

# Quantitative Methods for Studying Fruit Morphology in Strawberry

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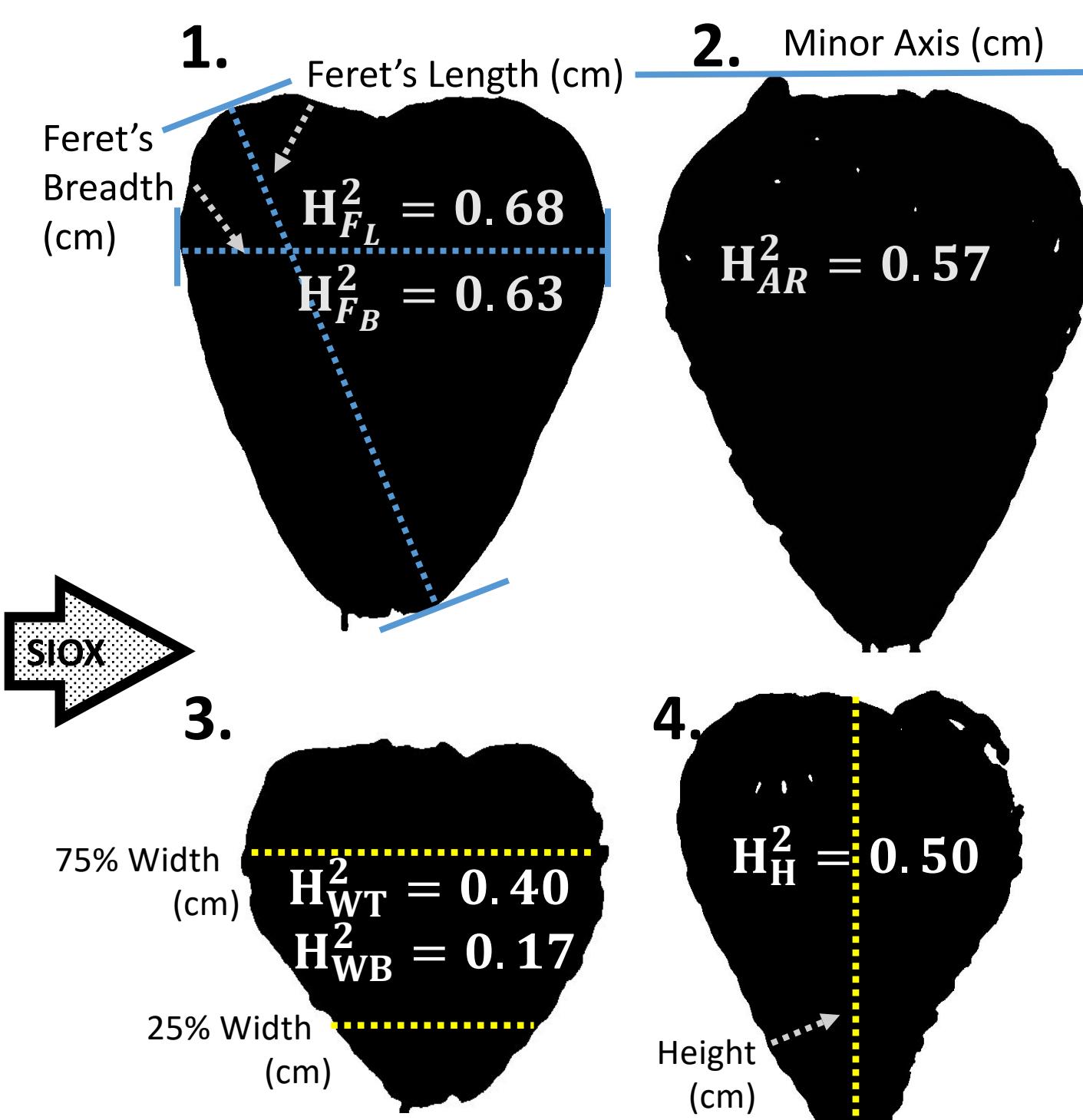
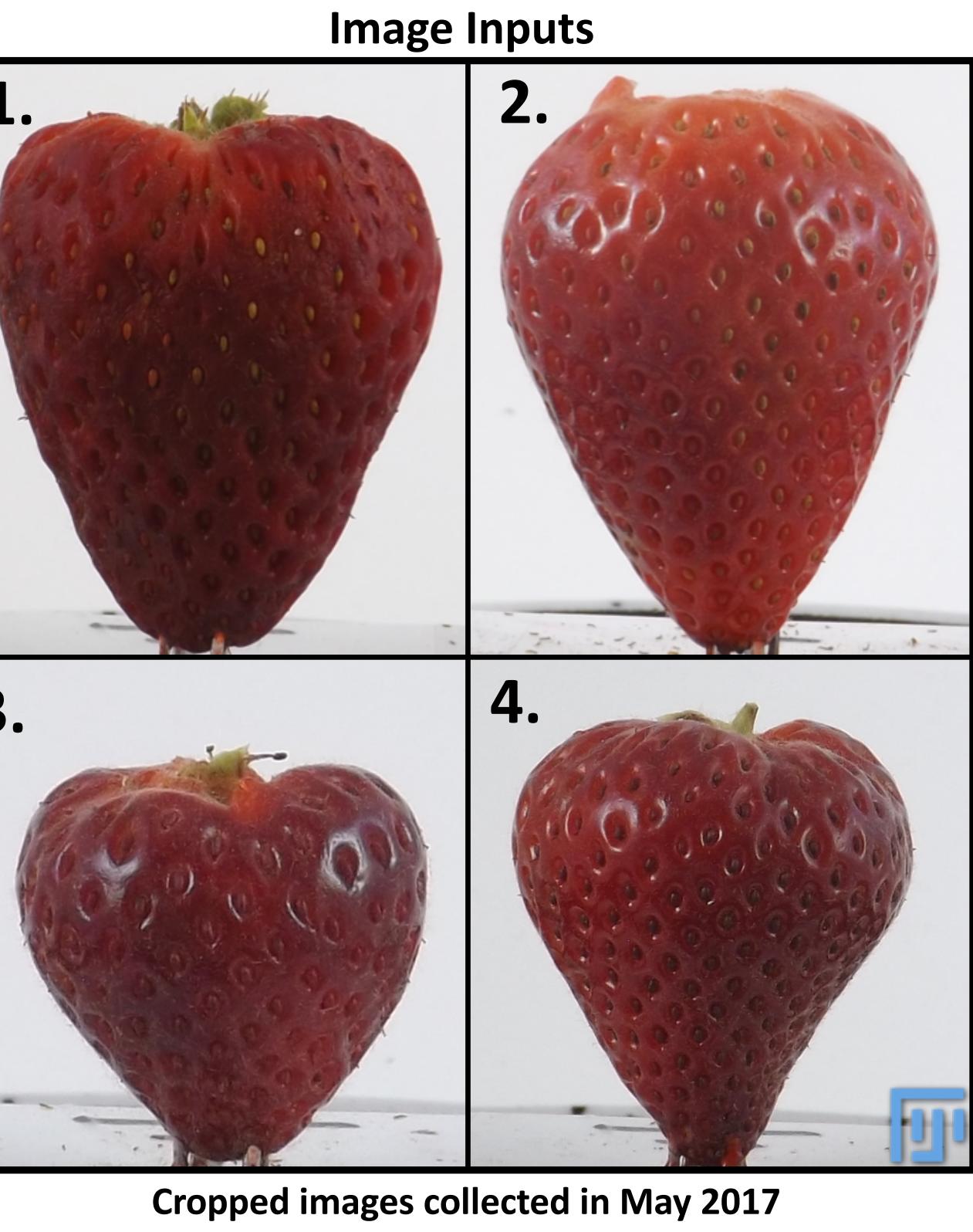
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## Introduction

Several phenotypic characteristics, including, shape, and external color, are determinants of both grower- and consumer-centric fruit quality in strawberry (*Fragaria × ananassa*). Strong artificial selection for superior shelf-life, increased yield of marketable fruit, and other commercial production traits has significantly changed fruit morphology and quality attributes to produce high yielding cultivars with large, ultra-firm fruit. The genotype-to-phenotype networks underlying these changes have not been investigated in depth, and genes targeted by selection have not yet been identified in strawberry. Moreover, it remains unclear what level of phenotypic complexity is necessary and sufficient to support genomic-based inquiries and discoveries, expand what is known about modern germplasm, and enhance breeding practices in strawberry. Here, we demonstrate the quantitative methods being deployed to study fruit morphology in strawberry.

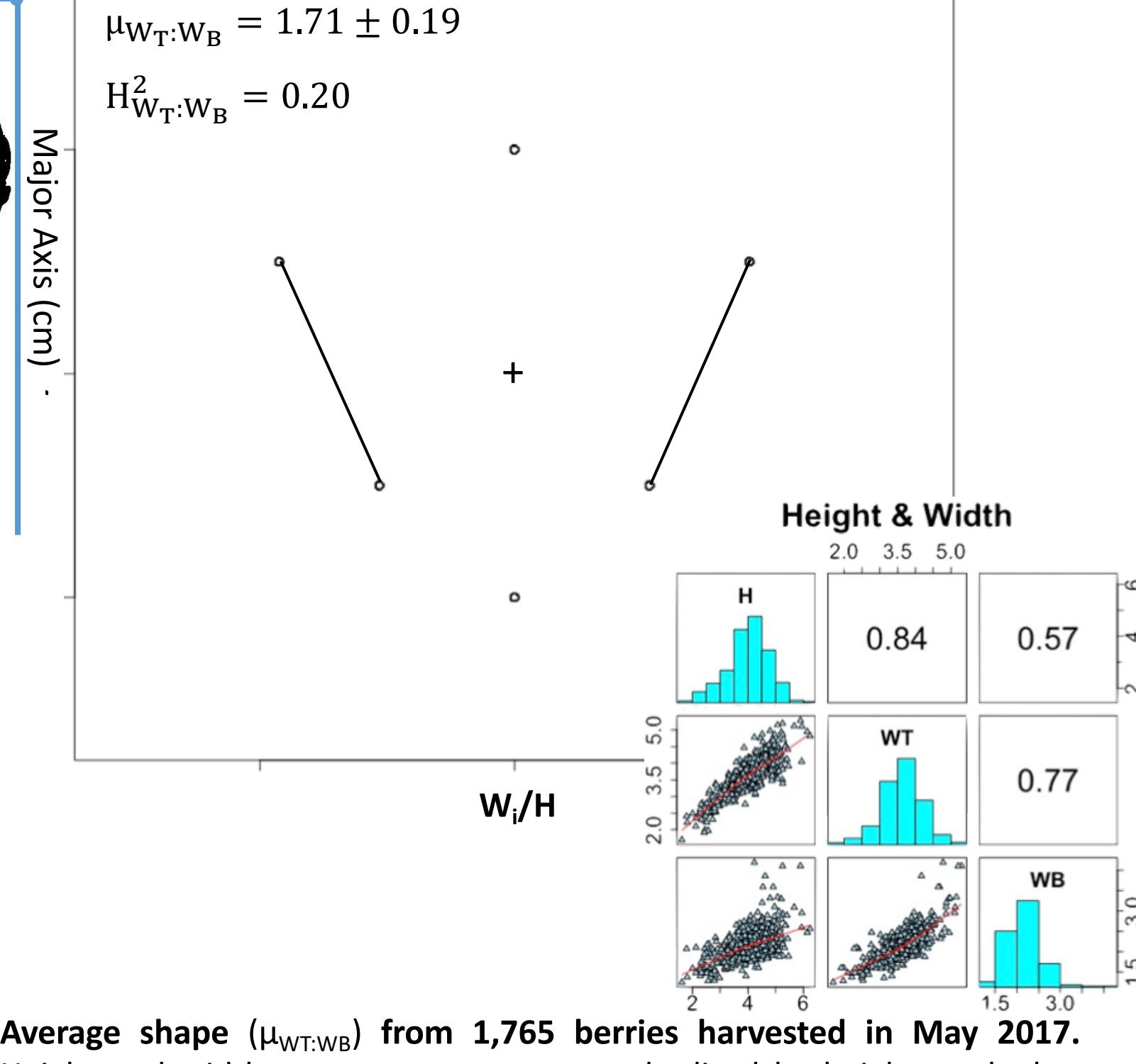
## Methods

### In One Dimension



Masks generated using the SIOX algorithm in FIJI [1]. Broad sense heritability of each trait estimated as  $H^2 = \sigma_G^2 / \sigma_P^2$

### Average Standardized Shape

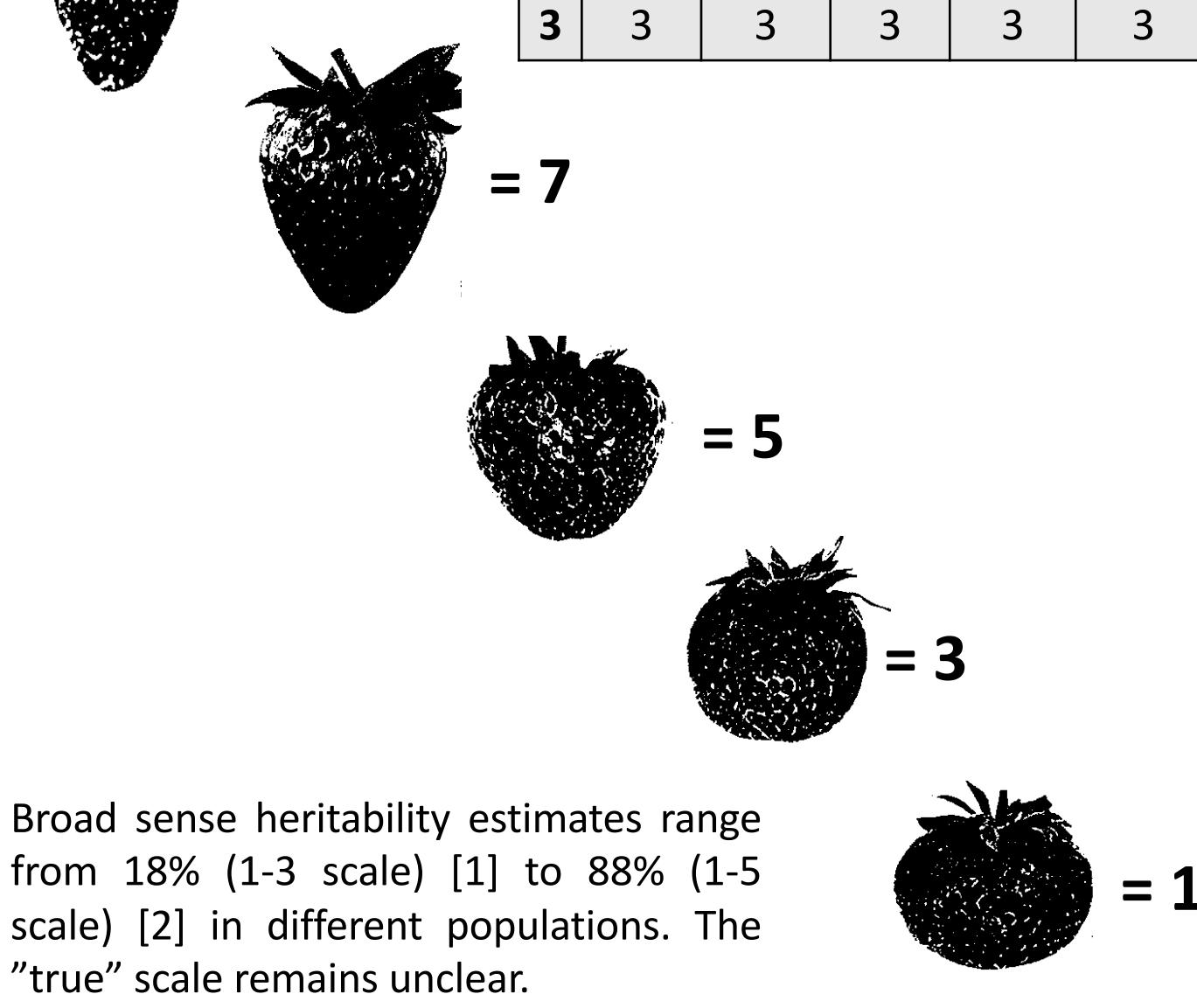


Average shape ( $\mu_{W_T:W_B}$ ) from 1,765 berries harvested in May 2017. Height and width measurements are standardized by height, such that the height of every berry is 1 cm.

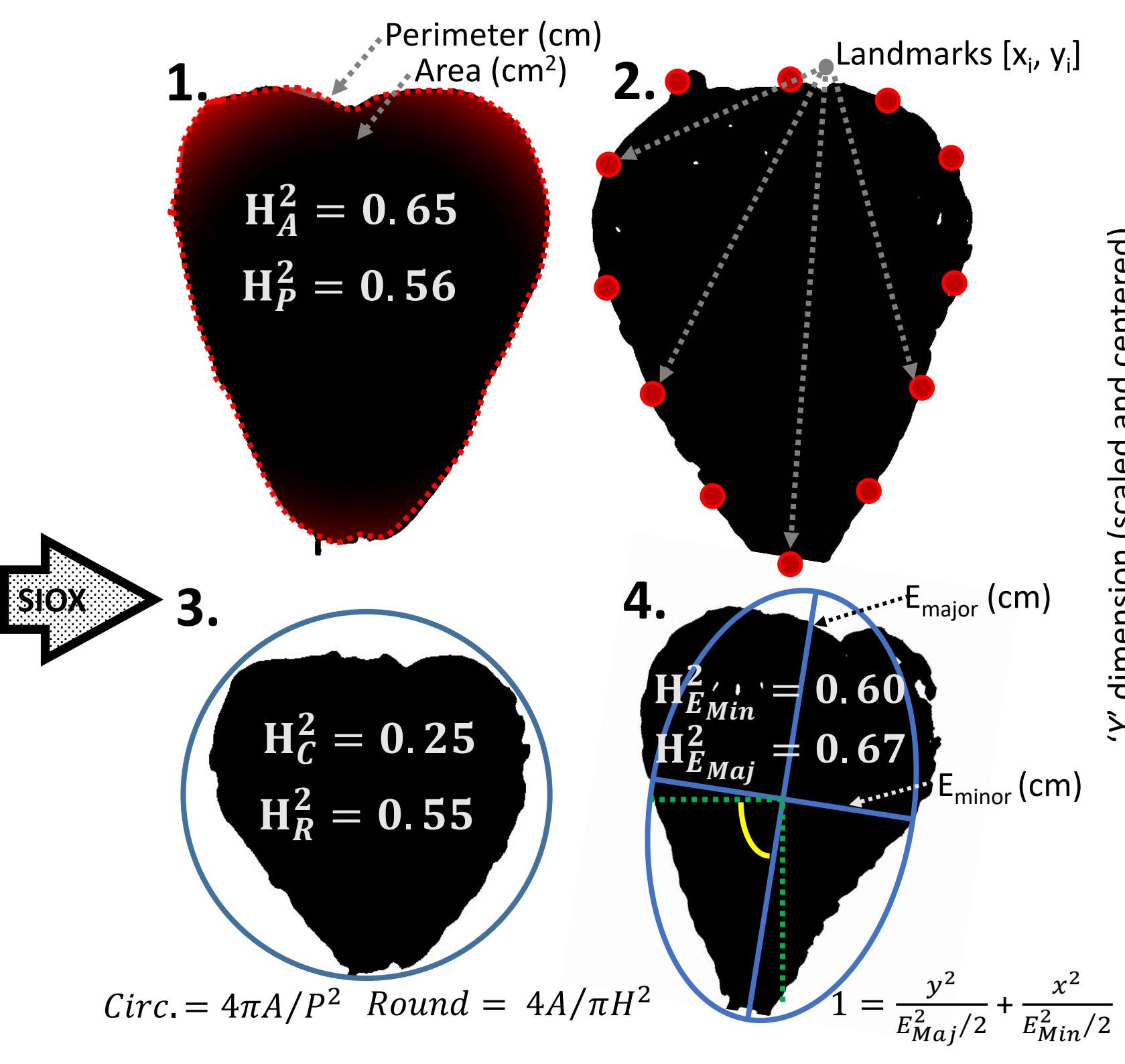
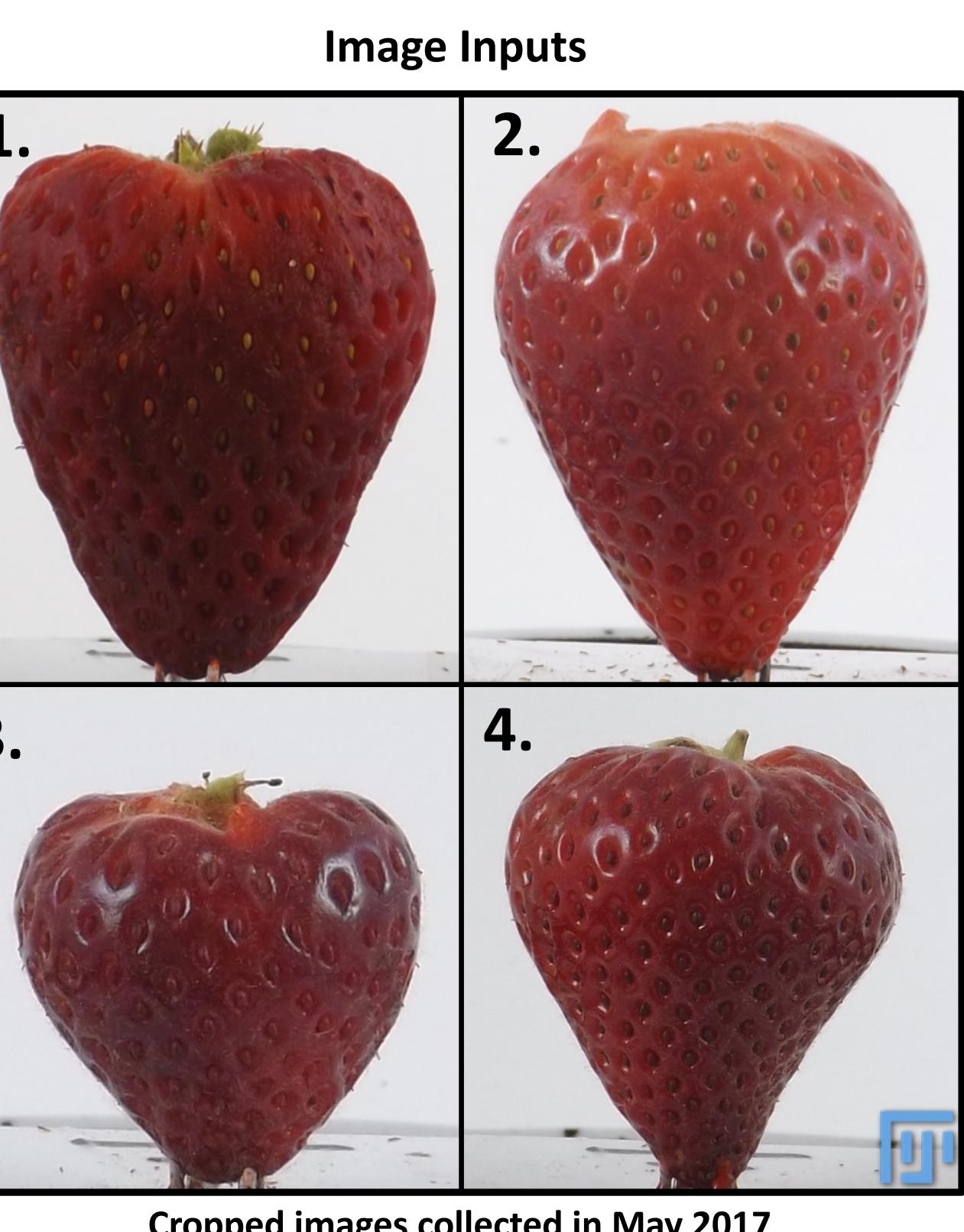
### Categorical

Current shape phenotyping protocols for strawberry rank fruit into categories (1-n).

#	ID1	ID2	ID3	ID4	$\mu$
1	1	2	1	1	1.25
2	2	2	2	1	1.75
3	3	3	3	3	3

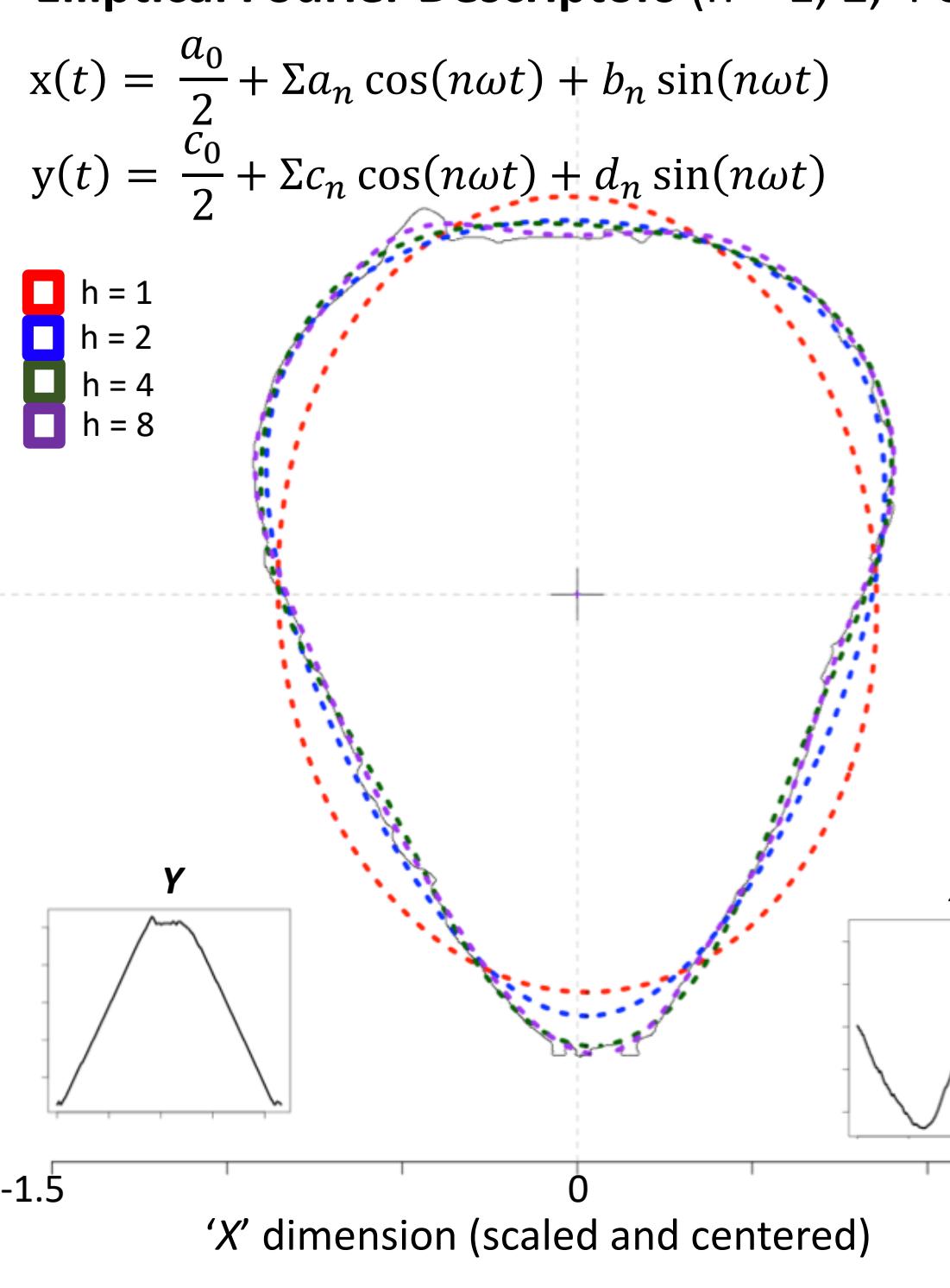


### In Two Dimensions



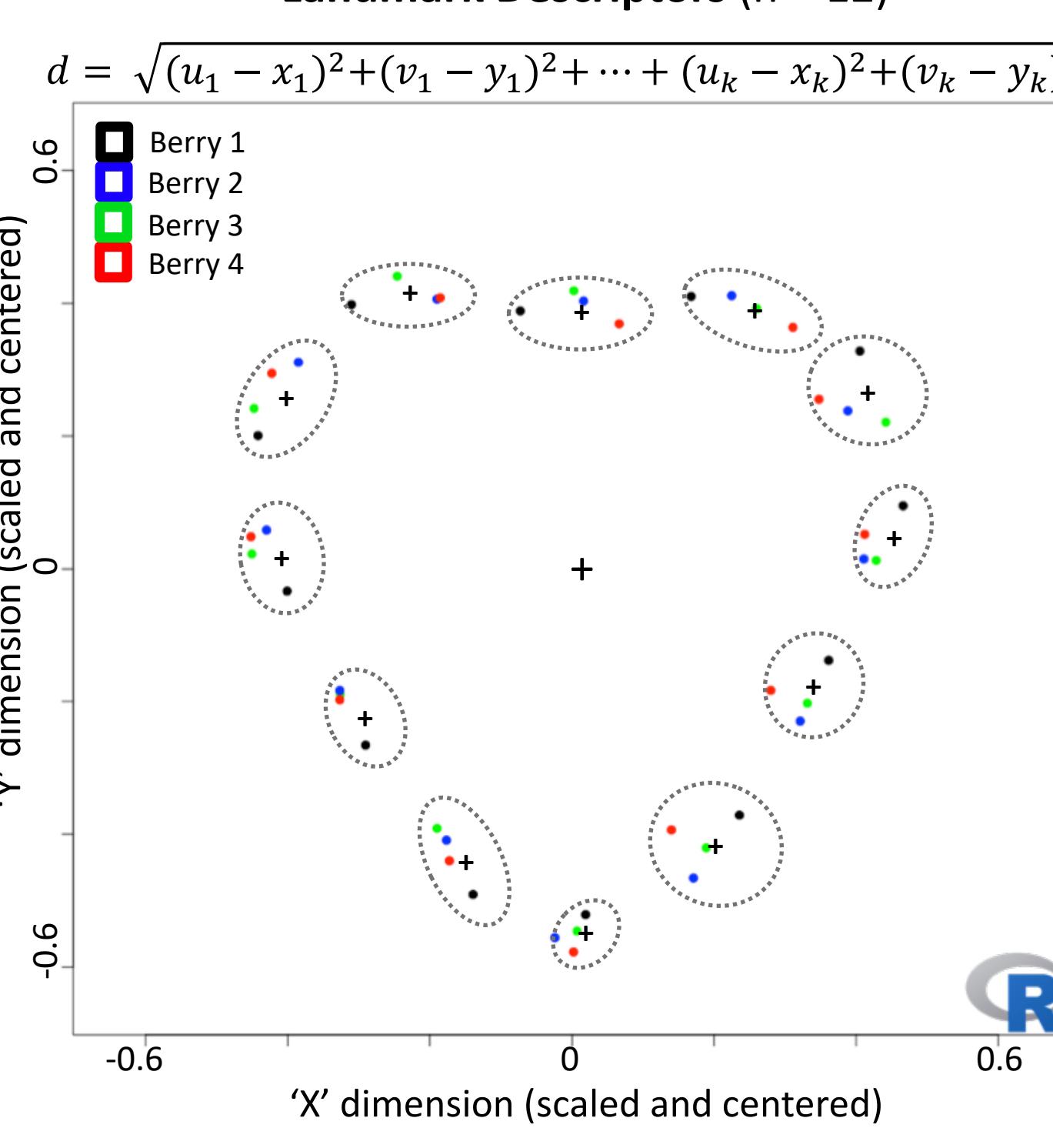
Masks generated using the SIOX algorithm in FIJI [1]. Broad sense heritability of each trait estimated as  $H^2 = \sigma_G^2 / \sigma_P^2$

### Elliptical Fourier Descriptors (h = 1, 2, 4 & 8)



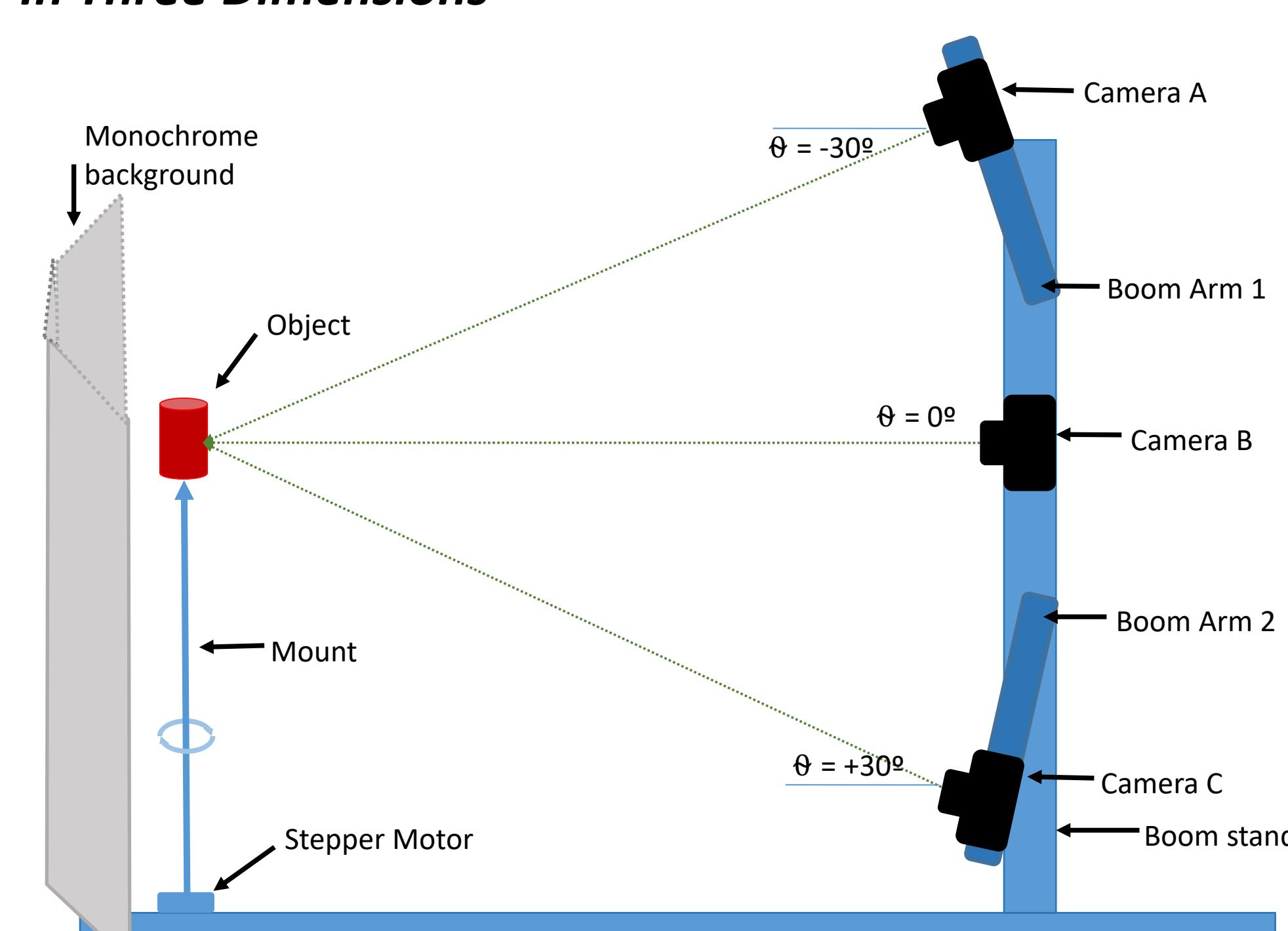
Elliptical Fourier Descriptors generated using "Momocs" in R [4]. The "Momocs" package in R provides a simple for calculating functional shape descriptors of closed form outlines.

### Landmark Descriptors (n = 12)



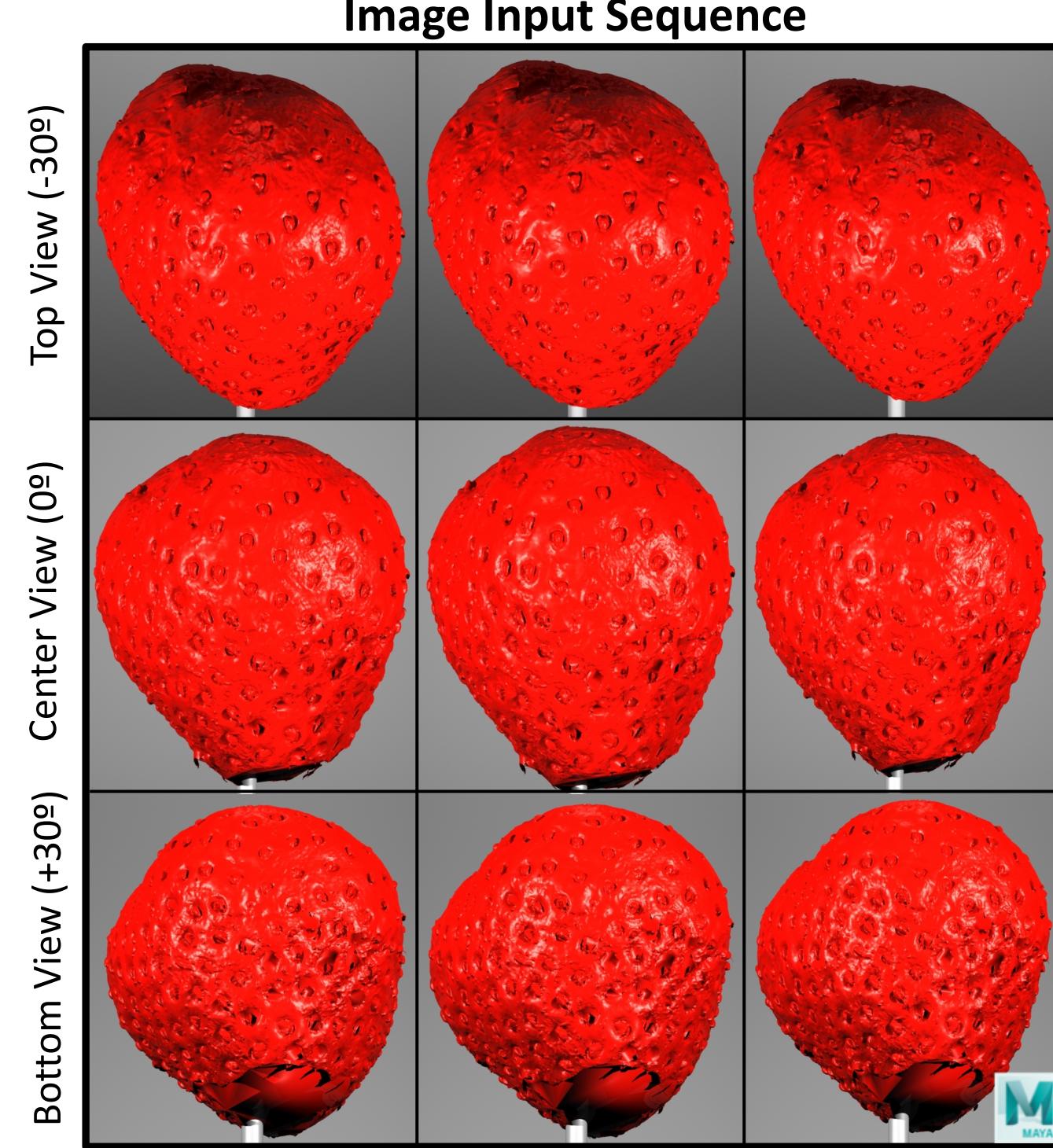
Unaligned pseudo-landmarks extracted in R. 12 evenly spaced points along the closed outline for the four strawberries are depicted along with centroid of each cluster.

### In Three Dimensions



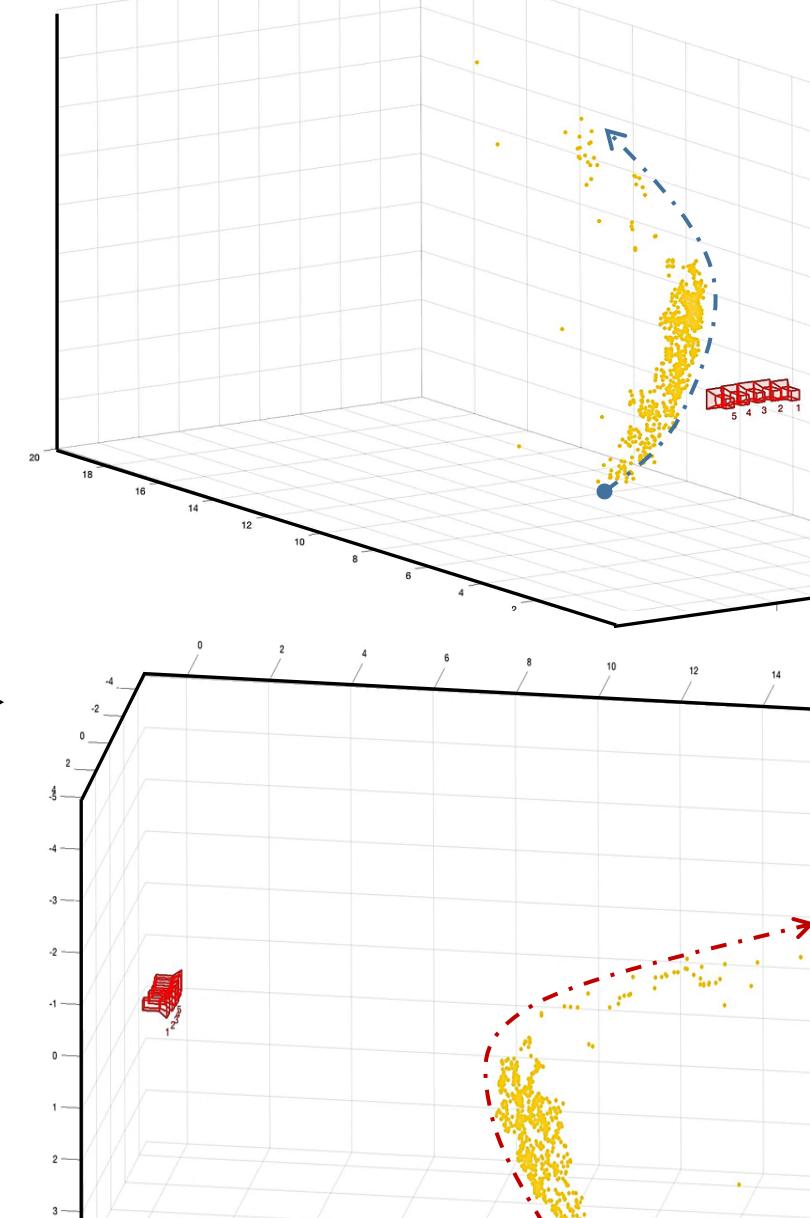
Initial design of imaging platform for automated image capture.

Digitally implemented in the AutoDesk® Maya® software to capture images from 3-D models.



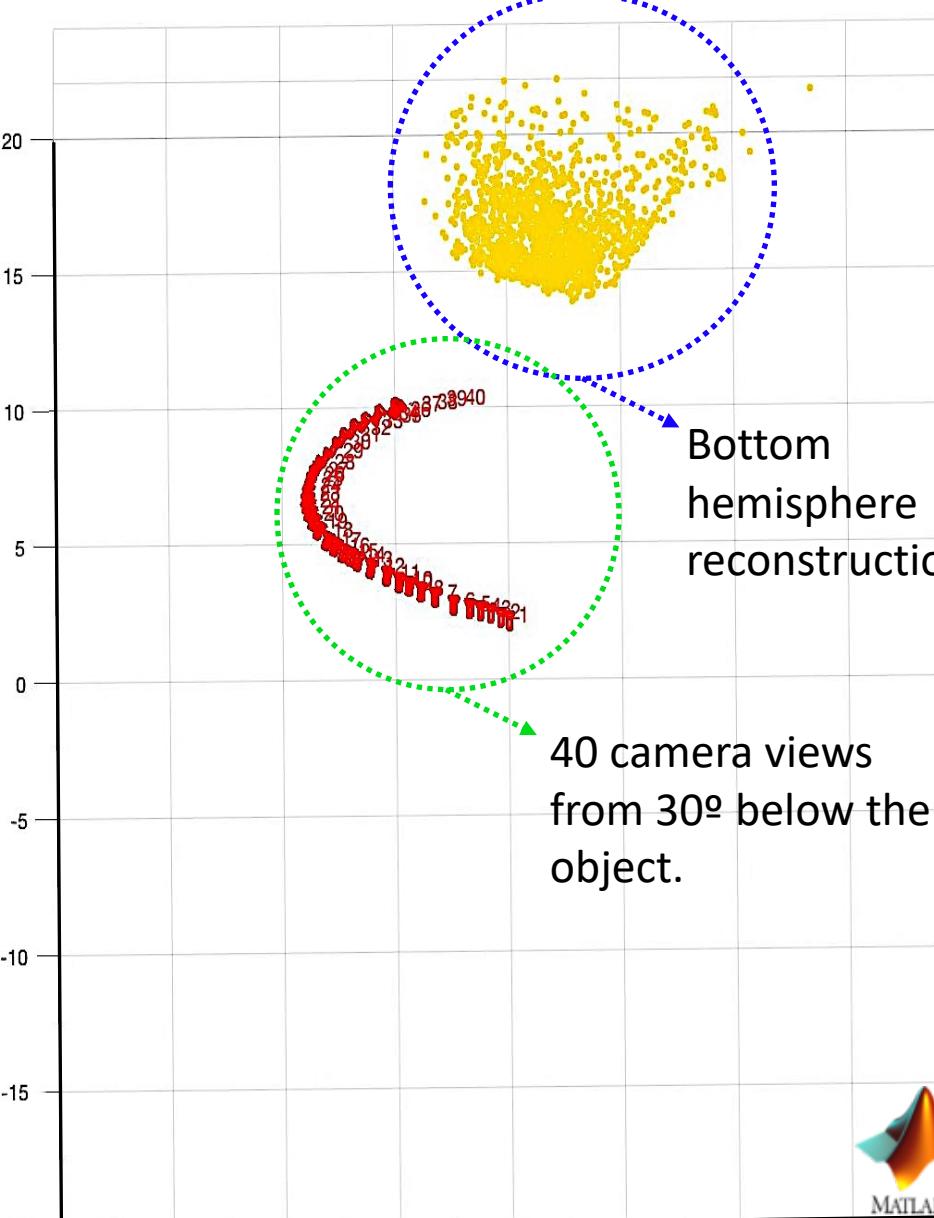
Images digitally rendered in Maya® by AutoDesk®. 60 views (6° between views) per rotation, per camera were captured for each digital object.

### A. Dense Reconstruction (5 views)



Camera calibration, key point detection, and 3-D sparse point-cloud rendered in MATLAB. Five centered views (A) and 40 bottom views (B) were used to check camera alignment using MATLAB. Observed a collapse in the angular spacing of our known camera positions

### B. Dense Reconstruction (40 views)



## Conclusions

- Both one and two dimensional traits, which are cheap and easy to acquire and assess, have broad sense heritability on the range of [0.17, 0.68] demonstrating the genetic control of these phenotypes.
- Multiple proprietary software have failed to detect and register key points during camera calibration for the 3-D reconstruction of strawberries giving credence to our work.
  - Images generated from 5 cameras seem to align well and generate dense clouds that resemble strawberries.
  - We are yet to obtain a full 3-D reconstruction of a strawberry as the angle between individual cameras seems to collapse from 6° to 4°.
- Three dimensional traits avoid the symmetry assumptions of both one and two dimensions and provide detailed topological information for performing functional data analytics and generating genomic insights.

## Future Directions (and Dimensions)

- Fix issues with camera calibration and validate accuracy of 3-D fruit models.
- Determine which morphological features are most relevant for classifying strawberries into distinct categories.
- Implement genome wide-association and genomic selection to determine signal in 1-D, 2-D, and 3-D parameterizations.
- Explore the biological development of morphological features through time and differential gene expression.

References: [1] Schindelin et al. Nat. Meth. (2012); [2] Whitaker et al. J. Amer. Soc. Hort. Sci. (2012); [3] Antanaviciute, L. Thesis. (2016); [4] Bonhomme et al. J. Stat. Soft. (2014);



United States Department of Agriculture National Institute of Food and Agriculture

Acknowledgments: This work is supported by the Specialty Crops Research Initiative (#2017-51181-26833) from the USDA National Institute of Food and Agriculture. Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the author(s) and do not necessarily reflect the view of the U.S. Department of Agriculture. This work is also supported by the Henry A. Jastro Graduate Student Research Award.

