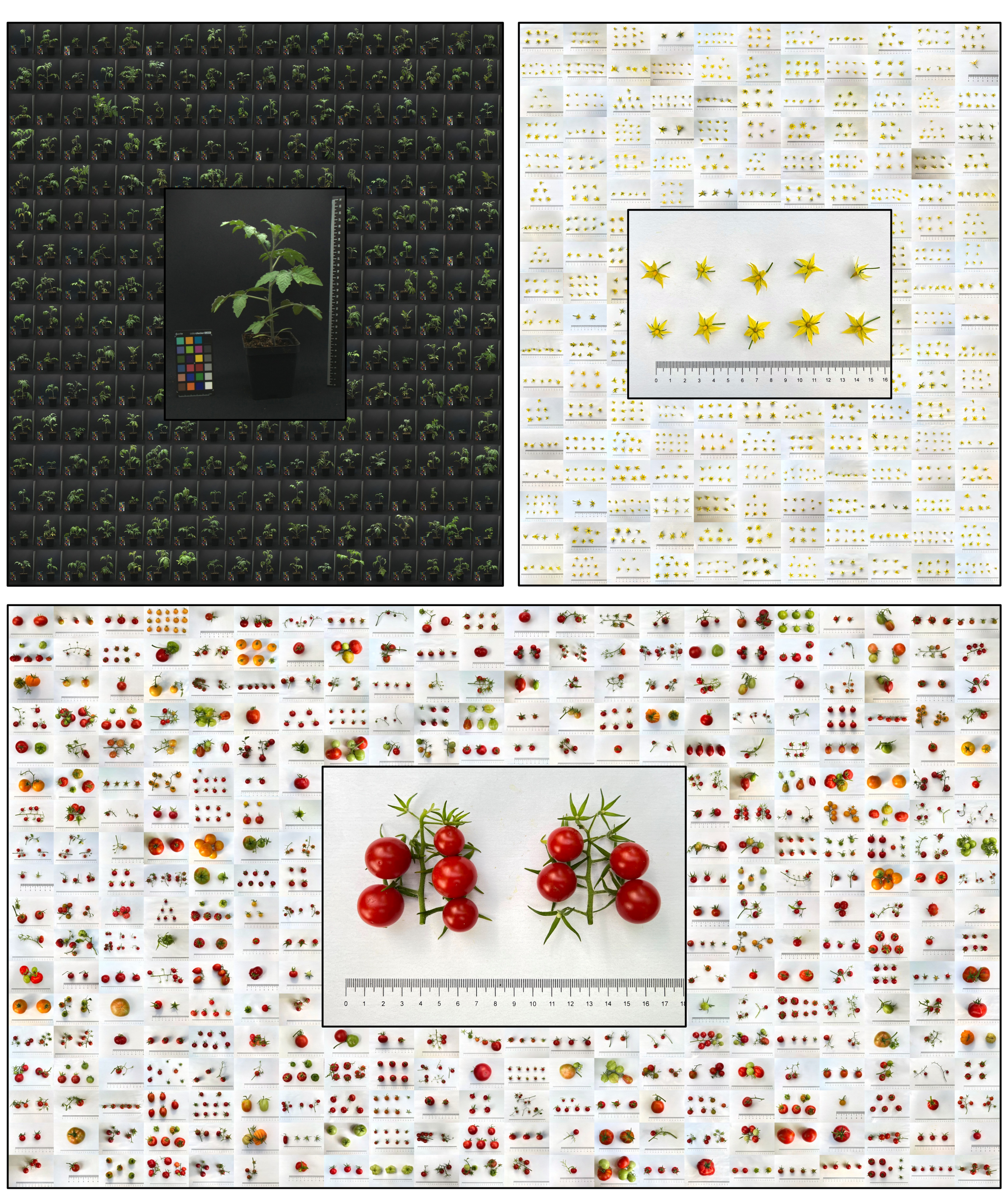
A phenotyping system quantifies pollen populations during heat stress using high-throughput microscopy and computer vision

Cedar Warman & Ravishankar Palanivelu
School of Plant Sciences, University of Arizona, Tucson, AZ

Abstract

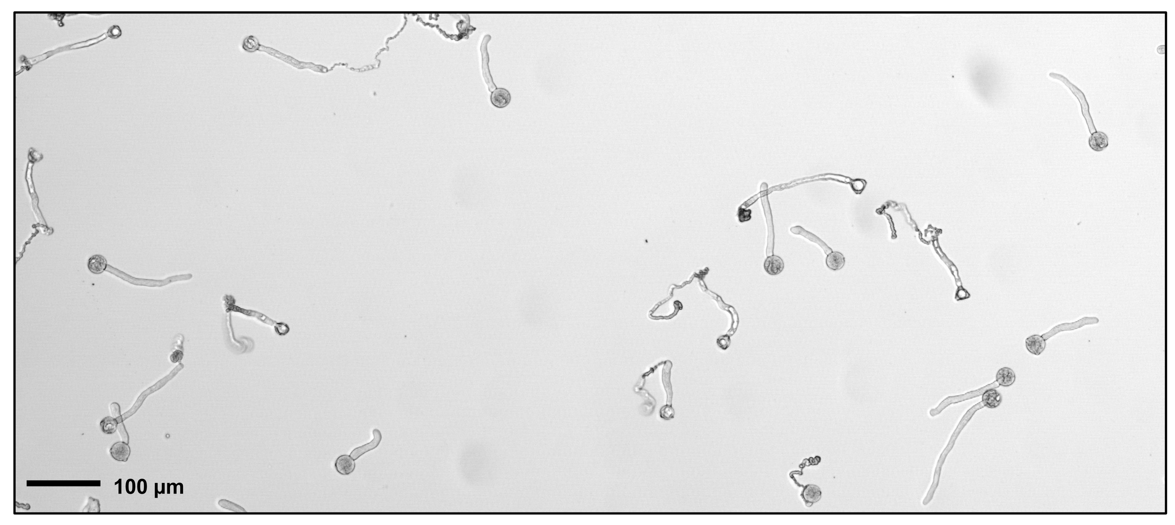
Plant reproduction is sensitive to heat stress. Pollen tube growth can be accelerated or arrested by high temperatures, leading to unstable tubes, failed sperm cell delivery, and ultimately crop yield loss. Pollen growth dynamics have historically been observed on the scale of individual pollen grains, but there are only a few studies surveying pollen populations across genotypes and environmental conditions. Here we describe a phenotyping system that quantifies tomato pollen characteristics on a large scale and under varied heat stress conditions. In this system, we combined high-throughput bright-field microscopy with automated object detection and tracking to understand the life of growing pollen tubes. We used this method to survey pollen from a diverse panel of 220 tomato and close wild relative accessions under different temperatures. This method can be readily adapted to pollen from different species, providing a rapid way to characterize heat stress responses and molecular functions in flowering plants.

220 accessions capture genetic diversity of tomato and wild relatives

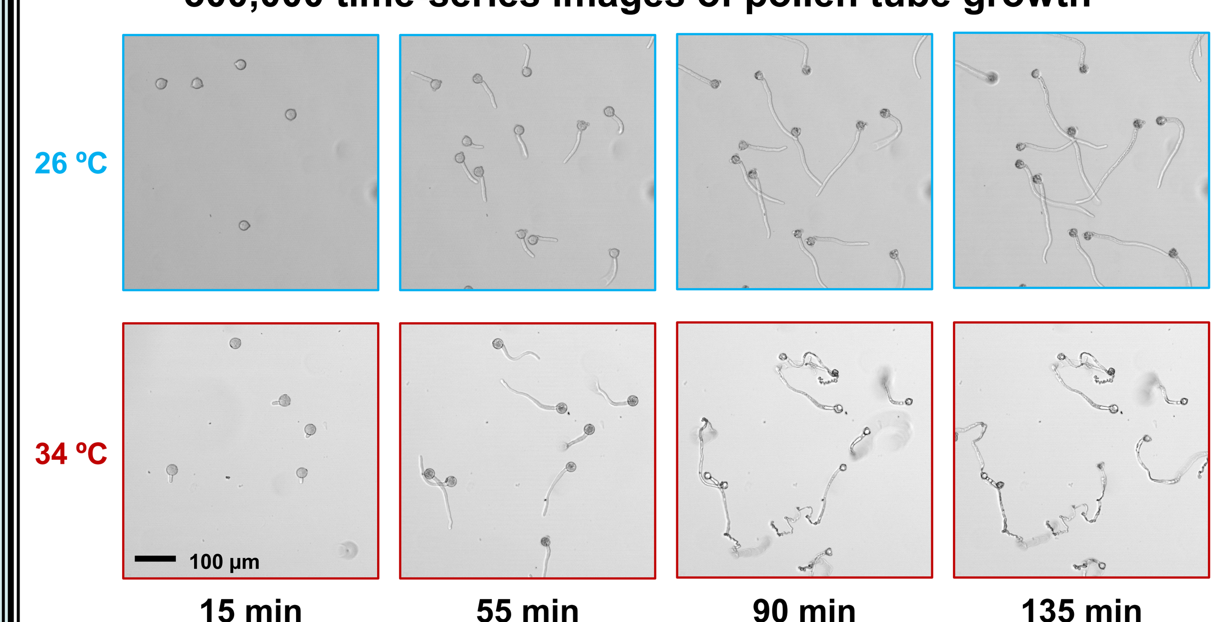


Open-source phenotyping systems, sensors, and web apps

Heat stress affects pollen tube growth



~300,000 time-series images of pollen tube growth



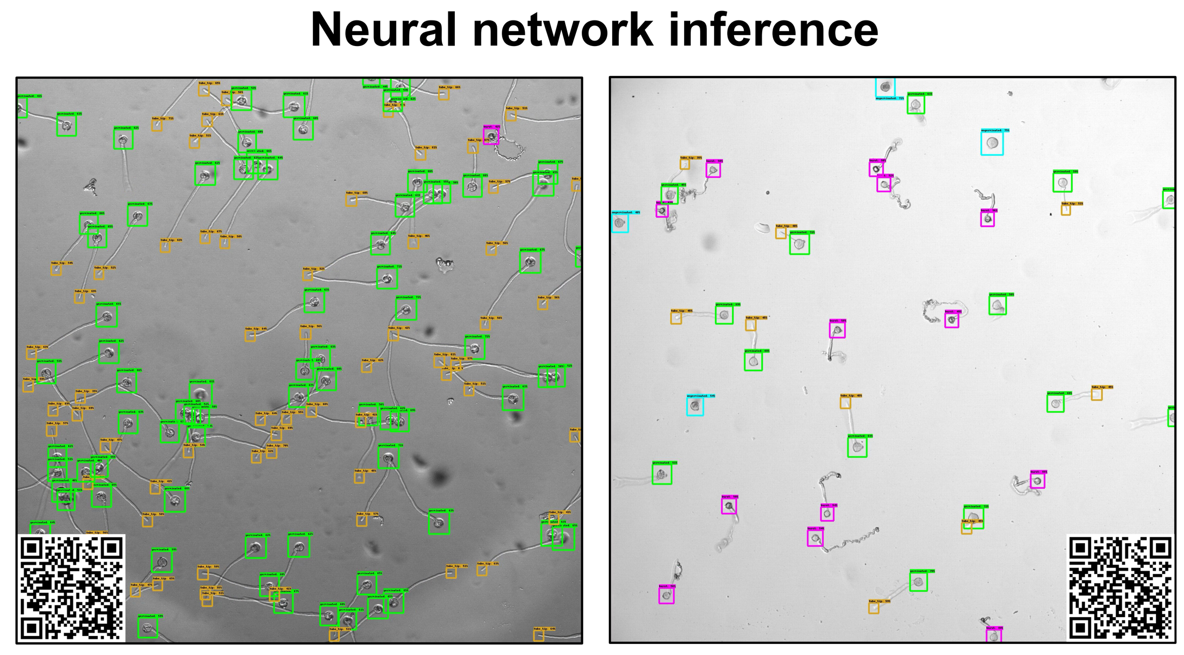
A convolutional neural network was trained to label pollen features

CenterNet Hourglass104

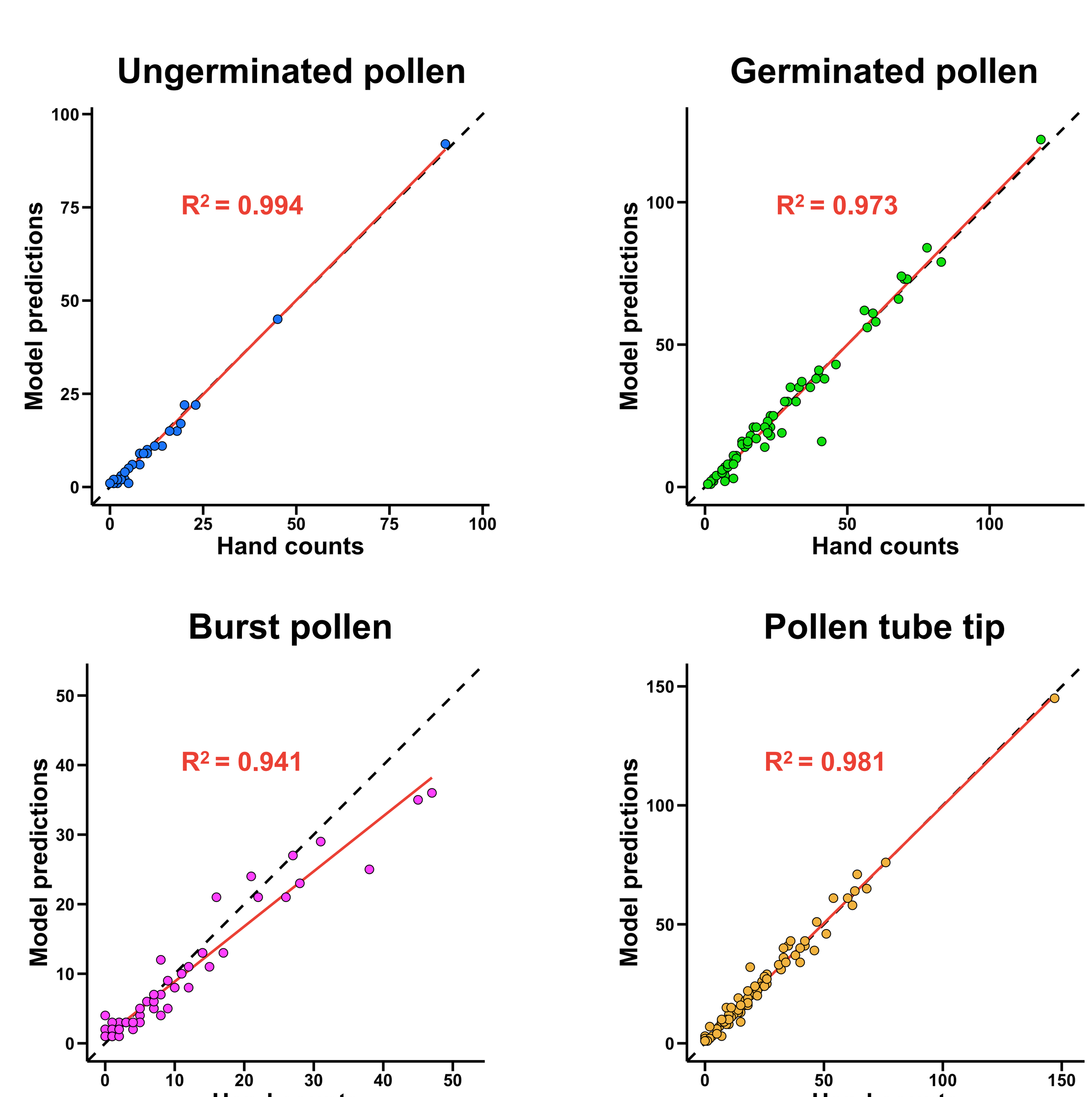
- 400 labeled images
  - ~30,000 labels
- 9 minutes per image labeling
- Trained on Nvidia A100 for 3 hours
- Inference on 4 Nvidia V100s
  - 19 hours for ~300,000 images
  - 35,000x human speed

TensorFlow
The University of Arizona High Performance Computing
Jetstream2

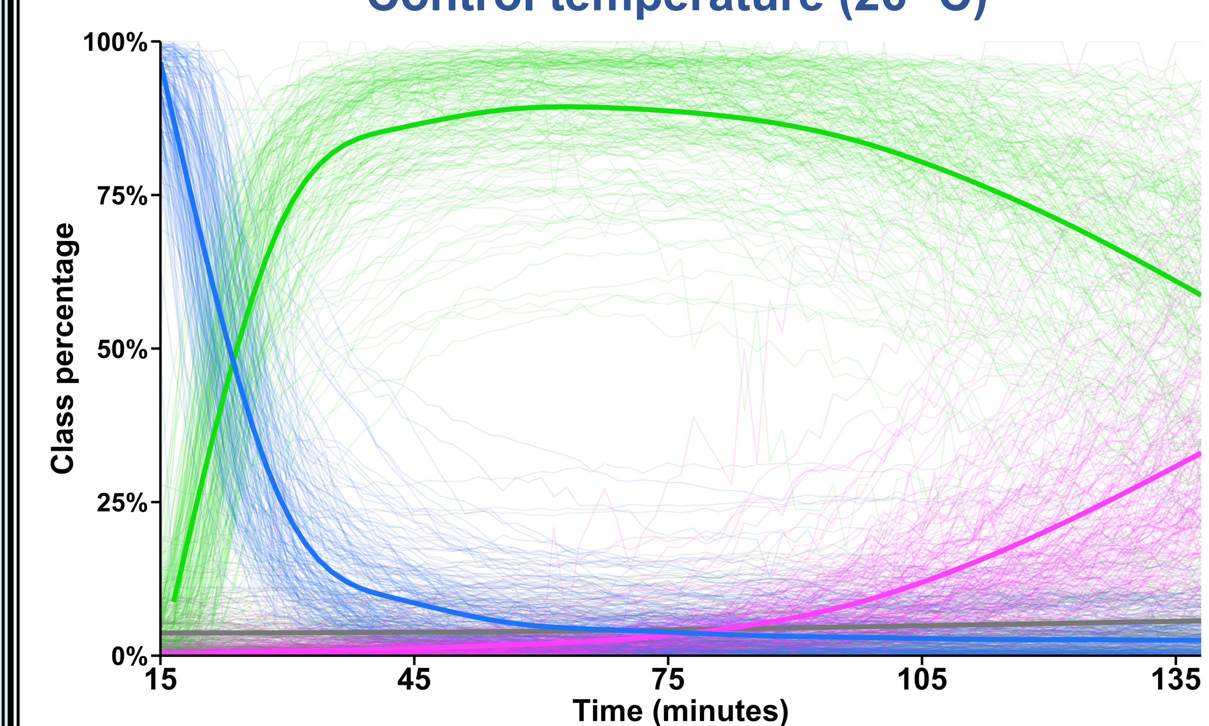
Neural network inference

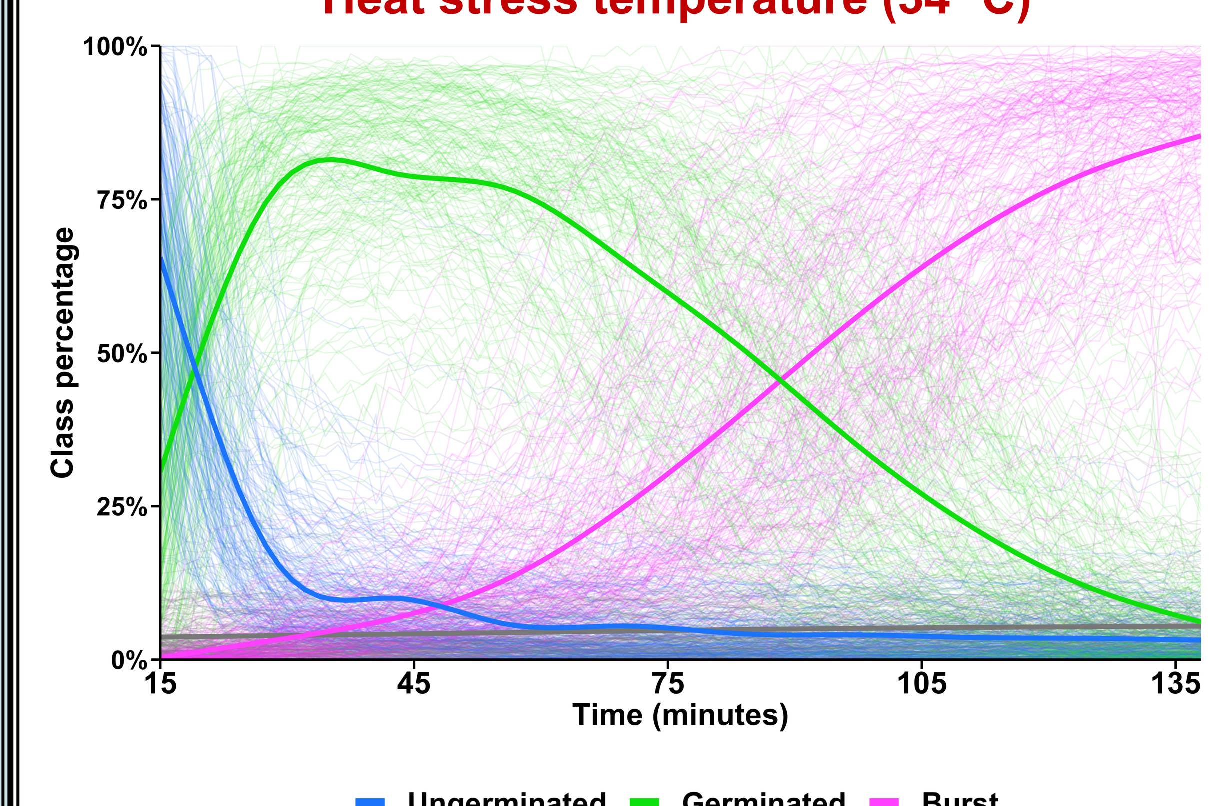


The neural network is accurate



Pollen populations were measured by the phenotyping system



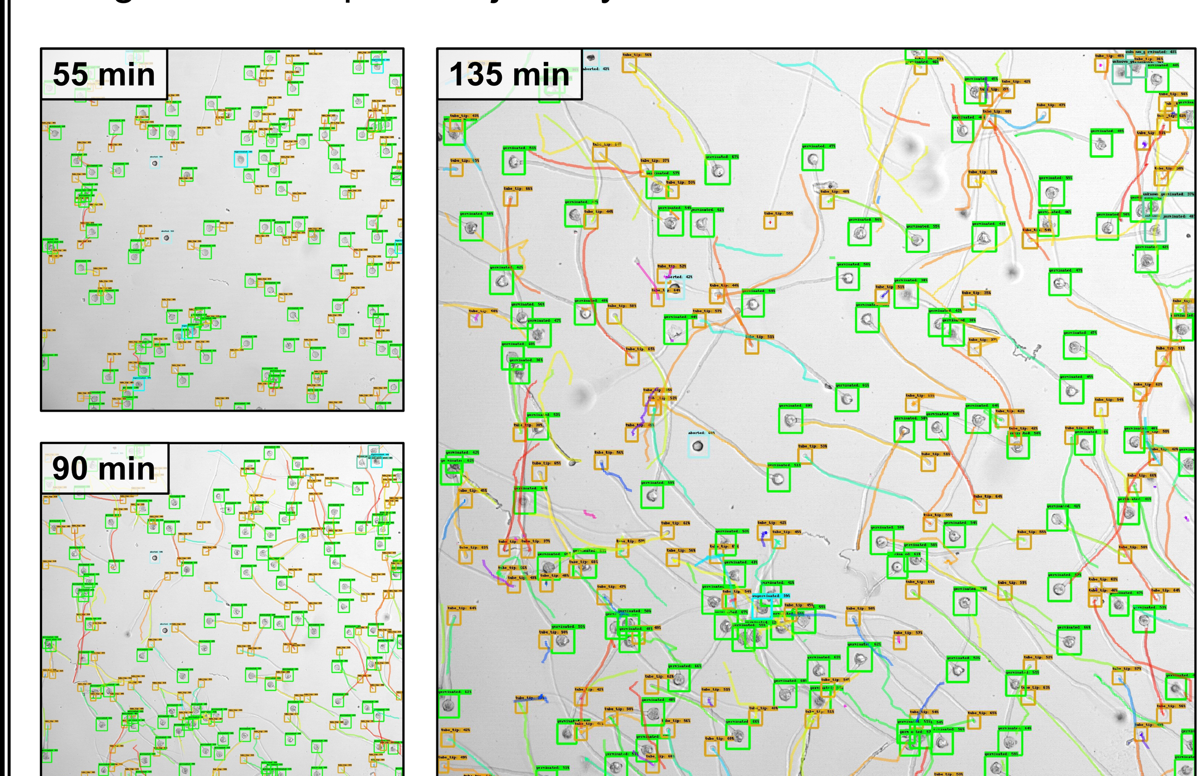


Tube tip tracking provides additional phenotypes

BayesianTracker

- Multiple object tracking reconstructs tube tip trajectories in crowded fields
- github.com/quantumjot/BayesianTracker

btrack
Lowe Lab, UCL



Acknowledgements

Thank you to Sara McKinley, Berenice Gonzalez, Yaire Gutierrez, Jorge Munoz, Kekhrie Tsurho, Xander Nelson, Christopher Nacion, and Katrina Zearley for technical assistance. Thank you to University of Arizona High Performance Computing and Indiana University Jetstream2 for computational resources. Thank you to the C.M. Rick Tomato Genetics Resource Center, the USDA National Plant Germplasm System, Esther van der Knaap, and Zachary Lippman for tomato germplasm. This work was funded by National Science Foundation grants IOS-1939255 (Mark Johnson, Ravishankar Palanivelu, Gloria Muday, James Pease, & Ann Loraine) and IOS-2109832 (Cedar Warman).

This poster is available online:

@cedarwarman