

Persistent Homology for Data of Plant Morphology

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Outline

- 1 Motivation
- 2 Introduction
- 3 Application to Plant Morphology Analysis
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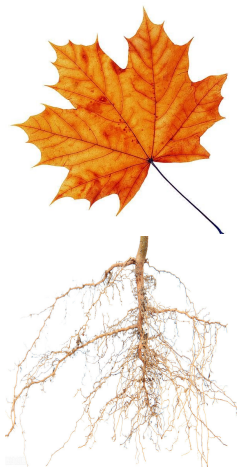
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Motivation

The local morphology of plants, such as roots, branches and leaves, has obvious geometric and topological features.

Most of the leaves are flat, hence we only need to study the 2D shape of leaves. For roots, capturing its morphology can be difficult sometimes, because roots are highly branched structure lacking easily identifiable nodes and rarely fully quantified. But using topological methods(e.g., PH, TDA), we can distinguish the root structure of plants.

Motivation



Motivation

Mao Li presented a morphometric technique based on topology, using a persistent homology framework, to measure the morphology of leaves and classify them by plant family(2017). This method (1) comprehensively measures local and global shape features, (2) can compare different shapes, (3) is robust to common noises in shape data.

Combined with analysis methods (e.g., canonical variant analysis (CVA), principal component analysis(PCA)), persistent homology can be used to classify the morphology of plants. Topological features provide a framework to quantify leaflets, roots and branching architectures of plants comprehensively.

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Persistent Homology

Filtration is a collection $K = \{K_\lambda\}_{\lambda \geq 0}$ of simplicial complexes with $K_\lambda \subset K_{\lambda'}$ for all $\lambda \leq \lambda'$.

Let (X, d) be a metrix space of finite points, define the **Rips complex**:

$$R_\lambda(X, d) = \{(x_0, x_1, \dots, x_n) \in X \mid d(x_i, x_j) < \lambda, 0 \leq i, j \leq n, n \in \mathbb{N}\}$$

Rips filtration is an increasing sequence of sets with the form

$$R(X, d) = \{R_{\lambda_k}(X, d) \mid k = 1, \dots, N, 0 < \lambda_k < \lambda_{k+1}\}$$

Persistent Homology

- (1) The input is a finite set of points (point cloud) embedded in Euclidean space or other metric space. For any real number $r > 0$, consider the union of all spheres of radius r centered at fixed points in the point cloud. As the radius r increases, the union of balls provides a filtration.
- (2) The input is a real valued function on space X . For instance, X can be a Euclidean space. Considering the sublevel set $\{x \in X \mid f(x) \leq r\}$, the filtration is obtained as the threshold r increases.

Persistent Homology

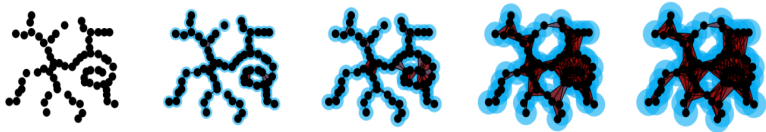


FIGURE 1. A dataset, the surrounding union of balls, and its Čech complexes at different choices of scale.

Persistent Homology

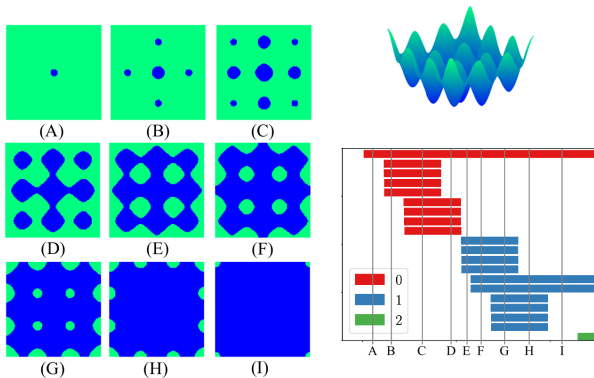


FIGURE 2. (Top right) An energy function for the molecule pentane. The domain is a torus, i.e. a square with periodic boundary conditions, as there are two circular degrees of freedom (dihedral angles) in the molecule. (Left) Nine different sublevel sets of energy. (Bottom right) The sublevel set persistent homology of this energy function on the torus, with 0-dimensional homology in red, 1-dimensional homology in blue, 2-dimensional homology in green. Image from [Mirth et al. \[2020\]](#).

Persistent Homology

Persistent homology can be represented in two equivalent ways: either as a **persistence barcode** or as a **persistence diagram**;

Persistence barcode is a collection of bars whose left end points and right end points are birth and death respectively.

Each interval in the persistence barcode is represented in the persistence diagram by a point in the plane, with its **birth coordinate** on the horizontal axis and with its **death coordinate** on the vertical axis. Since the death of each feature is after its birth, persistence diagram points all lie above the diagonal line $y = x$.

Persistent Homology

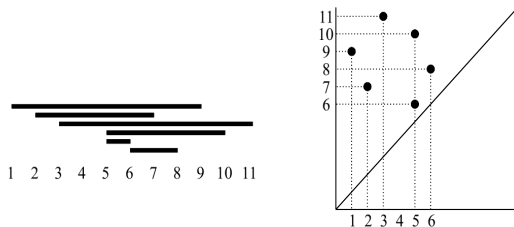


FIGURE 3. (Left) A persistent homology barcode, with the birth and death scale of each bar indicated on the horizontal axis. (Right) Its corresponding persistence diagram, i.e. a collection of points in the first quadrant above the diagonal, with birth coordinates on the horizontal axis and death coordinates on the vertical axis.

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Steps of the PH method

Steps of the PH method

1. Extracting point cloud datasets from images
2. Converting point clouds to functions
3. Forming filtrations
4. Computing persistent homology
5. Analyzing persisting results(e.g., persistent barcode/diagram, Betti curve and Euler characteristic)

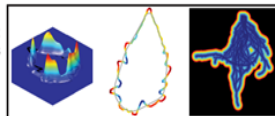
Steps of the PH method

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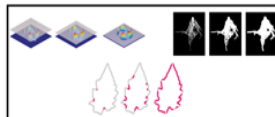
1. Extracting point clouds from images



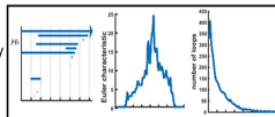
2. Converting point clouds to functions



3. Forming filtrations



4. Computing persistent homology



Process of analysis

1. Combine PH with statistical framework to diverse morphologies in the same tomato plants of a near-isogenic *S. pennellii* introgression line population (compare the introgression line IL4-3 to the cvM82 parent).
2. Apply statistical methods such as multidimensional scaling (MDS), principal component analysis (PCA), and canonical variant analysis (CVA) to turn the barcode information into a single value that describes leaf shape, leaflet serrations, and root architecture, to demonstrate the versatility of this approach.

Process of analysis

Persistent Homology Can Discriminate between Genotypes with Larger Effect Sizes Than Conventional Univariate Traits and Shows Heritability Results Similar to Those Obtained by Conventional Multivariate Approaches.

Persistent Homology Reveals Novel QTLs Not Identified Using Conventional Univariate or Multivariate Traits.

Results

1. the PH QTLs explained a relatively large amount of shape variation in our data set.
2. Multivariate analyses (whether with conventional traits or PH) always outperform univariate traits. For leaf shape, four univariate traits together can identify 16 QTLs, while the multivariate trait can detect 27 QTLs. For root architecture, four univariate traits together can identify 43 QTLs, while the multivariate trait can detect 57 QTLs.
3. Shoot and root architectures, when analyzed with a metric capable of quantifying multivariate features across scales, are under concerted genetic control.

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References

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Mao Li et al. Characterizing 3D inflorescence architecture in grapevine using X-ray imaging and advanced morphometrics: implications for understanding cluster density, Journal of Experimental Botany, Volume 70, Issue 21, 1 November 2019, Pages 6261–6276;

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