# ISBI 2023 Tutorial Proposal

# Title: Topological Data Analysis for Biomedical Imaging Data

## Keywords

Topological data analysis, Persistent homology, Time delay embedding, Dynamic-TDA, Wasserstein distance, persistent diagrams

## Brief description

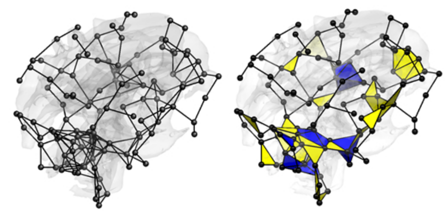

Figure 1: The traditional graph representation of brain networks (left) and the simplical complex representation of brain networks used in persistent homology (right). 2-simplices (yellow triangles) show the connectivity of three regions while 3-simplices (blue tetrahedrons) show the connectivity of four regions. Standard graph data structure cannot encode such complex connectivity patterns directly *without* additional models or data structure.

The era of big data in biology and medicine brings exciting opportunities for new scientific discoveries and challenges in biomedical image processing and analysis. Yet, valuable information in the sheer amount of complex imaging data may be hidden in patterns that cannot be decoded easily with standard tools. Recently, topological data analysis (TDA) has been a promising new avenue of research in extracting such hidden patterns in biomedical images (Figure 1). TDA characterizes topological changes of multivariate representations of imaging data in multidimensional scales. In doing so TDA reveal the persistent topological patterns in data only visible on a multiscale level. The overall topological changes hold more significance in TDA features over fleeting structures also makes the approach particularly robust at the presence of image noise and artifacts. The unique powers of TDA are demonstrated by a decade worth of theory development and various applications in computer vision and biomedical imaging [Zomorodian and Carlsson, 2005; Singh et al., 2008; Ghrist, 2008; Carlsson and Memoli, 2008; Edelsbrunner and Harer, 2008; Petri et al., 2014; Sizemore et al., 2018]. However, leading medical imaging conferences such as SPIE, ISBI and MICCAI never had any tutorial on TDA.

## Expected Aims, Structures & Audiences

This workshop is aimed at educating the state-of-the-art in TDA methodolods with hand-on tutorials from three leading experts (Moo K. Chung, Soheil Kolouri and Hernando Ombao) in the field. Chung will give an introductory overview of basic concepts in TDA followed by two more advanced lectures on state-of-arts by Kolouri and Ombao. The focus of the tutorial will be on computations, algorithms and codes as well as theory behind computations. Distributable imaging data will be used to demonstrate key relevant topics in TDA with practical know-hows on obtaining computed results for biomedical applications. The tutorial will consist of three major topics covered for one hour each for total 3 hour duration. The tutorial will consists of brief theoretical review on the topics with hand-on computer demonstration. *Even at the minimum, audiences will know how to extract topological features, compute the topological distances and use in various statistical and machine learning applications using provided codes and scripts at the end of tutorial.*

The expected audiences are graduate students and researchers trying to learn TDA for their biomedical applications. The audiences are expected to be familiar with basics of linear algebra and computer programming. However, the knowledge in TDA or topology is not needed and the tutorial will be self-contained. It is hoped that the tutorial session will provide a forum for quick painless exposure to TDA. Considering the recent surge of interest and practical use of topological loss in deep learning [Clough et al., 2019a,b], we expect sizable number of audiences.

The last time Chung organized a related workshop for ISBI in year 2020 (Interaction of Topology and Geometry in Biomedical Imaging), there were more than 90+ Zoom participants in the early morning session. We expect similar number of audiences and success.

## Lecturers & Biosketch

**Moo K. Chung** (http://www.stat.wisc.edu/~mchung) will give an introductory lecture on the **simplical homology** and **persistent homology**. Chung is an exert on TDA applications in brain imaging and has published more than 30 papers on TDA since 2009. Chung wrote the first persistent homology paper in biomedicial imaging [Chung et al., 2009] and the first persistent homology paper on brain networks in ISBI [Lee et al., 2011]. Chung is an Associate Professor in the Department of Biostatistics and Medical Informatics at the University of Wisconsin-Madison. He is also affiliated with the Waisman Laboratory for Brain Imaging and Behavior and the Department of Statistics. He participated in the World Class University Project at Seoul National University in South Korea as a faulty between 2009-2013. Dr. Chung's research focuses on topological data analysis, spectral geometry, computational neuroimaging and brain network analysis. His research concentrates on the methodological development required for quantifying and contrasting brain functional, anatomical shape and network variations in both normal and clinical populations using various mathematical, statistical and computational techniques. He has published three books on neuroimage computation including Brain Network Analysis in 2019 [Chung, 2019]. The book has few chapters in persistent homology and TDA. Chung is an active member of ISBI and published more than 20 papers in ISBI since 2004.

**Soheil Kolouri** will give an introductory lecture on the **Wasserstein distance between persistent diagrams**. Kolouri is an expert on the scalable computation Wasserstein distance using the sliced-Wasserstein distance [Kolouri et al., 2019, 2020; Naderializadeh et al., 2021]. Kolouri is an Assistant Professor of Computer Science at Vanderbilt University, Nashville, USA and the director of Machine Intelligence and Neural Technologies (MINT) lab (http://skolouri.github.io). His research interests include continual learning, bio-inspired machine learning, geometric deep learning, and computational optimal transport. Before joining Vanderbilt University, he was a research scientist and principal investigator at HRL Laboratories, Malibu, CA, where he was the PI and the Co-PI on multiple DARPA programs involving next-generation machine learning. Soheil obtained his Ph.D. in Biomedical Engineering from Carnegie Mellon University where he received the Bertucci Fellowship Award for outstanding graduate students from the College of Engineering in 2014 and the Outstanding Dissertation Award from the Biomedical Engineering Department in 2015. Kolouri recently received the best paper award from ICASSP on sliced probability metrics [Kolouri et al., 2022].

**Hernando Ombao** (https://www.kaust.edu.sa/en/study/faculty/hernando-ombao) will give an introductory lecture on the **Dynamic-TDA** and **time delay embedding** for dynamically changing biomedical images. Ombao is the Chair and Professor of Statistics Program at King Abdullah

University of Science and Technology (KAUST), Saudi Arabia. He was formerly a Statistics Professor at University of California-Irvine. He is an Elected Fellow of the American Statistical Association (ASA) and served as former chair of the Section on Imaging within the ASA. Ombao has extensive experience developing novel time series methods for analyzing functional brain signals and images [Ombao et al., 2018; Ombao and Van, 2008; Samdin et al., 2017]. Ombao also co-edited a book on state-of-the-art statistical methods for structural imaging, fMRI and electroencephalogram [Ombao et al., 2016]. Recently, Ombao has been developing dynamic-TDA and topological dependency of signals will provide necessary expertise on dynamic-TDA to the tutorial [Bourakna et al., 2022a,b].

## Course Material & Coursepacks

All the tutorial material will be available through github https://github.com/laplcebeltrami/ISBI2023TDA. The downloadable course pack will include lecture notes, slides, example data that were used as illustrations, all the computer codes and scripts generating example studies. All the material will be free from copyright issues. The following lecture topics will be covered.

### Lecture 1. Simplical homology and persistent homology

The tutorial will be given by Chung. The tutorial will cover simplical complex data structures (including Rips complex), boundary operators, spectral-TDA through the Hodge Laplacian [Dakurah et al., 2022]. Then data visualization techniques such as persistent diagrams and barcodes will be introduced. Diffusion, gradient computation, convolution and kernel computation over simplical complices will be given as an application [Anand et al., 2022].

### Lecture 2. Wasserstein distance between persistent diagrams

The tutorial will be given by Kolouri. The tutorial consists of introduction to Wasserstein distances and its sliced version. Persistent diagrams will be represented as an empirical distributions using the Dirac delta functions. Then the algorithmic detail on the computation of the Wasserstein distance between persistent diagrams will be presented [Carriere et al., 2017]. Its scalable version called the sliced-Wasserstein distance will be also introduced [Kolouri et al., 2019]. Various machine learning applications including deep learning will be presented [Kolouri et al., 2020; Naderializadeh et al., 2021]. In deep leaning, mainly the sliced-Wasserstein distance is used as a loss function [Hu et al., 2019].

### Lecture 3. Dynamic topological data analysis

The tutorial will be given by Ombao. The tutorial consists of the concept of time delay embedding that embed time series data and biological signals into the time series of scatter points [Anderson et al., 2006]. The dependency structures of data will then be modeled through persistent homology [Bourakna et al., 2022a,b]. The topological dependency of dynamic imaging data has been rarely investigated but the direction of TDA is moving toward modeling the topology of dynamics or the dynamics of topological changes in functional imaging such as MEG, EEG and fMRI [Songdechakraiwut and Chung, 2020].

## Organizer

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The brief biosketch of Chung is given in the Lecturers section.

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