



Using robots to characterize genotype by environment interactions through developmental time

jlg374@cornell.edu



Joseph Gage¹, Nicholas Lepak², Michael A. Gero¹, Edward S. Buckler^{1,3,4}

¹Institute for Genomic Diversity, Ithaca, NY 14853

²USDA-ARS, Ithaca, NY 14853

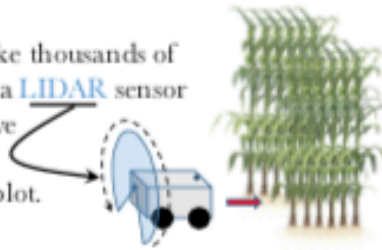
³School of Integrative Plant Sciences, Plant Breeding and Genetics Division, Cornell University, Ithaca NY 14853

By facilitating daily, field-scale data collection with millimeter precision, rover-based phenotyping will enable unprecedented temporal resolution for studying **interactions between genotype (G), environment (E), and developmental time (T)**.

Rovers are affordable, autonomous, and scalable.



Rovers make thousands of scans with a **LIDAR** sensor as they drive through each field plot.



LIDAR data are processed to produce 3D reconstructions of field plots.



LIDAR data are summarized by dimensionality reduction to produce heritable descriptors of whole-plant architecture that are not constrained to human-defined traits like plant height or leaf count.



Rovers enable longitudinal data collection at densely spaced timepoints in NY. The same germplasm is also grown in dozens of environments as part of Genomes to Fields. These data allow comparison of genotype interactions with different dimensions: spatial and temporal.



Hypothesis:

Common genetic control determines both differential developmental trajectories and differential response to environments between genotypes



- Drivers of phenotypic plasticity
- Important targets for crop resiliency

The information, data, or work presented herein was funded in part by USDA-ARS, the Genomes to Fields Initiative, and the Advanced Research Projects Agency-Energy (ARPA-E), U.S. Department of Energy under Award Number DE-AR0000596. This material is based upon work supported by the NSF Postdoctoral Research Fellowship in Biology under Grant No. IOS-1806119.



Cornell University

