Persistent homology analysis of brain artery trees

Ezra Miller

Duke University, Department of Mathematics

ezra@math.duke.edu

joint with

Paul Bendich & Aaron Pieloch (Duke Math)

J.S. Marron & Sean Skwerer (Chapel Hill Stat/Oper.Res.)

[arXiv:stat.AP/1411.6652]

Joint Mathematics Meetings, San Antonio
11 January 2015



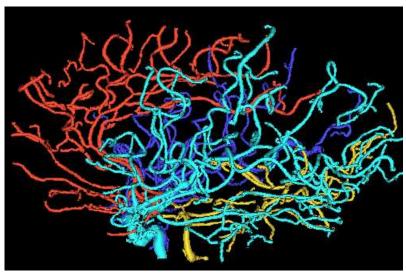




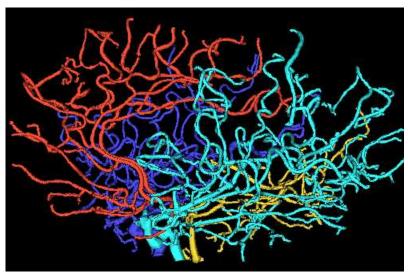
Brain artery trees

Goal: Statistical analysis taking 3D geometry into account

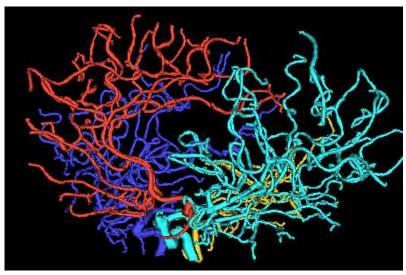
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[Bullitt and Aylward, 2002]



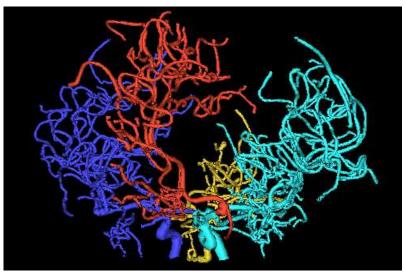
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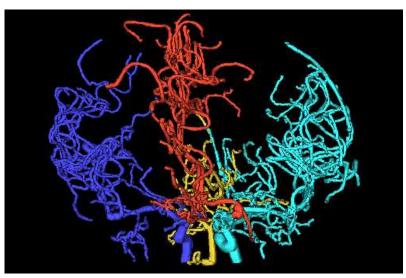
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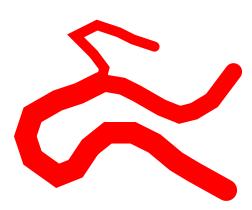
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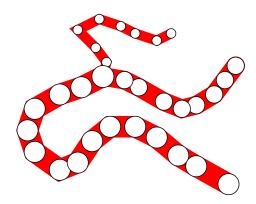


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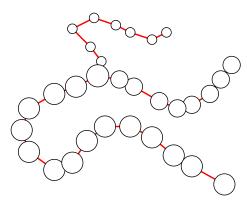
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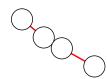
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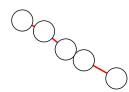
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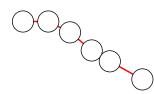
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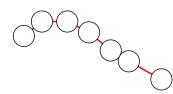
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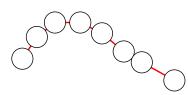
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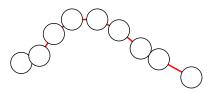
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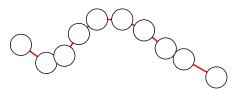
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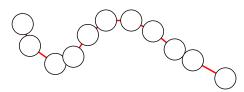
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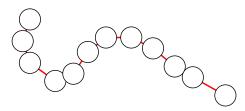
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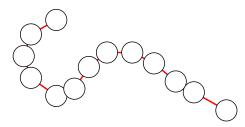
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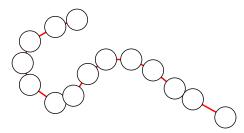
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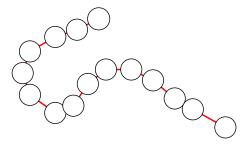
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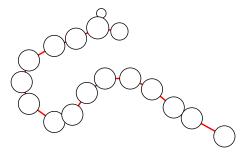
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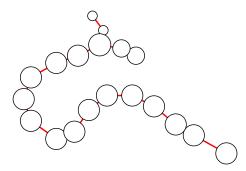
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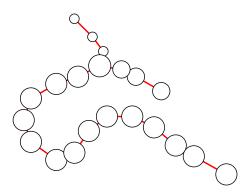
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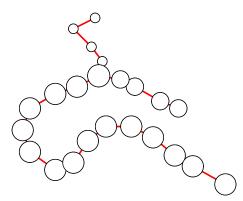
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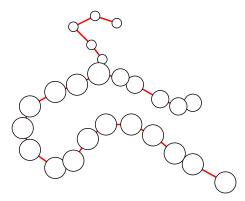
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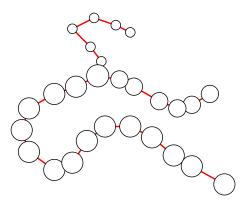
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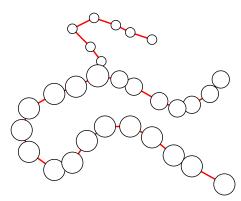
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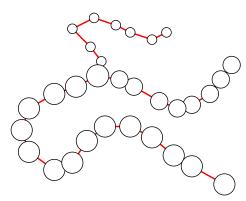
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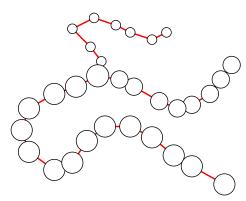
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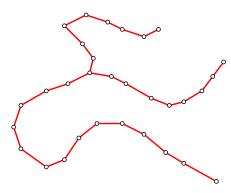
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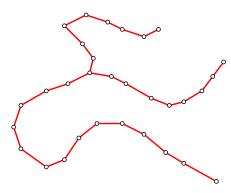
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Persistent homology

Fix a topological space X

- build X step by step
- measure evolving topology

Def. Let X_{\bullet} be a filtered space, meaning $\emptyset = X_0 \subset X_1 \subset \cdots \subset X_m = X$. The persistent homology H_iX_{\bullet} is $H_iX_1 \to H_iX_2 \to \cdots \to H_iX_m$, a sequence of vector space homomorphisms.

Examples:

- 1. Given a function $f: X \to \mathbb{R}$, let $X_k = f^{-1}((-\infty, t_k])$. Good choice of $t_0, \ldots, t_m \in \mathbb{R}$: the values of t across which H_iX_t changes.
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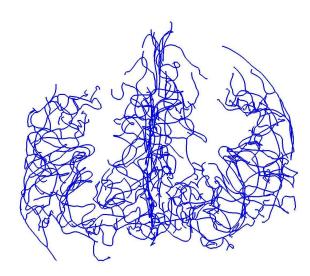
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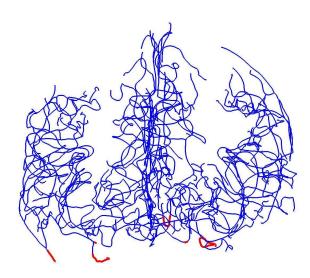
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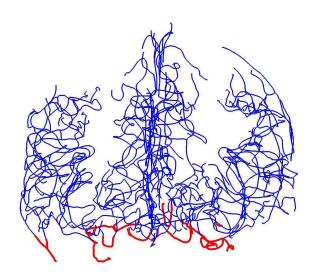
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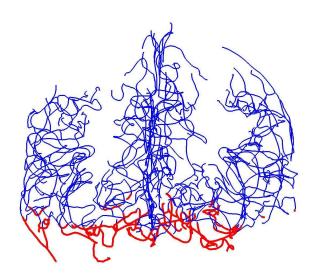
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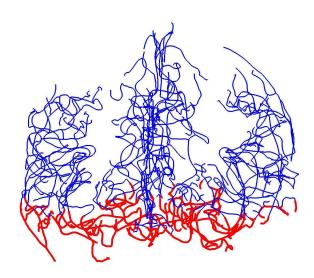
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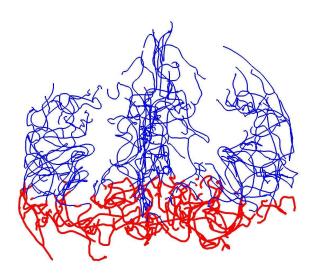


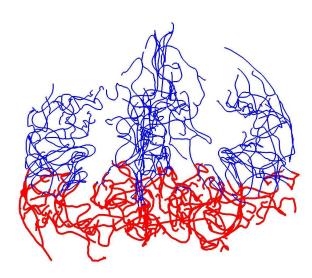


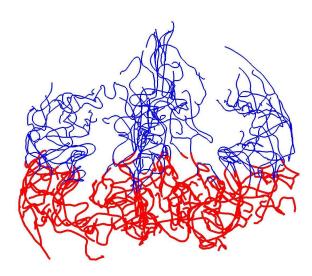


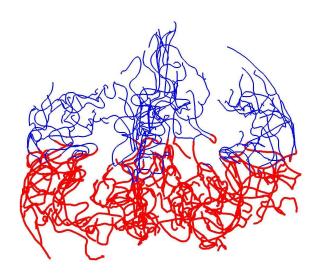


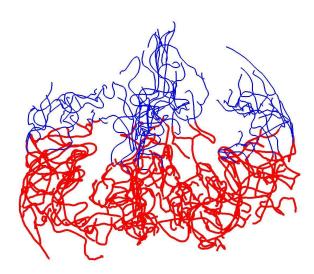


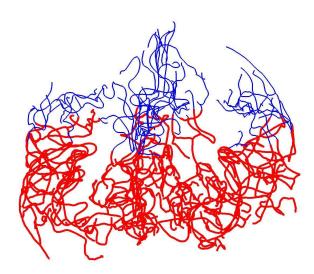


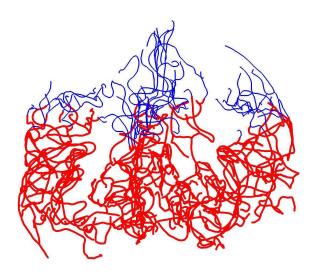


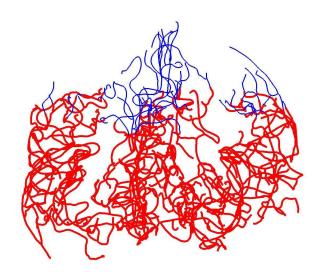


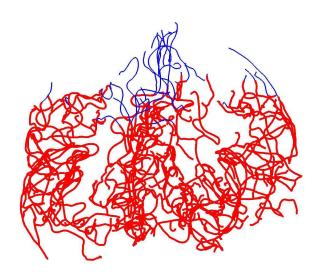


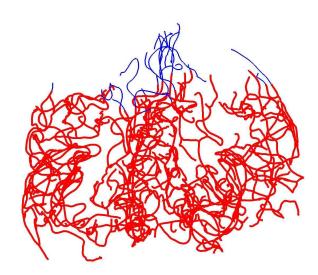


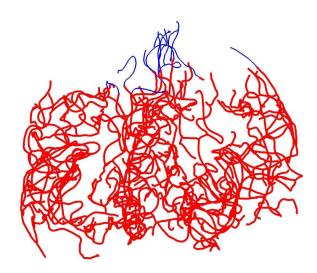


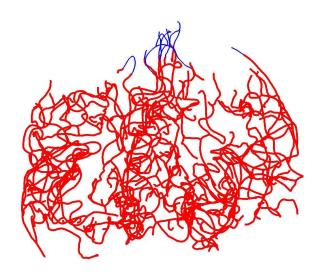


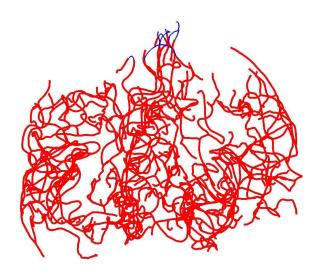


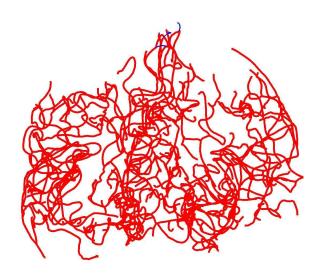


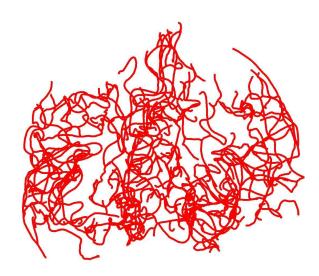












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Sweep filtration

Goal: statistical analysis taking into account

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

Sweep filtration

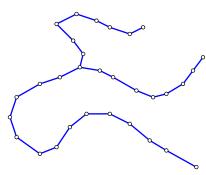
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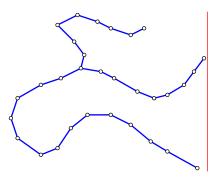
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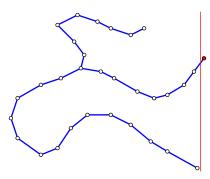
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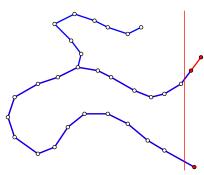
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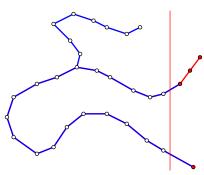
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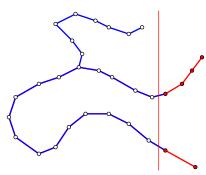
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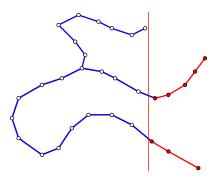
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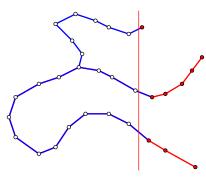
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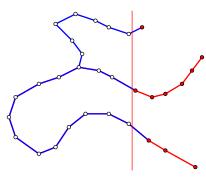
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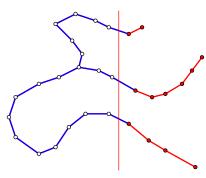
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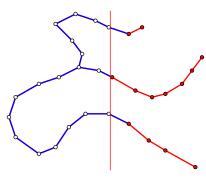
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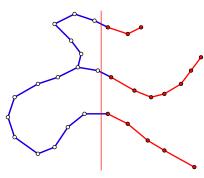
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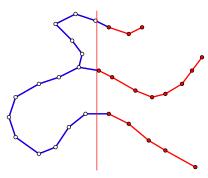
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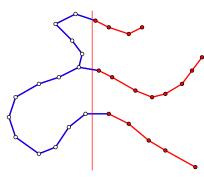
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Sweep filtration

Goal: statistical analysis taking into account

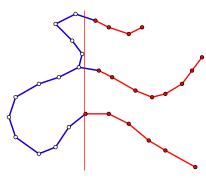
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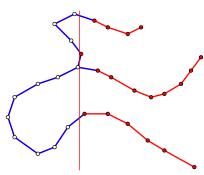
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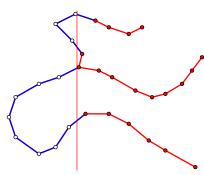
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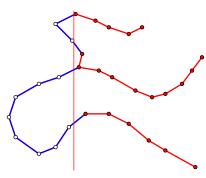
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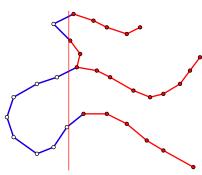
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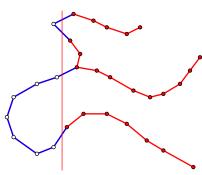
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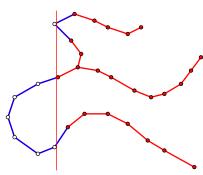
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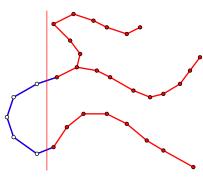
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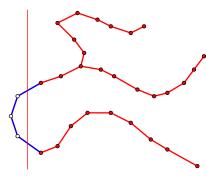
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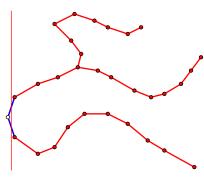
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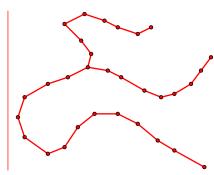
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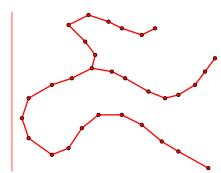


Sweep filtration

Goal: statistical analysis taking into account

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Filter by sweeping across with a plane:



- birth time of each new component
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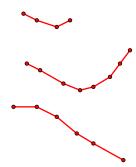
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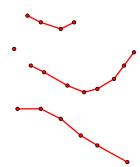
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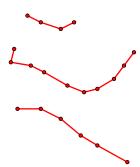
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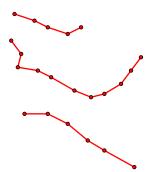
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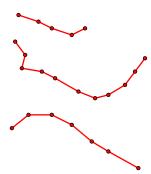
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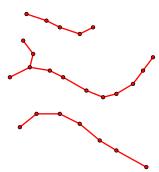
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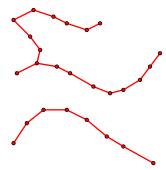
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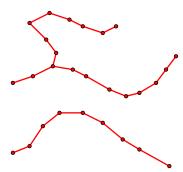
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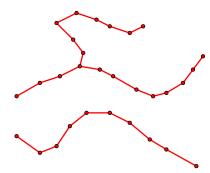
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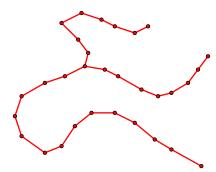
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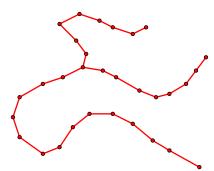
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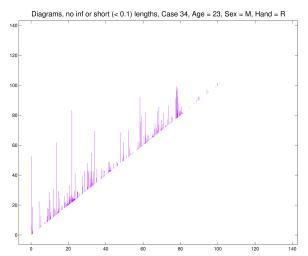


Record:

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

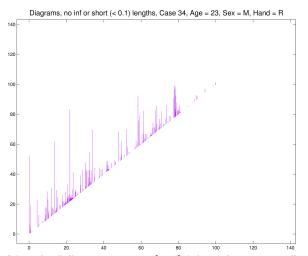
Easily computable if $\dim X$ is low; \dim of ambient space is irrelevant.

Bar codes



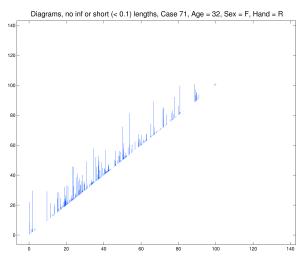
- multiset of (vertical) line segments [t, t'] (plotted at x-coordinate t)
- one for each class with birth time t and death time t'.

Bar codes



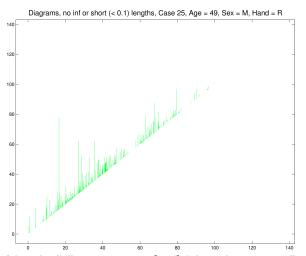
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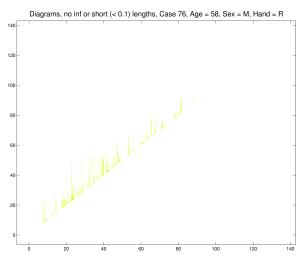
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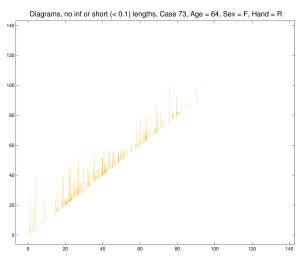
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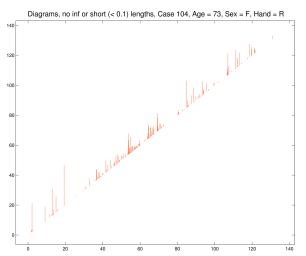
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Statistical analysis

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

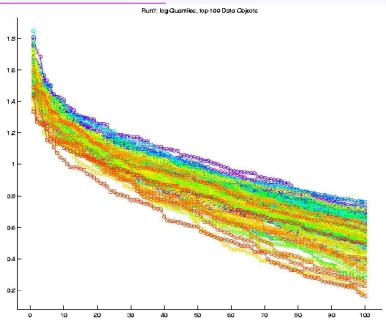
Conclusions [Bendich, Marron, M.—, Pieloch, Skwerer 2014] Longest bars in older brains tend to be shorter and later.

- 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)
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Top 100 bars: log scale



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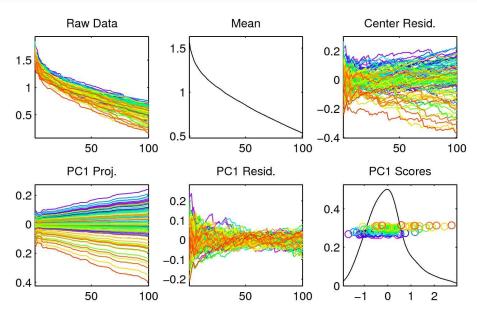
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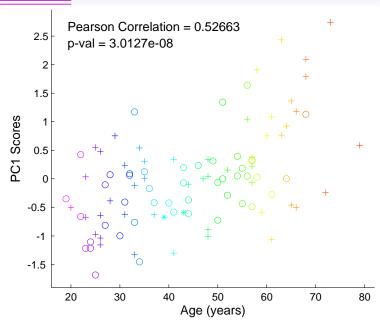
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Age vs. PC1



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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?

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 future studies they might not.
 (Challenge problem: detect meaningful minute features.)
- · While biggest features are important,
- they hinder strength of correlation.

- Importance
 ⇒ significance for geometric features.
- Persistent homology can detect significant features lying between important and noise.

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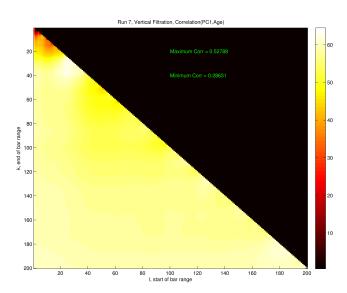
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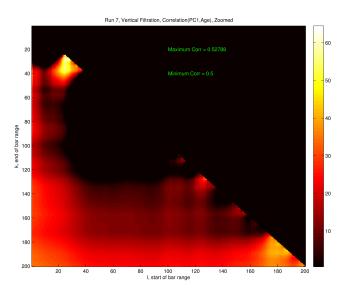
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Persistent homology mantra: most significant features

- are "biggest"
- live "far from the diagonal" in bar codes.

For brain artery trees.

- While biggest features are important,
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- Importance ⇒ significance for geometric features.
- Persistent homology can detect significant features lying between important and noise.

Reflections on persistent homology

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Discrete methods [Aydin, et al. 2009]

- disregard metric and embedding
- compare combinatorial structures
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Phylogenetic trees [SAMSI WG 2013]

- connect cortical surface landmarks to nearest leaves
- apply averaging algorithm [M.—, Owen, Provan; Bačák 2012] in tree space [Billera, Holmes, Vogtmann 2001]
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Dyck paths [Dan Shen and J.S. Marron, et al. 2014]

- pay attention to edge lengths but disregard 3D embedding
 - complicated tree pruning
 - Pearson correlation \sim .25

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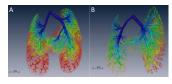
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fMRI. (with Lazar et al.): classification using persistent homology

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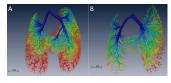




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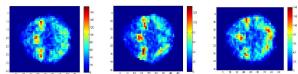
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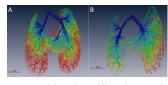
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Future directions

Lung vasculature. (with McLean et al., Bendich, Marron)





fMRI. (with Lazar et al.): classification using persistent homology







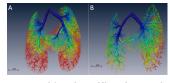
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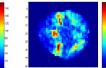
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Thank You