

# Modelling the effects of domestication in Wheat through novel computer-vision techniques

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### Introduction

This project aims to create a set of data, of novel phenotypic information, using a computer vision technique I developed at the National Plant Phenomics Centre for examining wheat grains using  $\mu$ -Computed Tomography [2]. This technique allows for a detailed extraction of 3-dimensional morphometric data of seeds in wheat and other crops.

I have been able to gain access to a wide range or primitive, non-domesticated wheat varieties as well as their cultivated relatives. These genotypes also provide a nice gradient of ploidy which could also provide great insight into how genome structure effects grains. I aim to use the outlined method to extract data from these crops and create statistical analysis software to answer various research questions.

### Research Aims

Primarily I have three main null-hypothesis which I hope this project will be able to reject:

- ▶  $H_0$  = Domestication has no effect on the morphometric properties of wheat
- ▶  $H_0$  = Ploidy has no effect on the morphometric properties of wheat
- ▶  $H_0$  = There is no difference in hulled and non-hulled genotypes

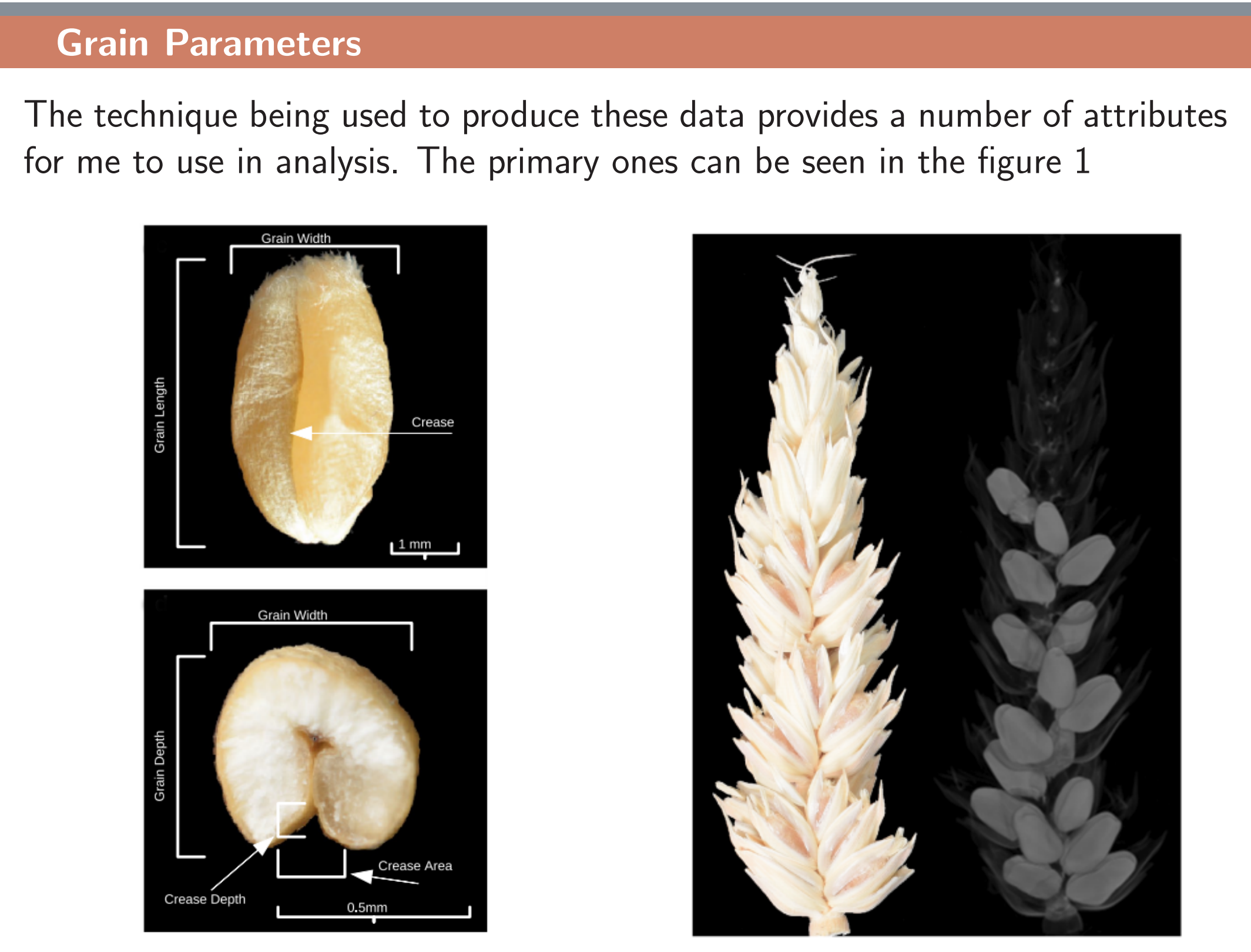


Figure 1: wheat grains labelled with data

Figure 2: wheat Spikes original (left) and scanned (right)

### Software Development Aims

In order to make this work reproducible, as I believe it will justify many further studies I am creating a software library which acts as a specialist tool for handling the type of data which CT-Scanners output.

To do this I am using the *PyQT* library to create a GUI framework which will be useable by non-programmers in order to test hypothesis and build systematic models of the given input data.

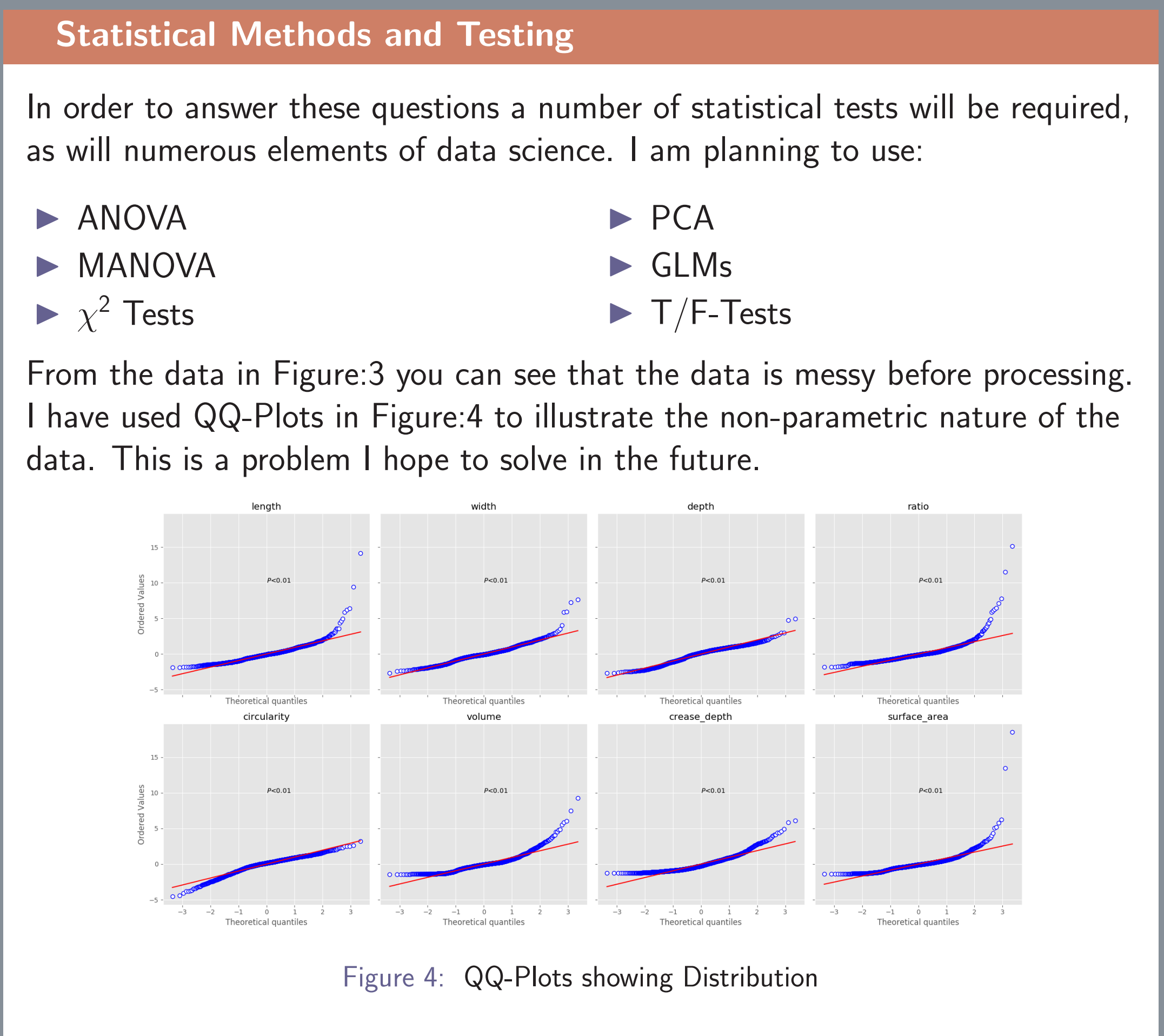
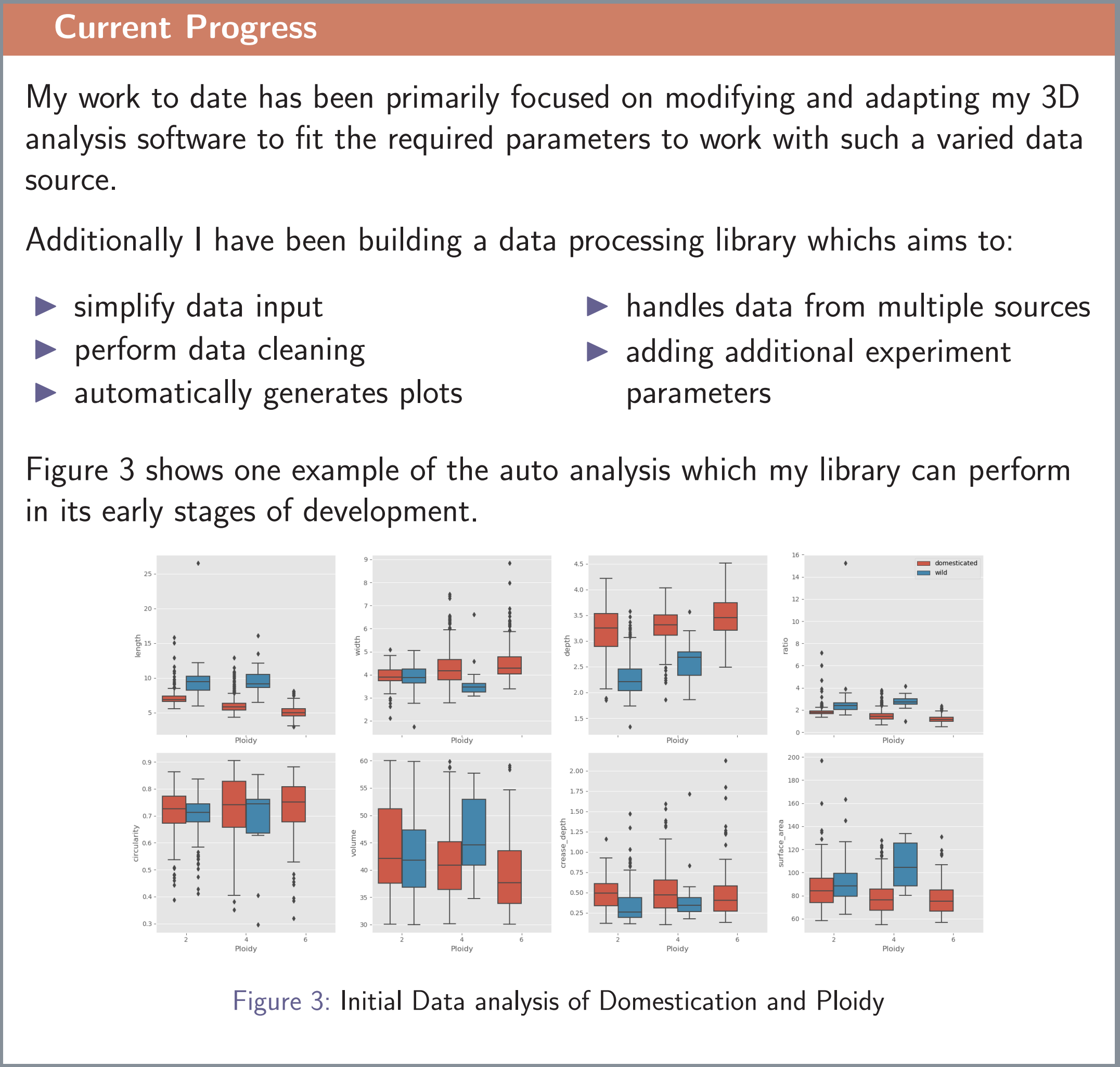
### Future Work

My main aims for the future is to fully implement my statistical library, once completed I can focus on testing my outlined hypothesis. I will also be aiming to make use of the *scipy* data models packages in Python in order to better model the data and to search for more vital underlying meanings in the data I've created.

Once this library is more complete, I shall be joining it into the GUI I have developed to allow for quick, easy and automatic analysis of future experiments. Should this project justify the need for more information, then it should be easily added through this additional application that I am developing with *PyQt*.

In order to address a broader picture, and to widen the scope of this research I am in the process of obtaining data used by Gegas et.al in 2011 to examine 2-Dimensional morphometric traits for a wide array of wheat that correlates nicely with what I have produced so far [1].

This would hopefully provide a lot of interesting information if the datasets were to compliment each other.



### Futher Information

For more information on this project I recommend keeping up-to-date with my development blog which can be found at <http://www.users.aber.ac.uk/nah26>

### Acknowledgements and Thanks

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- ▶ Dr. Kevin Williams

### References

V. C. Gegas, A. Nazari, S. Griffiths, J. Simmonds, L. Fish, S. Orford, L. Sayers, J. H. Doonan, and J. W. Snape. A genetic framework for grain size and shape variation in wheat. *The Plant Cell*, 22(4):1046–1056, 2010.

N. Hughes, K. Askew, C. P. Scotson, K. Williams, C. Sauze, F. Corke, J. H. Doonan, and C. Nibau. Non-destructive, high-content analysis of wheat grain traits using x-ray micro computed tomography. *Plant Methods*, 13(1), nov 2017.

H. R. Oliveira, M. G. Campana, H. Jones, H. V. Hunt, F. Leigh, D. I. Redhouse, D. L. Lister, and M. K. Jones. Tetraploid wheat landraces in the mediterranean basin: Taxonomy, evolution and genetic diversity. *PLoS ONE*, 7(5):e37063, may 2012.