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9. Paper 2

Estimation of probability for the presence of claw and hoof diseases by combing cow- and herd-level information using a Bayesian network

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Submitted for publication

Estimation of probability for the presence of claw and hoof diseases by combing cow- and herd-level information using a Bayesian network

Abstract

Cross sectional data on the prevalence of claw and (inter) digital skin diseases on 4854 Holstein Friesian cows in 50 Danish dairy herds was used in a Bayesian network to create herd specific probability distributions for the presence of three lameness causing diseases. Parity and lactation stage are identified as risk factors on cow level, for the prevalence of the three lameness causing diseases digital dermatitits (DD), other interdigital diseases (OID) and hoof horn diseases (HHD). Four herd level risk factors have been identified; herd size, the use of footbaths, a grazing strategy and total mixed ration. Besides, the data has been used to estimate the random effect of herd on disease prevalence and to find conditional probabilities of cows being lame, given the presence of the three diseases. By considering the 50 herds representative for the Danish population, the estimates for risk factors, conditional probabilities and random herd effects are used to formulate cow-level probability distributions of disease presence in a specific Danish dairy herd. By step-wise inclusion of information on cow- and herd-level risk factors, lameness prevalence and clinical diagnosis of diseases on cows in the herd, the Bayesian network systematically adjusts the probability distributions for disease presence in the specific herd. Information on population-, herd- and cow-level is combined and the uncertainty in inference on disease risk is quantified.

Key words: Lameness; dairy cattle; probability distribution; Bayesian network

9.1 Introduction

Dairy cattle lameness is a health disorder caused by a broad spectrum of diseases to the cow's hoof, (inter) digital skin and legs. Lameness is an important problem for the modern dairy industry due to its economic impact (Enting et al., 1997; Ettema and Østergaard, 2006a) and effects on animal welfare (Whay et al., 1998; Metz and Bracke, 2003) . In order for the farmer to decide whether to implement preventive or curative actions against the lameness causing diseases, an estimate of the diseases' true prevalence is essential. Definition and consequently identification of (clinical) cases in a herd is subject to personal opinion. Methodologies to score a cow's claw and locomotion differ both in practice and science (Whay, 2002). The animal's true disease state is therefore never known with certainty.

In case disease risk is described with a point estimate, which we claim to be real and fixed, uncertainty about the true disease state is ignored. By describing disease risk with a probability distribution, the degree of belief in the quantity of interest is expressed. Probability distributions can be created systematically by using Bayesian statistics, using Markov Chain Monte Carlo (MCMC) based methods, i.e. Winbugs (Spiegelhalter et al., 2004). A characteristic of Bayesian data analysis is quantification of uncertainty in inferences based on statistical data analysis (Gelman et al. 2004). An overview of the extensive use of Bayesian statistics for estimating animal- and herd-level disease risk is given by Branscum et al. (2004). The objective of our study is to develop a framework that can describe disease risk in a specific herd by a distribution based on prior knowledge on disease prevalence in the entire population, combined with herd specific knowledge.

The diseases in question are three lameness causing diseases to the cow's claw and (inter) digital skin. Herd specific knowledge can be information on the presence of herd level risk factors for the claw and skin diseases. Clear associations have been found between presence of these diseases and herd size (Rodriguez-Lainz et al., 1999), implementation of a grazing strategy compared to zero-grazing (Somers et al. 2003), periodic implementation of footbaths (Somers et al. 2005a) and feeding strategy (Manson and Leaver, 1989; Wells et al., 1995). Knowledge on beforehand on the presence of these risk factors changes our belief in the actual risk level of the diseases in the herd under study. A second type of herd specific knowledge is the presence of clinically lame cows in the herd observed by a visual locomotion score. Not all diseases are painful enough to alter the cow's gait and standing position. Whay et al. (1998) have demonstrated a difference in the degree of painfulness between claw and skin diseases. Manske et al. (2002a) found different associations between the presence of claw and skin diseases and clinical lameness. Clearly the presence of claw and skin diseases does not provide solid evidence for the presence of lame cows; reversely the presence of lameness does not supply perfect knowledge on the presence of claw and skin diseases. However, in case the probability of a cow being lame, conditional on the presence of a disease is known, evidence on lameness can change our belief in the presence of diseases. A third type of herd specific knowledge is clinical observation of the diseases on the cow's claw and skin during (routine) claw trimming. The three types of knowledge differ in collecting ease and informative value. By using Bayesian statistics the *value* of each source of evidence gets reflected in the posterior distribution, which accordingly can be used by the decision maker. A decision can either be based directly on

the probability distribution or on the output of a decision support model, which uses the hyper parameters of the distributions as parameter values for disease risk.

9.2 Material and Methods

9.2.1 Data set

The data used in this study comes from a cross sectional study on the prevalence of hoof and skin diseases recorded at periodic hoof trimming. Of all professional claw trimmers that were asked to join the study, only four agreed. The claw trimmers included all client herds that met eligibility criteria: predominantly Holstein Friesian (HF) cows housed in free-stalls with concrete floors and cubicles. Only herds where all cows were routinely trimmed during the visit were included in the study. These herds were visited once during the housing season from October 2002 to April 2003; all cows trimmed were inside at the time of trimming in order to minimize variation caused by season. In total the recordings on 4854 cows in 50 Danish dairy herds were included in the analysis.All skin and horn lesions related to the distal part of all four limbs were recorded. This included heel horn erosion (HHE), sole haemorrhage (SH), sole ulcer (SU), interdigital dermatitis (ID), digital dermatitis (DD), interdigital hyperplasia (IH), white line abscess (WLA), white line disease (WLD) and double sole (DS).

For the purpose of modelling lameness in a decision support model as a cause of three aggregations of diseases (Ettema and Østergaard, 2006b) the diseases were aggregated by aetiology and agreement in risk factors. The diseases WLD, WLA, SH, SU and DS were aggregated as hoof horn diseases (HHD). The remaining diseases IH, HHE, ID, and DD have an infectious origin. DD was maintained as a separate outcome and IH, HHE, and ID were aggregated as other infectious diseases (OID). A more thorough support for the aggregation can be found in Ettema et al. (2007) in which the same aggregation is used. A more thorough description of the dataset can be found in the same article. Besides the clinical diagnoses of hoof diseases, the cows' locomotion was scored as the cows walked towards the trimming shute. Conditions for locomotion scoring were sub-optimal and properly performed in only three herds. Locomotion was scored according to Sprecher et al. (1997) by one observer, where cows with score >2 were qualified as lame, which is moderately lame or worse.

Parity and lactation stage were included in the analysis as the two covariates on cow level. Cows were either of parity 1, 2 or 3 and up. Stage of lactation was divided in 0 to 60 days in milk (DIM1), 61 to 120 days in milk (DIM2) or >120 days in milk (DIM3). On beforehand the absence of a linear relationship between lactation stage and disease occurrence was assured. Lactation stage was therefore divided in three stages of which the second and third stage have earlier been defined as high and low risk period, respectively (Manske et al., 2002b; Holzhauer et al., 2008b).
Thirty three herd level variables were collected at hoof trimming. The GENMOD procedure in SAS (SAS, 2001) was used to identify the herd level risk factors that had the strongest association with the diseases' prevalence. Covariates (risk factors) were not included based on a significant association, but on the magnitude of the parameter estimate. Initially, four

dichotomous covariates for every disease were included in the analysis. Herd size was either below or above 125 cows. A grazing strategy was either absent, i.e. zero-grazing or in any way implemented during a limited period of the year. Footbath use was categorized into regular use, compared to never using a footbath or only when needed. Finally, feeding type was either the use of a total mixed ration (TMR) or concentrate stations. Table 1 shows an overview of distribution of risk factors on cow and herd level.

Table 1
Distribution in absolute numbers and percentages in brackets of risk factors on cow level (n=4854) and herd level (n=50)

Cow level risk factors				Herd level risk factors			
Parity	1	1953	(40%)	Herd size	<125	18	(36%)
	2	1363	(28%)		>125	32	(64%)
	3+	1953	(32%)	Grazing	Zero	20	(40%)
					Summer	30	(60%)
DIM[a]	1	838	(17%)	Footbath	Regular	28	(56%)
	2	880	(18%)		Not regular	22	(44%)
	3	3136	(65%)	TMR	Yes	19	(38%)
					No	31	(62%)

[a] DIM 1: 0-60 days in milk, DIM 2: 61-120 days in milk, DIM 3: >120 days in milk

9.2.2 Bayesian data analysis

9.2.2.1 Markov Chain Monte Carlo

The idea behind Bayesian statistics is inference on a parameter (*θ, theta)* conditional on observed data, *y* and summarizing the result in a probability statement. This posterior probability, notated as P(*θ*|*y*), is estimated using computer intensive algorithms. The method used in this study is Markov Chain Monte Carlo (MCMC) and is based on drawing samples of *θ* from approximate distributions and then correcting those draws to better approximate the target posterior distribution (Gelman et al., 2007). Samples are drawn sequentially where each time step depends on the previous one until the stationary, marginal posterior distribution is reached. The Gibbs sampler is the particular Markov chain algorithm used to generate the sequence of samples from the joint probability distribution (Casella and Gettinby, 1992). The software used in this study is Winbugs (Spiegelhalter et al., 2004).

9.2.2.2 Statistical model

A graphical presentation of the Bayesian network used for the analysis is presented in figure 1.

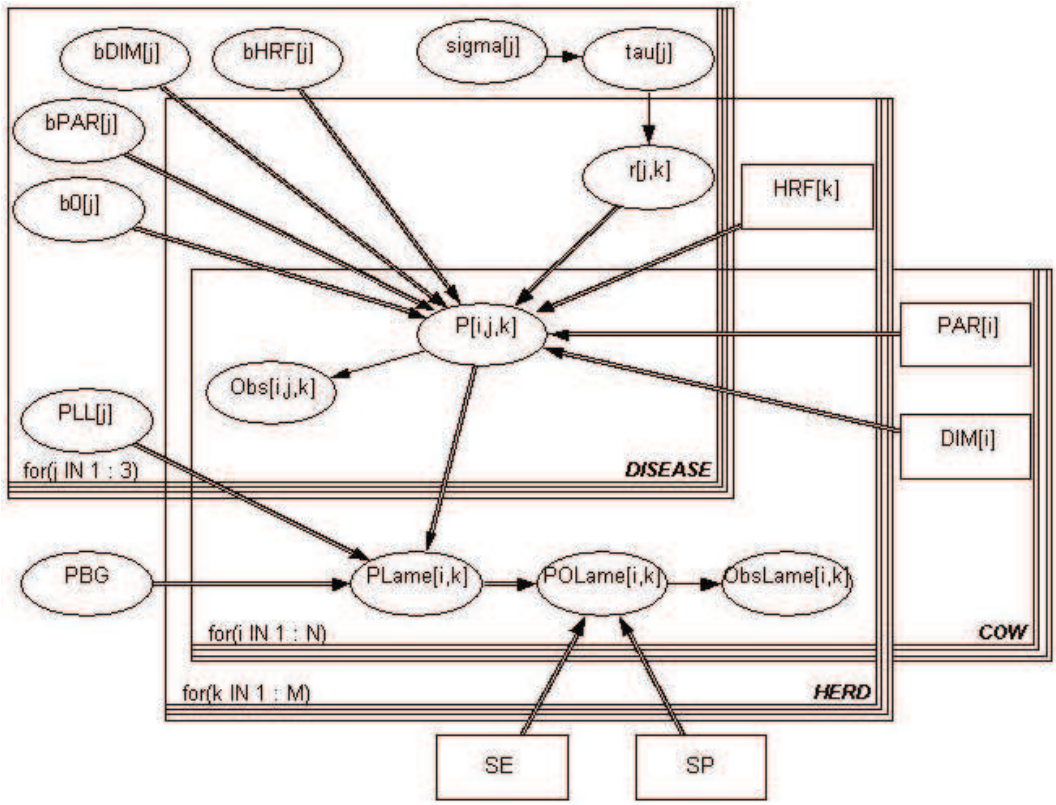

Fig. 1: Graphical presentation of the Bayesian network. *Obs[i,j,k]* is the test outcome of the clinical observation at claw trimming of the *j*th lesion on the *i*th cow in the *k*th herd. *P[i,j,k]* is the probability of the cow's disease state being positive. The components of the regression models are the intercept *b0[j]*, parameters *bPAR[j]* and *bDIM[j]* representing the *i*th cow's parity (PAR) and lactation stage (DIM) as a risk factor, respectively, *bHRF[j]* representing a herd level risk factor (HRF, of which there are four) and the random effect *r[j,k]* of herd *k*. *ObsLame[i,k]* is the test outcome of locomotion scoring being either positive or negative. *POLame[i,k]* is the probability of lameness being observed, where *SPlame* and *SElame* represent the sensitivity and specificity of the diagnosis. *PLame [i,k]* is the probability of the latent disease state being positive. Probability of the *j*th lesion causing clinical lameness is represented by *PLL[j]*. A back ground probability of being lame *(PBG)* is specified, representing any other cause of lameness.

The probability of the *i*th cow in the *k*th herd having the *j*th disease at periodic claw trimming is represented by the node P_{ijk} . This node, together with all edges directed at it, represents a random effects logistic regression model (Gelman and Hill, 2007).

$$Logit(P_{ijk}) = \beta_{0j} + \beta_{parity_j} * PAR_i + \beta_{\dim j} * DIM_i + \beta_{footbath_j} * FB_k + \beta_{herdsizej} * HS_k + \beta_{grazing_j} * GR_k + \beta_{TMRj} * TM_k + Rherd_{jk}$$

$$Rherd_{jk} \sim \mathrm{N}(0, \sigma_j^2)$$

The parameters β_{parity_j} and $\beta_{\dim_j}$ are the effect of parity and lactation stage, respectively, on the presence of the *j*th disease. The parameters $\beta_{footbath_j}$, $\beta_{herdsize_j}$, $\beta_{grazing_j}$ and β_{TMR_j} represent the association of the herd-level risk factors footbath strategy, herd size, grazing strategy and TMR-use, respectively, with the presence of the *j*th disease. The random effect of herd *k* on the presence of the *j*th disease is represented by $Rherd_{jk}$.

The test outcome Obs_{ijk}, i.e. whether the *j*th disease was diagnosed or not during trimming of the *i*th cow in the *k*th herd, was Bernoulli distributed with probability parameter depending on the *i*th cows disease state: ~Bern(P_{ijk}). Furthermore, a causal diagram is represented in figure 1, connecting lameness with its four causes.

$$PLame_{ik} = 1 - (1 - PBG) * (1 - PLL_j P_{ijk})$$

The probability of the *i*th cow in the *k*th herd being clinically lame ($PLame_{ik}$) is dependent on the probabilities of the *i*th cow having the *j*th disease; P_{ijk}. Not every disease is *painful* enough to result in clinical lameness, which in this study is defined as a locomotion score (Sprecher et al. 1997) of 3 and up. Therefore, nodes representing the conditional probability of being lame given the presence of a disease (P(lame|disease$_j$), noted as PLL_j) were included for every disease. Besides, a background probability (*PBG*) was included that represents any other cause of lameness. This structure uses the assumption of noisy or (Jensen, 2001) and is simplified in figure 2. The four nodes represent all causes of lameness. Each cause results in lameness unless an inhibitor, with probability $q_{1..4}$, prevents it. It is hereby assumed that the inhibitors are independent and the background event is always present.

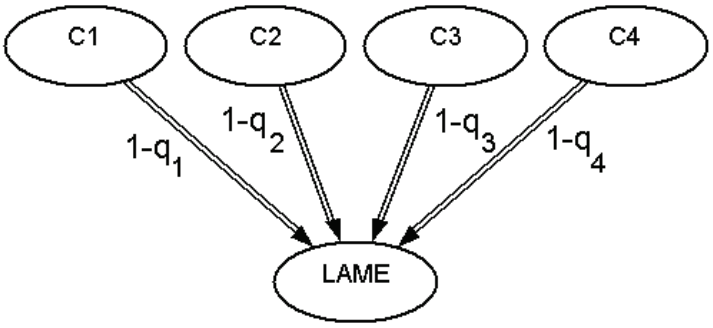

Figure 2: Simplified causal diagram of lameness and its 4 causes assuming *noisy or*; q_n is the probability that the effect of cause Cn is inhibited.

Besides modeling the probability of causing lameness (PLL) for the three single diseases, nodes representing every 2-way combination of diseases causing lameness were explored in the network.

The probability of observing a cow lame ($POLame_{ik}$) depends on $PLame_{ik}$ and on the probability of diagnosing an animal as diseased given a positive disease state (sensitivity, SE) and the probability of diagnosing an animal as healthy given a negative disease state (specificity, SP).

$$POLame_{ik} = SE * PLame_{ik} + (1 - SP) * (1 - PLame_{ik})$$

Both *SP* and *SP* should be considered observer specific. In the dataset used in this study, one hoof trimmer scored the cows' locomotion on different farms. In order to estimate *SP* and *SE* of a clinical diagnosis without prior knowledge on any of the models parameters, data on more than two independent tests (hoof trimmers) performed in more than two populations should be available (Branscum et al., 2005). This was not the case; therefore it was not possible to estimate sensitivity and specificity of the individual hoof trimmer (or the population of hoof trimmers) as is done by Baadsgaard and Jørgensen (2005). For *SP* and *SE* point estimates were used of 0.95 and 0.76, respectively (Thomsen, 2005). This study used a Bayesian threshold model to evaluate inter-observer agreement for diagnosing lameness using the same scoring system and cut-off value as this study. Test outcome $ObsLame_{ik}$, i.e. whether lameness was diagnosed or not by locomotion scoring, was Bernoulli distributed with probability parameter depending on the disease state: ~Bern($POLame_{ik}$).

9.2.2.3 Prior distributions

Flat normal distributions (~dnorm(0.0, 0.001)) were used for every parameter but the variance component of the logistic regression models. Prior distributions for the variance components on herd level for every disease were uniform (~dunif(0.001, 5)). Prior distributions for the three conditional probabilities of being lame given the presence of a disease, along with the background probability of lameness, were given a non-informative beta distribution (~dbeta(1,1)).

9.2.2.4 Model selection and convergence diagnosis

Candidate models were compared by monitoring the Deviance Information Criteria (DIC) (Spiegelhalter et al., 2002) where the model with the lowest value was considered best in predicting a dataset with a structure comparable to the one under study. The DIC was used to decide on inclusion of covariates in the regression model and inclusion of nodes representing the probability of the three single diseases, and every 2-way combination of them, causing lameness. Additionally, model goodness-of-fit was assessed by studying the differences between observed and predicted prevalence on herd level of the three diseases. These residuals were examined graphically (gg-plot and q-plot) and the Kolmogorov-Smirnov test for normal distribution of residuals was performed (probability ≥ 0.05 of D-statistic being larger than the critical D-statistic) (Weisstein, 2006).

Two chains were run with different initial values. To assess convergence, the four formal convergence tests at the core of the convergence diagnostic and output analysis (CODA) package were used (Best et al., 1995). The Raftery and Lewis' diagnostic (Raftery and Lewis, 1992) was used to determine the number of iterations needed to obtain desired precision in parameter estimates. It was decided to run 90.000 iterations, with a thinning factor of 20, of which the first 5000 were discarded as burn-in and the following 85.000 were used for posterior inference.

9.2.3 Herd level prevalence of lameness

Diagnosis of clinical lameness by locomotion scoring was done in 3 herds. The observed prevalence of lameness in the remaining 47 herds could be estimated directly as the mean of

the relevant individual $POLame_{ik}$'s. This estimate for observed lameness prevalence in the *k*th herd is referred to as ELP_k.

9.2.4 Illustration of application

The Bayesian data analysis was performed to get estimates on risk factors, herd level variance and lameness probabilities conditioned on disease presence. This analysis was the necessary first step in reaching the study's objective of describing the probability of having three lameness causing diseases with a hyper distribution for a cow in a new herd. In this new herd, which from here on will be referred to as the *specific herd of interest,* we want to infer on cow-level disease risk. In order to use the results of the 50 herds in estimating disease risk in the *specific herd of interest*, the entire dataset, supplemented with information on the *specific herd of interest,* was reanalyzed. To illustrate how the resulting probability distributions of cows in *the specific herd* are affected by information available on *the specific herd*, the data were reanalyzed 7 times. In every analysis, different types and different amounts of information were included.

In the first analysis 16 herds were added to the dataset, all with missing values for both observed diseases and lameness. The 16 herds represent 16 possible combinations of herd level risk factors. Apart from information on management, no further information was available on prevalence of diseases or clinical lameness. The 16 herds were analyzed together at the same time; since they did not contain any information, estimates on population level would remain unchanged.In analysis 2 to 7 *the specific herd* was analyzed as a herd with a herd size (H) over 125, regular use of footbaths (F), implementation of zero-grazing (G) and the use of a total mixed ration (T). Results of lameness observation by locomotion were added, signifying a low and high prevalence of lameness in analysis 2 and 3, respectively. Thereafter the entire dataset was reanalyzed with clinical observation performed on 45 cows during hoof trimming, indicating a low and high prevalence of diseases in analysis 4 and 5, respectively. For analysis 6 and 7 the same information was available, only on more cows.

Addition of a new herd to the dataset would also result in new estimates on population level; we were not interested in these new estimates since the information on the *specific herd of interest* is fictitious. We also did not want the new estimates influencing the *estimates in the specific herd* of interest; all seven analyses were therefore performed one at a time.

9.3 Results

9.3.1 Descriptive statistics

In table 2 the cow- and herd-level prevalence of diseases and clinical lameness are displayed. Lameness was diagnosed properly in only 3 herds. However, the prevalence of observed lameness (ELP) among all 4854 cows and in all 50 herds was estimated through simulation.

Table 2
Prevalence of digital dermatitis (DD), other interdigital diseases (OID) and hoof horn diseases (HHD) diagnosed at periodic claw trimming and prevalence of observed lameness (LAME) and estimated prevalence of observed lameness (ELP)

Cow level prevalence		Herd level prevalence						
		Mean	S.D.	Min	Q1	Median	Q3	Max
DD[1]	0.22	0.20	0.14	0	0.09	0.17	0.32	0.55
OID[1]	0.31	0.31	0.22	0	0.11	0.27	0.46	0.92
HHD[1]	0.15	0.15	0.13	0.01	0.09	0.12	0.19	0.85
LAME[2]	0.14	0.19	0.19	0.04	-	0.12	-	0.40
ELP[3]	0.12	0.12	0.04	0.07	0.10	0.11	0.13	0.33

[1] DD, OID and HHD were diagnosed on 4854 cows in 50 herds
[2] Lameness was observed on 285 cows in 3 herds
[3] Lameness Prevalence was estimated for 4854 cows in 50 herds

Lameness was observed in three herds with an average prevalence of 0.19 on herd level. When lameness prevalence was estimated for all 50 herds, a mean of 0.12 was found.

9.3.2 Logistic regression analysis

The median posterior odds ratios of the fixed effects on cow and herd level, along with their 95% credibility posterior intervals, are presented in table 3.

Table 3
Median posterior odds ratios (OR) and 95% credibility posterior intervals (95% CPI) for the odds of being diagnosed with Digital Dermatitis (DD), Other Interdigital Diseases (OID) and Hoof Horn Diseases (HHD) at periodic claw trimming on cow (n=4854) and herd level (n=50).

			OR	95% CPI	
				$Q_{0.025}$	$Q_{0.975}$
DD	Cow level	Parity 2 [a]	1.05	0.88	1.25
		Parity 3 [a]	0.86	0.72	1.03
		DIM 1 (0-60 days) [b]	0.79	0.64	0.97
		DIM 2 (61-120 days) [b]	1.28	1.06	1.55
	Herd level	No regular footbath [c]	0.50	0.24	1.00
		Herd size >125 [d]	2.09	1.03	4.45
		TMR [e]	1.76	0.85	3.75
OID	Cow level	Parity 2 [a]	1.31	1.11	1.56
		Parity 3 [a]	1.32	1.11	1.55
		DIM 1 (0-60 days) [b]	0.99	0.82	1.19
		DIM 2 (61-120 days) [b]	1.25	1.04	1.49
	Herd level	Zero grazing [f]	1.76	0.73	4.37
		No regular footbath [c]	0.60	0.27	1.27
		Herd size >125 [d]	1.87	0.78	4.48
		TMR [e]	3.17	1.45	7.17
HHD	Cow level	Parity 2 [a]	1.18	0.93	1.47
		Parity 3 [a]	3.02	2.48	3.70
		DIM 1 (0-60 days) [b]	0.64	0.50	0.82
		DIM 2 (61-120 days) [b]	0.87	0.70	1.09
	Herd level	Zero grazing [f]	1.79	0.90	3.47
		Herd size >125 [d]	1.47	0.76	2.92
		TMR [e]	1.72	0.93	3.18

[a] versus parity 1
[b] versus DIM 3 (>120 days in milk)
[c] versus regular use of footbaths
[d] versus herd size below 125
[e] versus the use of concentrate stations
[f] versus grazing in summer

Parity was the strongest risk factor for HHD and the weakest for DD. In case a significant association is defined as an estimate of which the 95% credibility posterior interval does not include figures both below and above 1, lactation stage (DIM) was a significant covariate for the presence of all three diseases. In case footbaths were not regularly used, the odds of diagnosing DD in a herd were half compared to a herd that regularly used footbaths. A herd size above 125 cows was the other significant risk factor on herd level for DD. The use of a

total mixed ration was the only risk factor significant on herd level for the prevalence of OID. In case a trend is defined as an estimate of which the 90% credibility posterior interval (not shown) does not include figures both below and above 1, there was a trend for TMR being a risk factor for HHD with a median OR of 1.79 (90% CPI: 1.03, 2.87). A zero-grazing strategy was positively associated with the prevalence of both OID and HHD; only for HHD there was a trend with a median OR of 1.79 (90% CPI: 1.02, 3.14). The posterior estimates for the standard deviation of the herd level variance for every disease (not shown in table 3) were 1.14, 1.24 and 0.93 for DD, OID and HHD, respectively. The random effect of herd was largest for OID and smallest for HHD.

Besides the coefficients in the logistic regression model, analysis of the data with the network presented in figure 1 resulted in three probabilities of being lame given the presence of disease and a background probability of being lame. The summary of the posterior estimates is presented in table 4.

Table 4
Posterior estimates of the background probability of lameness (PBG) and the probability (PLL) of Digital Dermatitis (DD), Other Interdigital Diseases (OID) and Hoof Horn Diseases (HHD) causing lameness

	Mean	SD	$Q_{0.025}$	Median	$Q_{0.975}$
PBG	0.012	0.012	0.000	0.009	0.044
PLL DD	0.046	0.045	0.001	0.033	0.165
PLL OID	0.020	0.019	0.001	0.014	0.070
PLL HHD	0.481	0.096	0.302	0.478	0.678

The background event is the cause of lameness that is present at all times for all cows whether they have a disease or not. The probability that this event causes lameness was 0.012 (1-(1-PBG)). Diseases DD, OID or HHD caused lameness with a probability of 0.046, 0.020 and 0.481, respectively. The conditional probability of being lame given the presence of DD, P(LAME|DD+) was 0.057 (1-(1- PBG)*(1- PLLDD)). In the same way it can be calculated that the probability of a cow being lame given the presence of all three diseases was 0.521.

9.3.3 Illustration of application

Posterior estimates for the probabilities' logit values of a cow in *the specific herd* of interest having the three diseases are presented in table 5. The 16 different rows represent all possible combinations of herd-level risk factors of *the specific herd* of interest being either present (1) or absent (.). Besides this information on herd level, there was no other information gathered on cow-level prevalence of diseases or clinical lameness. All estimates represent a third parity cow, in the third stage of lactation (>120 days in milk).

Table 5
Posterior estimates of the logit of the probability of a third parity cow, in the third stage of lactation having digital dermatitis (DD), other interdigital diseases (OID) and hoof horn diseases (HHD) in 16 different herds with information only on herd level; herd size >125 (H=1), no regular use of footbaths (F=1), zero grazing (G=1) and TMR use (T=1).

					DD		OID		HHD	
	H	F	G	T	mean	sd	mean	sd	mean	sd
1	1	1	1	1	-1.44	1.23	0.15	1.36	-0.34	1.00
2	1	1	1	.	-2.01	1.21	-1.01	1.32	-0.88	0.98
3	1	1	.	1	-1.45	1.23	-0.41	1.35	-0.92	1.02
4	1	.	1	1	-0.76	1.24	0.67	1.35	-0.33	1.01
5	1	1	.	.	-2.01	1.21	-1.58	1.34	-1.46	1.01
6	1	.	1	.	-1.32	1.19	-0.49	1.30	-0.88	0.97
7	1	.	.	1	-0.76	1.24	0.10	1.38	-0.91	1.02
8	1	.	.	.	-1.32	1.19	-1.06	1.35	-1.46	1.01
9	.	1	1	1	-2.19	1.20	-0.47	1.38	-0.73	1.02
10	.	1	1	.	-2.76	1.21	-1.63	1.37	-1.27	1.00
11	.	1	.	1	-2.19	1.20	-1.05	1.30	-1.31	0.97
12	.	.	1	1	-1.50	1.21	0.04	1.35	-0.73	1.02
13	.	1	.	.	-2.76	1.21	-2.21	1.31	-1.85	0.97
14	.	.	1	.	-2.07	1.19	-1.12	1.33	-1.27	0.99
15	.	.	.	1	-1.50	1.21	-0.53	1.31	-1.30	0.97
16	.	.	.	.	-2.06	1.19	-1.69	1.31	-1.84	0.97

In case the only thing known about a herd is the fact that herd size is above 125, footbaths are not used regularly, cows are not grazed in summer and TMR is used the best guess for the probability's logit value for the presence of DD was -1.44 with a standard deviation of 1.23. On the p-scale (not shown), the distribution had a mean of 0.24, a standard deviation of 0.19 and it was 95% certain that the probability was
between 0.02 and 0.73. Figure 3 shows the posterior distribution of both the probability and the respective logit value for the presence of DD.

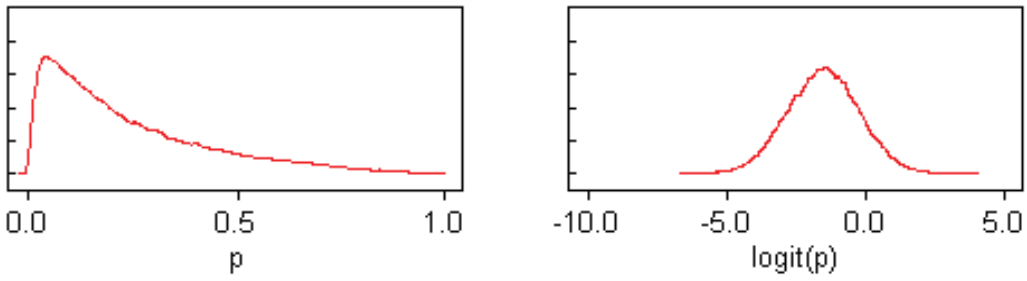

Figure 3: Distribution for the probability (p) of having DD and its logit value for a cow of parity 3, in the third stage of lactation in a herd of which only herd level risk factors are known

The posterior estimates in table 6 represent the logit values of the probabilities of a cow in *the specific herd* of interest of having the three diseases in case the data was reanalyzed

after adding information on *the specific herd* of interest. Logit values are presented, instead of the respective probabilities. This is done because all logit-values are normally distributed and can therefore be presented by two figures (mean, sd). To get an impression of the shape of a skewed distribution on the respective p-scale (figure 3), the median, the 2.5% and 97.5% percentiles need to be presented as well.

Table 6
Posterior estimates of the logit of the probability of a third parity cow, in the third stage of lactation having digital dermatitis (DD), other interdigital diseases (OID) and hoof horn diseases (HHD) in 7 different analyses where information on the specific herd concerned information on only herd level*(1), lameness observations (2,3) and disease diagnoses at trimming (4-7).

						DD		OID		HHD	
	DD	OID	HHD	LAME	N	mean	sd	mean	sd	mean	sd
1	-	-	-	-	-	-1.44	1.23	0.15	1.36	-0.34	1.00
2	-	-	-	0%	45	-1.70	1.19	-0.03	1.37	-1.65	0.77
3	-	-	-	40%	45	-1.30	1.26	0.23	1.34	1.49	0.70
4	7%	7%	7%	-	45	-2.62	0.52	-2.33	0.50	-1.58	0.48
5	40%	40%	40%	-	45	-0.60	0.31	-0.37	0.31	0.34	0.31
6	7%	7%	7%	-	180	-2.76	0.30	-2.56	0.29	-1.83	0.29
7	40%	40%	40%	-	180	-0.54	0.17	-0.38	0.17	0.36	0.18

*Herd size >125, no regular use of footbaths, zero grazing and the use of TMR

The seven rows represent seven analyses in which different types and different amounts of information on *the specific herd* were available; in the first row only information on herd-level risk factors was known (as the first row in table 5). Before observing lameness, the mean values of the posterior probability distributions for having DD, OID and HHD (not shown) were 0.24, 0.52 and 0.43, respectively. From table 6 it becomes clear that observing 0 out of 45 cows lame changed our belief in the presence of all three diseases (analysis 2 versus 1). On the probability scale the posterior distributions had mean values of 0.21, 0.49 and 0.17, respectively. The probability of a cow having HHD changed the most. Besides, the degree of belief reflected by the standard deviations in table 6 increased for the presence of HHD only. Making clinical observations of diseases at hoof trimming clearly changed both our belief and degree of belief in the expected probability of having diseases (analysis 4 and 5). In case the same evidence was available on a four fold number of cows, the degree of belief further increased (analysis 6 and 7).
In figure 4 the effect of different types and amounts of information on the posterior estimate for the probability and its logit value of having HHD is illustrated.

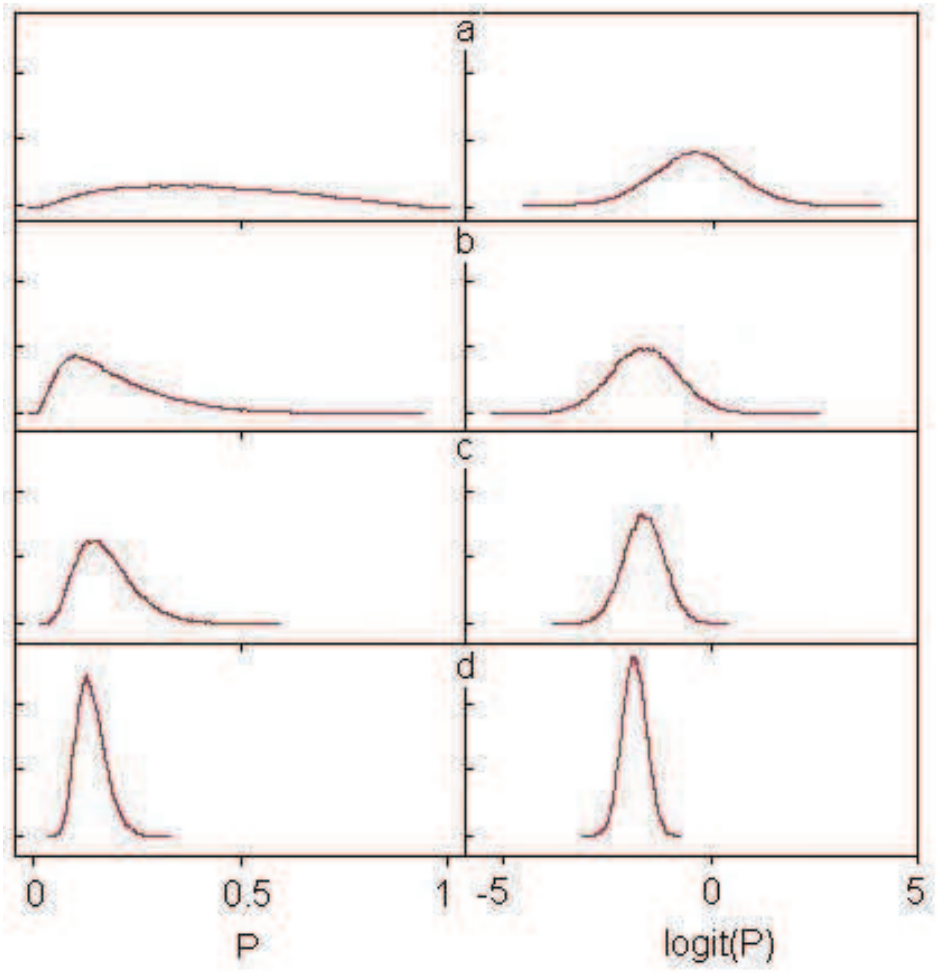

Figure 4a-d: Poster distributions of the probability (P) of having HHD and its logit value in the specific herd of interest in case only herd-level information is available (a), 45 cows are locomotion scored (b), 45 and 180 cows are clinically diagnosed for lesions (c and d, respectively)

9.4 Discussion

9.4.1 Variation on herd level caused by trimmer

Four trimmers collected the data in this cross sectional study. From the inclusion of trimmer as a fixed effect in the logistic regression model (results not shown) it became clear that the probability of observing a disease was depended on trimmer, yet only significant for OID. However, it was decided not to include trimmer in the final analysis as a fixed effect because of the higher purpose of this analysis; i.e. describing the full uncertainty of the probability of having one of three diseases. In case trimmer would have been included as a fixed effect, the reference category would have been representative for only one trimmer. This claims certainty about the observer. This was undesirable, since the trimmer of the cows in any specific herd of interest, i.e. in a future application of the network, will not be known. Including both herd and trimmer as a random effect was not possible; every trimmer visited only a limited number of farms and distinction could therefore not be made between variation caused by farm and trimmer.

9.4.2 Bayesian analysis

For interpretation of the results of the Bayesian analysis, the previously discussed variation on herd level caused by trimmer should be kept in mind. Estimates for the single claw trimmers are possibly different. The quantification of parity as a risk factor for the claw and hoof diseases is in agreement with the ones previously reported. Low parity was also quantified as risk factor for DD by Holzhauer et al. (2006) and Somers et al. (2005a). For both OID and HHD the opposite effect of parity was observed. The same was found for interdigital dermatitis, in our study aggregated into OID, by Somers et al. (2005b). Sole ulcers, hemorrhages and separations were all aggregated into HHD in this study; high parity was quantified as a risk factor for all three diseases by Manske et al. (2002b). A negative association was found between the prevalence of HHD and DD and the first 60 days in milk. Both Holzhauer et al. (2006) and Somers et al. (2005a) reported this stage of lactation as low risk period for digital dermatitis. Sole ulcer was also observed least during the first 60 days in the study of Holzhauer et al. (2008b) and Manske et al. (2002b).

A herd size above 125 cows was quantified as a risk factor for all diseases, though only significant for DD with an OR of 2.09. A statistically significant OR of 1.01 for the proportional increase in the odds of DD for a cow, for each unit increase in herd size (ranging from 44 to 361) was reported by Rodriguez-Lainz et al. (1999). Somers et al. (2005a, 2005b) didn't find a significant association between herd size and the prevalence of DD and ID, the latter was aggregated into OID in this study. Neither did Holzhauer et al. (2006) for the association between DD and SU, the latter was aggregated into HHD in this study. Significantly negative associations between large herd size and white line fissures and heel horn erosion were reported by Sogstad et al. (2005). Not using footbaths or only when necessary, i.e. a non-regular use of footbaths, was negatively associated with the prevalence of DD, compared to a regular use of footbaths. This might imply that the absence of a footbaths strategy indicates the absence of problems. A similar result and explanation was reported by Somers et al. (2005a). Rodriguez-Lainz et al. (1999) on the other hand, found a negative association between footbath use and prevalence of DD; they reported an OR of 0.34 compared to not using footbaths. Any inference on causal relationship should be done with great care in cross sectional studies like these.

Implementation of a zero-grazing strategy was omitted from the DD model and quantified as a non-significant risk factor for OID and HHD, although a trend was present for the latter. This positive association of zero grazing with the prevalence of HHD might be explained by reduced hoof wear during summer on pasture, which makes the claw less susceptible for trauma in the housing season. Hoof wear is an important risk factor for hoof horn diseases (Blowey, 2005). The lack of significance can be explained by the fact that all cows were trimmed during the housing season; any positive effect of grazing during summer might not be noticeable anymore once the cows are inside. For the occurrence of both DD and ID during the pasture period, restricted grazing was a strong risk factor compared to a full grazing system (Somers et al., 2005a; Somers et al., 2005b). This same relation was not found in this study when cows were trimmed during the housing season. Rodriguez-Lainz et al. (1999) also reported a housing system with only pasture as the lowest risk category for DD, in comparison to loose (straw) housed cows, open corrals and free-stalls.

The implementation of a Total Mixed Ration had a positive association with the prevalence of all three diseases in our study. For OID this relationship was significant and for HHD there was a trend. On beforehand the strongest relationship was expected between TMR and HHD, due to the role of nutrition in the etiology of hoof horn diseases (Manson and Leaver, 1989; Webster, 2001; Bergsten, 2003). In a study by Livesey et al. (1998) sole hemorrhage and white line disease (both aggregated into HHD in our study) were exacerbated by a high concentrate diet, compared to a low concentrate diet. This effect was not found for heel horn erosion (aggregated into OID in our study). In a study on clinical lameness, where no distinction was made on the causing diseases, a higher incidence was found in herds that used a total mixed ration for lactating cows compared to those who didn't (25.5 vs 13.9%) (Wells et al., 1995). In case of a TMR, the concentrate-forage ratio is constant; the intake of extra roughage without extra concentrate is not possible. Livesey and Fleming (1984) showed that forage restriction compared to free access to forage resulted in an 8 fold increase in both laminitis and sole ulcer. In both treatments the same amount of concentrates were fed. More important than the concentrate-ratio being constant is the ratio not being too high. For this study however, we did not have additional information on the TMR composition.

The probabilities of lameness (moderately or worse) given the presence of diseases indicated to be highest for HHD (table 4). Both OID and DD had a low probability of resulting in lameness. Manske et al. (2002a) found the risk of lameness to be significantly increased (OR) for cows with a sole ulcer (6.02), separations (2.77) and hemorrhages (2.35); all of which are aggregated into HHD in this study. Murray et al. (1996) and Green et al. (2002) also reported sole ulcer as the number one cause of lameness. *Dermatitis* did not significantly increase the risk of lameness in the study of Manske et al. (2002a). In their aggregation of *dermatitis* both heel-horn erosion and erosive dermatitis were included, together with verrucose dermatitis. The latter is a synonym for digital dermatitis, which was considered separate in our study. Whay et al. (1998) showed that the nociceptive threshold, a measure for responsiveness to a harmful stimulus, was lowest (not significant) for animals with acute digital tissue infection compared to sole ulcers and white line disease. This test was however performed *after* the animals were diagnosed as clinically lame. It shows that of all lame cows, the ones with digital tissue infection are going through the most pain, which does not contradict the findings in our study. 28 days after the animals were treated in the study of Whay et al. (1998), the cows with tissue infection had a significant higher threshold compared to cows lame due to the other diseases, indicating fast recovery after treatment. This shows that these diseases are acute and painful for a shorter period of time. This agrees with a low probability of finding a lame cow due to an infectious disease in a cross sectional study. Holzhauer et al. (2008a) differentiated different stages of DD in an intervention study. Of all cases of DD, around 20% were categorized as erosive dermatitis and painful at palpation and 80% of all lesions were superficial, recovering or recovered and neither of them painful. Most studies agree that interdigital dermatitis and heel horn erosion are highly prevalent but not explicitly associated with lameness (Toussaint Raven and Cornelisse, 1971; Blowey and Sharp, 1988). Both diseases constitute the vast majority of the other interdigital diseases in this study (Ettema et al., 2007).

Another aspect that should be noted when interpreting the low probabilities of causing lameness for both DD and OID is that the predictive ability of this model was weak and based on only 285 cows in 3 herds. The observed level of lameness in the 3 herds was 0.04, 0.12 and 0.40. The estimated prevalence for the three herds was 0.10, 0.18 and 0.33, respectively.

9.4.3 Prior distribution

The occurrence of separation is often observed in fitting a logistic regression model if one or more parameters diverge to extreme negative or positive values (Heinze and Schemper, 2002; Gelman et al., 2008). This typically occurs in small samples. Separation was not observed in this analysis when flat, normal distributions were used for all components, except the random variance component, of the logistic regression model. Parameter estimates and history plots did not differ when uniform distributions were used that only allow variation in the *relevant* range, as for example done by Nielsen and Toft (2007).

Jørgensen (2003) warns against the use of flat priors on the logit scale since it results in a non-flat prior on the p-scale with a peak at both 0 and 1. This would make the occurrence of separation even more likely. As said before, separation was not a problem in this analysis. Gelman et al. (2008) defined an informative empirical prior distribution that can be used for any logistic regression analysis. According to this paper a Cauchy distribution with center 0 and scale 2.5 for every coefficient in the logistic regression model should be used, except the intercept for which a Cauchy distribution with center 0 and scale 10 should be used. Unfortunately the software used in this study does not enable the use of a Cauchy distribution; these priors were therefore not used in this analysis.

9.4.4 Model selection and convergence diagnosis

Based on the Deviance Information Criteria (DIC) it was decided to exclude grazing strategy and the use of footbaths from the regression model of DD and HHD, respectively. The occurrence of clinical lameness was modeled by including a node for every disease representing the disease's probability of resulting in lameness (PLL). Nodes representing every 2-way combination of diseases causing lameness were also explored in the network. By studying the DIC and comparing the predicted with the actual prevalence of observed lameness it was decided to drop any combination of diseases causing lameness.The four formal convergence tests at the core of the convergence diagnostic and output analysis (CODA) package indicated that the samples drawn for inference were drawn from the converged posterior distributions. The same conclusion was drawn when the history plots and Gelman and Rubin diagnostic plots (Gelman and Rubin, 1992) were studied as demonstrated by Toft et al. (2007). The residuals of predicted herd prevalence were normally distributed for DD and OID, but not for HHD. The observed herd level prevalence of HHD was very positively skewed compared to the other two; extreme values were predicted less good by the model.

9.4.5 Illustration of application

Due to the low probability of OID and DD resulting in lameness (table 4), indicating a low association between the diseases and lameness, the belief and degree of belief got little updated when observations on clinical lameness are done in the specific herd of interest. A high or low prevalence of lameness did clearly not tell us much about the prevalences of these infectious diseases. Whereas, the expected probability of a cow having HHD changed from 0.43 to 0.17 in case 0 cows out of 45 were diagnosed as moderately lame or worse. The conditional probability of lameness given the presence of this disease was 0.49 (1-(1-PBG)*(1-PLLHHD) (table 4). Since the probability of anything else (OID, DD and the background event) causing lameness was low, the absence of observable clinical lameness in a herd reduced our belief in HHD being a big problem in this herd.

In case observations were done on claw level on 45 cows in the herd, belief of all three diseases got updated, illustrated by the different values for the means and sd's in table 6 when analysis 1 is compared to 4 and 5. What is not shown in this table is the effect caused by herd. In case no observations on claw or cow level were done in the specific herd of interest and the only information available was on herd level risk factors (analysis 1), the herd level effect in the *specific herd* for DD had a mean value of 0 and a standard deviation of 1.14. This value for the standard deviation was earlier reported in paragraph 3.3 as standard deviation of herd level variance. In case 45 cows are trimmed and DD is diagnosed on only three of them (7%, analysis 4) the effect on herd level had a mean value of -1.02 and a standard deviation of 0.63. In case the same prevalence was observed on 180 cows (analysis 6) the effect on herd level had a mean value of -1.09 and a standard deviation of 0.53. The more information there was available on cows in a herd, the more certain the effect of herd. This was reflected in both the estimates of herd level effect and the smaller standard deviations of the estimates on cow level when comparing analysis 1, 4 and 6.

9.4.6 Hyper parameters in Monte Carlo simulation models

In case the economic impact is to be modeled of the diseases in question with the simulation model Simherd (Østergaard et al., 2004), it may be important to consider the full uncertainty around the most important parameters of the state of nature; i.e. disease risk. Using point estimates in the state of nature of a stochastic simulation model represents the uncertainty between animals since the occurrence of the event is triggered stochastically. However, risk in decision making is underestimated (Jørgensen, 2000) since the point estimate is assumed certain. In the approach of sampling a disease risk from a probability distribution for every single replicate of the simulation model, the additional uncertainty around the state of nature is represented. Kristensen and Pedersen (2003) have clearly demonstrated the influence of the uncertainty concerning true parameter values on a simulation models output.

9.5 Conclusion

A framework is created that describes disease risk in a specific herd by a distribution. By using a Bayesian network, prior knowledge on disease prevalence in the entire population is combined with herd specific knowledge in a systematic way.

Demonstration of the effect of three different types of herd specific knowledge, on the estimate of disease risk, is performed in order of collection ease; gathering information on the herd's management strategies is easiest and trimming individual cows is most time consuming. As ease of collection goes down, the degree of which the evidence changes our belief goes up. The resulting probability distribution can either directly be used by a decision maker for assessment of the health problem in the herd, or the hyper-parameters can be used by a Monte Carlo simulation model.

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