CONFERENCE SCHEDULE

2021 13th International Conference on Bioinformatics and Biomedical Technology (ICBBT 2021)

&

2021 International Workshop on Frontiers of Graphics and Image Processing (FGIP 2021)

May 21-23, 2021, Xi'an, China

Co-organized by

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Conference Introduction

2021 13th International Conference on Bioinformatics and Biomedical Technology (ICBBT 2021) with its workshop-2021 International Workshop on Frontiers of Graphics and Image Processing (FGIP 2021) will be held during May 21-23, 2021 in Northwestern Polytechnical University, Xi'an, China. Previously, ICBBT series had been successfully held in Chengdu, China in 2010, Sanya, China in 2011, Singapore in 2012, Macau in 2013, Gdansk, Poland in 2014, Singapore in 2015, Barcelona, Spain in 2016, Lisbon, Portugal in 2017, Amsterdam, The Netherlands in 2018, Stockholm, Sweden in 2019, online in 2020.

ICBBT 2021 is to bring together innovative academics and industrial experts in the field of Bioinformatics and Biomedical Technology to a common forum. The primary goal of the conference is to promote research and developmental activities in Bioinformatics and Biomedical Technology. Another goal is to promote scientific information interchange between researchers, developers, engineers, students, and practitioners working in China and abroad. The conference will be held every year to make it an ideal platform for people to share views and experiences in Bioinformatics and Biomedical Technology and related areas.

Papers will be published in the following proceedings or journal:

International Conference Proceedings by ACM (ISBN: 978-1-4503-8965-5), which will be archived in ACM Digital Library, indexed by Ei Compendex and Scopus, and submitted to be reviewed by Thomson Reuters Conference Proceedings Citation Index (ISI Web of Science).

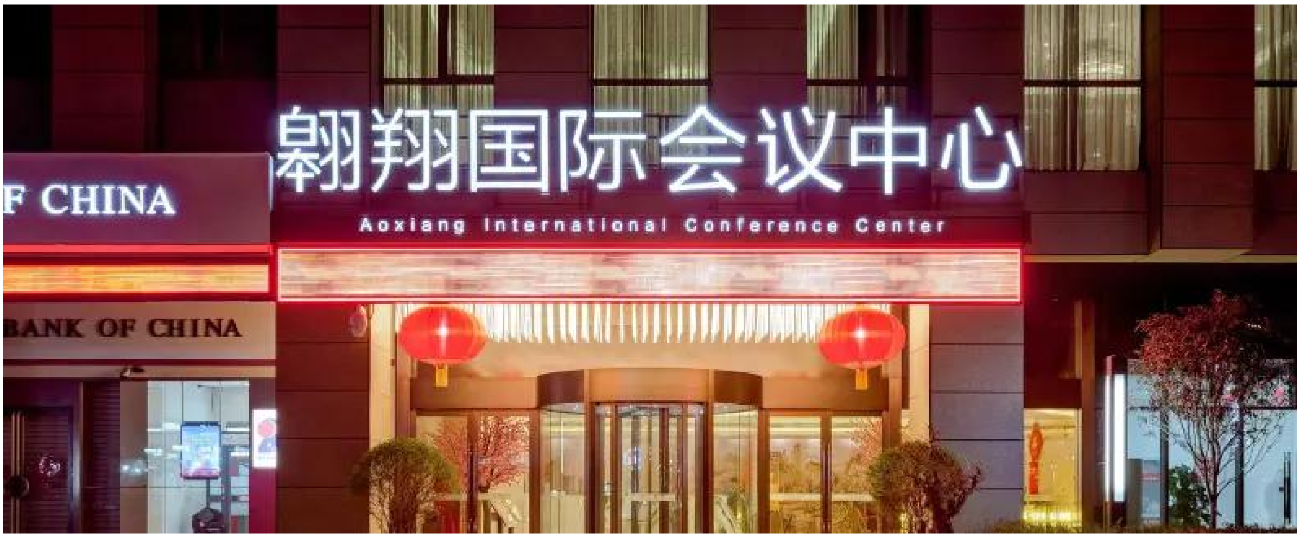
International Journal of Pharma Medicine and Biological Sciences (IJPMBS, ISSN: 2278-5221), which will be indexed by Embase (Under elsevier), ProQuest; International Committee of Medical Journal Editors (ICMJE); Health sciences library (NYU); HINARI Access to Research in Health Programme; etc.

ICBBT 2021 Conference website and email: www.icbbt.org; icbbt@cbees.org

Conference Venue

Aoxiang International Conference Center（西安翱翔国际会议中心）

地址：西安市碑林区劳动南路西工大创新大厦B座



西安翱翔国际会议中心位于西安市劳动南路，北邻西工大校区，处于大唐西市文化旅游商圈，靠近西高新技术产业开发区，地处地铁5号线6号线换乘站处，交通便利，地理位置优越。酒店以“归园田居”为设计理念，深厚的东方禅意文化底蕴为核心，用现代手法将东方文化的传统要素一一提炼，导入设计的每个细节中，使原本色彩古朴的装修与现代的理念相结合，展示东方的静谧安逸和简单利落的现代风格，体现心境空灵，悠然自得的精神诉求。

翱翔国际会议中心交通路线指南
咸阳机场到酒店
1、打车：距离约36公里、打车费约110元、车程时间约50分钟。（正常不堵车情况下）
2、机场大巴到酒店：机场大巴西高新区线到志成丽柏大酒店，向北步行约10分钟到达酒店，距离机场车程时间约50分钟。
西安火车站到酒店：乘坐201路、206路、608路公交到劳动南路或西工大西门站下车。
西安北站（高铁站）到酒店：地铁2号线南稍门站换乘地铁5号线西北工业大学站下车（E口出）。
城西客运站到酒店：乘坐106路、212路到劳动南路站下车
城东客运站到酒店：地铁1号线劳动路站换乘公交322路劳动南路站下车；地铁1号线洒金桥站换乘公交107路、10路劳动南路站下车；地铁1号线劳动路站换乘公交24路西工大西门站下车
城南客运站到酒店：乘坐106路劳动南路站下车
城北客运站到酒店：乘坐1路劳动南路站下车；乘坐211路桃园路口站下车
酒店到西安市中心（钟鼓楼）公交路线：29路、43路、游7。

Presentation Guideline

Presentation Requirement

- At least one author should present for each abstract/full paper during the session.

Time Zone

- The time shown in this schedule is **Greenwich Mean Time (GMT+08:00) – China Standard Time**.

Warm Tips for Presentation

- English is the official language.
- Get your presentation PPT/Slides prepared.
- Keynote Speech: about 35 Minutes of Presentation and 5 minutes of Q&A.
- Invited Speech: about 15 Minutes of Presentation and 5 minutes of Q&A.
- Oral Presentation: about 12 Minutes of Presentation and 3 minutes of Q&A.
- One Best Oral Presentation will be selected from each session, and the result will be announced at the end of the session.

Onsite Presentation Instruction

- **Devices Provided by the Conference Organizer:** (a) Laptop Computer (MS Windows Operating System with MS PowerPoint and Adobe Acrobat Reader). (b) Digital Projectors and Screen. (c) Laser Stick. (d) Materials Provided by the Presenters: PowerPoint or PDF Files (Files should be copied to the Conference laptop at the beginning of each Session.)
- **Instruction for Poster Presentation:** Materials Provided by the Conference Organizer: The place to put posters. Materials Provided by the Presenters: (a) Home-Made Posters: Submit the poster to the staff when signing in. (b) Maximum poster size is A1. (c) Load Capacity: Holds up to 0.5 kg.
- **Conference Material:** All presented papers will be issued with hard copy of conference materials: Receipt/Invoice, Participation and presentation certificate, Conference program book, etc.
- **Dress Code:** Please wear formal clothes or national representative of clothing.

Personal Insurance

- Along with your registration, you will receive your name badge, which must be worn when attending all conference sessions and activities. Participants without a badge will not be allowed to enter the conference venue.
- For your safety, please do not lend your name badge to the persons who are not involved in the conference and bring the irrelevant persons into the conference venue.
- The conference organizers cannot accept liability for personal injuries, or for loss or damage of property belonging to conference participants, either during, or as a result of the conference. Please check the validity of your own insurance.

Online Presentation Instruction

- **Equipment Needed:** (a) A computer with an internet connection (wired connection recommended). (b) USB plug-in headset with a microphone (recommended for optimal audio quality). (c) Webcam (optional): built-in or USB plug-in. (d) Please set up your laptop time in advance.

Presentation Guideline

- **Download the ZOOM:** https://zoom.us/download; https://www.zoom.com.cn/download.
- **Learn the ZOOM skills:** https://support.zoom.us/hc/en-us/articles/201362033-Getting-Started-on-Windows-and-Mac.
- **How to use ZOOM:** (a) Set the language. (b) Test computer or device audio. (c) Join a meeting: Join the meeting with "meeting ID" provided in the program, tap the name as "paper ID+name", eg.: "XA0007-Olia Lai" “TA0002”, then click "Join". (d) Get familiar with the basic functions: Rename, Chat, Raise Hands, Start Video, Share Computer Sound and Share Screen, etc.
- **Environment Requirement:** (a) Quiet Location. (b) Stable Internet Connection. (c) Proper Lighting.
- **Test Session:** On May 19, there are test sessions. On that day, all the above functions will be taught including how to use ZOOM. If you don’t know how to use, please do not worry. However, please do download ZOOM and log in the meeting room in advance, then, you can join the conference.
- **Voice Control Rules during the Presentation:** (a) The host will mute all participants while entering the meeting. (b) The host will unmute the speakers' microphone when it is turn for his or her presentation. (c) Q&A goes after each speaker, the participant can raise hand for questions, the host will unmute the questioner. (d) After Q&A, the host will mute all participants and welcome next speaker.
- To effectively control the time and avoid some unexpected situations, it is suggested that you should record your presentation ahead of time, play the video or do the live oral presentation online while it's your turn for presentation.

  Step 1: Author records a video introduction with their own image, speaking to the camera, introducing themselves: name, affiliation, brief description of scope of their work.

  Step 2: Author then switches to their slides and provides a voiceover describing images in each slide.

  Step 3: Author needs to be able to upload these presentations to a location specified by YOU in advance. Send the video to the staff in advance.
- **Conference Material:** All presented papers will be issued with soft copy of conference materials: Receipt/Invoice, Participation and presentation certificate, etc.
- **Notes:** (a) Log in the meeting room 15 minutes ahead of the session. (b) Learn the zoom skills. (c) Your punctual arrival and active involvement in each session will be highly appreciated. (d) The conference will be recorded; we will appreciate your proper behavior.

Contact Us

- Contact us by We-chat for any inquires.

Program-at-a-Glance

Test Session-May 19, 2021 (Wednesday)

Meeting ID:	**Duration**
Opening Remarks--Prof. Xiaoyi Feng, Northwestern Polytechnical University, China	10:00-10:10
Keynote Speaker--Prof. Tatsuya Akutsu, Kyoto University, Japan	10:10-10:20
Keynote Speaker--Prof. Taesung Park, Seoul National University, South Korea	10:20-10:30
Keynote Speaker--Prof. Hongbing Lu, Fourth Military Medical University, China	10:30-10:40
Invited Speaker--Prof. Jiyun Li, Donghua University, China	10:50-11:00
Invited Speaker--Assoc. Prof. Xiuying Wang, The University of Sydney, Australia	11:00-11:10
Invited Speaker--Assoc. Prof. Sansanee Auephanwiriyakul, Chiang Mai University, Thailand	11:10-11:20
Invited Speaker--Lei Zhang, Principal Curator of Omics Data at China National Gene Bank Data Base, China	11:20-11:30
Invited Speaker--Dr. Faez Iqbal Khan, University of Electronic Science and Technology of China, China	11:30-11:40
Keynote Speaker--Prof. Fabio Roli, University of Cagliari, Italy	11:40-11:50
Keynote Speaker--Prof. Tuan D. Pham, Prince Mohammad Bin Fahd University, Saudi Arabia	11:50-12:00
Poster Session 1	12:00-12:15
Meeting ID:	**Duration**
Oral Session 1 Topic: Clinical Medicine and Health Information System	10:00-10:30
Oral Session 2 Topic: Computational Biology and Image Processing	10:30-11:10
Oral Session 3 Topic: Bioinformatics	11:10-12:15
Break Time	12:15-14:20

Meeting ID:	**Meeting ID:**	**Duration**
Oral Session 4 Topic: Bioinformatics and Genomics	Oral Session 5 Topic: Machine Learning and Artificial Intelligence in Biomedicine	14:20-15:05
Oral Session 6 Topic: Bioinformatics and Computational Biology	Oral Session 7 Topic: Biomedical Signal Analysis and Biosystem Modeling	15:05-15:45
Oral Session 8 Topic: Medical Imaging and Image Processing	Oral Session 9 Topic: Biomedical Engineering and Technology	15:45-16:30

Tips: Please log in the meeting room in the specific test session on time. Oral presentation test: 5 minutes/per paper. Poster presentation test: 3minutes/per poster.

Program-at-a-Glance

Arrival Registration-May 21, 2021 (Friday)

Arrival Registration & Conference Material Collection	**Duration**
Venue: Hotel Lobby, 1st Floor	10:00-16:00

Tips: The arrival registration can be also done at any time during the conference on May 21-22, 2021.

Online Session-May 21, 2021 (Friday)

Meeting ID:	**Duration**
Opening Ceremony	14:00-14:10
Keynote Speech I--Prof. Tatsuya Akutsu, Kyoto University, Japan	14:10-14:50
Keynote Speech II--Prof. Taesung Park, Seoul National University, South Korea	14:50-15:30
Break	15:30-15:50
Keynote Speech III--Prof. Fabio Roli, University of Cagliari, Italy	15:50-16:30
Keynote Speech IV--Prof. Tuan D. Pham, Prince Mohammad Bin Fahd University, Saudi Arabia	16:30-17:10

Onsite Session-May 22, 2021 (Saturday)

Meeting Room: Juya Conference Hall-5F (5 楼聚雅厅)

Morning Conference	**Duration**
Opening Remarks--Prof. Xiaoyi Feng, Northwestern Polytechnical University, China	09:00-09:10
Keynote Speech V--Prof. Hongbing Lu, Fourth Military Medical University, China	09:10-09:50
Invited Speech I--Lei Zhang, Principal Curator of Omics Data at China National Gene Bank Data Base, China	09:50-10:10
Invited Speech II--Dr. Faez Iqbal Khan, University of Electronic Science and Technology of China, China	10:10-10:30
Group Photo & Poster Session 1: XA0027, TA2018, TA1012N, XA0026, XA0011	10:30-10:55
Oral Session 1--Topic: Clinical Medicine and Health Information System XA0018, TA0010, XA1009, TA3001, XA0013, XA0031	10:55-12:25
Lunch: Heyanju-2F (2 楼和筵居)	12:25-13:40
Afternoon Conference	**Duration**
Oral Session 2--Topic: Computational Biology and Image Processing XA0048, TA0009, TA2019, XA0050, XA0038, XA0020, XA1007, XA0012	13:40-15:40
Break	15:40-16:00
Oral Session 3--Topic: Bioinformatics XA0049, XA0045, XA1001, XA1006, TA2021, TA2008, TA2020, XA0044, XA2001	16:00-18:15
Dinner: Heyanju-2F (2 楼和筵居)	18:30-20:00

Tips: Please log in the ZOOM Room or arrive at the Conference Room 15 minutes ahead of the session.

Program-at-a-Glance

Online Session-May 23, 2021 (Sunday)

Morning Conference		
Meeting ID:		**Duration**
Invited Speech III--Assoc. Prof. Sansanee Auephanwiriyakul, Chiang Mai University, Thailand		09:00-09:20
Invited Speech IV--Assoc. Prof. Xiuying Wang, The University of Sydney, Australia		09:20-09:40
Invited Speech V--Prof. Jiyun Li, Donghua University, China		09:40-10:00
Break		10:00-10:10
Meeting ID:	**Meeting ID:**	**Duration**
Oral Session 4 Topic: Bioinformatics and Genomics XA0008, XA1014, TA2013, XA1004, XA0028, XA0030, XA1010, XA0029, TA2015	Oral Session 5 Topic: Machine Learning and Artificial Intelligence in Biomedicine XA0014, XA1011, TA4002, TA2011, TA2006, XA1013, TA0008, TA2022-A, TA0011N	10:10-12:25
Break		12:25-13:30
Afternoon Conference		
Meeting ID:	**Meeting ID:**	**Duration**
Oral Session 6 Topic: Bioinformatics and Computational Biology XA0006, XA0019, XA0035, XA0040, TA2010, XA0034, XA0046, TA0006	Oral Session 7 Topic: Biomedical Signal Analysis and Biosystem Modeling TA0001, TA2007-A, TA0002, XA1008, TA0004, TA2003, XA0007, TA3002	13:30-15:30
Break		15:30-15:45
Oral Session 8 Topic: Medical Imaging and Image Processing TA2009, XA2003, XA2002, XA0010, TA2004, XA1003, TA2023-A, XA1016, TA2014	Oral Session 9 Topic: Biomedical Engineering and Technology TA0013, TA0007, XA0033-A, XA0004, TA5002-A, XA1015, TA1010-A, XA1005, XA0047	15:45-18:00

Tips: Please log in the meeting room 15 minutes ahead of the session.

Keynote Speech I

Duration: 14:10-14:50, May 21, 2021 (Friday)
Meeting ID:

Prof. Tatsuya Akutsu
Kyoto University, Japan

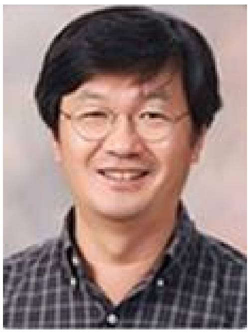
Tatsuya Akutsu received B.Eng. and M.Eng. in Aeronautics and D.Eng. in Information Engineering from University of Tokyo, in 1984, 1986 and 1989, respectively. From 1989 to 1994, he was with Mechanical Engineering Laboratory. From 1994 to 1996, he was an Associate Professor in the Department of Computer Science at Gunma University. From 1996 to 2001, he was an Associate Professor in Human Genome Center, Institute of Medical Science, University of Tokyo. Since 2001, he has been a Professor in Bioinformatics Center, Institute for Chemical Research, Kyoto University. He is a fellow of Information Processing Society of Japan (IPSJ), and was an editor-in-chief of IPSJ Transactions on Bioinformatics for 2006-2009. His research interests include bioinformatics, complex networks, and dicrete algorithms.

Speech Titile: Graph Theoretic Approaches to Analysis and Control of Biological Networks

Abstract: Development of control theory for biological systems is one of major goals in systems biology and bioinformatics. Recently, several graph theoretic concepts have been utilized for finding driver nodes that can control the entire state of a network. In particular, maximum matching (MM), minimum dominating set (MDS), and feedback vertex set (FVS) have been widely utilized. In this talk, we briefly review and conceptually compare these approaches. Then, we present various extensions of the MDS-based method that have been developed by us. Although it is difficult to directly apply graph theoretic approaches to control of real biological systems. they are useful for finding important genes and proteins. Indeed, MDS has been applied to analysis of various kinds of biological networks by us and others, which include protein-protein interaction networks, drug-target protein network, non-coding RNA-protein network, and cancer metabolic network. We overview these applications too. This talk is based on joint work with Jose Nacher in Toho University.

Keynote Speech II

Duration: 14:50-15:30, May 21, 2021 (Friday)
Meeting ID:



Prof. Taesung Park
Seoul National University, South Korea

Prof. Taesung Park received his B.S. and M.S. degrees in Statistics from Seoul National University (SNU), Korea in 1984 and 1986, respectively and received his Ph.D. degree in Biostatistics from the University of Michigan in 1990. From Aug. 1991 to Aug. 1992, he worked as a visiting scientist at the NIH, USA. From Sep. 2002 to Aug. 2003, he was a visiting professor at the University of Pittsburgh. From Sep. 2009 to Aug. 2010, he was a visiting professor in Department of Biostatistics at the University of Washington. From Sep. 1999 to Sep. 2001, he worked as an associate professor in Department of Statistics at SNU. Since Oct. 2001 he worked as a professor and currently the Director of the Bioinformatics and Biostatistics Lab. at SNU. He served as the chair of the bioinformatics Program from Apr. 2005 to Mar. 2008, and the chair of Department of Statistics of SNU from Sep. 2007 and Aug. 2009. He has served editorial board members and associate editors for the international journals including Genetic Epidemiology, Computational Statistics and Data Analysis, Biometrical Journal, and International journal of Data Mining and Bioinformatics. His research areas include microarray data analysis, GWAS, gene-gene interaction analysis, and statistical genetics.

Speech Title: Deep Learning-Based Pathway Analysis using Hierarchical Structural Component Models

Abstract: Many statistical methods for pathway analysis have been used to identify key genes and proteins within previously known pathways associated with a given disease, or to detect novel pathways from proteins known to be disease-related. It is well known that pathways overlap and are highly correlated. However, most pathway methods do not consider this correlation between pathways, which may cause false negative or positive errors. Recently, a hierarchical structural component model (HisCoM) was proposed to take this correlation into account by fitting all pathways in one model simultaneously. However, since HisCoM assumes linear contributions of biological factors to the effect of a pathway, it does not fully project the complexity of relationships between biological factors. We propose DeepHisCoM which uses deep learning to find complex contributions of biological factors to the effect of a pathway. DeepHisCoM has all advantages of HisCoM such as using the hierarchical structured information in pathways. Through simulation studies, DeepHisCoM was shown to have higher power in the non-linear pathway effect and comparable power for the linear pathway effect, when compared to the conventional pathway methods. Application to a Hepatocellular Carcinoma (HCC) dataset demonstrated that DeepHisCoM successfully identified well known pathways that are highly associated with HCC such as Tryptophan metabolism and Primary bile acid biosynthesis.

Keynote Speech III

Duration: 15:50-16:30, May 21, 2021 (Friday)
Meeting ID:

Prof. Fabio Roli
University of Cagliari, Italy

Fabio Roli is a Full Professor of Computer Science at the University of Cagliari, Italy, and Director of the Pattern Recognition and Applications laboratory (https://pralab.diee.unica.it/). He is partner and R&D manager of the company Pluribus One that he co-founded (https://www.pluribus-one.it). He has been doing research on the design of pattern recognition and machine learning systems for thirty years. His current h-index is 71 according to Google Scholar (April 2021). He has been appointed Fellow of the IEEE and Fellow of the International Association for Pattern Recognition. He was a member of NATO advisory panel for Information and Communications Security, NATO Science for Peace and Security (2008 – 2011). Prof. Roli is the recipient of the 2020 Pattern Recognition Medal of the international scientific journal Pattern Recognition, and the 2020 IAPR Pierre Devijver Award, granted to an outstanding scientist who has significantly contributed to the field of statistical pattern recognition.

Speech Titile: From Known Knowns to Unknown Unknowns in AI: Historical and Technical Issues

Abstract: AI has been originally developed for *closed-world*, and *noise-free*, problems where the possible states of natures and actions that a rationale agent could implement were perfectly known. One could argue that, at that time, AI dealt with *known knowns*. Since the 1980s, when machine learning became an experimental science, AI researchers started to tackle pattern recognition problems with noisy data, using probability theory to model uncertainty and decision theory to minimize the risk of wrong actions. This was the era of *known unknowns*, characterized by the rise of benchmark data sets, larger and larger year after year, and the belief that real world problems can be solved collecting enough training data. However, recent results have shown that available data sets have often a limited utility when used to train pattern recognition algorithms that will be deployed in the real world. The reason is that modern machine learning has often to face with *unknown unknowns*. When learning systems are deployed in adversarial environments in the *open world*, they can misclassify (with high-confidence) never-before-seen inputs that are largely different from known training data. *Unknown unknowns* are the real threat in many security problems (e.g., zero-day attacks in computer security). In this talk, I give a historical and technical overview of the evolution of AI and machine learning for pattern recognition, and discuss how this evolution can be regarded as a transition from *known knowns* to *unknown unknowns*, and the key role that adversarial machine learning plays to make AI safer.

Keynote Speech IV

Duration: 16:30-17:10, May 21, 2021 (Friday)

Meeting ID:

Prof. Tuan D. Pham

Prince Mohammad Bin Fahd University, Saudi Arabia

Tuan D. Pham currently holds positions as Professor in AI and Founding Director of the Center for Artificial Intelligence at Prince Mohammad Bin Fahd University, Saudi Arabia. The Center for Artificial Intelligence is equipped with state-of-the-art computing facilities and infrastructure. His previous position was Professor of Biomedical Engineering at Linkoping University, University Hospital Campus, Linkoping, Sweden. He was appointed as Professor and Leader of the Aizu Research Cluster for Medical Engineering and Informatics, and the Medical Image Processing Lab, both at the University of Aizu, Japan. Before his appointments in Japan, he was appointed as Associate Professor and the Bioinformatics Research Group Leader at the University of New South Wales, Canberra, Australia. His current research focuses on AI and machine learning methods for image processing, time-series analysis, complex networks, and pattern recognition applied to medicine, biology, and mental health. He serves as an Associate/Section Editor for several scholarly journals, series, and conference proceedings. In 2020, Dr. Pham is selected as an Expert in Artificial Intelligence by the U.S. Food and Drug Administration (FDA) Center for Devices and Radiological Health (CDRH) Network of Digital Health Experts Program (NoDEx).

Speech Title: Recurrence Analysis in Deep Learning of Medical Images and Physiological Signals

Abstract: Time-frequency and time-space properties of medical images and physiological time series are introduced as a robust tool for deep learning-based classification. Experimental results obtained from the classification of benign and malignant mediastinal lymph nodes in lung cancer on computed tomography and sensor-induced physiological signals of Parkinson's disease and heart irregularity show the effectiveness of the use of recurrence analysis in deep learning. The proposed approach has the potential for 1) achieving very high classification accuracy, 2) saving tremendous time for data learning, and 3) being cost-effective and user-comfortable for clinical trials by reducing multiple wearable sensors for data recording.

Opening Remarks

Duration: 09:00-09:10, May 22, 2021 (Saturday)

Meeting Room: Juya Conference Hall-5F (5 楼聚雅厅)

General Chair
Prof. Xiaoyi Feng
Northwestern Polytechnical University, China

Xiaoyi Feng received the M.S. degree from the Northwest University, Xi'an, China, in 1994. She received her Ph.D. degree from the Northwestern Polytechnical University, Xi'an, China, in 2001. She is currently a professor with the School of Electronics and Information, Northwestern Polytechnical University since 2008. She has authored or co-authored more than 80 papers in journals and conferences such as IEEE TIP/TMM/TIFS/TAC, IJCAI, FG and ICIP. She was co-program chair for International Conference on Biomedical Engineering and Applications (ICBEA 2020) and International Conference on Image Processing Theory, Tools and Applications (IPTA2018). Her current research interests include computer vision, image process, radar imagery and recognition.

Keynote Speech V

Duration: 09:10-09:50, May 22, 2021 (Saturday)
Meeting Room: Juya Conference Hall-5F (5 楼聚雅厅)

Prof. Hongbing Lu
Fourth Military Medical University, China

Hongbing Lu, Ph.D., professor and director, Faculty of Biomedical Engineering, Fourth Military Medical University. Her research interests cover a spectrum from medical image reconstruction to image analysis for computer-aided detection and diagnosis, including brain network analysis for mental disorder. As the principal investigator of near twenty projects including key projects funded by the National Science Foundation of China, by Ministry of Science and Technology, and by the Military Research Foundation, she has published over 170 research papers including leading journals like Biomaterial, IEEE Trans Med Imag, Euro Radiol, and IEEE Trans Biomed Eng (with single highest citation over 420), holds more than ten US and Chinese licensed patents, and awarded by many prizes including the First Prize of State Science and Technology Award. She is currently the committee chair of the Shaanxi Society of Biomedical Engineering, and has served as an associate editor of IEEE Transactions on Medical Imaging and Medical & Biological Engineering & Computing.

Speech Title: Towards Quantitative in-vivo Imaging with Cone-beam X-ray Luminescence Computed Tomography (CB-XLCT)

Abstract: As a molecular imaging tool with high sensitivity, optical imaging has been widely used for in-vivo monitoring of cancer development. However, limit penetration depth of light in tissues makes it difficult to image deep-seated cancer in-vivo. Recently, with the development of X-ray excited nanophosphors, X-ray luminescence computed tomography (XLCT) has shown its potential in imaging deep-seated tissues in-vivo. To achieve quantitative XLCT imaging with high sensitivity and spatial resolution, there are some challenges to be solved, including inaccurate forward model, slow and limited imaging, and inaccurate reconstruction. In this talk, we report some solutions for quantitative and fast cone-beam XLCT imaging.

Invited Speech I

Duration: 09:50-10:10, May 22, 2021 (Saturday)
Meeting Room: Juya Conference Hall-5F (5 楼聚雅厅)

Lei Zhang

Principal Curator of Omics Data at China National GeneBank DataBase, China

Lei Zhang received her B.S degree in computer science and M.S. degree in Biochemistry and Molecular Biology from HUST (Huazhong University of Science and Technology). She severed as project manager for Signal Transduction and Transcriptome Engineering in China-UK HUST-RRes Genetic Engineering and Genomics Joint Laboratory, executive director of Tivoli Education Technical Support in IBM GPSG RDC (Wuhan) (as internee). She joined CNGBdb as a research scientist in data curation and mining. Broad project experience in whole genome sequencing analysis of Model plants and animals, Genome-Wide Association Studies about Individuals and Groups, metagenome analysis of microbiome, rare disease associated SNPs detection and Pharmacogenomics research. She has published 5 academic papers and conference reports, owns 6 invention patents. Her current interests include biological big data mining, integration, management and sharing, aiming to provide all-in-one data service integrated data processing, data archiving, data online analysis and data application in Life Sciences.

Speech Title: CNGBdb: An Integrated Data Platform for Multi-Omics Data Sharing and Analysis in Life Science

Abstract: Dramatic advancement of DNA Sequencing technology has revolutionized the research approaches and benefits human health, agricultural science, and pandemic control. Here, **CNGBdb** provides a comprehensive solution of data sharing, workflow management, elastic cloud computing resource and trusted collaboration environment for research and industries in life science. At this stage, three unique datasets including the CNSA, COVID-19 genome sequence datasets and CODEPLOT automatic analysis system are available and made ready for use in the CNGBdb platform. Compared with other relevant resources, CNGBdb is featured by the advantage of three aspects. Firstly, CNGB Sequence Archive system, Scientific databases and key data resources corporation are incorporated to provide a highly efficient and user-friendly framework to create data submission workflows and perform data sharing in this platform. Meanwhile, CODEPLOT provide an enterprise level of elastic cloud computing resource to run parallel jobs in batch mode, based on highly scalable, high-performance, enterprise-class Kubernetes clusters and Docker container technology. Furthermore, the cutting-edge technologies like data encryption, block-chain and secure multiparty computing are employed in this platform to provide a highly secure and reliable environment for data sharing and collaboration. In short, CNGBdb is a reliable and flexible bioinformatics data platform in life science, which aims to promote the efficient sharing, cooperation, and utilization of omics data in research and industries.

Invited Speaker II

Duration: 10:10-10:30, May 22, 2021 (Saturday)

Meeting Room: Juya Conference Hall-5F (5 楼聚雅厅)

Dr. Faez Iqbal Khan

University of Electronic Science and Technology of China, China

Dr. Faez Iqbal Khan obtained his PhD degree in Computational Chemistry (Bioinformatics) in 2015 from Durban University of Technology, South Africa. He got his B.Sc. and M.Sc. degrees in Biomedical Science and Bioinformatics. He was a postdoctoral researcher and visiting scholar in 2016 at Henan University of Technology and South China University of Technology. Dr. Khan joined the Computational Mechanistic Chemistry and Drug Discovery group at Rhodes University South Africa in 2017 as a postdoctoral researcher and part time lecturer. He was a postdoctoral research fellow at University of Electronic Science and Technology of China (UESTC) from February 2019 to March 2021. He joined UESTC as Assistant researcher/ Foreign Teacher from 1st April 2021. He has expertise in the field of Bioinformatics, Biotechnology, Biochemistry, and Computational chemistry. He is well equipped with various molecular biology techniques as well as bioinformatics programs such as Cloning of gene using E. coli/ P. Pastoris, Protein Expression, Protein Purification, AMBER, Discovery Studio, Material Studio, AutoDock, Modeler, MMPBSA and GROMACS. He has published more than 60 papers in SCI journals. He is active reviewer of several scientific journals.

Speech Title: Sphingosine Kinase 1 Inhibitors as Therapeutics against Cancer

Abstract: Sphingosine kinase 1 (SphK1) is a promising therapeutic target against several diseases including mammary cancer. The aim of present work is to identify a potent lead compound against breast cancer using ligand-based virtual screening (LBVS), molecular docking, Molecular Dynamics (MD) simulations, and the Molecular Mechanics Poisson-Boltzmann Surface Area (MMPBSA) calculations. The LBVS in molecular and virtual libraries yielded 20,800 hits, which were reduced to 621 by several parameters of drug-likeness, lead-likeness, and PAINS. Furthermore, 55 compounds were selected by ADMET descriptors carried forward for molecular interaction studies with SphK1. The binding energy (DG) of three screened compounds namely ZINC06823429 (–11.36 kcal/mol), ZINC95421501 (–11.29 kcal/mol), and ZINC95421070 (–11.26 kcal/mol) exhibited stronger than standard drug PF-543 (–9.9 kcal/mol). Finally, it was observed that the ZINC06823429 binds tightly to catalytic site of SphK1 and remain stable during MD simulations. This study provides a significant understanding of SphK1 inhibitors that can be used in the development of potential therapeutics against breast cancer.

Invited Speaker III

Duration: 09:00-09:20, May 23, 2021 (Sunday)
Meeting ID:

Assoc. Prof. Sansanee Auephanwiriyakul
Chiang Mai University, Thailand

Sansanee Auephanwiriyakul (S'98–M'01) received the Ph.D. degree in computer engineering and computer science, both from the University of Missouri, Columbia, in 2000, respectively. After receiving her Ph.D. degree, she worked as a post-doctoral fellow at the Computational Intelligence Laboratory, University of Missouri-Columbia. She is currently an Associate Professor in the Department of Computer Engineering and an associate director of the Biomedical Engineering Institute, Chiang Mai University, Thailand. Dr. Auephanwiriyakul is a senior member of the IEEE. She is an Associate Editor of the IEEE Transactions on Fuzzy System, the IEEE Transactions on Neural Networks and Learning Systems, ECTI Transactions on Computer and Information Technology. She was an Editorial Board of several prominent journals. She was a general chair of the IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2016). She was a Technical Program Chair, Organizing Committee in several major conferences including the IEEE International, Conference Fuzzy Systems. She is a member of several important IEEE CIS technical committees.

Speech Title: Fuzzy Pattern Recognition in Data Analysis

Abstract: Data Analysis is a process to analyze data in terms of representing, describing, evaluating, interpreting the data using statistical methods. Data can come in the form of statistical representation or a vector of numbers in which numeric pattern recognition algorithms can deal with this type of data set. Another type of data can be in the form of syntactic data. For this type of data set, there is another research branch in pattern recognition called syntactic pattern recognition that is able to analyze it. Each sample in syntactic data set is normally represented as a string. The strings in the same data set can have different lengths. Also, the string does not have any mathematical meaning that we can calculate as if they are vectors of numbers. One of the popular theories used in data analysis is Fuzzy set theory, an extension of the classical set introduced by Lotfi Zadeh in 1965. Since then, there are many theories and applications developed based on Fuzzy set theory. In this talk, there are three parts on the utilization of the Fuzzy pattern recognition in data analysis. First, we will show how to develop a fuzzy algorithm in a decision making when the data are a collection of fuzzy vectors (a vector of fuzzy numbers). Another is how to incorporate the Fuzzy set theory into a set of feature generation in the classification problem. The last part of the talk is how to incorporate the Fuzzy set theory into string grammar pattern recognition. All algorithms in this talk are developed at Computational Intelligence Research Laboratory, Chiang Mai University. In each part of the talk, we will show applications of these algorithms in several real-world problems, e.g., sign language translation system, face recognition, health applications and person identification.

Invited Speaker IV

Duration: 09:20-09:40, May 23, 2021 (Sunday)
Meeting ID:

Assoc. Prof. Xiuying Wang
The University of Sydney, Australia

Assoc. Prof Xiuying Wang received her PhD in Computer Science from the University of Sydney in 2006. She is currently the Associate Director of Multimedia Lab, School of Computer Science, The University of Sydney. Her research focuses on quantitative data analysis and fusion as relates to biomedical imaging data computing. She broadly researches in areas such as image processing and radiomic analysis, clustering and segmentation, image registration for biomedical and multimedia applications, saliency detection, identification, and visual analytics of medical and health data.

Speech Title: AI-Enabled Computing and Fusion for understanding Heterogeneous Data

Abstract: The abundance of data generated by revolutionary technologies at a high velocity is central to modern industry, education, health service and social life. 'Big data' are a new form of capital in current enterprises because the insights into their inherent values will support more efficient and effective decision-making. Integrative fusion and analysis of big data will pave the new paths to discover the new values and knowledge in a broader spectrum. This talk will introduce innovative methods addressing the critical AI questions raised by high dimensionality and multi-view fusion. In particular, it will focus on AI-enabled computing and fusion approaches to harness feature engineering and data analytics to predict treatment prognosis for personalized precision medicine.

Duration: 09:40-10:00, May 23, 2021 (Sunday)

Meeting ID:

Prof. Jiyun Li

Donghua University, China

Dr. Jiyun Li is a full professor in School of Computer Science and Technology at Donghua University and research director of Shanghai Urban perspective data hub. Her research interests focus on health data engineering and intelligent medical modelling.

Speech Title: Attention Based Cooperative Diagnosis of Breast Cancer with Two-View Mammograms

Abstract: Mammography is the most commonly used breast cancer screening method. Most current one view based models are suffered from high false positive rate. In this talk, we propose an attention based cooperative diagnosis model of breast cancer with two-view mammograms (cranial caudal and mediolateral oblique) by referring to the radiologists' way of reading images. First, two-view images were registered to a standard template separately. Then the features of two-view images were fused by the attention mechanism for the classification of lesions in the images. Finally, the lesions on two-view images were identified and matched, so as to lower the false positive rate.