

## Identifying trichomes on digital images of soy leaves

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**Motivation and aim:** Trichomes are extensions of the aforementioned epidermal cells in plants. Soybean leaf trichome plays an important biological role in resisting pests and adapting to the environment and exhibits a wide range of phenotypic variation. Currently, the typical method used to collect trichome data is qualitative visual counting using lenses, which is labor- and time-intensive, another method is the use of scanning electron microscope (SEM), which is costly, time-consuming and not conducive to high-throughput analysis. As more and more plant and trait parameters need to be measured quickly and accurately, various types of computer vision algorithms, immaterialage processing and machine learning classification methods are increasingly used in plant phenomics data analysis. In this work, we suggest method for an automated identification of trichomes on the surface of soybean leaves through machine vision segmentation algorithms and semantic segmentation based on neural network.

**Materials and methods:** The soybean trichome microscopic images, totaling over 500, were obtained from Sirius in Sochi. Among them, 146 images with manually annotated pixel-level masks were selected and divided into training (87 images), validation (29 images), and test (30 images) sets in a 60:20:20 ratio. To increase sample size and match the neural network's input requirements, all images and masks were sliced into non-overlapping patches of 128×128 pixels. These image patches served as inputs for training and evaluation in the subsequent model development stage. A U-Net convolutional neural network was constructed using the TensorFlow framework. The model accepts 128×128×3 RGB image patches and outputs 128×128×4 probability maps representing four pixel classes. During training, accuracy and loss were recorded for each epoch on both the training and validation sets. After optimization, the best-performing model was used to predict trichomes on full-sized images by segmenting them into patches, performing inference, and stitching predictions back together. In post-processing, only trichome pixels were retained, and a Gaussian filter was applied to smooth the binary output. Finally, trichome regions were detected and counted using the findContours function in OpenCV, enabling automated quantification and visualization.

**Results:** The U-Net model demonstrated high performance in the semantic segmentation of soybean trichome images. During training, the average accuracy reached 98.28% on the training set and 98.31% on the validation set, with both average loss values below 0.06. These results indicate that the model effectively learned to distinguish trichome structures from the background. The predicted masks retained accurate pixel-level details, and the post-processing pipeline successfully identified and counted individual trichomes across images, confirming the robustness and generalization ability of the proposed method.

**Conclusions:** By analyzing the number, length and other characteristic of trichomes, we will explore the association between these microstructures and the function and growth status of soybean leaves, and further reveal the important role of trichomes in plant adaptation and growth and development. By combining machine vision counting and plant phenomics research, we expect to provide important data support for geneticists to study soybean growth and development.

**Funding:** The study is supported by the Kurchatov Genome Center of the Institute of Cytology and Genetics of Siberian Branch of the Russian Academy of Sciences, in agreement with the Ministry of Science and Higher Education of the Russian Federation, No. 075-15-2019-1662.