

# Semi-Automated Feature Extraction from RGB Images for Sorghum Panicle Architecture

## RFR-A18103

Seyed Vahid Mirnezami, grad student  
Baskar Ganapathysubramanian,  
associate professor  
Department of Mechanical Engineering  
Yan Zhou, Aaron Kusmec, and  
Qi Fu, grad students  
Srikant Srinivasan and Lakshmi Attigala,  
scientists  
Maria Salas-Fernandez, associate professor  
Patrick Schnable, distinguished professor  
Department of Agronomy

## Introduction

Because structural variation in the inflorescence architecture of cereal crops can influence yield, it is of interest to identify a means to better evaluate inflorescence architecture across genotypes and thereby facilitate breeding efforts. Manual collection of inflorescence phenotypes can be time consuming and can be technically challenging for some traits. For these reasons, a semi-automated phenotyping pipeline, TIM (Toolkit for Inflorescence Measurement), was developed and used to extract trait data from sorghum panicles.

## Materials and Methods

A total of 1,064 mature sorghum panicles from 272 genotypes were collected from two Iowa State University field sites—the Kelly Farm and the Burkey Farm. Panicles were mounted upright near a reference scale and imaged with a high-resolution camera in a light box. First taken was a front view, then the panicle was rotated 90 degrees to image a side view (Figure 1).

A pipeline was developed, TIM (available at the Schnable Lab's GitHub

<https://github.com/schnablelab>), to semi-automatically extract traits from panicle images. The trait extraction via TIM involved the following steps: 1) segmentation of the panicle and the reference scale from the background using a custom-built MATLAB application, 2) measurement of traits on the segmented panicle, and 3) conversion of trait values from pixels to metric measurements using a reference scale. Trait measurement was performed in a fully automated manner using standard image-processing algorithms.

Eight panicle traits were extracted from front and side plane images of the 1,064 panicles: length, width (2 views), area (2 views), volume, and solidity (2 views) i.e. loosely or tightly packed panicle.

## Results and Discussion

To evaluate the accuracy of the semi-automated image-processing method, the team manually measured the length and width of single panicles from 17 genotypes randomly selected from the set. The resulting trait values were compared with the corresponding values automatically extracted from images of the same panicles. The coefficient of determination ( $r^2$ ) between the values of the auto-extracted length and width versus ground truth were 0.93 and 0.89, respectively (Figure 2), indicating the pipeline can accurately extract panicle length and width.

## Acknowledgements

Thanks to Lisa Coffey (Schnable Lab) and Nicole Lindsey (Salas-Fernandez Lab) for field design and coordination; graduate student Zihao Zheng (Schnable Lab) for panicle harvest; and undergraduates (Schnable Lab) Stephanie Shuler, Jodie Johnson, and Katherine Lenson for collecting image data.

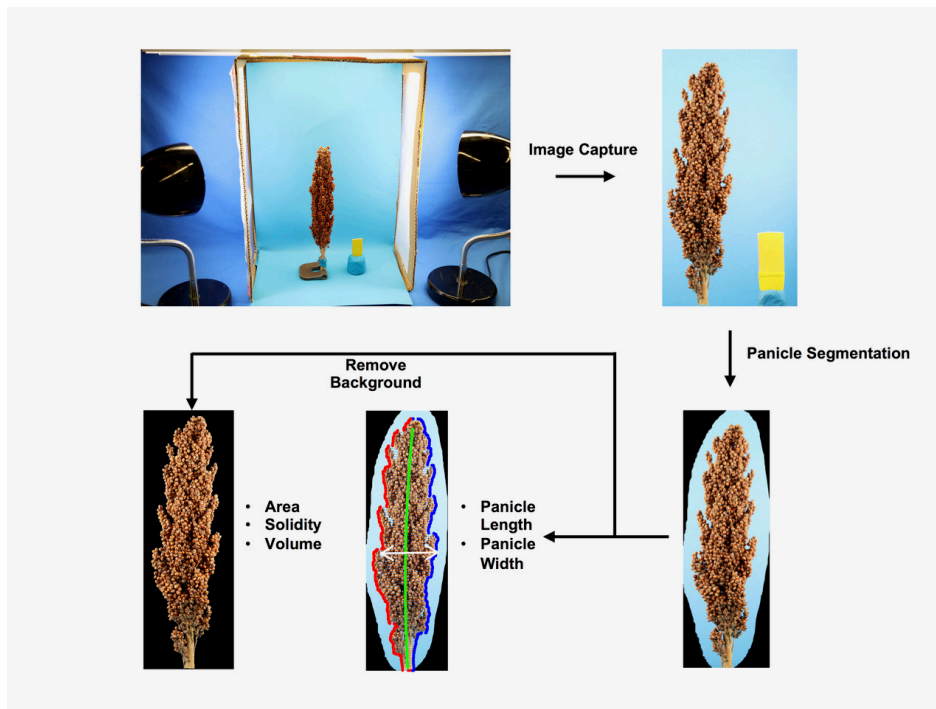


Figure 1. Phenotyping pipeline used to extract traits from 1,064 panicles of 272 genotypes. Each panicle was photographed from both the front and side planes. Segmentation was conducted manually for subsequent automatic trait extraction.

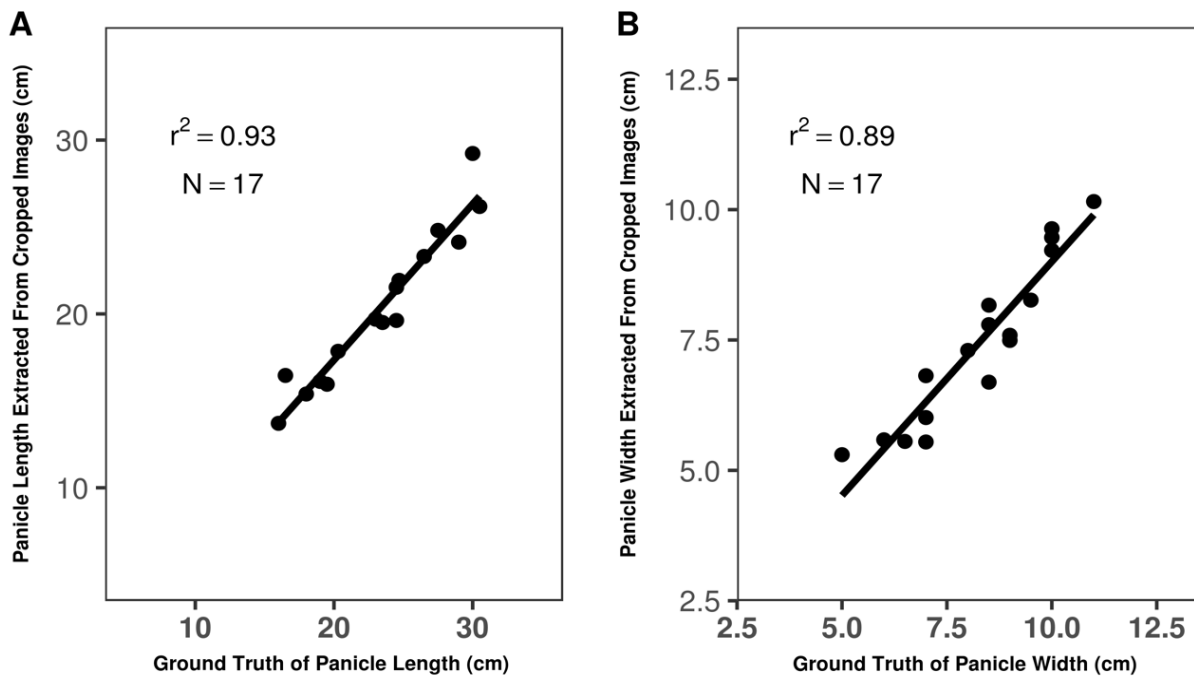


Figure 2. Comparison of ground-truth measurements and trait values extracted from images of 17 randomly chosen panicles. A, Panicle length. B, Panicle width of front plane.