Master thesis: Phenomic Selection with Sugar Beet NIRS data

This thesis will be a joint project between the University Hohenheim and Strube Research.

Within the last very recent years, the plant breeding toolbox has been enhanced with a new approach: phenomic selection. The basic principle is similar to genomic selection, but here spectral data replace the genotyping. Near-Infrared Spectroscopy (NIRS) has been routinely used in agriculture since more than 60 years. However, the huge potential of this new approach is to use electromagnetic wavelengths as an alternative to molecular markers to build relationship matrices and predictive models. Under certain conditions, phenomic selection has been shown to be as accurate as genomic selection or to outperform it in the prediction of certain traits. Furthermore, since NIRS data can capture plot-to-plot and environment-to-environment variation, it seems to perform well for modelling genotype-environment effects, opening new perspectives of application. Additionally, phenomic selection brings the enormous advantage to be very low cost while high throughput in the production of data.

The aim of this master thesis is to develop a predictive model for two phenotypic traits essential in sugar beet breeding, namely root yield and sugar content. During every harvest campaign from Strube Research, NIR spectral data are collected from each sugar beet plot. For each of the traits mentioned, NIR data of test hybrids from two given consecutive years will be used to develop a predictive model. This model will be applied to newly combined hybrids tested in a third year. This third-year hybrids will contain at least one of the inbred lines of the hybrids tested in years 1 and 2. The phenotypic dataset will therefore encompass a rich collection of genotypes and environments and will be provided by Strube Research. The main focus will be on predicting the genotypic value of tested hybrids. In addition, this thesis will explore the additional opportunity that NIRS data offer in modelling and predicting other effects, most importantly genotype-environment interaction.

References
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