Description of Topic

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- Description of Topic
- Materials and Image Capture Setup
- Completed Work
- Work in Progress
- 6 Additional Aims
- 6 References

# What is the project?

The project is aiming to use computational methods to answer biologically significant questions on wheat grain morphology and domestication using  $\mu CT$  images.

To do this, I will be using:

- Computer vision on 3D image sets
- Statistical analysis and data science
- Scientific theory to create reproducible results

#### Research Question:

Is it possible to use  $\mu$ CT imaging to answer questions about Wheat domestication?

I hope so!

#### **Null-Hypothesis**

- $\bullet$   $H_0$  = Domestication has no effect on the morphometric properties of wheat
- ullet  $H_0 = \text{Ploidy has no effect on the morphometric properties of wheat}$
- $\bullet$   $H_0$  = There is no difference in hulled and non-hulled genotypes
- \*Hulling is a trait associated with domestication

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# Materials (Plant)

I have a wide range of Wheat genotypes, these are:

- Ranged between diploid, tetraploid and hexiploid
- 12 total genotypes
- Divided between domestication status



Figure 1: A Primitive Wheat Spike

# Methods (Image Generation)

### Capture Methods

In order to generate this data a  $\mu\text{CT}100$  scanner (ScancoMedical, Switzerland) was used Each spike was:

- ~1000 slices (51 slices per stack),
- ullet 125 projections/180° were taken and a
- binning of 6 was used.
- $\bullet$  Output images are a 0.2 megapixel (512 x 512) resolution (68.8  $\mu/\text{pixel}$ )

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# Data Gathering

#### MATLAB Software

Data has been extracted from the  $\mu$ CT images using a method I previously developed at IBERS [1]. A lot of additions and novel augmentations have been added in order to work with the range of Wheat genotypes.

- This is done via separating non-grain from grain ROIs in the image data
- Measurements are taken on a per grain level
- Measurements are in mm, mm<sup>2</sup> and mm<sup>3</sup> based on type
- Data is exported as CSV files

# Improved Watershedding Algorithm

#### Algorithm

$$|x_1 - x_2| + (\sqrt{2} - 1), |x_1 - x_2| > |y_1 - y_2| (\sqrt{2} - 1) |x_1 - x_2|, \text{ otherwise}$$
 (1)

#### Visual Example

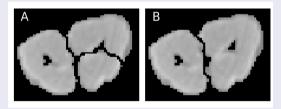


Figure 2: A showing the chessboard method, B improved quasi-euclidean method

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# Data Analysis WIP

#### Statistical Methods to be implemented

These will be implemented in Python using the library SciPy [2]

- ANOVA
- MANOVA
- GLMs

- $\chi^2$  Tests
- PCA
- T/F-Tests

#### Graphing Methods to be implemented

All Graphing is being implemented using Matplotlib [3]

- Box
- Swarm
- Scatter / LM

- Violin
  - Correlation Maps
  - Frequency/Histograms

# Reproducible Analysis GUI - 1 WIP

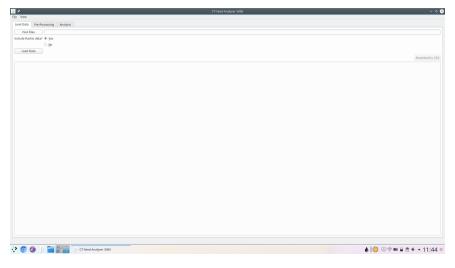


Figure 3: Inital GUI

# Reproducible Analysis GUI - 2 WIP

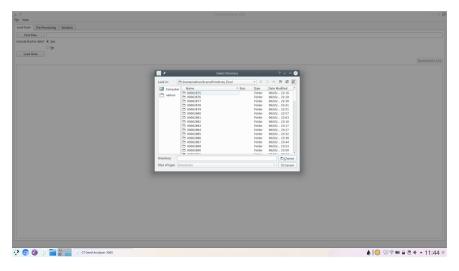


Figure 4: GUI select folders to search for data

## Reproducible Analysis GUI - 3 WIP

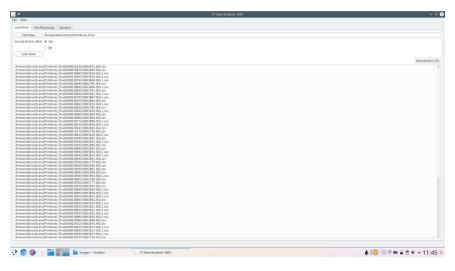


Figure 5: GUI with data loaded sucessfully

# Reproducible Analysis GUI - 4 WIP

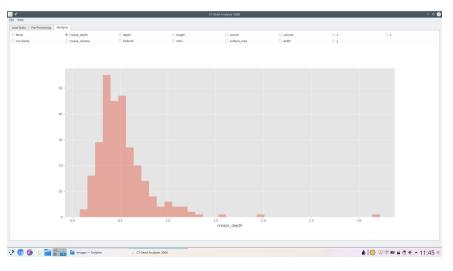


Figure 6: GUI dynamically graphing crease\_depth

# Reproducible Analysis GUI - 5 WIP

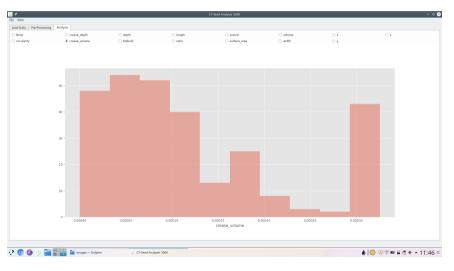


Figure 7: GUI dynamically graphing crease\_volume

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#### Additional Aims

#### Not yet started, but would like to implement by end of project

- Automate error finding and identification
- Visually Display Errors in Data
- Write testing suite for software

#### Ideas for future work

- Test software library on other datasets
- Grow more plants and create more replicates for more robust study

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References O•

#### References

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- [1] Nathan Hughes, Karen Askew, Callum P Scotson, Kevin Williams, Colin Sauze, Fiona Corke, John H Doonan, and Candida Nibau.
  - Non-destructive, high-content analysis of wheat grain traits using X-ray micro computed tomography. *Plant Methods*, 13, 2017.
- [2] Eric Jones, Travis Oliphant, and Pearu Peterson. {SciPy}: open source scientific tools for {Python}. 2014.
- [3] J. D. Hunter. Matplotlib: A 2d graphics environment. Computing In Science & Engineering, 9(3):90–95, 2007.