Public Abstract
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Plant root phenotyping is a key component in plant breeding and selection for desireable root properties. Preferable root traits can not only help a plant to grow faster but also allow for more dense and deep root system architectures (RSA) that aid in making the plant resistant to drought conditions. In this thesis, an efficient high-throughput plant root phenotyping system that can take the images of RSA from various angles using multiple cameras is presented. This system needs to be a high-throughput system such that is can be used to phenotype up to hundreds or thousands of plant roots quickly.

In this research, a novel multi-camera root imaging system and a phenotyping procedure, which can extract traits that correlate better than a single- camera root imaging system, is introduced. The system consists of a set of six cameras that take images of a plant root from six different directions. A segmentation procedure using the Expectation-Maximization (EM) algorithm is developed and employed to iteratively distinguish plant root pixels from background pixels. It is also shown that this proposed method provides a better segmentation results of plant root images when compared to the thresholding methods used in previously published research. Another novel contribution in this thesis is the automated extraction of root traits from the imagery collected. It is shown that these automated traits correlate to manually measured traits that have been previously shown to have strong relationships with genes associated with RSA. Results also show that merging of the autonomously extracted traits from multiple cameras provide higher correlation with the manual traits as opposed to traits measured from only one camera. The data for the plant roots are collected over a period of 3 years, each year improving the imaging system and the underlying software used to control the system. Further, it is shown that the traits are extracted with a much faster implementation using the multi-camera imaging system when compared to a previous plant root phenotyping platform.