

# Unified Big Data in Genomics and Phenomics for Plant Breeding

**Project Lead:** Jared Crain, Kansas State University, USA

## Approach

Pairing phenomic data with genomic data has the potential to revolutionize plant breeding. The optimal integration of these two fields have not been fully explored, and one overlooked area has been in field-based single plant phenotyping within early generations. High-throughput evaluation of single plants that enables breeders to select as well as advance populations during early generations, could increase the rate of genetic gain and resource efficiency within plant breeding. This project will focus on advancing the field of high-throughput phenotyping to the scale of single plants using unmanned aerial vehicles (UAVs) equipped with high-resolution sensors. Using digital imagery throughout the growing season, data from single plants (wheat) will be collected and evaluated. Methods to evaluate single plants from digital imagery will be developed in open-source pipelines and repositories allowing for real-time data sharing and evaluation. The initial population evaluated will be an association mapping panel of publically available lines, creating an artificial segregating population to refine single plant analysis methods. Along with evaluating the association mapping panel, segregating lines from a breeding program will also be assessed. A key component of this research will be open source nature of the project and the expected deliverables of documented research guides for researchers to use within their own programs. The methods developed will also be relevant for researchers that are screening populations looking for key phenotype changes that may come from populations, such as mutation breeding, double haploid, or genetic engineering, where there is insufficient seed to evaluate full size test plots.