### Schedule

#### December 16, 2024, Monday

Time&Date	Welcome to TSIMF	
7:30-8:30	Breakfast (60 minutes)	
Chair: Stephen ST. Yau( 丘成栋 )		
9:00-9:30	<b>Yiqin Gao</b> ( 高毅勤 ) Modeling of bio-related molecules with the help of AI	
9:30-10:00	John Z.H. Zhang( 张增辉 ) Protein-ligand binding energy and molecular solvation	
10:00-10:30	Zhigang Yao( 姚志刚 ) Single-cell analysis via manifold fitting: A framework for RNA clustering and beyond	
10:30-11:00	Coffee Break (within 30 minutes)	
Chair: Qi Wa	ang(王奇)	
10:20-11:10	<b>Xiaofan Li</b> ( 李晓璠 ) Finite difference approximation with ADI scheme for two-dimensional keller-segel equations	
11:10-12:00	Xiaoqin Zou( 邹晓勤 ) An iteratively derived knowledge-based scoring function at atomic level for Protein-DNA Complexes Evaluations	
12:00-14:00	Lunch break (120 minutes)	
Chair: John	Z.H. Zhang( 张增辉 )	
14:00-14:30	Shi-Jie Chen( 陈世杰 ) Kinetic pathway of HIV-1 TAR cotranscriptional folding	
14:30-15:00	Mengcen Guan( 关梦岑 ) A novel representation for proteins related to phosphorylation process	
15:00-15:30	Changjun Chen( 陈长军 ) Efficient clustering on a super large collection of molecular structures on a multiple GPU platform	
15:30-16:00	Coffee Break (within 30 minutes)	
Chair: Shi-Jie Chen( 陈世杰 )		
16:00-16:30	Dmytro Kozakov	
17:30-19:00	Dinner	

# December 17, 2024, Tuesday

Time&Date	Welcome to TSIMF	
7:30-8:30	Breakfast (60 minutes)	
Chair: Yiqin Gao( 高毅勤 )		
9:00-9:30	Qi Wang( 王奇 ) Motion of active elastic particles driven by self-generatedforce couples	
9:30-10:00	Yongshuai Jiang( 姜永帅 ) RABC: Rheumatoid Arthritis Bioinformatics Center	
10:00-10:30	Hongyu Yu( 余泓谕 ) Chromosomal fusion recognition based on the alignment-free natural vector method	
10:30-11:00	Coffee Break (within 30 minutes)	
Chair: Shi H		
10:20-11:10	Yishuai Niu( 牛一帅 ) A Novel Framework for Predicting Genome Sequences and Gene Mutations Based on Natural Vector and Convex Hull Theory	
11:10-12:00	Zhaoming Wang( 王朝明 ) Molecular epidemiological investigation of adverse late effects among survivors of childhood cancer	
12:00-14:00	Lunch break (120 minutes)	
Chair: Zhaoming Wang( 王朝明 )		
14:00-14:30	Shi Huang( 黄石 ) Testing the molecular models of modern human origins	
14:30-15:00	Qi Wu( 吴琦 ) A mechanic program for phenotypic evolution	
15:00-15:30	Xiao He( 何晓 ) ChemGPT: An AI-Driven Molecular Synthesis Platform	
15:30-16:00	Coffee Break (within 30 minutes)	
Chair: Yishuai Niu( 牛一帅 )		
16:00-16:30	Jinqiao Duan( 段金桥 ) Early Warning Indicators for Critical Transitions in Stochastic Biological Systems	
16:30-17:00	Tao Zhou( 周涛 ) Exploring the convex hull principle in scRNA-seq scenarios	
18:00-20:00	Banquet	

### December 18, 2024, Wednesday

Time&Date	Welcome to TSIMF
7:30-8:30	Breakfast (60 minutes)
Chair: Shan	Zhao(赵山)
9:00-9:30	Dong Xu( 许东 ) Protein language models and their prompt-based learning
9:30-10:00	Jiahui Chen( 陈嘉会 ) Integrating differential operators and deep learning in biology application
10:00-10:30	Minghui Yang( 杨明晖 ) Investigation of biochemical reaction through quantum computing
10:30-11:00	Coffee Break (within 30 minutes)
Chair: Buyo	ng Ma( 马步勇 )
10:20-11:10	<b>Zixuan Cang</b> ( 仓子暄 ) Modeling Single-cell and Spatial Transcriptomics Data Using Optimal Transport
11:10-12:00	Guoqing Hu( 胡国庆 ) Asymmetric Natural Vector Method for Predicting Ambiguous Nonstandard Base Codes
	Group photo
12:00-14:00	Lunch break (120 minutes)
13:30-17:00	Free Discussion 13:30-17:00
17:30-19:00	Dinner

## December 19, 2024, Thursday

Time&Date	Welcome to TSIMF	
7:30-8:30	Breakfast (60 minutes)	
Chair: Jie W	/u(吴杰)	
9:00-9:30	Jianhua Xing( 邢建华 ) Learning governing equations of cellular dynamics from single cell data	
9:30-10:00	Xinqi Gong( 龚新奇 ) Sable: Bridging the Gap in Protein Structure Understanding with an Empowering and Versatile Pre-training Paradigm	
10:00-10:30	Shan Zhao( 赵山 ) A new boundary condition for the nonlinear Poisson-Boltzmann equation in electrostatic analysis of proteins	
10:30-11:00	Coffee Break (within 30 minutes)	
Chair: Dong Xu( 许东 )		
10:20-11:10	Yi Xiao( 肖奕 ) Integrated approach to DNA 3D structure prediction	
11:10-12:00	Jian Jiang( 江健 ) Mathematical AI for virtual screening of drug discovery	
12:00-14:00	Lunch break (120 minutes)	
Chair: Yi Xi	ao(肖奕)	
14:00-14:30	Jie Wu( 吴杰 ) IntComplex for high-order interactions	
14:30-15:00	Yuanzhen Shao( 邵元桢 ) Ensemble average solvation energy functional and its computational model	
15:00-15:30	Jinyong Ying( 应金勇 ) Deep learning methods for elliptic problems and the applications in predicting electrostatics	
15:30-16:00	Coffee Break (within 30 minutes)	
Chair: Xinqi	Gong( 龚新奇 )	
16:00-16:30	<b>Zhijie Tan(</b> 谭志杰) Physics-principle-based prediction for RNA 3D structures	
16:30-17:00	Xin Zhao( 赵鑫 ) IGHV3-53 Sequence Characteristics and Neutralizing Activity: Predictive Modeling and Broad-Spectrum Antibody Design Against SARS-CoV-2	
17:30-19:00	Dinner	

### December 20, 2024, Friday

Time&Date	Welcome to TSIMF		
7:30-8:30	Breakfast (60 minutes)		
Chair: Jianhua Xing( 邢建华 )			
9:00-9:30	Buyong Ma( 马步勇 )		
	Deep learning of protein energy landscape and conformational		
	dynamics from experimental structures in PDB		
	Xue Gong( 公雪 )		
9:30-10:00	Topology-enhanced machine learning model for anticancer peptide		
	prediction		
10:00-10:30	Jinzhi Lei( 雷锦志 )		
	Quantitative cancer-immunity cycle modeling for predicting disease		
	progression in advanced metastatic colorectal cancer		