A Case Study of the Application of Artificial Intelligence to Aid in the Clinical Detection of Porcine Reproductive and Respiratory Syndrome Virus in Sow Farms

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ABSTRACT

The introduction of a pathogen into a livestock population is the cause devastating losses in swine farms. The early detection of disease plays an essential role in limiting the effects of a pathogen introduction on a population. While the use of routine lab-based molecular testing for antigens can aid in rapid pathogen detection, the number of samples statistically required, and the associated expense make its frequent use unrealistic. For these reasons, researchers continue to develop additional tools to aid in disease detection. This project proposes a predictive tool that overcomes the limitations of inherent biological variation by utilizing current machine learning advancements to detect disease quickly and accurately within a population.

The early identification of a pathogen on a sow farm facilitates timely management decisions to slow pathogen transmission and reduce the severity of disease. Producers' decisions encompass a broad range of tactics to limit spread through the feed, people, supply, or animal movements. Prompt implementation of these tactics is essential for minimizing both the individual producer's and the industry's short- and long-term financial losses.

Described is a tool that facilities sensitive syndromic surveillance for sow farms by applying machine learning to historical individual sow production records to predict of the outcome of an individual breeding event. The tool predicts which sow breeding events will yield piglets (farrow) and subsequently monitors the outcome of the breeding event. If more services result in failure than expected, as defined by the model's error, the model signals a disruption (presence of disease). To compare the sensitivity of the tool to the established Statistical process control approach (SPC), retrospective data from two sow farms that experienced a Porcine reproductive and respiratory syndrome virus (PRRSv) introduction were assessed.

While both the machine learning based tool and SPC detected PRRSv introduction on each farm, the average detection was 1 and 3 weeks before the farm reported a disease event using the novel machine learning-based method and 2 weeks after and 1 week before using SPC. In addition to identifying the PRRSv introduction, the machine learning approach identified production disruption resulting from changes to the electronic sow feeding system on the farm. SPC failed to identify this disruption. These two test cases demonstrate that the novel machine learning-based method maybe more sensitive for the surveillance of swine farms for pathogen and non-pathogen related disruptions to average production compared to previously described SPC based approach. The machine learning based technique is broadly applicable to economically important diseases, and most importantly can serve as an early alert for novel pathogens where industry level monitoring is not conducted routinely.

General Terms

Artificial Intelligence, Algorithm, Case Study

Keywords

Machine learning, surveillance, swine, disease, SPC, epidemiology

1. INTRODUCTION

The timely and sensitive detection of a novel pathogen is the foundation any infectious disease control and management plan for the infected population, be it human or animal. For global pig production, early detection of infectious diseases in commercial swine herds facilitates timely management decisions to limit the spread of a disease outbreak within a specific farm or production system and, more broadly, at a regional or industrial level. [1]-[3] In modern swine production systems, a single farm site typically specializes in only one phase of production (breeding or growing) with many of the support services (feed, semen, supplies, transportation, and maintenance) shared between farms. Growing pigs from a single breeding herd are often raised on multiple farms that are separate from the breeding herd source and from each other. The growing pigs arrive at the farm after being weaned from their dams, at approximately three weeks of age, and remain there until they are sold for harvest at a pork processing facility. The total time between weaning and harvest is typically 26 weeks. Therefore, at these growing farms, there may be pigs on site that arrived from the breeding herd any time from one to 26 weeks prior. This farming structure results in the frequent movement of feed, people, supplies, and pigs between farms. As the time between pathogen entry and detection increases in a breeding herd, the number of movements that occurred also increases, resulting in additional primary and secondary transmission events due to contact with the infected, but undetected, breeding farm. These contact transmission events can serve as means of pathogen introduction directly with pig movement or indirectly with fomites between farms, increasing the probability of additional disease outbreaks.[4]

Disease outbreaks in swine herds lead to morbidity and mortality which are costly to the pig farmer. Financial losses suffered from infectious diseases are substantial in the US swine industry. Porcine Reproductive and Respiratory Syndrome (PRRS), a viral disease that results in abortions and pneumonia, results in a loss of \$664 million per year to the US swine industry.[5] While remarkable, these financial losses from PRRS alone are a fraction of the forecasted potential losses associated with a foreign animal disease introduction.[6] Early pathogen identification for rapid control and eradication of an outbreak is pivotal for limiting both the economic losses on farms and those financial losses associated with the inability to access foreign export markets.[7] Therefore, to reduce loss of income and market access, accurate surveillance protocols for early detection of disease to prevent outbreak spread are needed. Unfortunately, the practical and economic constraints associated with the large sample size required to ensure accurate surveillance for an infectious disease via diagnostic, i.e., laboratory assays forces veterinarians and farmers overseeing the herds to rely on clinical observation as a method for identifying a novel infectious disease in a herd.[8] Regrettably, this approach is fraught with challenges due to non-specific clinical signs and the difficulty associated with intense, repeated, individual observation in large populations. Combined, this makes the rapid and accurate identification of novel and clinically significant pathogens practically difficult.[9],[10] To address this challenge, veterinarians and scientists are adapting the technical and analytical tools broadly applied to detect system-level changes in other industries, such as statistical process control, for the rapid and accurate detection of infectious disease in swine populations.

Statistical process control (SPC) monitors a system for disruptions to a process, i.e., a production cycle.[11] SPC compares current process outcomes to historical variation around the mean. If the current data indicates a shift from the historical mean that is greater than the expected normal variation, an "SPC signal" is generated. This signal implies the existence of a production disruption, which the operator can then investigate further.[12] This use of structured, objective assessment employing the statistical concept of the mean (average) and variance (variation around a mean) is also applicable to swine production systems. The presence of stringent controls over farm management, nutrition, and environment can be used to keep the herd's production outcomes within steady and predictable boundaries. А common cause of disruption of production outcomes in agricultural animal systems is the physiological disorders within the population due to disease outbreaks. The resulting morbidity and mortality from a disease incursion results in production outcomes that deviate from predicted boundaries.[12] The ability to systemically identify the deviation of a production outcome from the historical average can thus serve as a useful indicator of the introduction of a novel pathogen into the population. Indeed, SPC has been implemented for use in animal agricultural industries, such as within swine farms and pork production, to both monitor production outcomes and as an indirect method to detect disease. Examples within the swine industry include the use of SPC to monitor changes in abortion rate and frequency within sow farms which enabled detection of PRRSv infection one to four weeks before conventional diagnostic methods.[13] In addition, SPC monitoring of water intake data detected disease in young piglets one day before clinical observation of a change in drinking behavior.[14]

For these reasons, research into additional modalities to monitor outcomes that can function in systems with a high degree of variation is needed. Machine learning (ML) is one such modality that can create accurate predictions of the outcome parameters of a process.[15] The robustness of ML algorithms in predicting outcomes within variable processes[16] creates the opportunity to compare a predicted outcome to the actual result. The comparison of an outcome to the predicted outcome from ML better represents current system performance than comparison to historical averages which, by definition, do not take the current system performance into consideration but rely heavily on previous performance to inform the parameters. Many industries, such as crop agriculture, forestry, energy, and manufacturing have adopted ML approaches to monitor changes in productivity.[17]-[22] However, the adoption of ML-driven techniques in animal agriculture [23]-[29] while possible, is limited.

This paper describes a machine learning based tool to monitor the production process within sow farms, namely pregnancy failure events, as a method of clinical sign detection and signal the need for further diagnostic confirmation during a disease outbreak. The goal of this analytical tool is to reduce the time between the introduction and detection of a new infectious disease in a swine breeding herd.

2. MATERIAL AND METHODS

This study creates a non-specific syndromic surveillance method for sow farms to monitor the normal production cycle's disruptions by comparing actual reproductive outcomes to predicted outcomes. The following sections outline the steps taken to develop the tool.

2.1 Data Collection

The data set consists of sow breeding records from two approximately 6000 female breeding herds located in the Midwestern United States and contains approximately thirteen years of retrospective production data. This data consisted of records from individual sow services exported from the farm's record management system (Porcitec®, Agritec, Barcelona, Spain).

In addition, any major event with the potential of disrupting production was recorded during the study timeframe (2019-2020). This study refers to the farms as Farm 1 and Farm 2. Both farms experienced outbreaks of PRRS following the introduction of a novel, unrelated variant of the PRRS virus (PRRSv). Both farms are considered "high health" status and are free of A. pleuropneumoniae and swine dysentery. Each farm adheres to intensive biosecurity systems and practices, including shower in-shower out, dedicated supply delivery, dedicated, washed, and thermally assisted dried live animal transport. M. hyopneumoniae and Influenza A virus (IAV) infections are present in both herds. Both farms have common management, feed, and semen sources but independent external sources of replacement breeding females.

Farm 1 utilizes group-based housing for gestating sows after 40-45 days of pregnancy until farrowing. Sows are housed individually during lactation, the pre-breeding period and for the first 40-45 days of gestation. The farm made a change to the equipment used to feed sows in group housing with installation starting in January and ending in April 2019. This farm has been historically free from PRRSv infection. In week 12 of 2020 an IAV-H1N1 gamma cluster virus that had not been previously identified on the farm resulted in an outbreak of clinical respiratory disease typical of influenza. Two weeks later, week 14, 2020, an outbreak of PRRS was confirmed though standard molecular diagnostic methods, reverse transcription-polymerase chain reaction (rt-PCR), and clinical investigation by the herd veterinarian. 1 contains the complete history of Farm 1.

Farm 2, all sows are housed individually across all phases of production. There was significant maintenance activity on the farm during the late summer and early fall of 2019, resulting

in the movement of sows at abnormal times during gestation. In week 2 of 2020 an IAV- H1N1 gamma cluster virus that had not been previously identified on the farm resulted in an outbreak of clinical respiratory disease typical of influenza. Historically the farm was endemically infected with PRRSv but was free from detectable clinical signs and PRRSv nucleic acids in routine sampling and testing of pigs during lactation from December 2018 until week 19 of 2020. In week 19 of 2020 an outbreak of PRRS due to a new PPRSv variant was confirmed though standard molecular diagnostic methods (rt-PCR, genomic sequencing) and clinical investigation by the herd veterinarian. 2 contains the complete history of Farm 2.

2.2 Data Cleaning

Once collected, the raw data is subject to data cleaning to address missing data, outliers, and errors. The goal of this exercise is to ensure that all entries are both valid, formatted and have adequate nonblank entries as required for the prediction model. This data cleaning process utilized a standardized technique across all observation in both data frames. All duplicate observations were removed from the dataset. A duplicate observation was defined as any observations with an identical ID and a service date less the 21 days apart, the normal length of a reproductive cycle of a sow. Then variables with any structural errors, and formatting within the entries were addressed. Outliers within the dataset were identified when any when any numerical production variable was greater than three z scores from the mean of that production variable. Individual service records (observations) were censored if containing an outlier. For this analysis variables missing more than 60% of the entries were excluded for their limited predictive value to the problem. Finally records with biologically implausible outcomes, outside an appropriate range based on technical knowledge, were assumed to be errors and the observation was removed.

2.3 Feature Engineering

Following an initial round of cleaning, feature engineering generated additional variables and information to identify potential complex relationships to enhance the model's predictive value. Featuretools, a publicly available python library, was utilized to perform feature engineering on the datasets. Featuretools uses the deep feature synthesis algorithm[30] to automatically generate additional features from rational datasets. The deep feature synthesis algorithm is a method used to automate and standardize the feature creation process and uses various mathematical functions (e.g., transformations, aggregation) to calculate new variables.

After the entity set was built, normalization occurred to create additional datasets for different subsets or groups. These subsets were individual sows, parities (number of recorded litters), and service groups (all the sows bred in one calendar week), allowing information to be grouped by subset to generate additional combinatory features, such as the mean of a category, to improve accuracy. Finally, a target entity, dataset, consisting of three objects: ID, cutoff time, and target was defined? where ID is the unique service ID, cutoff time, or time in which the model will make a prediction is the service date, and the target for the model is the service result. After completing all entities, automated deep-feature synthesis on the data set, with $max_depth = 3$, finalized the feature engineering process. In total, 33 variables split into four entity sets entered automated feature engineering, resulting in 495 additional features. After feature engineering, the dataset underwent data quality analysis, as previously described.

These steps maximized the usefulness of the raw data to train a supervised classification model. Before training, standardization was performed on all numerical features so that features lie between -1 and 1. Dummy variables represent all categorical variables because the classification algorithm does not permit text data.

2.4 Exploratory Data Analytics

Multiple data visualization techniques in Python's Seaborn and Matplotlib libraries to investigate relationships were applied before creating the model. Multicollinearity was defined as variables the have a Pearson's correlation coefficient greater than 0.9. For highly correlated variables, the second variable was removed. This cut-off value (0.9) was only selected to ensure that nearly duplicate data did not exist, as multicollinearity do not affect decision trees and thus will not impact the selected algorithm.

2.5 Machine-Learning Model Training

When predicting the outcome of a service (farrow/not farrow), the target variable is categorical. Therefore, a supervised classification model, in this case gradient boosting algorithm, XGBoost, was employed. Supervised classification models allow the user to train an algorithm to predict group membership by providing historical data and known outcomes for the algorithm to train from.

XGBoost, allowed for accurate predictions on a large complex tabular data set without excessive computer processing requirements. Gradient boosting is a method wherein the final prediction model comprises multiple weak prediction models. Combining multiple weak predictors creates a single strong predictor. [31]

Model training utilized the SciKitLearn library within Python.[32] Exclusion of the parity 0 animals in the dataset occurred before training. Gilts (Parity 0 animals) in these farms have no historical data recorded before breeding precluding analysis. For training, a randomized 80% of the instances comprised the training dataset, with the remaining 20% serving as the test dataset to measure the accuracy of the model's predictions. The model was trained to the default XGBoost classification algorithm to predict whether a sow will farrow at the time of breeding. Features of the greatest importance to the model were parity, previous lactation length, previous gestation length, and previous number of liveborn piglets.

Assessment of the model for accuracy, precision, and recall followed model training. Accuracy is the percentage of predictions made correctly. Precision is the percentage of sows that farrowed of those that the model predicted to farrow. The recall is the percentage of sows that the model predicted to not farrow that actually failed to farrow. Accuracy of the overall model was greater than 90% for both farms, precluding the need for model tuning.

Following the initial model's completion, a 5-fold cross validation was performed. From each training set, the mean and standard deviation of the algorithm's weekly error were used to generate an X bar SPC chart to monitor the model error fluctuations over time. Weekly error represents the number of incorrect predictions discovered during that calendar week divided by total number of sows with predictions. The arithmetic mean of the weekly error is then calculated by calculated the average of a weeks within the study timeframe. Standard deviation was calculated in a similar fashion. The workflow of the machine learning process can be seen in Figure 1.



Figure 1. Workflow of the machine learning process

2.6 Error Rate Technique for Process Disruption

The cumulative error of the predictions for each day over the most recent twelve months of data were plotted on an X bar chart for each farm to monitor potential production disruptions. Cumulative error was defined as the number of sows that failed to maintain pregnancy that were expected to complete a successful pregnancy to term (farrow) for sows that had a service event in the prior 115 days divided by the total number of sows that had a service event in the prior 115 days.

The plotted cumulative error was evaluated with a standardized set of rules to signal aa production disruption in the farm. The rules utilized to determine a signal were as follows:

- anytime the weekly cumulative error stays above one standard deviation away from the mean for five or more weeks, a signal is triggered,
- 2. anytime the weekly cumulative error of the model remains two standard deviations above the mean for three or more weeks, a signal is activated,
- 3. anytime the cumulative weekly error of the model surpasses three standard deviations above the mean, a signal is triggered.

SPC chart creation employed the R statistical environment.[33]

2.7 Abortion Based EWMA Model

On the available data, a previously described exponentially weighted moving average (EWMA) techniques was implemented based on the reported abortions from each farm. This analysis served as the "gold standard" for comparison of the Machine Learning Error Rate Technique's ability to detect process disruptions. Chart parameters followed those described 13, with sigma equal to 3 and the smoothing parameter equivalent to 0.40. The baseline average for abortions for the SPC chart used 21 weeks of data before the final 18 months of data. EWMA SPC chart creation employed the R statistical environment.[33]

2.8 Comparison of Detection Methods

An extensive history of disease outbreaks, major process changes (e.g. changes in feed, health program additions or removals, or management practices), major construction events, and unforeseen natural disasters for both farms. The detected signals on each farm were compared to the farm's histories to determine if the timing of signals were correlated with known changes on the farm. Both farms rely on detection of clinical signs followed by confirmatory diagnostic testing to detect the presence of PRRSv. Both the machine learning based model and the EWMA model were then compared to the date that diagnostic samples were taken. The days until clinical observations were compared for the two systems.

3. RESULTS

When comparing this novel approach and the previously described EMWA SPC chart for abortions as a syndromic surveillance method, the mean detection time was 2.5 weeks later for the EMWA SPC method for abortions than the Weekly Cumulative Error SPC generated from the machine learning approach, Table 1. Although slower the EMWA SPC method detected the same number of disruptions as the Weekly Cumulative Error SPC.

Table 1. Comparison of EWMA SPC to cumulative errorSPC as weeks before clinical observation.

	EWMA SPC	Cumulative Error SPC
Farm 1	-2 weeks	1 week
Farm 2	1 week	3 weeks

3.1 Farm 1

Following data cleaning, processing, and feature engineering, the Farm 1 dataset contained 448 features and 151,451 instances, where each instance represented a service event. After five independent training runs of the algorithm, the maximum accuracy observed was 91.1%, and the minimum was 90.2%. The mean accuracy, precision of farrowing prediction, and recall of farrowing prediction, of all five trials was 90.4%, 90.2%, and 99%, respectively (Table 1). The mean weekly cumulative error of the model was 0.63%, with a mean-standard deviation of 0.58%.

Table 2. Performance metrics of machine learning modelon farm 1. F1 scores represent the harmonic mean of the
precision and recall for the row.

	Precision	Recall	F1
Farrow	90.2%	99.0%	94.6%
Failure	44.7%	51.3%	48.0%
Overall			94.0%

3.2 Farm 2

After data cleaning, processing, and feature engineering, the Farm 2 dataset contained 459 features and 151,541 instances. After the five unique training runs of the algorithm, the maximum accuracy observed was 92.7%, and the minimum was 92.1%. The mean accuracy, precision of farrowing prediction, and recall of farrowing prediction, of all five trials was 92.5%, 92.3%, and 99.1%, respectively (Table 2). The mean weekly cumulative error of the model was 0.48%, with a mean-standard deviation of 0.46%.

Table 3. Performance metrics of machine learning modelon farm 2. F1 scores represent the harmonic mean of the
precision and recall for the row.

	Precision	Recall	F1
Farrow	92.3%	99.1%	94.6%
Failure	66.3%	74.6%	70.5%
Overall			92.7%

3.3 Signal of Production Disruption

The Weekly Cumulative Error Xbar Chart for Farm 1 (Figure 2), with sigma equal to 0.58%, reveals one signal of production disruption in the 18-month timeframe. This signal occurred in week 13 of 2020. The farm's veterinarian detected Casual a novel PRRSv infection in week 14, 2020. observation of the Xbar chart revealed a continuous increase in model error starting in week 10, 2020. The Weekly Cumulative Error Xbar-R Chart for Farm 2 (Figure 3), with sigma equal 0.46%, revealed four production disruption signals over the 18-month timeframe. These signals of disruption occur in weeks 9-2019, 23-2019, 43-2019, and 16-2020-three of the four signals correlated to events in the farm history. Extensive on-farm maintenance (equipment repairs requiring the abnormal movement of sows between individual pens) potentially explain the signal during week 23-2019. The farm performed multiple vaccinations for IAV and PRRSv, potentially explaining the unexpected pregnancy failures in week 43-2019. Finally, the signal in week 16-2020 occurs three weeks before detecting a novel PRRSv infection on the farm.



Figure 2. Weekly cumulative error of farm 1, as compared to 1, 2, and 3 sigmas from the mean error of the predictive model. Signal is highlighted by the yellow arrow. The solid red vertical line highlights the clinical observation of PRRSv.



Figure 3. Weekly cumulative error of farm 2, as compared to 1, 2, and 3 sigmas from the mean error of the predictive model. Signal is highlighted by the yellow arrow. The solid red vertical line highlights the clinical observation of PRRSv.

3.4 SPC Chart of Abortions

The EWMA SPC chart of the farm's abortions, as previously described, was used to identify potential disruptions. Farm 1 had three signals (Figure 4). The first in week 5-2019 may correlate with the beginning of the change in electronic gestating sow feeding systems. The second signal in week 24-2019 does not correlate with any known events. The final signal during week 16 of 2020 occurs two weeks after PRRSv detection.

The EWMA chart for Farm 2 identifies two signals (Figure 5) during week 43-2020, which correlates with multiple mass vaccinations of the herd in weeks 40-2019 and 42-2019, and in week 18-2020, one week before the detection of a novel PRRSv.



Figure 4. EWMA of number of weekly abortions occurring in farm 1. Red dots represent an EWMA outside of the control limit and the solid red line represents the week of PRRSy observation





4. DISCUSSION

Historically, producers and veterinarians have relied on clinical observation by farm staff to identify disease in a farm. More recently, they have used more advanced approaches such as Statistical process control (SPC) to detect disease-related disruptions within a production system. While both methods can accurately detect disease within a population, their reliance on biological and clinical parameters with a high degree of intrinsic variation limits their effectiveness in signal detection. Further limiting SPC's value are the subtle clinical effects of endemic diseases such as PRRSv and Influenza, in the face of high intrinsic variation in production outcomes present in commercial production.

While SPC can be a useful tool for monitoring health and production in livestock systems, limitations of its use exist. SPC was initially developed to detect disruptions within tightly regulated processes; however, its capacity to recognize disturbances in systems with high intrinsic variability, i.e., biological systems like animal agriculture especially in the area of reproduction, is limited.[11] Furthermore, the use of SPC in livestock systems has been applied to several commonly measured production outcomes such as the percentage of pregnant animals that successful give birth or the number of abortions in a fixed population of pregnant animals. Changes in these outcomes are often multifactorial and include not only infectious diseases, but also nutrition, animal care, and environmental conditions. In addition, changes in production outcomes are not specific to a single infectious disease as most diseases have overlapping patterns of change or clinical signs. Furthermore, in herds endemically infected with one or more pathogens, the clinical diseases present cause changes to measured production outcomes continuously but with varying degrees of severity. Since the production parameters vary as a direct result of clinical disease prevalence, the sensitivity of SPC to detect disease within the population diminishes.[11] This means that in populations endemically infected with one or more pathogens, subtle changes in production outcomes that occur shortly after a novel pathogen introduction may go undetected because the resulting impact is less than the variation in production outcomes already occurring from the preexisting, endemic pathogens, since SPC relies on historical information to monitor a process for disruptions.[11]

Applications of advanced data analytics, particularly machine learning, can facilitate the processing of large complex datasets to identify complex relationships quickly and accurately within a system. In this application, machine learning overcame the problems that a highly variable system creates for identifying production disruptions, such as those caused by novel pathogen entry. Development, training, and validation demonstrated that the trained machine learning algorithm could predict correctly 92.7% of the time if an individual sow will farrow at the time of breeding. Changes in the algorithm's accuracy facilitated monitoring sow populations for unexplained reproductive failure throughout gestation in herds with a known health and management history.

Overall, the Weekly Cumulative Error SPC performed well. While the accuracy of on farm detection is unknown, we believe both farms represent a typical trained farm staff within the US, this in combination with routine diagnostic surveillance ensure the identification of disease. In herds that experience fewer recent disruptions, the advantage in detection time compared to clinical signs observation may be more significant. The difference in model detection timing compared to clinical conformation between the two farms is most likely due to the farm's inherent variability before the outbreak's onset. Farm 1's event history is such that the target variable, service outcome, is more variable in nature, as events have impacted farrowing rates previously. Farm 1 was going through the remodeling of the gestation feeding system, resulting in error substantially larger than the historical mean during this period decreasing the sensitivity of the Weekly Cumulative Error SPC. Because of this increased variability, prediction of such a variable is made harder, resulting in a lower overall performance of the model. The effects of remodeling on top of the increased inherent variation in the production data from Farm 1, resulted in the farrowing prediction model only obtaining a mean accuracy of 90.4%

The results suggest the EMWA SPC for abortions is slower to detect disease outbreaks than the Weekly Cumulative Error SPC tool. While the EMWA SPC for abortions method may be a more specific tool in identifying abortion-inducing events, the Weekly Cumulative Error SPC tool has a faster detection time. However, the Weekly Cumulative Error SPC tool failed to identify an IAV introduction in one farm over this period.

Even with the Weekly Cumulative Error SPC tool performing well in this study further validation is needed, both on a larger number of farms and for a wider number of ailments, whether pathogen or management induced. This paper is meant to describe the potential use of a machine learning technique to drive diagnostic testing decision on farms, while larger studies are needed to calculate meaningful sensitivity and specificity of disease processes on farm. The presence of IAV on both farms prior to PRRSv could also potentially reduce vigilance of farm staff in clinical detection, again reinforcing the need of further validation. In addition, the use of a such a tool requires real-time access to farm data to ensure that a disruption is identified as early as possible. The number of farms currently able to enter farm data in real-time is limited, as many still use paper records on farm that get uploaded to an electronic form at a future date. This lag between paper and the electronic records system may negate the benefit noted on some farms. While currently a major limitation, such technologies the prove beneficial may entice farms to adopt faster alternative methods of data collection.

While Weekly Cumulative Error SPC tool comes with limitations, it holds the ability to quickly identify productionrelated disturbances within farms holds tremendous promise. Although there are many potential causes for a signal, the Weekly Cumulative Error SPC may serve as a sensitive method to detect numerous production disruptions, including disease. While specificity is poor for a singular disease, due to the vague clinical signs monitored, reproductive failure, the ability to accurately conduct syndromic surveillance on farms is a step rate change in the ability to mitigate the impact of disease in a herd, system, region, and country. This method has the potential to detect clinical disruptions that may impact conception or gestation of a litter on a farm, including but not limited to diseases that cause anorexia or pyrexia. The Weekly Cumulative Error SPC does not replace the skills and knowledge of a veterinarian, producer, or confirmatory diagnostic testing but serves alongside them to enhance their abilities and focus their efforts.

While other methods currently exist to make predictions about the occurrence of PRRSv or PEDv on swine farms, [34]-[36] this is the first described using existing production data routinely collected on sow farms. While other methods are able to detect disease accurately within a farm, the application of the Weekly Cumulative Error SPC may allow for easier adoption as it only relies on a singular farm's data, and not the neighborhood characteristics. While there are advantages and disadvantage of each method, the ability that machine learning shows when predicting disease from differing data types is impressive and shows the potential for such a technology within the industry. As the swine industry continues to collect more and more data, the combination of the many datasets used within each method may lead to a superior model as both individual farm performance and the regional risk profile are accounted for.

This project achieved its objective to develop a novel, datadriven approach to production record analytics that utilizes machine learning techniques to improve clinical disruption detection times shortening the time to diagnostic confirmation within a sow farm. While limited in scale, we believe that Weekly Cumulative Error SPC serves as a foundation for detecting changes in swine health/production at the farm, system, and industry level in the presence of normal production variation. With the ability to accurately predict an individual sow's breeding service outcome, unexpected variation (more than the model's expected error) serves as a quick and accurate process disruption signal which may help guide diagnostic surveillance on farm.

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