

Soybean Root Phenomics

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Introduction

Since the beginning of domesticated agriculture, plants have been selected based on phenotypic characteristics visually observed above ground. Often roots and soil root interactions are less commonly studied and observed. Some breeders now are starting to investigate beyond the generally known knowledge of root system architecture (RSA). Legume crops present a unique, often hidden relationship, underground. Historically, researchers and farmers rarely quantify the number of nodules present on a soybean root. Nodules are the structural component of a soybean root where *Bradyrhizobium japonicum* lives in a symbiotic relationship with a legume to fix nitrogen for the plant. For breeders to more effectively quantify and study this beneficial relationship, a new tool has been developed called SNAP—Soybean Nodule Acquisition Program—which uses computer vision and machine learning to identify and quantify the nodules in a 2D soybean root image.

Materials and Methods

In order to develop SNAP, two field trial locations were established at the ISU Horticulture Research Station, Ames, Iowa, and the ISU Muscatine Island Research Farm,

Fruitland, Iowa. These locations were selected for their sandy soil profiles to enable easier mechanical root extraction. Six genotypes were replicated 10 times at seven unique time points at each location throughout the growing season related to the growth and development stages of soybeans. Roots were manually extracted, cleaned, and imaged. A sample of the nodules were identified and labeled in the images. These labeled images were randomly patched into 128 x 128 images and input into a Faster-RCNN neural network. The convolutional neural layers enable the development of a classifier, which can be used to identify nodules in images the computer has not seen before.

Results and Discussion

Currently, SNAP successfully enables researchers to quantify the nodules on a soybean root from the V1-V6 stages of growth and development. Work is continuing to enable nodule quantification in the R1-R8 development stages. Through the use of SNAP, breeders and producers will be able to quantify nodulation to empower stronger breeding decisions and crop input choices. Further, when combined with RSA tools, such as ARIA (Automated Root Image Analysis), SNAP will enable researchers to further study the locations and interactions of nodules across the root mass.

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Figure 1. Nodules classified by SNAP.

In this figure, bounding boxes and their respective class scores show the confidence of the box containing a nodule on soybean roots.

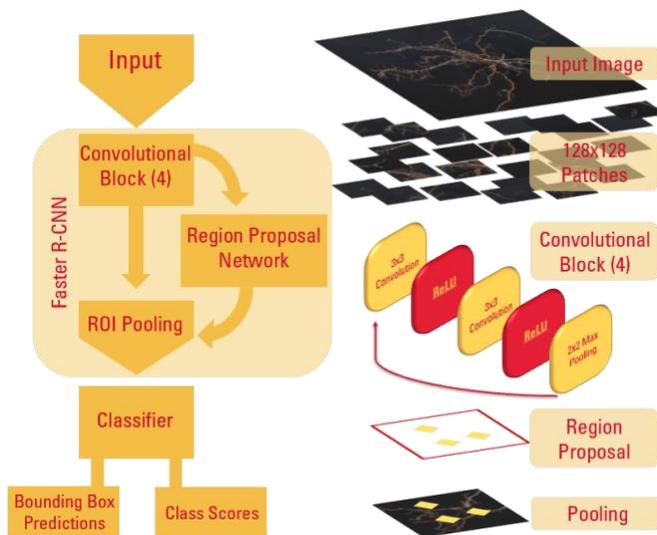


Figure 2. Process of building the SNAP classifier.

This figure shows the steps used after labeling the nodules in an input image to build the SNAP classifier for future images. First the input image is cropped into random patches, then processed in a Faster R-CNN generating region proposal. These regions then are pooled together to develop the classifier with bounding box predictions and class scores.