the difference in values before and after treatment was statistically significant (P < .001). CRP concentrations of dogs in complete remission (median, 1.91; range, 0.2–103) were significantly different (P = .031) from those of dogs with partial remission (median, 2.48; range, 0–89), stable disease (median, 1.77; range, 1.03–42.65), or progressive disease (median, 8.7; range, 0–82.5). There was profound variation of CRP measurements within each dog.

Conclusions: CRP is useful in determining complete remission status after treatment with cytotoxic drugs. However, the individual variation between dogs means CRP concentration is not sufficiently different in other remission states to permit its use in monitoring progression of the disease. Greater reliability in determining remission status might be achieved by combining CRP concentration with other serum markers.

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Scopus rating (2007): SJR 1.531 SNIP 1.673
The effect of lameness treatments and treatments for other health disorders on the weight gain and feed conversion in boars at a Danish test station

Lameness in finishers can cause economic losses to farmers and lameness affects the welfare of pigs. In order to study the economic losses, we investigated the effect of lameness on productivity, measured as the mean daily weight gain (MDWG) and the feed conversion ratio (FCR), and evaluated the importance of these effects. The study design was observational of a cross sectional type and data was collected from a Danish boar test station during February 2002 and December 2004. A total of 10,473 boars were included in the study. We adapted a quantitative interpretation of lameness, using the number of lameness treatments of the individual animal, and generated the new variable: "lameness treatments". All treatments other than lameness were recoded as "non-lameness treatments". Multivariable hierarchical analyses were performed to assess the association between the risk factors: number of lameness treatments, records of non-lameness treatments (yes/no), breed (Duroc, Hampshire, Landrace, Yorkshire) and weight at 4 weeks with each of the outcome variables: MDWG and FCR. In order to improve the assumption of normality, we used a quadratic transformed MDWG and an inverse transformed FCR in the analyses. Lameness treatments had a significant effect on the transformed MDWG (p < 0.0001). Boars with one to three lameness treatments had a significant reduction in the MDWG, which corresponded to a reduction of 27 g per day. Boars with four and five lameness treatments did not have a significant reduction in the MDWG. More than five lameness treatments caused the largest reduction in the MDWG corresponding to 40 g per day. There was no significant association between lameness treatments and the transformed FCR (p = 0.14). Records of non-lameness treatments, breed and weight at 4 weeks were all significantly associated with the transformed MDWG and -FCR. Boars with records of non-lameness treatments had a reduction in the MDWG of 56 g per day and an increase in the FCR of 0.04 feed units per kg live weight. At the test station, the prevalence of boars with records of lameness treatments was 4% whereas the prevalence of records of non-lameness treatments was 65%.

General information
Publication status: Published
Organisations: Danish Pig Production/Danish Meat Association, Aarhus University, University of Copenhagen
Contributors: Jensen, T. B., Baadsgaard, N. P., Houe, H., Toft, N., Østergaard, S.
Number of pages: 9
Pages: 34-42
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: Livestock Science
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Scopus rating (2007): SJR 0.587 SNIP 1.129
Web of Science (2007): Indexed yes
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Keywords: Boars, Lameness treatments, Non-lameness treatments, Weight gain, Feed conversion ratio
DOIs:
10.1016/j.livsci.2007.01.153
Research output: Contribution to journal › Journal article – Annual report year: 2007 › Research › peer-review

Age-specific characteristics of ELISA and fecal culture for purpose-specific testing for paratuberculosis
Paratuberculosis is a chronic infection, and animals are not equally affected by it. Therefore, diagnostic tests that are able to detect different stages of the infection are needed for objective decision making. A longitudinal study was carried out to describe the ability of 2 tests to predict 2 conditions in dairy cattle: "infection" and "infectious," exemplifying 2 different purposes of testing. "Infection" is the term of choice for certification and eradication purposes, and "infectious" is more relevant for control purposes. In the study period of 3 yr, repeated sampling of milk (n = 23,219) and feces (n = 8,832) was performed. A total of 1,985 Danish dairy cows provided material for the study. Milk samples were analyzed for antibodies using an ELISA, and fecal samples were analyzed for mycobacteria by culture. A reference test to correctly classify cattle antemortem does not exist; thus, "infection" and "infectious" were defined by repeated testing using one test as the condition to be detected by the other test. Fecal culture responses were evaluated against antibody status, and ELISA responses were evaluated against detected bacterial shedding. The results of this study indicate that the ability of both tests to detect "infection" increases almost linearly from 2 to 5 yr of age, whereas the ability of both tests to detect "infectious" is not affected by age. Purpose-specific tests are required to appropriately interpret and use test results for
management of paratuberculosis, and relevant covariates, such as age, should be included when possible.

**General information**
- **Publication status:** Published
- **Organisations:** University of Copenhagen
- **Contributors:** Nielsen, S. S., Toft, N.
- **Number of pages:** 11
- **Pages:** 569-579
- **Publication date:** 2006
- **Peer-reviewed:** Yes

**Publication information**
- **Journal:** Journal of Dairy Science
- **Volume:** 89
- **Issue number:** 2
- **ISSN (Print):** 0022-0302
- **Ratings:**
  - Scopus rating (2006): SJR 1.158 SNIP 1.638
- **Web of Science (2006):** Indexed yes
- **Original language:** English
- **URLs:**
  - http://www.scopus.com/record/display.url?eid=2-s2.0-32444433048&origin=inward&txGid=8013B69168B054389E2E2CB3435C2C4.kqQeWtawXauCyC8ghhRGJg%3a1

**Evaluation of three 3ABC ELISAs for foot-and-mouth disease non-structural antibodies using latent class analysis**

**BACKGROUND:** Foot-and-mouth disease (FMD) is a highly contagious viral disease of even-toed ungulates. Serological diagnosis/surveillance of FMD presents several problems as there are seven serotypes worldwide and in the event of vaccination it may be necessary to be able to identify FMD infected/exposed animals irrespective of their vaccination status. The recent development of non-structural 3ABC protein (NSP) ELISA tests has greatly advanced sero-diagnosis/surveillance as these tests detect exposure to live virus for any of the seven serotypes of FMD, even in vaccinated populations. This paper analyses the performance of three NSP tests using a Bayesian formulation of the Hui-Walter latent class model to estimate test sensitivity and specificity in the absence of a "gold-standard" test, using sera from a well described cattle population in Cameroon with endemic FMD.

**RESULTS:** The analysis found a high sensitivity and specificity for both the Danish C-ELISA and the World Organisation for Animal Health (O.I.E.) recommended South American I-ELISA. However, the commercial CHEKIT kit, though having high specificity, has very low sensitivity. The results of the study suggests that for NSP ELISAs, latent class models are a useful alternative to the traditional approach of evaluating diagnostic tests against a known "gold-standard" test as imperfections in the "gold-standard" may give biased test characteristics.

**CONCLUSION:** This study demonstrates that when applied to naturally infected zebu cattle managed under extensive rangeland conditions, the FMD ELISAs may not give the same parameter estimates as those generated from experimental studies. The Bayesian approach allows for full posterior probabilities and capture of the uncertainty in the estimates. The implications of an imperfect specificity are important for the design and interpretation of sero-surveillance data and may result in excessive numbers of false positives in low prevalence situations unless a follow-up confirmatory test such as the enzyme linked immunoelectrotransfer blot (EITB) is used.

**General information**
- **Publication status:** Published
- **Organisations:** University of Edinburgh, Pan-American Foot-and-Mouth Disease Center, Danish Institute for Food and Veterinary Research, Pirbright Institute, Regional Centre of Wakwa, University of Liverpool, University of Copenhagen
- **Contributors:** Bronsvoort, B. M. D., Toft, N., Bergmann, I. E., Sørensen, K., Anderson, J., Malirat, V., Tanya, V. N., Morgan, K. L.
- **Number of pages:** 1
- **Pages:** 30
- **Publication date:** 2006
- **Peer-reviewed:** Yes

**Publication information**
- **Journal:** B M C Veterinary Research
- **Volume:** 2
- **ISSN (Print):** 1746-6148
- **Ratings:**
  - Scopus rating (2006): SJR 0.359 SNIP 1.098
Guidelines for improved disease recording and recommendations for use of data

The Danish Veterinary Cancer Registry: an update

The effect of correlation structures on the properties of diagnostic tests for paratuberculosis

The Gamma-Poisson model as a statistical method to determine if micro-organisms are randomly distributed in a food matrix
matrix. In this study, we analyse the Gamma-Poisson model to explore some of the properties of the Gamma-Poisson model left unexplored by the previous study. The conclusion of our analysis is that the Gamma-Poisson model distinguishes poorly between variation at the Poisson level and the Gamma level. Estimated parameter values from simulated data-sets showed large variation around the true values, even for moderate sample sizes (n = 100). Furthermore, at these sample sizes the likelihood ratio is not a good test statistic for discriminating between the Gamma-Poisson distribution and the Poisson distribution. Hence, to determine if data are randomly distributed, i.e., Poisson distributed, the Gamma-Poisson distribution is not a good choice. However, the ratio between variation at the Poisson level and the Gamma level does provide a measure of the amount of overdispersion. (c) 2005 Elsevier Ltd. All rights reserved.

General information
Publication status: Published
Organisations: University of Glasgow, University of Copenhagen
Contributors: Toft, N., Innocent, G. T., Mellor, D. J., Reid, S. W. J.
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Publication date: 2006
Peer-reviewed: Yes

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Journal: Food Microbiology
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Scopus rating (2006): SJR 1.06 SNIP 1.619
Web of Science (2006): Indexed yes
Original language: English
DOIs:
10.1016/j.fm.2005.01.014
Research output: Contribution to journal – Journal article – Annual report year: 2006 – Research – peer-review

A framework for decision support related to infectious diseases in slaughter pig fattening units
This paper analyzes the problem faced by managers of pig fattening units when the pigs are subject to common epidemic diseases, such as respiratory diseases or Swine Influenza. The problem is defined as a simultaneous optimization of the delivery policy and control strategies for disease control. As some disease controls, such as vaccination, are implemented at the batch level and last through the lifetime of the vaccinated pigs, the problem requires that decisions are addressed at multiple timescales. Using the framework of multi-level hierarchic Markov processes a general framework was defined. The elements defining the framework were the decisions at the tactical (batch) level and the operational (daily) level. Decisions at the strategic level, e.g., decisions lasting longer than the length of a batch, were considered as constraints to the lower levels of the decision problem and not optimized. The major components of the general framework were a stochastic growth model, an epidemic model to handle within-batch spread of disease, a transition model to handle the between-batch spread of disease, and link between the growth model and the disease model and a general set of control measures. The model was illustrated using an example with Swine Influenza in an all-in-all-out production system. Results show that the optimal delivery policy and control strategies for disease interact. This suggests that decision support must adopt an integrated approach to modelling the decision complex in pig production in order to represent the full complexity of the system. (c) 2004 Elsevier Ltd. All rights reserved.

General information
Publication status: Published
Organisations: University of Copenhagen, Danish Institute of Agricultural Sciences
Contributors: Toft, N., Kristensen, A. R., Jørgensen, E.
Number of pages: 18
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Publication date: 2005
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Publication information
Journal: Agricultural Systems
Volume: 85
Issue number: 2
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Ratings:
Scopus rating (2005): SJR 0.695 SNIP 1.293
A stochastical model of chick and grower survival in smallholder poultry production

Continuous-data diagnostic tests for paratuberculosis as a multistage disease

Diagnosing diagnostic tests: evaluating the assumptions underlying the estimation of sensitivity and specificity in the absence of a gold standard
the size of the difference between disease prevalences within the populations influences the precision of the estimates. It is also illustrated by a simulation study how a difference in a test sensitivity between populations may result in estimates that are biased towards the sensitivity of the test in the population with highest disease prevalence, since that population estimate is supported by most of the data. It is shown that the assumption of conditional independence between tests in general cannot be ignored in latent class models. Failure to impose conditional independence will result in a model that lacks identifiability in a way that cannot be handled by adding more tests or dividing the sample into more populations. (c) 2005 Elsevier B.V. All rights reserved.

General information
Publication status: Published
Organisations: Danish Institute of Agricultural Sciences, University of Copenhagen
Contributors: Toft, N., Jørgensen, E., Højsgaard, S.
Number of pages: 15
Pages: 19-33
Publication date: 2005
Peer-reviewed: Yes

Publication information
Journal: Preventive Veterinary Medicine
Volume: 68
Issue number: 1
ISSN (Print): 0167-5877
Ratings:
Scopus rating (2005): SJR 0.92 SNIP 1.441
Web of Science (2005): Indexed yes
Original language: English
DOIs:
10.1016/j.prevetmed.2005.01.006
Research output: Contribution to journal › Journal article – Annual report year: 2005 › Research › peer-review

Spatial distribution of Escherichia coli O157-positive farms in Scotland
Using a sample of 949 Scottish farms with finishing cattle, the spatial distribution of Escherichia coli O157-positive farms was investigated using disease mapping models. The overall prevalence of E. coli O157-positive farms was estimated as 22%. The regions used in this study were the 16 postcode areas of Scotland. For each region, the posterior relative risk (RR) was estimated as a model-based alternative to the saturated standardized morbidity ratio (SMR), i.e., the ratio between observed and expected cases in a region. Three Bayesian hierarchical models with generalized linear modeling of the area-specific risks were used to estimate the posterior relative risk of E. coli O157-positive farms in the postcode areas: a random-effects model incorporating only spatially uncorrelated heterogeneity; a model incorporating both spatially correlated and uncorrelated heterogeneity; and a pseudo-mixture model with unstructured correlation and a weighted mix of two variance components representing the spatial correlation and a jump structure. None of the models identified any areas with a significant increase or decrease in risk. The deviance information criteria slightly favored the simplest model (RR range: 0.92-1.09). However, this model appeared to smooth out more of the variation in the RR compared to the pseudo-mixture model, which gave a more informative pattern of the posterior relative risks (range: 0.81-1.22). (c) 2005 Elsevier B.V. All rights reserved.

General information
Publication status: Published
Organisations: University of Glasgow, Biomathematics & Statistics Scotland, SAC Veterinary Science Division, University of Copenhagen
Contributors: Toft, N., Innocent, G. T., McKendrick, I. J., Ternent, H. E., Mellor, D. J., Gunn, G. J., Synge, B., Reid, S. W. J.
Number of pages: 12
Pages: 45-56
Publication date: 2005
Peer-reviewed: Yes

Publication information
Journal: Preventive Veterinary Medicine
Volume: 71
Issue number: 1-2
ISSN (Print): 0167-5877
Ratings:
Scopus rating (2005): SJR 0.92 SNIP 1.441
Web of Science (2005): Indexed yes
Evaluating diagnostic tests

Aims: To evaluate a conventional bacteriological test based on faecal culture and an indirect serum ELISA for detection of S. Dublin infected cattle. To compare the predictive values of the two tests in relation to the prevalence.

Methods and Results: A total of 4531 paired samples from cattle in 29 dairy herds were analysed for presence of S. Dublin bacteria in faeces and immunoglobulins directed against S. Dublin lipopolysaccharide in an indirect serum ELISA. Sensitivity and specificity were estimated at two ELISA cut-off values using a validation method based on latent class models, which presumably provides less biased results than traditional validation methods. Stratification of data into three age groups gave significantly better estimates of test performance of the ELISA. Receiver operating characteristic (ROC) curves were constructed for comparison of overall performance of the ELISA between the three age groups. The sensitivity of the faecal culture test was low (6-14%). ELISA appeared to have a higher validity for animals aged 100-299 days of age than older or younger animals. Overall, the negative predictive value of the ELISA was 2-10 times higher than for the faecal culture test at realistic prevalence of infection in the test population.

Conclusions: The diagnostic sensitivity of the faecal culture test for detection of S. Dublin is poor, the specificity is 1. The superior sensitivity and negative predictive value of the serum ELISA makes this test preferable to faecal culture as an initial screening test and for certification of herds not infected with S. Dublin.

Significance and Impact of the Study: A quantitative estimate of the sensitivity of a faecal culture test for S. Dublin in a general population was provided. ELISA was shown to be an appropriate alternative diagnostic test. Preferably, samples from animals aged 100-299 days of age should be used as these give the best overall performance of the ELISA. Plots of ROC curves and predictive values in relation to prevalence facilitates optimisation of the ELISA cut-off value.
Measures of association and effect

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N., Agger, J. F. G., Bruun, J.
Number of pages: 13
Pages: 95-107
Publication date: 2004

Host publication information
Title of host publication: Introduction to veterinary epidemiology : internationally reviewed
Place of publication: Frederiksberg
Publisher: Biofolia
Editors: Houe, H., Ersbøll, A. K., Toft, N.
ISBN (Print): 87-9131-921-8
Source: LIFE
Source-ID: 7958652
Research output: Chapter in Book/Report/Conference proceeding › Book chapter – Annual report year: 2004 › Education

Measures of disease frequency

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N., Agger, J. F. G., Houe, H., Bruun, J.
Number of pages: 17
Pages: 77-93
Publication date: 2004

Host publication information
Title of host publication: Introduction to veterinary epidemiology : internationally reviewed
Place of publication: Frederiksberg
Publisher: Biofolia
Editors: Houe, H., Ersbøll, A. K., Toft, N.
ISBN (Print): 87-9131-921-8
Source: LIFE
Source-ID: 7958636
Research output: Chapter in Book/Report/Conference proceeding › Book chapter – Annual report year: 2004 › Education

Observational studies

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Ersbøll, A. K., Toft, N., Bruun, J.
Number of pages: 14
Pages: 47-60
Publication date: 2004
Sample size and sampling methods

General information
Publication status: Published
Organisations: Unknown
Contributors: Toft, N., Houe, H., Nielsen, S. S.
Number of pages: 23
Pages: 109-131
Publication date: 2004

Spatial statistical methods for estimating regions with increased risk of BVDV infection in Denmark

General information
Publication status: Published
Organisations: Technical University of Denmark, Danish Bacon and Meat Council, Danish Cattle Federation, University of Copenhagen, University of Prince Edward Island
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Publication date: 2004

Appendix A: Biostatistics

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Erskæll, A. K., Toft, N.
Number of pages: 5
Pages: 267
Publication date: 2003
Comparison of results from a classic and a latent class method for test validation of a Salmonella Dublin ELISA

General information
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Organisations: University of Copenhagen
Contributors: Nielsen, L. R., Toft, N., Ersbøll, A. K.
Number of pages: 4
Publication date: 2003
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Event:

Bibliographical note
Kode for udgivelsesland: 'dk' Kode for bibliotekets beholdning: 'ikke modtaget'
Source: LIFE
Source-ID: 69295 (000011697)
Research output: Chapter in Book/Report/Conference proceeding › Book chapter – Annual report year: 2003
Communication

Estimation of sero-prevalence of paratuberculosis with mixture models including covariates

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Nielsen, S. S., Toft, N., Bibby, B. M., Nielsen, A.
Number of pages: 3
Publication date: 2003
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Event:

Bibliographical note
Kode for udgivelsesland: 'cl' Kode for bibliotekets beholdning: 'modtaget' Ukendte organisationer '
'Epidemiologi', '
'Epidemiologi', '
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Source: LIFE
Source-ID: 71388 (000012119)
Research output: Contribution to conference › Paper – Annual report year: 2003
Research

Evaluating diagnostics tests

General information
Publication status: Published
Organisations: University of Copenhagen
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Pages: 137-155
Publication date: 2003

Host publication information
Title of host publication: Veterinary epidemiology : from hypothesis to conclusion
Place of publication: København
Publisher: Samfundslitteratur

Bibliographical note
Kode for bibliotekets beholdning: 'ikke modtaget'
Source: LIFE
Exploring disease definitions of *Salmonella* Dublin in latent class analysis

**General information**
Publication status: Published
Organisations: Research Center Foulum, University of Copenhagen
Contributors: Toft, N., Nielsen, L. R., Højgaard, S.
Number of pages: 3
Publication date: 2003
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**Bibliographical note**
Kode for bibliotekets beholdning: 'modtaget'
Source: LIFE
Source-ID: 71778 (000012190)
Research output: Contribution to conference › Conference abstract for conference – Annual report year: 2003 › Research

Prøveudtagning - hvilke dyregrupper og hvor mange?

**General information**
Publication status: Published
Organisations: Unknown
Contributors: Toft, N., Houe, H., Erskell, A. K.
Number of pages: 7
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Sider: 68-74
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Research output: Contribution to conference › Paper – Annual report year: 2003 › Research

Data analysis: chapter 13

**General information**
Publication status: Published
Organisations: University of Copenhagen
Contributors: Erskell, A. K., Bruun, J., Nielsen, A. C., Toft, N.
Number of pages: 37
Pages: 199-235
Publication date: 2002

**Host publication information**
Title of host publication: *Veterinary epidemiology: from hypothesis to conclusion*
Place of publication: Frederiksberg
Publisher: Center for Skov, Landskab og Planlægning/Københavns Universitet
Source: LIFE
Source-ID: 66883 (000011222)
Research output: Chapter in Book/Report/Conference proceeding › Book chapter – Annual report year: 2002 › Education

Data management

**General information**
Publication status: Published
Organisations: University of Copenhagen
Contributors: Houe, H., Erskell, A. K., Toft, N.
Diagnosing diagnostic tests: evaluating the precision of different approaches for estimation of sensitivity and specificity

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N., Jørgensen, E., Højsgaard, S.
Number of pages: 10
Pages: 137-146
Publication date: 2002

Diagnosing diagnostic tests: evaluating the precision of different approaches for estimation of sensitivity and specificity

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N., Jørgensen, E., Højsgaard, S.
Number of pages: 10
Pages: 137-146
Publication date: 2002

Diagnosis testing with multiple classifications

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N., Nielsen, S. S., Jørgensen, E.
Number of pages: 6
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Peer-reviewed: No
Event:

Estimation of farm specific parameters in a longitudinal model for litter size with variance components and random dropout

The estimation of farm specific parameters is often ignored in studies of decision support systems such as, e.g., sow replacement problems. This study concerns the specification and estimation of farm specific parameters in a model for litter size required by a replacement problem considering culling based on productive performance. This implies a joint distribution of the litter size at the parities under consideration. A non-linear parametric mean curve is used to model the expected litter size at different parities for sows within the same herd, The, covariance matrix is modeled using variance components of random effects, serial correlation and measurement error. Data from a total of 43 herds are used to devise a likelihood based inference, using maximum likelihood to obtain initial estimates for maximum posterior estimation of farm specific parameters. The maximum posterior approach is required to obtain reasonable estimates in the cases where on-farm registrations are inadequate. (C) 2002 Elsevier Science B.V. All rights reserved.
Optimisation of the validity of ELISA and faecal culture tests for paratuberculosis: selection of population or correction by population characteristics?

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Nielsen, S. S., Toft, N.
Number of pages: 6
Publication date: 2002
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Source: LIFE
Source-ID: 65772 (000011031)
Research output: Contribution to conference – Paper – Annual report year: 2002 – Research

Sample size and sampling methods: chapter 8

General information
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Organisations: Unknown
Contributors: Toft, N., Houe, H., Nielsen, S. S.
Number of pages: 19
Pages: 109-127
Publication date: 2002

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Title of host publication: Veterinary epidemiology: from hypothesis to conclusion
Place of publication: Frederiksberg
Publisher: Center for Skov, Landskab og Planlægning/Københavns Universitet
Source: LIFE
Source-ID: 66517 (000011156)
Research output: Chapter in Book/Report/Conference proceeding – Book chapter – Annual report year: 2002 – Education

Stikprøverstørrelser og indsamlingsmetoder

General information
Publication status: Published
Organisations: Unknown
Contributors: Houe, H., Toft, N.
Number of pages: 10
Publication date: 2002
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Source: LIFE
Source-ID: 66387 (000011140)
Research output: Contribution to conference – Paper – Annual report year: 2002 – Research

Veterinary epidemiology: from hypothesis to conclusion

General information
Publication status: Published
Organisations: Unknown
Tradeoffs in modeling epidemic disease in slaughter pig production

General information
Publication status: Published
Organisations: Danish Institute of Agricultural Sciences, University of Copenhagen
Contributors: Toft, N., Kristensen, A. R., Jørgensen, E.
Number of pages: 6
Pages: 391-396
Publication date: 2001

Host publication information
Title of host publication: Ikke angivet
Publisher: Agro
Editor: Steffe, J.
Edition: 1

Bibliographical note
Ukendte organisationer "90"
Source: LIFE
Source-ID: 52550 (000008567)
Research output: Chapter in Book/Report/Conference proceeding – Article in proceedings – Annual report year: 2001 – Research

A framework for decision support related to an infectious disease in slaughter pig production

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N., Kristensen, A. R., Jørgensen, E.
Number of pages: 9
Publication date: 2000
Peer-reviewed: No
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Bibliographical note
Source-ID: 50347 (000008125)
Research output: Contribution to conference – Paper – Annual report year: 2000 – Research

Elements of decision support systems in pig production

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N.
Number of pages: 92
Publication date: 2000

Publication information
Place of publication: Copenhagen
Publisher: [The Royal Veterinary and Agricultural University, [Dina]]
Estimation of farm specific parameters in a longitudinal model for litter size with variance components and random dropout

General information
Publication status: Published
Organisations: Danish Institute of Agricultural Sciences, University of Copenhagen
Contributors: Toft, N., Jørgensen, E., Dethlefsen, C.
Number of pages: 10
Pages: 127-136
Publication date: 2000

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Title of host publication: Pig Herd Management Modelling and Information Technologies Related
Publisher: L.M. Plà
Editors: Plà, L. M., Pomar, J. P.

Bibliographical note
Ukendte organisationer "90"
Source: LIFE
Source-ID: 48730 (000007849)
Research output: Chapter in Book/Report/Conference proceeding – Article in proceedings – Annual report year: 2000 – Research

Evaluation of SIR epidemic models in slaughter pig units using Monte Carlo simulation

General information
Publication status: Published
Organisations: Research Center Foulum, University of Copenhagen
Contributors: Jørgensen, E., Søllested, T. A., Toft, N.
Number of pages: 10
Pages: 27-36
Publication date: 2000

Host publication information
Title of host publication: Pig Herd Management Modelling and information technologies related
Publisher: L.M. Plà
Editors: Plà, L. M., Pomar, J.

Bibliographical note
Ukendte organisationer "90"
Source: LIFE
Source-ID: 49127 (000007908)
Research output: Chapter in Book/Report/Conference proceeding – Article in proceedings – Annual report year: 2000 – Research

Linking decisions on multiple time scales

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N.
Number of pages: 10
Publication date: 1999
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Bibliographical note
Modeling eating patterns of growing pigs using dynamic linear models

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N., N. Madsen, T.
Number of pages: 17
Publication date: 1998

Publication information
Place of publication: Copenhagen
Publisher: Dina, KVL
Original language: English

The dynamic aspect of the reproductive performance in the sow herd

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N.
Publication date: 1998

Publication information
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Publisher: Dina, KVL
Original language: English

Beslutningsstøttesystemer til håndtering af beslutninger med forskellige tidshorisonter

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N.
Number of pages: 1
Pages: 9
Publication date: 1997

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Title of host publication: Dina notat
Publisher: Den Kgl. Veterinær- og Landbohøjskole, Institut for Husdyrbrug og Husdyrsundhed, Dinas Forskerskole
Editor: Ringgaard Kristensen, A.

Bibliographical note
Kode for udgivesesland: 'dk'
Source: LIFE
Source-ID: 27304 (000003513)
Research output: Chapter in Book/Report/Conference proceeding – Article in proceedings – Annual report year: 1997 – Research

Illustration af sekventielt beslutningsproblem i soholdet

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N.
Model based decision support in sow herds with emphasis on linking decisions with different time horizons

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N.
Number of pages: 6
Pages: 55-60
Publication date: 1997

Host publication information
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The parameter input file for the multi-level hierarchic Markov Process

General information
Publication status: Published
Organisations: University of Copenhagen
Contributors: Toft, N., Kristensen, A. R.
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Projects:

Disease databases
The general purpose of the project is to explore the potential use and value of different data sources as a monitoring tool for detection of diseases in Danish swine herds. The project is a continuation of the PhD project "Veterinary Epidemiology with the focus on monitoring livestock disease using diagnostic databases", in which different databases and monitoring methods were explored in the context of endemic diseases.
As a starting point, the project will be focused on methods to detect changes in mortality and to find possible links among diseases occurrence, antibiotic usage, and other data streams (such as meat inspection and laboratory diagnostic data).
Lopes Antunes, A. C., Project Participant, National Veterinary Institute, Epidemiology
Jensen, V. F., Project Participant, National Veterinary Institute, Epidemiology
Toft, N., Project Manager, National Veterinary Institute, Epidemiology
01/01/2017 → 31/12/2019
Project: Research

Veterinary epidemiology with emphasis on the association between spatial proximity, contact structures, antibiotic consumption and antibiotic resistance
Birkøgaard, A. C., PhD Student, National Veterinary Institute
Toft, N., Main Supervisor
Hisham Beshara Halasa, T., Supervisor
Boklund, A., Examiner
Dewulf, J., Examiner
Nielsen, S. S., Examiner
Samfinansieret - Andet
01/12/2013 → 20/12/2017
Award relations: Veterinary epidemiology with emphasis on the association between spatial proximity, contact structures, antibiotic consumption and antibiotic resistance
Project: PhD

Undersøgelse af sammenhænge mellem sundhed, velfærd og antibiotikaforbrug hos danske husdyr
Fertner, M. E., PhD Student, National Veterinary Institute
Toft, N., Main Supervisor
Boklund, A., Supervisor
Christiansen, L. E., Supervisor
Jensen, V. F., Examiner
Pedersen, K. S., Examiner
Dewulf, J., Examiner
Stege, H., Supervisor
Technical University of Denmark
15/12/2011 → 17/11/2016
Award relations: Undersøgelse af sammenhænge mellem sundhed, velfærd og antibiotikaforbrug hos danske husdyr
Project: PhD

Development of a herd- and cow-specific decision support tool for control of mastitis
Gussmann, M. K., PhD Student, National Veterinary Institute
Hisham Beshara Halasa, T., Main Supervisor
Toft, N., Supervisor
Boklund, A., Examiner
Denwood, M., Examiner
Rajala-Schultz, P. J., Examiner
Nielsen, S. S., Supervisor
Samfinansieret - Andet
01/07/2015 → 30/09/2018
Award relations: Development of a herd- and cow-specific decision support tool for control of mastitis
Project: PhD

Simulation modeling of LA-MRSA dispersal and control between swine herds
Schulz, J., PhD Student, National Veterinary Institute
Hisham Beshara Halasa, T., Main Supervisor
Boklund, A., Supervisor
Toft, N., Supervisor
Jensen, V. F., Examiner
Baekbo, P., Examiner
Selhorst, T., Examiner
Offentlig finansiering
01/05/2015 → 21/02/2019
Award relations: Simulation modeling of LA-MRSA dispersal and control between swine herds
Project: PhD

The spread and control of LA-MRSA within Danish pig herds
Sørensen, A. I. V., PhD Student, National Veterinary Institute
Hisham Beshara Halasa, T., Main Supervisor
Novel methods for applied spatio-temporal risk assessment models of endemic and emerging vector borne diseases
Cuellar, A. C., PhD Student, National Veterinary Institute
Bødker, R., Main Supervisor
Kjær, L. J., Supervisor
Toft, N., Supervisor
Christiansen, L. E., Examiner
Konradsen, F., Examiner
Purse, B., Examiner
Technical University of Denmark
15/02/2015 → 15/01/2019
Award relations: Novel methods for applied spatio-temporal risk assessment models of endemic and emerging vector borne diseases
Project: PhD

Veterinary Epidemiology - biological models of vector borne diseases
Haider, N., PhD Student, National Veterinary Institute
Bødker, R., Main Supervisor
Kjær, L. J., Supervisor
Toft, N., Supervisor
Vigre, H., Examiner
Lindström, A. Å., Examiner
Mortensen, S., Examiner
Offentlig finansiering
15/02/2015 → 11/12/2018
Award relations: Veterinary Epidemiology - biological models of vector borne diseases
Project: PhD

Veterinary Epidemiology with focus on monitoring livestock disease using diagnostic databases
Lopes Antunes, A. C., PhD Student, National Veterinary Institute
Toft, N., Main Supervisor
Hisham Beshara Halasa, T., Supervisor
Jensen, V. F., Examiner
Revie, C. W., Examiner
Mortensen, S., Examiner
Offentlig finansiering
15/12/2013 → 26/04/2017
Award relations: Veterinary Epidemiology with focus on monitoring livestock disease using diagnostic databases
Project: PhD

Dynamics and mechanisms of antimicrobial resistance in animal husbandry
Clasen, J., PhD Student, Department of Systems Biology
Folkesson, A., Main Supervisor
Toft, N., Supervisor
Sternberg, C., Examiner
Johansen, P. J., Examiner
Regenberg, B., Examiner
Samfinansieret - Andet
15/12/2013 → 16/08/2018
Award relations: Dynamics and mechanisms of antimicrobial resistance in animal husbandry
Project: PhD
iCull: iCull
Herd-specific economic decision tool for farmers.
Kirkeby, C. T., Project Participant, National Veterinary Institute, Section for Epidemiology
Hisham Beshara Halasa, T., Project Manager, National Veterinary Institute, Section for Epidemiology
Græsbøll, K., Project Participant, Section for Veterinary Epidemiology and public sector consultancy, Department of Applied Mathematics and Computer Science, Dynamical Systems
Christiansen, L. E., Project Manager, Department of Applied Mathematics and Computer Science, Dynamical Systems
Toft, N., Project Manager, National Veterinary Institute, Section for Epidemiology
Saxmose, S., Project Manager
Project ID: 23176
01/11/2013 → 31/10/2015
Project: Research