TopTime Conference abstracts

Monday 27 October

9.30-10.30. Elizabeth Munch — Recent trends in persistence bundles

The field of Topological Data Analysis (TDA) has recently seen extensive interest in persistence bundles, defined as the study of maps $f : B \to \mathrm{Dgm}$ from a base space B to the space of (usually one-parameter) persistence diagrams. This framework encompasses a variety of structures, each with distinct origins and analytical considerations depending on the nature of B. Key instances include vineyards (where B is an interval, representing evolving filtrations), the family of persistent homology transforms (such as those based on directional filtrations for $B = \mathbb{S}^{d-1}$, or distance to affine subspaces where B is an affine Grassmannian, or even distance to a knot for $B = \mathbb{S}^1$). In this survey talk, we will provide an overview of current research trends on the subject, with a particular focus on the critical role of tracking and updating cycle representatives.

References:

1. Turner, K., Mukherjee, S., and Boyer, D. M. (2014). Persistent homology transform for modeling shapes and surfaces. Information and Inference: A Journal of the IMA, 3(4), 310–344.
2. Hickok, A. (2023). Persistence diagram bundles: A multidimensional generalization of vineyards. arXiv:2210.05124.
3. Arya, Giunti, Hickok, Kanari, McGuire, and Turner. (2024). Decomposing the persistent homology transform of star-shaped objects. arXiv:2408.14995.
4. Munch, E. (2025). An invitation to the Euler characteristic transform. The American Mathematical Monthly, 132.
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11.00-12.00. Denisse Sciamarella — Chaotic dynamics: A temporal cell complex called Templex

A templex encodes the structure of a semiflow in phase space via a non-simplicial cell complex called BraMAH, together with a directed graph whose nodes are the locally highest-dimensional cells of the complex and whose edges indicate flow-compatible connections between these cells. The BraMAH complex allows the extraction of the generators of the homology and torsion groups of the structure underlying the dataset. By construction, this complex identifies junction loci in a branched manifold. Once the complex is endowed with the directed graph, an equivalence relationship different from homology can be defined by declaring that all digraph cycles that flow into and out of a junction through the same nodes belong to the same class. The non-equivalent directed cycles starting and ending at a junction define the generatex set. I will review the history and conception of this framework and illustrate its applicability to fluid and climate dynamics. I will highlight how the generatex set can be interpreted as a family of topological modes of variability, and how a templex can be decomposed into fundamental dynamical units that can be bonded to yield different types of chaos. Perspectives on defining persistence for the generatex set will be outlined.

References:

1. G. D. Charó, D. Sciamarella, J. Ruiz, S. Pierini, M. Ghil. Topological modes of variability of the wind-driven ocean circulation. Chaos: An Interdisciplinary Journal of Nonlinear Science, 35(9) (2025)

2. D. Sciamarella, G. D. Charó. Chapter 9: New Elements for a Theory of Chaos Topology, in Topological Methods for Delay and Ordinary Differential Equations, edited by Pablo Amster & Pierluigi Benevieri, Series Title: Advances in Mechanics and Mathematics, Springer Birkhäuser Cham, Hardcover ISBN 978-3-031-61336-4 (2024)

3. C. Mosto, G. D. Charó, C. Letellier, D. Sciamarella. Templex-based dynamical units for a taxonomy of chaos. Chaos: An Interdisciplinary Journal of Nonlinear Science, 34(11) (2024)

4. M. Ghil, D. Sciamarella. Dynamical systems, algebraic topology and the climate sciences. Nonlinear Processes in Geophysics, 30(4), 399-434 (2023)

5. G. D. Charó, C. Letellier, D. Sciamarella. Templex: A bridge between homologies and templates for chaotic attractors. Chaos: An Interdisciplinary Journal of Nonlinear Science, 32(8) (2022)

13.30-14.30: Jānis Lazovskis — Persistent homology updates on dynamic data

Persistent homology, as a topological summary and feature indicator of a dataset, is a mainstay of applied topology. Computing the persistent homology barcode is computationally expensive, so in dynamic settings such as time-dependent, streaming, or noisy data, it is natural to consider methods which perform computations only concerning the data which has changed. We provide an overview of the field of dynamic peristent homology, and its development through mathematical objects and data structures. Recent advances in computational software also allow users to access and track the updates of the underlying objects that capture the persistent homology of a dataset. Insertion, rearrangement, and most recently, removal of data, have implementations which allow arbitrary changes to be requested and the persistent homology to be efficiently updated. This is joint work with Barbara Giunti, and is funded in part by the Latvian Council of Science grant 1.1.1.9/LZP/1/24/125.

References:

1. David Cohen–Steiner, Herbert Edelsbrunner, Dmitriy Morozov. Vines and vineyards by updating persistence in linear time. Symposium of Computational Geometry, 2006. `https://doi.org/10.1145/1137856.1137877`

2. Gunnar Carlsson, Vin de Silva. Zigzag Persistence. Foundations of Computational Mathematics, 2010. `https://doi.org/10.1007/s10208-010-9066-0`

3. Herbert Edelsbrunner, John Harer. Computational Topology: An Introduction. American Mathematical Society, 2010. https://bookstore.ams.org/mbk-69

4. Mustafa Hajij, Bei Wang, Carlos Scheidegger, Paul Rosen. Visual Detection of Structural Changes in Time-Varying Graphs Using Persistent Homology. Pacific Visualization Symposium, 2018. https://ieeexplore.ieee.org/document/8365984

5. Barbara Giunti, Jānis Lazovskis. Pruning vineyards: updating barcodes by removing simplices. arxiv, 2025. https://arxiv.org/abs/2312.03925

15.00-16.00. Hannah Schreiber — The TDA pipeline and Gudhi

Gudhi is a C++ and Python library for topological data analysis (TDA) and geometric understanding of data in higher dimensions. In this talk, I will explain and define the TDA pipeline that can be build with Gudhi: from the construction of complexes and filtrations, to the computation of persistent (co)homology and finally the possibilities of uses of the resulting persistence diagrams/barcodes. The more "theoretical" explanations will be followed by applied examples with time varying data and code demonstration.

References:

1. The GUDHI Project. *GUDHI User and Reference Manual.* GUDHI Editorial Board, 3.11.0 edition, 2025. `https://gudhi.inria.fr/doc/3.11.0/`

2. H. Edelsbrunner, D. Letscher, and A. Zomorodian. *Topological persistence and simpli cation.* Discrete & Computational Geometry, 28(4):511-533, 2002.

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Tuesday 28 October

9.30-10.30. Rob Hyndman — Anomaly detection using surprisals

I will discuss a probabilistic approach to anomaly detection based on extreme 'surprisal values' aka log scores, equal to minus the log density at each observation. The surprisal approach can be used for any collection of data objects, provided a probability density can be defined on the sample space. It can distinguish anomalies from legitimate observations in a heavy tail, and will identify anomalies that are undetected using methods based on distance measures. I will demonstrate the idea in various real data examples including univariate, multivariate, time series and regression contexts, and when exploring more complicated data objects. I will also briefly outline the underlying theory when the density is known, and when it is estimated using a kernel density estimate. In the latter case, an innovative bandwidth selection method is used based on persistent homology

References:

1. Kandanaarachchi, S., & Hyndman, R. J. (2022). Leave-one-out kernel density estimates for outlier detection. Journal of Computational and Graphical Statistics, 31(2), 586-599. https://robjhyndman.com/publications/lookout/

2. Hyndman, R. J. (2026?) That's weird: Anomaly detection using R. `OTexts.com/weird`. See, especially, ch 6.

11.00-12.00. Aurore Delaigle — Blockwise dynamic selection of smoothing parameters in density estimation for streaming data

We consider nonparametric density estimation from streaming data such as observations collected from sensor networks. Those data are characterized by their continuous collection over time in a high-velocity and often nonstationary environment, requiring near-real-time low-storage processing methods. We study the properties of an iterative estimator, which does not require storing data for long periods of time nor accessing them repeatedly. Then we suggest a procedure for implementing it in practice.

References:

1. Duda, P., Rutkowski, L., Jaworski, M. and Rutkowska, D. (2020). On the Parzen kernel-based probability density function learning procedures over time-varying streaming data with applications to pattern classification. IEEE Trans. Cybern., 5, 1683–1696

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5. Rutkowski, L. (1989). Non-parametric learning algorithms in time-varying environments. Signal Process., 18, 129–137. Vogt, M. (2012). Nonparametric regression for locally stationary time series. Ann. Statist., 40, 2601–2633.

6. Zhang, T. and Wu, W. B. (2015). Time-varying nonlinear regression models: Nonparametric estimation and model selection. Ann. Statist., 43, 741–768.

15.00-15.30. Dylan Peek — Time series analysis of spiking neural systems via transfer entropy and directed persistent homology

We present a topological framework for analysing neural time series that integrates Transfer Entropy (TE) with directed Persistent Homology (PH) to characterize information flow in spiking neural systems. TE quantifies directional influence between neurons, producing weighted, directed graphs that reflect dynamic interactions. These graphs are then analyzed using PH, enabling assessment of topological complexity across multiple structural scales and dimensions. We apply this TE+PH pipeline to synthetic spiking networks trained on logic gate tasks, image-classification networks exposed to structured and perturbed inputs, and mouse cortical recordings annotated with behavioral events. Across all settings, the resulting topological signatures reveal distinctions in task complexity, stimulus structure, and behavioral regime. Higher-dimensional features become more prominent in complex or noisy conditions, reflecting interaction patterns that extend beyond pairwise connectivity. Our findings offer a principled approach to mapping directed information flow onto global organizational patterns in both artificial and biological neural systems.

References:

1. Cliques of Neurons Bound into Cavities Provide a Missing Link between Structure and Function, Reimann et al.

2. Time Series Analysis of Spiking Neural Systems via Transfer Entropy and Directed Persistent Homology, Peek et al.

15.30-16.00. María Sánchez-Muñiz —Topological fingerprints of ENSO dynamics: From model to data

We use the Jin–Timmermann conceptual ENSO model as an idealized dynamical system to develop a topological data analysis (TDA) pipeline to detect regime shifts and understand climate dynamics. We reconstruct model trajectories in phase space via time-delay embedding and compute persistent homology using an efficient landmark-based approach. In particular, random subsampling is replaced by structured landmark selection methods (Max–Min and an ε-net cover), which ensure a uniform cover of the attractor and preserve its topology (by the nerve theorem). These landmark sets are used to build low-dimensional simplicial complexes—including Vietoris–Rips and Witness complexes—enabling tractable computation of persistence. We compare persistence diagrams across key model parameter regimes and identify robust topological features that serve as *fingerprints* of different dynamics. Additionally, we experiment with complementary TDA tools such as Ball Mapper and persistence-diagram distance heatmaps to visualize changes in attractor geometry and highlight regime transitions. Finally, we outline a pipeline from model to observations: initial tests on reanalysis data reveal an analogous low-dimensional structure (bistable El Niño vs. La Niña basins). Our work aims to build a rigorous and scalable topological framework to characterize ENSO regime changes and apply it to observational data.

Joint work with Rolando Kindelan- Nuñez, Margaret Brown, Mircea Petrache, Davide Faranda, Gisela D Charó and Pushpi Paranamana.

References:

1. G. Carlsson and M. Vejdemo-Johansson, *Topological Data Analysis with Applications.* Cambridge University Press, 2021.

2. A. Leitão and N. Otter, "Time-Optimal Persistent Homology Representatives for Univariate Time Series," *arXiv preprint arXiv:2412.08209*, 2024.

3. P. Dłotko, "Ball Mapper: A Shape Summary for Topological Data Analysis," *arXiv preprint arXiv:1901.07410*, 2019.

4. D. Faranda, Y. Sato, C. Dong, A. Gualandi, R. Noyelle, T. Alberti, B. Dubrulle, L. Féry, G. Messori, M. Vrac, P. Vaittinada Ayar, P. Yiou, and G. Mengaldo, "El Niño and Droughts in Southeast Asia: A Stochastic–Chaotic Modeling Approach," *HAL preprint hal-04928658*, 2024.

5. F.-F. Jin and A. Timmermann, "A Nonlinear Coupled Model of ENSO," *Geophysical Research Letters*, vol. 30, no. 24, 2003.

Wednesday 29 October

9.30-10.30. Firas Khasawneh — Topological approach for data assimilation (TADA)

Topological Data Analysis (TDA) is a collection of tools for studying structure and shape of spaces. It has been widely used to quantify topological invariants of spaces such as connectivity, loops, and voids in spaces by encoding that information in a mathematical construction called the persistence diagram. These diagrams provide a two dimensional summary of when those invariants appear and disappear as a scale parameter is varied. Despite the many successful applications of TDA to dynamical systems in many domains, a differential framework for persistence has only been recently discovered. The introduction of this framework has opened the door to many possibilities that include optimization and Data Assimilation (DA). In this talk I will show how persistence differentiation can be leveraged to incorporate measurements of dynamical systems with model outputs to improve prediction accuracy within DA pipeline. I will show how this Topological Approach for Data Assimilation (TADA) can lead to enhanced forecasting of dynamical systems. In addition to applying TADA to prototypical dynamical systems such as Lorenz, I also show an application to high-fidelity simulation of Hall Effect Thrusters (HETs). The operation of HETs involves complex processes such as ionization of gases, strong magnetic fields, and complicated solar panel power supply interactions. Therefore, their operation is extremely difficult to model thus necessitating Data Assimilation (DA) approaches for estimating and predicting their operational states. Because HET's operating environment is often noisy with non-Gaussian sources, this significantly limits applicable DA tools. I will show how TADA, which does not have the Gaussian noise assumption, produces accurate forecasts for HETs' states.

References:

1. Leygonie, J., Oudot, S. and Tillmann, U. "A Framework for Differential Calculus on Persistence Barcodes." Found Comput Math 22, 1069–1131 (2022).
2. Mathieu Carrière, Frédéric Chazal, Marc Glisse, Yuichi Ike, Hariprasad Kanna. "Optimizing persistent homology based functions," arXiv preprint arXiv:2010.08356. (2021).
3. Chumley, M. M., and Khasawneh, F. A. "Topological Approach for Data Assimilation." arXiv preprint arXiv:2411.18627. (2024).
4. Chumley, M. M., and Khasawneh, F. A. "Hall Effect Thruster Forecasting using Topological Approach for Data Assimilation." arXiv preprint arXiv:2504.06157. (2025).
5. Khasawneh et al. "Teaspoon: A Python Package for Topological Signal Processing." Journal of Open Source Software, 10(107), 7243. (2025).

11.00-12.00. Michael Small — Embedding and topology of time series data

Time delay embedding 2 provides a generic approach to transform time varying data into a cloud of points with topological properties (almost) guaranteed to share dynamical invariants with the underlying deterministic data generating process. One of the most popular invariants is the *correlation dimension*

$$d_c = \lim_{\epsilon \to 0} \frac{\log C(\epsilon)}{\log \epsilon}$$

which quantifies the spatial scaling of the correlation integral $C(\epsilon)$ defined to be the distribution of interpoint distances

$$C(\epsilon) = \text{Prob}(\|x_i - x_j\| < \epsilon).$$

Some time ago, a suite of methods were proposed to treat this temporal sequence of $x_i \in \mathbb{R}^n$ as a network — in various ways 1, starting with 5. These approaches connect dynamic invariants (such as correlation dimension) to structural properties of the networks, and the networks themselves are often highly evocative of the complex multiscale structure present in the original data. We describe straightforward applications of the persistence diagram of topological data analysis (TDA) to quantify the similarity between these embedded objects 3 (thereby providing a measure of model performance) and deduce appropriate parameters for a *good* embedding 2. We conclude by asking if there is more to be done — does TDA provide a multiscale generalisation of the correlation integral 4, and what exactly are the connections between these objects?

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2. Tan, E., Algar, S., Correa, D., Small, M., Stemler, T. and Walker, D., Selecting embed- ding delays: An overview of embedding techniques and a new method using persistent homology. Chaos 33 (2023) 032101.

3. Tan, E., Corrêa, D., Stemler, T. and Small, M., Grading your models: Assessing dynamics learning of models using persistent homology. Chaos 31 (2021) 123109.

4. Weng, T., Wu, M., Feng, S., Chen, X., Ren, Z., Liu, R. and Small, M., A generalized high-order correlation dimension for strange attractors. Chaos, Solitons and Fractals, 194 (2025) 116190.

5. Xu, X., Zhang, J. and Small, M., Superfamily phenomena and motifs of networks induced from time series. Proc Natl Acad Sc USA 105 (2008), 19601-19605.

Thursday 30 October

9.30-10.30. Vanessa Robins — The extended persistent homology transform for manifolds with boundary

The Persistent Homology Transform (PHT) is a topological transform introduced by Turner, Mukherjee and Boyer in 2014 1. Its input is a shape embedded in Euclidean space; then to each unit vector the transform assigns the persistence module of the height function over that shape with respect to that direction. The PHT is injective on piecewise-linear subsets of Euclidean space, and it has been demonstrably useful in diverse applications as it provides a landmark-free method for quantifying the distance between shapes 2. One shortcoming is that shapes with different essential homology (i.e., Betti numbers) have an infinite distance between them.

The theory of extended persistence for Morse functions on a manifold was developed by Cohen-Steiner, Edelsbrunner and Harer in 2009 to quantify the support of the essential homology classes 3. By using extended persistence modules of height functions over a shape, we obtain the extended persistent homology transform (XPHT) which provides a finite distance between shapes even when they have different Betti numbers.

It may seem that the XPHT requires significant additional computational effort, but recent work, 4, by Katharine Turner and myself shows that when A is a compact manifold with boundary X, embedded in Euclidean space, the XPHT of A can be derived from the PHT of X, and a signature for each local minimum. James Morgan has implemented the required algorithms for 2-dimensional binary images as an R-package. This talk will provide an outline of our results and illustrate their application to shape clustering, and symmetry quantification. These applications were studied by our former students Jency Jiang and Nicholas Bermingham 5.

References:

1. Turner, K., Mukherjee, S., Boyer, D.M.: Persistent homology transform for modeling shapes and surfaces. Inform. Inference: J. IMA 3(4), 310–344 (2014)
2. Amézquita, E.J., Quigley, M.Y., Ophelders, T., Landis, J.B., Koenig, D., Munch, E., Chitwood, D.H.: Measuring hidden phenotype: quantifying the shape of barley seeds using the Euler characteristic transform. In Silico Plants 4(1), diab033 (2022)
3. Cohen-Steiner, D., Edelsbrunner, H., Harer, J.: Extending persistence using Poincaré and Lefschetz duality. Found. Comput. Math. 9(1), 79–103 (2009)
4. Turner K, Robins V, Morgan J.: The extended persistent homology transform of manifolds with boundary. J. Ap. and Comp. Top. 8(7), 2111–54 (2024)
5. Bermingham, Nicholas, Robins, Vanessa, Turner, Katharine: Planar symmetry detection and quantification using the extended persistent homology transform. In Proceedings of IEEE Vis 2023 TopoInVis workshop, pages 1–9, Melbourne, Australia, (2023).

11.00-11.30. Elizabeth Thompson — A stable measure for conditional periodicity of time series using persistent homology

Given a pair of time series over the same time period, we study how the periodicity of one influences the periodicity of the other. There are several known methods to measure such time-series similarity. One commonly used measure is percent determinism (%DET) 4 , which measures how correlated the pairwise distances between two embeddings of a pair of time series are. We experimentally show limitations of %DET in practice, including its requirement of four parameters for its computation as well as its reliance on pairwise Euclidean distances which make it less robust to small perturbations in time series embeddings. Persistent homology has been utilized to construct a scoring function with theoretical guarantees of stability that quantifies the periodicity of a single univariate time series f_1, denoted score(f_1) 2, 3 . Building on this concept, we propose a conditional periodicity score that quantifies the periodicity of one univariate time series f_1 given another f_2, denoted score($f_1|f_2$), and derive theoretical stability results for the same. Dimension reduction techniques are often used on time series data to reduce computational costs. With this setting in mind, we prove a new stability result for score($f_1|f_2$) under orthogonal projection of the time series embeddings onto their respective first K principal components. We show that the change in our score is bounded by a function of the eigenvalues corresponding to the remaining (unused) $N - K$ principal components 1 and hence is small when the first K of them capture most of the variation in the time series embeddings. We derive a lower bound on the minimum embedding dimension to use in our pipeline which guarantees that any two such embeddings give scores that are linearly within ϵ of each other. We present a procedure for computing conditional periodicity scores and implement it on several pairs of synthetic signals. We experimentally compare our similarity measure to %DET, revealing greater robustness of score($f_1|f_2$) to added noise on several pairs of synthetic time series and highlighting the comparability of our score to %DET and the lack of robustness of %DET on several pairs of real time series describing the yearly proportion of incoming calls to a Washington police department per month of various types.

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2. Jose Perea and John Harer. Sliding Windows and Persistence: An Application of Topological Methods to Signal Analysis. Foundations of Computational Mathematics, 15:799–838, 2015. arXiv:1307.6188, doi:10.1007/s10208-014-9206-z.

3. Jose A. Perea, Anastasia Deckard, Steve B. Haase, and John Harer. SW1PerS: Sliding windows and 1-persistence scoring; discovering periodicity in gene expression time series data. BMC Bioinformatics, 16(1):257, 2015. doi:10.1186/s12859-015-0645-6.

4. S. Wallot and G. Leonardi. Analyzing multivariate dynamics using cross-recurrence quantification analy- sis (CRQA), diagonal-cross-recurrence profiles (DCRP), and multidimensional recurrence quantification analysis (MdRQA) — A tutorial in R. Front Psychol, 2018. doi:10.3389/fpsyg.2018.0223.

11.30-12.00. Aleksandr Kachura — Blurred magnitude homology of directed brain networks

A possible approach to analyzing multivariate time series with interdependent components is to construct a complete weighted graph with nodes corresponding to the components of the time series and edge weights representing the strength of dependence between the pair of components corresponding to their ends. Among the many fields where this methodology is popular, neuroscience can be distinguished. A prominent example is the analysis of functional connectomes 1, brain networks whose nodes represent brain regions. These networks exhibit non trivial structure, so their topological characteristics are useful for analysis. The level of interconnection between brain regions is usually measured using non-directional correlations, while the functional connections between brain regions are inherently directional.

Topological characteristics of graphs can be analyzed with persistent homology 2, an increasingly popular data analysis tool that can also be applied to graphs. The essence of this approach is to track the moments of the appearance and disappearance of topological structures as the scale varies, using algebraic invariants called homology. When applied to weighted graphs – including functional connectomes – persistent homology allows us to study how the topological structure of a graph changes as the edge filtering threshold varies. This enables identification of noise-robust topological features, which is crucial when the graph structure is not given a priori but estimated from data. Several homology theories exist. Simplicial homology – historically the first one used to compute persistent homology – cannot account for the directions of graph edges. The most direct generalization of this homology theory to digraphs is the homology of directed flag complexes 3. However, it still discards some directional information. One of the homology theories that makes it possible to preserve a large proportion of information about the directions of edges is blurred magnitude homology 4.

In this work we introduce a method for classifying directed functional connectomes using blurred magnitude homology, specifically its Betti curves, a popular numerical descriptor of persistent homology. As an example, we apply the developed technique to study graphs constructed from fMRI scans of individuals with ASD and typically developing controls.

We experimentally tested the approach on the ABIDE dataset. This work was supported by the Russian Science Foundation, Grant No. 24-68-00030.

References:

1. Uddin, L. Q., Yeo, B. T., & Spreng, R. N. (2019). Towards a universal taxonomy of macro-scale functional human brain networks. Brain topography, 32(6), 926-942.
2. Edelsbrunner, H., Harer, J. (2010). Computational topology: an introduction. American Mathematical Society.
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15.00-16.00. Konstantin Mischaikow: Homological dynamics

Data-driven dynamics suffers from a lack of precision; typically data is noisy and sparse and thus one should not expect precise statements about the associated dynamics. With this in mind I will discuss the concept of homological dynamics where the focus is on obtaining correct meaningful robust descriptions of the dynamics from finite information.

To describe homological dynamics I will discuss the following topics: (1) the underlying data structures, (2) order theory, (3) Morse graphs and attractors, and the (4) Conley index. In order to relate homological dynamics to classical dynamical systems I will review classical Conley theory and describe how characterizations of dynamics using homological dynamics can be transferred to understanding in the language of classical dynamics.

Finally, time permitting I will describe two simple examples to demonstrate how homological can be used in practice.

References:

1. W.D. Kalies, K. Mischaikow, and R.C.A.M. Vandervorst, Lattice structures for attractors I, J. Comput. Dyn. 1 (2014), no. 2, 307–338.
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4. Bogdan Batko, Marcio Gameiro, Ying Hung, William Kalies, Konstantin Mischaikow, and Ewerton Vieira, Identifying nonlinear dynamics with high confidence from sparse data, SIAM J. Appl. Dyn. Syst. 23 (2024), no. 1, 383–409
5. Marcio Gameiro, Tomáš Gedeon, Hiroshi, Kokubu, Konstantin Mischaikow, Hiroe Oka, Bernardo Rivas, Ewerton Vieira, and Daniel Gameiro, Global dynamics of ordinary differential equations: Wall labelings, Conley complexes, and ramp systems, 2024

17.30-18.30. Public Lecture: Philippa Pattison — The mathematics of social networks

In this lecture I describe how mathematical approaches have been used to build understanding of the structure of human social networks and their properties. Social networks can reflect social and economic ties of many types, such as who-socialises-with-whom, who-collaborates-with-whom, or who-offers-credit-to-whom. Starting with the simplest assumption of a social network as a random graph, I explain how the interplay between mathematical and empirical studies of networks has led to progressively more sophisticated and effective models. A number of case examples illuminate the trajectory of model development and illustrate that a key to successful progress has been to allow for endogenous local processes in the formation and dissolution of network ties. I also point to ways in which the current modelling suite can advance our understanding of some important social outcomes and then touch briefly on active areas of further model development.

Website of public lecture:

`https://maths.anu.edu.au/news-events/events/mathematics-social-networks`

Friday 31 October

9.00-10.00. Musashi Koyama — Degree-1 persistent homology on planar time varying point clouds

Persistent homology has been applied to static data sets in a wide array of contexts. Naturally the next step is to apply persistent homology to a time-varying point-cloud. For time-varying point-clouds, instead of a persistence diagram one has a persistence vineyard. A persistence vineyard can be thought of as a stack of persistence diagrams, each diagram corresponding to the point-cloud at a given time. In this talk we give a novel algorithm for computing the degree-1 Vietoris-Rips persistent vineyard of a time-varying point-cloud in the plane which makes use of properties of the relative neighborhood graph on a planar point set.

References:

1. D. Cohen-Steiner, H. Edelsbrunner, and D. Morozov, "Vines and vineyards by updating persistence in linear time," in Proceedings of the twenty-second annual symposium on Computational geometry, pp. 119–126, 2006. 1
2. G. T. Toussaint, "The relative neighbourhood graph of a finite planar set," Pattern Recognit., vol. 12, pp. 261–268, 1980. 1, 3

11.00-12.00. Agnese Barbensi — Topology, unknotting and optimal pathways

In this talk I discuss the concept of topological simplification, with a focus on knotting/unknotting of spatial curves and applications to proteins. The talk is partially based on results from the paper 1. For a review on knots/topology in biophysics, see the survey paper 2.

References:

1. Topologically Directed Simulations Reveal the Impact of Geometric Constraints on Knotted Proteins, A. Barbensi, A.R. Klotz, D. Gkountaroulis, 2025, `https://doi.org/10.48550/arXiv.2504.12659`
2. Topology in soft and biological matter, Tubiana et al, Physics Reports Volume 1075, 2024, Pages 1-137 `https://doi.org/10.1016/j.physrep.2024.04.002`