Computational Topology and Application, December 18- 22, 2023
Room A-110

Time&Date	**Monday** **(December 18)**	**Tuesday** **(December 19)**	**Wednesday** **(December 20)**	**Thursday** **(December 21)**	**Friday** **(December 22)**
7:30-8:30	*Breakfast (60 minutes)*				
Chair	Haibao Duan	Rongling Wu	Jianzhong Pan	Hongwei Lin	
9:00-9:30	Yuri Dabaghian	Guowei Wei	Kelin Xia	Stephen Theriault	HU, CHUAN-SHEN
9:30-10:00	Chao Chen	Fang Li	Yuri Muranov	Yaru Gao	Jie Wu
10:00-10:30	Discussions	Discussions	Discussions	Discussions	Discussions
10:30-11:00	*Coffee Break (within 30 minutes)*				
Chair	Stephen Theriault	Guowei Wei	Zhi Lv	Wilderich Tuschmann	
11:00-11:30	Bei Wang	Rongling Wu	Shiping Liu	Shaobo Di	
11:30-12:00	Mengmeng Zhang	Qinghai Zhang	Fengling Li	Bingxu Wang	
12:00-14:00	*Lunch break (120 minutes)*				
Chair	Yuri Muranov	Ximin Liu		Jie Wu	
14:00-14:30	Tianchen Gao	Pavel Wiegmann	Free Discussion 13:30-17:00	Beifang Chen	
14:30-15:00	Jingyan Li	MAGGS KELLY SPRY		Matthew Burfitt	
15:00-15:30	Discussions	Discussions		Discussions	
15:30-16:00	*Coffee Break (within 30 minutes)*			*Coffee Break (within 30 minutes)*	
Chair	Fei Han	Beifang Chen		Fengchun Lei	
16:00-16:30	Xiaoxi Lin	Wanying Bi		Hongwei Lin	
16:30-17:00	Ran Liu	Shuang Wu		Wenting Zhao	
17:00-17:30	Discussions	Discussions		Discussions	
17:30-19:00	*Dinner*		Banquet 18:00-20:00	*Dinner*	

Simplicial Representation Learning with Neural k-forms

MAGGS KELLY SPRY
EPFL, Switzerland

Geometric deep learning extends deep learning to incorporate information about geometry and topology data, especially in complex domains like graphs. In this talk, we will present a different approach to the dominant message- passing paradigm, focusing on leveraging geometric information from simplicial complexes embedded in Rn using node coordinates. We use differential k- forms in Rn to create representations of simplices, offering interpretability and geometric consistency without message passing. This approach also enables us to apply differential geometry tools and achieve universal approximation. Our method is efficient, versatile, and applicable to various input complexes, including graphs, simplicial complexes, and cell complexes.

Algebraic Topology and Distributed Computing

Stephen Theriault
University of Southampton

Algebraic topology has proved to be a useful tool in the study of distributed computing. In this talk we discuss how a geometric realization problem that arises in distributed computing can be formulated as a more general problem in algebraic topology. We go on to describe solutions in some initial cases and relate the solutions back to distributed computing. This is joint work with Xingwu Liu, Jie Wu and Yunguang Yue.

GLMY homology theory

Yuri Muranov
University of Warmia and Mazury in Olsztyn

In 2014 Grigor'yan, Lin, Muranov and Yau developed methods for constructing cohomolgy theories on discrete sets and described relations of these results to others (co)homology theories, such that simplicial (co)homology and Hochchild cohomology. This theory is titled GLMY theory and it describes relations between discrete and continuous algebraic topology. In this talk we discuss the main results of GLMY theory, open problems, and possible directions of development.

Some applications of persistent homology and persistent path homology

Hongwei Lin
Zhejiang University

Persistent homology is the main tool in computational topology, which is an effective method for calculating topological features at different scales. In this talk, we report a series of applications of persistent homology and persistent path homology, including the vectorization method of persistent diagram and its applications in the classification and retrieval of porous structures; 3D printing technology for porous structures based on persistent homology, such as thickness calculation method and slicing method for porous structures; topology understanding and curve reconstruction technology based on persistent homology; topologically aware surface reconstruction method. Finally, we report the singular pattern extraction method from a vector field via persistent path homology.

Several computational topology problems for numerical PDEs on moving domains

Qinghai Zhang
Zhejiang University

Given a time-dependent vector field $\boldsymbol{u} : \mathbb{R}^n \times \mathbb{R}^n \to \mathbb{R}^n$, a moving hyper- surface $\delta(t) \subset \mathbb{R}^n$, and a time interval $[t_0, t_e]$, we decompose the phase space $\mathbb{R}^n$ into flux sets so that all Lagragian particles in the flux set of index k at the initial time t_0, following the nonautonomous flow of u, will go across $\delta(t)$ for the same net number k of times.
Suppose a function $f : \mathbb{R}^n \times \mathbb{R}^n \to \mathbb{R}^n$ satisfes the scalar conservation law with respect to u. We prove the identity
$\int_{t_0}^{t_e} \int_{\mathcal{S}(t)} f(\mathbf{x},t)\left(\mathbf{u}(\mathbf{x},t) - \partial_t \mathcal{S}(t)\right) \cdot \mathbf{n}(\mathbf{x},t) \mathrm{d}\mathbf{x} \mathrm{d}t = \sum_{k \in \mathbb{Z} \setminus \{0\}} k \int_{\mathcal{D}_{\mathcal{S}}^k(t_0,t_e)} f\left(\mathbf{p}, t_0\right) \mathrm{d}\mathbf{p}$
where $\mathcal{D}_\delta^k\left(t_0, t_e\right)$ is the aforementioned flux set of index k. The above results lead to a rigorous analysis of volume-of-fluid methods widely used in moving boundary problems. They also yield efficient algorithms for calculating fluxes in conservation laws.
Finally, we propose a mathematical model for two- and three-dimensional continua, establishing a solid theoretical foundation for the study of their arbitrarily complex topology, large geometric deformations, and topological changes such as merging in the context of multiphase flows. Our modeling space, named the Yin space, consists of regular open semianalytic sets with bounded boundaries, and is further equipped with constructive and algebraic definitions of Boolean operations.
Key words:Regular open sets with bounded boundaries, hyperbolic conservation laws, Numerical PDEs on moving domains

Persistent path-spectral based machine learning for protein-ligand binding affinity prediction

Ran Liu
BIMSA

Molecular descriptors are essential to quantitative structure activity/property relationship (QSAR/QSPR) models and machine learning models. In this talk we will introduce our recently proposed persistent path-spectral (PPS), PPS- based molecular descriptors, and PPS-based machine learning model for the prediction of the protein-ligand binding affinity. For the graph, simplicial complex, and hypergraph representation of molecular structures and interactions, the path-Laplacian can be constructed and the derived pathspectral naturally gives a quantitative description of molecules. Further, by introducing the filtration process of the representation, the persistent path-spectral can be derived, which gives a multiscale characterization of molecules. Molecular descriptors from the persistent path-spectral attributes then are combined with the machine learning model, in particular, the gradient boosting tree, to form our PPS-ML model. We test our model on three most commonly used data sets, i.e., PDBbind-v2007, PDBbind-v2013, and PDBbind-v2016, and our model can achieve competitive results.
Key words: Simplicial complex; Persistent path-spectral; Molecular discriptor

The Homotopy Groups of Digraphs and Its Puppe Sequence

Mengmeng Zhang
BIMSA

Detecting and interpreting the high-order structure in digraphs draws a lot of interest in complex network. The GLMY homology theory of digraphs introduced by Grigor'yan-Lin-Muranov-Yau in 2012 already successfully applied in various fields in interpreting the high-order structure. Moreover, they also established the homotopy theory of digraphs. From the perspective of algebraic topology, the homotopy theory of digraphs deserves to be explored deeper to help us understand and dig more potential meaning in digraphs. In this talk, we will introduce the homotopy groups of digraphs given by a variation of that introduced by Grigor'yan, Lin, Muranov and Yau, which admits an intuitive grids description. Furthermore, we verify the digraph analogue of Puppe sequence.

Key words:Digraph; Homotopy group; Puppe Sequence

Applications of GLMY theory in metabolomic networks of complex diseases

Shuang Wu
Beijing Institute of Mathematical Sciences and Applications

Human diseases involve metabolic alterations. Metabolomic profiles have served as a biomarker for the early identification of high-risk individuals and disease prevention. However, current approaches can only characterize individual key metabolites, without taking into account their interactions.This work have leveraged a statistical physics model to combine all metabolites into bDSW networks and implement GLMY homology theory to analyze and interpret the topological change of health state from symbiosis to dysbiosis.The application of this model to real data allows us to identify several hub metabolites and their interaction webs, which play a part in the formation of inflammatory bowel diseases.

Key words:metabolic interaction, idopNetwork, GLMY homology theory

The magnitude homology of a hypergraph

Wanying Bi
Hebei Normal University & BIMSA

The magnitude homology, introduced by R. Hepworth and S. Willerton, offers a topological invariant that enables the study of graph properties. Hypergraphs, being a generalization of graphs, serve as popular mathematical models for data with higher-order structures. In this talk, we focus on describing the topological characteristics of hypergraphs by considering their magnitude homology. We begin by examining the distances between hyperedges in a hypergraph and establish the magnitude homology of hypergraphs. Additionally, we explore the relationship between the magnitude and the magnitude homology of hypergraphs. Furthermore, we derive several functorial properties of the magnitude homology for hypergraphs.

Lastly, we present the Kunneth theorem for the simple magnitude homology of hypergraphs.

Key words:Hypergraph, magnitude, magnitude homology, Künneth theorem

An application of topological data analysis in predicting sumoylation sites

Xiaoxi Lin
Dalian University of Technology & BIMSA

Sumoylation is a reversible post-translational modification that regulates certain significant biochemical functions in proteins. The protein alterations caused by sumoylation are associated with the incidence of some human diseases. Therefore, identifying the sites of sumoylation in proteins may provide a direction for mechanistic research and drug development. Here, we propose a new computational approach for identifying sumoylation sites using an encoding method based on topological data analysis. The features of our model captured the key physical and biological properties of proteins at multiple scales. In a 10-fold cross validation, the outcomes of our model showed 96.45% of sensitivity (Sn), 94.65% of accuracy (Acc), 0.8946 of Matthew's correlation coefficient (MCC), and 0.99 of area under curve (AUC). The proposed predictor with only topological features achieves the best MCC and AUC in comparison to the other released methods. Our results suggest that topological information is an additional parameter that can assist in the prediction of sumoylation sites and provide a novel perspective for further research in protein sumoylation.

Key words:topological data analysis, post-translational modification, persistent homology

On GLMY homology of Cayley digraphs and covering digraphs

Shaobo Di
Hebei Normal University & BIMSA

We develop a theory of covering digraphs, similar to the theory of covering spaces. By applying this theory to Cayley digraphs, we build a "bridge" between GLMY-theory and group homology theory, which helps to reduce path homology calculations to group homology. We show some cases where this approach allows us to fully express path homology in terms of group homology. To illustrate this method, we provide a path homology computation for the Cayley digraph of the additive group of rational numbers.

Key words:GLMY homology, cayley digraph, covering of digraph

Persistent Topological Laplacians

Guowei Wei
Michigan State University

In recent years, the impact of topological data analysis (TDA) in sciences and engineering has grown exponentially. The main tool of TDA, persistent homology (PH), helps bridge the gap between complex geometry and abstract topology through filtration. PH has been incredibly successful in handling intricately complex, high-dimensional, nonlinear, and multiscale data. However, it has some limitations, including its inability to handle heterogeneous information (i.e., different types of objects in the point cloud), its qualitative nature (e.g., a 5-member ring is counted the same as a 6-member ring), its lack of description of non-topological changes (i.e., homotopic shape evolution), its incapable of coping with directed networks and digraphs, and its inability to characterize structured data (e.g., self- organizations in data). To address these challenges, we introduce persistent topological Laplacians (PTLs), including persistent Laplacians, persistent path Laplacians, persistent sheaf Laplacians, persistent hypergraph

Laplacians, persistent hyperdigraph Laplacians, and evolutionary de Rham-Hodge theory. By combining these tools with state-of-the-art artificial intelligence (AI) algorithms, we have uncovered the mechanisms of SARS-CoV-2 evolution and accurately forecast emerging dominant SARS-CoV-2 variants.

Development and application of material property prediction methods based on digraph topology and GLMY theory

Bingxu Wang
School of Advanced Materials, Peking University, Shenzhen Graduate School

Topology, as a novel method for data analysis, can greatly simplify the complexity of data while retaining critical information and has recently become one of the most promising methods for analyzing the topology of materials in the field of materials science. However, traditional topological methods often struggle with the asymmetric interactions inherent in multi-elemental systems found in crystals and clusters of small inorganic molecules. Addressing this challenge, GLMY theory stands out as an advanced mathematical method specifically designed for oriented systems.

Its remarkable capacity to describe unbalanced or asymmetric relationships in data positions this approach as a key player in qualitatively analyzing intrinsic topological features present in materials and small inorganic molecules.

This presentation leverages digraph topology and GLMY theory in the analysis of inorganic small molecules and crystal structures to predict the physicochemical properties of materials. The methodology involves constructing digraphs for inorganic small molecules and crystal structures based on their atomic types and chemical bonding relationships. Subsequently, the sustained persistent GLMY homology of each directed graph is computed. The resulting topological features of material structures serve as inputs to a prediction model for both nonlinear and linear predictions of the physicochemical properties of materials. The findings demonstrate a significant improvement in prediction accuracy compared to traditional methods in materials science. This substantiates the superiority of GLMY theory, showcasing its potential to advance physicochemical properties prediction capabilities in materials science.

Key words:Persistent GLMY homology, Multi-element system, Cluster and crystalline materials

New graph invariants based on p-Laplacians

Shiping Liu
Univerity of Science and technology of China

As a classical nonlinear model equation on graphs, graph p-Laplacian provide finer informaiton about the network topology and plays an important role in spectral graph theory, geometric group theory, machine learning and image processing. We will discuss new spectrum-based graph invariants which we call the cut-off adjacency eigenvalues. Those new invariants are defined via certain monotonicity of the graph p-Laplacian variational eigenvalues. Those invariants are quite helpful to derive an asymptotic analysis of graph p-Laplacians.

Key words:graph p-Laplacian, signed graphs, Cheeger inequality

Gauss-Bonnet of polytopal manifold and topological classification of embedded graphs with nonnegative curvature

Beifang Chen
Hong Kong University of Science and Technology

A d-polytopal manifold is a manifold obtained by gluing a collection of d-polytopes along their isometric facets. For each vertex of a polytopal manifold, we define a discrete Gaussian curvature as the normal angle-sum with sign, extended over all polytopes at the given vertex. We obtain a gauss-Bonnet theorem when the absolute total curvature is finite. In particular, if a graph G (possibly infinite) is embedded in a 2-dimenional manifold M without boundary such that that every face has at least 3 sides, and if the combinatorial curvature is nonnegative everywhere, then the number of vertices with non-vanishing curvature is finite. Furthermore, if G is finite, then M has four topological patterns: sphere, torus, projective plane, and Klein bottle. If G is infinite, then M has three topological patterns: cylinder without boundary, plane, and projective plane minus one point.

A polynomial invariant for knotoids

Fengling Li
Dalian University of Technology

As a generalization of the classical knots, knotoids deal with the open- ended knot diagram in a surface. In recent years, many polynomial invariants for knotoids appeared, such as the bracket polynomial, the index polynomial and the $n\mathrm{th}$ polynomial, etc. In this talk, we aim to introduce a polynomial invariant for knotoids which will have potential applications in molecular biology.
Key words:knotoid; polynomial invariant; Gauss diagram

Statistical Mechanics and Topology of Aging

Rongling Wu
BIMSA

Aging is an accumulative process of interactions among many factors over ages. We propose a new norm of statistical mechanics for reconstructing interaction networks that drive aging and age-associated diseases. This norm is built on a system of mixed ordinary differential equations that decompose the overall behavior of each underlying factor into its independent component and dependent component through evolutionary game theory. We code the independent components as nodes and dependent components as edges into bidirectional, signed, and weighted networks. We implement GLMY homology theory to dissect the topological architecture of aging networks and trace key roadmaps of how each underlying factor governs the rate of aging processes. The new model could potentially provide results that help to prevent and even reverse aging by altering key pathways.
Key words:Complex network, aging, GLMY homology

Decision boundary volum

Matthew Burfitt
BIMSA

In a classification problem, the decision boundary of a deep neural network is the region learned by the network function bordering areas assigned different class labels. By definition, the decision boundary determines the classification effectiveness of the function and understanding its structure gives us important insights on effectiveness of the network.

Considering the decision boundary of a feed-forward neural network in a two class classification problem, the boundary is a codimension-1 submanifold. A classical theorem of Weyl gives a precise description of the volume of the tubular neighborhood of a compact embedded smooth manifold. In this talk we propose to measure the volume of a small neighborhood of the decision boundary. Given a search region, we achieve an estimate of a lower bound of this volume by employing a Monte Carlo method and determining if the sampled point are within a neighborhood of the boundary.

An immediate application lies in developing none-data dependent generalization measures. By applying neighborhood boundary volume measurements over varying hyper-parameter choices, we observe that optimal network generalization is often achieved at critical points in the geometric structure of the network decision boundaries.

This is joint work with Jacek Brodzki, and Pawel Dlotko.

Key words:Neural networks, Generalization, Weyl’s tube formula

Measure Theoretic Reeb Graphs and Reeb Spaces

Bei Wang
University of Utah

A Reeb graph is a graphical representation of a scalar field on a topological space that encodes the topology of the level sets. In this paper, we propose novel constructions of Reeb graphs that incorporate the use of a measure. Specifically, we introduce Reeb graphs of metric measure spaces. A metric measure space is a metric space equipped of a measure. Our main goal is to enhance the robustness of the Reeb graph in representing the topological features of a scalar field while accounting for the distribution of the measure. We first prove the stability of a measure theoretic Reeb graphs with respect to the interleaving distance. We then prove its stability with respect to the measure, defined using the distance to a measure or the kernel distance, respectively. Our results also extend to the setting of Reeb spaces. This is a joint work with Qingsong Wang, Guanqun Ma, and Raghavendra Sridharamurthy

Δ-Twisted Homology and Fiber Bundle Structure of Twisted Simplicial Sets

Jingyan Li
BIMSA

In this talk, I will introduce a new homology, called Δ-twisted homology, which applied to Δ sets with twisted structures on faces. Using the Δ- twisted ideas to Cartesian products, we introduce the notion of Δ-twisted Cartesian product on simplicial sets, which generalizes the classical work of Barratt, Gugenheim and Moore on twisted Cartesian products of simplicial sets. Under certain hypothesis, we show that the coordinate projection of Δ-twisted Cartesian product admits a fibre bundle structure.

Key words: homolog, fibre bundle, Δ-set

Presentations of mapping class groups and applications to cluster algebras from surfaces

Fang Li
Zhejiang University

In this paper, we give presentations of the mapping class groups of marked surfaces stabilizing boundaries for any genus. Note that in the existing works, the mapping class groups of marked surfaces were the isotopy classes of homeomorphisms fixing boundaries pointwise. The condition for stabilizing boundaries of mapping class groups makes the requirement for mapping class groups to fix boundaries pointwise to be unnecessary.

As an application of presentations of the mapping class groups of marked surfaces stabilizing boundaries, we obtain the presentation of the cluster automorphism group of a cluster algebra from a feasible surface (S,M) .

Lastly, for the case (1) 4-punctured sphere, the cluster automorphism group of a cluster algebra from the surface is characterized. Since cluster automorphism groups of cluster algebras from those surfaces were given in \cite{ASS} in the cases (2) the once-punctured 4-gon and (3) the twice-punctured digon, we indeed give presentations of cluster automorphism groups of cluster algebras from surfaces which are not feasible.

This is a joint work with Jinlei Dong.

Key words:mapping class group, cluster algebra from surface, presentation

Persistent hypergraph homology and its applications

Yaru Gao
Dalian University of Technology

Persistent homology is a standard topology data analysis tool for determining the importance of (or ranking of) entities in a connected system that is represented by a simplicial complex. However, many complex systems and datasets have natural multiway interactions that are more faithfully modeled by a hypergraph. Here we introduce a new topological feature, Hˆ homology, on hypergraphs and an efficient algorithm to compute both persistent H inf barcodes and Hˆ barcodes. Our theory is demonstrated by analyzing face-to- face interactions of different populations.

Key words:Topological data analysis, persistent homology, hypergraphs

Mathematical AI for molecular data analysis

Kelin Xia
Nanyang Technological University

Artificial intelligence (AI) based molecular data analysis has begun to gain momentum due to the great advancement in experimental data, computational power and learning models. However, a major issue that remains for all AI-based learning models is the efficient molecular representations and featurization. Here we propose advanced mathematics-based molecular representations and featurization (or feature engineering). Molecular structures and their interactions are represented as various simplicial complexes (Rips complex, Neighborhood complex, Dowker complex, and Hom-complex), hypergraphs, and Tor-algebra-based models. Molecular descriptors are systematically generated from various persistent invariants, including persistent homology, persistent Ricci curvature, persistent spectral, and persistent Tor-algebra. They are further combined with machine learning models and used in molecular data analysis. Finally, we will give a brief discussion about our recent works on geometric deep learning and topological deep learning.

Key words:Topological data analysis; molecular representation; machine learning

Evolutionary Game Theory Acts in the Dysbiotic Gut Microbiota

Gao Tianchen
Tsinghua University Yau Mathematical Sciences Center & Xiamen University

This report primarily discusses how evolutionary game theory can be used to interpret the dysbiotic gut microbiota of inflammatory bowel disease (IBD) patients. We will focus on one of two types of IBD - ulcerative colitis (UC). The pathogenesis of UC is believed to be closely related to the shift of the gut microbiota from symbiosis to dysbiosis, and this shift leads to the abnormal activation of the immune system and the occurrence of inflammation. Here, we integrate the principle of evolutionary game theory to formulate the mathematical equations describing how microbes interact with each other in the gut microbiota. These equations found a basis for the reconstruction of informative, dynamic, omnidirectional, and personalized networks (idopNetwork). The topological analysis of idopNetwork can help to identify key microbial interaction pathways underlying the shift of the gut microbiota from symbiosis to dysbiosis and vice versa. I will demonstrate this idea by analyzing a real dataset of the gut microbiota.

Key words:Evolutionary Game Theory, Gut Microbiota, IdopNetwork

Reconstruction of facial shape: genetics and epigenetics

Wenting Zhao
Institute of Forensic Science of China

Variance of facial phenotype underlies the uniqueness of human individuals and also associated with hundreds of genetic syndromes. Understanding the genetic architecture that form the diversity of facial shape remains challenging partly because of the high dimensionality and complexity of craniofacial morphology. In this talk, I will introduce our recent work about genetic and epigenetic variations that are significantly associated with data-driven facial features, as well as further analysis of the effects of these variants on facial morphology variance.

Key words:facial morphology, data-driven features, genetic varaints

Periodic topology on solar cell material analysis

HU, CHUAN-SHEN
Nanyang Technological University - NTU Singapore

With its extraordinary efficiency, cost-effectiveness, and impressive stability, 2D perovskite holds immense promise for transforming photovoltaic technology, particularly in solar cell development. However, the limitations of current material structure representations have significantly impeded AI-based perovskite design and discovery. This presentation introduces a novel framework that integrates topological data analysis (TDA), periodic geometry, and machine learning to represent 2D perovskite structures and predict their bandgaps effectively. This innovative approach enables the detection of the inherent periodic geometry and topology within the material's atomic system, surpassing the traditional focus on chemical interactions among atoms and unit cell periodicity. We employ mathematical tools such as persistent homology, quotient complexes, and density fingerprints to encode this essential periodicity in the topological and geometric aspects of the crystalline structure. Additionally, we provide a comprehensive and concise introduction to these tools in the context of TDA and periodic geometry.

Key words:Persistent homology, Periodic quotient complex, Periodic geometry

Topological Aspects of Hydrodynamics

PAVEL BORISOVICH WIEGMANN
University of Chicago

In this talk, I briefly and on an elementary level discuss a few topological phenomena in fluid mechanics, which have given rise to a branch of physics/mathematics focusing on topological aspects of fluid kinematics. Topological ideas are relevant to fluid kinematics since fluid flow involves continuous deformation of a transported field.

Aspects of topological approaches for data science

Jie Wu
BIMSA

We establish a new theory which unifies various aspects of topological approaches for data science, by being applicable both to point cloud data and to graph data, including networks beyond pairwise interactions. We generalize simplicial complexes and hypergraphs to super-hypergraphs and establish super-hypergraph homology as an extension of simplicial homology. Driven by applications, we also introduce super-persistent homology. This is a joint work with Jelena Grbic, Guowei Wei and Kelin Xia.

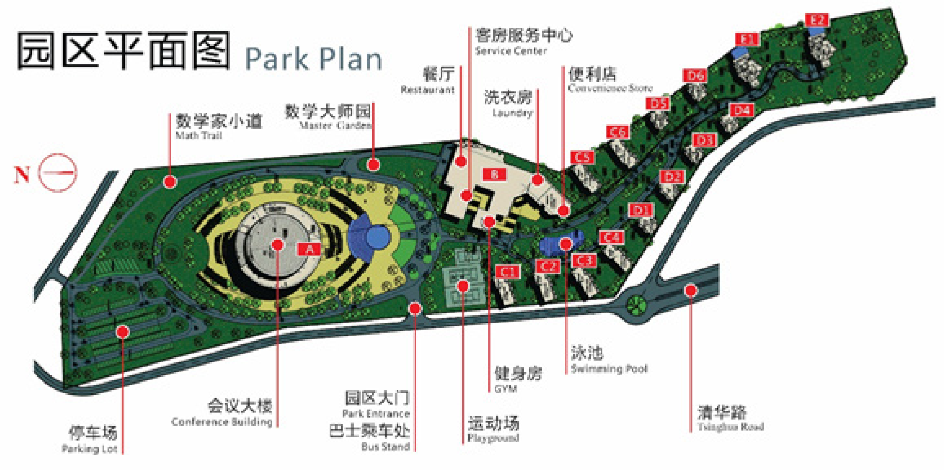
Key words:Topological data analysis, hypergraph, super-hypergraph, persistent homology, super persistent homology, simplicial complex, Delta set, scoring scheme.

Welcome to TSIMF

The facilities of TSIMF are built on a 23-acre land surrounded by pristine environment at Phoenix Hill of Phoenix Township. The total square footage of all the facilities is over 29,000 square meter that includes state-of-the-art conference facilities (over 10,000 square meter) to hold many international workshops simultaneously, two reading rooms of library, a guest house (over 10,000 square meter) and the associated catering facilities, a large swimming pool, gym and sports court and other recreational facilities.

Management Center of Tsinghua Sanya International Forum is responsible for the construction, operation, management and service of TSIMF. The mission of TSIMF is to become a base for scientific innovations, and for nurturing of innovative human resource; through the interaction between leading mathematicians and core research groups in pure mathematics, applied mathematics, statistics, theoretical physics, applied physics, theoretical biology and other relating disciplines, TSIMF will provide a platform for exploring new directions, developing new methods, nurturing mathematical talents, and working to raise the level of mathematical research in China.

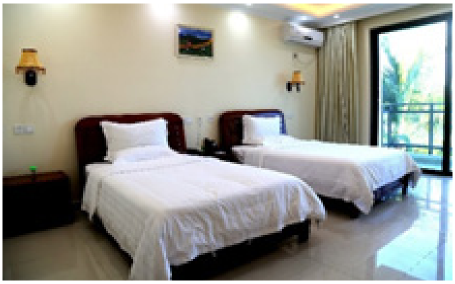
About Facilities



Registration

Conference booklets, room keys and name badges for all participants will be distributed at the front desk. Please take good care of your name badge. It is also your meal card and entrance ticket for all events.

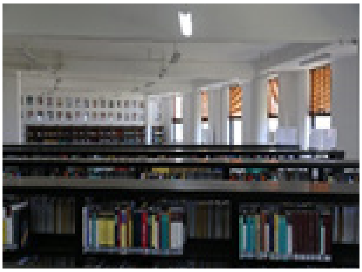
Guest Room



All the rooms are equipped with: free Wi-Fi, TV, air conditioning and other utilities.

Family rooms are also equipped with kitchen and refrigerator.

Library



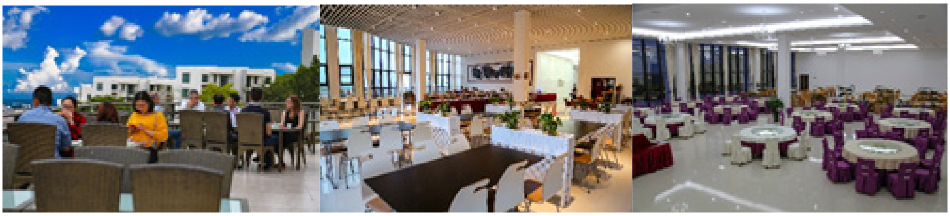
TSIMF library is available during the conference and can be accessed by using your room card. There is no need to sign out books but we ask that you kindly return any borrowed books to the book cart in library before your departure.

Opening Hours: 09:00am-22:00pm

In order to give readers a better understanding of the contributions made by the Fields Medalists, the library of Tsinghua Sanya International Mathematics Forum (TSIMF) instituted the Special Collection of Fields Medalists as permanent collection of the library to serve the mathematical researchers and readers.
So far, there are 234 books from 47 authors in the Special Collection of Fields Medalists of TSIMF library. They are on display in room A220. The participants are welcome to visit.

Restaurant

All the meals are provided in the restaurant (Building B1) according to the time schedule.



Breakfast	07:30-08:30
Lunch	12:00-13:30
Dinner	17:30-19:00

Laundry

The self-service laundry room is located in the Building 1 (B1).

Opening Hours: 24 hours

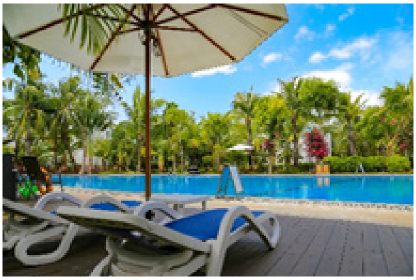
Gym

The gym is located in the Building 1 (B1), opposite to the reception hall. The gym provides various fitness equipment, as well as pool tables, tennis tables etc.

Playground

Playground is located on the east of the central gate. There you can play basketball, tennis and badminton. Meanwhile, you can borrow table tennis, basketball, tennis balls and badminton at the reception desk.

Swimming Pool



Please note that there are no lifeguards. We will not be responsible for any accidents or injuries. In case of any injury or any other emergency, please call the reception hall at +86-898-38882828.

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We provide free shuttle bus for participants and you are always welcome to take our shuttle bus, all you need to do is wave your hands to stop the bus.

Destinations: Conference Building, Reception Room, Restaurant, Swimming Pool, Hotel etc.

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