

# Forecasting early-lactation diseases in Holstein dairy cows using milk spectra and machine learning

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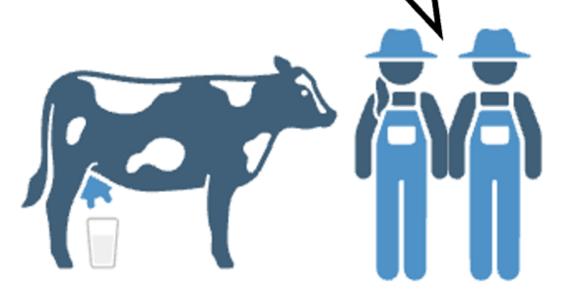




**Abstract #: 2621** 

#### Introduction

Can we use raw milk spectra and algorithms to monitor health of earlylactation cows?



- Dairy cows commonly experience health disorders in the early lactation period.
- Blood sampling and analysis is costly for farmers and invasive for cows. Thus, it's necessary to develop new methods.
- Milk sampling and analysis is cost-effective but its potential in non-invasive, forecasting early-lactation diseases has yet to be fully explored.

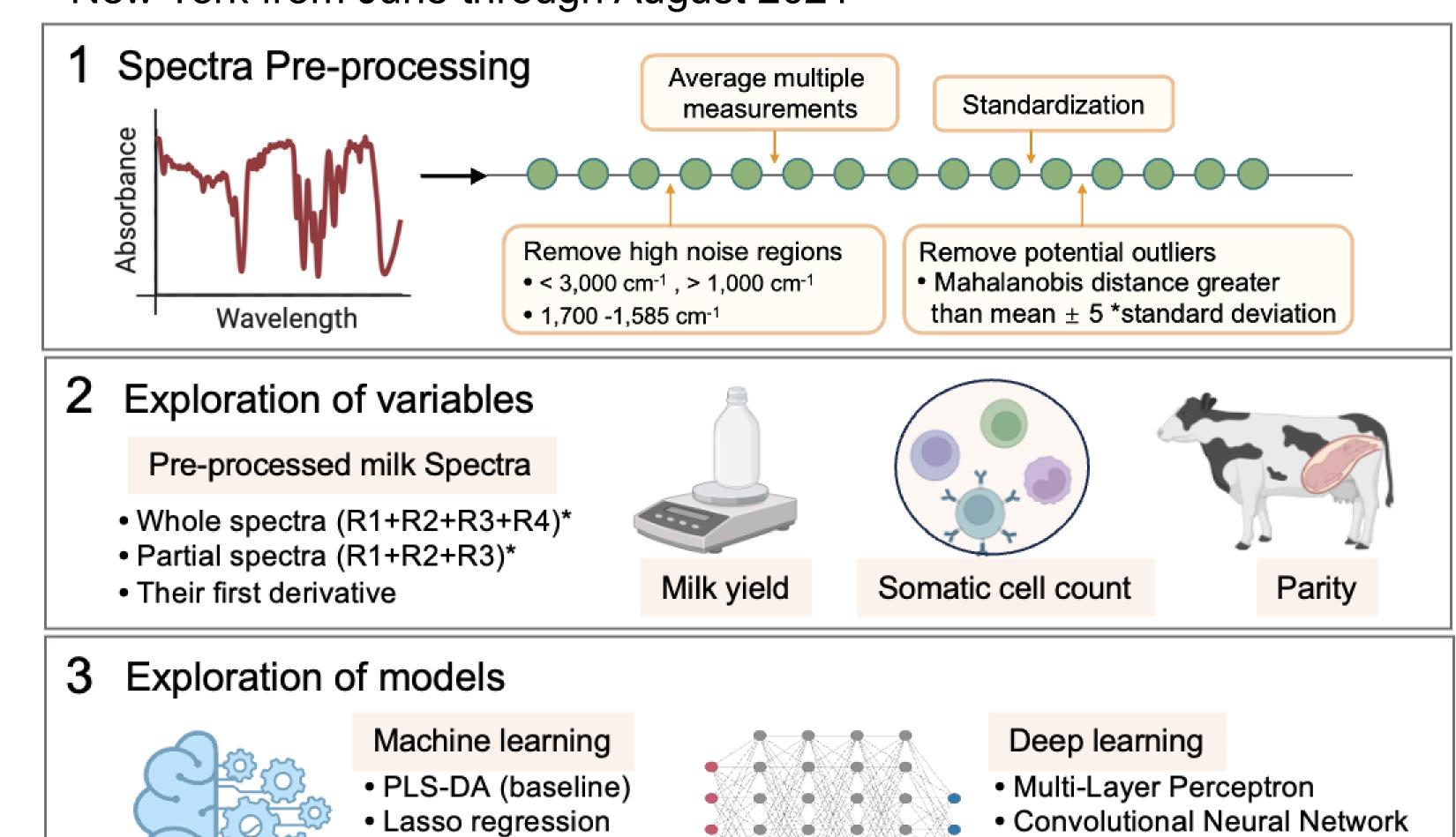
# Objectives

To fully explore the potential of milk FTIR spectra to forecast early-lactation disease in dairy cows, we set up two specific objectives:

- To evaluate whether milk spectra become more abnormal and more beneficial for prediction as disease diagnosis nears;
- To explore the performances of various machine learning and deep learning methods with some cow-level variables in forecasting disease diagnosis (metritis, displaced abomasum, ketosis, and mastitis) within the first 30 DIM.

### Materials & Methods

■ Dataset: 1,144 cows and 6,113 milk samples on 1 commercial herd in New York from June through August 2021



## Conclusions & Implications

 Progressive changes in spectral regions related to the absorbance of fat, protein, and lactose are correlated with disease progression.



- Progressive changes in specific spectral regions enhanced predictive accuracy with disease progression.
- Predictive performance peaked in all models at 1 d prior to disease diagnosis.
- Including milk yield, somatic cell count, and parity into the milk FTIR spectra-based models improved the predictive accuracy.
- Machine and deep learning models outperformed the baseline PLS-DA.

This study highlights the effectiveness of integrating raw milk FTIR spectra with cow-level variables to forecast health conditions in early-lactation Holstein dairy cows via machine and deep learning models.

#### Results

Elastic Net

Random forest

**Figure 1.** Descriptive statistics for (n=825) and disease group (n=289).

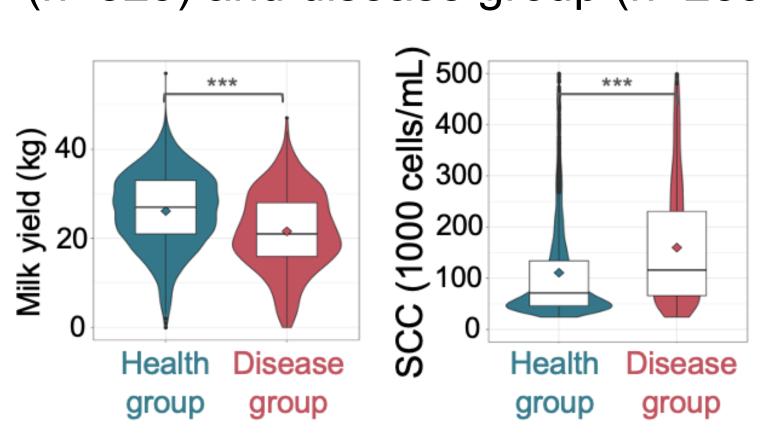


Figure 2. Absolute difference (mean ± SD) in the pre-processed milk FTIR cow-level variables in health group spectra (wavenumber ranging between 3,000-1,000 cm<sup>-1</sup>, mean ± SD) and four subregions (R1, R2, R3, R4) between health group and disease group.

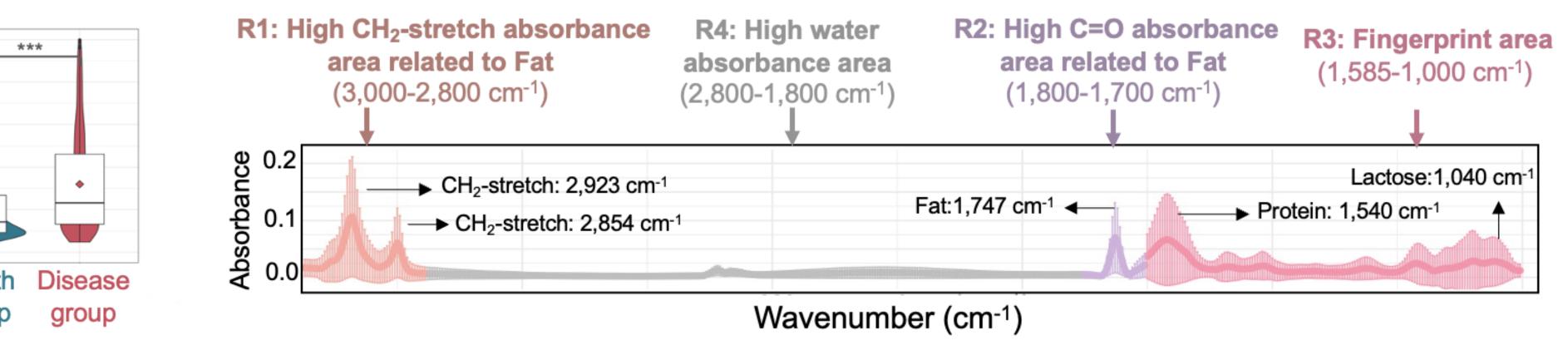


Figure 3. Comparison of predictive accuracy between models using different variables on different times prior to disease diagnosis (>14 d, 14 - 11 d, 10 - 8 d, 7 - 6 d, 5 - 4 d, 3 d, 2 d, and 1 d), based on cross-validation.

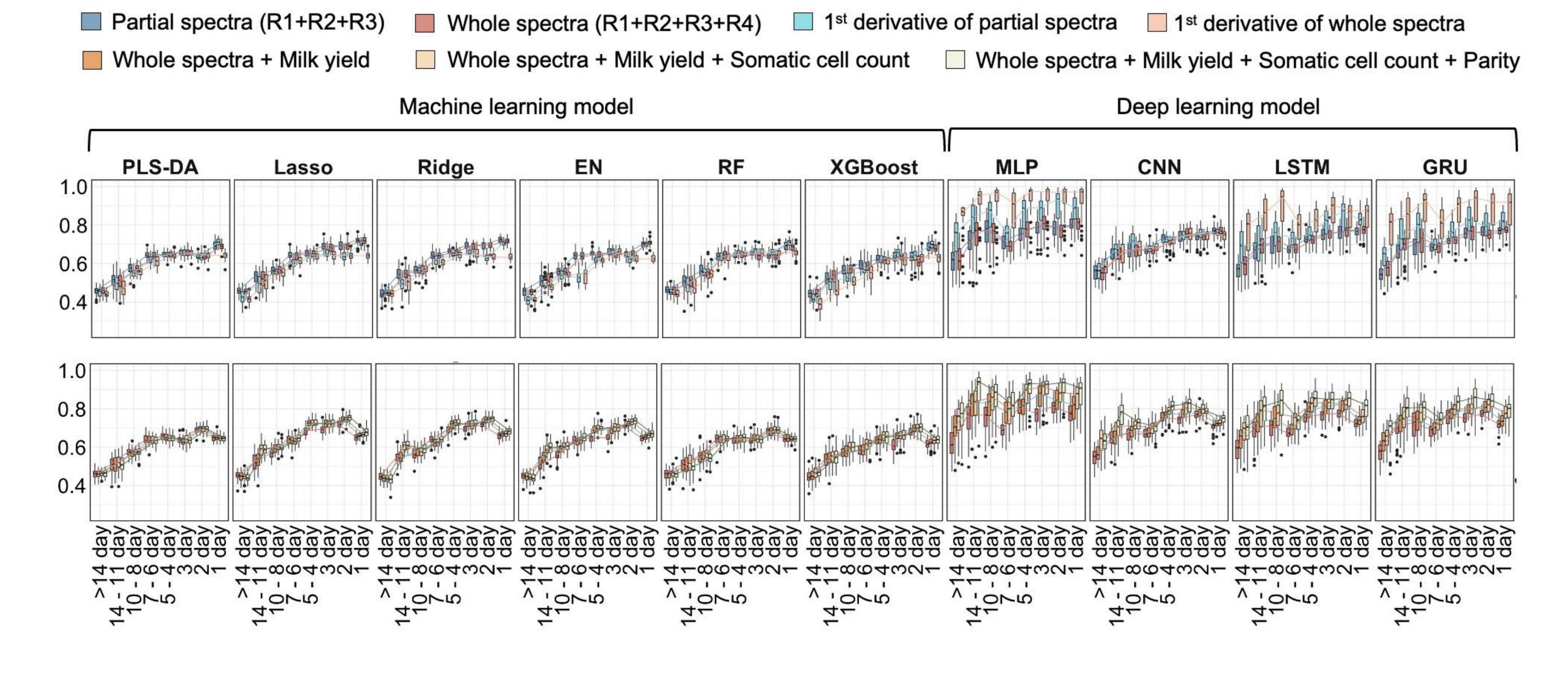


Figure 4. Predictive performance compared to PLS-DA of models using whole spectra, milk yield, SCC, parity as the predictors on different times prior to disease diagnosis (>14 d, 14 – 11 d, 10 – 8 d, 7 – 6 d, 5 – 4 d, 3 d, 2 d, and 1 d), based on cross-validation.

Long Short-Term Memory

Gate Recurrent Unit

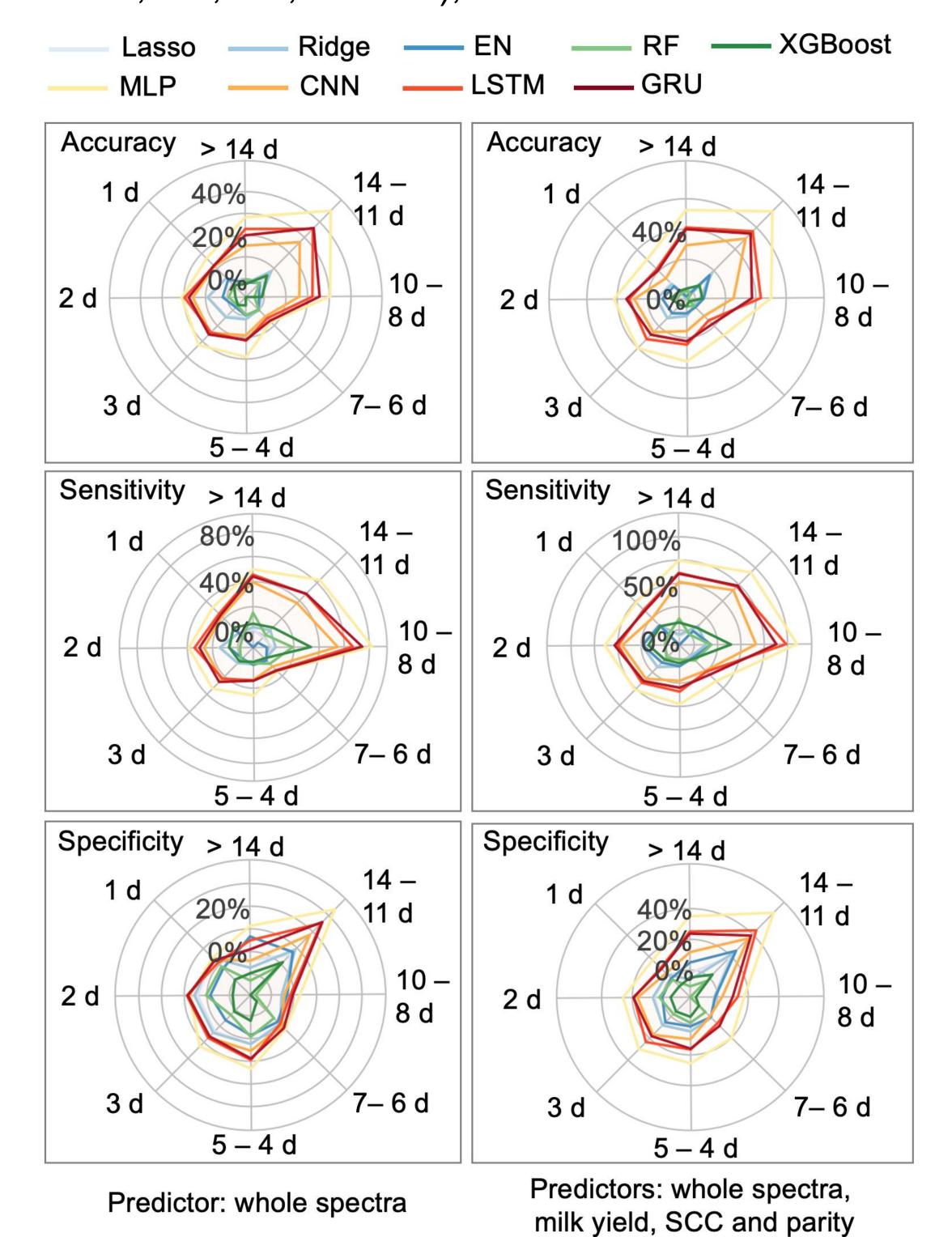


Figure 5. Visualization of four representative cows. As the disease diagnosis day neared, there was a steady escalation in the models' predictive probability for a subsequent disease, reaching its peak on 1 d prior to

