

Prompt Engineering on a Foundation Model to Segment Symptomatic *Arabidopsis Thaliana*

Anonymous ECCV 2024 Submission

Paper ID #18

1 Introduction

The pathosystem *Arabidopsis thaliana*/*Pseudomonas syringae* pathovar tomato DC3000 is commonly used as a model for plant-pathogen interaction [10]. The disease symptoms consist of stains of varied colors [5]. The advent of high-throughput phenotyping platforms allows for the simultaneous study of many plants in different conditions. However, segmentation of symptomatic plants remains difficult because brown symptoms may appear similar to the soil, and moss and algae have the same color as the plant [3]. Most articles related to *A. Thaliana*'s segmentation have used the standard CVPPP dataset containing healthy plants [2, 8]. At the moment the state-of-the-art is LS-Net [3]. Articles addressing symptomatic plants train new neural networks and are either destructive [7, 9] or need covers to help with segmentation [4]. This work aims to address the segmentation of symptomatic *A. thaliana* plants on natural soil without training a deep learning model and using the least possible amount of annotated images. To this end, we leverage on the Segment Anything Model (SAM) [6]. With SAM, pixels can be used as prompts by setting them as foreground or background. We propose a method to set these prompts automatically, using the lowest amount of annotated images possible.

2 Materials and Methods

The plants used in the experiment were grown in a high-throughput growth chamber with image acquisition from the top view. The created dataset contained 354 images, 59 containing healthy plants and 295 symptomatic plants. The dataset was divided into a training set (206 images), and, a test set (89 images).

In this method, we split the image's pixels into 3 classes: plant, background, and, unknown, using histograms, fig. 1b. We computed accumulated histograms for all training images for all channels in 4 color spaces: RGB, HSV, YIQ, and, LAB. We built separate histograms for healthy and infected photos. We then set 2 thresholds, the first one was set at 0.95 quantiles of the healthy plant's histogram, and all pixels under this value were assigned to the plant class. The second threshold was set at quantiles 0.995 of the infected plant's histogram, all pixels over this value were assigned to the background class. Pixels located between the 2 thresholds were assigned to the unknown class. These quantile

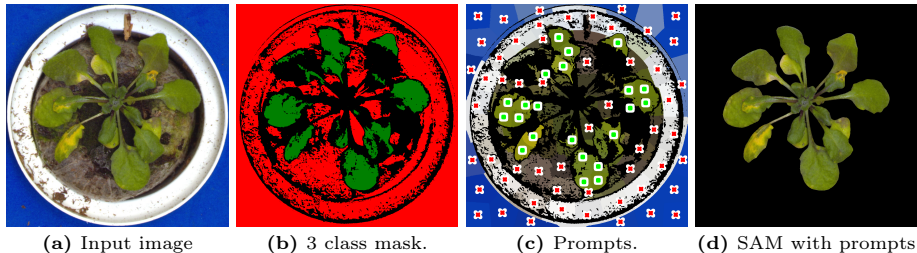


Fig. 1: Segmentation pipeline steps.

values were set so that the least amount of plant and background pixels would be swapped when assigning classes. The next step was creating separate thresholded images containing plant and background pixels, unknown pixels were discarded at this stage. Then, superpixels were created using the SLIC method [1] on each thresholded image, 200 for the plant image and 100 for the background image. With these quantities, plant superpixels could capture smaller leaves and background superpixels were kept to a reasonable amount. Superpixels not matching the target class were discarded. Each superpixel’s center was then used as a prompt, fig. 1c, to segment the input image with SAM, fig. 1d.

To assess the minimum number of images needed for good performance we performed the threshold search with the full training dataset using cross-validation and with subsets of the dataset containing 2, 10, and, 30 images using a validation dataset with the size of a cross-validation fold. Each experiment was performed 5 times.

3 Results and Discussion

When searching the thresholds with the full dataset the average cross-validation Dice was 0.9972 with an average standard deviation of 0.0001. When only using 2 samples, the average Dice was 0.9972 with a standard deviation of 0.0005. This shows that 2 annotated images are enough to calculate the thresholds. We also applied our method to the CVPPP dataset and, compared the results to the state-of-the-art [3], we obtained a Dice of 0.9841 on the test dataset compared to 0.9651, but, with a lower IoU score, 0.8771 versus 0.9339, due to segmentation errors in dataset A3.

4 Conclusion and Perspectives

In this work, we have presented a method to obtain good segmentation results with only 2 annotated images without training a new segmentation deep learning model. This nondestructive method will allow scientists to track the plant pathogen interaction over time. It would now be interesting to apply this method to other pathosystems and improve the results on the CVPPP dataset.

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