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Phenomic Prediction - Optimization of NIRS preprocessing

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In recent years, phenomic prediction has emerged as a new method in the plant breeding community. The method can be compared to genomic prediction, except that instead of marker data, NIR spectra are used to predict various traits. Phenomic prediction has been shown to have great potential. However, there are still many open questions regarding its practical application. For example, in the field of spectroscopy, it is standard practice to optimize the preprocessing of spectra, which so far has only been done to a limited extent for phenomic prediction. We therefore used three different data sets of breeding programs of soybean, triticale and maize to identify the best combinations of Savitzky-Golay filter parameters for preprocessing near-infrared spectra for phenomic prediction. We tested 677 combinations of polynomial order, derivative and window size and evaluated them with fivefold cross-validation.

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