

Applied Topology

Fabian Roll

Applied and Computational Topology Group - TUM

MDSI Research Seminar - 11.12.2023

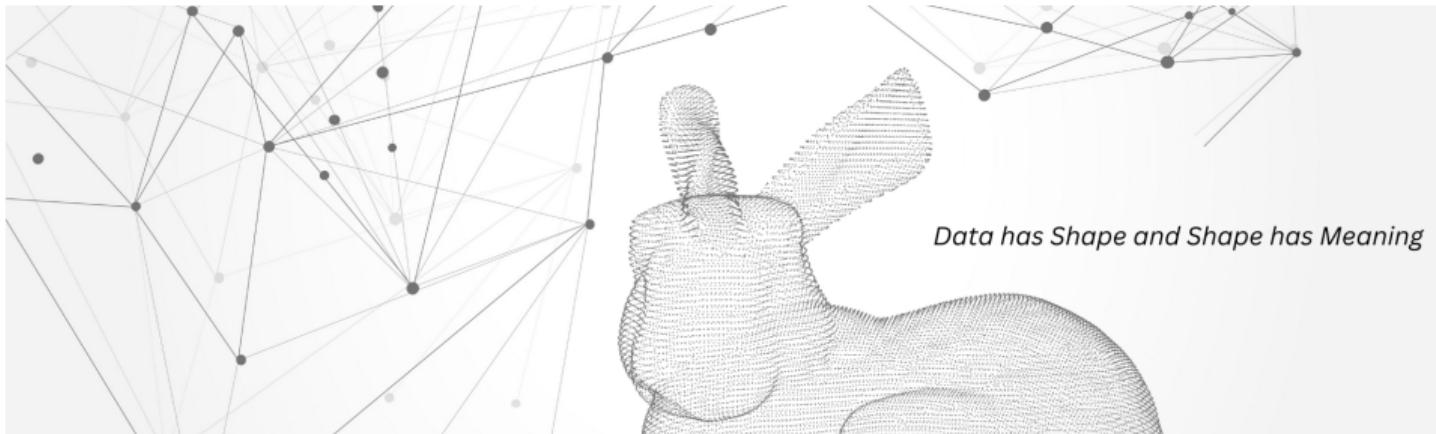
About myself

- B.Sc., M.Sc., Doctoral candidate in Mathematics at TUM
- Interested in the mathematical properties of geometric complexes and their use in topological data analysis
- Internship at Horváth (management consulting) in the Steering Lab
- 3 months research stay at the Ohio State University, USA
- Like travelling, hiking, skiing, cycling, sailing



fabian.roll@tum.de

What is Applied Topology?



-  [B. Giunti, J. Lazovskis, B. Rieck](#) donut.topology.rocks
-  [Applied Algebraic Topology Research Network](#) YouTube Channel
-  [F. Hensel, M. Moor, B. Rieck](#), A Survey of Topological Machine Learning Methods. *Frontiers in Artificial Intelligence*, doi: 10.3389/frai.2021.681108, 2021

What is Applied Topology?

Applied and Computational Topology



The research group around [Prof. Ulrich Bauer](#) deals with the computational analysis of topological structures arising in real world data.



Welcome

Welcome to the website of the AIDOS LAB at the [Institute of AI for Health](#), an institute of [Helmholtz Munich](#)! We are fascinated by discovering hidden structures in complex data sets, in particular those arising in healthcare applications.

Our primary research interests are situated at the intersection of **geometry, topology, and machine learning**. We want to make use of geometrical and topological information to imbue neural networks with more information in their respective tasks, leading to better and more robust outcomes. Along the way, we develop new **manifold learning** techniques, new **representation learning** algorithms, and much more.

pytorch-topological: A topological machine learning framework for pytorch

Collaboration

How can I help you?

- Connect you with other people in our field.
- Help you understand the mathematical concepts of algebraic topology and their use in topological data analysis.
- Help you use (or adapt) software/techniques: Ripser, CGAL, GUDHI, UMAP, ...

How can we collaborate?

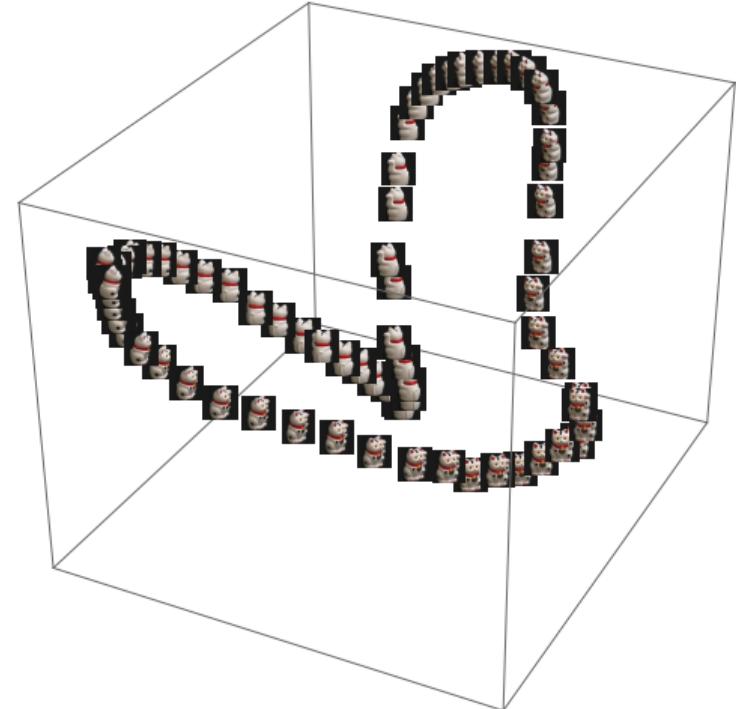
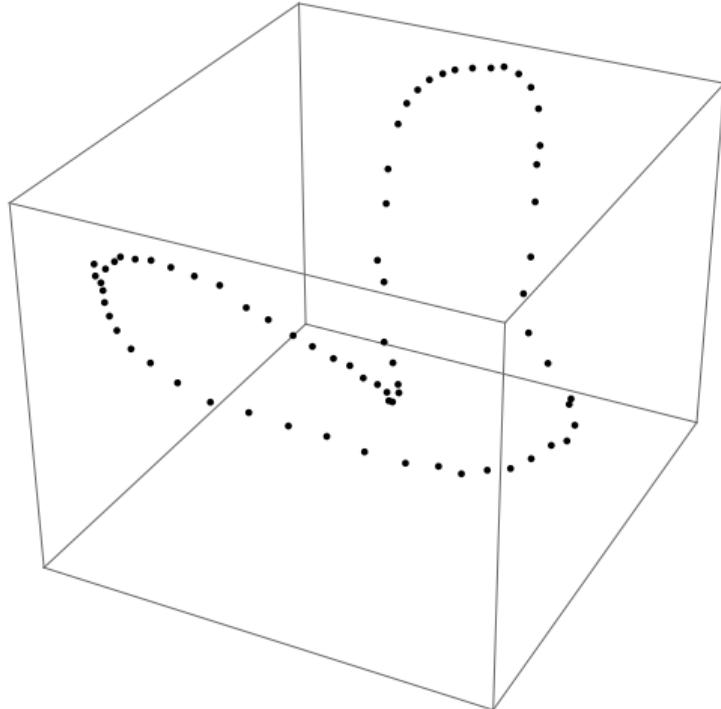
- If you have data and a reason to try out topological methods, I can help.
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What structures can our methods detect?

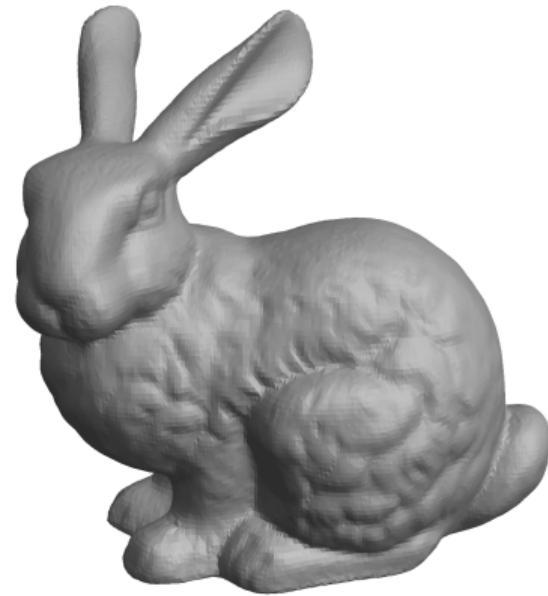
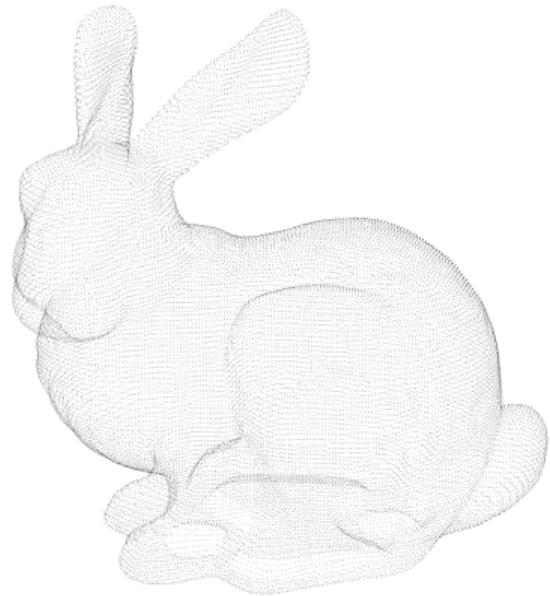


Source: Columbia University Image Library (COIL-100)

What structures can our methods detect?



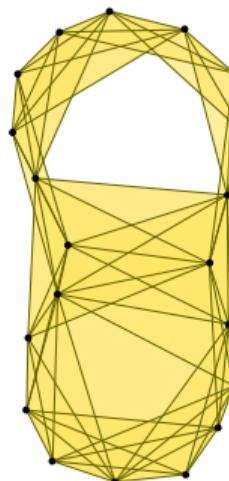
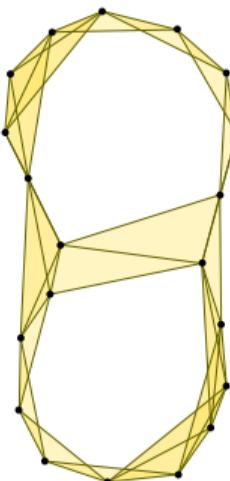
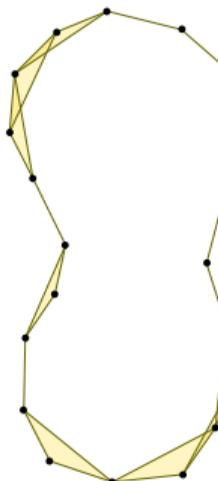
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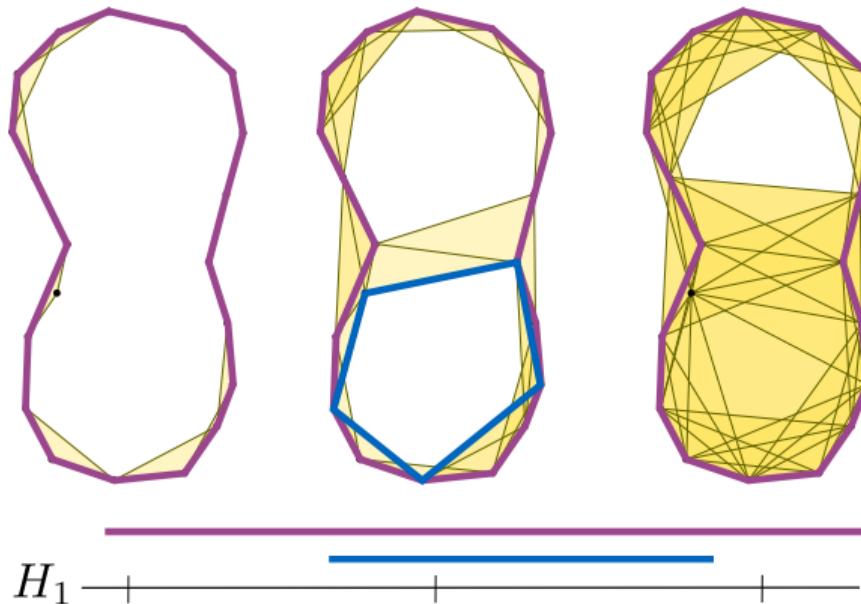
Connecting the dots

Definition. Let X be a metric space. The Vietoris-Rips complex at scale r is the simplicial complex

$$\text{Rips}_r(X) = \{S \subseteq X \text{ finite} \mid S \neq \emptyset, \text{ diam } S \leq r\}.$$



Persistent homology



Persistence diagrams discretely encode the multiscale connectivity of point clouds.

Persistent homology

Application to COVID-19 genetic evolution data

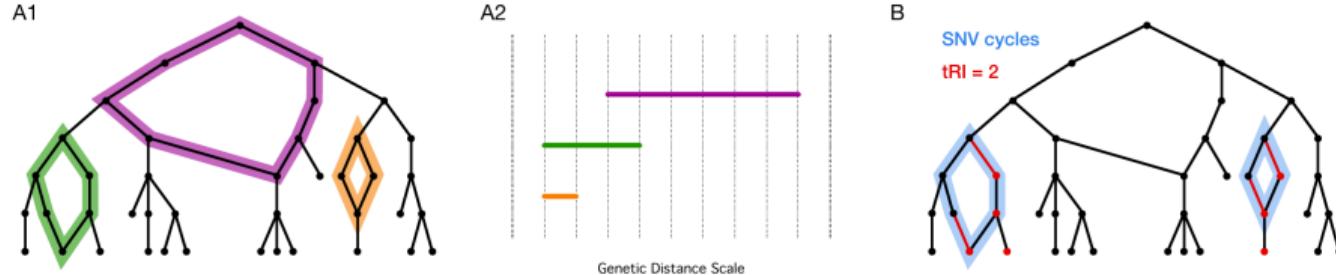


Figure 2. Topological data analysis quantifies convergent evolution. (A) Persistent homology detects reticulate events in viral evolution by means of a persistence barcode. Each bar in the barcode (A2) corresponds to a topological cycle in the reticulate phylogeny (A1). Bars at small genetic distance scales are expected to correspond mainly to homoplasies, while recombination events typically produce topological features at larger scales. (B) SNV cycles are topological cycles in the reticulate phylogeny for which adjacent sequences differ by single nucleotide variations (SNV) only. Under the assumption of single substitutions per site, any SNV in

 M. Bleher, L. Hahn, M. Neumann, J. A. Patino-Galindo, M. Carriere, U. Bauer, R. Rabidan, A. Ott
Topological data analysis identifies emerging adaptive mutations in SARS-CoV-2. Preprint, arXiv doi:
10.48550/arXiv.2106.07292, 2023

Persistent homology

COVID-19 genetic evolution data

covid data (≈ 15000 points)	Ripser's runtime
ordered chronologically	1 day



[U. Bauer Ripser: efficient computation of Vietoris–Rips persistence barcodes. Journal of Applied and Computational Topology, doi: 10.1007/s41468-021-00071-5, 2021](#)

Persistent homology

COVID-19 genetic evolution data

covid data (≈ 15000 points)	Ripser's runtime
ordered chronologically	1 day
ordered reversed chronologically	2 min



M. C. Escher, Circle Limit III



U. Bauer Ripser: **efficient computation** of Vietoris–Rips persistence barcodes. Journal of Applied and Computational Topology, doi: 10.1007/s41468-021-00071-5, 2021

Persistent homology

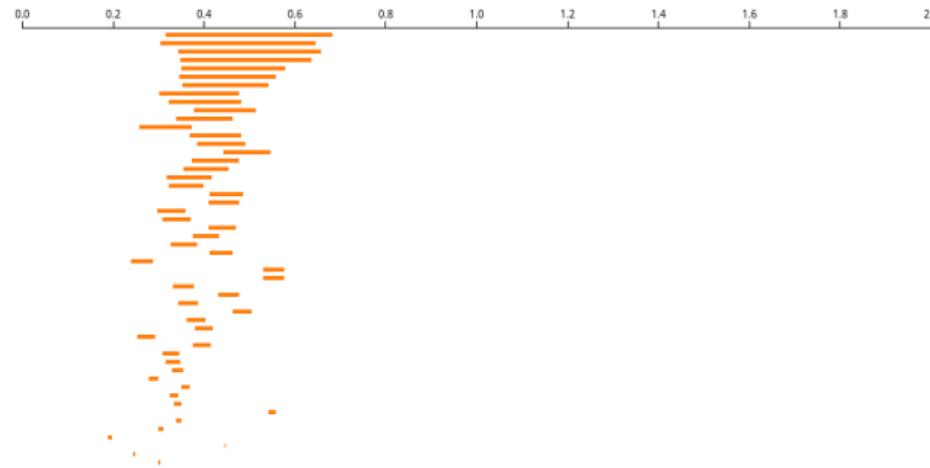
live.ripser.org

Ripser

Load a to compute Vietoris–Rips persistence barcodes in dimensions to and up to distance

No file selected.

Persistence intervals in dimension 1:



Persistence intervals in dimension 2:

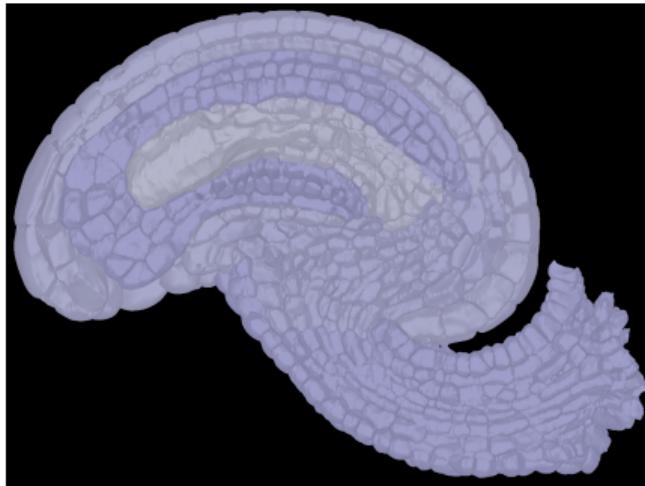


Elapsed time: 0.874 seconds

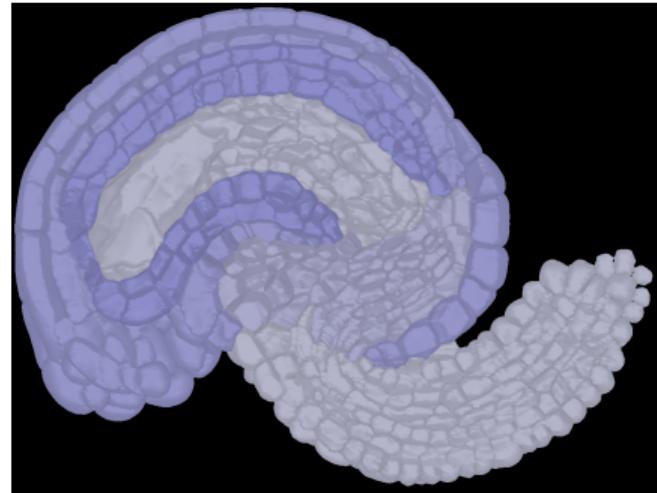
NADO

Nerve-based topological analysis of 3D digital ovules

Joint work with the Schneitz Lab (Plant Developmental Biology at TUM)



Cardamine hirsuta ovule



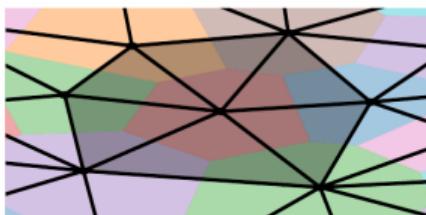
Arabidopsis thaliana ovule

NADO

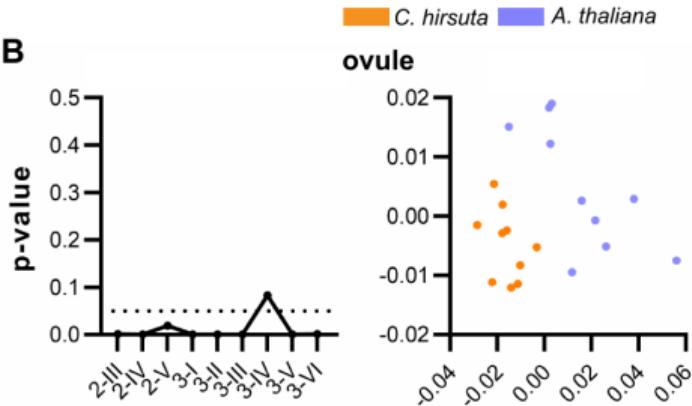
Nerve-based topological analysis of 3D digital ovules

A

Vertex star of a single cell



B



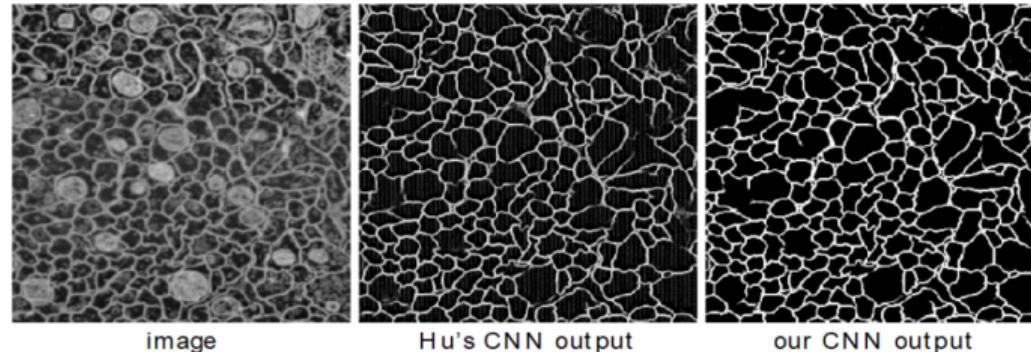
T.A. Mody, A. Rolle, N. Stucki, F. Roll, U. Bauer, K. Schneitz, Diverse 3D cellular patterns underlie the development of *Cardamine hirsuta* and *Arabidopsis thaliana* ovules Preprint, bioRxiv doi: 10.1101/2023.12.06.570408, 2023

SegMatch3D

Fast and Accurate 3D Image Segmentation by Matching Topological Features

My colleague Nico Stucki uses, as part of an MDSI project, topological information to train machine learning models:

$$l_{train}(\mathbf{L}, \mathbf{G}) = \alpha \underbrace{l_{\text{BM}}(\mathbf{L}, \mathbf{G})}_{\text{topological}} + \underbrace{l_{\text{dice}}(\mathbf{L}, \mathbf{G})}_{\text{classical}}$$



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