A large, modern greenhouse with multiple levels and rows of plants growing in soil. The structure has a translucent roof and walls, allowing sunlight to filter through. A metal walkway with railings runs along the side of the greenhouse.

PhytoOracle: A scalable, modular data processing pipeline for phenomic data

Emmanuel Gonzalez, Travis Simmons, Ariyan Zarei, Michele Cosi,
Nathan Hendlar, Holly Ellingson, Jeffrey Demieville, Duke Pauli, Eric Lyons

Domestication of teosinte and trait gathering



Domestication of teosinte and trait gathering



Traits of interest

- Morphological
 - Plant height
- Physiological
 - Photosynthetic efficiency, reflectance, canopy temperature
- Yield
 - Ear per plant, angle of ear, kernel number, kernel firmness
- Quality of yield
 - Kernel colour, sugar content



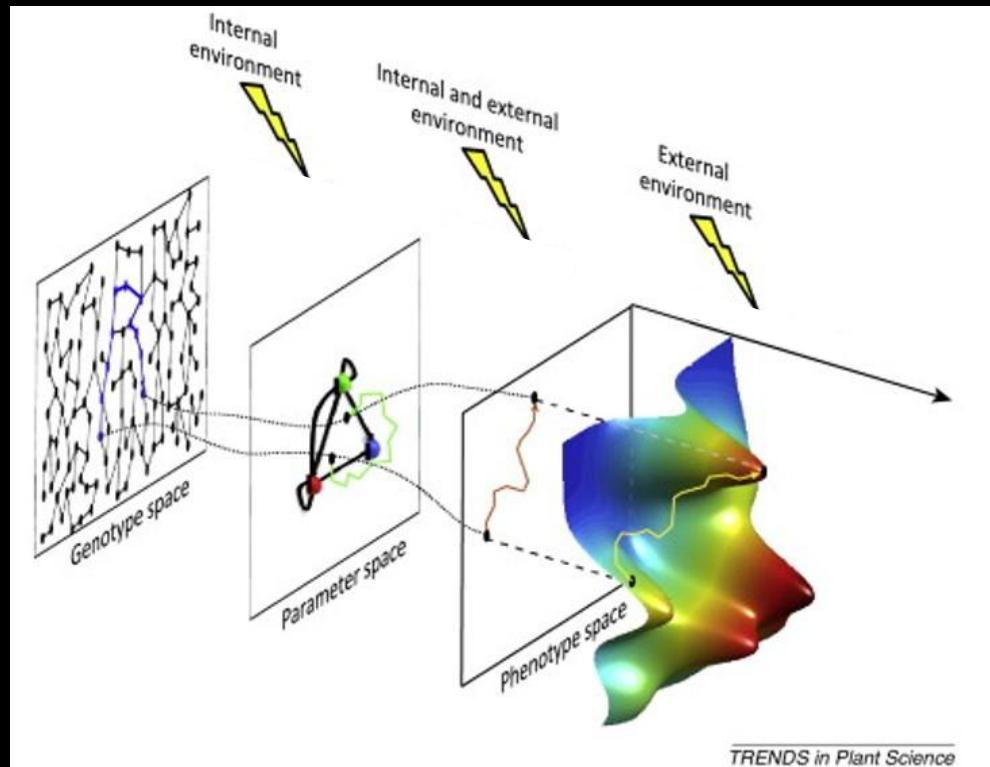
Trait gathering has modernized



Connecting genotype to phenotype

Gene combinations interact with the internal and environment to produce phenotypes

- Optimal to study phenotypes in the environment in which they are expressed



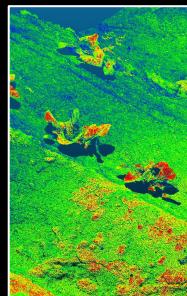
TRENDS in Plant Science

Obtaining and extracting high-quality phenomic data



Data volume:

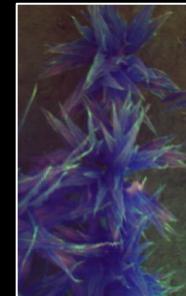
- Max: 10 TB/day
- Typical: 1.5 TB/day



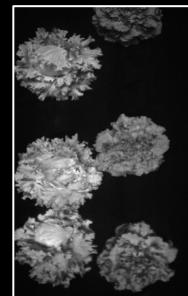
3D



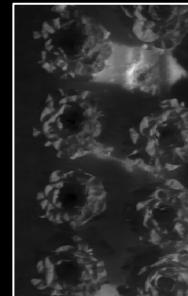
RGB



Hyperspectral



Fluorescence



Thermal



PhytoOracle



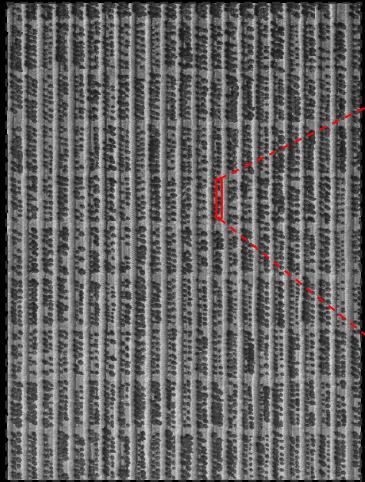
PhytoOracle pipeline workflow

Raw Images → GPS correction,
Orthomosaic,
Plot clipping → Phenotype
Quantification

Raw Images

GPS correction,
Orthomosaic,
Plot clipping

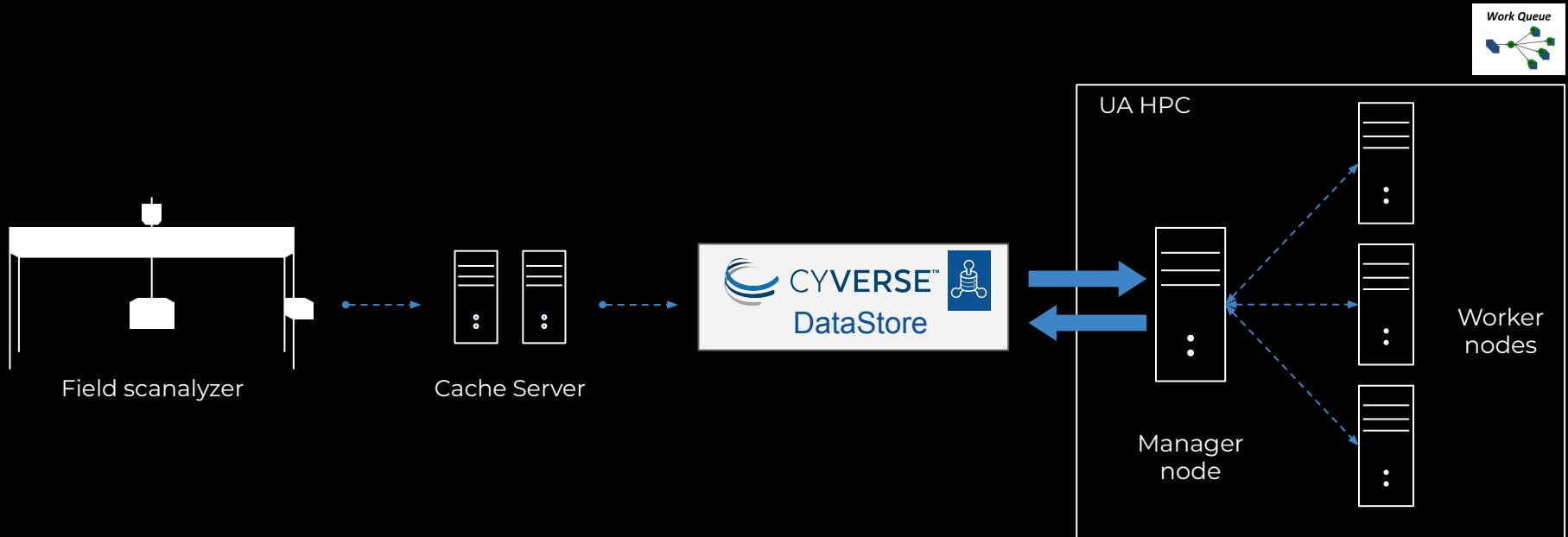
Phenotype
Quantification



date	treatment	genotype	roi_temp
2/3/2020	treatment 1	GRxI_1074	290.8565674
2/4/2020	treatment 1	GRxI_1074	280.3588867
2/5/2020	treatment 1	GRxI_1074	288.3753357
2/8/2020	treatment 1	GRxI_1074	298.1218567
2/11/2020	treatment 1	GRxI_1074	293.346344
2/12/2020	treatment 1	GRxI_1074	293.0809326
2/13/2020	treatment 2	Trianon	293.035553
2/14/2020	treatment 3	GRxI_1010	296.1292114
2/15/2020	treatment 1	GRxI_1074	296.0202637
2/16/2020	treatment 1	GRxI_1074	295.1908875
2/17/2020	treatment 1	GRxI_1074	298.5577393
2/18/2020	treatment 1	GRxI_1074	298.7333374
2/19/2020	treatment 1	GRxI_1074	299.1886902



Data flow and distributive framework



Scalability exponentially reduces data processing times

How much time would it take to process* a single season worth of RGB data (50TB) on a 4-core, regular lab computer?

55 years!

* From raw data to a quantifiable phenotype

How much time would it take PhytoOracle to process* a single season worth of RGB data (50TB)?

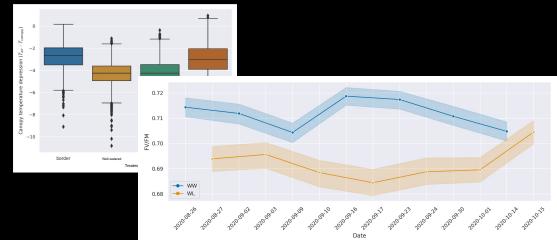
Only 6 days!

* From raw data to a quantifiable phenotype



Today's tutorial

- Running sections of PhytoOracle pipelines to extract thermal and reflectance data
- Visualizing intermediate and phenotypic trait outputs on a Jupyter Notebook





MegaStitch



GPS errors and image stitching

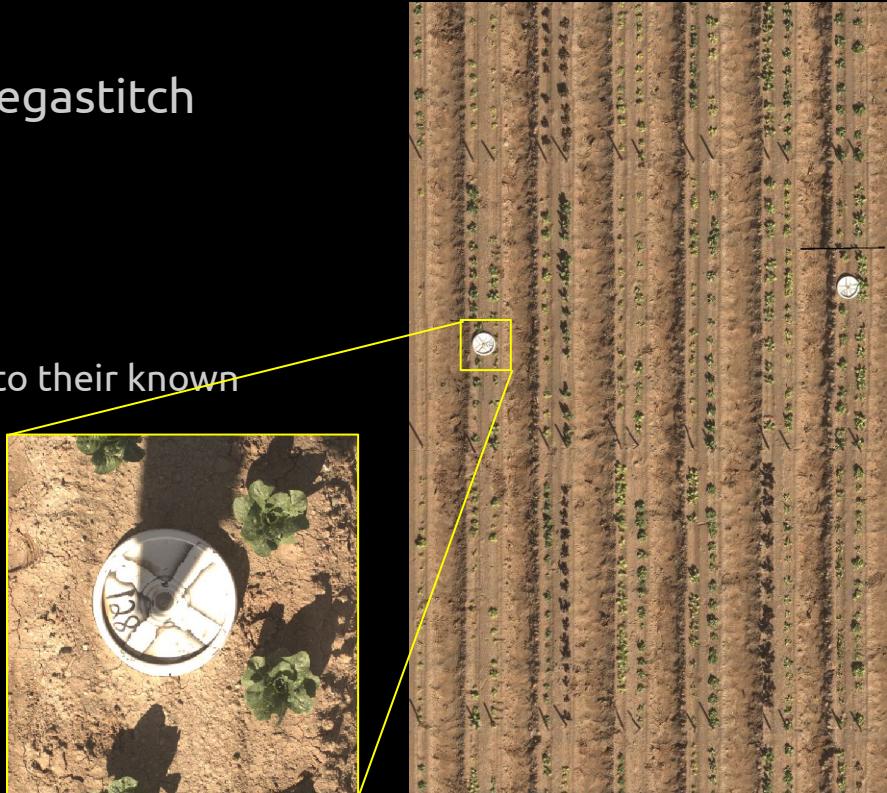
- **Noisy geo-references**
 - Relative coordinate system
 - Delays in triggering the cameras
 - Missing images
- **Naive stitching not possible**
 - GPS error not uniform





Geo-correction and using GPS metadata

- Large scale image stitching using Megastitch
 - Drift and inconsistency
 - White bucket lids come to rescue!
- Solution?
 - Use noisy GPS as priors
 - Anchor Ground Control Point (GCP) lids to their known location
 - Minimize error globally



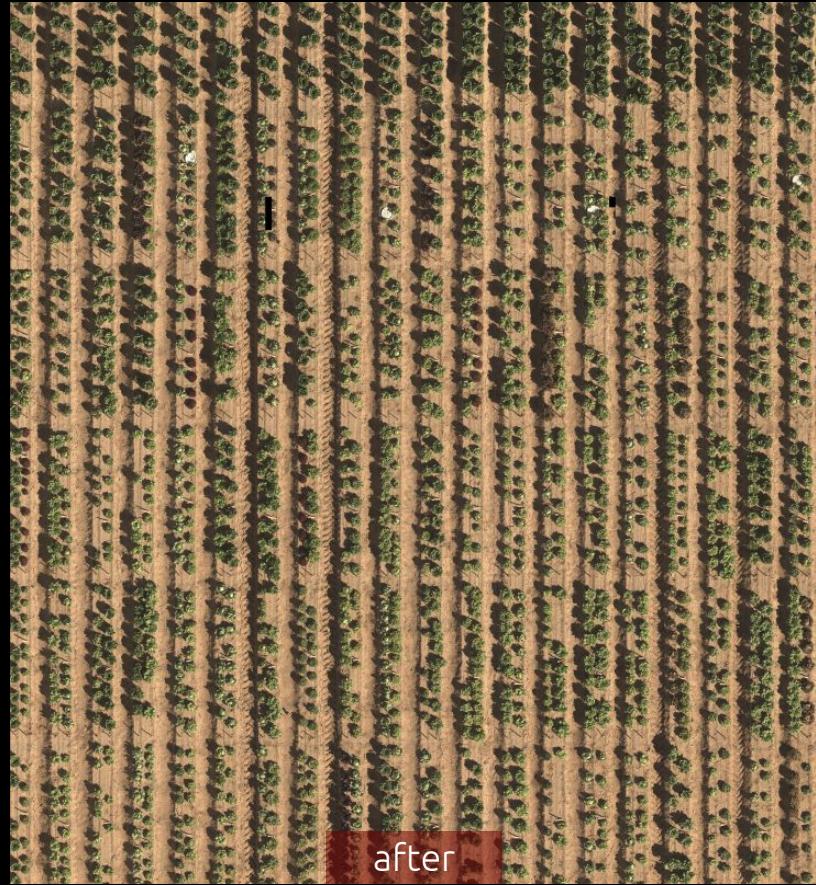
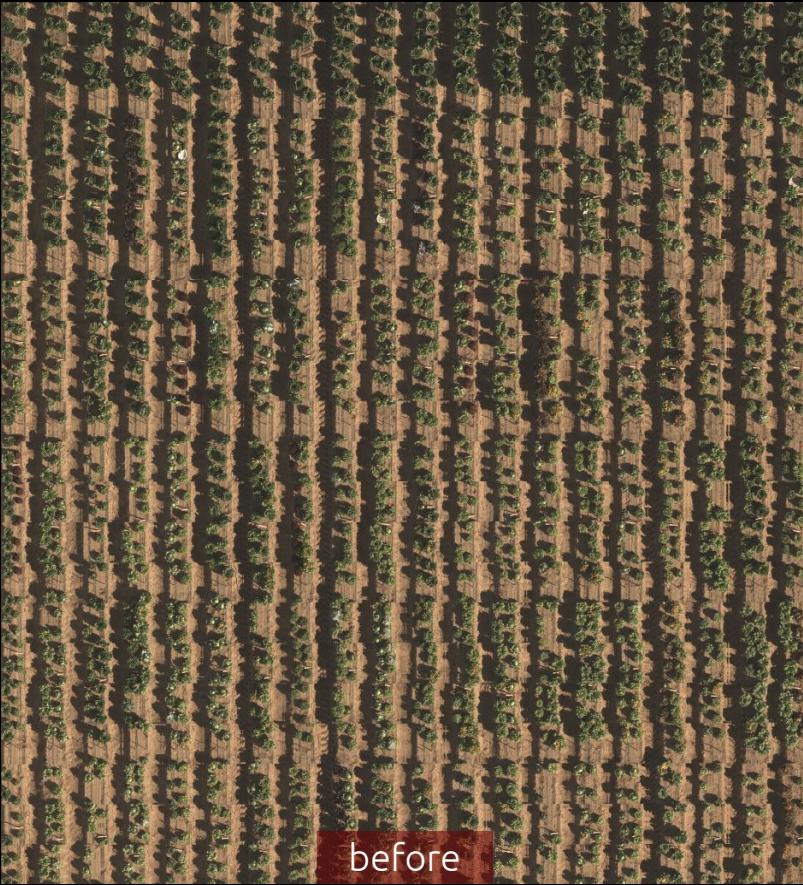


Impacts on phenotyping

- **Addressed problems**
 - Commercial software cannot stitch scanalyzer images
 - Low overlap and few distinct visual features
- **Impacts**
 - Accurate plot level orthos
 - Identify and match plants from different scans
 - Measure phenotypes accurately



Results





Labelbox Model Training

Image Labeling Example

TOOLS

Search or press /

negative 1

OBJECTS

No annotations yet

Use the tools above to start annotating.

Skip Submit

The image shows a user interface for image annotation. The central part of the interface displays a photograph of a row of young green plants, likely lettuce, growing in a field. To the left of the image is a sidebar titled 'TOOLS' which includes a search bar and a checkbox labeled 'negative'. Below the tools is another sidebar titled 'OBJECTS' which contains a small blue icon and a message indicating 'No annotations yet' along with instructions to start annotating. At the very bottom of the interface are two buttons: 'Skip' on the left and 'Submit' on the right.

Resources

Documentation:

<https://tinyurl.com/phytooracle-rtd>

Containers:

<https://github.com/phytooracle>

Workflows:

<https://github.com/LyonsLab/PhytoOracle>

Data:

<https://tinyurl.com/cyverse-datacommons>

Orthomosaics (10% resolution):

<https://tinyurl.com/bisque-orthomosaics>

ArcGIS map:

<https://tinyurl.com/arcgis-phytooracle>



Closing Remarks

We thank the AG2PI team.

We also thank the Cyverse staff for the iRODS and virtual machine troubleshooting.

We finally thank Drs. Duke Pauli, Kobus Barnard and Eric Lyons for their support and leadership.

