Program & Abstracts

Applied Algebraic Topology 2017

August 8 (Tue) – 12 (Sat), 2017　Hokkaido University

AIMR　JST　科研費 KAKENHI

ORGANIZERS

- Zin Arai (Chubu Univ.)
- Paweł Dłotko (INRIA)
- Kathryn Hess (EPFL)
- Yasuaki Hiraoka (Tohoku Univ.)
- Daisuke Kishimoto (Kyoto Univ.)
- Hiroshi Kokubu (Kyoto Univ.)
- Ran Levi (Univ. of Aberdeen)
- Dai Tamaki (Shinshu Univ.)
- Toru Ohmoto (Hokkaido Univ.)

SUPPORTS

- Faculty of Science, Hokkaido University (Host organization)
- Advanced Institute for Materials Research, Tohoku University
- EPFL start-up grant (Kathryn Hess)
- JST CREST TDA (Yasuaki Hiraoka)
- NIMS MI^2I (Yasuaki Hiraoka)
- JSPS KAKENHI Grant Number 15K04870 (Dai Tamaki)
- JSPS A3 Foresight Program (Yasumasa Nishiura)

Applied Algebraic Topology 2017

Program

- **Presentation time**

  Plenary lecture: 1 hour

  Contributed lecture: 30 minutes

- **Place**

  Plenary lecture: Auditorium (2F)

  Contributed lecture: Auditorium (2F) and Conference Room 1 (1F)

  Poster session: Hall (1F)

August 8 (Tuesday)

8:00 -	Registration	
9:00 - 10:00	Plenary lecture 1	
10:00 - 10:30	Coffee Break	
10:30 - 11:30	Plenary lecture 2	
11:30 - 14:00	*Lunch	
14:00 - 15:00	Plenary lecture 3	
15:30 - 16:00	Coffee Break	
15:30 - 17:00	Contributed Lecture 1	Contributed Lecture 2
17:30 - 18:30	Welcome Party	

*A3 members have a lunch meeting for A3 foresight.

August 9 (Wednesday)

9:00 - 10:00	Plenary lecture 4	
10:00 - 10:30	Coffee Break / Photo Session	
10:30 - 11:30	Plenary lecture 5	
11:30 - 14:00	*Lunch	
14:00 - 15:00	Plenary lecture 6	
15:30 - 16:00	Coffee Break	
15:30 - 17:00	Contributed Lecture 3	Contributed Lecture 4
17:00 - 17:30	Poster Session	

*A3 members have a lunch meeting for A3 foresight.

August 10 (Thursday)

9:00 - 10:00	Plenary lecture 7	
10:00 - 10:30	Coffee Break	
10:30 - 11:30	Plenary lecture 8	
11:30 - 17:30	*Excursion	
18:00 - 20:00	Banquet	

*A3 members have a lunch meeting for A3 foresight.

August 11 (Friday)

9:00 - 10:00	Plenary lecture 9	
10:00 - 10:30	Coffee Break	
10:30 - 11:30	Plenary lecture 10	
11:30 - 14:00	*Lunch	
14:00 - 15:30	Contributed Lecture 5	Contributed Lecture 6
15:30 - 16:00	Coffee Break	
16:00 - 17:00	Contributed Lecture 7	Contributed Lecture 8

*A3 members have a lunch meeting for A3 foresight.

August 12 (Saturday)

9:00 - 10:00	Plenary lecture 11
10:30 - 11:30	Plenary lecture 12
11:30 - 13:00	*Lunch

*A3 members have a lunch meeting for A3 foresight.

Information for Participants

Registration Desk

Date: Monday, August 8 (Open at 8:00 AM)

Venue: 2F Conference Hall, Hokkaido University (北海道大学学術交流会館 2 階)

Social Program

Welcome Party

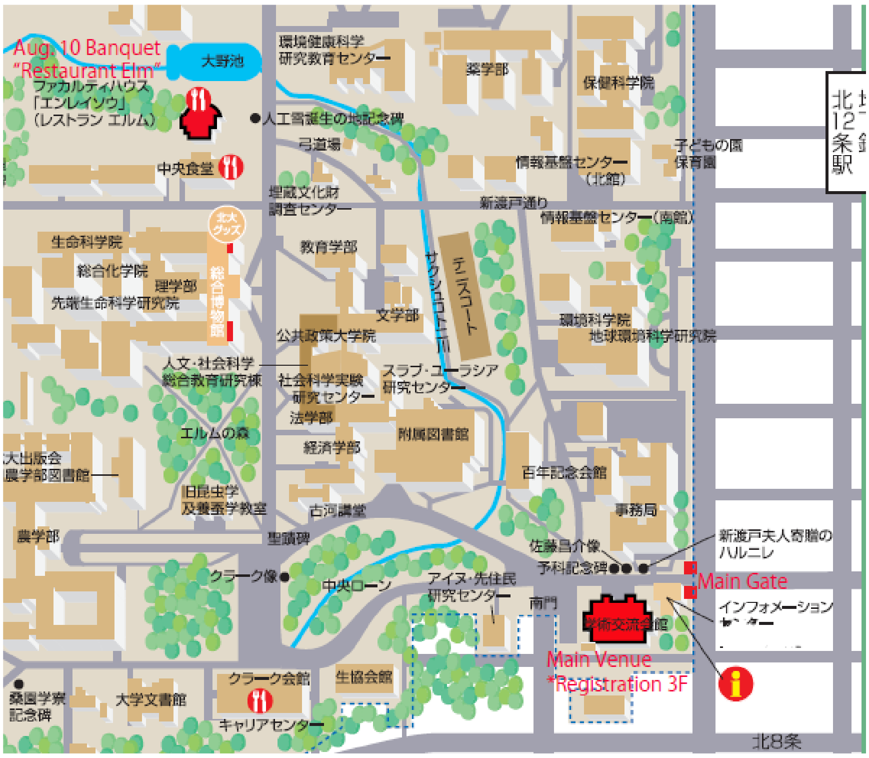
Date: 17:30-18:30, Tuesday, August 8

Venue: Conference Room 1 (北海道大学学術交流会館　第一会議室)

Banquet

Date: 18:00-20:00, Thursday, August 10

Venue: Faculty House Trillium "Restaurant Elm”, Hokkaido University



Excursion

Date: 11:30-17:30, Thursday, August 10

Itinerary: Transfer to Otaru by public transportation - Free time in Otaru - come back to Sapporo by yourself.

Please note that all expenses, such as transportation fee and admission fee, for excursion is at your own cost.

If you would like to join excursion, please register at the venue by August 9 (Wed).

Abstract

Plenary Lecture

The Rise and Spread of Algebraic Topology

John Baez[1]

[1]*Department of Mathematics*, University of California at Riverside

As algebraic topology becomes more important in applied mathematics it is worth looking back to see how this subject has changed our outlook on mathematics in general. When Noether moved from working with Betti numbers to homology groups, she forced a new outlook on topological invariants: namely, they are often *functors,* with two invariants counting as “the same” if they are *naturally isomorphic*. To formalize this it was necessary to invent categories, and to formalize the analogy between natural isomorphisms between functors and homotopies between maps it was necessary to invent 2-categories. These are just the first steps in the “homotopification” of mathematics, a trend in which algebra more and more comes to resemble topology, and ultimately abstract “spaces” (for example, homotopy types) are considered as fundamental as sets. It is natural to wonder whether topological data analysis is a step in the spread of these ideas into applied mathematics, and how the importance of “robustness” in applications will influence algebraic topology.

Local cohomology and stratification

Vidit Nanda
University of Oxford, The Alan Turing Institute

I will outline a method to automatically discover the canonical (or, coarsest possible) stratification of a given cell complex into cohomology manifolds, each of which is a union of cells. The construction proceeds by iteratively localizing the poset of cells about a family of subposets; these subposets are in turn determined by a collection of cosheaves which capture variations in local cohomology across cells in the underlying complex. The result is a finite sequence of categories whose colimit recovers the canonical strata (and hence, identifies all the topological singularities) of our complex via isomorphism classes of its objects. The entire process is amenable to efficient distributed computation.

Towards a Computational, Discrete Geometric Foundation for Nonlinear Dynamics

Konstantin Mischaikow[1]

[1] *Department of* Mathematics, Rutgers University

Abstract The current paradigm for nonlinear dynamics focuses on the existence and structure of invariant sets. As over a century of work shows this is an incredibly rich subject and perhaps, from the perspective of modern applications, too rich. For example, in general, invariant sets are not computable and structurally stable systems are not generic. As consequence it appears difficult to develop a natural methodology for analyzing dynamics in the context of scientific challenges driven by data as opposed to mathematical models.

In this talk I will describe an alternative approach to dynamics based on using order structures to identify gradient versus recurrent-like behavior and algebraic topology to characterize local and global structures of the dynamics. Using regulatory networks arising from systems biology as motivation I will demonstrate some advantages of this approach: it allows for finite queryable descriptions of global dynamics; it leads to natural decompositions of parameter space; it lends itself to efficient computations; and the results lead to mathematically rigorous statements about the possible dynamics of more traditional models based on differential equations.

Topology of complexes arising in models for Distributed Computing

Dmitry Feichtner-Kozlov

University of Bremen, Germany

We shall talk about various simplicial models for distributed computing. The main model consists of iterated chromatic subdivisions and corresponds to the well-used model in distributed computing. Using the Weak Symmetry Breaking as an example we shall translate questions of distributed computing into purely combinatorial-simplicial questions for the corresponding complex. We shall see how this approach leads to many interesting new and open questions in various fields of mathematics.

Materials TDA and random/statistical topology

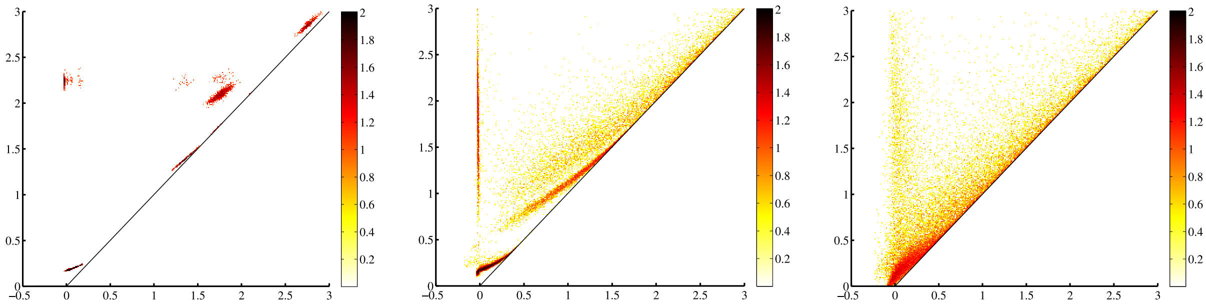
Yasu Hiraoka[1]

[1]*AIMR, Tohoku* University
hiraoka@tohoku.ac.jp

In this talk, I will briefly explain our recent activity of topological data analysis on materials science (e.g. [1,2]). Our main tool is the persistent homology, which is an emerging mathematical concept for characterizing shapes of data. In particular, it provides a tool called the persistence diagram that extracts multiscale topological features such as rings and cavities in atomic configurations and digital high dimensional images. I present a unified method using persistence diagrams for studying the geometry embedded in those data. Furthermore, I will also show a new framework of materials informatics by combining statistical and machine learning methods with persistence diagram.

Then, motivated from materials TDA project, I will also present a recent result [3] about convergence of persistence diagrams on stationary point processes in R^N. Several limit theorems such as strong laws of large numbers and central limit theorems for random cubical homology are also shown [4].

[1] Y. Hiraoka, T. Nakamura, A. Hirata, E. G. Escolar, K. Matsue, and Y. Nishiura. Hierarchical structures of amorphous solids characterized by persistent homology. Proceedings of the National Academy of Sciences of the United States of America 113 (2016), 7035–7040.
[2] Mohammad Saadatfar, Hiroshi Takeuchi, Nicolas Francois, Vanessa Robins, and Yasuaki Hiraoka. Pore configuration landscape of granular crystallisation. Nature Communications. 8:15082 (2017), DOI: 10.1038/ncomms15082.
[3] T. K. Duy, Y. Hiraoka, and T. Shirai. Limit theorems for persistence diagrams. arXiv:1612.08371.
[4] Y. Hiraoka and K. Tsunoda. Limit theorems for random cubical homology. arXiv:1612.08485.



Persistence diagrams of SiO2. Left: Crystal, Middle: Glass, Right: liquid.

Applied Topology from the point of view of Probability

Robert J Adler

Andrew and Erna Viterbi Faculty of Electrical Engineering,
Technion - Israel Institute of Technology

It is an undeniable fact that the moment any area of Pure Science, including Mathematics, meets data, randomness comes into play, whether it be as a result of sampling variance, measurement error, background noise, or any of a multitude of stochastic phenomena. Topology is no exception, but stands out from many other examples in that Topology and Randomness are two topics that have rarely appeared together, making the integration of statistical approaches into Applied Topology singularly challenging.

Driven, in a large part, by issues arising in Applied Topology, the past few years have seen considerable activity at the Topology/Probability and Topology/Statistics interfaces. I will describe a number of the results of this activity, mainly looking at them from the perspective of Probability, but also illustrating their potential importance to Applied Topology.

Among others, the (to some extent eclectic) results I hope to cover will come from the theory of random surfaces, mappings and embeddings; from problems related to learning the homology of manifolds when sampling from them in the presence of noise; and from the crucial problem of understanding randomness in persistence diagrams.

Efficient Signal Processing in Random Spiking Networks that Generate Variability

Taro Toyoizumi

RIKEN Brain Science Institute

Source of cortical variability and its influence on signal processing remain an open question. We address the latter, by studying two types of balanced random networks of quadratic integrate-and-fire neurons that produce irregular spontaneous activity patterns: (a) a deterministic network with strong synaptic interactions that actively generates variability by chaotic dynamics and (b) a stochastic network that has weak synaptic interactions but receives externally generated noise. These networks of spiking neurons are analytically tractable in the limit of a large network-size and channel-time-constant. Despite the difference in their sources of variability, spontaneous activity patterns of these two models are indistinguishable unless majority of neurons are simultaneously recorded. We characterize the network behavior with dynamic mean field analysis and reveal a single-parameter family that allows interpolation between the two networks, sharing nearly identical spontaneous activity. Despite the close similarity in the spontaneous activity, the two networks exhibit remarkably different sensitivity to external stimuli. The difference between the two networks is further enhanced if input synapses undergo activity-dependent plasticity, producing significant difference in signal to noise ratio. We show that, this difference naturally leads to distinct performance while integrating spatio-temporally distinct signals from multiple sources. Unlike its stochastic counterpart, the deterministic chaotic network activity can serve as a reservoir to perform near optimal Bayesian integration and Monte-Carlo sampling from the posterior distribution. We describe implications of the differences between deterministic and stochastic neural computation on population coding and neural plasticity. ・・・・・・・・・・・・End

Magnitude homology

Tom Leinster [1]

[1]*School of Mathematics, University of Edinburgh*

Magnitude homology is a homology theory of enriched categories, proposed by Michael Shulman late last year. It therefore specializes to (among other things) a homology theory of ordinary categories and a homology theory of metric spaces. This metric homology theory is something new, and is different from persistent homology. As a sample result, the first homology of a subset X of Euclidean space detects whether X is convex.

Like all homology theories, magnitude homology has an Euler characteristic, defined as the alternating sum of the ranks of the homology groups. Often this sum diverges, so we have to use some formal trickery to evaluate it. In this way, we end up with an Euler characteristic that is often not an integer. This number is called the *magnitude* of the enriched category. In the setting of compact metric spaces, magnitude is closely related to volume, surface area, curvature, and other classical invariants of geometry. In the special setting of finite metric spaces, magnitude appears to provide information of interest about point-sets, such as the apparent dimension and number of clusters at different length scales.

I will give an overview of these developments, assuming little categorical knowledge.

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End

Reeb Graph Smoothing via Cosheaves

Vin de Silva[1], Elizabeth Munch[2], Amit Patel[3], Dmitriy Smirnov[4], Song Yu[5]

[1,4,5]*Department of Mathematics, Pomona College,*
[2]*Department of Computational Mathematics, Statistics, and Engineering, Michigan State University*
[3]*Department of Mathematics, Colorado State University*

Abstract. Topological persistence is perhaps the most well-known aspect of applied algebraic topology. In this talk, I will give an introduction to the category-theoretic perspective that unifies several different constructions: persistence modules, merge trees, Reeb graphs. The case of Reeb graphs is particularly fruitful: these are ordinarily thought of as topological graphs equipped with a non-degenerate real-valued function, but one can also interpret them as cosheaves over the real line.

Whereas sheaves are widely used in algebraic geometry, the dual theory of cosheaves is perhaps less commonly exploited. Following [de Silva, Munch, Patel (2016)], I will explain the correspondence between Reeb graphs and Reeb cosheaves, and use it to define a metric on the class of all Reeb graphs, as well as a 1parameter semigroup of ‘smoothing’ operators that progressively simplify the topology of a given Reeb graph. Finally, I will present an algorithm [de Silva, Smirnov, Yu (2017, unpublished)] that produces, in a single calculation, the description of the smoothings of a given Reeb graph at all possible parameter values.

Topological organization of neural networks

Carina Curto

The Pennsylvania State University

Neural networks serve as data summaries and dynamic models of neural activity in the brain. Recently, methods from topological data analysis have been used to gain insights into the structure of such networks, using various types neural activity data. In this talk, we will turn our attention to how network structures uncovered by topological methods might shape dynamics. We will illustrate these ideas in the context of threshold-linear networks of simple neurons, whose dynamics are controlled purely by the pattern of connectivity as defined by a directed graph. This enables us to study directly the role of connectivity in shaping network dynamics, without worrying about effects stemming from the intrinsic properties of neurons. Here we find some interesting connections between topologically-relevant features of the network structure and its dynamic attractors. We also identify some aspects of the connectivity that are not picked up by standard tools, but may be amenable to new types of topological analyses.

Directed topology and Concurrency Theory

Lisbeth Fajstrup,

Department of Mathematics Aalborg University

Abstract:

Insights of a topological nature play a more and more prominent role in discovery and analysis of fundamental mechanism in engineering and science. This talk will be a survey of a specific development, namely in the modelling and analysis of concurrency, i.e., parallel structures in computer science.

About 20 years ago, we introduced directed algebraic topology, topological spaces with a “time”-direction, to study models of concurrent computing such as PV-models and Higher Dimensional Automata. The spaces model the joint states of the system and executions are (time)-directed paths. Executions are equivalent if the corresponding directed paths can be continuously deformed into each other via directed paths – they are homotopic through directed paths. Topology is certainly the right tool, but time directions have to be taken into account, hence, directed topology is needed. Both algorithms and insight have come out of this interplay between a new mathematical area and the applications.

This talk will give an introduction to this mathematical field and the applications in concurrency theory.

On Computing Persistent Homology

Robert Ghrist[1]

[1] *Departments of Mathematics & Electrical/Systems Engineering*
University of Pennsylvania

The past fifteen years has witnessed a dramatic increase in the applications of homological algebra to the applied sciences. Several challenges remain, including: (1) how to compute efficiently in homological algebra; (2) how to extend the set of current applications and methods; and, perhaps most importantly, (3) how to educate end-users in the meaning and proper use of homological tools.

This talk will present some new perspectives on computing homology and persistent homology (based on recent work of Greg Henselman) and point to advances beyond persistent homology.

Contributed Lecture

【CL1-1】

Graph persistence

Mattia G. Bergomi[1], Massimo Ferri[2], Lorenzo Zuffi[2]
[1]Champalimaud Foundation, Lisbon, Portugal, [2]University of Bologna, Italy

The main concepts of persistence are extended to weighted graphs. Two main ways are explored:

1) Various constructions of simplicial complexes out of sublevel subgraphs, filtered through the weight, and persistent homology of the resulting complexes. Here, particular attention is devoted to “dual” constructions (e.g. cliques and independent sets), which yield a form of extended persistence.
2) Persistence of purely graph-theoretical structures (blocks and edge-blocks).

A natural distance for weighted graphs is defined and compared with distances between the various persistence diagrams obtained by the above processes.

【CL1-2】

A Persistent Homological Analysis of Network Data Flow Malfunctions

Nicholas A. Scoville[1], Karthik Yegnesh[2]
[1]*Ursinus College,* [2]*Methacton High School*

Persistent homology has recently emerged as a powerful technique in topological data analysis for analyzing the emergence and disappearance of topological features throughout a filtered space, shown via persistence diagrams. In this presentation, we develop an application of ideas from the theory of persistent homology and persistence diagrams to the study of data flow malfunctions in networks with a certain hierarchical structure. In particular, we formulate an algorithmic construction of persistence diagrams that parametrize network data flow errors, thus enabling the potential for novel applications of statistical methods that are traditionally used to assess the stability of persistence diagrams corresponding to homological data to the study of data flow malfunctions.

【CL1-3】

Information topology and probabilistic graphical models

Juan Pablo Vigneaux and Daniel Bennequin
Institut de Mathématiques de Jussieu (UMR-CNRS 7586), Université Paris Diderot,
Sorbonne Paris Cité

Baudot et Bennequin [2] have introduced a cohomology adapted to information theory. To this end, they use the constructions of topos theory [1]: an "information topos" is a ringed topos on a suitable site whose objects are σ-algebras. One can define a family of sheaves Fq, with $q > 0$, such that Shannon's entropy generates $H^1(F1)$ and Tsallis' entropy S_q generates $H^1(Fq)$ when $q \neq 1$. Other information functions appear also as cocycles and the theory can be extended to the quantum case.

In this context, we identify the entropy as the solution of a problem of extension of algebras. We also present a combinatorial analogue of Shannon's axioms [5] for strings of size N with fixed type (the proportion of appearances of each symbol) that give the cocyle equation in the limit $N \to \infty$.

Each probabilistic graphical model [4] gives an information topos; accordingly, Bayesian networks, Markov fields and other interesting models find a place in our theory. The site is such that the usual Bethe-Kikuchi approximation is obtained by Möbius inversion on it, followed by a truncation [3]. We present a simplicial representation for factor graphs; the obstruction to find a global state (probability law) with prescribed marginals is strongly related to the topology of this representation. Some explicit examples will be discussed.

References

[1] M. Artin, A. Grothendieck, and J. Verdier. *Théorie des topos et coho- mologie étale des schémas: Séminaire de géométrie algébrique du Bois- Marie 1963/64 - SGA 4. Exposés I à IV, théorie des topos. Tome 1*. Lecture notes in mathematics. Springer-Verlag, 1972.

[2] P. Baudot and D. Bennequin. The homological nature of entropy. *En- tropy*, 17(5):3253–3318, 2015.

[3] R. Mori. New understanding of the bethe approximation and the replica method. *arXiv preprint arXiv:1303.2168*, 2013.

[4] A. Pelizzola. Cluster variation method in statistical physics and proba- bilistic graphical models. *Journal of Physics A: Mathematical and Gen- eral*, 38(33):R309, 2005.

[5] C. Shannon. A mathematical theory of communication. *Bell System Technical Journal*, 27:379–423, 623–656, 1948.

【CL2-1】

Investigating porous material with persistent homology

Senja Barthel[1], Paweł Dłotko[2], Kathryn Hess[3], Yongjin Lee[1], S Mohamad Moosavi[1], Berend Smit[1,5]

[1]Laboratory of molecular simulations, EPFL, [2]Mathematics, Swansea,
[3]Mathematics, EPFL, Chemistry, UC Berkeley

Material science is a field with many potential applications of persistent homology. Many properties of materials are related to shapes, for example the arrangement of atoms or that of potentials or densities. The talk will show the construction of a persistent homological descriptor for pore shapes of nano-porous materials to examine geometric similarities of these materials. This allows drawing conclusions on the material's gas adsorption and separation behaviour, in particular carbon capture and methane storage.

・・・・・・・・・・End

【CL2-2】

Computational Topology for Spreading Dynamics

Barbara Mahler[1], Ulrike Tillmann[1], Heather Harrington[1], Mason Porter[2]

[1] *Mathematical Institute, University of Oxford*
[2]*Department of Mathematics, University of California, Los Angeles*

We consider complex contagions on “ noisy geometric networks”. These are networks whose nodes are embedded in a manifold and have both “geometric edges” that respect the geometry of the underlying manifold and “non-geometric edges” that are not constrained by the geometry of the underlying manifold. In particular, we study a threshold contagion model on a noisy geometric network whose nodes are embedded in a torus. We investigate the pattern of propagation of the contagion and the extent to which it adheres to the structure of the underlying torus. Our methods involve using a “contagion map” to map the network nodes to a point cloud, which we analyze using tools from computational topology.

【CL2-3】

Applications of persistent homology to immunochemistry

Takashi Teramoto[1], Akihiro Takiyama[2]
[1]*School of Medicine, Asahikawa Medical University*
[2]*Hokkaido Bunkyo University*

Immunohistochemical data (IHC) plays an important role in clinical practice, and is typically gathered in a semi-quantitative fashion that relies on some degree of visual scoring. However, visual scoring by a pathologist is inherently subjective and manifests both intra-observer and inter-observer variability. In this study, we introduce a novel computer-aided quantification methodology for immunohistochemical scoring that uses the algebraic concept of persistent homology.

Using image data derived from 30 specimens of invasive ductal carcinoma of the breast, stained for the replicative marker Ki-67, we computed homology classes. These were then compared to nuclear grades and the Ki-67 labeling indices obtained by visual scoring. Combining this approach with biostatistical analysis, results in a diagram of homology classes classified into positive and negative groups. The new metrics for IHC staining were defined: the percentage of positive groups in all homology classes, called the Persistent Homology Index (PHI). Comparisons of PHI versus a pathologist-derived Ki-67 labeling index demonstrated a high Spearman correlation of 0.81 ($p < 0.001$), confirming that our novel approach yields highly similar data to that generated by visual evaluation, although PHI data are informed by a richer biologic dataset than conventional evaluation methods.

【CL3-1】

Topological Representation of Neuronal Morphologies

Lida Kanari, Pawel Dlotko, Martina Scolamiero, Ran Levi, Julian Shillcock, Kathryn Hess and Henry Markram

The shape of neuronal arborizations defines amongst other aspects their physical connectivity and functionality. Yet an efficient method for quantitatively analyzing the spatial structure of such trees has been difficult to establish. The wide diversity of neuronal morphologies in the brain, even for cells identified by experts as of the same type, renders an objective classification scheme a challenging task.

We propose a novel Topological Morphology Descriptor (TMD), inspired by Topological Data Analysis, to quantitatively analyze the branching shapes of neurons, which overcomes the limitations of existing techniques. The TMD of a tree is a filtration of the sub-level sets defined by a set of spheres of decreasing diameter, centered at the neuronal soma. The distance between the persistence barcodes of neuronal morphologies can be used as a metric of distance between the trees and hence it is useful for their objective separation into morphological groups.

This method is applicable to any tree-like structure, and we demonstrate this property by applying it to groups of mathematical random trees as well as neuronal trees. Our results show that the TMD of tree shapes is highly effective for reliably and efficiently distinguishing different groups of trees and neurons. Therefore, the TMD provides an objective benchmark test to asses the quality of any classification of branching cells into discrete morphological classes.

Finally, we propose a generalization of the TMD to study time series of tree. This method is used to track the morphological evolution of trees in time, in order to enhance our understanding of neuronal development.

【CL3-2】

Cliques of Neurons Bound into Cavities Provide a Missing Link between Structure and Function

Michael W. Reimann[1,6], Max Nolte[1,6], Martina Scolamiero[2], Katharine Turner[2], Rodrigo Perin[3], Giuseppe Chindemi[1], Paweł Dłotko[4,7], Ran Levi[5,7], Kathryn Hess[2,7,*] and Henry Markram[1,3,7,*,†]

[1]Blue Brain Project, École Polytechnique Fédérale de Lausanne (EPFL) Biotech Campus, 1202 Geneva, Switzerland, [2]Laboratory for Topology and Neuroscience, Brain Mind Institute, EPFL, 1015 Lausanne, Switzerland, [3]Laboratory of Neural Microcircuitry, Brain Mind Institute, EPFL, 1015 Lausanne, Switzerland, [4]DataShape, INRIA Saclay, 91120 Palaiseau, France, [5]Department of Mathematics, University of Aberdeen, Aberdeen AB24 3UE, UK, [6]These authors contributed equally to this work, [7]Co-senior author, [*]Correspondence: kathryn.hess@epfl.ch, henry.markram@epfl.ch, [†]Lead contact

The lack of a formal link between neural network structure and its emergent function has hampered our understanding of how the brain processes information. We have now established such a link by taking the direction of synaptic transmission into account, constructing graphs of a network that reflect the direction of information flow, and analyzing these directed graphs using algebraic topology. Applying this approach to a local network of neurons in the neocortex revealed a remarkably intricate and previously unseen topology of synaptic connectivity. The synaptic network contains an abundance of cliques of neurons bound into cavities that guide the emergence of correlated activity. In response to stimuli, correlated activity binds synaptically connected neurons into functional cliques and cavities that evolve in a stereotypical sequence towards peak complexity. We propose that the brain processes stimuli by forming increasingly complex functional cliques and cavities.

【CL3-3】

Cliques and cavities in the human connectome

Ann Sizemore[1,2], Chad Giusti[1], Ari Kahn[1], Jean M. Vettel[3,1,4],
Richard Betzel[1], Danielle S. Bassett[1,5]

[1]*Department of Bioengineering, University of Pennsylvania*
[2]*Broad Institute, Harvard University and the Massachusetts Institute of Technology*
[3]*Human Research & Engineering Directorate, U.S. Army Research Laboratory*
[4]*Department of Psychological and Brain Sciences, University of California, Santa Barbara*
[5]*Department of Electrical & Systems Engineering, University of Pennsylvania*

The complex tangles of neural wiring cooperate to support a diverse range of cognitive function. Efforts to understand neural architecture and its relation to function often study the connectome by translating this complex system into a network, with brain regions as nodes and white matter streamlines as edges. However, commonly applied graph theoretical tools are unable to capture mesoscale patterns of connections between brain regions which may be essential to cognition. Here we move to the language of algebraic topology in which we encode groups of all-to-all connected brain regions as cliques, which are both biologically relevant and allow us to see novel features such as topological cavities. While cliques of brain regions allow for rapid communication, topological cavities may promote parallel processing of information. Using an averaged connectome from eight healthy adults scanned in triplicate, we find a gradient of clique size along the anterior-posterior axis, consistent with previous studies of these areas. To find essential cavities we compute the persistent homology of the connectome and find topological cavities of different dimensions. We further investigate four long-lived persistent cavities and consistently detect these features across individual scans. We compare the persistent homology results to those obtained from a null model created by wiring minimization and find fewer and shorter-lived cavities arise in the averaged connectome. Yet we observe removing subcortical regions from the network yields similar persistence diagrams between the averaged connectome and null model, suggesting subcortical regions act as cone points within an efficiently wired cortical shell. We see most recovered minimal generators of persistent cavities link brain regions of early and late evolutionary origin, suggesting the importance of non-trivial loops in controlling higher brain function. Finally we speculate on the role of topological cycles in cognitive function and discuss the promise of applied topology in biological applications.

【CL4-1】

The Computation of the Erosion Distance

Brittany Terese Fasy[1], Amit Patel[2]
[1]*Montana State,* [2]*Colorado State University*

Persistence diagrams have been adopted by many mathematicians, computer scientists, statisticians, and data scientists as a convenient summary of a function over a topological space or of a point cloud. One of the bottlenecks currently in adoption of the persistence diagram as a standard data analysis tool is the computation of distances between persistence diagrams. In 2010, a new distance was introduced called the *Erosion Distance*, which takes a new view of the persistence diagram: instead of looking at a set of points in the extended plane, the erosion distance first takes a Möbius inversion of this point set, obtaining a function defined over the extended plane. This function is piecewise constant over a finite partition of the plane. We present an algorithm for computing the Erosion Distance that will take one step towards making the use of persistence diagrams more feasible for large data sets.

NOTE: This abstract is for a paper that we are currently writing. So, if accepted, I would likely want to submit a revised version of this abstract before it is publicly published.

【CL4-2】

New invariants for multi-parameter persistent homology

Nina Otter[1,2], Heather Harrington[1], Henry Schenck[3], Ulrike Tillmann[1,2]
[1]Mathematical Institute, University of Oxford, [2]The Alan Turing Institute,
[3]University of Illinois at Urbana–Champaign

Topological data analysis (TDA) is a field that lies at the intersection of data analysis, algebraic topology, computational geometry, computer science, and statistics. The main goal of TDA is to use ideas and results from geometry and topology to develop tools for studying qualitative features of data. One of the most successful methods in TDA is persistent homology (PH), a method that stems from algebraic topology, and has been used in a variety of applications from different fields, including robotics, material science, biology, and finance.

PH allows to study qualitative features of data across different values of a parameter, which one can think of as scales of resolution, and provides a summary of how long individual features persist across the different scales of resolution. In many applications, data depend not only on one, but several parameters, and to apply PH to such data one therefore needs to study the evolution of qualitative features across several parameters. While the theory of 1-parameter persistent homology is well understood, the theory of multi-parameter PH is hard, and it presents one of the biggest challenges of TDA.

In this talk I will briefly introduce persistent homology, give an overview of the complexity of the theory in the multi-parameter case, and then discuss how tools from commutative algebra give invariants able to capture homology classes with large persistence.

No prior knowledge on the subject is assumed.

This talk is based on joint work with Heather Harrington, Henry Schenck, and Ulrike Tillmann.

【CL4-3】

Multidimensional Persistence: Computation and Applications

Matthew Wright
Department of Mathematics, Statistics, and Computer Science, St. Olaf College

Multidimensional persistent homology is highly relevant in the analysis of noisy data, as it offers the ability to filter by two or more parameters simultaneously. However, the algebraic complexity of multidimensional persistence modules makes it difficult to extract useful invariants in this setting, and until recently there was no available software for using multidimensional persistence in practice. In this talk, I will describe current work, part of the RIVET software project, to enable the use of multidimensional persistence in real-world applications. This talk will describe recent algorithmic and computational advances related to RIVET, such as the parallelization of the main RIVET algorithm, as well as current work with students at St. Olaf College to apply RIVET to real data.

【CL5-1】

Applications of Persistent Homology to Simulated Turbulent Fluid Flows on a 3D Domain

Rachel Levanger[1], Takashi Ishihara[2], Paweł Dłotko[3], Miroslav Kramár[4], Konstantin Mischaikow[5]

[1]*Department of Electrical and Systems Engineering*, University of Pennsylvania,
[2]*Graduate School of Engineering*, Nagoya University,
[3]*Department of Mathematics*, Swansea University,
[4]*DataShape*, *INRIA S*aclay, [5]*Department of Mathematics*, Rutgers University

We use persistent homology to study two paradigms of complex turbulent fluid flows obtained by direct numerical simulations of the Navier Stokes equations on three-dimensional domains. First, we show how persistent homology can be used in conjunction with diffusion maps to study the properties of vorticity fields of fully-developed turbulence. We use these techniques to uncover a log-linear relationship between existing statistical quantities of vorticity, and also show how these quantities relate to statistics on the persistence diagrams themselves. Second, we use speed profiles in the space of persistence diagrams to study the turbulent combustion simulations of the Homogeneous Charge Compression Ignition process of an n-heptane and air mixture generated by the Tsurushima model, which tracks 35 chemical species across 38 elementary chemical reactions. Our method shows that persistent homology can be used to cluster together chemical species which share common reaction profiles in the low-temperature oxidation phase of the combustion process, as well as point to differences in the reaction process that are caused by different initial turbulence conditions. We compare our methods to the use of speed profiles in L^p space.

【CL5-2】

A Discrete Morse Theoretic Approach for Computing Connection Matrices

Kelly Spendlove[1], Shaun Harker[1], Konstantin Mischaikow[1], Rob Vander Vorst[2]
[1] Rutgers University, *[2] VU University*

Algebraic topology and dynamical systems are intimately related: the algebra may constrain or force the existence of certain dynamics. Morse homology is the prototypical theory grounded in this observation. Conley theory is a far-reaching topological generalization of Morse theory and a great deal of effort over the last few decades has established a computational version of the Conley theory. The computational Conley theory is a marriage of combinatorics, order theory and algebraic topology, and has proven effective in tackling dynamical problems.

Within the Conley theory the connection matrix is the mathematical object which transforms the approach into a truly homological theory; it is the Conley-theoretic generalization of the Morse boundary operator. We discuss how the connection matrix can be computed efficiently with discrete Morse theoretic techniques. We will introduce a software package for such computations. Finally, we demonstrate our techniques with an application of our theory and software to the setting of a Morse theory on spaces of braid diagrams introduced by R. Vandervorst et al.

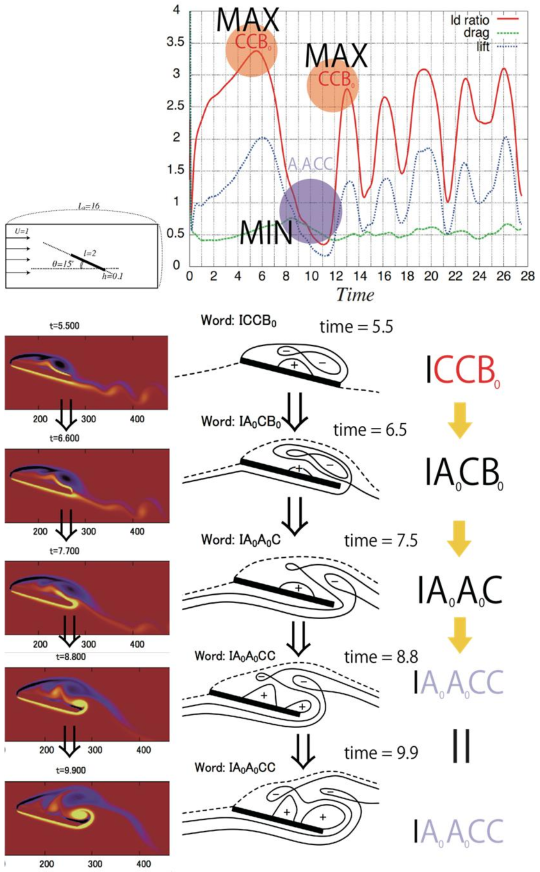
This application allows us to prove forcing theorems for stationary and periodic solutions and connecting orbits in a class of parabolic PDEs.

【CL5-3】

Finite representabilities of surface flows

Tomoo Yokoyama
Department of Mathematics, Kyoto University of Education

In this talk, we introduce finite representations of two dimensional incompressible flows. Applying the topological methods to an evolution of an incompressible and viscid flow around an inclined flat plate placed in a uniform flow, we can estimate when the lift-to-drag ratios of the plate are maximal and can determine transient streamline patterns between structurally stable streamline patterns. Moreover, we show that topological structures of generic two dimensional flows can be represented by finite combinational structures. In fact, a flow with non-degenerate singular points and with at most finitely many limit cycles but without quasi-minimal sets on a compact surface can be reconstructed by finite labeled graphs. Finally, we discuss the relations between topological structures and data structures.

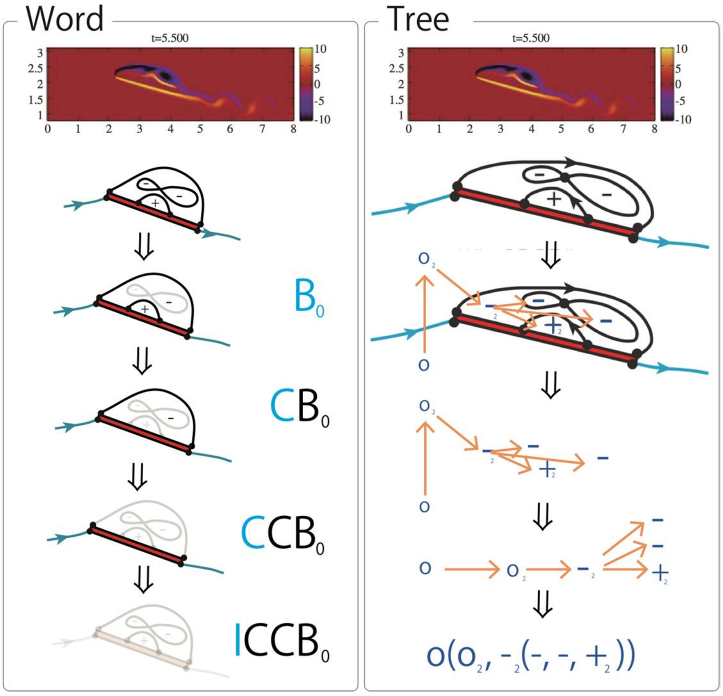


Surface flow → Tree

Local stream topological structure → Letter

Global stream topological structure → Label + Edge

{ Surface flow of finite type } → { Labelled Tree } "1 to 1"



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【CL6-1】

Two-Tier Mapper: a user-friendly clustering method for global gene expression based on topology

Rachel Jeitziner[1], Mathieu Carrière[4], Jacques Rougemont[2],
Steve Oudot[4], Kathryn Hess[3], and Cathrin Brisken[1]

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I will present a new method to analyze biological data, based on topological data analysis. I will introduce the mathematics underlying this new tool, illustrate its utility through examples, and describe theoretical aspects of its stability.

This method provides a first approximation to the variability in a dataset, describing divergences from sample to sample. It comprises a visualization tool that distinguishes the various clusters, giving an easy-to- grasp presentation of the variation between samples in the dataset as a colored graph.

The method, which is based on the well-known Mapper algorithm, can be applied reliably to both small and large datasets, which is a clear advantage in comparison with standard statistical tools, which perform reliably only on datasets of at least a certain minimal size. All parameters are determined either in a data-driven manner or by choosing reliable, user-independent default parameters.

【CL6-2】

The Least Squares Klein Bottle for Image Patches

Bradley Nelson[1], Gunnar Carlsson[2]
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[2]*Department of Mathematics, Stanford University*

It has been observed that an important subspace of high-contrast image patches has the topology of the Klein bottle. In this work, we offer a simple explanation why the Klein bottle appears when modeling edges in images, derived from properties of odd and even functions, and in doing so show that there are many Klein bottles that one may consider. We consider the task of inferring the best Klein bottle to fit a given set of image patches from a family of possibilities, and compare the ability of our proposed method to represent image patches to other dimension reduction techniques.

【CL6-3】

A topological view on Shape deformation

Shizuo KAJI

Department of Mathematical Sciences, Yamaguchi University, Japan / JST PRESTO

Manipulating shapes with computer has now become ubiquitous; Computer graphics (CG) is essential to film making, and so is Computer Aided Design (CAD) to industrial design. From a topological view point, a shape is a certain space (typically, a simplicial complex or a surface) and its deformation (animation) is a family of imbeddings into the ambient space (typically, R^3). In this talk, I will review some of my recent work to demonstrate how this topological view can actually be made into algorithms of shape deformation.

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【CL7-1】

Applications of classifying spaces in quantum computation

Cihan Okay[1], Robert Raussendorf[2], Stephen Bartlett[3], Sam Roberts[3]
[1]University of Western Ontario, [2]University of British Columbia, [3]The University of Sydney

In quantum computation an important class of observables are the Pauli observables. Commutativity properties of these observables determine fundamental features of quantum systems such as contextuality. Adem, Cohen, and Torres-Giese introduced a classifying space for principal bundles whose transition functions commute when simultaneously defined. I will talk about topological properties of these classifying spaces and applications to study contextuality in quantum computation.

【CL7-2】

Simplicial networks and effective resistance

Kang-Ju Lee, Woong Kook
Seoul National University

We introduce the notion of effective resistance for a *simplicial network* (X,R) where X is a simplicial complex and R is a set of resistances for the top simplices, and prove two formulas generalizing previous results concerning effective resistance for resistor networks. Our approach, based on combinatorial Hodge theory, is to assign a unique harmonic class to a *current generator* σ, an extra top-dimensional simplex to be attached to X. We will show that the harmonic class gives rise to the *current* I_σ and the *voltage* V_σ for $X \cup \sigma$, satisfying Thompson's energy-minimizing principle and Ohm's law for simplicial networks.

The effective resistance R_σ of a current generator σ shall be defined as a ratio of the σ-components of V_σ and I_σ. By introducing *potential* for voltage vectors, we present a formula for R_σ via the inverse of the weighted combinatorial Laplacian of X in codimension one. We also derive a formula for R_σ via weighted high-dimensional tree-numbers for X, providing a combinatorial interpretation for R_σ. As an application, we generalize Foster's Theorem, and discuss various high-dimensional examples. Moreover, as a tool for analyzing simplicial networks, we suggest a definition of information centrality for simplicial networks. This is a joint work with Woong Kook.

【CL7-3】

Topological complexity of subgroups of the braid groups

David Recio-Mitter, Mark Grant
University of Aberdeen

Topological complexity (TC) was introduced in the early 2000s by Michael Farber in the context of topological robotics. It is a numerical homotopy in- variant of a space which measures the instability of motion planning. More- over, TC can also be defined for a (discrete) group π, as the TC of its Eilenberg-Mac Lane space K(π,1). In particular the TC of the full braid group B_n is by definition equal to the TC of the unordered configuration space of n points on the plane.

In this talk the TC of groups will be introduced and calculated for some subgroups of the full braid groups, for instance mixed (or coloured) braid groups and congruence subgroups. The methods used in the calculations are algebraic rather than topological.

This is joint work with Mark Grant.

【CL8-1】

Injectivity results for the Persistent Homology Transform

Katharine Turne[1], Justin Curry[2], Sayan Mukherjee[2,3]

[1]*Laboratory for Topology and Neuroscience and Chair of Mathematical Statistics, Ecole Polytechnique Federal de Lausanne*, [2]*Department of Mathematics, Duke University,*
[3]*Department of Statistical Science, Duke University,*

The Persistent Homology Transform (PHT) was introduced in *Persistent homology transform for modeling shapes and surface* (Turner, et al. 2014) as a tool to performing statistical shape analysis with persistent homology. The PHT consists of the collection of persistence diagrams calculated from the sublevel sets of the height function in each direction. We showed that the PHT was injective over the domain of embedded finite simplicial complexes in 2 and 3 dimensional Euclidean space. In this talk I will present further injectivity results with some comments on how they are proved. In particular we will see how the PHT is injective over the domain of all semialgebraic subsets of a fixed Euclidean space, and that finitely many directions are sufficient if we restrict to finite simplicial complexes satisfying some reasonable geometric conditions.

【CL8-2】

The law of large number of the lifetime in random complex processes

Shu Kanazawa[1]

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We consider a higher dimensional generalization of Frieze's ζ(3)-limit theorem. Frieze's theorem states that the expected weight of the minimum spanning tree in the complete graph, whose edges are all independently weighted by uniform random variables over the interval [0, 1], converges to ζ(3) as the number of vertices goes to infinity. By using the terminology of persistent homology, Frieze's theorem can be regarded as the limiting theorem of the expected value of the 0-th lifetime sum in an increasing family of the Erdös—Rényi random graphs, which is called by the Erdös—Rényi process. At this point of view, Y. Hiraoka and T. Shirai studied the behavior of the expected lifetime sums in the Linial—Meshulam complex process and the clique complex process, which are higher dimensional generalizations of the Erdös—Rényi process [1].

we first establish a generalization of the cohomology vanishing theorem based on the quantitative approach. By using this estimate, we improve the upper bound of the order of the expected lifetime sum in the clique complex process, which was obtained in [1]. Especially, we determine the exact order of the expected lifetime sum in the clique complex process. Second, using the same estimate, we prove the law of large number of the lifetime in the (k+1)-Linial—Meshulam complex process with n vertices. Specifically, we prove the following three statements. The last two statements can be regarded as a higher dimensional generalization of Frieze's theorem.

1. The k-th expected lifetime sum L_k in the (k+1)-Linial—Meshulam complex process behaves in $O(n^k)$.
2. The expected value of the random variable L_k/n^k converges to a positive constant I_k as n goes to infinity.
3. The random variable L_k/n^k converges in probability to the constant I_k.

We remark that the first statement was proved in [1] by other method and the second statement was conjectured from a formal discussion.

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This is joint work with Masanori Hino.

Poster Session

P-01

The Shape of Chronic Obstructive Pulmonary Disease

Francisco Belchi-Guillamon[1], Mariam Pirashvili[1], Joy Conway[2], Michael Bennet[3],
Ratko Djukanovic[4], Jacek Brodzki[1]

[1]*School of Mathematics*, University of Southampton, [2]*Health Sciences*, University of Southampton,
[3]Respiratory Biomedical Research Unit (BRU), Southampton General Hospital, [4]Medicine, University of Southampton

Quantitative features that can be obtained from medical imaging are far from creating a complete picture of Chronic Obstructive Pulmonary Disease (COPD). This makes spirometry tests still be the current most common diagnostic technique in COPD. In this work, we create a more complete picture of the disease by extracting from chest CT scans novel quantitative features that encode the precise structure of the airways inside the lungs. These features are computed using Persistent Homology, allow us to distinguish patients at different stages of COPD without the need for normalising by size and are related to airway deflection, cavity quantification and length of the bronchial tree.

Our CT measurements differ substantially to those used in current research, most of which consist of the absolute or relative volume of some region in the lungs. Additionally, the size independence contrasts with the case of lung function measurements such as FEV1%.

P-02

Topological complexity and efficiency of motion planning algorithms

Zbigniew Błaszczyk[1], Jose Gabriel Carraquel Vera
Faculty Mathematics and Computer Science, Adam Mickiewicz University

We introduce a variant of Farber's topological complexity, defined for smooth compact Riemannian manifolds, which takes into account only motion planners with the lowest possible “average length” of the output paths. We prove that it never differs from topological complexity by more than 1, thus showing that the latter invariant addresses the problem of the existence of motion planners which are “efficient”.

P-03

Towards parameter free denoising

Mickaël Buchet[1*], Tamal. K. Dey[2], Jiayuan Wang[2], and Yusu Wang[2]

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In many data analysis applications, we are given a point set that is supposedly sampling an unknown object called the ground truth. This sample is corrupted by noise some of the points may lie far away from the ground truth, creating outliers also termed as ambient noise. One of the main goals of denoising techniques is to remove those points so that the error becomes bounded with respect to the Hausdorff distance. Popular denoising approaches such as deconvolution and thresholding require the input of several parameters by the user, either to define the algorithm or the noise model. We aim at lightening the burden put on the user by reducing the number of parameters to one in the general case and zero in the case of a uniform sampling.

We propose a one-step algorithm that, given a scale defining parameter, removes points that are outliers at this scale. The presence of this parameter cannot be avoided for general point sets as the definition of a scale is indispensable. However, if we add some uniformity in the data, then this uniformity can replace the notion of scale. In this case, we propose an algorithm alternating decluttering steps and resampling steps that denoise the data without knowing the correct scale.

This algorithm presents three interesting features. First, the decluttering is made in a way that is dual to classic algorithms. Usually, one select good points and then removed all points that are not closed to a good point as being irrelevant. In our approach, we look at all points and keep only those that are far from a good point, the notion of closeness being defined by the point currently being investigated. A good choice on the order in which points are investigated yield theoretical guarantees. Second, we introduce a new technique of resampling. The set of points obtained through the decluttering step is too usually too sparse. We hence add again some of the points we removed in order to obtain a denser sampling before iterating. Finally, our algorithm does not need any parameter and returns a theoretically guaranteed result without computing the correct scale, which is a very difficult question. Instead, we guarantee that after passing the unknown optimal scale, we will not worsen our sampling.

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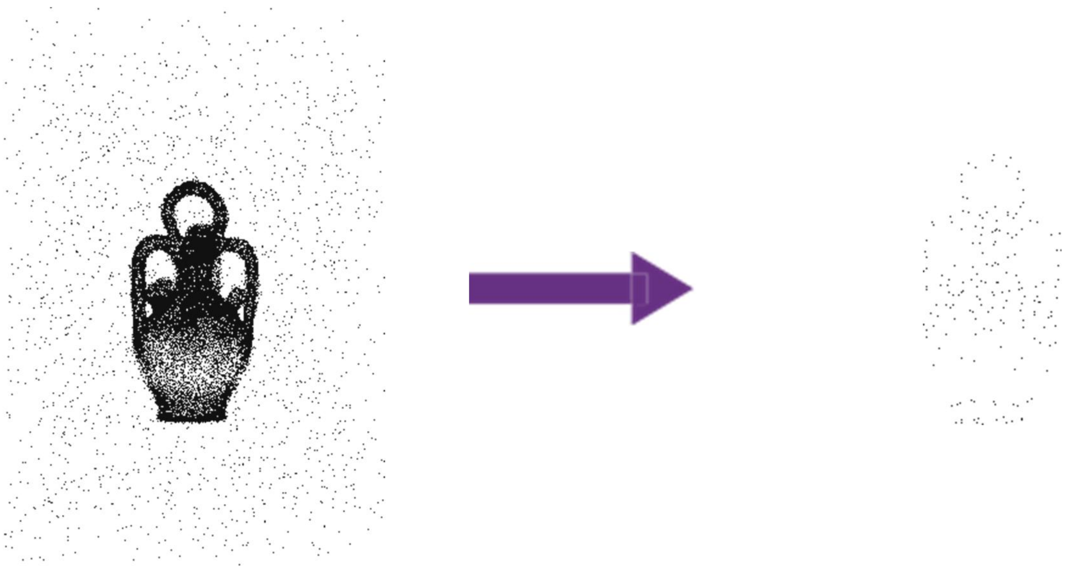

P-04

Integral free loop cohomology of complete flag manifolds

Matthew Burfitt
University of Southampton

A complete flag manifold is the quotient of a Lie group by its maximal torus and is one of the nicer examples of homogeneous spaces. Related objects are studied in different areas of mathematics and mathematical physics. In topology, the study of free loop spaces on manifolds has two folded motivation. First there is a relation between geometrically distinct periodic geodesics on a manifold and their free loop spaces, originally studied by Gromoll and Meyer in their 1969 paper. More recently the study of string topology, in particular the Chas-Sullivan loop product, has been an active area of research with connection to interesting areas in algebraic topology including topological quantum field theory, operads and topological cyclic homology. In this talk I will discuss my work on the cohomology of the free loop space of complete flag manifolds. I will explain my results in the case of the special unitary group $SU(n)$, as this is complicated enough case to illustrate the main ideas but at the same time technically the simplest one.

P-05

Categorical Constructions in Cellular Sheaf Theory

Samuel Carp
Department of Applied Mathematics, University of Pennsylvania

We provide a solution to the problem of generating random Cellular Sheaves over a Cell Complex via a simple categorical construction. The insights the construction provides lead to the consideration of several other functorial constructions whose connections and implications we explore. In particular, the existence of a certain adjunction leads us to consider a class of cellular sheaves with interesting properties.

P-07

Representation spaces for central extensions and almost commuting unitary matrices

Man Chuen Cheng[1], Alejandro Adem[2]
[1] *Department of Mathematics, The Chinese University of Hong Kong*
[2] *University of British Columbia*

The space Hom (Γ, G) of homomorphisms from a discrete group Γ to a Lie group G is studied in algebra, topology and physics. In the case of $\Gamma = \mathrm{Z}^n$, it is the space of ordered commuting n–tuples in G and has been analyzed using a variety of methods from algebraic topology and representation theory. We would like to consider the case where Γ is a central extension of the form $1 \to \mathrm{Z}^r \to \Gamma \to \mathrm{Z}^n \to 1$ and $G = U(m)$ is a unitary group. We enumerate and describe the structure of the connected components of Hom (Γ, $U(m)$) and the associated moduli spaces Rep (Γ, $U(m)$). This is joint work with Alejandro Adem.

P-08

Vietoris-Rips Realization of Indecomposable Persistence Modules of Large Dimension

Mickaël Buchet[1], Emerson G. Escolar[2]

[1, 2] *WPI-AIMR,* Tohoku University

In this work we exhibit an infinite family, parametrized by dimension order d, of pairwise non-isomorphic indecomposable persistence modules over the commutative ladder quiver with length 5. We then give a family of bifiltrations of topological spaces whose H_1 persistent homologies is the infinite family of persistence modules. Moreover, for each bifiltration we provide a pair of Vietoris-Rips filtrations linked by simplicial maps that realize it homologically. Our construction provides an elementary proof of the fact that the commutative ladders with length greater than or equal to 5 are representation-infinite. We aim by this example to show that indecomposables of high dimension can be easily realized topologically and should not be ignored.

P-09

Study of Neural Connectivity Pattern via Persistent Homology

Sungyeon Hong

Department of Mathematics, École Polytechnique Fédérale de Lausanne

Persistent homology is widely used in topological data analysis as it is effective in qualitative understanding of a network. More precisely, it can detect long-lasting (persistent) topological features within a weighted network through a nested sequence of simplicial complexes determined by the weights. Such persistent features contain robust mesoscopic connectivity information. Among the wide range of applications of persistent homology from natural image statistics[1] to material science, we are particularly interested in its usage in neuroscience. Taking a neuronal network of the somatosensory cortex of a rat (digitally reconstructed by the Blue Brain Project[2]) as a graph with neurons as nodes and their synaptic connections as edges, we adopt a graph-theoretic measure, local efficiency, as a weight parameter to create a filtration. In this *efficiency filtration*, each cortical neuron is weighted by its local efficiency value. We use this filtration to get layer-wise connectivity patterns in the structural organization of the neocortex divided into six layers, and then apply it to various models for comparison. This is a novel approach in a combining "classical" graph-theoretic measure with "recently" developed algebraic topological tool.

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[2] H. Markram et al. Reconstruction and Simulation of Neocortical Microcircuitry, Cell 163, 456-492 (2015)

P-10

A Higher-Dimensional Homologically Persistent Skeleton

Sara Kalisnik Verovsek[1], Vitaliy Kurlin[2], Davorin Lesnik[3]
[1]Brown University, [2]University of Liverpool, [3]University of Ljubljana

A data set is often given as a point cloud, i.e. a non-empty finite metric space. An important problem is to detect the topological shape of data

– for example, to approximate a point cloud by a low-dimensional non- linear subspace such as a graph or a simplicial complex. Classical clustering methods and principal component analysis work very well when data points split into well-separated groups or lie near linear subspaces. Methods from topological data analysis detect more complicated patterns such as holes and voids that persist for a long time in a 1-parameter family of shapes associated to a point cloud. These features were recently visualized in the form of a 1-dimensional homologically persistent skeleton, which optimally extends a minimal spanning tree of a point cloud to a graph with cycles. We generalize this skeleton to higher dimensions and prove its optimality among all complexes that preserve topological features of data at any scale.

P-11

Harmonic classes and data analysis

Younng-Jin Kim, Woong Kook
Department of Mathematical Sciences, Seoul National University

Discrete harmonic classes for a finite complex are the kernel of its combinatorial Laplacians, and they are isomorphic to the homology groups over a field by combinatorial Hodge decomposition. In our work, we will analyze geometric contents of these classes closely and explore their potential as a new method for data analysis. The main idea is that harmonic classes are supported typically by a larger collection of oriented cells than homology classes, and are helpful for local and global visualization. As a demonstration of this property, we unveil an intriguing combinatorial relation in discrete harmonic classes. To be specific, there are interpretations about coefficients of discrete harmonic classes in dimension 1 with the language of graph theory and combinatorics. Also, We will suggest application methods; a network embedding method, called harmonic mirroring, and an analysis on winding number, called harmonic winding analysis.

P-12

Kernel method for persistence diagrams via kernel embedding and weight factor

Genki Kusano

Graduate School of Science, Tohoku University

In topological data analysis (TDA), persistence diagrams are widely recognized as a useful descriptor of complicated data, and can distinguish robust and noisy topological properties. While persistence diagrams start to be applied to various problems, statistical or machine learning methods to analyze persistence diagrams are still limited. Hence, developing a statistical framework for persistence diagrams is a significant issue for further success of TDA. Since a persistence diagram is a point set of variable size, it is not straightforward to apply standard methods for statistical data analysis. Here, to introduce statistics into TDA, we construct kernel method for persistence diagrams.

Reference: Genki Kusano, Kenji Fukumizu and Yasuaki Hiraoka. "Persistence weighted Gaussian kernel for topological data analysis". Proceedings of the 33rd International Conference on Machine Learning (ICML), JMLR: W&CP volume 48, pp:2004--2013, 2016.
This is joint work with Kenji Fukumizu and Yasuaki Hiraoka.

P-13

Random Clique Topology of the Stochastic Block Model

Darrick Lee[1], Ann Sizemore[2], Robert Ghrist[1,3], Danielle S. Bassett[2,3]
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The stochastic block model (SBM) is an unweighted random graph model with labelled vertices in which edges are added with probability dependent the labels of the endpoints. Therefore, vertices with the same label will connect to other vertices in a similar manner. The SBM has recently been widely used in fields such as machine learning, neuroscience, and network science in general to detect clusters of vertices with similar connectivity patterns. This is achieved using inference algorithms to recover the most likely SBM parameters that would have generated a given graph.

Algebraic-topological tools such as persistent homology are beginning to be applied to networks to study their higher order structure. Recent work has been done to better understand the expected topological behaviour of well known random graph models such as the Erdös-Renyi graphs and random geometric graphs. This was done by proving the asymptotic properties of the Betti numbers for large graphs with various model parameters, from which we can obtain asymptotic Betti curves.

As many real-world networks are increasingly seen to be well-modelled by the SBM and analyzed using persistent homology, it is important to also study the asymptotic topological nature of these networks. In this work, we investigate the clique topology of the SBM by studying similar asymptotic properties such as requirements for vanishing and nonvanishing homology.

P-15

Homotopy types of gauge groups related to certain 7-manifolds

Ingrid Membrillo-Solis
Mathematical Sciences, University of Southampton, United Kingdom

Let X be a path-connected pointed topological space and let G be a topo- logical group. Given a principal G-bundle over X, P X, the gauge group is the group of G-equivariant automorphisms of P that fix X. The study of the topology of gauge groups when X is a low dimensional manifold has played a prominent role in mathematics and mathematical physics over the last thirty years. In 2011, however, Donaldson and Segal established the mathematical set- up to construct gauge theories using principal G-bundles over high dimensional manifolds. In this talk I will present some results on the homotopy theory of gauge groups when X is a manifold that arises as the total space of a S3-bundle over S4 and G is a simply connected simple compact Lie group.

P-16

Binarization of Spontaneous Neural Activities for Neural Ring Analysis

Momoka Tsuru, Keiji Miura
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Typical electrophysiological experiments in neuroscience examine the neural responses to sensory stimuli. That is, within the stimulus-response framework, how accurately the neural responses reflect the sensory stimuli has been characterized information theoretically. However, it is not necessarily clear if the neural responses actually responded only to the sensory stimuli the experimenters presented. For example, the neurons can actually respond to some hidden variables of which the experimenters are unaware. So, it is desirable to know in advance how much dimensions the "hidden stimulus space" for a neuron spans.

For that purpose, the systematic method of neural ring was proposed recently [1-3]. This novel, algebraic geometry-based method could uncover the information which conventional methods neglected. Meanwhile, the method of neural ring can be, in some sense, regarded as the distribution-free or nonparametric method and, therefore, the know-how for the application to noisy real data is lacking with few previous works.

Here we attempted to apply the neural ring method to the spontaneous neural activities in rat hippocampus [4-8]. The issues here can be that the real data is considerably noisy and that there are many possible ways to binarize the data so that the neural ring is applicable. By trying different styles of binarization, we discovered that some aspects of results are stable and did not change significantly. This suggests that, with the appropriate use, the neural ring can be a reliable data analysis method for obtaining stable biological conclusions.

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P-17

Segmentation of biomedical images by a computational topology framework

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The segmentation of patterns of cells in biomedical images constitutes a significant step towards the automated analysis of histological images. However, the presence of large numbers of cells and large cell patterns in whole slide images demands methods that are computationally tractable in addition to being efficient. This work presents a method for the robust segmentation of cell nuclei and cell patterns in histological whole slide images based on persistent homology. An abstract simplicial homology approach for image segmentation is established. The approach deals with the persistence of disconnected sets in the image thus identifying salient regions that express patterns of persistence. By introducing an image representation based on homological features, the task of segmentation is less dependent on variations in color and texture. This results in a novel approach that conceptualizes regions of interest (cell nuclei and cell group arrangements) pertinent to their topological features in a successful manner. The time cost of the proposed method is lower-bounded by an almost linear behavior and upper-bounded by $O(n^2)$ in a worst-case scenario. Time complexity matches a quasilinear behavior which is $O(n^{1+\varepsilon})$ for $\varepsilon < 1$. Images acquired from histological sections of liver tissue are used as a case study to demonstrate the effectiveness of the approach in cell nuclei segmentation. The histological landscape consists of hepatocytes and non-parenchymal cells. The accuracy of the proposed methodology is verified against an automated workflow created by the output of a conventional filter bank (validated by experts) and the supervised training of a random forest classifier. The results are obtained on a per-object basis. The proposed workflow successfully detected both hepatocyte and non-parenchymal cell nuclei with an accuracy of 84.6%, and hepatocyte cell nuclei only with an accuracy of 86.2%. A public histological dataset with supplied ground-truth data is also used for evaluating the performance of the proposed approach (accuracy: 94.5%). Further validations are carried out with a publicly available dataset, and ground-truth data from the Gland Segmentation in Colon Histology Images Challenge (GlaS) contest are used to demonstrate the effectiveness of the approach for the segmentation of cell structures. The proposed method is useful for obtaining unsupervised robust initial segmentations that can be further integrated into image/data processing and management pipelines.

P-18

Stiefel-Whintey class of a category and its application

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In a purely combinatorial context, we define Euler integrals and Stiefel-Whitney classes for finite posets and finite categories. This is an elementary toy example of combinatorial counterpart of characteristic classes for real algebraic orbifolds. We have implemented software for computing those invariants.

For finite categories, we propose a reasonable definition of constructible functions, which is modeled on such functions on a simplicial complex associated to a triangulated orbifold; the combinatorial substitute is the poset EA of elements associated to a functor ΔA→ **Monoids**, and then we associate the group F(EA;R) of (R-valued) constructible functions on the order complex of EA. We then introduce the Stiefel-Whitney class w_*(A) (:= $w_*(11_{E\mathrm{A}})$); it is defined as a natural transformation

$$w_* : \mathrm{F}^{eu}(E\mathrm{A};\mathrm{Z}_2) \rightarrow H_*(E\mathrm{A};\mathrm{Z}_2)$$

between a subfunctor F^{eu} of F and the Z_2-homology functor H_*. It may be compared with the Chern-Schwartz-MacPherson classes for quasi-projective Deligne-Mumford stacks X valued in the Chow group, formulated as a variant of Grothendieck-Riemann-Roch $c_* : \mathrm{F}(\mathrm{X};\mathrm{Z}) \rightarrow CH_*(\mathrm{X};\mathrm{Z})$, defined by the third author in algebraic geometry.

P-19

Digital Image Analysis using Persistent Homology and Machine Learning

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In this poster presentation, I will show you methods of digital image analysis using persistent homology and machine learning. Persistent homology enables us to describe the shape of data quantitatively from the viewpoint of homology and it is useful to study heterogeneous geometric structures. Machine learning enables us to detect characteristic patterns behind data. By the combination of persistence homology and machine learning, we can quantitatively and statistically find characteristic geometric pattern hidden behind the data. Persistence Image[1] and linear machine learning models are used for our methods. This combination gives us a very intuitive visualization of the learned result. “Inverse Problem” techniques for persistence diagrams are also effectively used to visualize the learned result. X-CT images of iron ore sinter are analyzed using the method.

This research is a joint work with M. Kimura (KEK) and Y. Hiraoka (WPI-AIMR, Tohoku Univ.).

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・・・・・・・・・・・・End

P-20

A New Algorithm for Calculating Homology Groups of Two-dimensional Digital Images and Its Implementation in a Computer Environment

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The Digital Topology is a sub branch of mathematics that rapidly developing since late of 1980. Basically Digital Topology perceived as making simulations of concepts in algebraic topology for digital images. In Digital Topology studies, it is aimed to obtain invariant for digital images. Homotopy and Homology groups are seen as fundamental invariant. Computation of Homotopy groups of digital images is very difficult. The calculation of homology groups is relatively easy and efficient. Therefore, homology groups are vital for determine the characteristics of digital images and able to distinguish between them. Digital homology groups were built on digital simplicial complexes. Calculation of homology groups of digital images has an important place in the digital topology. Although, there are many theoretical studies on the homology groups of the digital images in the literature but, yet not available to a robust computer algorithms. This study is targeted primarily to put forward the algorithm for calculating the homology groups of digital images. Then, this algorithm was realized in computer environment. C ++ is preferred as a programming language in transferring the algorithm to the computer environment. The application was done using sample images. Homology groups of previously defined digital simple closed curves and some other basic images were calculated. By calculating homology groups of more complex digital images, the power and effectiveness of the algorithm is observed. Analysis was done using application findings. In addition, two new adjacency relations for two-dimensional digital images are proposed in this study. According to this relation, simple digital closed curves were formed and the homology groups were examined and paralleled with others. It is envisaged that these adjacency relations will contribute to the solution of some problems and to the increase of the efficiency of the homology groups.

P-21

SOLUBILITY OF CHEMICAL COMPOUNDS

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This is a report on joint work with the Joining the Dots group at the University of Southampton.

Given a set of chemical compounds, we wish to predict their solubility in water. This is a regression problem that has been tackled by traditional machine learning methods previously. Some of their results were available to us and we were able to compare them with the topological methods we empoyed.

The data is given in two forms. The first is as a matrix of descriptors, or features, of logical, categorical and continuous type. The second is as molecular graphs – that is, as undirected, connected, labelled graphs. We built different models based on the form of the data. The output variable, solubility, is continuous.

Besides the task of predicting solubility, we also tried to discover the shape of the space of these molecules, to gain further insight into the chemical and physical properties of molecules that predict their solubility.

P-22

A COMBINATORIAL MODEL OF THE PATH FIBRATION

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For the path fibration $\Omega Y \rightarrow P\,Y \rightarrow Y$ on a path-connected poly- hedron $Y = \underset{\xi}{|}X|$ we construct a cellular model $|\mathbf{\Omega} X| \rightarrow |\mathbf{P} X| \rightarrow |X|$, where X is a simplicial complex, $\mathbf{\Omega} X$ is a monoidal cubical set and $\mathbf{P} X$ is a contractible cubical set. The restriction $\xi^{-1}(Y^{1}) \rightarrow Y^{1}$ of ξ to the 1-skeleton of Y is a simplicial approximation of the Cayley graph of the fundamental group $\pi 1(Y^{1})$. The chain algebra $C_{*}(\mathbf{\Omega} X)$ can be identified with the Cobar construction of the coalgebra $C_{*}(X)$. As a consequence the simply connectedness condition for certain constructions is reflexed. This is the joint work with Manuel Rivera.

P-23

Homotopy types of gauge groups over 4-manifolds

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Gauge groups originate from physics and they have many applications in physics and mathematics, for example Yang-Mills theory and the classification of 4-dimensional smooth manifolds. Given a Lie group G, a gauge group is defined to be the group of G-equivariant automorphisms of a principal G-bundle fixing its base manifold. In general gauge groups are difficult to calculate. In this talk, I will discuss a homotopy decomposition method and the homotopy types of gauge groups over certain non-simply connected 4-manifolds.

P-24

Homology-Based Immersions of Metric Objects

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Consider the surface of a hand naturally embedded in 3D space, and pick a point, say at the tip of the index finger. By considering intrinsic neighborhoods of increasing radius around this basepoint, and computing the associated persistent homology, one can extract a stable multi-scale point signature that encodes both global connectivity and local geometry. This construction was considered in a 2015 paper of Carriere, Oudot, and Ovsjanikov, and naturally leads to the question: "how does one pick the correct point? Surely some points give more information than others." We can deflect this question by refusing to choose a single point, instead allowing each point in our space to serve as a basepoint in its turn. What we obtain is an immersion of our metric object as a subset of barcode space. As a variant of this procedure, we can also start with a metric-measure object and subsequently obtain a probability distribution on barcode space. In the case of metric graphs, we show stability for these constructions in the appropriate metrics. It is a matter of ongoing research to determine how discriminative these constructions are and how they might be generalized to higher-dimensional spaces. This is joint work with Steve Oudot.

············End

P-25

K-theory and noncommutative geometry

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K-theory is an important tool from the view point of not only mathematics, but also physics. For example, it is the first example of generalized cohomology, it was used in the proof of Atiyah-Singer index theorem which is one of the greatest theorem in global analysis, and it has a relationship with string theory. *K*-theory has several variations including twisted one and equivariant one. Recently, it was pointed out that twisted *K*-theory is related with representation theory of loop groups of compact Lie groups due to Freed-Hopkins-Teleman theory. Fortunately (especially for me!), the first person in the three mathematicians is one of the invited speakers of this conference.

K-theory has several equivalent definitions just like ordinary cohomology theory. Although it was defined by use of vector bundles for compact Hausdorff spaces by Atiyah-Hirzebruch, it is correct to use classifying spaces to extend it to general spaces if one like *K*-theory to keep nice properties. However, there is another interesting way of generalization: **the formulation of noncommutative geometry (NCG for short).** In a word, NCG is an algebraic geometry of “locally compact crazy spaces”. Thanks to NCG, we can “geometrically” deal with various strange spaces including foliations and unitary duals of locally compact groups.

In this talk, I will begin with the core idea of NCG, introduce *K*-theory and compare it with classical one. Then, to show one of many merits of NCG, I will explain that several variation of *K*-theory including twisted one appears as “ordinary *K*-theory of strange spaces”.

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P-26

Stabilizing Auxiliary Persistence Information

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Persistent homology pairs critical values of a Morse function. These pairings are stable under perturbations of the Morse function, but the generically induced critical point pairings are unstable. A stable version of the critical point pairings can be obtained by convolving a corresponding real-valued function with an appropriate kernel. A continuous extension of this approach leads to a measure on the underlying manifold which reflects which parts of the manifold are responsible for a given region of the persistence diagram. This is work towards my PhD under the advisement of Dr. Peter Bubenik.

P-27

A Proof of Baez -Dolan Stabilization for Rezk's model of weak n-categories

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We will begin with an overview of an old problem, due to Baez and Dolan, that applied abstract homotopy theory to the study of mathematical physics (via topological quantum field theories). I will show how to reduce the statement of the Baez-Dolan Stabilization Hypothesis from a statement in higher category theory (we choose the setting of Rezk's Theta_n spaces) to one in abstract homotopy theory. I'll then sketch how to prove the Stabilization Hypothesis using model categories, operads, and left Bousfield localization. This is joint work with Michael Batanin.

P-28

Explore Heterogeneous Data Structures using Persistent Homology

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To explore the structural information of a heterogeneous dataset projected into lower dimensional representations, e.g. high-resolution microscopy where three dimensions (3D) marked histone position are projected into two dimensions (2D) focal plane, powerful tools to solve the following questions are highly wanted. 1) What kinds of robust measurements can make structures visible from structureless datasets? 2) Do projections conceal important structural information from the original data? 3) How can we characterize these structures?

To address this questions, we propose a topological method based on persistent diagrams (PDs). This method aims to capture multiscale shapes from model data. A well-known heterogeneous system, Lennard-Jones (LJ) is introduced as a physical model. Using molecular dynamics simulations, we generated a 3D LJ fluid as input. Several 2D projections are obtained from slices of different thickness of its linear system size. The resulting persistent homology calculations render up to two-dimensional PDs. Specific distributions in the PDs identify essential shape characteristics (cavities, tunnels) in the model atomic configuration. Physical properties like compressibility can be interpreted from the number and size of cavities in 3D and rings in 2D. Additional analysis is provided using three parameters from conventional methods in statistical mechanic: radial distribution function(RDF), the reduced fourth-order cumulant, isothermal compressibility. By comparing our approach with these conventional methods, we elucidate how we provide a unified approach that can not only classify topological features in all scale but also extract geometrical information in greater depth.

P-29

Persistent homology of time varying conditional independence networks

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Time varying brain activity networks have been studied using persistent homology, typically by estimating marginal interactions between network nodes via the linear Pearson correlation coefficient. Correlations give an indirect measure of link strength between each pair of network nodes, whereas classical graph analysis or topological data analysis techniques require the distance between nodes is a proper distance (metric), which corresponds to finding the conditional (in)dependence associations between network nodes.
In this work we present a new method for constructing large time varying conditional independence networks from multivariate time series. The networks are constructed by estimating the time varying inverse spectrum and calculating a distance between each pair of nodes at each time point. The method is demonstrated on fMRI data of resting state brain activity, and we show example results of the differences in time varying persistent homology between the new approach and standard time varying correlation networks.

P-30

The Persistent Homology of a Correspondence; A Viewpoint from Quiver Representations

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The theory of homology induced maps of correspondences proposed by Shaun Harker et al. is a powerful tool which allows the retrieval of underlying homological information from sampling data with noise or defects. In this study, we redefine induced maps of correspondences within the framework of persistence modules on commutative ladders, and provide more concise proofs of the main theorems in the original paper.

With this point of view, we easily extend these ideas to filtration analysis, which provides a new method for analyzing dynamical systems.