Improvement of mastitis detection, pathogen diagnosis and online decision support around treatment for automatic milking systems using additional non-automatic milking system data

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In automatic milking systems (AMS), clinical mastitis (CM) is currently detected by sensor measurements only. With these systems, the number of false-positive warnings for CM is currently too high. Additionally, the current systems can not predict the involved pathogen for CM. It is expected that further improvement of the detection of CM and the involved pathogen is possible by taking into account additional cow data, for instance, data on monthly somatic cell count (SCC) measurements and CM history.

In this project, models will be developed, based on additional cow data that could be combined with AMS data to improve the detection of CM. These models need to determine the risk of CM for individual cows. Additionally, for cows having CM, models will be developed that can predict the involved pathogen. For this part of the project, a dataset containing more than 8,000 CM cases with information on the involved pathogen was used.

In the first part of this project, a multivariate logistic regression model was developed including several cow-risk factors (non-AMS). The following cow-risk factors were significantly associated with the risk on CM: parity, month in lactation, season of the year, geometric mean SCC of previous lactation, SCC in the previous month, the accumulated number of CM cases in the previous month of the lactation and the accumulated number of CM cases in the month of lactation before the previous month of lactation. With the developed logistic regression model it is possible to determine the risk of CM for individual cows. This logistic regression model needs to be updated with daily information of the sensor measurements generated by the AMS. It became clear that for this purpose logistic regression models have several disadvantages. Logistic regression is not a flexible tool when new information becomes available and moreover, it can not handle missing values.

In the second part of the project, CM and the associated significant cow-risk factors will be analysed with Bayesian Networks to determine the risk of CM for individual cows. This statistical method is more flexible to include new information of the cow. This part of the project also includes the prediction of the involved pathogen. Naive Bayes classifiers are part of the Bayesian Networks and especially valuable for classification tasks. Therefore, these classifiers are currently used for the prediction of the involved pathogen for CM cases. For these analyses information on cow-risk factors and clinical signs of the CM case are used. First results show an accuracy of approximately 50% to distinguish between streptococcen, staphylococcen and *E. coli*.

Results of prediction models for the involved pathogen will be used for the third part of the project. In that part of the project, an online decision support model around the treatment of CM cases will be developed. In these decision support models, the farmer will be supported in the decision for different treatment options. Currently, work on this project has started.