**Title:** Plant phenotyping with limited annotation: Doing more with less

**Abstract**

Extracting diverse phenotypes from many plants can be a game-changer in understanding and adapting crops for climate change. Recent advances in computation and sensor technology have enabled the cheap collection of plant phenotype data. This continuous increase in data collection has made it possible to apply deep learning algorithms successfully in various challenging plant phenotyping tasks in laboratory and field conditions. In this thesis's first part, we develop deep learning models for disease identification in soybeans using RGB and hyperspectral data. One major challenge to training these DL models successfully for disease predictions was the requirement of copious amounts of annotated data. Because creating these large-scale annotated datasets for plant phenotyping problems generally requires non-trivial efforts, time, and resources. This annotation efficiency limitation has become a major bottleneck in deploying DL tools for plant science problems. In the second part of this thesis, we will present a variety of ways in which one can circumvent the need for large amounts of annotated datasets for training these DL models. We adopt, analyze and deploy various concepts in transfer learning, active learning, self-supervised learning, and domain adaption literature for annotation efficient plant phenotyping tasks in soybeans and maize. We show that utilizing these label-efficient approaches can lower the barrier to deploying DL tools for plant science applications.