



campus



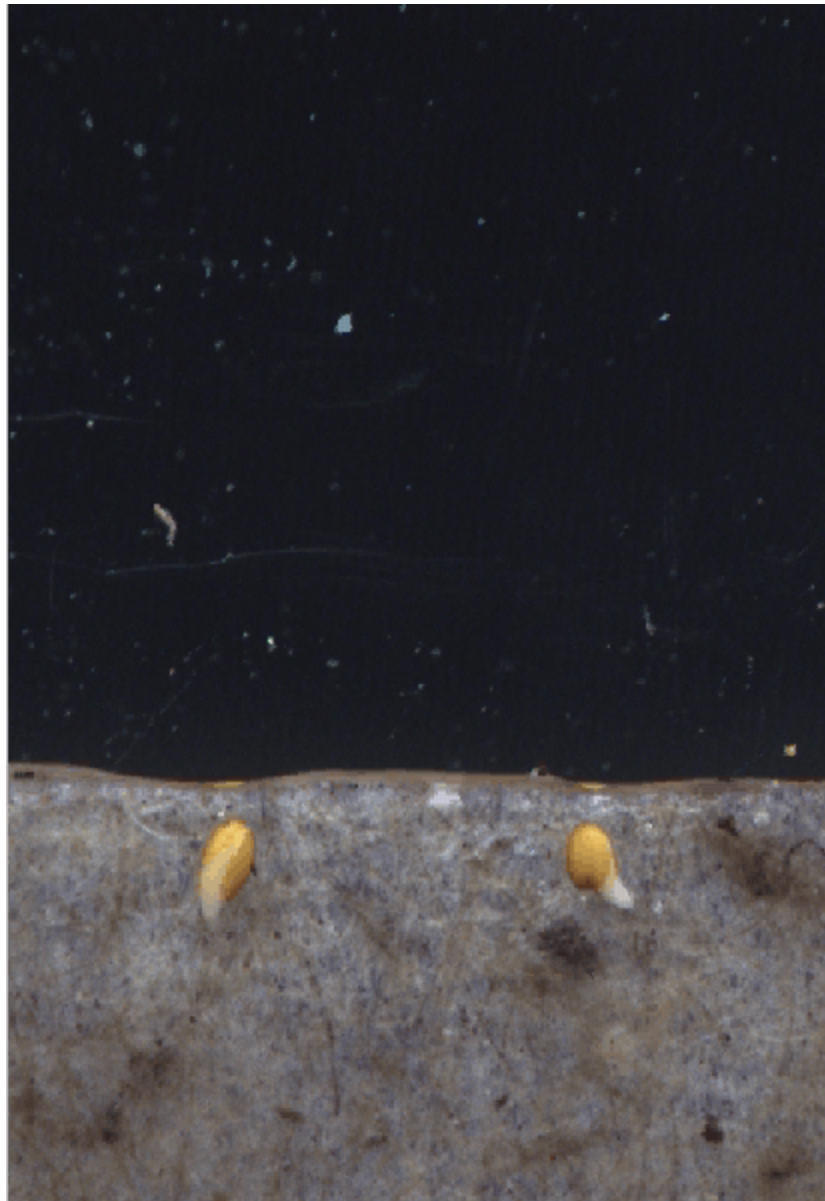
Botany Dept

Growth and development phenotypes in seedlings
measured by automated image analysis

Edgar Spalding

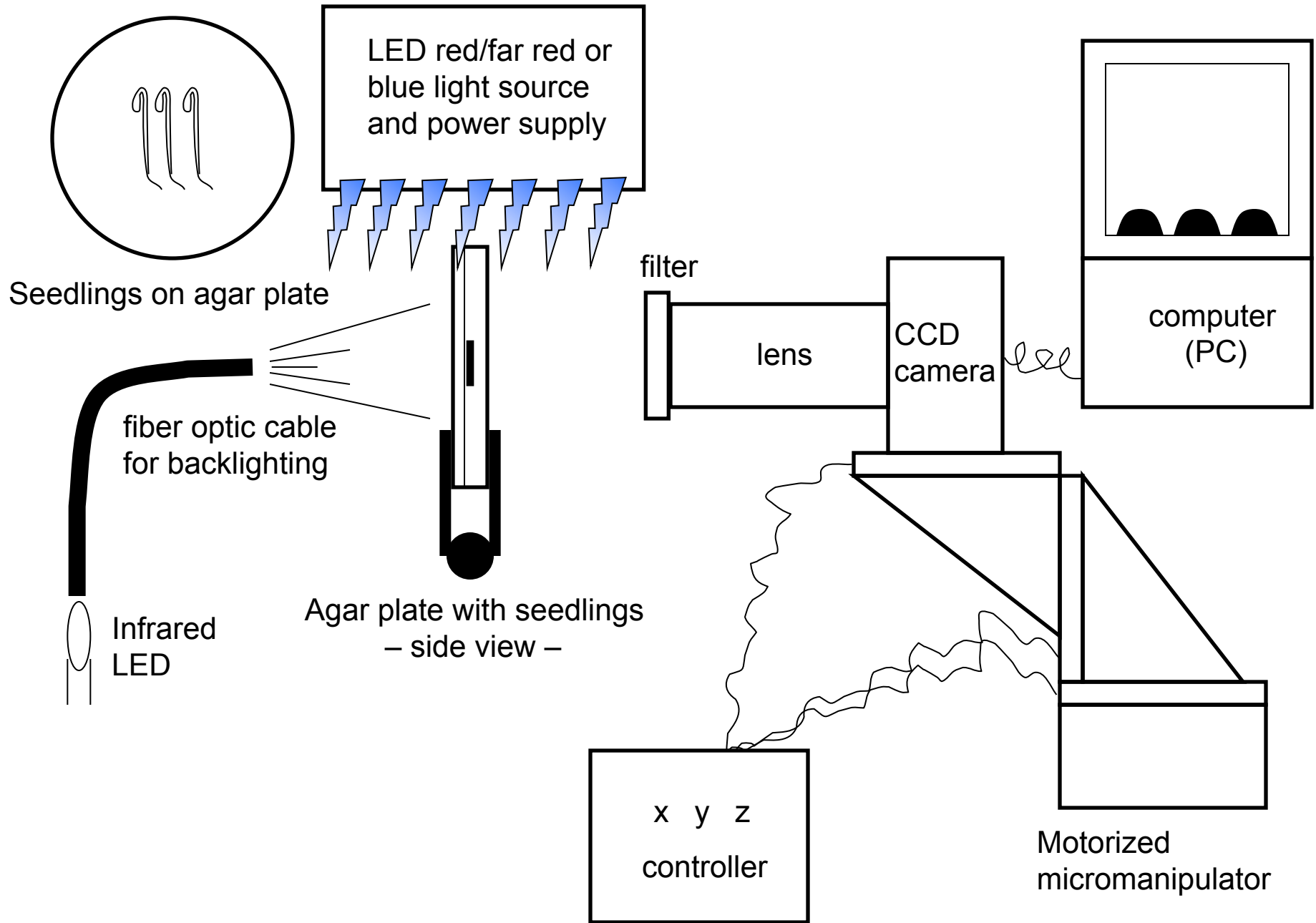
cry1

24,999 genes

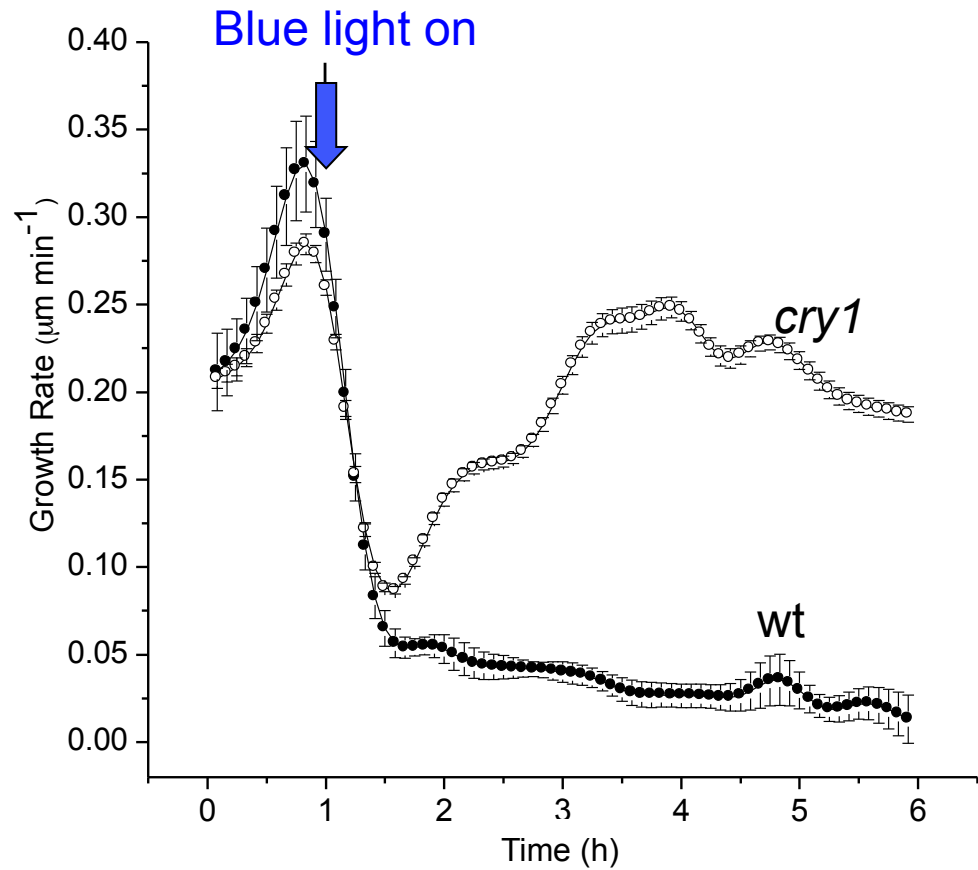
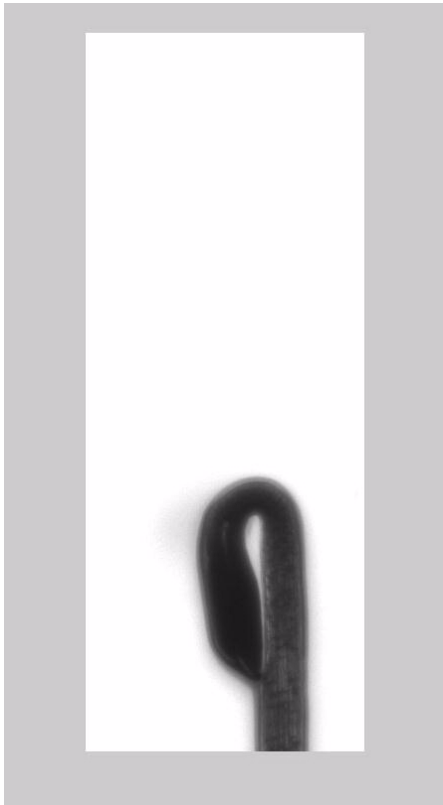
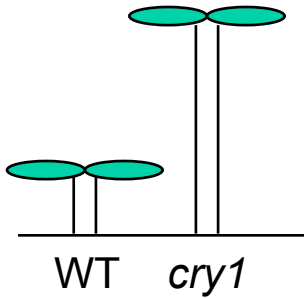


wild type

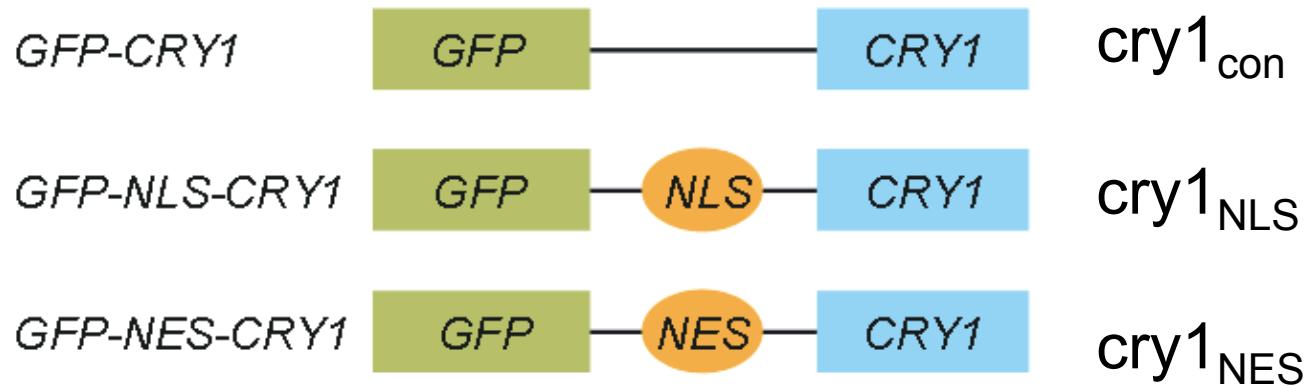
25,000 genes



Hypocotyl Growth Inhibition Induced by Blue Light



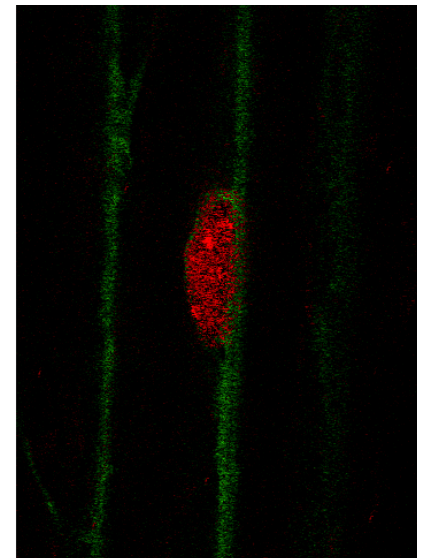
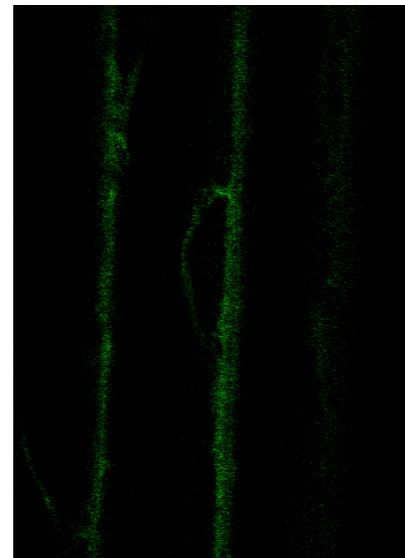
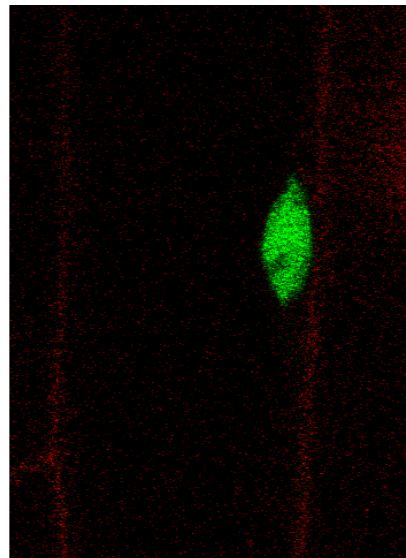
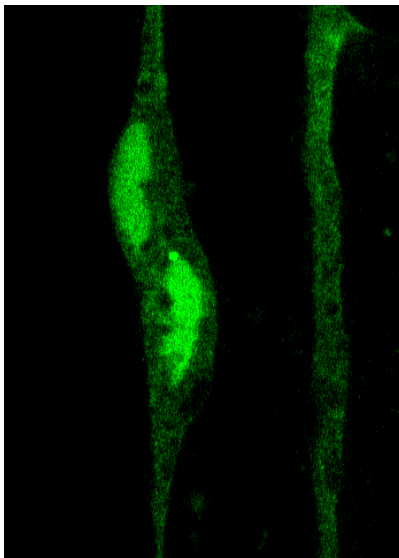
Engineering cry1 subcellular localization

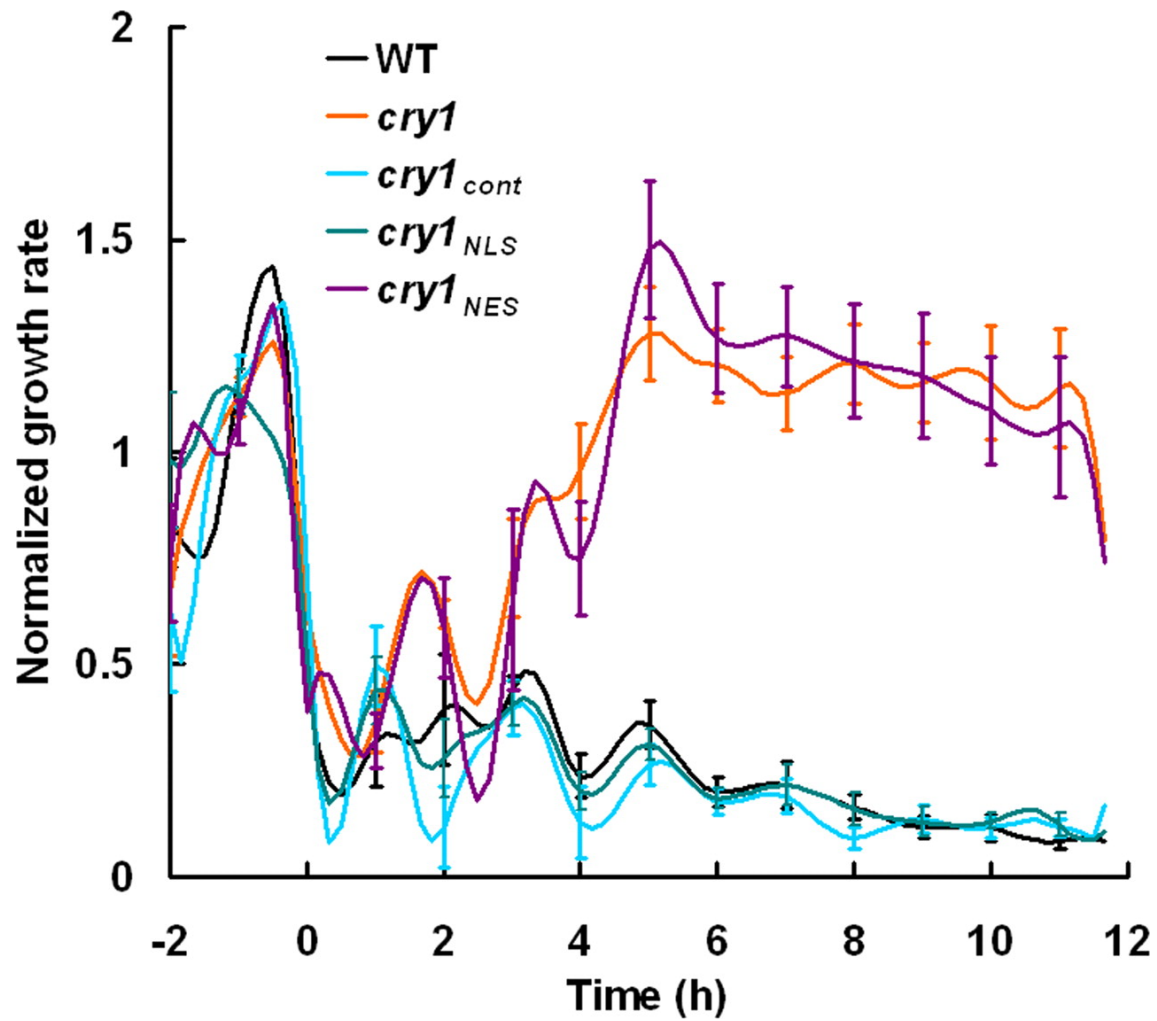


cry1_{con}

cry1_{NLS}

cry1_{NES}



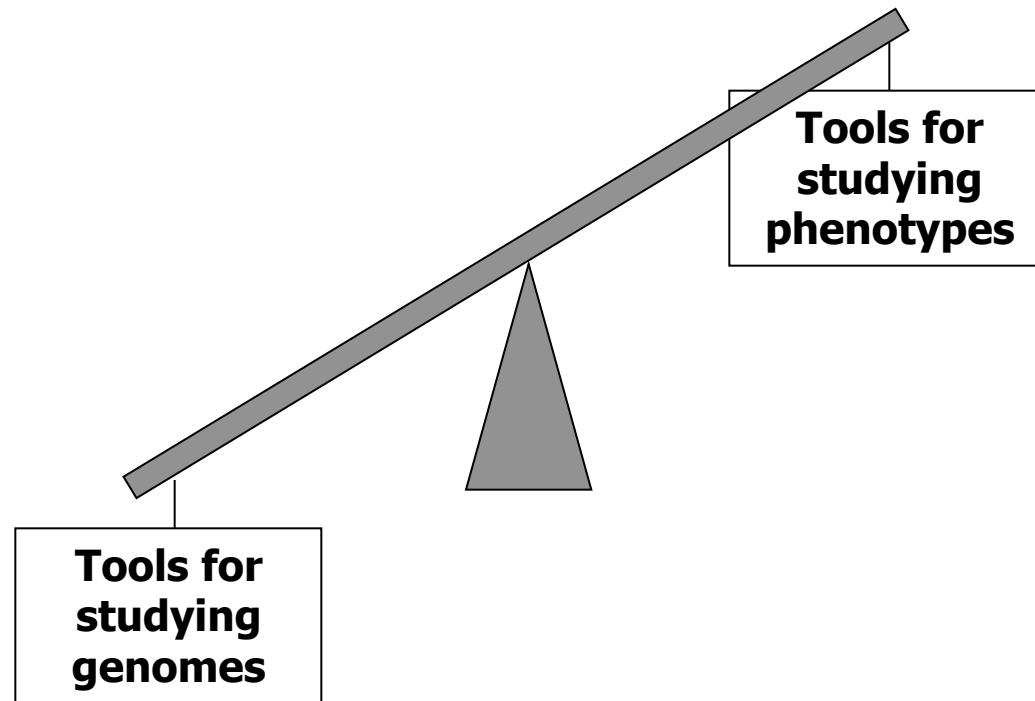




Guosheng Wu

What prevents scaling up to address genome-wide studies?

Motivation of the Phytomorph Project

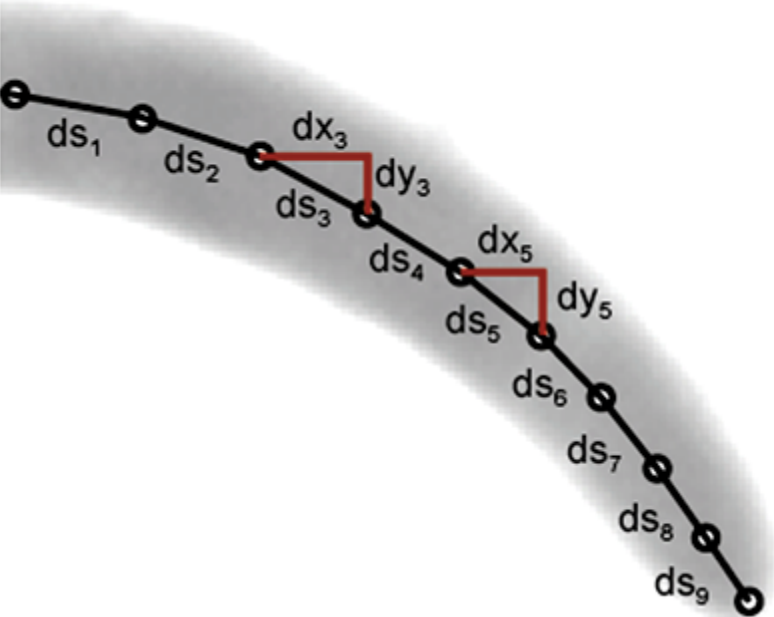


Root Gravitropism
measured every 2 minutes for 8 hours

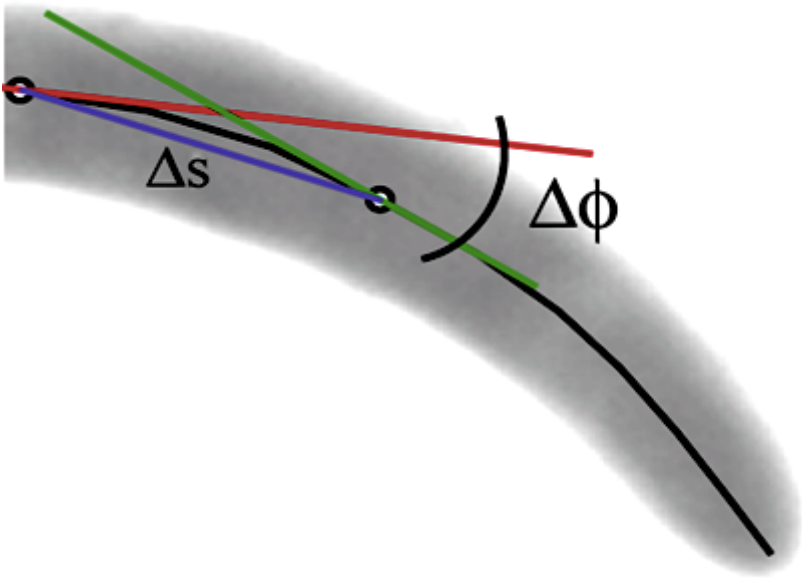


Parameters Derived from the Medial Axis

length



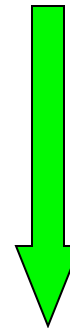
local curvature, $K = \Delta\phi/\Delta s$



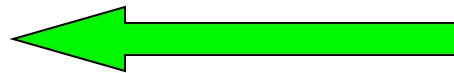
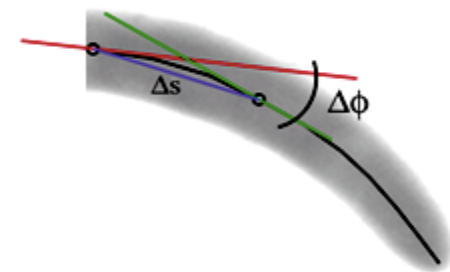
Our Automated Workflow



automated image acquisition
generates movies

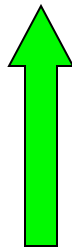


algorithmic feature
extraction and
quantification operates
on each object...

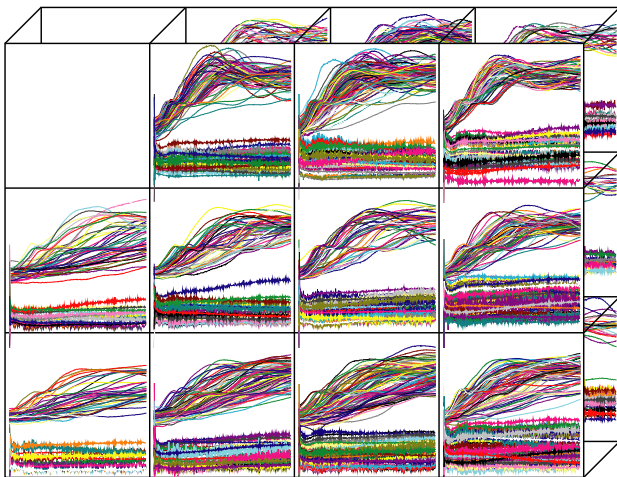


...resulting in large, high
dimension data sets...

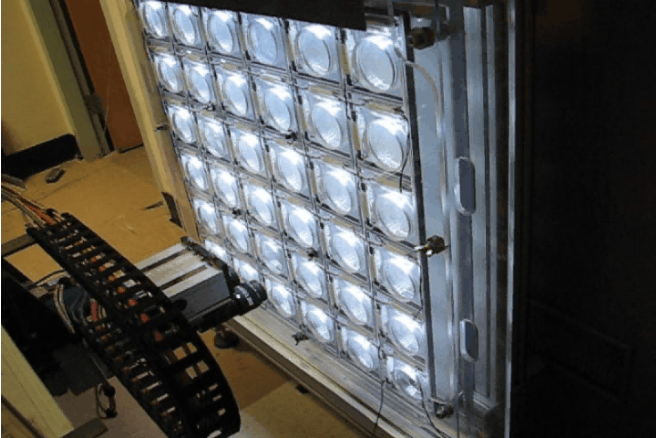
data mining



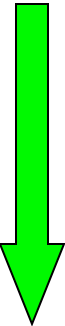
test new
hypotheses



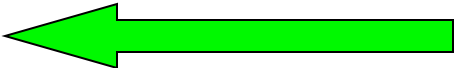
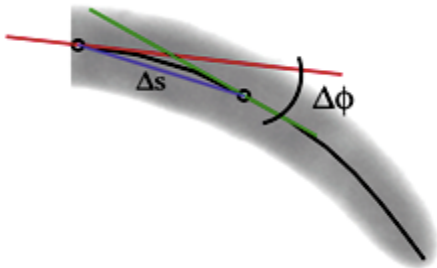
Our Automated Workflow



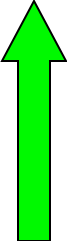
automated image acquisition
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algorithmic feature
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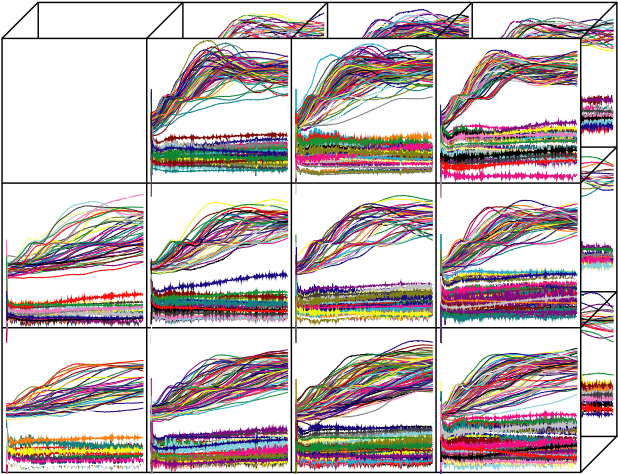


...resulting in large, high
dimension data sets...

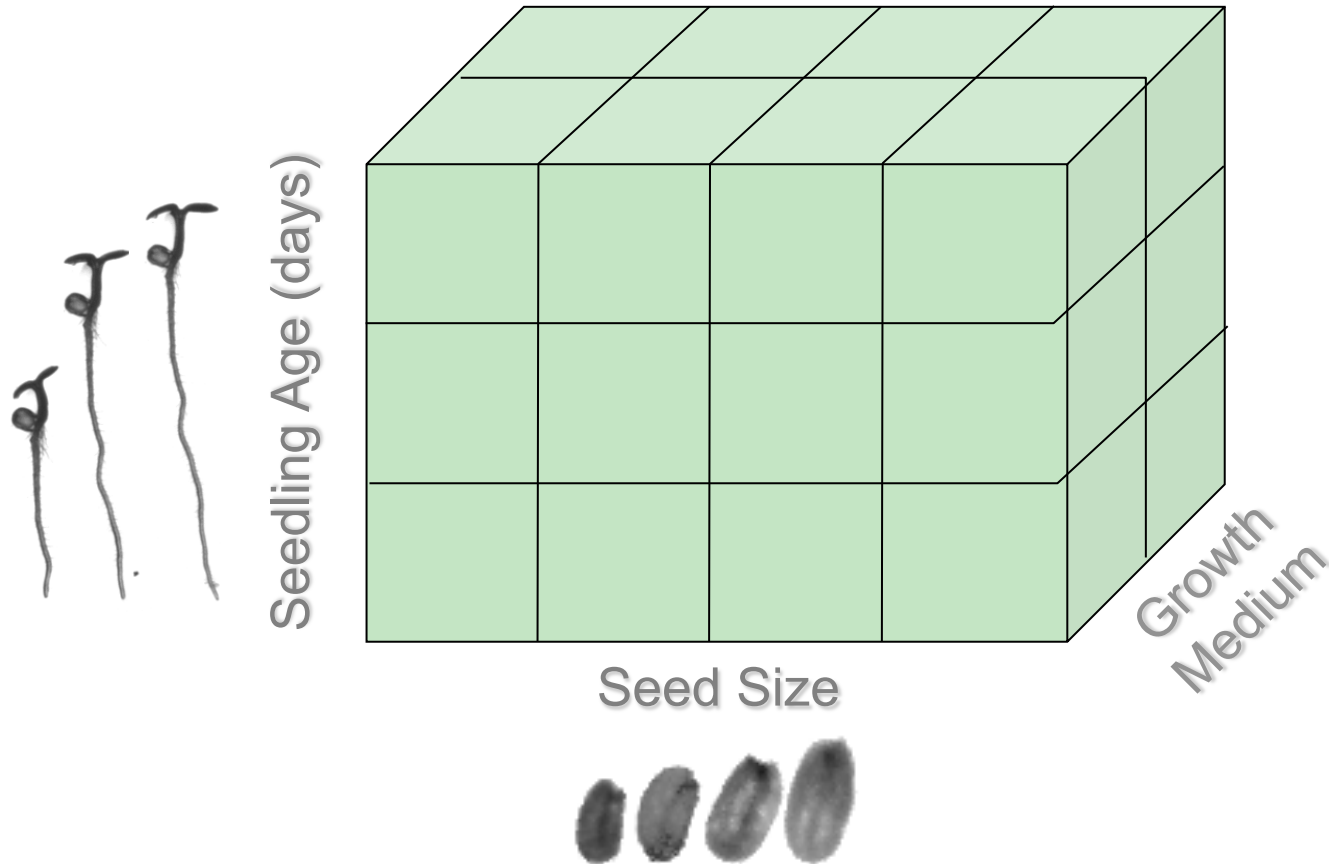


data mining

test new
hypotheses

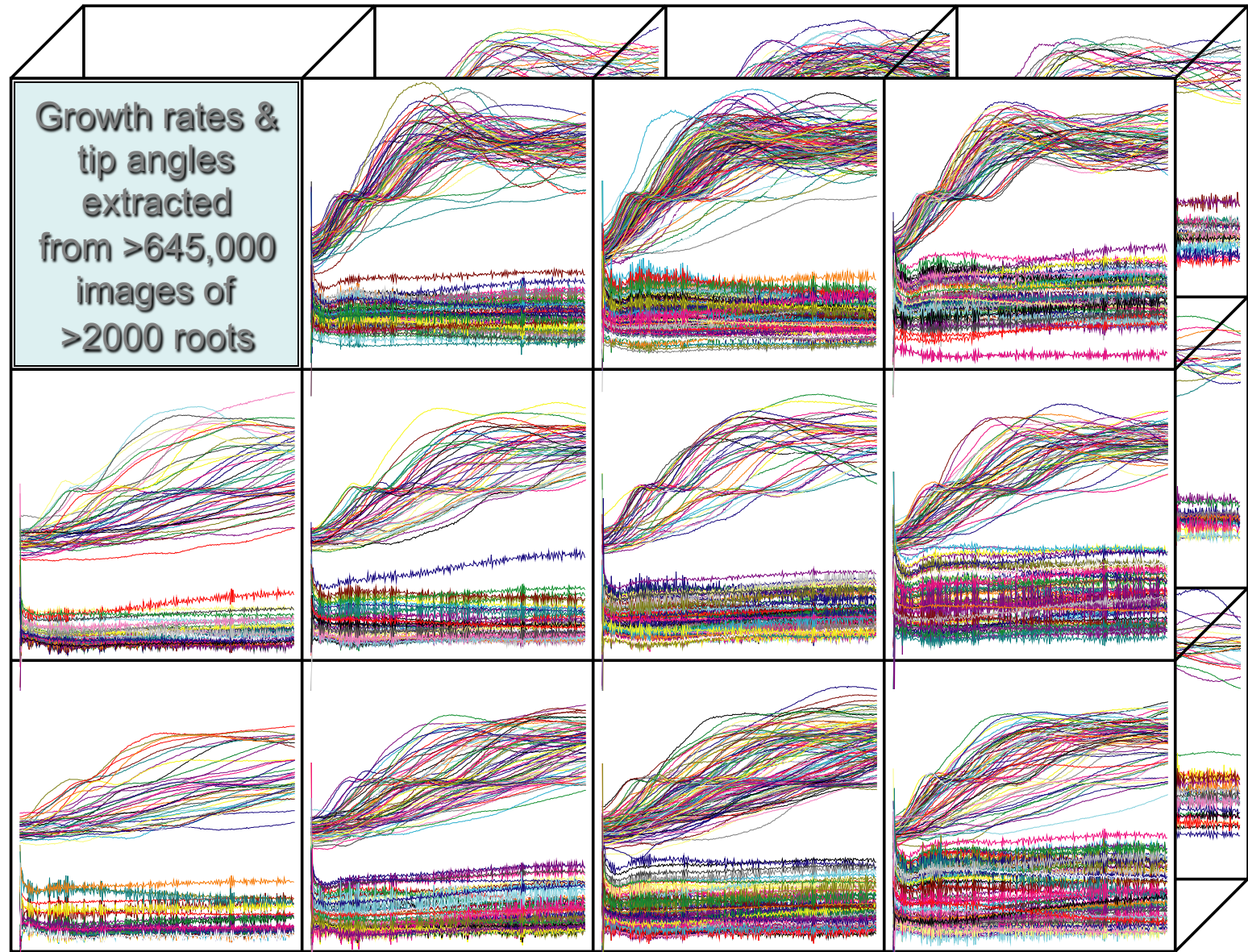


The Explored Condition Space

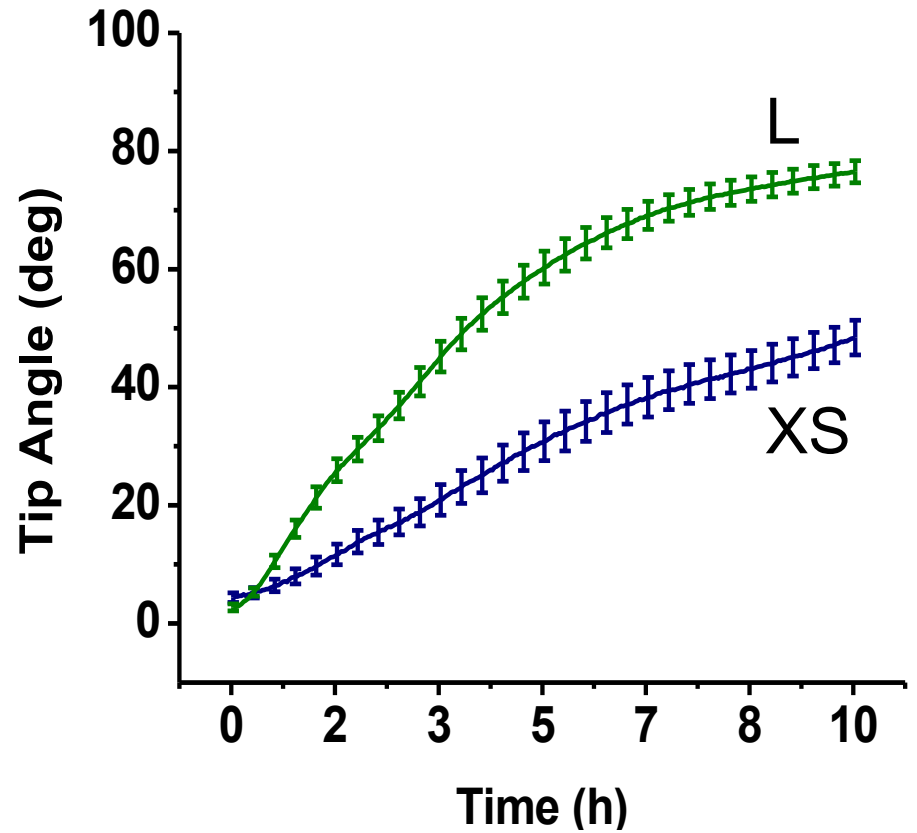
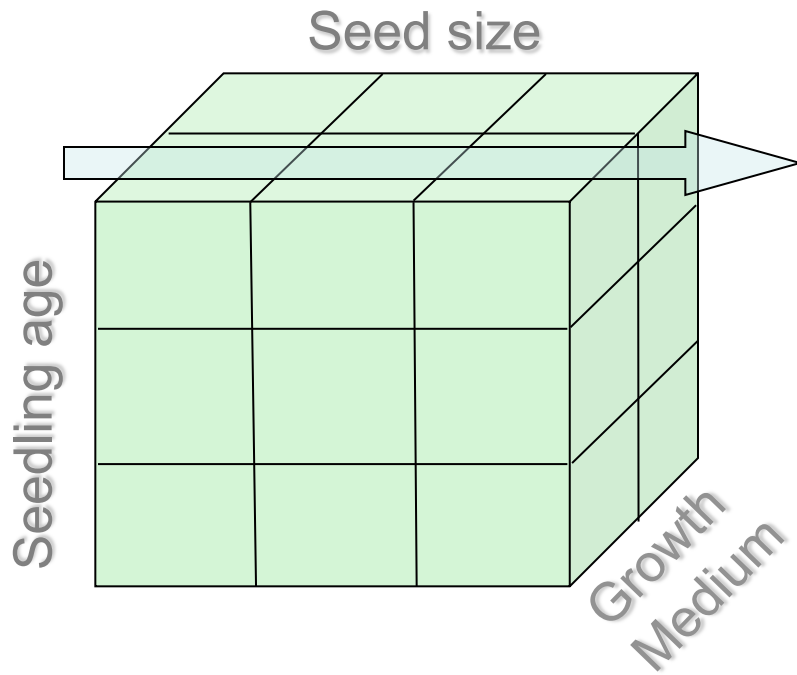


This '**response space**' was characterized with **2142** separate experiments each consisting of **301** time points for a total of **644,742** separate images, all analyzed automatically.

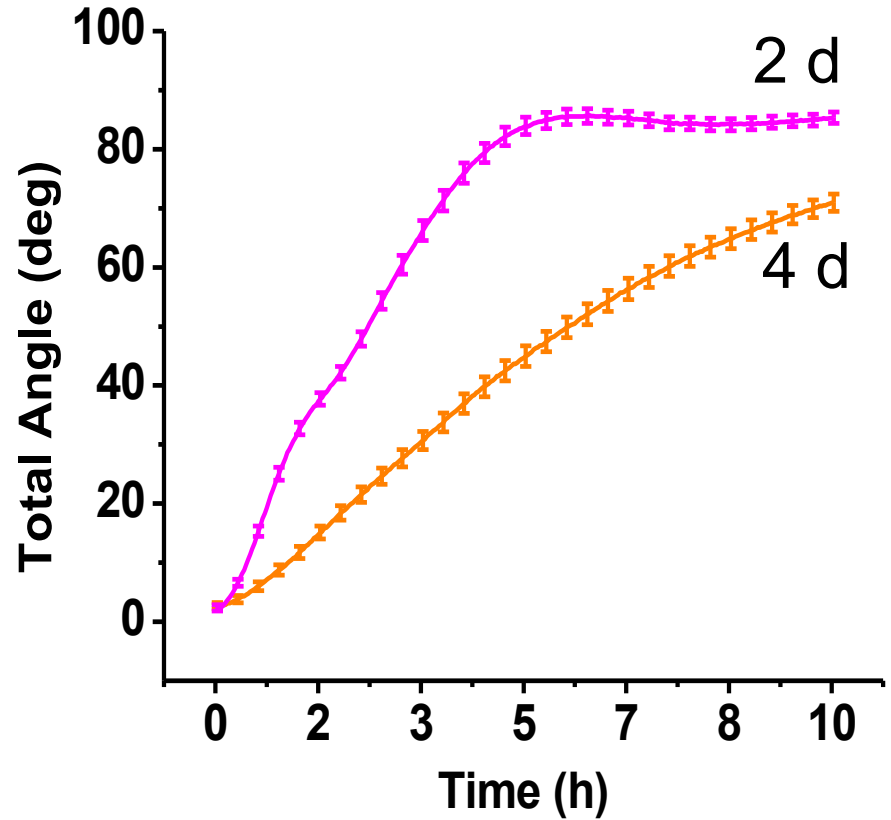
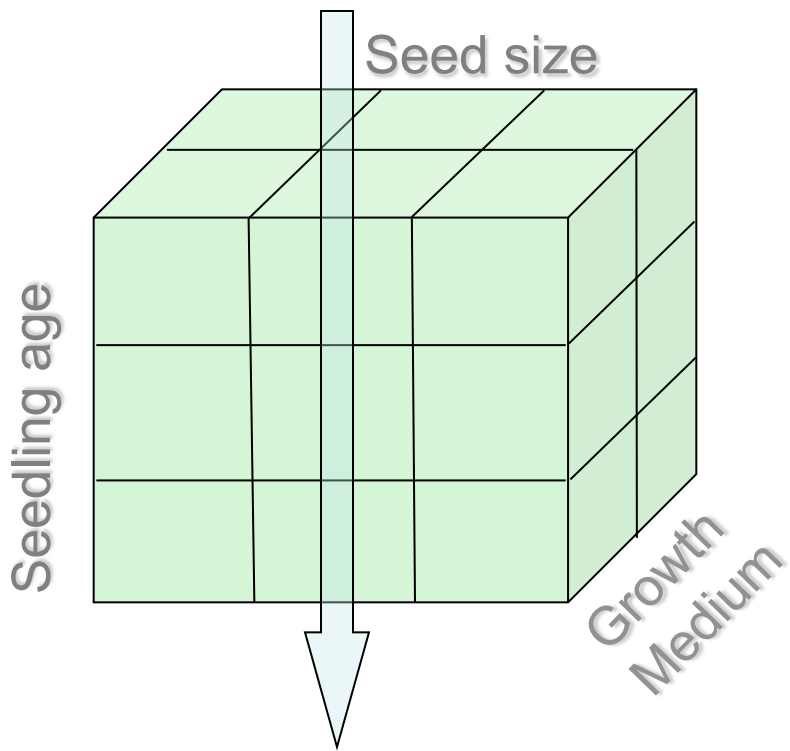
The Wild-Type Data Set



The Seed Size Axis



The Seedling Age Axis



The Key People

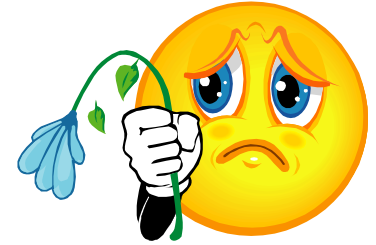
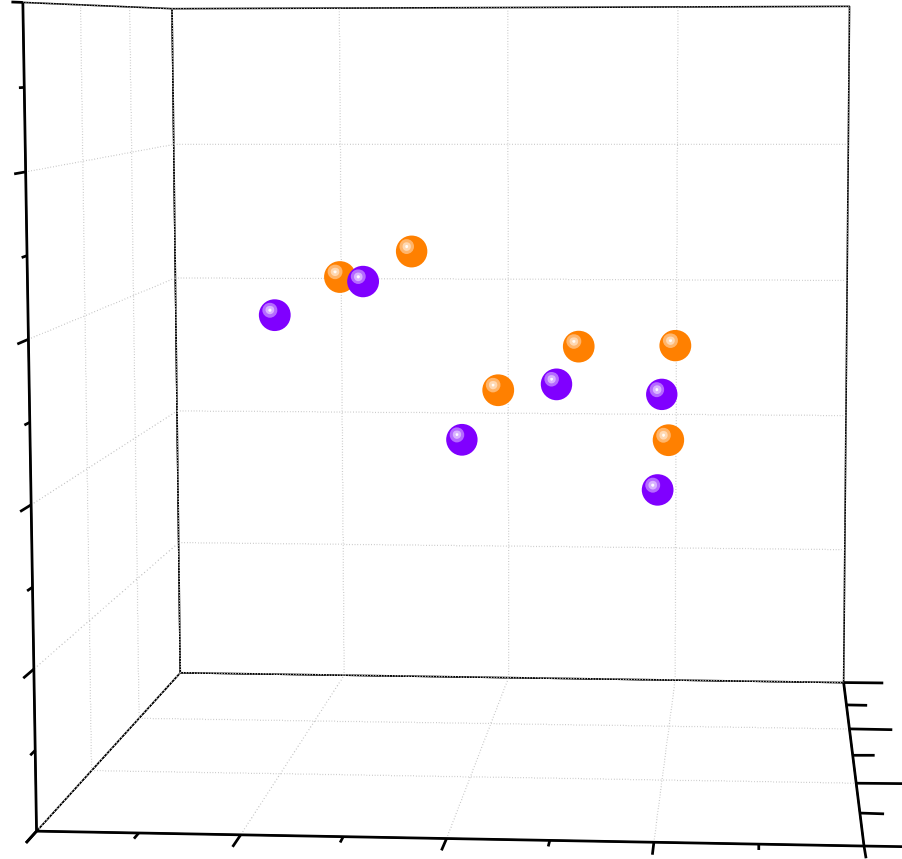


Nathan Miller

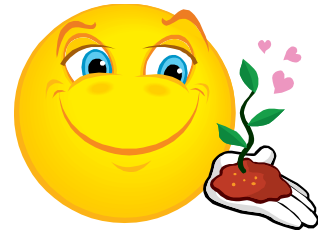
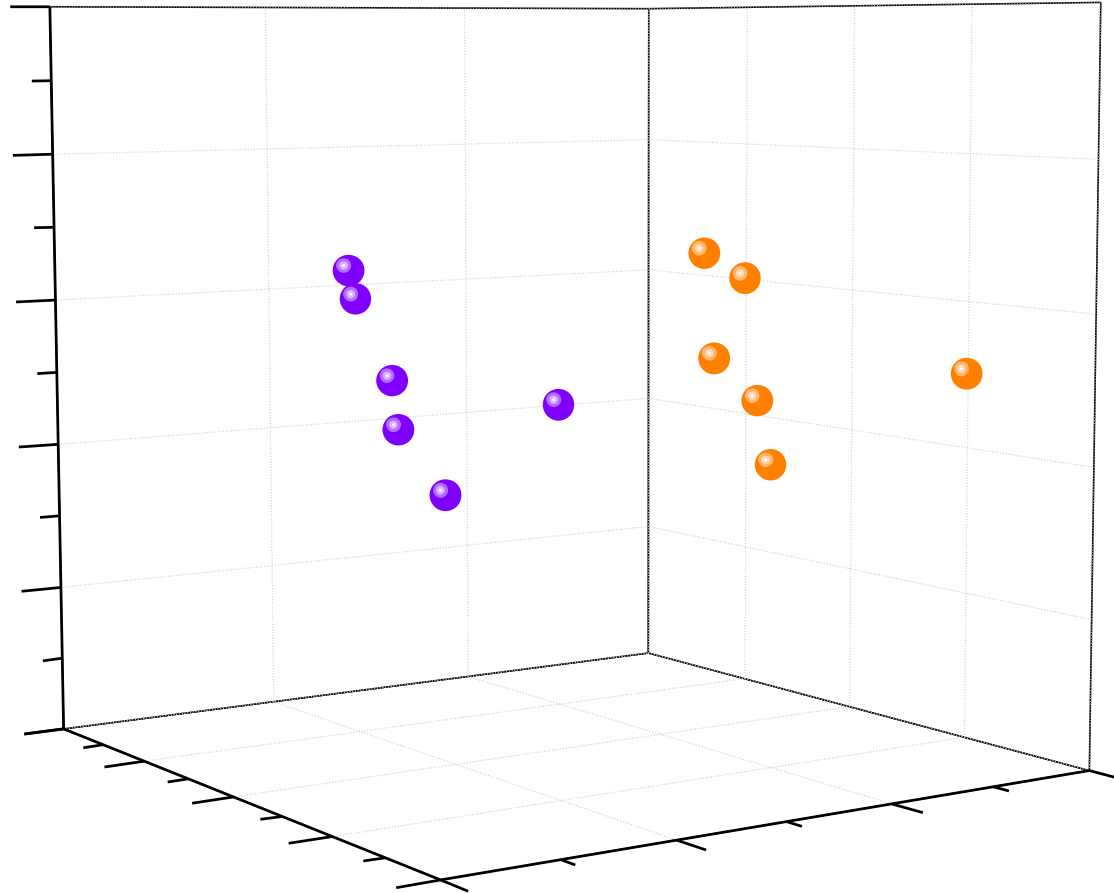


Tessa Durham Brooks

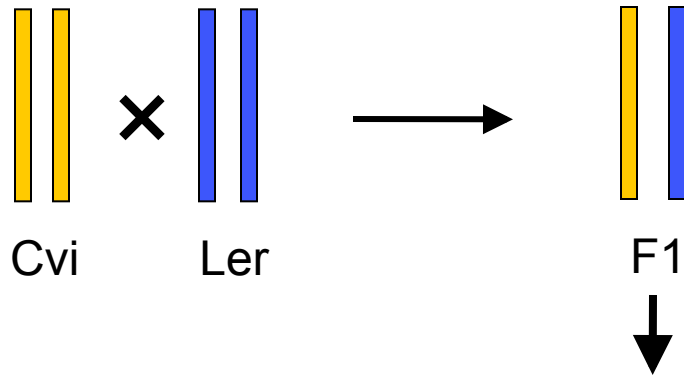
My mutant has no phenotype! #!*@!!^&#!



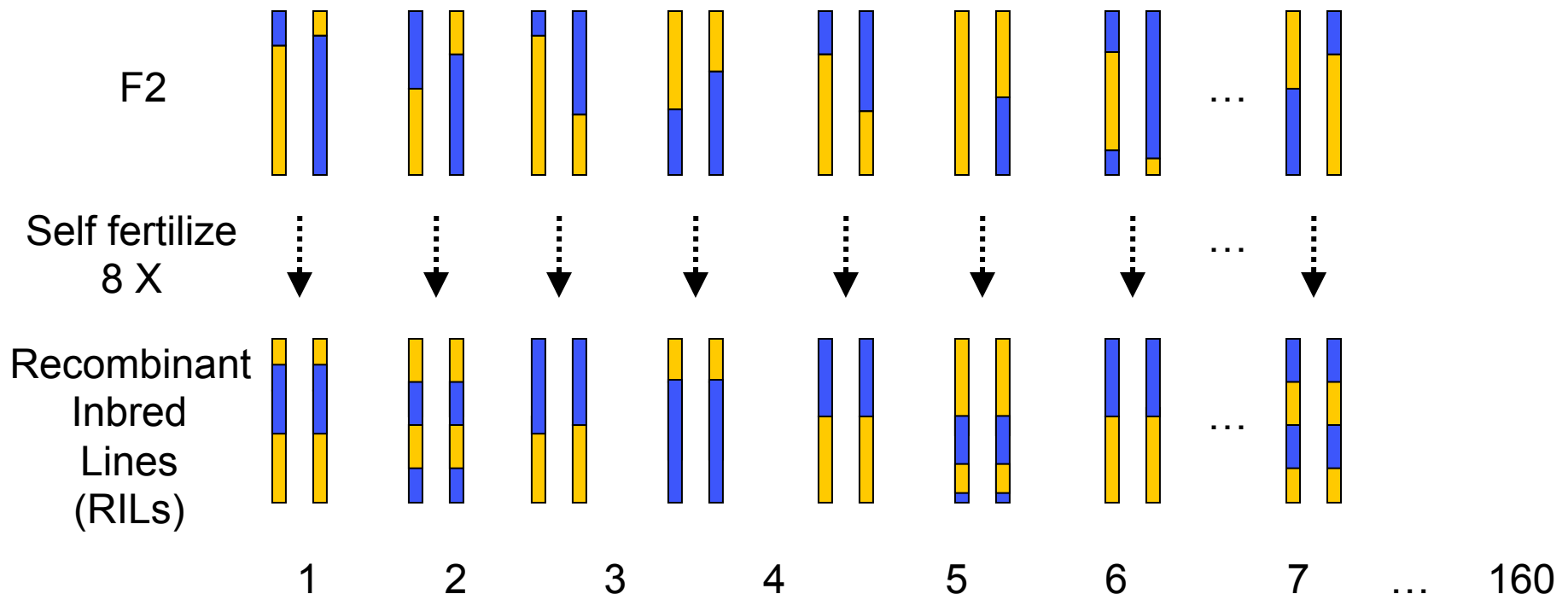
My mutant has a phenotype!



Germplasm is also needed for genome-wide studies

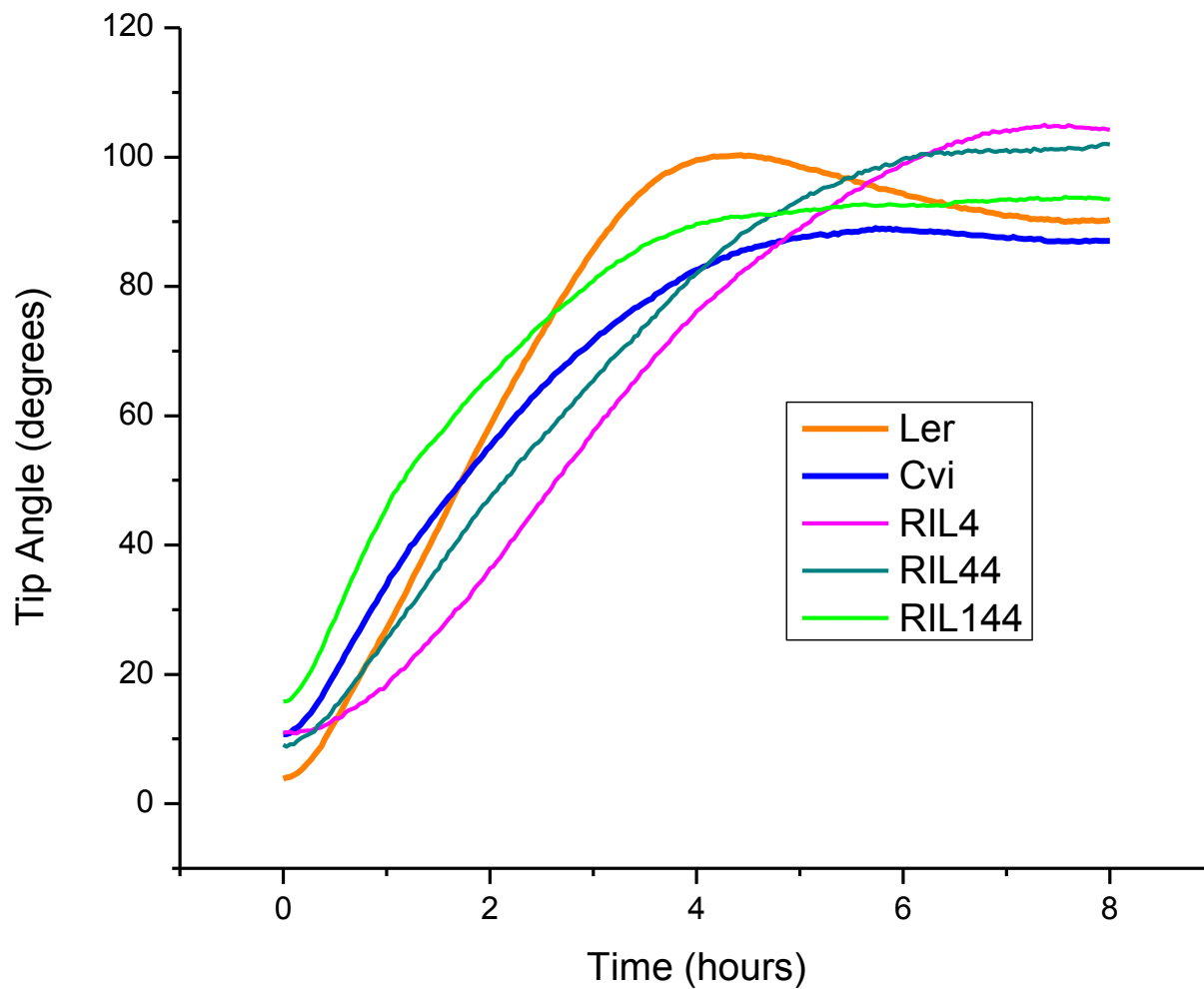


Populations useful for mapping phenotype to genotype have been created in many species. They are genetically well defined. **The current bottleneck is the rate of trait measurement.**

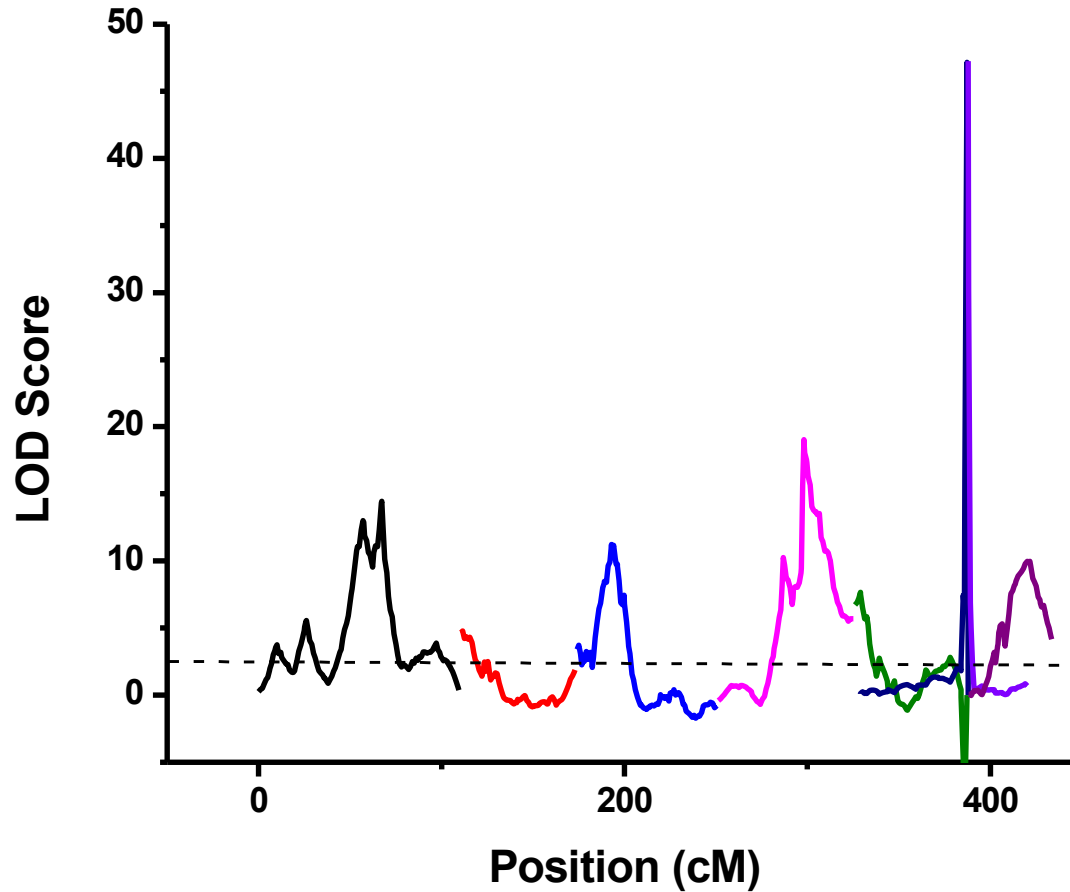


Machine Vision to Study Natural Genetic Variation

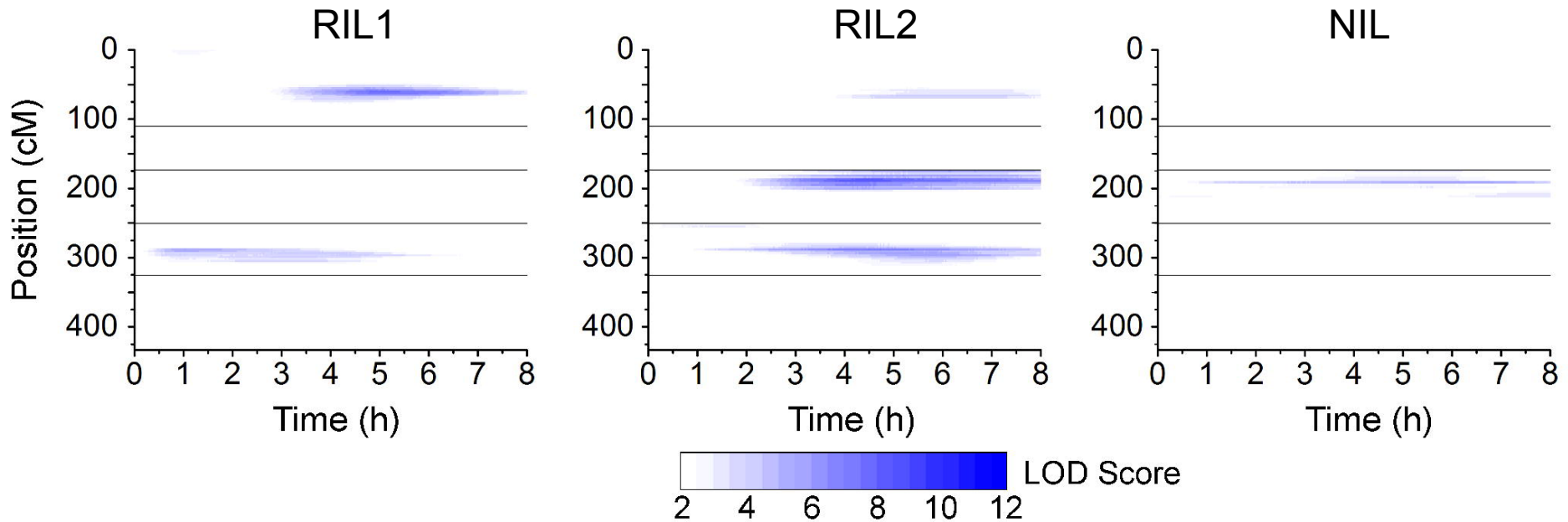
Treat each of the 241 time points as a separate 'trait'



A single QTL plot
(root tip angle at one point in time is the phenotype)



Time Course QTL Affecting Gravitropism



The Key People



Logan Johnson

Candace Moore

A Phenotype Pipeline

depends on a software continuum connecting three overlapping domains

Acquisition

produces *Raw Files*

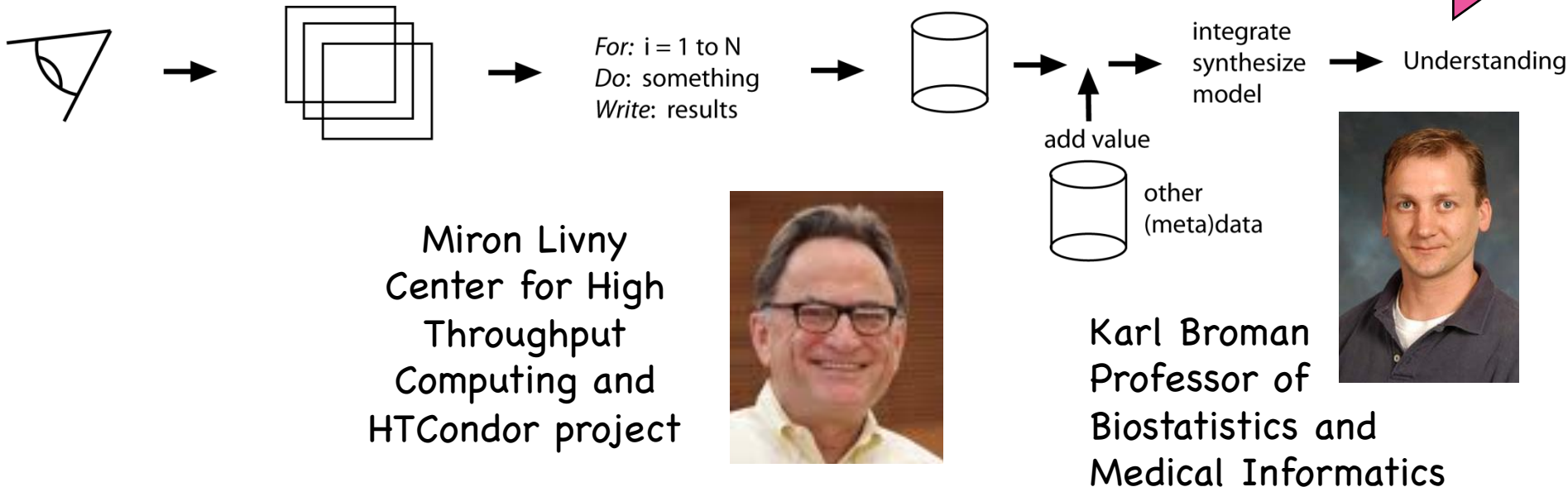
Algorithms

generate *Results*

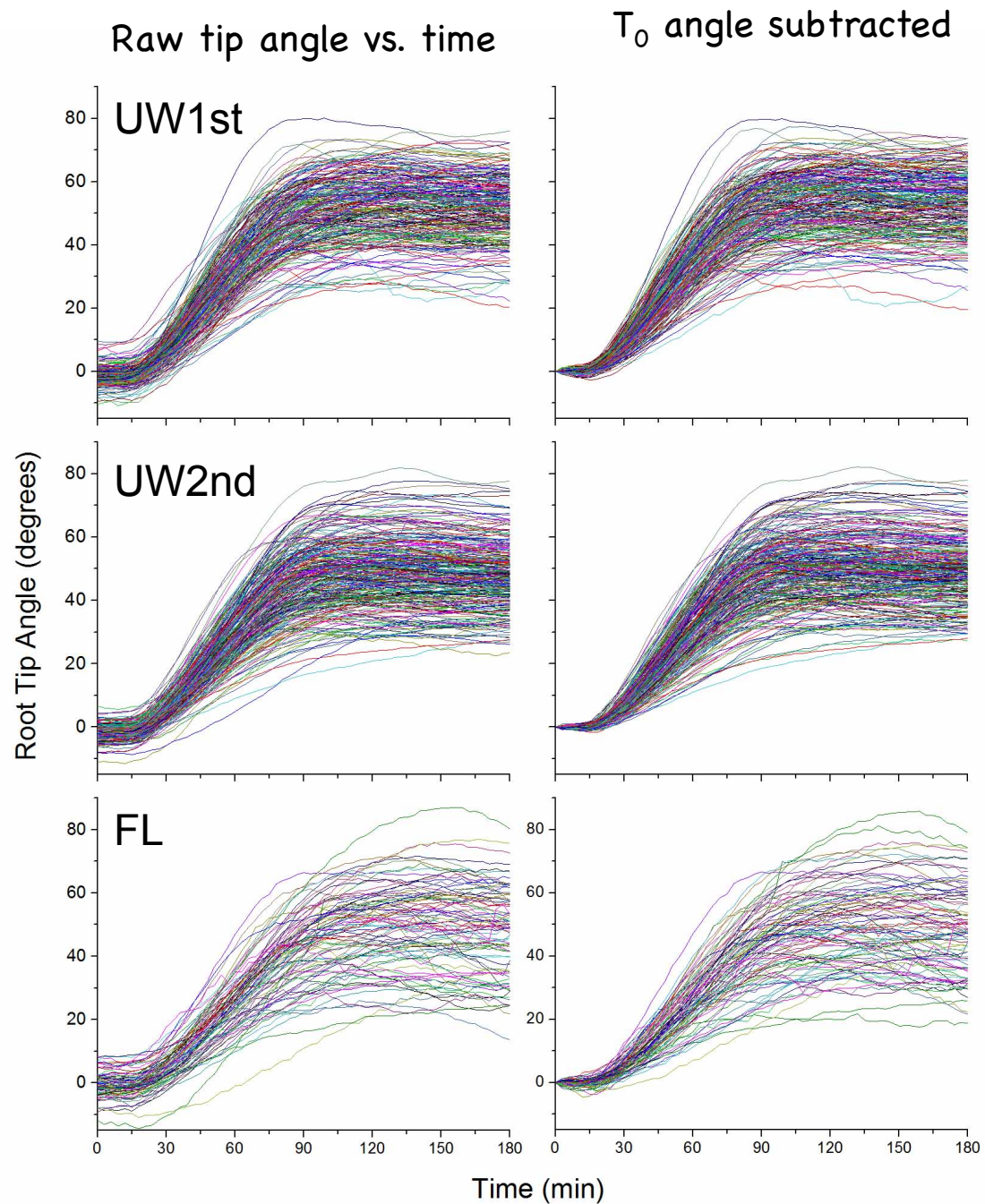
Modeling

generates *Understanding*

Acquisition produces Raw files from which an Algorithm extracts Results to be Modeled with other (meta)data to create Understanding

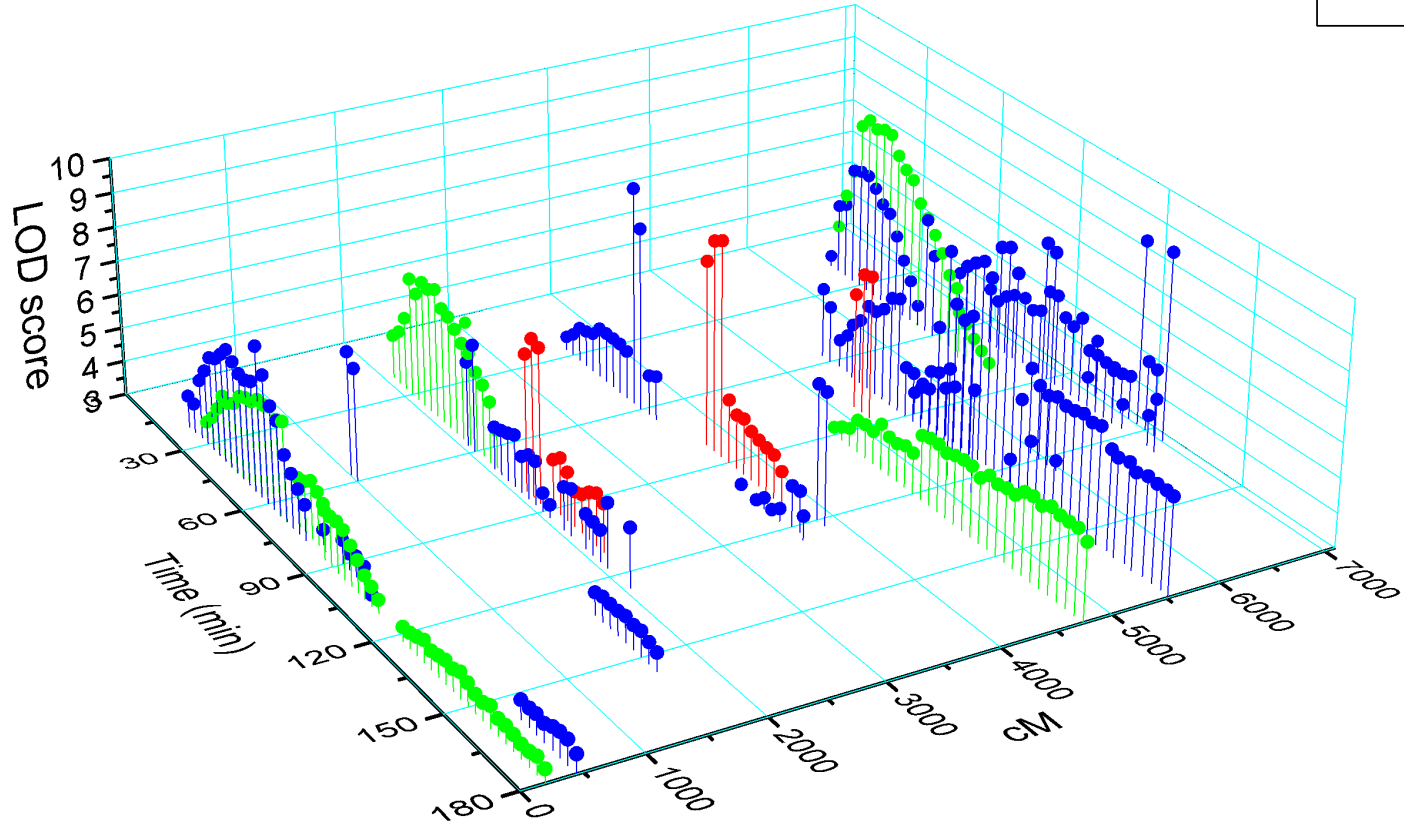


UW 1st set 239 lines
UW 2nd set 280 lines
FL 88 lines



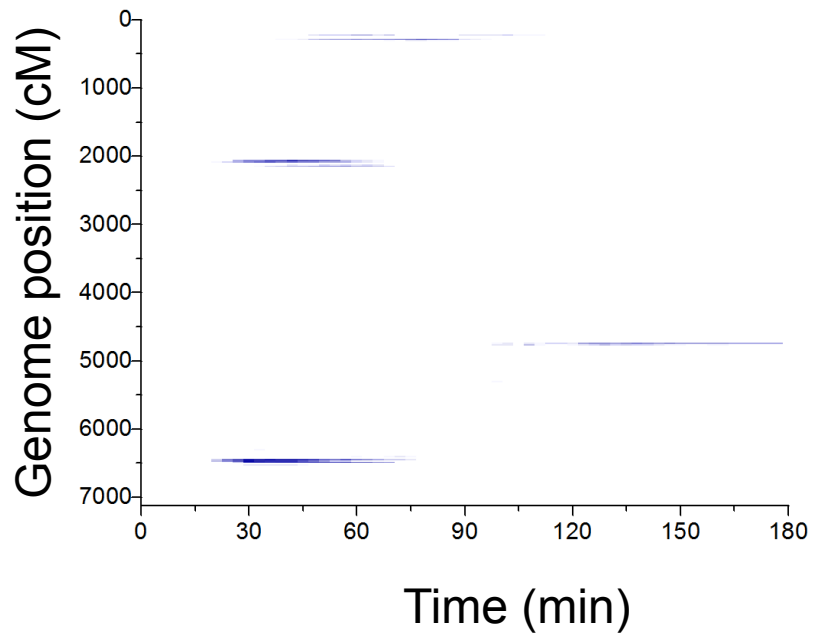
Maize root gravitropism time course QTL

- UW1st
- UW2nd
- FL

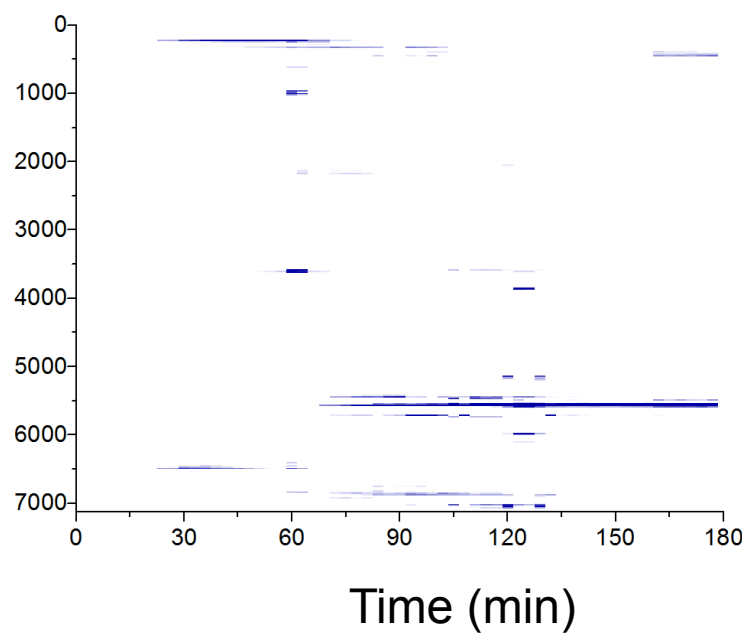


Maize gravitropism QTL

UW IBM302 RIL1



UW IBM302 RIL2



The Key People

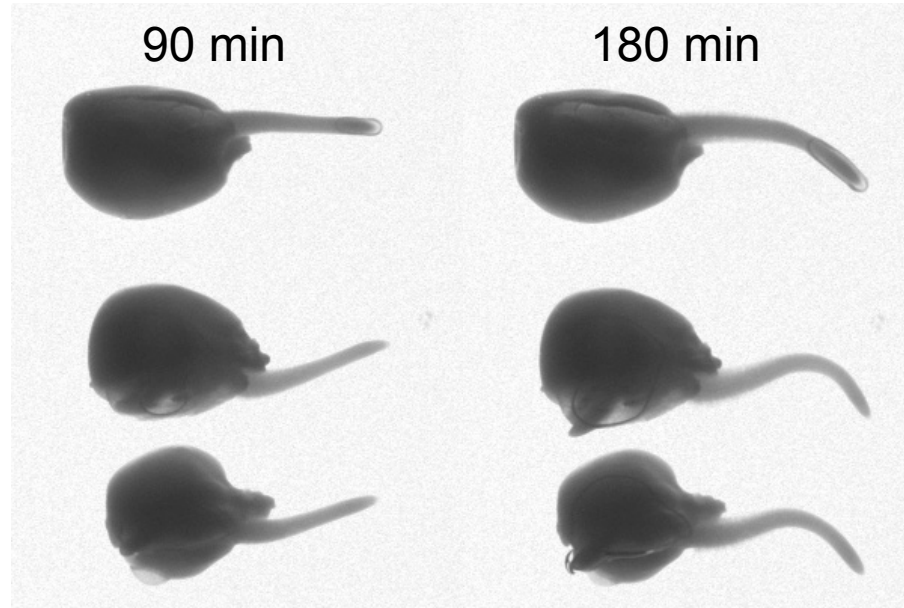


Takeshi Yoshihara

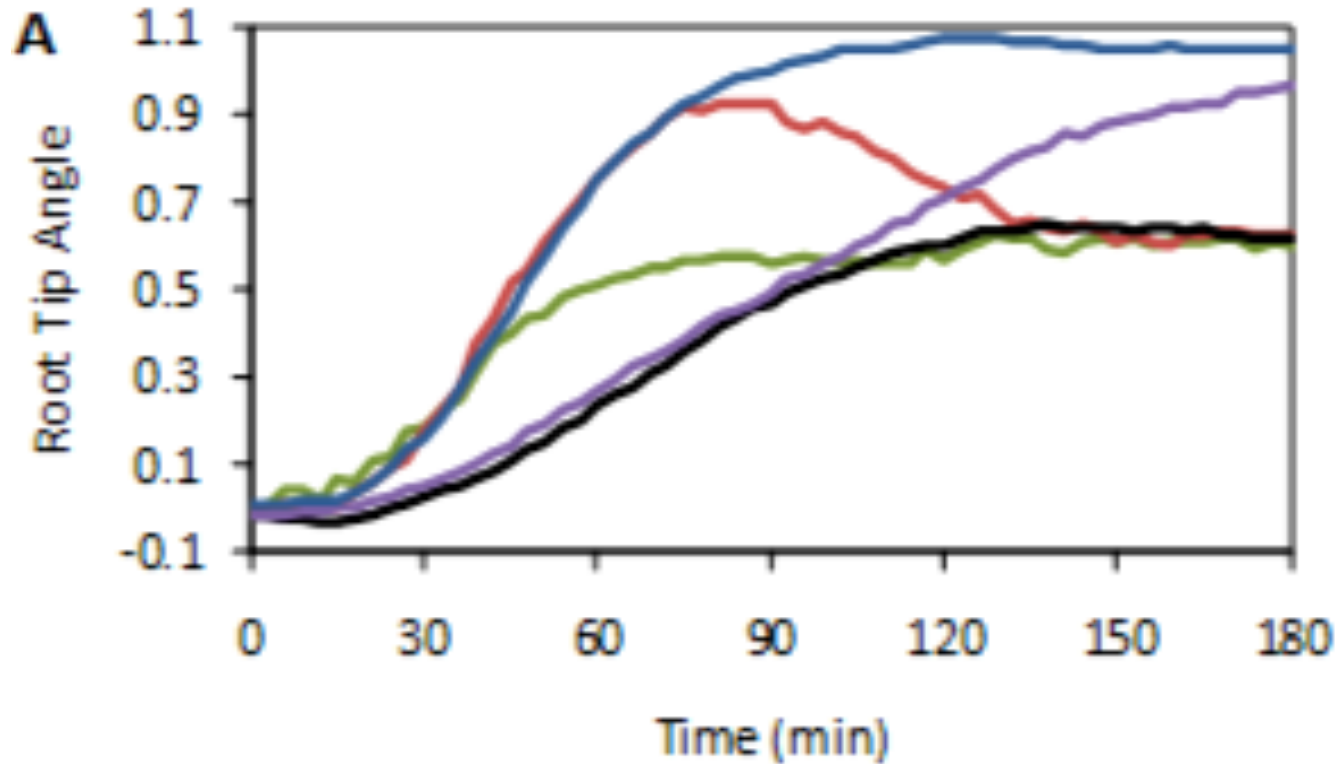


Nathan Miller

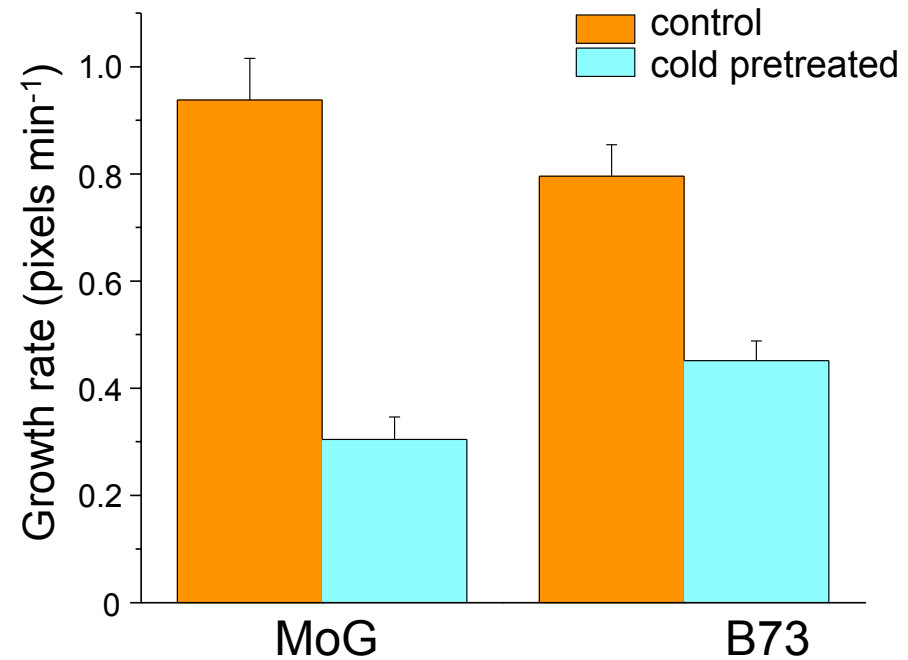
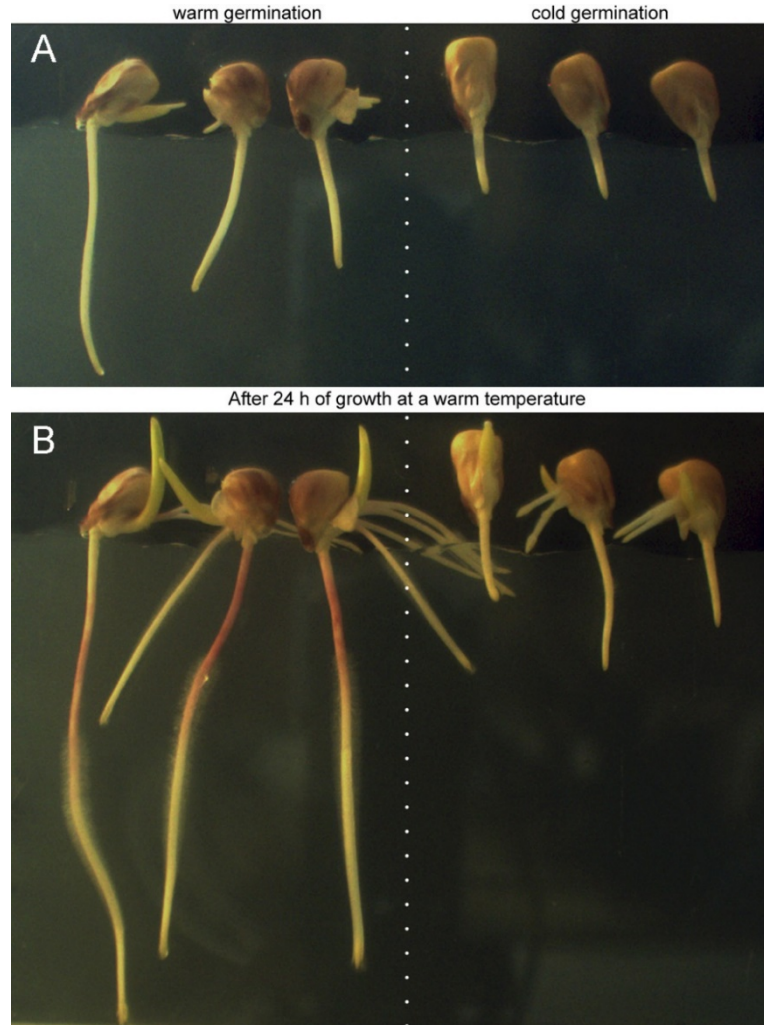
Maize Gravitropism QTL

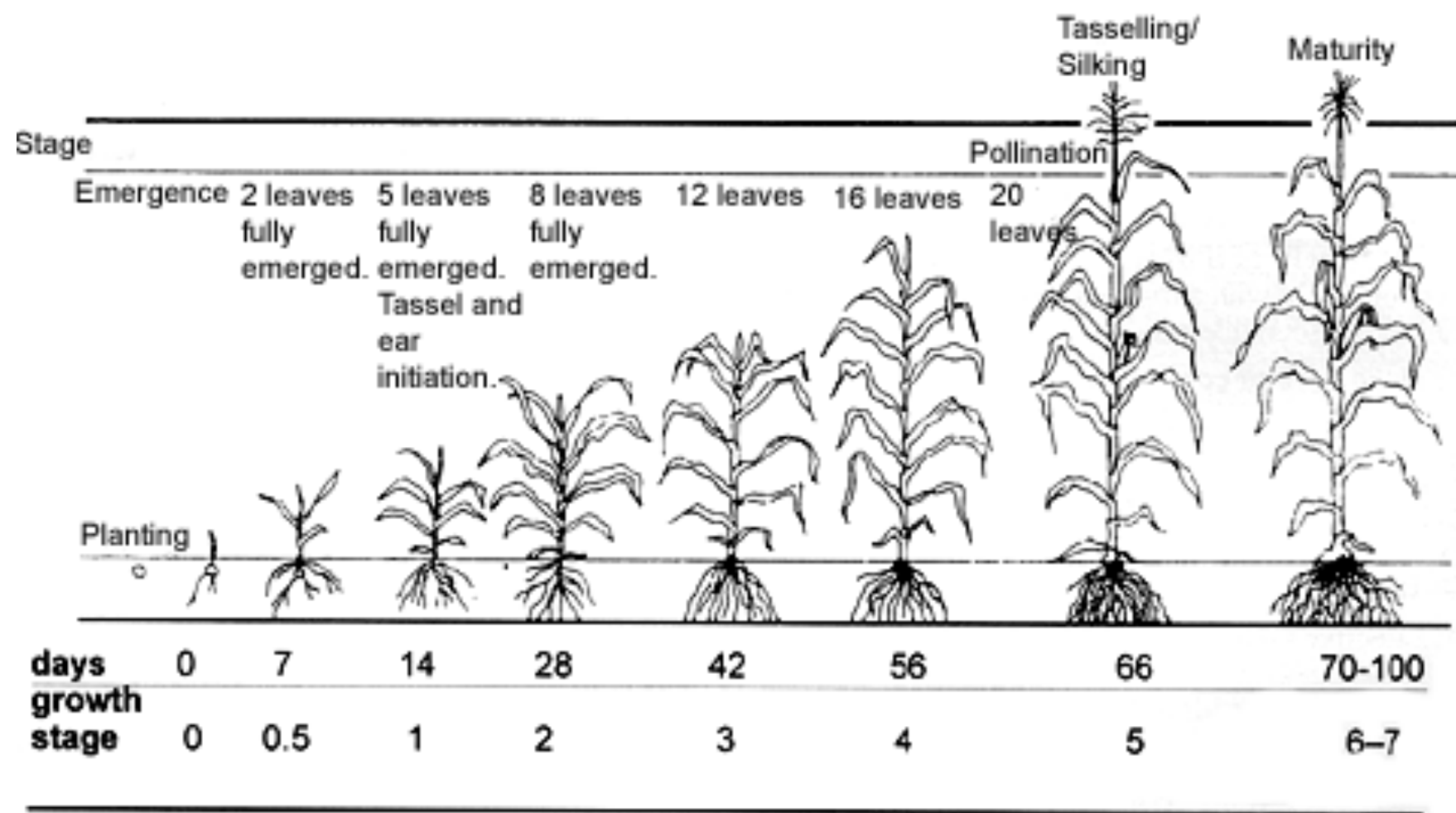


Variation within maize population of RILs

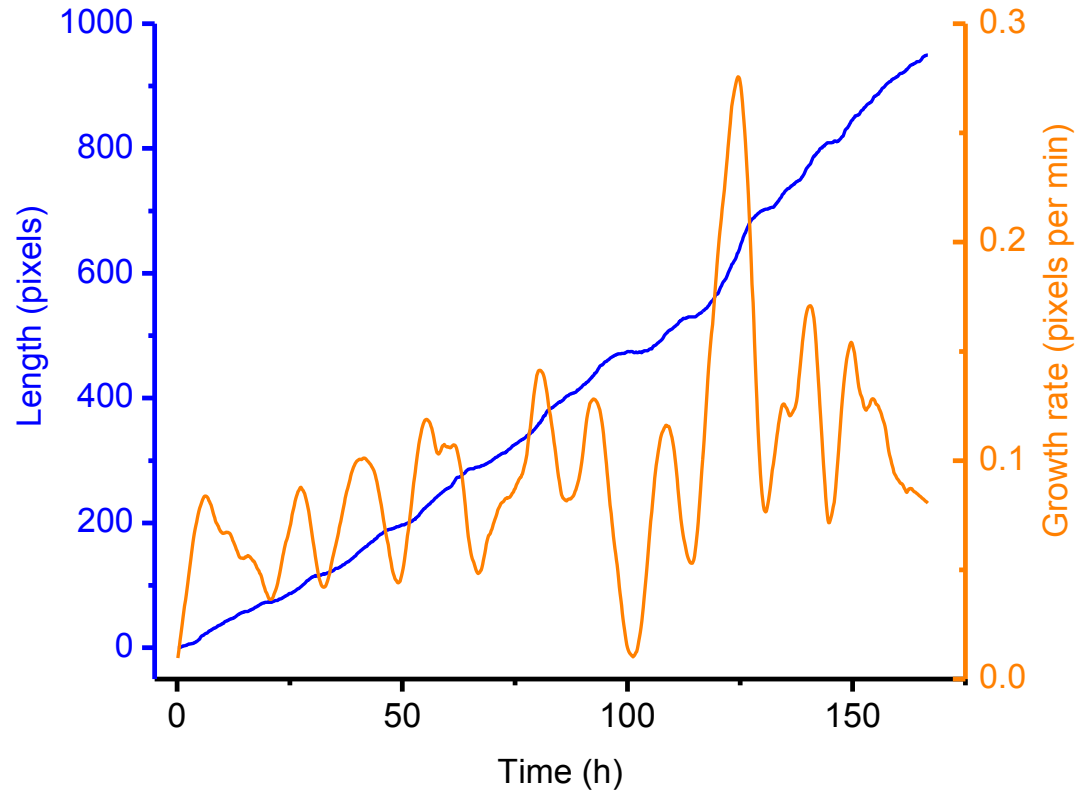


A cold pretreatment impairs growth over an ensuing 24 h warm period

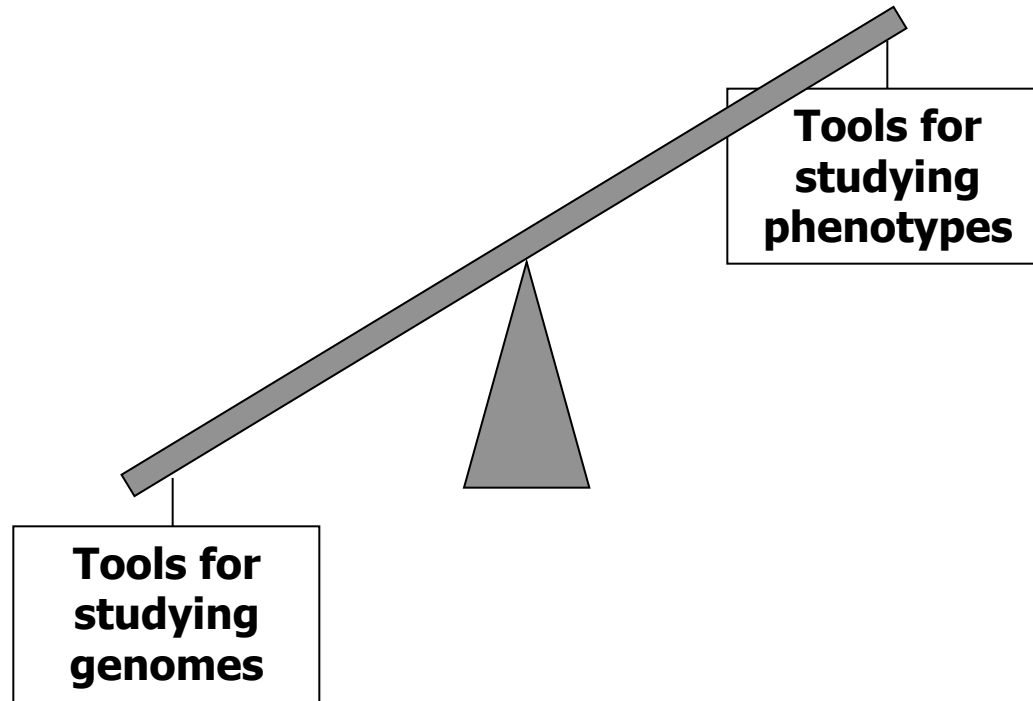




Measuring maize growth in the field



Motivation of the Phytomorph Project



Motivation of the Phytomorph Project

