### Persistent homology for biology

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## <u>Outline</u>

- 1. Data
- 2. Persistent homology
- 3. Ordinary persistence: one parameter
- 4. Multiple parameters: fruit fly wings
- 5. Tameness
- 6. History of persistent homology
- 7. Bar codes
- 8. Statistical analysis
- 9. Lessons on persistence
- 10. Future directions

## What kinds of data?

### Shapes

- 1D: curves (in  $\mathbb{R}^2$  or  $\mathbb{R}^3$ , say)
- 2D: photographs
- 3D: MRI, DTI, SPECT, PET, CAT, integrated photo
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- 4D: fMRI, or any time series of spatial 3D
- arbitrary D: abstract geometric structures from data
  - any bunch of isolated points in  $\mathbb{R}^n$  (!), especially for  $n \gg 0$
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## Fruit fly wings

### Normal fly wings [images from David Houle's lab]:



### Topologically abnormal veins:



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## A. apoplanos



courtesy Elen Oneal

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## Lung airways (COPD study)



[Belchi, Pirashvili, Conway, Bennett, Djukanovic, Brodzki 2018]

# Lung vessels (CDH study)



courtesy Sean McLean

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### Streamlines from Diffusion Tensor Imaging



courtesy Zhengwu Zhang

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25 30 35 40 45

40

#### courtesy Nicole Lazar

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$$\dim(H_0)=31$$

#### Example: expanding balls

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$$\dim(H_0)=26$$

### Example: expanding balls



 $\dim(H_0)=21$ 



$$\dim(H_0) = 12$$



$$\dim(H_0)=6$$

### Example: expanding balls



 $\dim(H_0)=2$ 



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- points in  $\mathbb{R}^n$ :  $Q = \{0, \dots, m\}$  or  $\mathbb{R}$  1-parameter ("ordinary") persistence
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# Fruit fly wings

#### Normal fly wings [images from David Houle's lab]:



# Fruit fly wings

#### Normal fly wings [images from David Houle's lab]:



#### Topologically abnormal veins:



# Fruit fly wings

#### photographic image



# Fruit fly wings



## What generates topological novelty?

[Houle, et al.]: selecting for certain continuous wing vein deformations yields

- skew toward more oddly shaped wings, but also
- much higher rate of topological novelty

Hypothesis. Topological novelty arises when directional selection pushes continuous variation in a developmental program beyond a certain threshold.

### Test the hypothesis

- "plot" wings in "form space"
- determine whether topological variants lie "in the direction of" continuous shape selected for, and at the extreme in that direction

Goal. Statistical analysis encompassing topological vein variation, giving appropriate weight to new singular points in addition to varying shape

- compare phenotypic distance to genotypic distance; needs
- metric specifying distance between topologically distinct wings

To proceed. Statistics with fly wings as data objects  $\rightsquigarrow$  statistics with multiparameter persistence diagrams as data objects

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Data Persistent homology Ordinary persistence Multiple parameters Tameness History Bar codes Statistical analysis Lessons Future directions Wing vein persistence [w/Houle, et al., ongoing]

Example. Encode fruit fly wing with 2-parameter persistence

- Ist parameter: distance from vertex set
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Sublevel set  $W_{r,s}$  is near edges but far from vertices  $\Rightarrow H_{r,s} = H_i(W_{r,s})$ 

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Example. Encode fruit fly wing with 2-parameter persistence

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A piece of fly wing vein



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discretized

How to write down multipersistence modules in general? Need finiteness....

Def [M.- 2017, see arXiv:math.AT/2008.00063]. A module M over an arbitrary poset Q admits a constant subdivision if Q is partitioned into

- constant regions A, each with vector space  $M_A \xrightarrow{\sim} M_a$  for all  $a \in A$ , having
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M is tame if it admits a finite constant subdivision and dim<sub>k</sub>  $M_q < \infty$  for all q. Example.  $k_0 \oplus k[\mathbb{R}^2]$  admits constant regions  $\{\mathbf{0}\}$  and  $\mathbb{R}^2 \setminus \{\mathbf{0}\}$ 

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#### Def. A module *M* over a poset *Q* has finite encoding $\pi : Q \to P$ if

- P is a finite poset,
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# Topology of probability distributions

[surface images from *Confidence sets for persistence diagrams*, by Fasy, Lecci, Rinaldo, Wasserman, Balakrishnan, Singh, Annals of Statistics **42** (2014), no. 6, 2301–2339.]

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Input. Topological space X filtered by set Q of subspaces:  $X_q \subseteq X$  for  $q \in Q$  $\Rightarrow Q$  is a partially ordered set:  $X_q \subseteq X_{q'} \Leftrightarrow q \preceq q'$ 

Def.  $\{X_q\}_{q \in Q}$  has persistent homology  $\{H_q = H(X_q; \Bbbk)\}_{q \in Q}$ . This is a

- Def. *Q*-module over the poset Q:
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# Examples

• points in  $\mathbb{R}^n$ :  $Q = \{0, \dots, m\}$  or  $\mathbb{R}$  1-parameter ("ordinary") persistence

1-parameter ("ordinary") persistence

- brain arteries:  $Q = \{0, \dots, m\}$  or  $\mathbb R$
- wing veins:  $Q = \mathbb{Z}^2$  or  $\mathbb{R}^2$  2 discrete or continuous parameters
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# History of persistent homology

# Ordinary persistence

- traces back to [Morse 1940s]
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- formally defined [Frosini, Landi 1999], [Robins 1999]
- efficient computation [Edelsbrunner, Letscher, Zomorodian 2002]
- applications [too many to list; a few early ones, but most roughly 2013-]

# Multiparameter persistence

- introduced [Carlsson, Zomorodian 2009]
- algorithms, presentations, visualizations, notions of noise, distance, ... [Bubenik, Carlsson, Chachólski, Lesnick, Scolamiero, Vaccarino, Wright, Zomorodian,...]
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# Essentially equivalent

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- 3D structure, in particular
- "bendiness", or "tortuosity"

#### Discrete methods [Aydin, et al. 2009]

- disregard metric and embedding
- compare combinatorial structures
- no correlations detected

#### Phylogenetic trees [SAMSI WG 2013]

- connect cortical surface landmarks to nearest leaves
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- too combinatorial again: found nothing but sticky mean at origin

#### Dyck paths [Shen & Marron, et al. 2014]

- pay attention to edge lengths but disregard 3D embedding
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#### Sweep filtration Filter brain arteries by sweeping across with a plane:

Record:

- birth time of each new component
- death of each component (when it joins to an older component)



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# <u>Bar codes</u>

#### Data structure: 3D tree $\rightsquigarrow$ bar code / lace array / persistence diagram:



multiset of (vertical) line segments [t, t'] (plotted at x-coordinate t)
one for each class with birth time t and death time t'.

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# Statistical analysis

Reduce to linear methods. 3D tree  $\rightsquigarrow$  bar code  $\rightsquigarrow$  vector in  $\mathbb{R}^{100}$ :

- top 100 bar lengths, in decreasing order, log scale
- correlate first principal component score vs. age

#### Conclusions [Bendich-Marron-M.-Pieloch-Skwerer 2014]

Longest bars in older brains tend to be shorter and later.

- Pearson correlation 0.52663
- *p*-value  $3.0127 \times 10^{-8}$  strongly significant

### Remarks. Results essentially unchanged after

- rescaling to account for natural variation in overall brain size (force standard deviation of the set of bar lengths to equal 1)
- rescaling to account for known correlation of age vs. total vessel length L [Bullitt, et al. 2005] (divide by L,  $\sqrt{L}$ , or  $\sqrt[3]{L}$ )
- repeating the analysis with residuals from regression between feature vector and total length.

## Top 100 bars



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## Top 100 bars: log scale

Run7: log Quantiles, top 100 Data Objects



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- top 100 bar lengths, in decreasing order, log scale
- correlate first principal component score vs. age

#### **Conclusions** [Bendich–Marron–M.–Pieloch–Skwerer 2014]

Longest bars in older brains tend to be shorter and later.

- Pearson correlation 0.52663
- *p*-value  $3.0127 \times 10^{-8}$  strongly significant

Remarks. Results essentially unchanged after

- rescaling to account for natural variation in overall brain size (force standard deviation of the set of bar lengths to equal 1)
- rescaling to account for known correlation of age vs. total vessel length L [Bullitt, et al. 2005] (divide by L,  $\sqrt{L}$ , or  $\sqrt[3]{L}$ )
- repeating the analysis with residuals from regression between feature vector and total length.

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# Age vs. PC1



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## Reflections on persistent homology

### Where did the best correlation occur?

- How did we choose top 100 bar lengths?
- What choices yield the best correlation? Why?
- Old persistent homology mantra: most significant features
  - are "biggest"
  - live "far from the diagonal" in bar codes.

### For brain artery trees

- Not surprising that very short bars ↔ noise, although in other studies they might not.
- While biggest features are important,
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- Importance  $\Rightarrow$  significance for geometric features.
- Persistent homology can detect significant features lying between important and noise.

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## Top 200 bars: heatmap



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### Implementation

- single preprocessing step for many multiPH computations; e.g., fly wings
- Lebesgue distance computations: no sampling for Riemann integration

Invariants

- E.g., what could "top 100 bar lengths" mean in multipersistence?
- E.g., boundaries of up- or downsets  $\rightsquigarrow$  "highly persistent" elements

Real L<sup>p</sup> distances [Bubenik-Scott-Stanley 2023], [Skraba-Turner 2023], [Bjerkevik-Lesnick 2021]

- integer parameters: match pairs of generators
- real parameters: sums  $ightarrow\infty$  with finer discrete approximation
- instead: use L<sup>p</sup> distances between boundaries of up- and downsets...
- ... from corresponding associated primes (same history or mortality type)

- resolve using upsets and/or downsets
- Conj:  $\mathbb{R}^n$ -modules have upset resolutions of length at most n-1.
- Compare [Geist-M.- 2023]:  $\mathbb{k}[\mathbb{R}^n_+]$  has global dimension n+1.

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