


# Quantifying barley morphology using Euler characteristic curves

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## Abstract

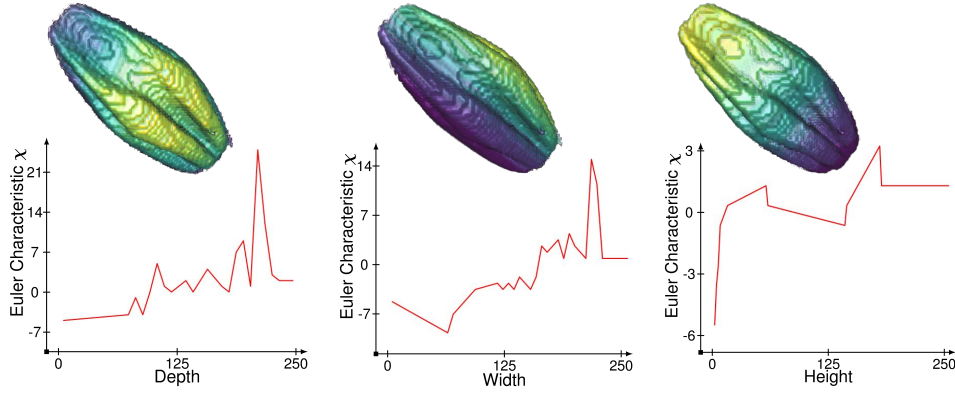
Shape is foundational to biology. Observing and documenting shape has fueled biological understanding, and from this perspective, it is also a type of data. The vision of topological data analysis, that data is shape and shape is data, will be relevant as biology transitions into a data-driven era where meaningful interpretation of large data sets is a limiting factor. We focus on quantifying the morphology of barley spikes and seeds using topological descriptors based on the Euler characteristic and relate the output back to genetic information.

**2012 ACM Subject Classification** Computing methodologies → Volumetric models

**Keywords and phrases** Topological Data Analysis; Euler characteristic transform; barley inflorescence

## 1 Introduction

Shape is data and data is shape. Biologists are accustomed to thinking about how the shape of biomolecules, cells, tissues, and organisms arise from the effects of genetics, development, and the environment. Traditionally, biologists use morphometrics to compare and describe shapes. The shape of leaves and fruits is quantified based on homologous landmarks (similar features due to shared ancestry from a common ancestor) or harmonic series from a Fourier decomposition of their closed contour. While these methods are useful for comparing many shapes in nature, they can not always be used: there may not be homologous points between samples or a harmonic decomposition of a shape is not appropriate. Topological data analysis (TDA) offers a more comprehensive, versatile way to quantify plant morphology. In particular, Euler characteristic curves [11] serve as a succinct, computationally feasible topological signature that allows downstream statistical analyses. For example, Li et al. [4] computed a morphospace for all leaves and used ECCs to predict plant family and location. Others have used the same filter and ECCs to determine the genetic basis of leaf shape in apple [9] and tomato [5] as well as the genetic basis of cranberry shape [3]. ECCs are sensitive enough to detect both complex and subtle effects of rootstock and climate on grapevine



■ **Figure 1** Three different Euler Characteristic Curves (ECCs) from three different filters. **(top)** X-ray CT scan of a barley seed. The symmetry of the seed encourages a filter by depth, width and height values. Slicing the barley seed in different directions produce **(bottom)** different corresponding ECCs.

leaf shape [8]. ECCs have also been used to measure the hairiness and shape of spikelets (arrangements of grass flowers) [7] and patterns of vegetation from satellite imagery [6].

## 2 Methods

In this project we are studying the morphology of barley seed and barley spikes (the branching inflorescence). The data arises from an artificial evolution experiment in which parental barley genotypes have been segregating for more than 60 years, corresponding to 60 different generations. In collaboration with Dr. Dan Koenig (UC Riverside), we have access to the seeds of progeny resulting from crosses of the original founders from each generation. Using X-ray CT scanning technology, we have created voxel-based 3D reconstructions of over 875 spikes, from which we have isolated individual seeds from each spike. Given the large number of seeds and voxels per seed, we use of the Euler Characteristic Transform as in [11] to quantify the morphology of each barley spike.

Consider each voxel-based image as a cubical complex  $X$  of dimension  $d = 3$  as in [10]. For a fixed direction  $\nu \in S^{d-1}$ , and a height value  $h$ , we define

$$X(\nu)_h = \{\Delta \in X : \langle x, \nu \rangle \leq h \text{ for all } x \in \Delta\}, \quad (1)$$

to be the subcomplex containing all cubical simplices below height  $h$  in the direction  $\nu$ . The Euler characteristic at height  $h$  is  $\chi(X(\nu)_h) = V - E + S - C$  where  $V, E, S, C$  are the number of vertices, edges, squares and cubes in  $X(\nu)_h$  respectively. The Euler characteristic curve (ECC) of direction  $\nu$  is defined as  $\{\chi(X(\nu)_h)\}_{h \in \mathbb{R}}$ . Turner et al. [11] proved that the collection of all ECCs corresponding to all possible directions effectively summarizes all the morphological information of 3D shapes in general. Moreover, with such collection we would be able to reconstruct the original object. A finite bound on the number of necessary directions for general 3D shapes has been proven [2], although the idea of efficiently reconstructing arbitrary 3D objects solely from ECCs [1] remains elusive.

Using a reduced number of ECCs as descriptors combined with known machine learning techniques, we explore the differences between founders phenotypes and their resulting progeny. This will provide insight into how selection pressures in a common environment alter the morphology of barley varieties originating from across the globe. From the X-ray CT scans we also extract traditional measurements for each barley seed, such as their volume,

surface area, and angle between the seed and the stalk (rachis). Using these measurements as descriptors, we can compare how machine learning techniques fare when using topological information vs. traditional, morphometric information.

### 3 Conclusions

Natural variation in barley, like all crops, encompasses differences in yield and adaptation to diverse climates and terrains. Understanding how differences in morphology affect these traits is vital to improve barley through breeding. TDA combined with X-ray CT scans offers a novel insight into the plant form and its evolution. As a long term plan, we will compare the topological descriptors to available genetic information of each barley sample. This analysis can further our understanding of the relationship between phenotype and genotype.

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