Using differential somatic cell count to improve udder health

R.H. Fourdraine, A. Samia Kalantari, J. Amdall and A.D. Coburn

AgSource Cooperative Services, 135 Enterprise Drive, Verona, WI 53593, United States

Abstract

Mastitis continues to be one of the costliest diseases found on US dairy farms. Routine milk analysis for Somatic Cell Count (SCC) has provided a valuable and inexpensive means to monitor udder health. New technologies such as PCR analysis of preserved milk samples have provided additional detail by determining which pathogens may be present allowing a more pinpoint approach in addressing mastitis. Although PCR is a valuable tool the costs for routine analysis of milk samples is too expensive for US dairy farmers. Differential Somatic Cell Count (DSCC) data can now be obtained as part of a regular milk analysis for SCC. Using monthly and weekly collected data AgSource has started the process to determine where DSCC can provide additional value and be incorporated in AgSource information management services. Although several trends have been observed regarding future udder health status, no conclusive results have been obtained using a machine learning approach. To improve the predictive capabilities more weekly milk samples will need to be collected and combined with PCR milk analysis results in order to get more detailed information about the type of infections.

Keywords: Fourdraine, Somatic Cell Count, differential somatic cell count, udder health, prediction, machine learning.

Introduction

Milk recording organizations and milk laboratories have offered individual cow mastitis screening using Somatic Cell Count (SCC) analysis for over 30 years. As management practices have improved so has udder health and herds have seen a decrease in cases of mastitis. US dairy farms have seen a steady decline in bulk tank SCC values. Although significant improvements have been made, mastitis is still one of the costliest disease farms have to deal with. AgSource herds typically use SCC analysis on all cows on a monthly basis and this has proven to be a very cost-effective measurement to monitor udder health. Typically cows are considered at risk for mastitis when the SCC value exceeds 200,000, cows with SCC less than 200,000 are considered healthy and not further diagnosed. Follow up diagnostics for cows exceeding 200,000 such as PCR and bacteriological testing can be used to more accurately pinpoint the specific mastitis causing pathogens. These methods are typically too expensive to use in a whole herd testing scheme. The question therefore is are there other cost-effective methods that can supplement SCC that can be used to easily screen cows and detect onset of mastitis at an earlier point where typically SCC may not have exceeded 200,000.

A possible opportunity may lie in the new Differential Somatic Cell Count (DSCC) measurement that is offered through the Fossomatic 7 DC from Foss Denmark. The DSCC represents the combined proportion of Polymorphonuclear Neutrophils (PMN) and lymphocytes in percent. The percentage of macrophages is 100 - DSCC. DSCC values can be provided for cows that have a SCC value that exceeds 50,000. Past research projects have shown the positive correlation between increased DSCC values as cows are subjected to mastitis causing pathogens. Cows considered healthy typically express low DSCC values (i.e. high percentage of Macrophages). Stage of lactation and parity have also shown to play a factor in DSCC measurements. To date most research was focused on establishing the relationship between changes in DSCC and infection, however little effort has been given to developing a practical application of DSCC in commercial milk testing schemes.

Materials and methods

Little is known about the value DSCC provides above and beyond SCC when included in regular milk recording. In order to build a practical application it was necessary to learn more about the data and any trends we could discover before specific areas of value could be determined. DSCC is only measured on cows with a SCC value of 50,000 or greater, typically in the US dairy industry a SCC value below 150,000 or 200,000 is considered a healthy cow with little concern. As cows exceed 200,000, concerns about infection increases as the SCC value increases. In addition to the magnitude of the SCC value, the duration and frequency of high SCC values is also a concern and typically expressed as new infections, chronic infections, repeat infections and fresh cow infections.

In order to learn more about the value DSCC provides, two tracks of exploration were chosen. The first track involved a preliminary data analysis of regular monthly individual cow milk samples providing insights on potential trends. While the second track involved a six weeks research trial collecting weekly milk samples from a 1,800 cow dairy farm. Cows of interest were selected for follow up PCR to determine if specific pathogens were present. Using cow data from the field trial a machine learning approach was used to determine if the combination of SCC and DSCC has any predictive characteristics to determine the future health status of the cow.

Collected data included, SCC, DSCC, milk composition and individual cow data such a parity, calving date, days in milk, and health events.

For the preliminary data analysis, the monthly sample data set included 124,747 test day milk analysis results, collected since December 2018, that have both SCC and DSCC values. Within this data set there were 39,135 cows at different parity and stages of lactation that had two or more consecutive data points. For the research trial the total number of weekly observations collected was 10,964 records on 2,080 cows from which 1,591 cows had six consecutive weeks of data.

Results

The monthly data analysis is a snapshot of the data that was collected through April 2019. The weekly data used in this analysis only contains data from a single herd. However additional data is being collected on a weekly basis from herds that have milking robots with automated sampling units and will be included at a later date.

Preliminary data analysis

Individual cow SCC data has been the primary tool in the dairy industry to determine if a cow should be considered as potentially infected or not. Past presentations about DSCC values collected by the Fossomatic 7 DC indicated that DSCC has a strong correlation with SCC, if that is the case the first question then becomes what is the correlation and if it is very high, what additional value does DSCC provide over SCC at the individual cow level? Using the monthly data set, the correlation between SCC and DSCC for cows with a SCC value greater than 50,000 was only 0.17 indicating that the relationship is not as high. This should be considered as good news because the combination of DSCC and SCC could point at additional findings that we would not be able to receive from SCC alone. Based on the percent of PMN and macrophages, one of the values DSCC could provide is the early indication that a cow may be potentially infected but has not elevated the SCC value to a level it would raise concern and place the cow on an attention list. A second value would be in determining if an infected cow is healing or responding to treatment that is not captured in the SCC value.

DSCC is measured as a percent of PMN, however little is known about what a normal range would be where the cow is providing an immunity response or is in a healing phase. Based on information gathered from FOSS Denmark, a DSCC value that is greater than 70 should be considered as high on PMN indicating the cow is showing an increased immunity response. Therefore the first interest was to evaluate if healthy cows (SCC score below 200,000) show differences in pathways of becoming infected based on previous month DSCC value. Using the dataset with repeat measures on a single cow, cows were grouped based on DSCC values, results are shown in figure 1. At this time there was not enough data to break out the results by days in milk or parity.

Results in figure 1 show that as DSCC increases a higher percent of cows considered healthy return the next month with a SCC above the threshold of 200,000. This could provide some early insights that cows with SCC <200,000 but DSCC above 70 do not require intervention right away but should be more closely monitored.

The second area of interest involves cows previously listed as infected (SCC>=200,000) and evaluated based on the previous DSCC value if these cows are improving. Figure 2 shows the response from previous to current test day based on the same DSCC categories as Figure 1.

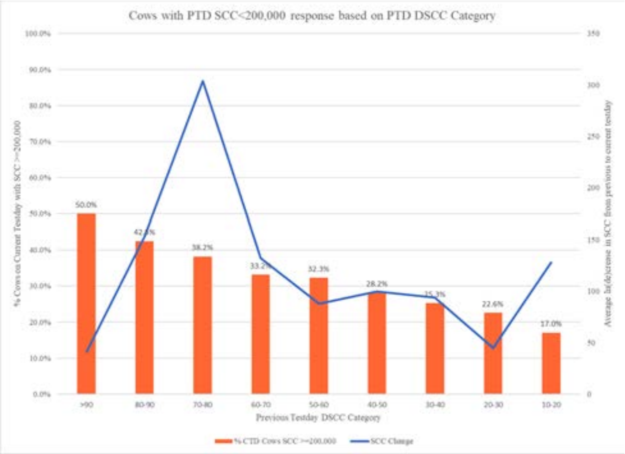

Figure 1. SCC response for clean cows from previous to current test day based on previous test day DSCC

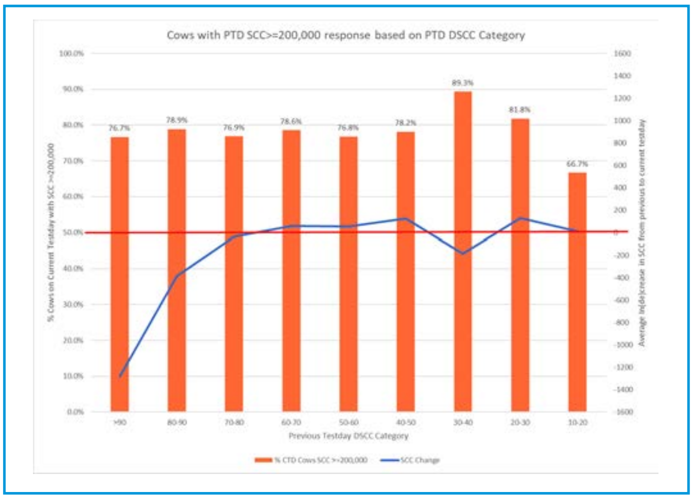

Figure 2. SCC response for infected cows from previous to current test day based on previous test day DSCC

Results shown in figure 2 indicates that regardless of DSCC category almost the same percentage (75%) of cows have SCC greater then 200,000 on the next test day. Although the percent is similar across DSCC categories, the cows that had the highest previous test day DSCC (DSCC greater than 80) showed the greatest reduction in SCC while cows with low DSCC (DSCC less than 70) showed little or no improvement. This raises the question if cows have a SCC of for example 1,000,000 or higher but a DSCC value between 40 and 60, are these cows healing or more likely to return the next month as still infected.

The current AgSource udder health summary provides multiple analysis that look at various groups of cows based on SCC, based on the SCC, the three main groupings of cows are:

- Newly Infected - SCC below 200,000 previously, now above 200,000
- Chronic infected - SCC above 200,000 in 2 consecutive test days
- Cured - SCC above 200,000 previously, now below 200,000

Using the three groupings Figure 3 shows the distribution of cows based on current test day DSCC category.

Results from figure 3 show that cows that are newly infected or chronic have a distribution that has far more cows with DSCC values of 80 or above compared to cured cows. DSCC values between 70 and 80 are somewhat a transition zone while DSCC values below 70 have a greater percentage of cows considered cured. As more data is collected one area to delve deeper into would be the cows considered cured but still exhibiting a high DSCC value and determine if they were truly cured or return to a higher SCC level. A second area are cows listed as newly infected or chronic but exhibiting low DSCC values.

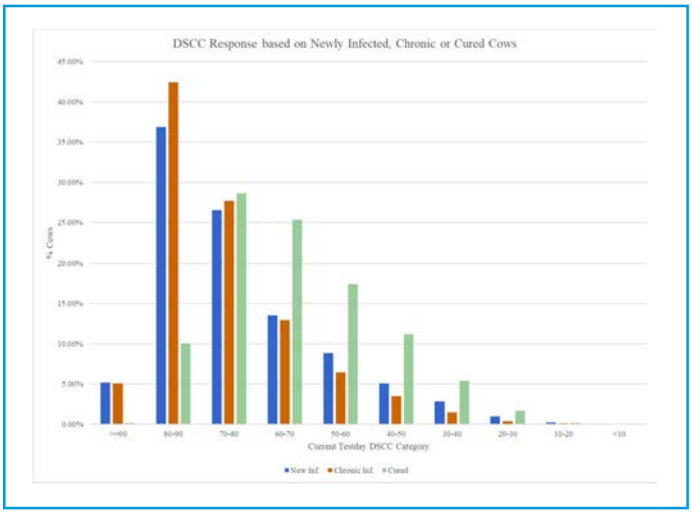

Figure 3. Distribution of cows by current test day DSCC score and infection status.

Research trial results

Utilizing the results from monthly SCC and DSCC data some early insights were gained in regards to which areas DSCC may provide additional value. Correlations between the SCC and DSCC values for the weekly samples were 0.3 which was slightly higher than the correlations observed using the monthly observations but still low enough to indicate there may be opportunity to consider DSCC as additional value over SCC.

Based on this information cows were grouped in several categories. These categories formed the initial starting point that would be used to assess where DSCC might provide possible value as it relates to monitoring udder health. PCR analysis was used to determine if cows in the different categories had any environmental or contagious pathogens present. Table 1 shows a matrix using different categories of SCC and DSCC and impact DSCC may have on udder health. Figure 4 shows the relationship between the weekly SCC and DSCC values for each cow as they fit in the five categories listed in table 1.

The total length of the field trial was 6 weeks and the first couple weeks were used to learn more about the data and identify cows in each of the categories listed above. Tables 2 through 6 show examples of cows with weekly SCC and DSCC values that qualify them for one of the 5 categories mentioned in table 1.

Using week 4 SCC and DSCC data cows were selected based on the criteria in table 1 and using the week 5 samples of those cows PCR analysis was performed on the pooled samples. The process was repeated with cows selected on week 5 and samples

Table 1. DSCC impact matrix.

Category	SCC	DSCC	Possible impact
1	Low (<200,000)	Low (~<70)	Healthy
2	Low (<200,000)	High (~>70)	Early warning
3	Medium (200,000-800,000)	Low (~<50)	Chronic problem
4	High (>800,000)	Low (~<50)	Not responding
5	Medium and High (>200,000)	High (~>70)	Responding to infections

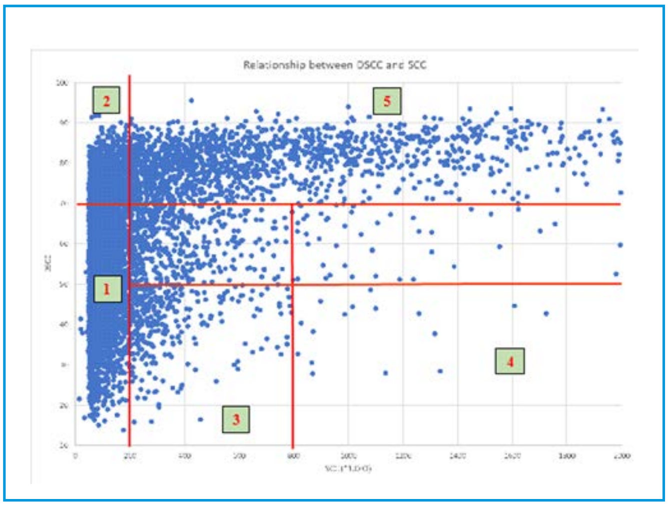

Figure 4. Relationship of DSCC and SCC and udder health category.

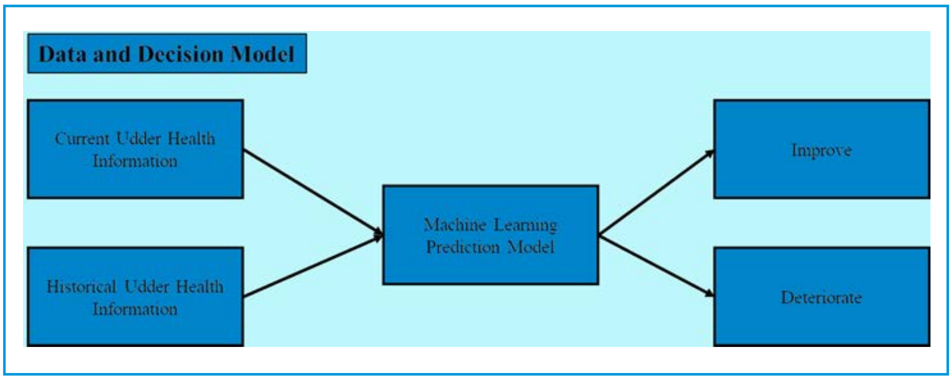

Figure 5. Machine Learning Predictive model.

collected on week 6 were run for PCR analysis. The week 6 samples were pooled and upon detection of any pathogens in the pooled sample individual cows were tested. The goal of the PCR analysis was to determine if any pathogens could be detected and if these were environmental or contagious. Results from week 6 showed that all pools tested positive for *Enterococcus* pathogen. No additional pathogens were found in the cows in category 2. Category 3 had two cows that tested positive for *Strep uberis* and one tested positive for Staph Aureus. Category 4 showed no additional pathogens and category 5 showed cows positive for *Staph aureus* and *Strep uberis*.

Predictive model

Analysis of the monthly and weekly data led the team to consider building a predictive model for future udder health status. Predictions are single cow based and use the most current and prior data on a single cow. The basis of the prediction model is shown in Figure 5.

Table 2. SCC and DSCC values for a cow considered healthy and in category 1.

ID	Date	SCC	DSCC
8892	2/7/2019	9	0
8892	2/14/2019	16	0
8892	2/21/2019	6	0
8892	2/28/2019	17	0
8892	3/7/2019	13	0
8892	3/14/2019	15	0

Table 3. SCC and DSCC values for a cow considered healthy but potentially at risk and in category 2.

ID	Date	SCC	DSCC
5986	2/7/2019	177	86.1
5986	2/14/2019	128	75.3
5986	2/21/2019	200	80.2
5986	2/28/2019	185	79.2
5986	3/7/2019	113	76.1
5986	3/14/2019	144	77.1

Table 4. SCC and DSCC values for a cow that could be chronic infected and in category 3.

ID	Date	SCC	DSCC
527	2/7/2019	379	45.9
527	2/14/2019	259	49.6
527	2/21/2019	217	42.9
527	2/28/2019	343	46.6

Table 5. SCC and DSCC values for a cow that could be infected and not responding in category 4.

ID	Date	SCC	DSCC
1403	2/7/2019	644	46.3
1403	2/14/2019	743	51.9
1403	2/21/2019	932	52.3
1403	2/28/2019	988	42.6
1403	3/7/2019	1725	42.8

Table 6. SCC and DSCC values for a cow considered infected and in category 5.

ID	Date	SCC	DSCC
1136	2/7/2019	1176	84
1136	2/14/2019	2169	83.6
1136	2/21/2019	3021	81.6
1136	2/28/2019	2312	85.1
1136	3/7/2019	2348	85.4
1136	3/14/2019	2140	78.8

Utilizing the field trial data set the number of observations based on the breakdown of the categories listed in Table 1 resulted in some categories having a limited number of observations limiting what can be achieved using a machine learning approach. Several approaches were used with the existing data and shared below.

Weekly observations were used to develop predictive models for flagging animals based on their previous weekly records. This was set up as a classification problem (subset of machine learning methods concerned with learning classes of target variables by provided target from training data). The target variables were created by mapping the observed SCC to 0 and 1. 0 was used for healthy cows (SCC < 200,000) and 1 was used to signal cows at-risk for mastitis (SCC >= 200,000).

After cleaning weekly observations total of 10,763 records were used as the dataset for this classification. From all the available features in the original dataset few were selected as the main features for this study and other features were engineered by transformation of these main features. SCC, DSCC, LACT, DIM, age (days), age at calving were included directly from the dataset, and linear score, Macrophage count, and PMN counts were calculated from the corresponding features. Other features were added to this dataset by merging and adding the number of each health events (abortion, displaced abomasum, ketosis, mastitis, metritis, milk fever, retained placenta) that happened before the current test, with inclusion of the total number of health events. To be able to classify the current SCC category, 3 lagged variables of key features including SCC, DSCC, and linear score was created. These variables were simply the data from the previous records up to 3 weeks prior to the current test. Furthermore, mean and standard deviation of SCC, linear score, DSCC, PMN and Macrophage counts, which include all the previous records of individual animals (excluding the last weekly record), were added to the dataset.

After removing the first week, because of lack of any previous records, and filling the missing values created by generating the lagged variables with the corresponding column median, total of 8,726 data points was divided into 75% train set and 25% test set, randomly. The training and testing sets were created in a way that each set had the same proportion of the target variable (stratifying by target to keep the proportion of target the same in both test and train sets), which was approximately 77% SCC < 200,000 and 23% with SCC >= 200,000. All the models were built on the training dataset and model evaluation was done by 5-fold cross validation, test set was just used to report the performance of the models here.

Different classification algorithms were applied to the training data and the models were evaluated according to their f1-score (weighed harmonic mean of recall (sensitivity) and precision). F1-score was used because for a good classification model both recall (the ability of the model to identify the at-risk cows) and precision (the ability of the model not to incorrectly classify at-risk cows as healthy cows) are important, and F1-score takes both metrics into account. In addition, recall and precision are especially important when there is an imbalanced dataset (as it is in the current dataset 77% healthy vs 23% at-risk cows) and accuracy of the model alone does not prove a good classifier.

From all the models tested the best model was the Gradient Boosting classifier, which is an example of boosting algorithm and subset of broader category of ML models called ensemble models. These are models that could outperform most other models on wide category of datasets by creating series of prediction models (usually tree models in the classification) sequentially. The classification errors at each step are evaluated and more weight is being put on those misclassified records, so the next model could further reduce the misclassification. Predictions of the final ensemble model would be the weighted sum of all the predictions from all individual tree built previously. Another significance of gradient boosting is the fact that it could create a relative importance of the features for classification. Results showed that the most important features for classifying healthy and at-risk cows in the current model setting, was mean linear score, mean SCC and their standard deviations, which means the cows previous average weekly SCC values is the most significant predictor of its future values (ModelAll). In this case DSCC adds almost nothing to the predictions. However, if we do not consider the mean and standard deviation of previous records in case we do not have it available, previous test SCC alongside PMN counts (generated from DSCC) were important (ModelPart1). Top 10 features sorted by their importance for the above models (ModelAll, ModelPart1) are sorted by their relative importance and can be seen in Table 7.

Based on the relative importance in Table 7 and applying feature selection some features (for example health events and all the categories created by binning the features were excluded) and a model with best subsets were developed.

The model based on the best subsets of features resulted a 79% f1-score with other scores plotted in Figure 6 across both classes. This resulted in a 0.859 area under the ROC curve (AUC), which shows the overall model performance and could be used to compare to other models. This can be compared with a model without any DSCC related features on right panel of Figure 6, which resulted in 0.853 AUC.

Table 7. Relative importance of top 10 features from ModelAll and ModelPart1.

Feature Name	**Relative Importance**	**Feature name**	**Relative importance**
mean_linear_score	0.777	lag_1_Cells	0.616
mean_Cells	0.106	lag_1_linear_score	0.08
sd_Cells	0.028	lag_1_PMN_cnt	0.059
sd_linear_score	0.015	lag_2_Cells	0.056
sd_DSCC	0.007	lag_1_Macrophage_cnt	0.043
lag_1_Cells	0.007	lag_3_Cells	0.023
DIM	0.006	lag_2_PMN_cnt	0.018
lag_3_PMN_MAC_ratio	0.005	DIM	0.017
age_days	0.005	lag_3_Macrophage_cnt	0.015
mean_Macrophage_cnt	0.004	scc_cat_lag_2	0.014

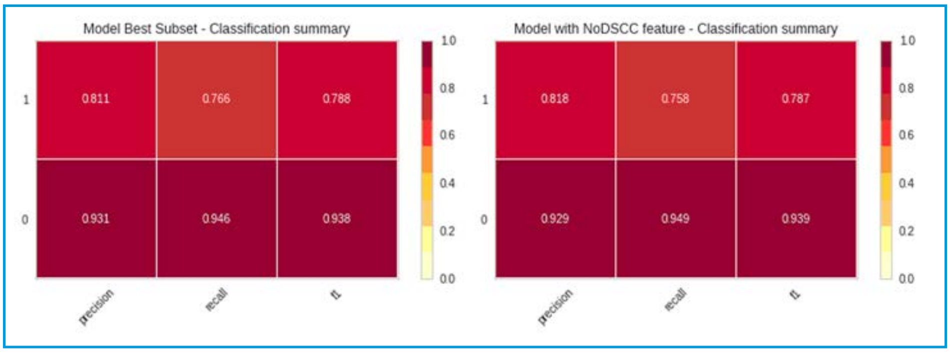

Figure 6. Best performing gradient boosting algorithm (left) vs. Model with no added feature from DSCC. Performance shown is evaluated on the unseen test data separated by respective class 0 as healthy cows (SCC < 200,000) and 1 at-risk cows (SCC >= 200,000)

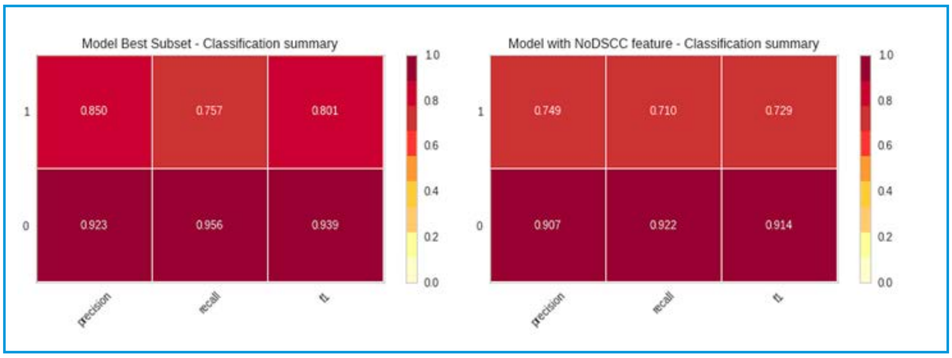

Figure 7. Best performing gradient boosting algorithm (left) vs. Model with no added feature from DSCC. Performance shown is evaluated on the unseen test data separated by respective class 0 as healthy cows (DSCC < 70) and 1 at-risk cows (DSCC >= 70)

A similar analysis was performed predicting DSCC instead of SCC. Therefore, the dataset target variable was changed to use DSCC >= 70 to classify at-risk cows and DSCC < 70 as healthy cows. This showed slightly better F1-score when considering best subset of features in the model and lower F1-score when no DSCC features were used in the model. The AUC of the best subset model, 0.856, was as high as the original models (using the SCC categories as target variables) but the model without any DSCC related features had a lower AUC of 0.817.

Table 8. Relative importance of top 10 features from ModelAll and ModelPart1 when DSCC was used to create target variable.

Feature Name	Relative Importance	Feature Name	Relative Importance
mean_DSCC	0.064	mean_PMN_pct	0.077
sd_DSCC	0.005	sd_PMN_pct	0.007
mean_Cells	0.004	lag_2_Cells	0.003
sd_linear_score	0.002	lag_3_Cells	0.003
lag_2_DSCC	0.002	lag_1_Cells	0.002
lag_1_Cells	0.002	age_days	0.002
age_days	0.001	lag_1_DSCC	0.001
DIM	0.001	DIM	0.001
lag_1_DSCC	0.001	age_at_calving	0.001
lag_3_DSCC	0.000	dim_cat	0.001

Conclusions

Based on the monthly and weekly data analysis, sofar no conclusive results have been reached regarding the use of DSCC. Although patterns in the data suggest that SCC combined with DSCC can identify some cows that may be considered healthy based on SCC alone the addition of DSCC can in some cases point at cows at risk. Using the data collected sofar, a machine learning approach predicting the future status of a single cows was not able to prove that DSCC provides a significant contribution over using SCC only. Future efforts will focus on collecting more weekly milk samples and look for additional relationships between DSCC and health status of the cow. Repeat analysis of monthly milk samples on the same cow will also increase the understanding of SCC and DSCC as it relates to parity and stage of lactation. Further understanding of the impact different environmental or contagious pathogens or impact of other (non-udder) health conditions on SCC and DSCC will be helpful in determining where DSCC can provide additional value.