CAT 2015
Topological Data Analysis: New developments and challenges
Oxford, 19-20 June 2015

Schedule

Friday

tea

16:00-17:00   *Colloquium: Gunnar Carlsson*
The Shape of Data

reception

[17:30-18:30   *Nomura Lecture: Ester Duflo*
Social Capital and Microfinance]

Saturday

registration

09:00-09:45   *Ulrich Bauer:*
Induced Matchings and the Algebraic Stability of persistence Barcode

coffee

10:15-11:00   *Claudia Landi:*
Discrete Morse theory for reducing complexes in Multidimensional Persistence

11:10-11:40   *Mikael Vejdemo-Johansson:*
Towards a topos foundation for persistent homology

11:50-12:20   *Ran Levi:*
Neurotopology - the topology of neural systems

lunch

14:00-14:45   *Frédéric Chazal:*
Persistent homology for geometric complexes: stability and statistical aspects

14:50-15:10   *Heather Harrington:*
Topological data analysis for investigating contagions on networks

15:10-15:30   *Rachel Jeitziner:*
Progression Analysis of disease and its application to breast cancer research

tea

16:00-16:45   *Gunnar Carlsson:*
Structures on Spaces of Persistence Barcodes

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organisers: ***Peter Grindrod, Heather Harrington, Mason Porter, Ulrike Tillmann***

Abstracts

Ulrich Bauer

Title: Induced Matchings and the Algebraic Stability of persistence Barcode

Abstract: We define a simple, explicit map sending a morphism f : M → N of pointwise finite dimensional persistence modules to a matching between the barcodes of M and N. Our main result is that, in a precise sense, the quality of this matching is tightly controlled by the lengths of the longest intervals in the barcodes of ker f and coker f.

As an immediate corollary, we obtain a new proof of the algebraic stability theorem for persistence barcodes, a fundamental result in the theory of persistent homology. In contrast to previous proofs, ours shows explicitly how a δ-interleaving morphism between two persistence modules induces a δ-matching between their barcodes. Our main result is based a structure theorem for submodules and quotients of persistence modules, and yields a novel "single-morphism" characterization of the interleaving relation on persistence modules.

Gunnar Carlsson

Colloquium title: The Shape of Data

Colloquium abstract: There has been a great deal of attention paid to "Big Data" over the last few years. However, often as not, the problem with the analysis of data is not as much the size as the complexity of the data. Even very small data sets can exhibit substantial complexity. There is therefore a need for methods for representing complex data sets, beyond the usual linear or even polynomial models. The mathematical notion of shape, encoded in a metric, provides a very useful way to represent complex data sets. On the other hand, Topology is the mathematical sub discipline which concerns itself with studying shape, in all dimensions. In recent years, methods from topology have been adapted to the study of data sets, i.e. finite metric spaces. In this talk, we will discuss what has been done in this direction and what the future might hold, with numerous examples.

Title: Structures on Spaces of Persistence Barcodes

Abstract: There are a number of situations where databases of "unstructured data" contain elements which themselves have geometric structure. In this situation, it becomes important to study not only individual barcodes, but there placement in a space of such barcodes. There are different notions of these spaces and we will talk about a number of possibilities for them, including some theorems which can be useful in translating topological methods into a more traditional machine learning framework.

Frédéric Chazal

Title: Persistent homology for geometric complexes: stability and statistical aspects

Abstract:: Persistent homology plays a fundamental role in Topological Data Analysis to extract multiscale topological features from data. In this talk we will present stability results for the persistent homology of filtered simplicial complexes built on top of totally bounded metric spaces. We will show how these results can be exploited to obtain statistical properties of persistence information in Topological Data Analysis.

Heather Harrington

Title : Topological data analysis for investigating contagions on networks

Abstract : The spread of a contagion, whether social or biological, can exhibit complicated dynamics on a network. Often the structure of a network is affected by its spatial constraints. For example, the spread of a contagion could require face-to-face interaction, which may lead to an underlying geometry such as the Earth's surface, in the network. It is unclear how the dynamics will reflect the geometry when long-range (i.e., non-geometric) edges are present; we explore this by using the Watts threshold model for complex-contagion dynamics (whereby a node adapts a contagion if the network exposure surpasses a threshold value). We embed the nodes of this network on a manifold (e.g the Euclidean plane) and we use the word "geometric" to describe edges of the generative model and the term "non-geometric" to describe other edges. Depending on the threshold, we classify the contagion phenomena via a bifurcation diagram. We study the extent to which a contagion adheres to the underlying network geometry even with 'noisy' edges by embedding the network nodes as points in a metric space (based on the node-to-node contagion transit times) and analyse the geometrical and topological properties. Surprisingly, we also find that our results give rise to a nonlinear dimension reduction technique.

This work is in collaboration with Florian Klimm, Miro Kramar, Konstantin Mischaikow, Peter Mucha, Mason Porter, and Dane Taylor.

Rachel Jeitziner

Title: Progression Analysis of disease and its application to breast cancer research.

Abstract: After having described the method developed by Monica Nicolau and Gunnar Carlsson called Progression Analysis of disease, we will see its application to several biological research questions. A quick overview on what standard tools would have told us on the same datasets will hopefully convince most of the participants that topological data analysis is or will become an unavoidable source of information on the data.

Claudia Landi

Title: Discrete Morse theory for reducing complexes in Multidimensional Persistence

Abstract: Forman's discrete Morse theory appeared to be useful for providing filtration--preserving reductions of complexes in the study of persistent homology. So far, the algorithms computing discrete Morse matchings have only been used for one--dimensional filtrations. In this talk some attempts in the direction of extending such algorithms to multidimensional filtrations are presented. Initial framework related to Morse matchings for the multidimensional setting is proposed. Moreover, matching algorithms working for 1-dimensional persistence are extended to work in the multidimensional setting. The correctness of the algorithms is proved, and its complexity analyzed. Such algorithms are used for establishing a reduction of a simplicial complex to a smaller cellular complex. First experiments with filtrations of triangular meshes are presented.

Ran Levi

Title: Neurotopology - the topology of neural systems

Abstract: The brain is without a doubt the most complicated complex system science ever studied. However,

at a basic level, the brain, or any part of it, is a network of neurons which can be described as a directed graph. It is also natural to think about connections among various brain regions in graphical terms. Electrical activity in the brain can similarly be viewed as highlighting certain subgraphs of an ambient graph. This approach has been used by theoretical neuroscientist for a while, employing mostly the tools of classical graph theory.

The Blue Brain model is an intricate and biologically accurate computer simulation of the neocortical column - a formation of roughly 31,000 simulated neurons. The data used in our study arises from forty two columns in six clusters of seven columns each, generated by the Blue Brain algorithm. The first five clusters are based on biological data extracted from five individual rats, while the sixth cluster is based of the data averaged across the five individuals. In each case the algorithm is ran seven times to create the columns. Like in a biological brain the resulting models are similar, but not identical, as the algorithm is in part stochastic in nature. The simulation allows scentists to ask questions of the model which are intractable by wet lab techniques. In particular, it is very easy to get the entire connectivity matrices of these columns, as well as activate them and obtain information about emergent chemical and electrical properties.

Combinatorial and algebraic topology are naturally suited to associating various invariants and metrics to directed graphs. In this talk I will report on an ongoing collaboration with the Blue Brain team. In particular I will show how rather naive techniques of algebraic topology are used to extract useful information from the system. These techniques can also be used in the study of neurological fMRI data and other large networks. This project is the practical, experimental part of a larger initiative which includes a highly theoretical component.

Mikael Vejdemo-Johansson

Title: Towards a topos foundation for persistent homology

Abstract: Persistent homology has been formalized with several different approaches to the underlying algebraic structures: persistence modules have been defined as graded modules over k[t], or as graded modules over a quiver of type A_n. Each of these formalizations have brought extensions of both algorithmics and the scope of what TDA methods can be envisioned and studied.

Recently, more attention have been generated to sheaf- or cosheaf-based perspectives on persistence. Most research in this direction focuses on persistence modules as vector space-valued sheaves over some choice of a base space that encodes the structure of persistent homology.

We explore a topos-based approach to foundations for persistent homology: the category of set-valued sheaves over a base space forms a topos, and therefore generates a set-theory. We can demonstrate a Heyting algebra that produces a topos that seems to exhibit the same features we are expecting from a persistent topology. Within the set theory of this topos, we can develop semi-simplicial sets, chain complexes, and a combinatorial homology theory that reimplements classical persistent homology by introducing the persistence aspects already at the level of set theory.

Finally, we describe some ideas on how a choice of a different base Heyting algebra can generate other shapes of a persistence theory, thus potentially unifying multidimensional, tree-based, DAG-based, circular and zig-zag persistence under a common foundation.