AI IN DAIRY FARMING

Aivancity | Substrate AI

AI IN DAIRY FARMING

AI CLINIC REPORT

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I. PROBLEMATIC

The dairy farming industry is continually evolving, driven by the need to enhance milk quality and production efficiency. As consumer demand for high-quality dairy products grows, farmers are increasingly seeking innovative solutions to optimize their operations and improve the nutritional profile of their milk. One promising approach to achieving these goals is the development of intelligent systems that can predict and recommend suitable botanical supplements for dairy animals. These botanical pills are formulated based on various parameters such as milk yield, species, protein content, fat content, lactose levels, and other relevant factors.

This project focuses on leveraging Artificial Intelligence (AI) and the Internet of Things (IoT) to develop a system capable of predicting the most suitable botanical supplement for dairy animals. By analyzing comprehensive data collected from dairy farms, the system aims to provide tailored recommendations that enhance milk quality, improve animal health, and increase overall farm productivity. The specific objectives of this project include:

1. Collecting and analysing data: Gather extensive data from dairy farms, including parameters such as milk quantity, species, protein rate, fat rate, lactose levels, and other relevant factors.
2. Developing predictive models: Utilize AI to create predictive models that analyze the collected data and recommend the most effective botanical supplements.
3. Enhancing milk quality: Implement the system to improve the nutritional quality of milk by optimizing the botanical supplements given to the animals.
4. Supporting farmer decision-making: Provide farmers with actionable insights and recommendations to help them make informed decisions about supplementing their dairy animals' diets.

However, a critical aspect of this project is to determine the necessity of Machine Learning (ML) in achieving these goals. While ML offers powerful tools for predictive analytics, it is essential to explore whether simpler, non-ML approaches can also meet the project's objectives effectively. By evaluating different methodologies, we aim to identify the most practical and efficient solution for predicting suitable botanical supplements in dairy farming.

The central problem this project addresses is the optimization of botanical supplements to improve milk quality, considering the diverse and dynamic factors influencing dairy production. The challenge lies in accurately predicting the right supplement for each animal, based on real-time data and individual characteristics. Through this project, we aim to develop a robust system that empowers dairy farmers with precise recommendations, ultimately leading to better milk quality and enhanced farm productivity.

II. DATA

1. Data extraction

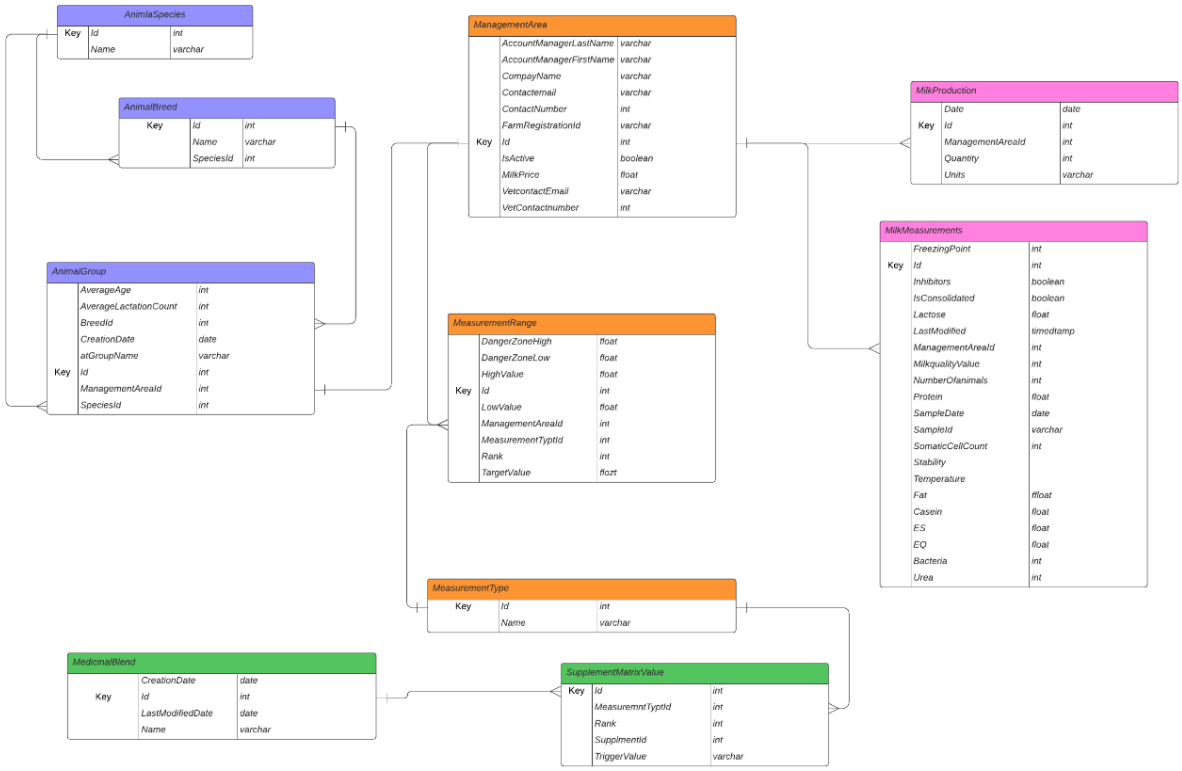


Figure 1 - Relational diagram of the tables used in our project

To extract data for the report, we first establish a connection to the production database using a connection string. The connection string specifies the server's name, database name, and security details such as user ID and password. Once connected, we can access the various tables in the database, those are shown in Figure 1.

The data consists of multiple Excel sheets, each with a specific purpose:

- **ManagementArea**: List of farms for which we are picking date.
- **MilkMeasurements**: Each row represents a milk laboratory analysis for a single farm from a single date.
- **MilkProduction**: Each row represents a single milk quantity got from a group of animals for a single farm on a single date.
- **MedicinalBlend**: Each row represents a single botanic pill.
- **MeasurementType**: Each row represents a single milk parameter that is being used in our analysis.
- **MeasurementRange**: Represents the list of rules of TargetValues (TV) that each farm has decided to apply to each milk parameter.

- **SupplementMatrixValue**: Represents or recommendation matrix. Each row links each botanic pill (SupplementId) with a milk parameter (MeasurementTypeId) indicating that it is recommended when the parameter is either Low / High, and its importance (Rank).
- **AnimalSpecies**: The list of animal species.
- **AnimalBreed**: The list of animal breeds and their corresponding species.
- **AnimalGroup**: The table that links animals with their corresponding farms.

2. Data processing and analysis

The data extracted, we then focused on analysis and preprocessing. Following the previous diagram, we applied all necessary merges to gather all relevant information in a single table that's going to be exploited further.

MilkMeasurements is the pivotal table in our work, it's where all data used to predict the milk quality is stored. Information from other tables is going to be appended to this one. After merging the data with the farms table (**ManagementArea**) to exclude potential measures coming from unknown sources since the intervals used to qualify the criticality level of each parameter depend on the different farms, we deleted some columns from **MilkMeasurements**:

- **NumberOfAnimals**: its value, always set at 0, does not allow us to exploit it, as it is used in the denominator of the calculation used to qualify the criticality level of the milk quantity
- **Lactose**, **Casein**: they are not involved in the recommendation process (moreover, almost all the values (resp. 42 and 84%) are 0, an equaivalent for Null value)
- **Inhibitors**, **MilkQualityValue**, **IsConsolidated**: they are not understandable
- **SampleId**, **LastModified**: the information contained is not relevant

Further, we noticed and corrected some formatting errors in the **FreezingPoint** column: one value was negative, and almost all values (75%) are in range [356, 639] instead of being < 1. We divided the values by 1000 to normalize the latter.

Although this information is not used in the recommendation algorithm, we felt it necessary to add information on the breeds and species of animals producing the milk studied. Data was retrieved from **AnimalBreed**, **AnimalSpecies**, and **AnimalGroup**, and the species names was then converted from Spanish to English. It's worth noting that animals from two farms were not identified in our database leading to a slight loss of information (179/3529 records or 5% of the records). As we can observe in Table 1, almost all animals in the study are goats of different breeds. Only one breed of sheep and cow are considered.

Species	Breed	NumberOfFarms
Goat	Florida	5
Goat	Malagueña	6
Goat	Murciano-granadina	3
Goat	Payoya	3
Sheep	Assaf	1
Cow	Frisona	1

Table 1 - Number of farms for each species and breed

In what follows, we'll be tackling the measurements that feed directly into the botanical pill recommendation algorithm proposed by our partners. A first operation we need to perform concerns measurement names which are saved in English in the main table, but in Spanish in the **MeasurementType** table that matches the milk characteristics labels to their ids. We then translate Spanish names to English ones. Secondly, we evaluate for each record the number of null values represented by a "0". Rows with strictly more than 2 missing values were then dropped. After this operation we kept 3148/3350 records (about 95%).

As each measured value is categorized according to intervals defined by the veterinarians of each farm (**MeasurementRange**), we associate each observed value on each parameter with a trigger value: **Danger Zone Low**, **Low**, **Adequate**, **High**, and **Danger Zone High**.

Figure 2 - Trigger values and zones

Note again that a value at 0 isn't admissible in the recommendation process, as well as values of the following columns: **Quantity**, **NumberOfAnimals**, **Casein**, and **Lactose**.

To perform this action, we need to melt the actual table to obtain a longer representation of it. In fact, each line of our table represents a milk measurement record with all its characteristics: **Fat**, **Protein**, **ES**[1], **EQ**[2], **Bacteria**, **SomaticCellCount**, **Urea**, and **FreezingPoint**. Knowing the farm from which that measurements come from, we now need to map each of the observed values with its corresponding trigger value, such that:

This initial record[3]

ManagementAreaId	Fat	Protein	ES	EQ	Bacteria	SomaticCellCount	Urea	FreezingPoint
1000	6	4	9	0	200	100	500	0

Table 2 - Data sample (1)

With these measurement ranges

ManagementAreaId (or Farm)	Danger Low Value	Low Value	High Value	Danger High Value	Measurement
1000	3	4	7	8	Fat
1000	3	5	7	10	Protein
1000	6	7	10	12	ES
1000	6	8	11	14	EQ
1000	6	10	50	100	Bacteria
1000	200	400	1500	2500	SomaticCellCount
1000	400	450	550	600	Urea
1000	0.45	0.55	0.59	0.66	FreezingPoint

Table 3 - Measurement ranges example

[1] Extracto Seco or Dry Extract
[2] Extracto Quesero or Chesse Extract
[3] This tabular data and all following are fake while representive of our dataset.

Leads to this melted result

Farm	Measurement	TriggerValue
1000	Fat	Adequate
1000	Protein	Low
1000	ES	Adequate
1000	EQ	*Not included (value = 0)*
1000	Bacteria	Danger Zone High (**DZ High**)
1000	SomaticCellCount	Danger Zone Low (**DZ Low**)
1000	Urea	Adequate
1000	FreezingPoint	*Not included (value = 0)*

Table 4 - Data sample (1) trigger values

From the 3148 input records at this step, we come out with 2761 (12% of data loss) rows after merging the data since the **MeasurementRange** table doesn't provide classification intervals for 12 farms.

This is the first step in the botanical pill recommendation algorithm, if required. But before going into detail about this process, let's highlight a few results from the data analysis.

- **Data recording period**

Figure 3 outlines that the start dates of measurements varied significantly across farms, ranging from March 2022 to July 2023. In contrast, the end dates were more consistent, falling between September and November 2023. This variation in starting periods might have implications on the volume of data collected, we will carry out an in-depth analysis to address this question.

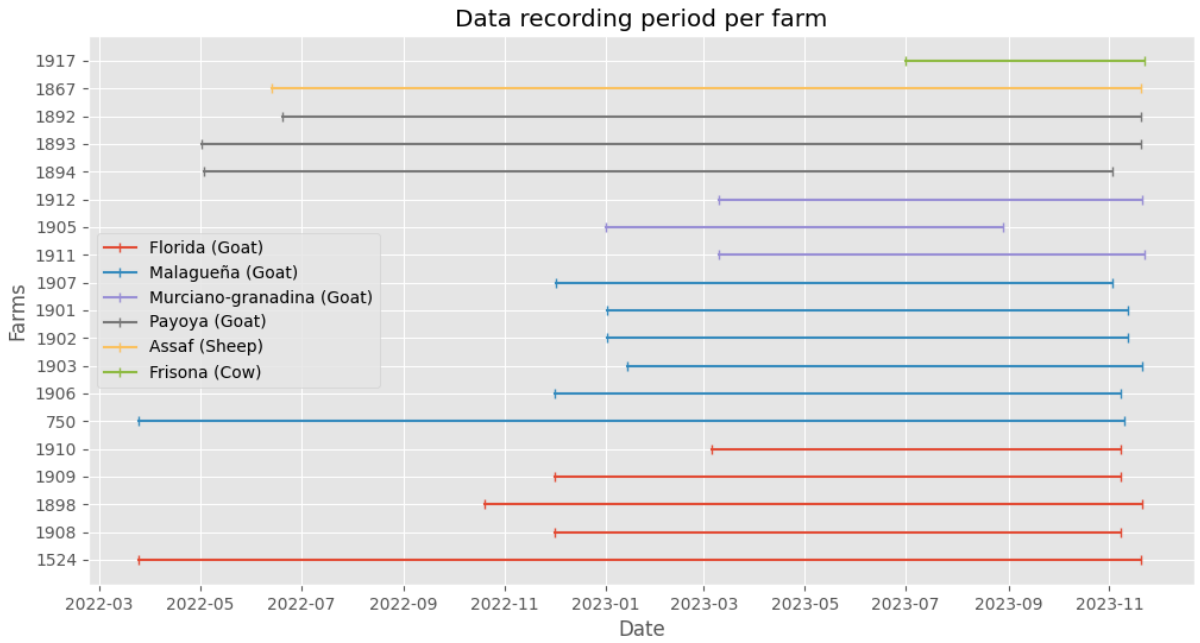


Figure 3 - Data recording period per farm

- **Number of samples per farm and breed**

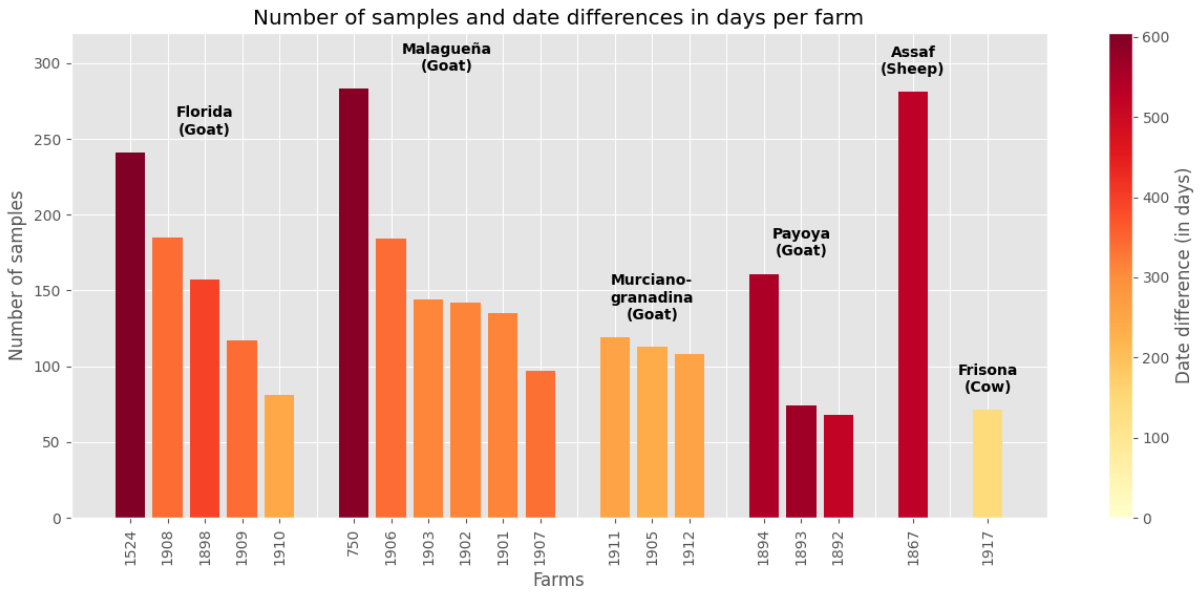


Figure 4 - Number of samples and date differences per farm

There is a strong correlation between the study period and the number of samples collected across most farms, indicating that longer periods lead to more data collection (Figure 4). However, the data collected for the Payoya goat breed is rather special in that many milk samples were analyzed over relatively short periods of time. It has been verified that in most cases only one milk measurement is made per day; the rule was broken only 13 times.

If we look at the number of days between two successive measurements, we see that while on average this gap is around 2 days for all breeds, it rises to 6 days for Payoya farms (Figure 5).

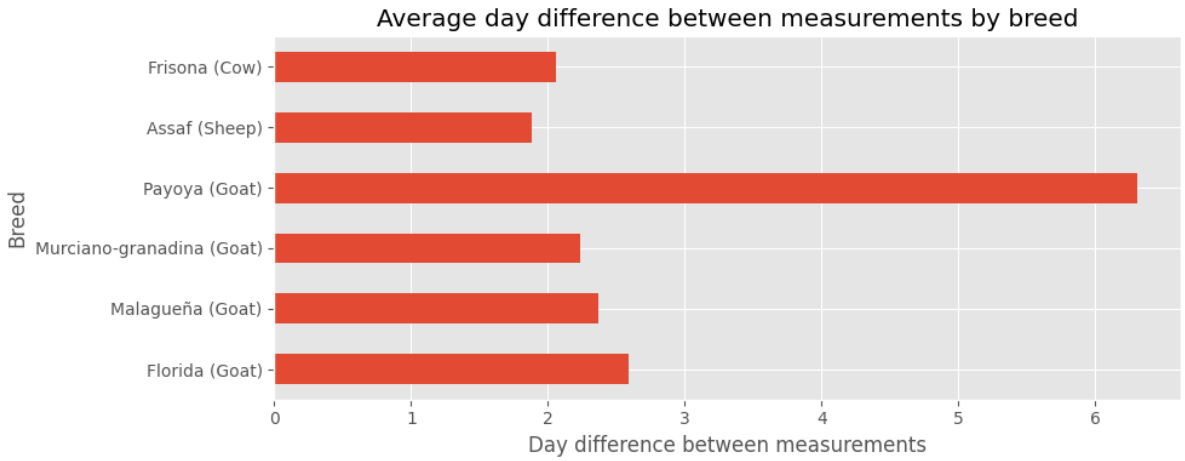


Figure 5 - Average day difference between measurements

- **Measurements distributions per farm, species, and breed**

The analysis of milk characteristics reveals significant variability across different farms and breeds for parameters such as **EQ**, **Fat**, **FreezingPoint**, **Protein**, and **Urea**. This suggests that species or breed can indeed impact these milk characteristics. More specifically, we can observe a strong correlation between the values and the species. Farm 1867, which raises sheep, shows very high overall parameter values. In contrast, Farm 1917, which raises cows, exhibits very low overall parameter values. However, some parameters like **Bacteria** and **SomaticCellCount** show uniformity across different breeds and farms, indicating that these specific characteristics might be less influenced by the breed or farm-specific factors. Finally, the **ES** distribution across farms is very atypical: farms 1902, 1901 (all Malagueña, Goat), and 1905 (Murciano-granadina, Goat) have surprisingly high values. It would be prudent to explore the influence of breed on milk parameters to determine if there are underlying genetic or environmental factors contributing to these variations. Relevant graphics are in Appendix A.

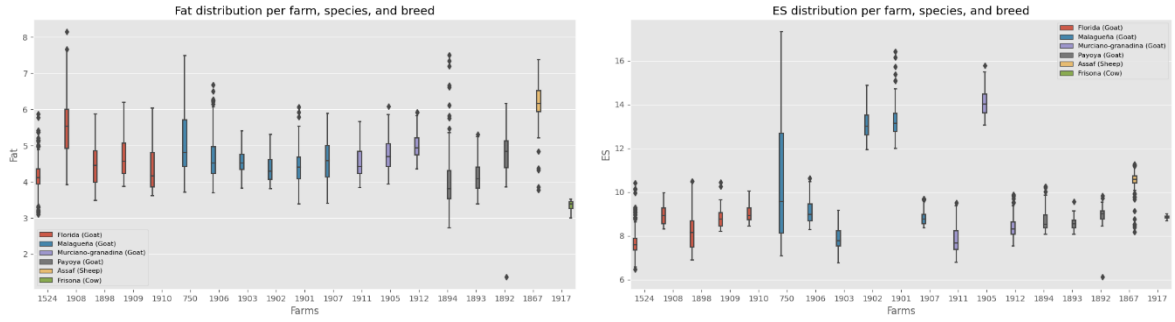


Figure 6 - Distribution of some parameters per farm

- **Measurement trigger values per farm**

The graphs show significant variations across the different parameters and farms. Some parameters such as **FreezingPoint** and Bacteria show high inter-farm consistency, suggesting uniform control practices. Other parameters such as **Urea**, **Protein** and **Bacteria** show considerable differences between farms and clusters, indicating that a clustered approach to the evaluation and improvement of management practices is required. It's worth noting that one more time farms 1867 and 1917 which have different type of animal species (resp. sheep and cow) stand out in this trigger values also: the first one have higher boundary values for **Protein**, **Fat** and **EQ**, while the second one has lower values for **Urea**, **SomaticCellCount** and **Bacteria**, which aligns with the previous distribution plots. More details can be found in Appendix B.

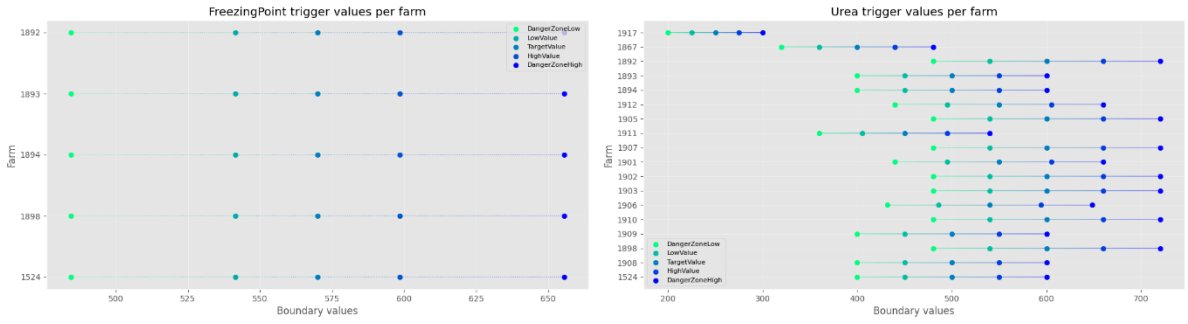


Figure 7 - Measurement trigger values per farm

Finally, we observe that the measurement ranges of certain params for some farms are missing:

Farm	1524	1908	1898	1909	1910	750	1906	1903	1902	1901	1907	1911	1905	1912	1894	1893	1892	1867	1917
Bacteria																			
ES																			
EQ																			
Fat																			
FP*																			
Protein																			
SCC*																			
Urea																			

*FP: FreezingPoint
**SCC: SomaticCellCount

Table 5 - Availability of measurement ranges per farms (red color = missing)

- **Distribution of trigger values per farm**

We have examined the distribution of trigger values for each parameter across all farms to analyze in detail the value zones and their distribution.

First, we note that the values for the **Bacteria** parameter are generally in the adequate zone, with a significant portion of the data relatively evenly distributed in the **High** and **Danger Zone High** areas. The **EQ**, **Fat**, and **Protein** parameters mostly have their values concentrated in the **Low** zone, then in the **Adequate** zone, while the **FreezingPoint** is generally **Adequate** and occasionally in the **Low** zone. Along with **Bacteria**, the parameters **SomaticCellCount** and **Urea** often have extreme values, particularly in the **Danger Zone High**. Most of the values for **SomaticCellCount** are in the **High** zone, while the distribution of these values across farms is quite random. A similarly random distribution is also observed for the **ES** parameter, with different profiles depending on the farms.

Overall, we notice that most of the parameters are often problematic (quantities below or above the recommended standards), except for **FreezingPoint**, which mostly has values in the **Adequate** zone. It is also important to highlight that the variables **Bacteria**, **SomaticCellCount**, and **Urea** are very often responsible for human intervention due to their values indicating an extremely concerning situation with excessively high levels (**Danger Zone High**). Appendix C contains other matrixes for further analysis.

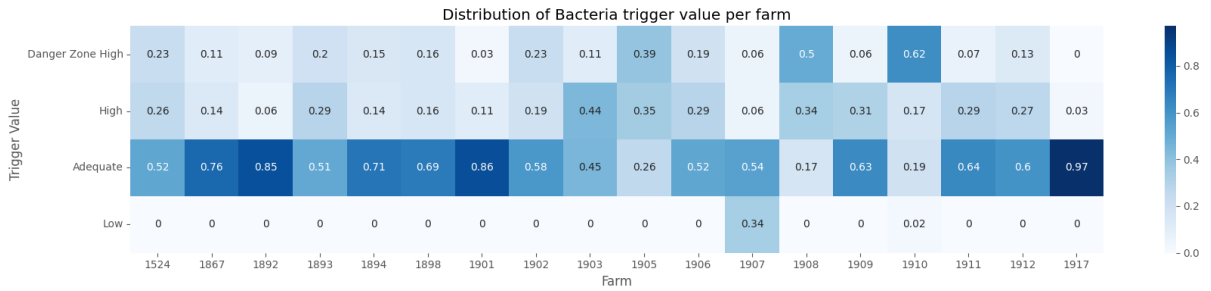


Figure 8 - Distribution of Bacteria trigger value per farm

III. APPROACHES

1. Expert algorithm

The following algorithm represents the sequential steps provided by the company. It is used to process and generate the final dataset used for predicting botanic pills efficacy in our machine learning models. The algorithm is structured as follows:

a) Collection of information

- List of farms
- List of feeds
    - For each feed, list of feed recommendation allocation rules
      E.g.: feed **BP_X** recommended when Fat is high, and Protein is low
- Milk quality and quality data
    - Milk quality is obtained from the data of the last laboratory analysis
    - The average milk production per animal per day is calculated with a formula including the number of animals, which is always set to zero, which is why this variable is not considered in our solution
- Targets/Critical values for each parameter by farm

b) Computational matrix creation algorithm

For each observation of a parameter in a farm sample, a result is computed:

- **Appropriate value:** The parameter is in normal values, no action is required
- **Danger Zone value:** The parameter is in a dangerous range (**much higher or lower** than normal), a notification for human intervention is generated
- **Inadequate value:** The parameter is in an inadequate range (**a little higher or lower** than normal), we may delve into the recommendation algorithm to assign a botanic pill to solve the problem

IMPORTANT: Any parameter whose value is 0 is ignored and is not considered for the generation of recommendations

c) Result assignment algorithm

The algorithm compares the results for all parameters of each farm and chooses one of the following cases:

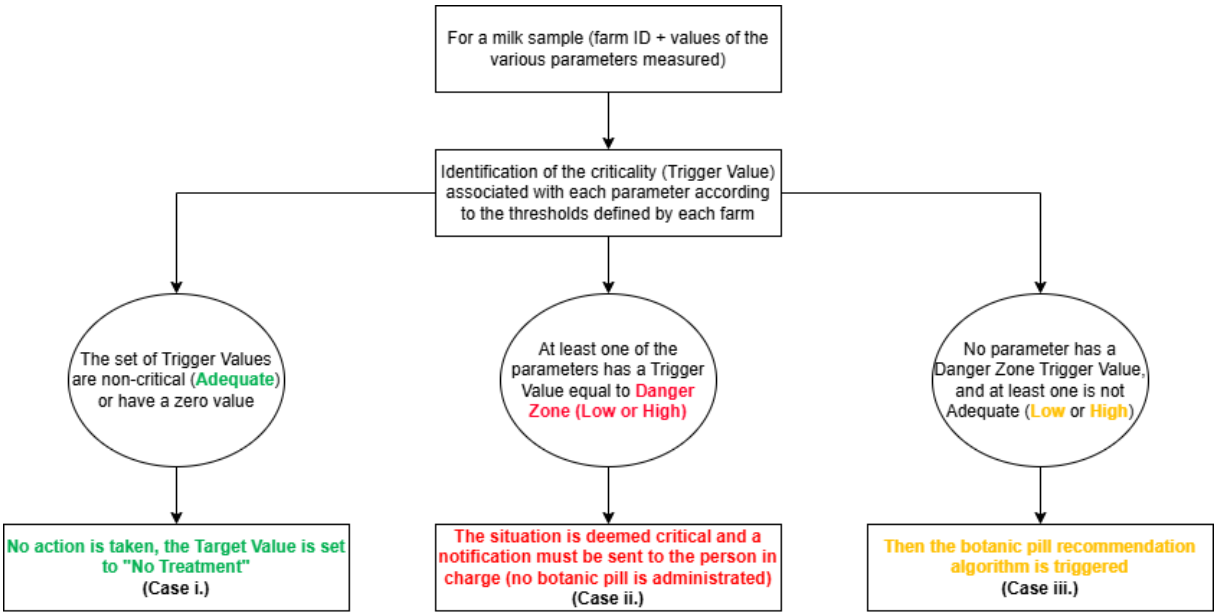


Figure 9 - Result assignment process

i. All parameters have appropriate values

Nothing is done, all parameters are correct.

Considerate our following melted data obtained after transformations in data preparation:

Farm	Measurement	Value	Danger Low Value	Low Value	High Value	Danger High Value	Trigger Value
1000	Fat	5	3	4	7	8	Adequate
1000	Protein	5.3	3	5	7	10	Adequate
1000	ES	8	6	7	10	12	Adequate
1000	EQ	0	6	8	11	14	*Not included*
1000	Bacteria	30	6	10	50	100	Adequate
1000	SomaticCellCount	600	200	400	1500	2500	Adequate
1000	Urea	455	400	450	550	600	Adequate
1000	FreezingPoint	0.57	0.45	0.55	0.59	0.66	Adequate

Table 6 - Data sample (2) and trigger values

Then the output is:

Farm	Target
1000	No treatment

Table 7 - Data sample (2) target

ii. At least one parameter is in Danger Zone

Notification is generated for human intervention.

Let's take an example:

Farm	Measurement	Value	Danger Low Value	Low Value	High Value	Danger High Value	Trigger Value
1000	Fat	5	3	4	7	8	Adequate
1000	Protein	2.5	3	5	7	10	DZ Low
1000	ES	8	6	7	10	12	Adequate
1000	EQ	0	6	8	11	14	*Not Included*
1000	Bacteria	4	6	10	50	100	DZ Low
1000	SomaticCellCount	600	200	400	1500	2500	Adequate
1000	Urea	700	400	450	550	600	DZ High
1000	FreezingPoint	0.57	0.45	0.55	0.59	0.66	Adequate

Table 8 - Data sample (3) and trigger values

Output:

Farm	Target
1000	Veterinarian intervention

Table 9 - Data sample (3) target

iii. All other cases (no parameters in Danger Zone, at least one parameter with inappropriate value)

Feed allocation algorithm is passed.

Let's look at the example below:

Farm	Measurement	Value	Danger Low Value	Low Value	High Value	Danger High Value	Trigger Value
1000	Fat	5	3	4	7	8	Adequate
1000	Protein	3.5	3	5	7	10	Low
1000	ES	8	6	7	10	12	Adequate
1000	EQ	0	6	8	11	14	*Not Included*
1000	Bacteria	70	6	10	50	100	High
1000	SomaticCellCount	600	200	400	1500	2500	Adequate
1000	Urea	555	400	450	550	600	High
1000	FreezingPoint	0.57	0.45	0.55	0.59	0.66	Adequate

Table 10 - Data sample (4) and trigger values

First, we must determine for each feed which parameter assignment rules have been met:

Botanic Pill (BP)	Measurement	Criteria	Trigger Value (inputs)	Rank of BP
BP_1	Protein	Low	Low	3
	Bacteria	Low	High	4
	Urea	High	High	5
BP_2	FreeZingPoint	Low	Adequate	8
	Bacteria	High	High	9
BP_3	Protein	Low	Low	7
	EQ	Low	Adequate	1
	Urea	High	High	5

Table 11 - Botanic pills and related criteria

The feed with the highest score (sum of ranks of the inadequate parameters) is recommended:

BP	Measurement	Criteria	Trigger Value	Rank of BP	Sum of Rank
BP_1	Protein	Low	Low	3	**8**
	Bacteria	Low	High	4	
	Urea	High	High	5	
BP_2	FreeZingPoint	Low	Adequate	8	**9**
	Bacteria	High	High	9	
BP_3	Protein	Low	Low	7	**12**
	EQ	Low	Adequate	1	
	Urea	High	High	5	

Table 12 - Comparison of the sum of ranks per botanic pill

Output:

Farm	Target
1000	BP_3

Table 13 - Data sample (4) target (1)

In case of a tie, the one with the highest number of inappropriate parameters is assigned:

BP	Measurement	Criteria	Trigger Value	Rank of BP	Σ of Rank	# of Params
BP_1	Protein	Low	Low	3	**12**	**3**
	Bacteria	Low	High	4		
	Urea	High	High	5		
BP_2	FreeZingPoint	Low	Adequate	8	**9**	**-**
	Bacteria	High	High	9		
BP_3	Protein	Low	Low	7	**12**	**2**
	EQ	Low	Adequate	1		
	Urea	High	High	5		

Table 14 - Comparison of the number of inadequate parameters

Output:

Farm	Target
1000	BP_1

Table 15 - Data sample (4) target (2)

NB: The company's algorithm ignores ties between feeds with the same inappropriate parameters. We chose to output all tied feeds:

BP	Measurement	Criteria	Trigger Value	Rank of BP	Σ of Rank	# of Params
BP_1	Protein	Low	Low	3	**12**	**2**
	Bacteria	Low	High	4		
	Urea	High	High	9		
BP_2	FreeZingPoint	Low	Adequate	8	**9**	**-**
	Bacteria	High	High	9		
BP_3	Protein	Low	Low	7	**12**	**2**
	EQ	Low	Adequate	1		
	Urea	High	High	5		

Table 16 - Sum of ranks and number of inadequate parameters all equal

Output:

Farm	Target
1000	[BP_1, BP_3]

Table 17 - Data sample (4) target (3)

2. Machine Learning

The resulting data frame after the algorithm application represents for each row, each milk laboratory analysis, corresponding to a single farm on a specific date. Due to an imbalanced target value (Table 18), we decided to group samples where the predicted class was a given botanic pill as a single **Treatment** value, and to drop the **No treatment** class. Consequently, we have two unique values as target: **Treatment**, and **Veterinarian intervention**.

Target		Count
Veterinarian intervention		**1136**
No treatment		**15**
Treatment	1	1017
	42	5
	45	1
	[38, 39, 40, 42, 46, 47]	337
	[38, 40, 42]	101
	[38, 39, 42]	78
	[39, 42]	40
	[38, 42]	20
	[44, 45]	6
	[38, 39, 40, 41, 42, 43, 44, 45, 46, 47]	2
	[1, 38, 39, 40, 42, 46, 47]	1
	[38, 40, 41, 42, 43]	1
	[38, 39, 42, 43]	1
	Total	**1610**

Table 18 - Target distribution

The following features are considered in the database:

Features	Type	Unit	Description
Fat	float	Percentage	Fat proportion
Protein	float	Percentage	Protein proportion
Dry Extract (ES)	float	Percentage	Residual mass after drying the milk
Cheese extract (EQ)	float	Percentage	Residual mass for cheese making
Bacteria	int	Colony-forming unit / Milliliter*1000	Quantity of bacteria
SomaticCellCount	int	Cells / milliliter*1000	Number of cells of type “somatic”
Urea	float	Milligram per Liter	Quantity of urea
FreezingPoint	float	Degree Celsius	Freezing temperature of the milk
Breed	object	-	Animal breed
Species	object	-	Animal species
Target	object	-	Whether to give a treatment, notify a veterinary, and do nothing

Table 19 - Machine learning models features

We developed three machine learning models: Decision Tree, Random Forest, and XGBoost. The data preparation steps are as follows:

- Drop **Id** and **ManagementAreaId** columns from the transformed data
- Split the data into training (70%) and testing (30%) sets
- Encode the training and testing features splits (X_train & X_test):
    - Encode categorical features using **OneHotEncoder**
    - Encode numerical features using **OrdinalEncoder**
- Encode the training and testing labels splits (y_train & y_test) using **LabelEncoder**

Here are the results:

Models	Accuracy	Precision (w. avg)	Recall (w. avg)	F1-score (w. avg)
Decision Tree	91%	91%	91%	91%
Random Forest	92%	92%	92%	92%
XGBoost	94%	94%	94%	94%

Table 20 - Prediction metrics

The confusion matrixes (**T: Treatment - VI: Veterinary intervention**):

Decision Tree

True \ Predicted	T	VI
T	443	40
VI	37	304

Random Forest

True \ Predicted	T	VI
T	461	22
VI	41	300

XGBoost

True \ Predicted	T	VI
T	464	19
VI	32	309

Table 21 - Prediction confusion matrixes

Considering overall performance and confusion matrices, **XGBoost** appears to be the best model with an overall **accuracy of 94%**. The **same performance** is observed in **precision**, **recall**, and **f1-score**. Though Random Forest and Decision Tree also demonstrate good performance, XGBoost consistently outperforms them in all metrics and offers the most reliable predictions, it's thus the best performing model for this scenario.

When considering XGBoost for the final model selection, it's crucial to understand the impact of different features on its performance, as illustrated in Figure 10. **Bacteria** and **SomaticCellCount** are the most significant features, **each contributing more than 40% to the model's feature importance**. These variables play a critical role in the model's decision-making process. Urea and ES also make contributions, albeit much smaller compared to the top two features. All other features have negligible importance in the model. The significant reliance on Bacteria and SomaticCellCount highlights these as critical variables impacting the model's predictions.

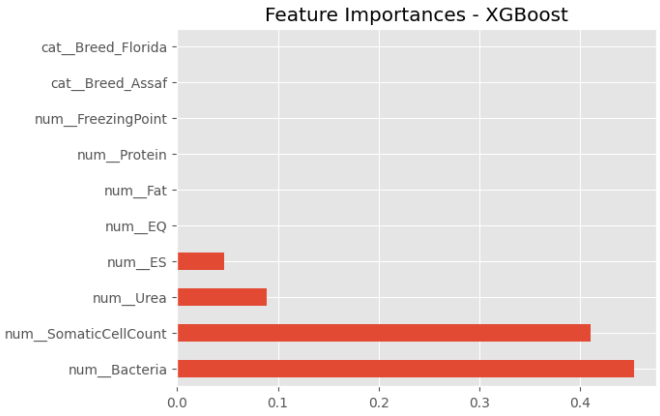


Figure 10 - XGBoost feature importance

IV. CONCLUSION

This project demonstrates the potential of using AI in dairy farming to optimize the nutritional quality of milk through recommendations for botanical supplements. By integrating milk measurements, animal species and breeds data, and farm-specific parameters, we developed a system capable of providing farmers insights on the need of a treatment or to a veterinarian intervention.

We gathered and processed a vast amount of data from multiple sources, ensuring that the final data set was comprehensive and representative of different farms and animal breeds. The initial approach utilized an expert-driven algorithm provided by our partner to recommend botanical supplements based on observed milk parameters. This rule-based method provided a clean dataset, the basis of our machine learning experimentations. We explored the use of three ML models - Decision Tree, Random Forest, and XGBoost - to predict the need for treatment or veterinarian intervention. The XGBoost model outperformed the others, achieving a 94% accuracy rate, and proved to be the most reliable in making predictions. Key features driving the model's predictions were identified, with Bacteria and SomaticCellCount being the most influential. While the expert algorithm provided a straightforward approach to recommendations, it lacked the necessary validation from our partner. The absence of a thorough validation process raises concerns about the reliability of the recommendations, particularly in real-world scenarios. Moreover, the challenges were further compounded by the presence of missing data, particularly in the measurement ranges and the identification of certain farms and animals, and the exclusion of important parameters like milk quantity. These gaps in data meant that the algorithm's output could not make full use of all the available information, potentially leading to suboptimal recommendations.

Future work could involve integrating more diverse data sources, such as environmental conditions, feed composition, and animal health records, to further refine the predictive models, and even collect enough data to build a bill recommendation system that predicts the right botanic pills in case a treatment is required. Moreover, while ML has shown great promise, exploring other statistical or heuristic methods could provide additional insights or alternative solutions, especially for farms with limited data. Finally, conducting long-term studies to assess the impact of the recommended botanical supplements on milk quality and farm productivity would provide valuable feedback for continuous improvement of the system.

V. APPENDIX

Appendix A

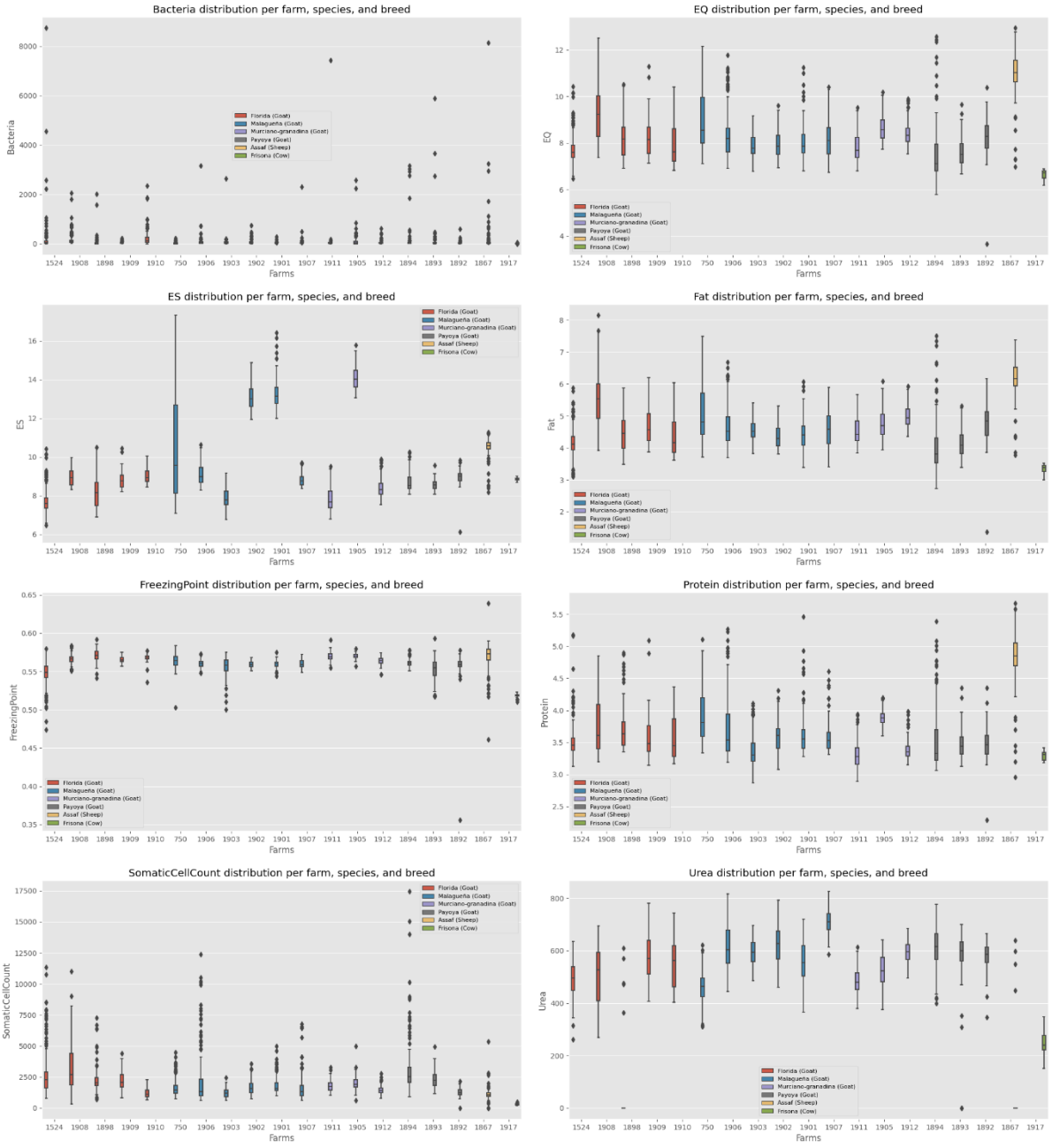


Figure 11 - Measurements' distributions per animal species

Appendix B

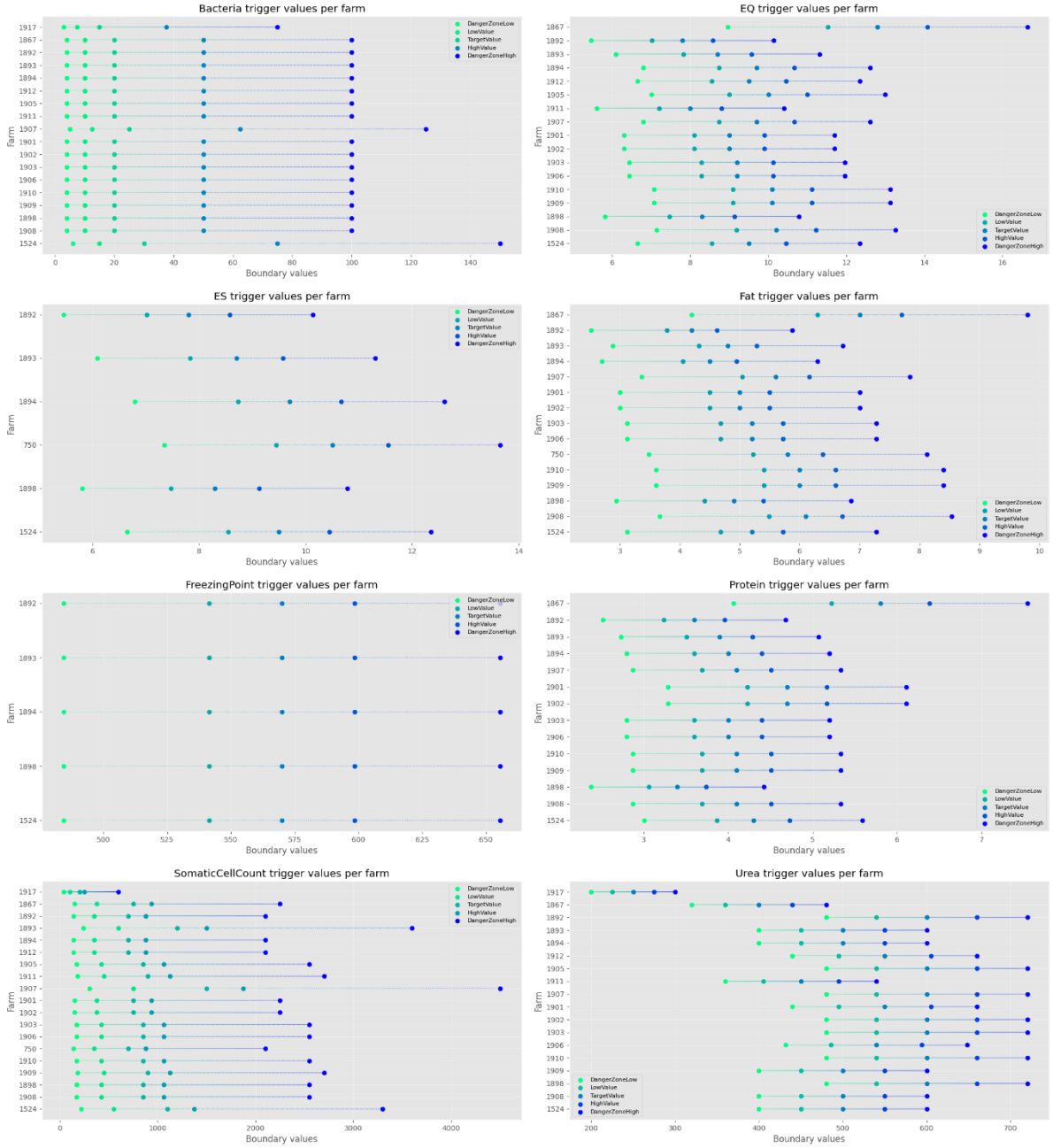
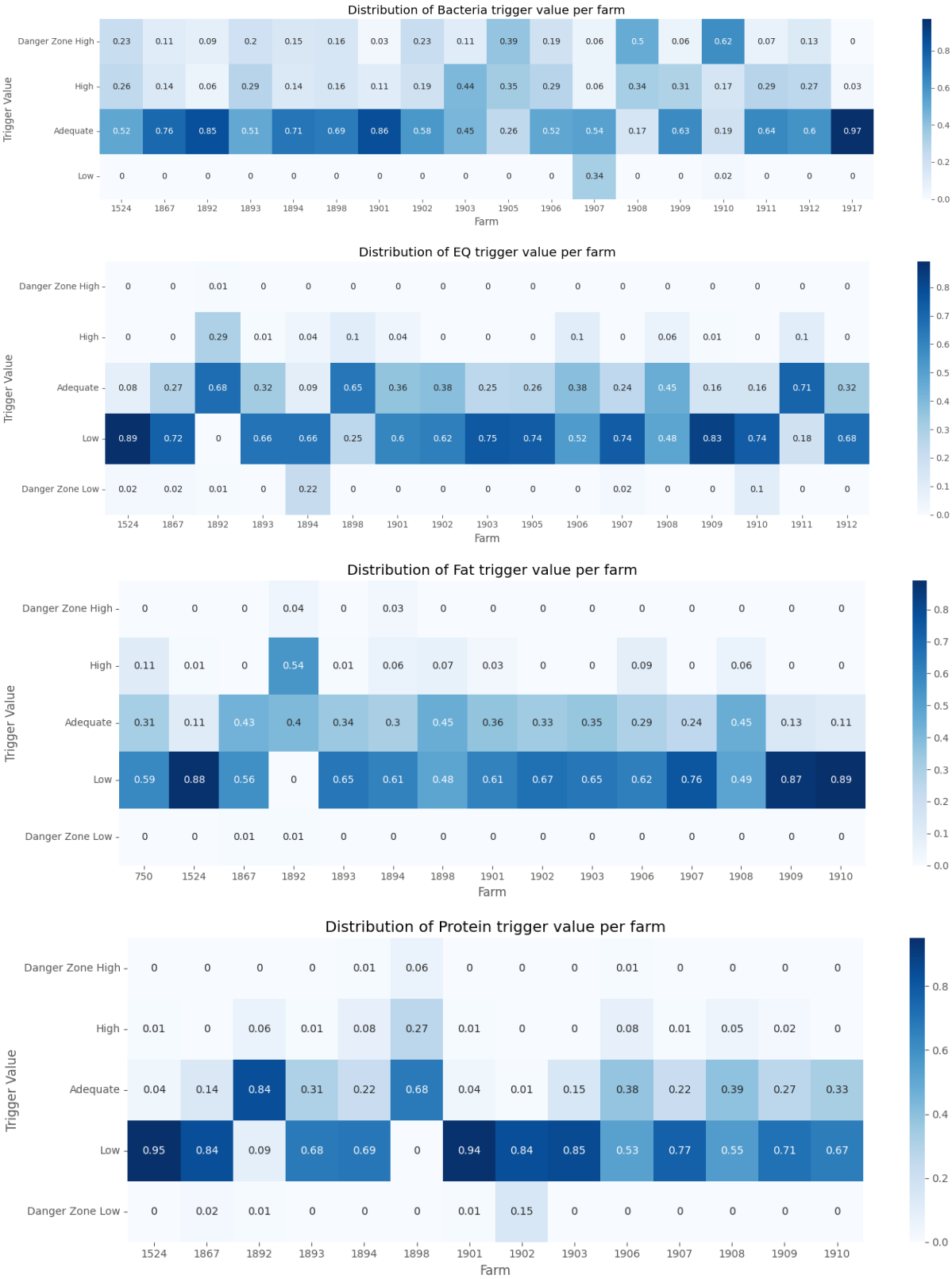


Figure 12 - Trigger values' ranges per farm

Appendix C


Distribution of Bacteria trigger value per farm
Trigger Value
Danger Zone High
High
Adequate
Low
0.23 0.11 0.09 0.2 0.15 0.16 0.03 0.23 0.11 0.39 0.19 0.06 0.5 0.06 0.62 0.07 0.13 0
0.26 0.14 0.06 0.29 0.14 0.16 0.11 0.19 0.44 0.35 0.29 0.06 0.34 0.31 0.17 0.29 0.27 0.03
0.52 0.76 0.85 0.51 0.71 0.69 0.86 0.58 0.45 0.26 0.52 0.54 0.17 0.63 0.19 0.64 0.6 0.97
0 0 0 0 0 0 0 0 0 0 0 0.34 0 0 0.02 0 0 0
1524 1867 1892 1893 1894 1898 1901 1902 1903 1905 1906 1907 1908 1909 1910 1911 1912 1917
Farm
0.0 0.2 0.4 0.6 0.8
Distribution of EQ trigger value per farm
Trigger Value
Danger Zone High
High
Adequate
Low
Danger Zone Low
0 0 0.01 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0.29 0.01 0.04 0.1 0.04 0 0 0 0.1 0 0.06 0.01 0 0.1 0
0.08 0.27 0.68 0.32 0.09 0.65 0.36 0.38 0.25 0.26 0.38 0.24 0.45 0.16 0.16 0.71 0.32
0.89 0.72 0 0.66 0.66 0.25 0.6 0.62 0.75 0.74 0.52 0.74 0.48 0.83 0.74 0.18 0.68
0.02 0.02 0.01 0 0.22 0 0 0 0 0 0 0.02 0 0 0.1 0 0
1524 1867 1892 1893 1894 1898 1901 1902 1903 1905 1906 1907 1908 1909 1910 1911 1912
Farm
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8
Distribution of Fat trigger value per farm
Trigger Value
Danger Zone High
High
Adequate
Low
Danger Zone Low
0 0 0 0.04 0 0.03 0 0 0 0 0 0 0 0 0
0.11 0.01 0 0.54 0.01 0.06 0.07 0.03 0 0 0.09 0 0.06 0 0
0.31 0.11 0.43 0.4 0.34 0.3 0.45 0.36 0.33 0.35 0.29 0.24 0.45 0.13 0.11
0.59 0.88 0.56 0 0.65 0.61 0.48 0.61 0.67 0.65 0.62 0.76 0.49 0.87 0.89
0 0 0.01 0.01 0 0 0 0 0 0 0 0 0 0 0
750 1524 1867 1892 1893 1894 1898 1901 1902 1903 1906 1907 1908 1909 1910
Farm
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8
Distribution of Protein trigger value per farm
Trigger Value
Danger Zone High
High
Adequate
Low
Danger Zone Low
0 0 0 0 0.01 0.06 0 0 0 0.01 0 0 0 0
0.01 0 0.06 0.01 0.08 0.27 0.01 0 0 0.08 0.01 0.05 0.02 0
0.04 0.14 0.84 0.31 0.22 0.68 0.04 0.01 0.15 0.38 0.22 0.39 0.27 0.33
0.95 0.84 0.09 0.68 0.69 0 0.94 0.84 0.85 0.53 0.77 0.55 0.71 0.67
0 0.02 0.01 0 0 0 0.01 0.15 0 0 0 0 0 0
1524 1867 1892 1893 1894 1898 1901 1902 1903 1906 1907 1908 1909 1910
Farm
0.0 0.2 0.4 0.6 0.8

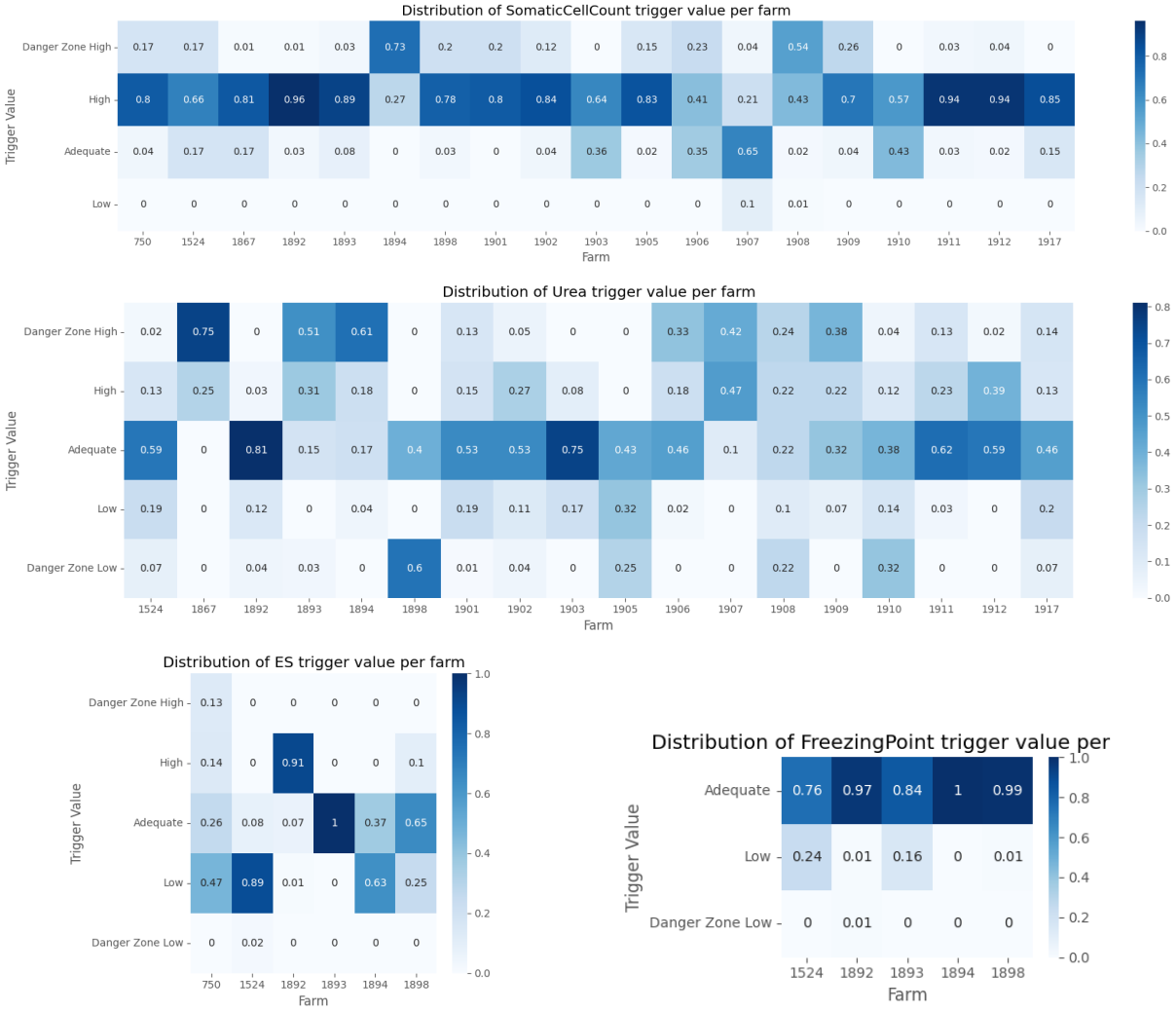


Figure 13 - Trigger values' distributions per farm