



# **2016 IEEE International Conference on Bioinformatics and Biomedicine**

**Dec 15-18, 2016, Shenzhen, China**

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# IEEE BIBM 2016

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# Dining Guide

用餐时间 Time for breakfast/lunch/dinner	用餐地点 (Location)
Breakfast Dec.15-18	贵宾楼：2楼凤凰阁、自助餐厅 2 <sup>nd</sup> floor FENGHUANGHALL and CAFETERIA
Lunch Dec.15-18	贵宾楼：2楼凤凰阁、1楼梧桐阁 2 <sup>nd</sup> floor FENGHUANG HALL and 1 <sup>st</sup> floor WUTONG HALL
Banquet Dec.16	二楼麒麟厅 (2 <sup>nd</sup> floor KYLIN HALL)
Dinner Dec.15-18	贵宾楼：2楼凤凰阁、1楼梧桐阁 2 <sup>nd</sup> floor FENGHUANG HALL and 1 <sup>st</sup> floor WUTONG HALL

## Transportation manual

报到地点：深圳麒麟山庄

**Registration Site:** Kylin Villa Hotel

会场：深圳麒麟山庄

**Conference Venue:** Kylin Villa Hotel

住宿：深圳麒麟山庄 & 维也纳酒店（深圳大学城店）

**Hotel:** Kylin Villa Hotel & Vienna Hotel Shenzhen College City

Please **print this NOTE** and show the note to the taxi driver if you take a taxi at Shenzhen. The driver will take you to the destination:

- **Please take me to the Kylin Villa Garden Hotel Luxury at 4599 Qinyuan Rd, Shenzhen, China.**  
(Chinese: 请送我到深圳市南山区沁园路 4599 号深圳麒麟山庄)
- **Please take me to the Shenzhen Bao'an International Airport**  
(Chinese: 请送我到深圳宝安国际机场)

国内的参会者，可以参考以下交通信息，也可以使用高德等导航软件获取帮助。

起点 \ 终点	深圳麒麟山庄	维也纳酒店 (深圳大学城店)
深圳宝安国际机场	机场 8 号线 (机场新航站楼→科苑立交南桥) →49 路公交车 (清华信息港→麒麟山庄接待处)	地铁 11 号线 (机场站→前海湾) →地铁 5 号线 (前海湾站→大学城站 C 口)
	打车预计需要 72 元	打车预计需要 64 元
深圳西站	M492 路 (大新村站上→麒麟山庄接待处)	36 路 (南头火车西站→桃源康复中心)
	打车预计需要 43 元	打车预计需要 36 元
深圳北站	地铁 5 号线 (深圳北站→大学城站 C 口) →49 路公交车 (丽山路南站→麒麟山庄接待处)	5 号线 (深圳北站→大学城站 C 口)
	打车预计需要 35 元	打车预计需要 32 元
深圳火车站	地铁 1 号线 (罗湖站→白石洲) →66 路公交车 (白石洲 3→麒麟山庄接待处)	387 路公交车 (火车站→黄贝岭地铁站 1) →地铁 5 号线 (黄贝岭站→大学城站 C 口)
	打车预计需要 79 元	打车预计需要 66 元
深圳东站	地铁 5 号线 (布吉站→大学城站) →49 路公交车 (丽山路南→麒麟山庄接待处)	地铁 5 号线 (布吉站→大学城站 C 口)
	打车预计需要 72 元	打车预计需要 64 元

起点 \ 终点	深圳宝安国际机场	深圳西站	深圳北站	深圳火车站	深圳东站
深圳麒麟山庄	B797 路公交车 (麒麟山庄接待处→新围村) →地铁 5 号线 (西丽站→前海湾) →地铁 11 号线 (前海湾→机场站)	66 路公交车 (麒麟山庄接待处→白石洲 3) →地铁 1 号线 (白石洲→大新村站) →b682 路公交车 (前海花园→南头火车西站)	49 路公交车 (麒麟山庄接待处→红花岭站) →地铁 5 号线 (大学城站→深圳北站)	66 路公交车 (麒麟山庄接待站→白石洲 3) →地铁 1 号线 (白石洲→罗湖站)	49 路公交车 (麒麟山庄接待站→红花岭站) →地铁 5 号线 (大学城站→布吉站)
	打车预计需要 72 元	打车预计需要 43 元	打车预计需要 35 元	打车预计需要 79 元	打车预计需要 72 元
维也纳酒店 (深圳大学城店)	地铁 5 号线 (大学城站→前海湾站) →地铁 11 号线 (前海湾→机场站)	36 路 (哈工大园区→南头火车西站)	5 号线 (大学城站→深圳北站)	43 路公交车 (哈工大园区→白石洲 3 站) →地铁 1 号线 (白石洲→罗湖站 E2 口)	地铁 5 号线 (大学城站→布吉站 B 口)
	打车预计需要 64 元	打车预计需要 36 元	打车预计需要 32 元	打车预计需要 66 元	打车预计需要 64 元

# Emergency Contact

Dr. Peng Ren (任鹏): +86 18634505064

Dr. Jiajie Peng (彭佳杰): +86 18745137124

Dr. Hansheng Xue(薛寒生): +86 13751036105

Dr. Renjie Tan (谭仁杰): +86 18745048341

Dr. Yang Hu (胡杨): +86 15045666752

Prof. Qinghua Jiang (蒋庆华): +86 13836019402

Prof. Xiaohua Hu (胡小华): +86 15071457605

Prof. Yadong Wang (王亚东): +86 18645118639

## IEEE BIBM 2016 Program Schedule

### Program

- [December 15, 2016](#)
- [December 16, 2016](#)
- [December 17, 2016](#)
- [December 18, 2016](#)

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Keynote Lecture: 60 minutes ((about 45 minutes for talk and 15 minutes for Q and A)

Invited Talk: 40 minutes (about 30 minutes for talk and 10 minutes for Q and A)

Tutorial: 115 minutes (about 100 minutes for talk and 15 minutes for Q and A)

Main Conference Regular Paper: 20 minutes (about 15 minutes for talk and 5 minutes for Q and A)

Main Conference Short Paper: 15 minutes (about 12 minutes for talk and 3 minutes for Q and A)

<b>Wednesday, December 14</b>	
2:00– 8:00 pm	<b>Registration</b>

<b>Thursday, December 15 (Workshops)</b>			
7:20am – 6:30pm	<b>Registration</b> <i>Hotel lobby</i>		
10:30-10:50am and 3:30-3:50pm	<b>Coffee Break</b>		
12:00-1:30pm	<b>Lunch</b> ( <i>provided by conference</i> )		
1:30-6:00pm	<b>Poster Session</b> ( <i>Set Up</i> )		
8:00-12:00pm	<b>Workshops</b>	<b>Session Chair</b>	<b>Location</b>
	<b>The 3rd Workshop on High Performance Computing on Bioinformatics (HPCB 2016)</b>	<b>Che-Lun Hung, Huiru Zheng, Chuan Yi Tang, Yuan Lin, Chang Gung</b>	二楼紫云阁 1 ZIYUN Hall 1 (2 <sup>nd</sup> floor)
	<b>2016 International Workshop on Biomedical and Health Informatics (BHI 2016)</b>	<b>Illhoi Yoo,</b>	一楼木棉厅 MUMIAN Hall(1 <sup>st</sup> floor)
	<b>Molecular networks and network pharmacology</b>	<b>Xingming Zhao</b>	二楼紫云阁 2 ZIYUN Hall 2 (2 <sup>nd</sup> floor)
	<b>The First International Workshop on Semantics-Powered Data Analytics (SEPDA 2016)</b>	<b>Zhe He, Cui Tao, Michel Dumontier, Jiang Bian,</b>	一楼杜鹃厅 DUJUAN Hall (1 <sup>st</sup> floor)
	<b>2016 Workshop on Health Informatics and Data Science (HI-DS 2016)</b>	<b>Xiong Liu, Rong Liu, Chunhui Hou</b>	二楼紫荆厅 ZIJING Hall (2 <sup>nd</sup> floor)
	<b>2016 International Workshop on Biomolecular Networks and Human Diseases</b>	<b>Min Li, Haiying Wang, Jianxin Wang, FangXiang Wu</b>	二楼彩云阁 CAIYUN Hall (2 <sup>nd</sup> Floor)
	<b>2016 Workshop on Accelerator-Enabled Algorithms and Applications in Bioinformatics (WACEBI 2016)</b> <b>Data mining in translational biomedical informatics</b>	<b>Yongchao Liu Dr. Qian Zhu, <u>Shimei Pan</u></b>	二楼龙腾阁 LONGTENG Hall (2 <sup>nd</sup> Floor)
1:30-6:00pm	<b>Workshops</b>	<b>Session Chair</b>	<b>Location</b>
	<b>The 7th Workshop on High Performance Bioinformatics and Biomedicine (HiBB)</b>	<b>Prof. Mario Cannataro</b>	二楼紫云阁 1 ZIYUN Hall 1 (2 <sup>nd</sup> floor)
	<b>International Workshop on Biological Network Analysis and Integrative Graph-Based Approaches (IWBNA 2016)</b>	<b>Mingon Kang, Dongchul Kim, Young-Rae Cho</b>	二楼彩云阁 CAIYUN Hall (2 <sup>nd</sup> Floor)
	<b>Data mining from genomic variants and its application to genome-wide analysis 2016</b>	<b>Taesung Park</b>	一楼杜鹃厅 DUJUAN Hall(1 <sup>st</sup> floor)

	<b>2016 International Workshop on Biomedical and Health Informatics (BHI 2016)</b>	<b>Illhoi Yoo,</b>	一楼木棉厅 MUMIAN Hall (1 <sup>st</sup> floor)
	<b>Molecular networks and network pharmacology</b>	<b>Xingming Zhao</b>	二楼紫云阁 2 ZIYUN Hall 2 (2 <sup>nd</sup> floor)
	<b>2016 Workshop on Health Informatics and Data Science (HI-DS 2016)</b>	<b>Xiong Liu, Rong Liu, Chunhui Hou</b>	二楼紫荆厅 ZIJING Hall
	<b>Semantic Data Analytics and Machine Learning in Bioinformatics and Medical Informatics (SMBM2016)</b>	<b>Dr. Haiying Wang</b>	二楼龙腾阁 LONGTENG Hall (2 <sup>nd</sup> Floor)
6:20-8:00pm	<b>Dinner (provided by conference)</b>		



Friday, December 16			
8:00am-6:00pm	<b>Registration</b>		
8:45-9:00am	<b>Welcome and Opening Session</b> Chairs: Yadong Wang, Kevin Burrage, Tianhai Tian, Shinichi Morishita, Yunlong Liu, Xiaohua Hu Kylin Hall(2 <sup>nd</sup> floor) 二楼麒麟厅		
9:00-10:00am	<b>Keynote Lecture 1 (Chair: Xiaohua Hu)</b> <b>“Trajectory Analysis -- Linking Genomic and Proteomic Data with Disease Progression”</b> Prof. Aidong Zhang Kylin Hall(2 <sup>nd</sup> Floor) 二楼麒麟厅		
10:00-11am	<b>Keynote Lecture 2 (Chair: Xiaohua Hu)</b> <b>“Whole genome sequencing of disease animal models”</b> Prof. Yixue Li Kylin Hall(2 <sup>nd</sup> floor) 二楼麒麟厅		
11:00-11:20am	<b>Coffee Break</b>		
10:20-12:30pm	<b>Sessions</b>	<b>Session Chair</b>	<b>Location</b>
	<b>Session 1: Next-Gen Sequencing (I)</b>	<b>Feng Luo</b>	一楼木棉厅 MUMIAN Hall (1 <sup>st</sup> floor)
	<b>Session 2: Networks/Pathway Analysis (I)</b>	<b>Taesung Park</b>	二楼紫荆厅 ZIJING Hall (2 <sup>nd</sup> floor)
	<b>Session 3: Biomedical Intelligence (I)</b>	<b>Qian Zhu</b>	二楼龙腾阁 LONGTENG Hall (2 <sup>nd</sup> Floor)
	<b>Session 4: Data-Mining and Visualization (I)</b>	<b>Jianxin Wang</b>	二楼紫云阁 1 ZIYUN Hall 1 (2 <sup>nd</sup> floor)
10:20-7pm	<b>Poster Session Setup and Display</b>		
12:30-2:00pm	<b>Lunch provided by conference</b>		
2:00-3:40pm	<b>Sessions</b>	<b>Session Chair</b>	<b>Location</b>
(including Invited talks)	<b>Session 5: Next-Gen Sequencing (II)</b>	<b>Kai Tan</b>	一楼木棉厅 MUMIAN Hall (1 <sup>st</sup> floor)
	<b>Session 6: Networks/Pathway Analysis (II)</b>	<b>Sun Kim</b>	二楼紫荆厅 ZIJING Hall (2 <sup>nd</sup> floor)
	<b>Session7: Biomedical Intelligence (II)</b>	<b>Gregory Chirikjian</b>	二楼龙腾阁 LONGTENG Hall (2 <sup>nd</sup> Floor)
	<b>Session 8: Data-Mining and Visualization (II)</b>	<b>Juan Huan</b>	二楼紫云阁 1 ZIYUN Hall 1 (2 <sup>nd</sup> floor)

	<b>Biological ontologies and knowledge bases</b>	<b>Jiajie Peng</b>	二楼紫云阁 2 ZIYUN Hall 2 (2 <sup>nd</sup> floor)
3:40-4:00pm	<b>Coffee Break</b> <i>Meeting Room Foyer</i>		
4:00-6:00pm	<b>Sessions</b>	<b>Session Chair</b>	<b>Location</b>
	<b>Session 9: Next-Gen Sequencing</b>	<b>De-Shuang Huang</b>	一楼木棉厅 MUMIAN Hall (1 <sup>st</sup> floor)
	<b>Session 10: Networks/Pathway Analysis (III)</b>	<b>Fang-Xiang Wu</b>	二楼紫荆厅 ZIJING Hall (2 <sup>nd</sup> floor)
	<b>Session 11: Signalling/Image Analysis (I)</b>	<b>Xing-Ming Zhao</b>	二楼龙腾阁 LONGTENG Hall (2 <sup>nd</sup> Floor)
	<b>Session 12: Text Mining and Oncology (I)</b>	<b>Hongfei Lin</b>	二楼紫云阁 1 ZIYUN Hall 1 (2 <sup>nd</sup> floor)
	<b>Biological ontologies and knowledge bases</b>	<b>Jiajie Peng</b>	二楼紫云阁 2 ZIYUN Hall 2 (2 <sup>nd</sup> floor)
7:00-9:00pm	<b>Banquet (Ticket required)</b>		
	<ol style="list-style-type: none"> <li>1. Best Paper Award ( Chairs:PC Chairs and Conference Chair)</li> <li>2. Best Student Paper Award (Chairs: PC Chairs and Conference Chair )</li> <li>3. Introduction of BIBM 2017 Host City (Chairs: Xiaohua Tony Hu, Dr. Chi-Ren Shyu)</li> </ol>		

<b>Saturday, December 17</b>			
8:00am-6:00pm	<b>Registration</b>		
9:00-10:00am	<b>Keynote Lecture 3</b> (Chair: Tianhai Tian) <b>Information and Decision-Making in Dynamic Cell Signaling (Tianhai, Tian)</b> Prof. David Rand Kylin Hall(2 <sup>nd</sup> floor)二楼麒麟厅		
10:00-11am	<b>Keynote Lecture 4</b> (Chair: De-Shuang Huang) <b>“Computational Psychophysiology Based Research Methodology for Mental Health”</b> Prof. Bin Hu Kylin Hall(2 <sup>nd</sup> floor)二楼麒麟厅		
11:00-11:20am	<b>Coffee Break</b>		
10:20am-12:30pm	<b>Sessions</b>	<b>Session Chair</b>	<b>Location</b>
	<b>Session 13: Transcriptomics (I)</b>	<b>Yufeng Wang</b>	一楼木棉厅 MUMIAN Hall (1 <sup>st</sup> floor)
	<b>Session 14: Genome-Phenome Analysis</b>	<b>Jean Gao</b>	二楼紫云阁 2 ZIYUN Hall 2 (2 <sup>nd</sup> floor)
	<b>Session15: Modelling and Data Integration (I)</b>	<b>Sarah ElShal</b>	二楼龙腾阁 LONGTENG Hall (2 <sup>nd</sup> Floor)
	<b>Session16: Signalling/Image Analysis (II)</b>	<b>Gianfranco Politano</b>	二楼紫云阁 1 ZIYUN Hall 1 (2 <sup>nd</sup> floor)
12:30-2:00pm	<b>Lunch provided by conference</b>		
	<b>Poster Session</b>		
2:00-3:40pm	<b>Sessions</b>	<b>Session Chair</b>	<b>Location</b>
	<b>Session 17 Phylogeny</b>	<b>Habtom Resson</b>	一楼木棉厅 MUMIAN Hall (1 <sup>st</sup> floor)
	<b>Session 18 Networks/Pathway Analysis (IV)</b>	<b>Hector Zenil</b>	二楼紫云阁 2 ZIYUN Hall 2 (2 <sup>nd</sup> floor)
	<b>Session 19 Signalling/Image Analysis (III)</b>	<b>Chi-Ren Shyu</b>	二楼龙腾阁 LONGTENG Hall (2 <sup>nd</sup> Floor)
	<b>Session 20 Data-Mining and Visualization (III)</b>	<b>Sanguthevar Rajasekaran</b>	二楼紫云阁 1 ZIYUN Hall 1 (2 <sup>nd</sup> floor)
	<b>Computational Approach to Study the Molecular Cell morphology and DNA /RNA, Protein Structure</b>	<b>Prof.Mahua Bhattacharya</b>	二楼彩云阁 CAIYUN Hall (2 <sup>nd</sup> Floor)

	<b>The 7th Integrative Data Analysis in Systems Biology (IDASB 2016)</b> <b>International Workshop on Biological Network Driven Analysis</b>	<b>Dr. Huiru (Jane) Zheng, Prof. Zhongming Zhao, Dr. Rui Jiang Fiona Browne</b>	一楼杜鹃厅 DUJUAN Hall (1 <sup>st</sup> floor)
3:40-4:00pm	<b>Coffee Break</b>		
4:00-6:00pm	<b>Sessions</b>	<b>Session Chair</b>	<b>Location</b>
	<b>Session 21 Protein/RNA Structure (I)</b>	<b>John Rogers</b>	一楼木棉厅 MUMIAN Hall (1 <sup>st</sup> floor)
	<b>Session 22 Signaling/Image Analysis (IV)</b>	<b>Stefan Jaeger</b>	二楼紫云阁 2 ZIYUN Hall 2 (2 <sup>nd</sup> floor)
	<b>Session 23 Modelling and Data Integration (II)</b>	<b>Antonios Lalas</b>	二楼龙腾阁 LONGTENG Hall (2 <sup>nd</sup> Floor)
	<b>Session 24 Healthcare Informatics</b>	<b>Jake Chen</b>	二楼紫云阁 1 ZIYUN Hall 1 (2 <sup>nd</sup> floor)
	<b>Computational Approach to Study the Molecular Cell morphology and DNA /RNA, Protein Structure</b>	<b>Prof. Mahua Bhattacharya</b>	二楼彩云阁 CAIYUN Hall (2 <sup>nd</sup> Floor)
	<b>The 7th Integrative Data Analysis in Systems Biology (IDASB 2016)</b>	<b>Dr. Huiru (Jane) Zheng, Prof. Zhongming Zhao, Dr. Rui Jiang</b>	一楼杜鹃厅 DUJUAN Hall (1 <sup>st</sup> floor)
6:20-8:00pm	<b>Dinner ( provided by conference )</b>		

<b>Sunday, December 18</b>			
8:00-10:00am	<b>Registration</b>		
9:00-10:40am	<b>Sessions</b>	<b>Session Chair</b>	<b>Location</b>
	<b>Session 25 Transcriptomics (II)</b>	<b>Min Li</b>	一楼木棉厅 MUMIAN Hall (1 <sup>st</sup> floor)
	<b>Session 26 Proteomics/PTM/Metabolomics</b>	<b>Shuai Cheng Li</b>	二楼紫云阁 2 ZIYUN Hall 2 (2 <sup>nd</sup> floor)
	<b>Session 27 Biomedical Intelligence (III)</b>	<b>Moumita Bhattacharya</b>	二楼龙腾阁 LONGTENG Hall (2 <sup>nd</sup> Floor)
	<b>Session 28 Modelling and Data Integration (III)</b>	<b>Jingshan Huang</b>	二楼紫云阁 1 ZIYUN Hall 1 (2 <sup>nd</sup> floor)
8:00-10:30am	<b>The 2016 Computational Structural Bioinformatics Workshop</b>	<b>Jing He</b>	紫薇厅 Ziwei Hall (2 <sup>nd</sup> floor)
	<b>Machine Learning and Big Data Research for Disease Classification and Phenotyping</b>	<b>Jinbo Bi</b>	一楼杜鹃厅 DUJUAN Hall (1 <sup>st</sup> floor)
	<b>Formal Methods for Biological and Biomedical Systems</b>	<b>Edmund M. Clarke, Natasa Miskov-Zivanov, Qinsi Wang</b>	二楼彩云阁 CAIYUN Hall (2 <sup>nd</sup> Floor)
10:00-12:20am	<b>Poster Display</b>		
10:40-11:00am	<b>Coffee Break</b>		
11:00am-12:30pm	<b>Sessions</b>	<b>Session Chair</b>	<b>Location</b>
	<b>Session 29 Protein/RNA Structure (II)</b>	<b>Jing He</b>	一楼木棉厅 MUMIAN Hall (1 <sup>st</sup> floor)
	<b>Session 30 Signalling/Image Analysis (V)</b>	<b>Yuanyuan Sun</b>	二楼紫云阁 2 ZIYUN Hall 2 (2 <sup>nd</sup> floor)
	<b>Session 31 Modelling and Data Integration (IV)</b>	<b>Sungmin Rhee</b>	二楼龙腾阁 LONGTENG Hall (2 <sup>nd</sup> Floor)
	<b>Session 32 High Performance Computing</b>	<b>Mira Park</b>	二楼紫云阁 1 ZIYUN Hall 1 (2 <sup>nd</sup> floor)
	<b>Machine Learning and Big Data Research for Disease Classification and Phenotyping</b>	<b>Jinbo Bi</b>	一楼杜鹃厅 DUJUAN Hall (1 <sup>st</sup> floor)
	<b>Formal Methods for Biological and Biomedical Systems</b>	<b>Edmund M. Clarke, Natasa Miskov-Zivanov, Qinsi Wang</b>	二楼彩云阁 CAIYUN Hall (2 <sup>nd</sup> Floor)

# Conference Paper Presentations

Session 1 Next-Gen Sequencing (I)	
Regular	B320 "CAMIL: Clustering and Assembly with Multiple Instance Learning for Phenotype Prediction" Nathan LaPierre, Mohammad Arifur Rahman, and Huzefa Rangwala
Regular	B418 "A de novo Genome Assembler based on MapReduce and Bi-directed de Bruijn Graph" Yuehua Zhang, pengfei xuan, Yunsheng Wang, Pradip Srimani, and Feng Luo
Short	B213 "Hybrid Error Correction approach and DeNovo Assembly for MinIon Sequencing Long Reads" mehdi kchouk and mourad Elloumi
Short	B341 "Mining structural variations of Heduo12 using paired-end reads" Huiqiang Jia, Haichao Wei, Daming Zhu, Jingjing Ma, Ruizhi Wang, and Xianzhong Feng

Session 2 Networks/Pathway Analysis (I)	
Regular	B203 "Semi-supervised graph cut algorithm for drug repositioning by integrating drug, disease and genomic associations" Guangsheng Wu, Juan Liu, and Caihua Wang
Regular	B226 "A computationally inferred regulatory heart aging model including post-transcriptional regulations" Gianfranco Politano, Federica Logrand, Mara Brancaccio, and Stefano Di Carlo
Short	B540 "A Framework for Robust Differential Network Modular Structure Discovery from RNA-seq Data" Tianle Ma and Aidong Zhang
Short	B502 "Inference and Differential Analysis of Extended Core Networks: a way to study Anti-Sense Regulation" Marc Legeay, Béatrice Duval, and Jean-Pierre Renou

Session 3 Biomedical Intelligence (I)	
Regular	B269 "Drug side effect prediction through linear neighborhoods and multiple data source integration" Wen Zhang, Yanlin Chen, Shikui Tu, Feng Liu, and Qianlong Qu
Short	B291 "Risk feature assessment of readmission for diabetes" Qian Zhu, Anirudh Akkati, and Pornpoh Hongwattanakul
Regular	B328 "A Conditional Probabilistic Model for Joint Analysis of Symptoms, Diagnoses, and Herbs in Traditional Chinese Medicine Patient Records" Sheng Wang, Edward Huang, Runshun Zhang, Xiaoping Zhang, Baoyan Liu, Xuezhong Zhou, and ChengXiang Zhai

Short	B315 "Traditional Chinese Medicine Formula Evaluation Using Multi-instance Multi-label Framework" Yongchun Li, Hong Li, Qian Wang, Chongjun Wang, and Xinsheng Fan
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Session 4 Data-Mining and Visualization (I)	
Regular	B387 "Construction of the spatial and temporal active protein interaction network for identifying protein complexes" Xiangmao Meng, Min Li, Jianxin Wang, Fang-Xiang Wu, and Yi Pan
Regular	B382 "Latent factor model with heterogeneous similarity regularization for predicting gene-disease associations" Xiangxiang Zeng, ningxiang ding, and Quan Zou
Short	B236 "A Realistic and Reliable 3D Pronunciation Visualization Instruction System for Computer-Assisted Language Learning" Jun Yu and Zeng-Fu Wang
Short	B390 "A Novel Phylogeny-Based Pattern Selection Algorithm and Its Application to Microbiomic Data" Nancy Huang and Yen-Jen Oyang

Session 5 Next-Gen Sequencing (II)	
Invited Talk I	<b>Computational tools for studying gene regulation in the 3-dimensional genome</b> <b>Dr. Kai Tan</b>
Regular	B461 "Accurate Annotation of Metagenomic data without species-level references" Haobin Yao, T.W. Lam, H.F. Ting, S.M. Yiu, Yadong Wang, and Bo Liu
Short	B265 "Eliminating heterozygosity from reads through coverage normalization" ZHAO Zicheng, Ng Yen Kaow, Xiaodong Fang, and Shuai Cheng Li
Short	B307 "Multi-norm Constrained Optimization Methods for Calling Copy Number Variants Calling in Single Cell Sequencing Data" Changsheng Zhang, Hongmin Cai, Jingying Huang, and Bo Xu

Session 6 Networks/Pathway Analysis (II)	
Invited Talk II	<b>Networks and Models for the Integrated Analysis of Multi Omics data</b> <b>Dr. Sun Kim (Chair: Tianhai Tian)</b>
Regular	B427 "Inference of genetic regulatory network for stem cell using single cells expression data" Jiangyong Wei, Xiaohua Hu, and Tianhai Tian
Short	B522 "DeepSplice: Deep Classification of Novel Splice Junctions Revealed by RNA-seq" Yi Zhang, Xinan Liu, James MacLeod, and Jinze Liu

Short	B452 "DASE: condition-specific Differential Alternative Splicing variants Estimation method without reference genome sequence, and its application to non-model organisms" Kouki Yonezawa, Tsukasa Mori, Shu-ichi Shigeno, and Atsushi Ogura
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Session 7 Biomedical Intelligence (II)	
Invited III	<b>Clinical application of precision medicine: Zhongshan Hospital Strategy</b> <b>Dr. Xiangdong Wang (Chair: Xiaohua Hu)</b>
Regular	B496 "A Time-series Similarity Method for QRS Morphology Variation Analysis" Liping Wang, Junjie Yao, Linpeng Jin, Jiawei Zhang, and Xia Liu
Regular	N204 " <i>Assiting humans to achive optimal sleep by changing ambient temperature</i> " "VIVEK GUPTA, SIDDHANT MITTAL, Sandip Bhaumk, and Raj Roy
Short	B354 "Naive-Bayes Ensemble: A New Approach to Classify Unlabeled Multi-Class Asthma Subjects" Seo-Jin Bang and Wei Wu

Session 8 Data-Mining and Visualization (II)	
Invited IV	<b>High Performance Computational Biology and Drug Design on TianHe Supercomputers</b> <b>Shaoliang Peng (Chair: Xingpeng Jiang)</b>
Regular	B406 "The Feature Selection Algorithm Based on Feature Overlapping and Group Overlapping" Xiaohui Lin, Huanhuan Song, Meng Fan, Weijie Ren, Lishuang Li, and Weihong Yao
Regular	B417 "DeepEnhancer: Predicting Enhancers by Convolutional Neural Networks" Xu Min, Ning Chen, Ting Chen, and Rui Jiang
Short	B334 "Sparse Canonical Correlation Analysis via Truncated l1-norm with Application to Brain Imaging Genetics" Lei Du, Tuo Zhang, Kefei Liu, Xiaohui Yao, Jingwen Yan, Shannon L. Risacher, Lei Guo, Andrew J. Saykin, and Li Shen

Session 9 Next-Gen Sequencing	
Regular	B472 "Concod: Accurate Consensus-based Approach of Calling Deletions from High-throughput Sequencing Data" Xiaodong Zhang, Chong Chu, Yao Zhang, Yufeng Wu, and Gao Jingyang
Regular	B485 "Learning Regulatory Motifs by Direct Optimization of Fisher Exact Test Score" Lin Zhu, Ning Li, and De-Shuang Huang
Short	B347 "Estimating Isoform Abundance by Particle Swarm Optimization" Jin Zhao and Haodi Feng
Short	B415 "Characterizing the roles of long non-coding RNA in rat alcohol preference" Ao Zhou and Yunlong Liu
Short	B527 "Compressing Genome Resequencing Data via the Maximal Longest Factor" Richard Beal, Aliya Farheen, and Don Adjeroh



Short	B549 "Comparative Analysis of Transcriptome Assembly Pipeline for Diploid Wheat" Natasha Pavlovikj, Kevin Begcy, Sairam Behera, Malachy Campbell, Harkamal Walia, and Jitender Deogun
Short	B563 "ERDS-exome: a hybrid approach for copy number variant detection from whole-exome sequencing data" Qinghua Jiang

Session 10 Networks/Pathway Analysis (III)	
Regular	B366 "The MSS of complex networks with centrality based preference and its application to biomolecular networks" Lin Wu, Min Li, Jianxin Wang, and Fang-Xiang Wu
Regular	B376 "Deep Pathway Analysis Incorporating Mutation Information and Gene Expression Data" Yue Zhao, Tham Hoang, Pujan Joshi, Seung-Hyun Hong, and Dong-Guk Shin
Regular	B561 "DeeperBind: Enhancing Prediction of Sequence Specificities of DNA Binding Proteins" Hamid Reza Hassanzadeh and May D. Wang
Short	B541 "Towards Constructing "Super Gene Sets" Regulatory Networks" Michael Neylon, Zongliang Yue, Thanh Nguyen, Timothy Ratliff, and Jake Chen
Short	B548 "Achieving High k-Coverage and k-Consistency in Global Alignment of Multiple PPI Networks" Bo Song, Jianliang Gao, Wemao Ke, and Xiaohua Hu
Regular	B372 "Analysis of Rumen Microbial Community in Cattle through the Integration of Metagenomic and Network-based Approaches" Haiying Wang, Huiru Zheng, Fiona Browne, Rainer Roehle, Richard Dewhurst, Felix Engel, Matthias Hemmje, and Paul Walsh

Session 11 Signalling/Image Analysis (I)	
Regular	B247 "Automatic Schizophrenia Discrimination on fNIRS by Using PCA and SVM" Hong Song, Iordachescu Ilie Mihaita Bogdan, and Shuliang Wang
Regular	B330 "Cardiac Image Registration by Combining Point Set Matching with Surface Structure Features" Xuan Yang, Cong Tan, and Hao Yang
Regular	B434 "Analyzing epileptic network dynamics via time-variant partial directed coherence" Bowen Liu, Junwei Mao, Yejun Shi, Qinchi Lu, Peiji Liang, and Puming Zhang
Short	B237 "A Three-Stage Decision Framework for Multi- Subject Emotion Recognition Using Physiological Signals" Jing Chen, Bin Hu, Yue Wang, Yongqiang Dai, Yuan Yao, and Shengjie Zhao
Short	B231 "Nonlinear Dynamic Analysis of Alpha Resting EEG: Novel Biomarkers for Heroin Addicts" Qinglin Zhao, Bin Hu, Wenhua Lin, Zhixue Li, Quanying Liu, Hua Jiang, Zhong Xue, and Hongqian Li
Regular	B275 "A SHAPE MODEL FOR CONTOUR EXTRACTION OF DROSOPHILA EMBRYOS" Qi Li and Yongyi Gong

Session 12 Text Mining and Oncology (I)	
Short	B273 "Biomedical Event Extraction via Long Short Term Memory Networks along Dynamic Extended Tree" Lishuang Li, Jieqiong Zheng, Jia Wan, and Degen Huang
Short	B538 "Improving Clinical Case Search Using Semantic Based Query Reformulations" Mohammad Alsulmi and Benjamin Carterette
Short	B474 "Measuring Phenotype Semantic Similarity using Human Phenotype Ontology" Jiajie Peng, Hansheng Xue, Yukai Shao, Xuequn Shang, Yadong Wang, and Jin Chen
Short	B377 "Analysis of Temporal Constraints in Qualitative Eligibility Criteria of Cancer Clinical Studies" Zhe He, Zhiwei Chen, and Jiang Bian
Short	B369 "TOPIC MODELLING OF BIOMEDICAL TEXT: FROM WORDS AND TOPICS TO DISEASE AND GENE LINKS" Sarah ElShal, Mithila Mathad, Jaak Simm, Jesse Davis, and Yves Moreau
Short	B358 "BAMOKNN: A Novel Computational method for Predicting the Apoptosis Protein Locations" Xiangtao Li, Shijing Ma, and Yunhe Wang
Short	B338 "ML-CNN: a novel deep learning based disease named entity recognition architecture" zhehuan zhao, zhihao Yang, luo Ling, yin Zhang, yuxia Li, Hongfei Lin, and Jian Wang
Short	B357 "Biomedical Event Extraction Based on Distributed Representation and Deep Learning" Anran Wang, Jian Wang, Hongfei Lin, Jianhai Zhang, Zhihao Yang, and Kan Xu
Short	B316 "A Neural Joint Model for Extracting Bacteria and Their Locations" Fei Li, Meishan Zhang, Guohong Fu, Tao Qian, and Donghong Ji

Session 13 Transcriptomics (I)	
Regular	B473 "Just-in-time expression of influential genes in the cellular networks of the malaria parasite Plasmodium falciparum during the red blood cycle" Xinran Yu, Hao Zhang, Timothy Lilburn, Hong Cai, Jianying Gu, Turgay Korkmaz, and Yufeng Wang
Regular	B479 "Top-k Utility-based Gene Regulation Sequential Pattern Discovery" Morteza Zihayat, Heidar Davoudi, and Aijun An
Short	B499 "A New System for Human MicroRNA Functional Evaluation and Network" Jiachun Han, Jiang Shu, and Juan Cui

Session 14 Genome-Phenome Analysis	
Regular	B217 "Mathematical and computational analysis of CRISPR Cas9 sgRNA off-target homologies" Michael Zhou, Daisy Li, Xiaoli Huan, Joseph Manthey, Ekaterina Lioutikova, and Hong Zhou
Regular	B362 "Robust Inductive Matrix Completion Strategy to Explore Associations between LincRNAs and Human Disease Phenotypes" Ashis Kumer Biswas, Dongchul Kim, Mingon Kang, and Jean Gao
Regular	B467 "Imaging-Genetic Data Mapping for Clinical Outcome Prediction via Supervised Conditional Gaussian Graphical Model" Xinliang Zhu, Jiawen Yao, Guanghua Xiao, Yang Xie, Jaime Rodriguez Canales, Edwin Parra, Carmen Behrens, Ignacio I. Wistuba, and Junzhou Huang
Short	B500 "Building Bayesian Networks from GWAS Statistics Based on Independence of Causal Influence" Lu Zhang, Qiuping Pan, Xintao Wu, and Xinghua Shi

Session 15 Modelling and Data Integration (I)	
Regular	B234 "Learning with Positive and Unknown Features" Chao Lan, Sai Nivedita Chandrasekaran, and Jun Huan
Short	B300 "Online Multi-Instance Multi-Label Learning for Protein Function Prediction" Feng Wu, Qiong Liu, Tianyong Hao, Xiaojun Chen, and Qingyao Wu
Regular	B392 "Copula particle filter algorithm for inferring parameters of regulatory network models with noisy observation data" Zhimin Deng and Tianhai Tian
Short	B309 "Maximizing Systolic Array Efficiency to Accelerate the PairHMM Forward Algorithm" Johan Peltenburg, Shanshan Ren, and Zaid Al-Ars

Session 16 Signalling/Image Analysis (II)	
Regular	B285 "Fluorescence and Bright-field 3D Image Fusion Based on Sinogram Unification for Optical Projection Tomography" xiaoqin Tang, Merel Hoff, Jerry Hoogenboom, Yuanhao Guo, Fuyu Cai, and Fons Verbeek
Regular	B465 "A Modified Rough-Fuzzy Clustering Algorithm with Spatial Information for HEP-2 Cell Image Segmentation" Pradipta Maji and Shaswati Roy
Regular	N206 <i>SeqMaker: A Next Generation Sequencing Simulator with Variations, Sequencing Errors and Amplification Bias Integrated</i> Chen, Yue Han, Lanting Guo, Jingjing Hu, and Jia Gu,
Short	B268 "Robust Retinal Vessel Segmentation via Clustering-Based Patch Mapping Functions" haiying xia, shuaifei deng, Minqi Li, and frank jiang

Session 17 Phylogeny	
Invited Talk 5	<b>Multi-Omic Approaches for Liver Cancer Biomarker Discovery</b> <b>Dr. Habtom Resson (Chair: Xiaohua Hu)</b>
Regular	B448 "HPTree: reconstructing phylogenetic trees for ultra-large unaligned DNA sequences via NJ model and Hadoop" Quan Zou and Xiangxiang Zeng
Short	B263 "COLT: Constrained Lineage Tree Generation from Sequence Data" Keke Chen, Venkata Gogu, Di Wu, and Ning Jiang
Short	B302 "COSPEDTree-II: Improved Couplet based Phylogenetic Supertree" Sourya Bhattacharyya and Jayanta Mukhopadhyay

Session 18 Networks/Pathway Analysis (IV)	
Invited Talk 6	<b>An Algorithmic-Information Calculus for Reprogramming Biological Networks</b> <b>Dr. Hector Zenil</b>
Regular	B250 "Optimal Control for Context-Sensitive Probabilistic Boolean Networks with Perturbation using Probabilistic Model Checking" Ou Wei, Zonghao Guo, Yun Niu, and Wenyuan Liao
Regular	B274 "The prediction of human splicing branchpoints by multi-label learning" Wen Zhang, Xiaopeng Zhu, Yu Fu, Junko Tsuji, and Zhiping Weng
Short	B348 "Reconstructing Gene Regulatory Network Based on Candidate Auto Selection Method" Linlin Xing, Maozu Guo, Xiaoyan Liu, and Chunyu Wang

Session 19 Signaling/Image Analysis (III)	
Invited Talk 7	<b>Semi-Hypothesis Guided Exploratory Analysis for Biomedical Applications</b> <b>Dr. Chi-Ren Shyu</b>
Regular	B446 "Construction of Retinal Vascular Trees via Curvature Orientation Prior" Xingzheng Lyu, Qifan Yang, Shunren Xia, and Sanyuan Zhang
Short	B482 "Learning Schizophrenia Imaging Genetics Data Via Multiple Kernel Canonical Correlation Analysis" Owen Richfield, Md. Ashad Alam, Vince Calhoun, and Yu-Ping Wang
Short	B460 "Corner Detection and Matching Methods for Brain Medical Image Classification" Linlin Gao, Haiwei Pan, and Jinming Han

Session 20 Data-Mining and Visualization (III)	
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Invited Talk 8	<b>Deep-Learning: Investigating Feed-Forward Deep Neural Networks for Modeling High Throughput Chemical Bioactivity Data</b> <b>Dr. Jun Huan</b>
Regular	B425 "Multi-View Clustering Microbiome Data by Joint Symmetric Nonnegative Matrix Factorization with Laplacian Regularization" Yuanyuan Ma, Xiaohua Hu, Tingting He, and Xingpeng Jiang
Regular	B501 "qPMS10: A Randomized Algorithm for Efficiently Solving Quorum Planted Motif Search Problem" Peng Xiao, Soumitra Pal, and Sanguthevar Rajasekaran
Short	B436 "Mining Protein Complexes Based on Topology Potential from Weighted Dynamic PPI Network" Xiujuan Lei, Yuchen Zhang, Fang-Xiang Wu, and Aidong Zhang

Session 21 Protein/RNA Structure (I)	
Regular	B331 "PredRBR: Accurate Prediction of RNA-binding Residues in Proteins Using Gradient Tree Boosting" Diwei Liu, Yongjun Tang, Chao Fan, Zhigang Chen, and Lei Deng
Regular	B428 "InfDisSim: a novel method for measuring disease similarity based on information flow" Yang Hu, Meng Zhou, Hongbo Shi, Hong Ju, Qinghua Jiang, and Liang Cheng
Regular	B556 "A Map of Binding Cavity Conformations Reveals Differences in Binding Specificity" Ziyi Guo and Brian Chen
Short	B279 "Improved protein residue-residue contacts prediction using learning-to-rank" Xiaoyang Jing and Qiwen Dong
Short	B245 "A novel algorithm for identifying essential proteins by integrating subcellular localization" YETIAN FAN, Xiaohua Hu, Xiwei Tang, Qing Ping, and Wei Wu
Short	B491 "Accelerating Protein-Protein Complex Validation by GPU based Funnel Generation" Michael Zabejansky and Haim Wolfson
Short	B523 "Semidefinite Facial Reduction and Rigid Cluster Interpolation in Protein Structure Elastic Network Models" Xiao-Bo Li, Forbes Burkowski, and Henry Wolkowicz

Session 22 Signalling/Image Analysis (IV)	
Regular	B333 "FPGA Implementation of the Coupled Filtering Method" Chen ZHANG, Tianzhu LIANG, Philip MOK, and Weichuan Yu
Short	B356 "3D Tracking Swimming Fish School using a Master View Tracking First Strategy" Shuo Hong Wang, Xiang Liu, Jingwen Zhao, Ye Liu, and Yan Qiu Chen
Regular	B363 "Coarse-to-Fine Stacked Fully Convolutional Nets for Lymph Node Segmentation in Ultrasound Images" Yizhe Zhang, Michael T. C. Ying, Lin Yang, Anil T. Ahuja, and Danny Z. Chen
Regular	B454 "Emotion Recognition from Multi-Channel EEG through Convolutional Recurrent Neural Network" Xiang Li, Dawei Song, Peng Zhang, Guangliang Yu, Yuexian Hou, and Bin Hu
Short	B371 "Deep Learning for Malaria Blood Smear Image Classification with Convolutional Neural Network" Zhaohui Liang, Stefan Jaeger, George Thoma, Jimmy Huang, Peng Guo, Andrew Powell, Komorat Silamut, Iker Ersoy, Mahdiah Poostchi, Kannappan Palaniappan, and Richard Maude
Short	B394 "Prediction of neonatal amplitude-integrated EEG based on LSTM method" Lizhe Liu, Weiting Chen, and Guitao Cao

Session 23 Modelling and Data Integration (II)	
Regular	B246 "Identifying protein complexes via multi-network clustering" Le Ou-Yang, Hong Yan, and Xiao-Fei Zhang
Short	B401 "Weighted Multi-view Learning for Predicting Drug-Disease Associations" Sai Nivedita Chandrasekaran and Jun Huan
Regular	B296 "A Predictive Model of Gene Expression Using a Deep Learning Framework" Rui Xie, Andrew Quitadamo, Jianlin Cheng, and Xinghua Shi
Regular	B517 "Numerical Assessment of Airflow and Inhaled Particles Attributes in Obstructed Pulmonary System" Antonios Lalas, Stauros Nousias, Dimitrios Kikidis, Aris Lalos, Konstantinos Moustakas, Konstantinos Votis, Omar Usmani, and Dimitrios Tzovaras
Short	B409 "Predicting disease-microbe association by random walking on the heterogeneous network" Xianjun Shen, Yao Chen, Xingpeng Jiang, Xiaohua Hu, Tingting He, and Jincai Yang

Regular	B441 "Identifying Drug-pathway Association Pairs Based on L2,1-Integrative Penalized Matrix Decomposition" Dong-Qin Wang, Chun-Hou Zheng, Ying-Lian Gao, Jin-Xing Liu, and Sha-Sha Wu
Short	B470 "Variable selection and prediction of clinical outcome with multiply-imputed data via Bayesian model averaging" Guozhi Jiang, Claudia H.T. Tam, Andrea O.H. Luk, Alice P.S. Kong, Wing-Yee So, Juliana C.N. Chan, Ronald C.W. Ma, and Xiaodan Fan

Session 24 Healthcare Informatics	
Regular	B294 "Inferring Social Influence of Anti-Tobacco Mass Media Campaigns" Qianyi Zhan, Jiawei Zhang, Philip Yu, Sherry Emery, and Junyuan Xie
Short	B408 "An Ensemble Embedded Feature Selection Method for Multi-Label Clinical Text Classification" Yumeng GUO, Fulai Chung, and Guozheng Li
Short	B311 "How to Record the Amount of Exercise Automatically? A General Real-Time Recognition and Counting Approach for Repetitive Activities" Shugang Zhang, Zhen Li, Jie Nie, Lei Huang, Shuang Wang, and Zhiqiang Wei
Regular	B327 "Implementation of a City-Wide Health Information Exchange Solution in the Largest Metropolitan Region in China" Guangjun Yu, Li Zhou, David Bates, Hui Lu, and Wenbin Cui
Short	B495 "MR Brain Tumor Detection Employing Laplacian Eigen Maps And Kernel Support Vector Machine" MAHUA BHATTACHARYA and Rahul Singh
Short	B292 "An Integrated Medical CPS for Early Detection of Paroxysmal Sympathetic Hyperactivity" Zuxing Gu, Hong Song, Yu Jiang, Jeonghone Choi, Hongjiang He, Lui Sha, and Ming Gu
Regular	B475 "Learning to Diagnose Cirrhosis via Combined Liver Capsule and Parenchyma Ultrasound Image Features" Shuo Hong Wang, Xiang Liu, Jingwen Zhao, Jia Lin Song, Jian Quan Zhang, and Yan Qiu Chen

Session 25 Transcriptomics (II)	
Regular	B560 "Feature selection based on functional group structure for microRNA expression data analysis" Yang Yang, Tianyu Cao, and Wei Kong
Short	B221 "A Sparse Network-regularized Singular Value Decomposition Approach for Specific Functional Module Discovery" Wenwen Min, Juan Liu, and Fei Luo
Short	B310 "Predicting MicroRNA-disease associations by walking on four biological networks" Wei Peng, Wei Lan, Jianxin Wang, and Yi Pan

Session 26 Proteomics/PTM/Metabolomics
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Regular	B504 "Metabolomic data deconvolution using probabilistic purification models" Minkun Wang, Cristina Di Poto, Alessia Ferrarini, Guoqiang Yu, and Habtom Ressom
Short	B229 "A framework for identifying disease genes by incorporating the subcellular localization information into the protein-protein interaction networks" Xiwei Tang and Xiaohua Hu
Short	B299 "Bacterial Biological Mechanisms for Functional Module Detection in PPI Networks" Cuicui Yang, Junzhong Ji, and Aidong Zhang
Short	B512 "Network-based analysis of reverse phase protein array data" Rency Varghese, Yiming Zuo, Yi Zhao, Yong-Wei Zhang, Sandra Jablonski, Mariaelena Pierobon, Emanuel Petricoin, Habtom Ressom, and Louis Weiner
Short	B374 "ILSES: Identification Lysine Succinylation-sites with Ensemble Classification" Wenzheng Bao and De-Shuang Huang

### Session 27 Biomedical Intelligence (III)

Short	B380 "Identifying Patterns of Associated-Conditions through Topic Models of Electronic Medical Records" Moumita Bhattacharya, Claudine Jurkovitz, and Hagit Shatkay
Short	B464 "Answering Diabetic Patients' Questions Using Expert-vetted Online Resources: A Case Study" yuqun Zeng, Liwei Wang, Hongfang Liu, Yanshan Wang, and Xusheng Liu
Short	B395 "LCM-DS: a Novel Approach of Predicting Drug-Drug Interactions for New Drugs via Dempster-Shafer Theory of Evidence" Jian-Yu Shi, Ke Gao, Xuequn Shang, and S.M. Yiu
Short	B388 "SAFS: A Deep Feature Selection Approach for Precision Medicine" Milad Zafar Nezhad, Dongxiao Zhu, Xiangrui Li, and Phillip Levy
Short	N202 "IXAmed-IE: on-line medical entity identification and ADR event extraction in Spanish" Arantza Casillas, Arantza Díaz De Ilarraza, Kike Fernandez, Koldo Gojenola, Maite Oronoz, Alicia Pérez and Sara Santiso

### Session 28 Modelling and Data Integration (III)

Regular	B230 "Unconstrained Optimization in Projection Method for Indefinite SVMs" Hao Jiang, Wai-Ki Ching, Yushan Qiu, and Xiaoqing Cheng
Regular	B384 "A P-Norm Singular Value Decomposition Method for Robust Tumor Clustering" Xiang-Zhen Kong, Jin-Xing Liu, Chun-Hou Zheng, and Mi-Xiao Hou



Regular	B404 "Innovative microRNA-lncRNA-mRNA co-expression analysis to understand the pathogenesis and progression of diabetic kidney disease" Lihua Zhang, Rong Li, Jingshan Huang, Qiuping Yang, Yanan Wu, and Bin Wu
Short	B345 "Evaluation of CD-HIT for constructing non-redundant databases" Qingyu Chen, Yu Wan, Yang Lei, Justin Zobel, and Karin Verspoor
Short	B544 "A Distributed and Privatized Framework for Drug-Target Interaction Prediction" Chao Lan, Sai Nivedita Chandrasekaran, and Jun Huan

#### Session 29 Protein/RNA Structure (II)

Regular	B435 "Predicting microRNA-environmental factor interactions based on bi-random walk and multi-label learning" Wei Lan, Jianxin Wang, Min Li, Chengqian Lu, Fang-Xiang Wu, and Yi Pan
Regular	B492 "CNNsite: Prediction of DNA-binding Residues in Proteins Using Convolutional Neural Network with Sequence Features" Jiyun Zhou, Qin Lu, Ruifeng Xu, Lin Gui, and Hongpeng Wang
Regular	B526 "Deep Convolutional Neural Networks for Protein Secondary Structure Detection in 3D Cryo-Electron Microscopy Images" Rongjian Li, Dong Si, Tao Zeng, Shuiwang Ji, and JING HE
Short	B361 "Symmetrical Rigid Body Parameterization for Biomolecular Structures" Jin Seob Kim and Gregory Chirikjian
Short	B373 "Towards Recognition of Protein Function based on its Structure using Deep Convolutional Networks" Amirhossein Tavanaei, Anthony Maida, Arun Kaniyammattam, and Rasiah Loganantharaj

#### Session 30 Signalling/Image Analysis (V)

Regular	B346 "An ant colony optimization algorithm for learning brain effective connectivity network from fMRI data" Jinduo Liu, Junzhong Ji, Aidong Zhang, and Peipeng Liang
Regular	B381 "Joint Distribution Adaptation Based TSK Fuzzy Logic System for epileptic EEG Signal Identification" Hao Feng, Yaxin Peng, Guixu Zhang, and Chaomin Shen
Short	B426 "ELM-Based Classification of ADHD Patients Using a Novel Local Feature Extraction Method" Yang Li, Zhichao Lian, and zhonggeng Liu
Short	B444 "A Texture Descriptor Combining Fractal and LBP Complex Networks" Jundong Yan, Yuanyuan Sun, Yawen Guan, and Xiaopeng Hu

Short	B456 "Deep Convolutional Neural Networks for Survival Analysis with Pathological Images and Clinical Data" Xinliang Zhu, Jiawen Yao, and Junzhou Huang
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Session 31 Modelling and Data Integration (IV)	
Regular	B359 "Integration of multiple heterogeneous omics data" Liu Juan, Zhang Chuanchao, Zeng Tao, and Chen Luonan
Regular	B321 "Computational Identification of Regions that Influence Activity of Transposable Elements in the Human Genome" Lingling Jin, Ian McQuillan, and Longhai Li
Regular	B375 "Unsupervised Single-Cell Analysis in Triple-Negative Breast Cancer: A Case Study" Arjun Athreya, Alan Gaglio, Junmei Cairns, Krishna Kalari, Richard Weinshilbom, Liewei Wang, Zbigniew Kalbarczyk, and Ravishankar Iyer
Regular	B317 "Finding More Effective Microsatellite Markers for Forensics" Bowen Tan, Zicheng Zhao, Zhe Zhang, Shengbin Li, and Shuai Cheng Li
Short	B437 "Iterative segmented least square method for functional microRNA-mRNA module discovery in breast cancer" Sungmin Rhee, Sangsoo Lim, and Sun Kim
Short	B509 "Visual Orchestration and Autonomous Execution of Distributed and Heterogenous Computational Biology Pipelines" Xin Mou, Hasan Jamil, and Robert Rinker

Session 32 High Performance Computing	
Regular	B450 "HiGene: A High-Performance Platform for Genomic Data Analysis" Liqun Deng, Guowei Huang, Yuzheng Zhuang, Jiansheng Wei, and Youliang Yan
Regular	B480 "mAMBER: A CPU/MIC Collaborated Parallel Framework for AMBER on Tianhe-2 Supercomputer" Shaoliang Peng, Xiaoyu Zhang, Yutong Lu, Xiangke Liao, Weiliang Zhu, and Dongqing Wei
Regular	B490 "BioNimbuZ: A Federated Cloud Platform for Bioinformatics Applications" Aletéia Araújo, Breno Moura, Edward Ribeiro, Guilherme Vergara, Lucas Santos, Maria Emília M. T. Walter, Maristela Holanda, and Michel Rosa
Short	B335 "VinaSC: Scalable Autodock Vina with Fine-grained Scheduling on Heterogeneous Platform" Lang Yu, Zhongzhi Luan, Hailong Yang, Xiangzheng Sun, and Zhe Wang
Short	B505 "DMcompress: dynamic Markov models for bacterial genome compression" Rongjie Wang, Yadong Wang, and Tianyi Zang
Short	B529 "Accelerating Large Scale Genomic Analysis with Spark" Xueqi Li

## Keynote Lectures

### Keynote 1: Computational Psychophysiology Based Research Methodology for Mental Health

**Speaker:**

Prof. Dr. Bin Hu

**Abstract:**

Computational psychophysiology is a new direction that broadens the field of psychophysiology by allowing for the identification and integration of multimodal signals to test specific models of mental states and psychological processes. Additionally, such approaches allows for the extraction of multiple signals from large-scale multidimensional data, with a greater ability to differentiate signals embedded in background noise. Further, these approaches allows for a better understanding of the complex psychophysiological processes underlying brain disorders such as autism spectrum disorder, depression, and anxiety. Given the widely acknowledged limitations of psychiatric nosology and the limited treatment options available, new computational models may provide the basis for a multidimensional diagnostic system and potentially new treatment approaches.

**Short Bio:**



Prof. Dr. Bin Hu is currently professor, dean in the School of Information Science and Engineering, Lanzhou University, adjunct professor in Tsinghua University, P. R. China. He is also IET Fellow, Chair of IEEE SMC TC on Computational Psychophysiology, and Chair of ACM China SIGBio, Vice President of International Society for Social Neuroscience (China committee) etc. His research interest includes computational theories and pervasive technologies in cognitive science and psychophysiology. His work has been funded as a PI by the Ministry of Science and Technology(973 project), National Science Foundation China, European Framework Programme 7, EPSRC, and HEFCE UK, etc, also, published more than 200 papers in peer reviewed journals, conferences, and book chapters.

### Keynote 2: Whole genome sequencing of disease animal models

**Speaker:**

Prof. Yi-Xu Li

**Abstract:**

Whole genome sequencing of disease animal models together with population genetics methodology is a powerful technology for deciphering new variations which associated with disease phenotypes. Here we show our studies on camel, dog, and rabbit. Whole genome sequencing data were generated from those animals, and then population genetics methodology was used in dealing with these whole genome sequencing date. Some important genetic variations were discovered which shown a strong associations with disease related phenotypes.

**Short Bio:**



Yi-Xue Li was born in Xinjiang, China. Currently, he is a Professor and Director of Big Bio-Medical Data Center in CAS-MPG Partner Institute of computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, a Director of Department of Bioinformatics and Biostatistics, Shanghai Jiaotong University, Director of Shanghai Center for Bioinformation Technology. Dr. Li received his BSc. and Msc. degrees in theoretical physics from Xinjiang University, China, in 1982 and 1987, respectively, and his Ph.D. degree in theoretical physics from Heidelberg University, Germany in 1996. After Dr. Li got his Ph.D. degree he worked as a bioinformatics research staff in European Molecular Biology Laboratory (EMBL) from 1997-2000, and came back to Shanghai, China in the middle of 2000.

Dr. Li has published more than 260 peer review journal papers in various international scientific journals, such as Science, Nature, Nature Genetics, Nature Biotechnology, Nature Communications, Lancet, Genome Research, PNAS, Bioinformatics, Diabetes, Nucleic Acids Res, Plos Computational Biology, Molecular Systems Biology, Molecular Biology & Evolution, Molecular Cellular Proteomics, Oncogene, Genome Biology, Journal of Molecular Cell Biology, etc., and his research results have been cited by more than 30000 researchers worldwide in books, theses, journal and conference papers, reach the H index 66 (by Google). He has served as a reviewer/panelist for many national research foundations/agencies such as the Chinese National Science Foundation, the National High-Tech Program(863) and National Key Basic Research Program(973). Dr. Li has served as an editorial board member for 5 scientific journals. He has organized several international conferences and workshops and has also served as a program committee member for several major national and international conferences like GIW, IBW, HUPO and National Bioinformatics Conference etc.

**Keynote 3:  
Information and Decision-Making in Dynamic Cell Signalling**

**Speaker:**

Dr. David Rand

**Abstract:**

I will discuss a new theoretical approach to information and decisions in signalling systems and relate this to new experimental results about the NF-kappaB signalling system. NF-kappaB is an exemplar system that controls inflammation and in different contexts has varying effects on cell death and cell division. It is activated by various stress stimuli, including inflammatory cytokines such as TNFalpha and IL-1beta and is regarded as one of the most important stress response pathways in the mammalian cell. In a variety of conditions it displays oscillatory dynamics when stimulated, with the transcription factor entering the nucleus in a pulsatile fashion with a period of roughly 100 minutes. It is commonly claimed that it is information processing hub, taking in signals about the infection and stress status of the tissue environment and as a consequence of the oscillations, transmitting higher amounts of information to the hundreds of genes it controls. My aim is to develop a conceptual and mathematical framework to enable a rigorous quantifiable discussion of information in this context in order to follow Francis Crick's counsel that it is better in biology to follow the flow of information than those of matter or energy. In my approach the value of the information in the signalling system is defined by how well it can be used to make the "correct decisions"

when those "decisions" are made by molecular networks. As part of this I will introduce a new mathematical method for the analysis and simulation of large stochastic non-linear oscillating systems. This allows an analytic analysis of the stochastic relationship between input and response and shows that for tightly-coupled systems like those based on current models for signalling systems, clocks, and the cell cycle this relationship is highly constrained and non-generic.

**Short Bio:**



Dr. David Rand's earlier research work in nonlinear dynamics was distinguished by its breadth and the fact that he made lasting contributions not only to pure and applied dynamical systems, but also to theoretical physics, fluid dynamics, and ecology and epidemiology. His current work is on the interface between mathematics and systems biology where he has developed substantial collaborations with a number of leading experimental biologists in what are examples of the approach advocated for systems biology in areas such as inflammation, immunology, circadian biology, cancer, endocrinology, and gene regulation. In parallel, in collaboration with Bärbel Finkenstädt and others he has developed new statistical techniques and mathematical tools for the analysis of the sort of biological systems models and data found in these biological areas. He has

extensive management and administrative experience (in particular as a head of Warwick's Mathematics Institute and its Systems Biology Centre). His prizes and distinctions include the LMS Whitehead prize, the UK's top prize for mathematicians under 40, and a prestigious EPSRC Senior Research Fellowship.

## **Keynote 4: Trajectory Analysis -- Linking Genomic and Proteomic Data with Disease Progression**

**Speaker:**

Dr. Aidong Zhang

**Abstract:**

Biological networks are dynamic and modular. Identifying dynamic functional modules is key to elucidating biological insight and disease mechanism. In recent years, while most researchers have focused on detecting functional modules from static protein-protein interaction (PPI) networks where the networks are treated as static graphs derived from aggregated data across all available experiments or from a single snapshot at a particular time, temporal nature of context-specific transcriptomic and proteomic data has been recognized by researchers. Meanwhile, the analysis of dynamic networks has been a hot topic in data mining and social networks. Dynamic networks are structures with objects and links between the objects that vary in time. Temporary information in dynamic networks can be used to reveal many important phenomena such as bursts of activities in social networks and evolution of functional modules in protein interaction networks. In this talk, I will address several critical challenges to construct robust, dynamic gene interaction networks, and present our computational approaches to identify disease-relevant functional modules and to track the progression patterns of modules in dynamic biological

networks. Significant modules which are correlated to phenotypes of interest can be identified, for example, those functional modules which form and progress across different stages of a cancer. Through identifying these functional modules in the progression process, we are able to detect the critical groups of proteins that are responsible for the transition of different cancer stages. Our approaches can also discover how the strength of each detected modules changes over the entire observation period. I will also demonstrate the application of our approach in a variety of biomedical applications.

***Short Bio:***



Dr. Aidong Zhang is currently on leave from the State University of New York (SUNY) at Buffalo and serving as a program director in the Information & Intelligent Systems division of the Directorate for Computer & Information Science & Engineering, National Science Foundation, USA. Dr. Zhang is a SUNY Distinguished Professor of Computer Science and Engineering. Her research interests include data mining/data science, bioinformatics, health Informatics, multimedia and database systems, and content-based image retrieval. She has authored over 290 research publications in these areas. She has chaired or served on over 160 program committees of international conferences and workshops, and currently serves on several journal editorial boards. She has published two books “Protein Interaction Networks: Computational Analysis” (Cambridge University Press, 2009) and “Advanced Analysis of Gene Expression Microarray Data” (World Scientific Publishing Co., Inc. 2006). Dr. Zhang is an IEEE Fellow.



## Invited Talks

### Invited Talk 1:

### Deep-Learning: Investigating Feed-Forward Deep Neural Networks for Modeling High Throughput Chemical Bioactivity Data

**Speaker:**

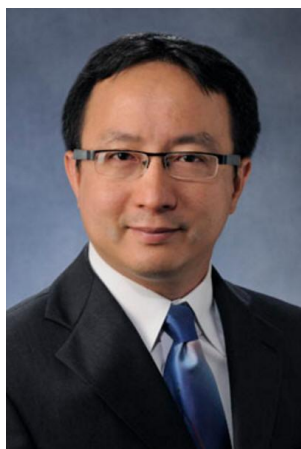
Dr. Jun (Luke) Huan

**Abstract:**

In recent years, research in Artificial Neural Networks (ANNs) has resurged, now under the Deep-Learning umbrella, and grown extremely popular due to major breakthroughs in methodological and computing capabilities. Deep-Learning methods are part of representation-learning algorithms that attempt to extract and organize discriminative information from the data. Recently reported success of DL techniques in crowd-sourced QSARs and predictive toxicology competitions has showcased these methods as powerful tools for drug-discovery and toxicology research. Nevertheless, reported applications of Deep Learning techniques for modeling complex bioactivity data for small molecules remain still limited.

In this talk I will present our recent work on optimizing feed-forward Deep Neural Nets (DNNs) hyper-parameters and performance evaluation of these methods as compared to shallow methods. In our study 48 DNNs, 24 Random Forest, 20 SVM and 6 Naïve Bayes arbitrary but reasonably selected configurations were compared employing 7 diverse bioactivity datasets assembled from ChEMBL repository combined with circular fingerprints as molecular descriptors. The non-parametric Wilcoxon paired signed-rank test was employed to compare the performance of DNN to RF, SVM and NB. Overall it was found that DNNs with 2 hidden layers, 2,000 neurons per each hidden layer, ReLU activation function and Dropout regularization technique achieved strong classification performance across all tested datasets. Our results demonstrate that DNNs are powerful modeling techniques for modeling complex bioactivity data.

**Short Bio:**



Dr. Jun (Luke) Huan is a Professor in the Department of Electrical Engineering and Computer Science at the University of Kansas. He directs the Data Science and Computational Life Sciences Laboratory at KU Information and Telecommunication Technology Center (ITTC). He holds courtesy appointments at the KU Bioinformatics Center, the KU Bioengineering Program, and a visiting professorship from GlaxoSmithKline plc. Dr. Huan received his Ph.D. in Computer Science from the University of North Carolina. Dr. Huan works on data science, machine learning, data mining, big data, and interdisciplinary topics including bioinformatics. He has published more than 100 peer-reviewed papers in leading conferences and journals and has graduated more than ten graduate students including seven PhDs. Dr. Huan serves the editorial board of several international journals including the Springer Journal of Big Data, Elsevier Journal of Big Data Research, and the International Journal of Data Mining and Bioinformatics. He regularly serves the program committee of top-tier international conferences on machine learning, data mining, big data, and bioinformatics. Dr. Huan's research is recognized internationally. He was a recipient of the prestigious National Science Foundation Faculty Early Career Development Award in 2009. His group won the Best Student Paper Award at the IEEE International Conference on Data Mining in 2011 and the Best Paper Award (runner-up) at the ACM International Conference on Information and Knowledge Management in 2009. His work appeared at mass media including Science Daily,

R&D magazine, and EurekAlert (sponsored by AAAS). Dr. Huan's research was supported by NSF, NIH, DoD, and the University of Kansas. Starting January 2016, Dr. Huan serves as a Program Director in NSF at its Intelligent and Information Division in the Computer and Information Science and Engineering Directorate.

## **Invited Talk 2: Networks and Models for the Integrated Analysis of Multi Omics data**

### ***Speaker:***

Dr. Sun Kim

### ***Abstract:***

These days, genome-wide measurements of genetic and epigenetics events, a.k.a omics data, are routinely produced; epigenetics is control mechanisms of genetics events as epi- means 'on' or 'upon'. As a result, a huge amount of omics data measured from different genetic and epigenetic events are available. For example, the amount of data at The Cancer Genome Atlas(TCGA) alone exceeds 2.5 peta byte as of October 2016. Unfortunately, the dimensions of omics data is huge, typically tens to hundreds or even millions of thousands while the number of samples are limited typically a few to thousands. Thus mining genetic and epigenetic data measured in different phenotype conditions is a very challenging problem, that is, small data sets on extremely high dimensions. Furthermore, all genetic and epigenetic events are inter-related. Thus it is necessary to perform integrated analysis of omics data sets of different types, which is even more challenging. To address these technical challenges, the bioinformatics community has used virtually all known network based analysis techniques, including recently developed deep neural networks. My group has been trying the network based integrated analysis of omics data at three different levels. First, we have been investigating on computational methods for associating different genetic and epigenetic events, which can be viewed as methods for defining edges in the network. Second, we have been developing mining sub-networks on the phenotype and time dimensions. Third, we have recently begun to investigate on the use of deep learning techniques for the integrated analysis of omics data. An important goal of our research is to combine network analysis and deep learning techniques to construct models or draw maps of cancer cells at multiple levels such as genomic mutations, gene activation/suppressions, epigenetic events including DNA methylation, histone modifications, and miRNA interference, biological pathways, and finally at the whole cell level including tumor heterogeneity and clonal evolution.

### ***Short Bio:***



Dr. Sun Kin is a professor and the director of Bioinformatics Institute of Seoul National University. He got his Bachelor degree in Computer Science and Statistics from Seoul National University, and got his Master degree in Computer Science from KAIST, and got his Ph.D. in Computer Science from University of Iowa. His research interests include Bioinformatics, Machine Learning, String Matching Algorithm.



## Invited Talk 3: High Performance Computational Biology and Drug Design on TianHe Supercomputers

### *Speaker:*

Dr. Shaoliang Peng

### *Abstract:*

Extremely powerful computers are needed to help scientists to handle high performance computational biology and drug design problems. The world's largest genomics institute BGI currently generates 6 TB data each day. The European Bioinformatics Institute (EBI) in Hinxton currently stores 20 petabytes (1 petabyte is 1015 bytes) of data and back-ups about genes, proteins and small molecules. TianHe supercomputers can speed up computational biology and drug design processing. In 2013, 2014, and 2015, Tianhe-2 topped the TOP500 list of fastest supercomputers in the world. Many well-known bioinformatics and drug design softwares (BWA, DOCK, SOAP3-dp, SOAPdenovo, SOAPsnp etc.) are developed and running on TH-2. The talk focuses on two main areas: 1. Drug Design: mD3DOCKxb is a largest high throughput molecular docking platform and finishes the docking of all the purchasable molecules (about 42 million) on earth within 24 hours. It has a parallel efficiency of over 70% using 192,000 CPU cores and 1,368,000 MIC cores. It gains the Gold Award of PAC 2015 (Parallel Application Challenge Competition) and is reported by CCTV 1, ScienceNet, China Science and Technology News, and 2015 Top 10 News of Hunan Province of China. 2. Genetic Engineering: The "Human Whole Genome Re-sequencing Analysis Software Pipeline" is firstly designed by applicant. The whole analyzing procedure takes 4 hours to finish the analysis of a 300 TB dataset of whole genome sequences from 2,000 human beings. The speedup is about 1200X.

TianHe Supercomputers can handle 3 kinds of computational biology and drug design problems: computation intensive, memory intensive, and communication intensive. In future, TH-2 will be open online to all the scientists not only in China but also all over the world.

### *Short Bio:*



Dr. Shaoliang Peng is a professor in National University of Defense Technology (NUDT, Changsha, China) and an adjunct professor of BGI. He was a visiting scholar at CS Department of City University of Hong Kong (CityU) from 2007 to 2008 and at BGI Hong Kong from 2013 to 2014. His research interests are high performance computing, bioinformatics, virtual screening, and biology simulation. He has participated in many keystone projects in China such as TianHe supercomputers. He gains the Gold Award twice of PAC 2014 and 2015 (Parallel Application Challenge Competition) and is reported by CCTV 1, ScienceNet, China Science and Technology News, and 2015 Top 10 News of Hunan Province of China (1. Human Whole Genome Re-sequencing Analysis Software Pipeline, 2. mD3DOCKxb: largest high throughput molecular docking platform). He also gains the Finalist Awards of 2015 IEEE International Scalable Computing Challenge, SCALE 2015. He has published 3 books and over 50 papers in ISC 2015, ACM/IEEE Transactions, Nature Communications, Cell AJHG, BMC Bioinformatics, IPDPS, and SCIENCE CHINA. The downloading times of software are over 50000. He is Executive Editor and Associate Editors of several international journals (Interdisciplinary Sciences: Computational Life Sciences, IJCSE, IJHPCN, and IJES). Moreover, he is the PI of several key projects including 973, 863 and National Natural Science Foundation of China (NSFC).

## Invited Talk 4:

## Multi-Omic Approaches for Liver Cancer Biomarker Discovery

**Speaker:**

Dr. Habtom W. Resson

**Abstract:**

Omic technologies offer the opportunity to characterize liver cancer at various molecular levels. In particular, characterizing the association of biomolecules such as metabolites and glycoproteins with liver cancer is a promising strategy to discover clinically relevant biomarkers. Metabolites are molecular fingerprints of what cells do at a particular point in time; they can reveal early signs of cancers when the chances for cure are highest. Also, the analysis of protein glycosylation is relevant to liver pathology because of the major influence of this organ on the homeostasis of blood glycoproteins. This talk will focus on the application of multi-omic approaches to identify biomarkers for early detection of liver cancer in patients with liver cirrhosis. Specifically, I will present transcriptomic, proteomic, glycomic/ glycoproteomic, and metabolomic (TPGM) studies we conducted by analysis of samples from HCC cases and cirrhotic controls using multiple omic platforms such as next generation sequencing, liquid chromatography-mass spectrometry (LC-MS), and gas chromatography-mass spectrometry (GC-MS). In addition to candidate biomarkers discovered by evaluating the changes in the levels of transcripts, proteins, glycans, and metabolites between HCC cases and cirrhotic controls, I will present network-based methods we developed for integrative analysis of multi-omic data to identify aberrant pathways/network activities and biomarkers for early detection of liver cancer.

**Short Bio:**



Dr. Resson is a Professor of Oncology at Georgetown University Medical Center (GUMC). His research focuses on using multi-omic approaches for liver cancer biomarker discovery. His laboratory collects biospecimens from human research participants, designs workflows for multi-omic studies, and develops computational methods for omic data analysis. Dr. Resson is the Director of GUMC's Genomics and Epigenomics Shared Resource (GESR), which provides various services including next generation sequencing, SNP genotyping, copy number variation analysis, DNA methylation analysis, and mRNA/miRNA expression analysis.

## Invited Talk 5: Semi-Hypothesis Guided Exploratory Analysis for Biomedical Applications

**Speaker:**

Dr. Chi-Ren Shyu

**Abstract:**

Medical research and clinical trials are often based on hypotheses that were observed from clinical practice with noticeable evidence. Forming clinically significant hypotheses will greatly benefit the success of clinical research and ensure both external and internal validity of the trial. In this talk, I will introduce a knowledge discovery

approach to automatically identify populations of subjects with commonly occurred comorbidities, genotypes, and phenotypes that present statistically high contrast between populations. To focus on a confined set of medical problems as most of medical researchers would like to target (hypertension and diabetes versus all chronic diseases), this approach is able to take a set of selected attributes of interest and expand knowledge discoveries from the initial set. The computational approach consists of a forward floating search method for population selection, a hierarchical frequent pattern mining tree to efficiently handle dense associations, contrast mining for identifying actionable plans, and accumulated contrast (ac-)index for ranking mining results for biomedical researchers. I will present exploratory analysis process and results from the Simon's Simplex Collection (SSC) by the Simons Foundation Autism Research Initiative (SFARI) which comprises data representing 11,560 individuals from 2,591 families. Putative autism subtypes were explored by partitioning families based on demographics and autism phenotypes. An extended contrast mining procedure identified genetic combinations showing preferential association for one of the contrasted subgroups, emphasizing combinations novel to the autistic proband within each family tree. Potentials for other biomedical applications will also be discussed.

### ***Short Bio:***



Dr. Chi-Ren Shyu is the director of the University of Missouri Informatics Institute. He holds the Paul K. and Dianne Shumaker Endowed Professorship of Biomedical Informatics. He received his Ph.D. in Electrical and Computer Engineering from Purdue University. Since joining University of Missouri-Columbia in 2000, Shyu has received several awards including the National Science Foundation CAREER award, Engineering Faculty Research Award, Engineering Teaching Excellence Award, the 2014 University of Missouri Faculty Interdisciplinary Entrepreneurial Award, the 2016 UM System President's Leadership Award. He actively serves the international research community, which includes organizing the IEEE HealthCom 2011 conference in Columbia as general chair, co-chairing technical program committee of the Second IEEE BigMM2016 and IEEE BIBE2016. He will serve as the general chair for the IEEE BIBM 2017 in Kansas City, Missouri, USA. Dr. Shyu also leads an interdisciplinary team of 22 researchers from veterinary medicine, engineering, human medicine to train doctoral students through the NIH BD2K's T32 Biomedical Big Data Science program (2016-2021) to tackle One Health Big Data challenges – translating discoveries from animal model to human health. His research interests include massive data analytics, biomedical informatics, mHealth and eHealth, visual knowledge reasoning and search engine design. Project sponsors, in addition to the NSF, include the National Institutes of Health, National Library of Medicine, the U.S. Department of Education and other for-profit and nonprofit organizations.

## **Invited Talk 6: Computational tools for studying gene regulation in the 3-dimensional genome**

### ***Speaker:***

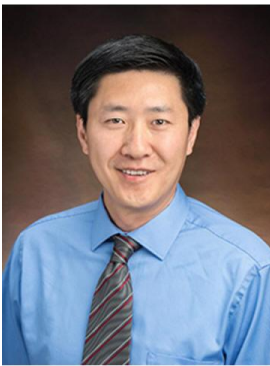
Dr. Kai Tan

### ***Abstract:***

Determining the 3-dimensional structure of the genome and its impact on gene expression has been a long-standing question in cell biology. Recent development in mapping technologies for chromatin interactions has led to a rapid increase in this kind of interaction data, revealing a hierarchical organization of the 3D genome, from large

compartments spanning multiple chromosomes, to mega-base-sized topological associated chromatin domains, to individual long-range chromatin loops mediating enhancer-promoter interactions. With the explosion of chromatin interaction data, there is a pressing need for analytical tools. In this talk, I will describe two computational algorithms for analyzing chromatin interaction data at different scales. I will first present a fast algorithm for identifying large-scale, hierarchical chromatin domains. I will demonstrate how the algorithm enables studies of chromatin subdomains in gene regulation. Accurate knowledge of enhancer-promoter interactions is a pre-requisite to understanding regulatory output of enhancers. I will present an algorithm for predicting enhancer-promoter interactions by integrating genomic, transcriptomic, and epigenomic data. Using data from multiple human cell types, I will demonstrate how the algorithm can help decipher the mechanisms underlying enhancer-promoter communication.

**Short Bio:**



Dr. Kai Tan is an associate professor in the Departments of Pediatrics, Genetics, Cell and Developmental Biology at the University of Pennsylvania and Children's Hospital of Philadelphia. He received his PhD degree in computational biology from Washington University in Saint Louis, followed by postdoctoral training in systems biology at the University of California San Diego. Dr. Tan's research focuses on understanding gene regulatory networks in normal and disease development. His laboratory has developed a number of algorithms for modeling and analyzing gene regulatory networks. He serves on the editorial board of PLoS Computational Biology and BMC Genomics. He is a member of Genomics, Computational Biology and Technology study section of NIH. He has served on the organization and program committees of international conferences including

BIBM, ISMB, and RECOMB.

**Invited Talk 7:  
Clinical application of precision medicine: Zhongshan Hospital Strategy**

**Speaker:**

Dr. Xiangdong Wang

**Abstract:**

Tomorrow's genome medicine in lung cancer should focus more on the homogeneity and heterogeneity of lung cancer which play an important role in the development of drug resistance, genetic complexity, as well as confusion and difficulty of early diagnosis and therapy. Chromosome positioning and repositioning may contribute to the sensitivity of lung cancer cells to therapy, the heterogeneity associated with drug resistance, and the mechanism of lung carcinogenesis. The CCCTC-binding factor plays critical roles in genome topology and function, increased risk of carcinogenicity, and potential of lung cancer-specific mediations. Chromosome reposition in lung cancer can be regulated by CCCTC binding factor. Single-cell gene sequencing, as part of genome medicine, was paid special attention in lung cancer to understand mechanical phenotypes, single-cell biology, heterogeneity, and chromosome positioning and function of single lung cancer cells. We at first propose to develop an intelligent single-cell robot of human cells to integrate together systems information of molecules, genes, proteins, organelles,

membranes, architectures, signals, and functions. It can be a powerful automatic system to assist clinicians in the decision-making, molecular understanding, risk analyzing, and prognosis predicting..

**Short Bio:**



Xiangdong Wang, MD, PhD, is a Distinguished Professor of Medicine at Fudan University, Director of Shanghai Institute of Clinical Bioinformatics, Executive Director of Clinical Science Institute of Fudan University Zhongshan Hospital, Director of Fudan University Center of Clinical Bioinformatics, Deputy Director of Shanghai Respiratory Research Institute, and visiting professor of King's College of London. His main research is focused on clinical bioinformatics, disease-specific biomarkers, lung chronic diseases, cancer immunology, and molecular & cellular therapies.

In addition, Dr Wang serves as the Executive Vice President of International Society for Translational Medicine, Chairman of Executive Committee of International Society for Translational Medicine, Deputy President of Chinese National Professional Society of Insurance & Health and a senior advisor of Chinese Medical Doctor Association, and Director of National Program of Doctor-Pharmacist Communication. Dr Wang was appointed as the Principal Scientist, Global Disease Advisor, Medical Monitor and Director, and Chairman of Director Board in a number of pharmaceutical companies, e.g. Astra Draco, AstraZeneca, PPT, and CatheWill. He was the professor of Molecular Bioscience at North Carolina State University, professor of Clinical Bioinformatics at Lund University, and the active member of American Thoracic Society International Health Committee, USA.

He serves as an Editor-in-Chief of Cell Biology and Toxicology (IF=2.84) and co-Editor-in-Chief of Clinical & Translational Medicine; Editor of Serial Book: Translational Bioinformatics; Asian Editor of Journal of Cellular Molecular Medicine (IF=4.99); Section Editor of Disease Biomarkers of Journal of Translational Medicine (IF=3.68); Associate Editor of Expert Review of Clinical Pharmacology (IF=2.48); and the editorial member of international journals, e.g. American Journal of Pulmonary Critical Care Medicine (IF=13), American Journal of Cellular & Molecular Biology (IF=5). He is the author of more than 200 scientific publications with the impact factor about 600, citation number about 5372, h-index 41, i10-index 138, and cited journal impact factor about 5000.

**Invited Talk 8:  
An Algorithmic-Information Calculus for Reprogramming Biological Networks**

**Speaker:**

Dr. Hector Zenil

**Abstract:**

Despite extensive attempts to characterize systems and networks based upon metrics drawn from traditional statistics, Shannon entropy, and graph theory to understand systems and networks to reveal their causal mechanisms without making too many unjustified assumptions remains still as one of the greatest challenges in complexity

science and science in general, specially beyond traditional statistics and so-called machine learning. Knowing the causal mechanisms that govern a system allows not only the prediction of the system's behaviour but the manipulation and controlled reprogramming of the system. Here we introduce a formal interventional calculus based upon universal principles drawn from the theory of computability and algorithmic probability, thereby enabling better approaches to the question of causal discovery. By performing sequences of fully controlled perturbations, changes in the algorithmic content of a system can be classified into the effects they have according to their shift towards or away from algorithmic randomness, thereby inducing a ranking of system's elements. This spectral dimension unmasks an algorithmic separation between components conditioned upon the perturbations and endowing us with a suite of powerful parameter-free algorithms to reprogram the system's underlying program. The predictive and explanatory power of these novel conceptual tools are introduced and numerical experiments are illustrated on various types of networks. We show how the algorithmic content of a network is connected to its possible dynamics and how the instant variation of the sensitivity, depth, and the number of attractors in a network is accessible by an analysis of its algorithmic information landscape. The results demonstrate how to unveil causal mechanisms to infer essential properties, including the dynamics of evolving networks. We introduce measures and methods for system reprogrammability even with no, or limited, access to the system kinetic equations or probability distributions. We expect this interventional calculus to be broadly applicable for predictive causal interventions and we anticipate it to be instrumental in the challenge of causality discovery in science from complex data.



## Workshops

<b>International Workshop on Biological Network Analysis and Integrative Graph-Based Approaches (IWBNA 2016)</b>		
<i>Session Chairs: Mingon Kang, Dongchul Kim, and Young-Rae Cho</i>		
Time	Title	Presenter/Author
<b>13:30-15:30</b>	<b>Session 1 (25-minute presentation and 5-minute Q &amp; A.)</b> Session Chair: Mingon Kang	
	Transcriptional Responses to Ultraviolet and Ionizing Radiation: An Approach Based on Graph Curvature	Yongxin Chen, Jung Hun Oh, Romeil Sandhu, Sangkyu Lee, Joseph Deasy, and Allen Tannenbaum
	2Path: a terpenoid metabolic network modeled as graph database	Waldeyr Silva, Marcelo Brígido, Danilo Vilar, Daniel Souza, Maria Emília Walter, and Maristela Holanda
	Individual Metabolic Network for the Accurate Detection of Alzheimer's Disease Based on FDG-PET imaging	Zhijun Yao, Bin Hu, Huailiang Nan, Weihao Zheng, and Yuanwei Xie
	Diagnosing Schizophrenia by Integrating Genomic and Imaging Data through Network Fusion	Su-Ping Deng, Dongdong Lin, Vince D. Calhoun, and Yu-Ping Wang
<b>15:30-16:00</b>	<b>Coffee Break</b>	
<b>16:00-17:00</b>	<b>Session 2 (25-minute presentation and 5-minute Q &amp; A.)</b> Session Chair: Mingon Kang	
	Filtering Association Rules in Gene Ontology Based on Term Specificity	Yong Shui and Young-Rae Cho
	Integrative Gene Regulatory Network Inference Using Multi-omics Data	Neda Zarayeneh, Jung Hun Oh, Donghyun Kim, Chunyu Liu, Jean Gao, Sang C. Suh, and Mingon Kang
<b>17:00</b>	Closing Remarks	

<b>2016 International Workshop on Biomolecular Networks and Human Diseases</b>		
<i>Session Chairs: Min Li, Jiangxin Wang, Haiying Wang, and FangXiang Wu</i>		
Time	Title	Author
08:20 – 10:30	<b>Session 1 (15 minutes for presentation + 5 minutes for Questions and discussion for each speaker)</b>	
8:20-8:30	<b>Opening</b>	
	<b>Disease-specific protein complex detection in the human protein interaction network with a supervised learning method</b>	Ziwei Zhou, yingyi Gui, zhihao Yang, xiaoxia Liu, lei Wang, yin Zhang, Hongfei Lin, and Jian Wang

	<b>Cancer genes discovery based on integrating transcriptomic data and the impact of gene length</b>	Pi-Jing Wei, Di Zhang, Junfeng Xia, and Chun-Hou Zheng
	<b>Identifying Disease Genes from PPI Networks Weighted by Gene Expression under Different Conditions</b>	Ping Luo, Li-Ping Tian, Jishou Ruan, and Fang-Xiang Wu
	<b>A novel identified temporal protein complexes strategy inspired by density-distance and brainstorming process</b>	Shen Xianjun, Zhou Jin, Jiang Xingpeng, Hu Xiaohua, He Tingting, Yang jincai, Xie Dan, and Xie Dan
	<b>Pervasive EEG Diagnosis of Depression using Deep Belief Network with Three-Electrodes EEG Collector</b>	Hanshu Cai, Xiaocong Sha, Xue Han, Shixi Wei, and Bin Hu
	<b>Epistasis detection using a permutation-based gradient boosting machine</b>	Kai Che, Xiaoyan Liu, Maozu Guo, Junwei Zhang, Lei Wang, and Yin Zhang
<b>10:30 – 10:50</b>	<b>Coffee Break</b>	
<b>10:50 – 12:10</b>	<b>Session 2(15 minutes for presentation + 5 minutes for Questions and discussion for each speaker)</b>	
	<b>Walking in the PPI network to identify the risky SNP of osteoporosis with decision tree algorithm</b>	Jincai Yang, Huichao Gu, Xingpeng Jiang, Qingyang Huang, Xiaohua Hu, and Xianjun Shen
	<b>Identifying Protein Complexes in Dynamic Protein-Protein Interaction Networks Based on Cuckoo Search Algorithm</b>	Jie zhao, Xiujuan Lei, and Fang-Xiang Wu
	<b>An EEG-based study on coherence and brain networks in mild depression cognitive process</b>	Li Xiaowei, Jing Zhuang, Hu Bin, and Sun Shuting
	<b>Robust Graph Regularized Discriminative Nonnegative Matrix Factorization for Characteristic Gene Selection</b>	Ling-Yun Dai, Chun-Mei Feng, Jin-Xing Liu, Chun-Hou Zheng, and Mi-Xiao Hou
<b>12:10-12:15</b>	<b>Closing</b>	

<b>Biomedical &amp; Health Informatics (BHI)</b>		
<i>Thursday, 12/15 at MUMIAN Hall</i>		
<i>Chair: Illhoi Yoo</i>		
	<b>Title</b>	<b>Presenter/Author</b>
9:20 am	<b>Welcome Illhoi Yoo (Workshop Chair)</b>	
9:30	MICS: a medical visual system for large-scale brain CT image classification	Li Wenbo, Pan Haiwei, Xie Xiaoqin, Zhang Zhiqiang, and Han Qilong
9:50	Clinical text mining for efficient extraction of drug-allergy reactions	Arantza Casillas, Koldo Gojenola, Alicia Pérez, and Maite Oronoza



10:10	The Design and Implementation of the Privacy Protection System of a Regional Health Information Platform	Shan Hu, Zhaosheng Gao, Lin Zhou, Nan Dong, Jing Xu, Zhiwei Liang, and Yi Zhou
10:30	<b>Break</b>	
10:50	Practical approach for disease similarity calculation based on disease phenotype, etiology, and locational clues in disease names	Mai Omura, Noboru Sonehara, and Takashi Okumura
11:10	Design and Development of ICU Intelligent Medicine Management System based on MVC	Siyuan Tang
11:25	Learning to Predict the Performance of Clinical Queries Using An Integrated Approach	Mohammad Alsulmi and Benjamin Carterette
11:45	Assisting humans to achieve optimal sleep by changing ambient temperature	VIVEK GUPTA, SIDDHANT MITTAL, Sandip Bhaumik, and Raj Roy
12:00	<b>Lunch</b>	
1:30 pm	Modular Reconfiguration of Metabolic Brain Networks in Health and Cancer: A Resting-State PET Study	Zhijun Yao, Bin Hu, Xuejiao Chen, Yuanwei Xie, and Lei Fang
1:50	Multi-label Classification for Intelligent Health Risk Prediction	Runzhi Li, Hongling Zhao, Yusong Lin, Andrew Maxwell, and Chaoyang Zhang
2:10	Reducing Surgical-Site Infections for Coronary Artery Bypass Graft Patients	Eva Lee, Zhuonan Li, Michael Wright, and Alexander Dr. Quarshie
2:30	Periodicity Intensity for Indicating Behaviour Shifts from Lifelog Data	Feiyan Hu and Alan Smeaton
2:50	Acoustic emission sonification and magnetic resonance imaging-based kinematics for exploratory analysis of knee joints	Lik-Kwan Shark, Kai Huang, Wei Quan, Michael Bowes, John Waterton, and John Goodacre
3:10	CIDExtractor: a chemical-induced disease relation extraction system for biomedical literature	Zhiheng Li, Yingyi Gui, Zhihao Yang, Yin Zhang, Lei Wang, Hongfei Lin, and Jian Wang
3:30	<b>Break</b>	
3:50 Pm	Android Application for Therapeutic Feed and Fluid Calculation in Neonatal Care - A Way to Fast, Accurate and Safe Health-care Delivery	Arunava Biswas, Romil Roy, Jayanta Mukhopadhyay, Deepak Khaneja, Sangeeta Das Bhattacharya, and Sourya Bhattacharyya
4:10	Exploring the Shared Neural Basis between the Positive and Negative Syndromes of Schizophrenia Using Multi-task Regression under the Stability Selection Frame	Heng Chen, Junjie Zheng, Zhiliang Long, Youxue Zhang, Xiaonan Guo, and Huafu Chen
4:25	Is EEG Causal to fNIRs?	Borzou Alipourfard, Jean Gao, Hanli Liu, and Olajide Babawale
4:45	Learning to Predict the Performance of Clinical Queries Using An Integrated Approach	Mohammad Alsulmi and Benjamin Carterette

5:05	A Compact Electronic Medical Record System for Regional Clinics and Health Centers in China: Design and Its Application	Lijun Pan, Xiaoting Fu, Fangfang Cai, Yu Meng, and Changjiang Zhang
5:25	Triptolide Targets on MYC towards Testis may Induce Male Reproductive Toxicity	Guang Zheng
5:40	GIDAC: a prototype for bioimages annotation and clinical data integration	Patrizia Vizza, Giuseppe Lucio Cascini, Pietro Hiram Guzzi, Rosario Curia, Loredana Sisca, and Pierangelo Veltri
5:55	Self-adjusting Nuclei Segmentation (SANS) of Hematoxylin-Eosin Stained Histopathological Breast Cancer Images	Yuxin Cui and Jianjun Hu

## Formal Methods for Biological and Biomedical Systems

*Session Chairs: Edmund M. Clarke, and Oinsi Wang*

Time	Title	Presenter/Author
9:00am - 9:50am	Invited Talk: The Pathway Logic Formal Modeling System: Diverse views of a formal	<b>Carolyn Talcott</b>
9:50am - 10:40am	Invited Talk: Energy-based Modeling in BioNetGen	John A.P. Sekar, Justin S. Hogg, and <b>James R. Faeder</b>
<b>10:40am - 11:00am</b>	<b>Coffee Break</b>	
11:00am - 11:30am	Parameter Estimation of Rule-based Models using	<b>Bing Liu</b>
11:30am - 12:00pm	CyberCardia Project: Modeling, Verification and Validation of Implantable Cardiac Devices	Md. Ariful Islam, Hyunkyung Lim, Nicola Paoletti, Houssam Abbas, Zhihao Jiang, Jacek Cyranka, Rance Cleaveland, Sicun Gao, Edmund Clarke, Radu Grosu, Rahul Mangharam, Elizabeth Cherry,
12:00pm - 12:30pm	Multi-scale Cardiac Modeling Reveal Tachyarrhythmias Induced by Abrupt	<b>Jieyun Bai</b> , Kuanquan Wang, and Henggui

## Workshop on Semantic Data Analytics and Machine learning in Bioinformatics and Medical Informatics

*Session Chair: Dr. Haiying Wang*

*1:30pm – 6:090pm, 15<sup>th</sup> December 2016, LONGTENG Hall*

Time	Title	Presenter/Author
13:30-13:35	<b>Opening Remarks</b>	
13:35-14:10	<b>Invited talk:</b> Talk title (TBC)	

<b>14:10-15:30</b>	<b>Session I (approximately 20 mins for each talk)</b>	
	A Self-adapting Method for RBC Count from Different Blood Smears Based On PCNN and Image Quality	Rong Ma
	Cardiac Left Ventricular Volumes Prediction Method Based on Atlas Location and Deep Learning	Gongning Luo, Suyu Dong, Kuanquan Wang, and Henggui Zhang
	A Novel Semantics-based Approach to Medical Literature Search	Chenhao Yang and Ben He
	DELTA: a Model Based Deep Clustering Approach	Yu Shang, Qiong Yu, Huansheng Cao, Guoqing Liu, Xiufeng Liu, Hao Wu, Yan Wang, and Ying Xu
<b>15:30-15:50</b>	<b>Coffee Break</b>	
<b>15:50-17:50</b>	<b>Session II ( approximately 20 mins for each talk)</b>	
	Modelling Enteric Methane Emissions from Milking Dairy Cows with Bayesian Networks	Huiru Zheng, Haiying Wang, and Tianhai Yan
	A Novel Saliency Detection Method via Manifold Ranking and Compactness Prior	Libo Zhang, Zakir Ullah, Yihan Sun, and Tiejian Luo
	A Fast and Precise Speech-Triggered Tongue Animation System by Combining Parameterized Model and Anatomical Model	Jun Yu, Chen Jiang, and Zengfu Wang
	Prediction and Analysis of Hot Region in Protein–Protein Interactions	Xiaoli Lin and Xiaolong Zhang
	Computational Identification of cis-Regulatory Genomic Elements via Machine Learning Approaches	Melissa Woghiren, Yifeng Li, and Alioune Ngom
	Prediction of Calmodulin Binding Proteins Using Short Linear Motifs	Yixun Li, Mina Maleki, Nicholas Carruthers, Luis Rueda, Paul Stemmer, and Alioune Ngom
<b>17:50</b>	<b>Closing Remarks</b>	

## The 1<sup>st</sup> International Workshop on Semantics-Powered Data Analytics (SEPDA 2016)

*Session Chair: Zhe He, Jiang Bian, Cui Tao, Michel Dumontier*

<b>Time</b>	<b>Title</b>	<b>Presenter/Author</b>
<b>08:00-08:10</b>	<b>Opening Remarks</b>	
<b>08:10-09:00</b>	<b>Keynote: Dr. Hua Xu (University of Texas Health Center at Houston)</b>	
<b>09:00-09:10</b>	Short Break	

<b>09:10-10:30</b>	<b>Session 1 (20 minutes for each talk, including Q&amp;A)</b> Session Chair: Dr. Zhe He	
	Classification of Status for Supplement Use in Clinical Notes	Yadan Fan, Lu He, and Rui Zhang
	The utilization of the OmniSearch semantic search tool to explore various microRNA regulation mechanisms in osteoarthritis	Jingshan Huang, Bi Liu, Yang Liu, and Ji Chen
	Dependency-based convolutional neural network for drug-drug interaction extraction	Shengyu Liu, Kai Chen, Qingcai Chen, and Buzhou Tang
	Exploiting Distributional Semantics to Benefit Machine Learning in Automated Clinical Text Classification: An Initial Study	Wenxin Ning and Ming Yu
<b>10:30-10:50</b>	Coffee Break	
<b>10:50-12:10</b>	<b>Session 2(20 minutes for each talk, including Q&amp;A)</b> Session Chair: Dr. Jiang Bian	
	Towards an obesity-cancer knowledge base: biomedical entity identification and relation detection	Juan Antonio Lossio-Ventura, William Hogan, François Modave, Amanda Hicks, Joshua Hanna, Yi Guo, Zhe He, and Jiang Bian
	A comprehensive (biological and computational) investigation on the role of microRNA::mRNA regulations performed in chronic obstructive pulmonary disease and lung cancer	Jingshan Huang, Dejing Dou, Jun She, Andrew Limper, Yanan Yang, and Ping Yang
	A Representational Analysis of Temporal Uncertainty in Clinical Events	Mohcine Madkour, Hsing-yi Song, Jingcheng Du, and Cui Tao
	Ontological Features of Electronic Health Records Reveal Distinct Association Patterns in Hepatocellular Carcinoma and Liver Metastasis	Lawrence Chan, Cesar Wong, and Keith Chiu
<b>12:10</b>	<b>Closing</b>	

<b>Workshop on Molecular networks and network pharmacology</b> <i>(20 minutes for each talk, including Q and A)</i> Session Chairs: Xingming Zhao, Kang Ning		
Time	Title	Presenter/Author
	<b>Session 1</b> Session Chair: Xingming Zhao Co-chair: Kang Ning	
	<b>Opening Remarks</b>	
09:00 – 10:30	Detecting Coordinated Regulations of Pathways By Higher Logic Analysis	Yansen Su, Xingyi Zhang, and Linqiang Pan
	Network based study for the anti-rheumatic mechanism of Tibetan medicated-bath therapy	Jian Yang, Tianhong Wang, Xiaona Shen, Xing Chen, Kehui Zhao, Jing Wang, Yi Zhang, Jing Zhao, and Yang Ga

	A novel scoring estimator to screening for oncogenic chimeric transcripts in cancer transcriptome sequencing	Jian-lei Gu, Yao Lu, Shi-yi Liu, Cong Liu, and Hui Lu
	Developing a robust colorectal cancer (CRC) risk predictive model with the big genetic and environment related CRC data	Chunqiu Zheng, Lei Xing, Tian Li, Tingting Li, Huan Yang, Jia Cao, Badong Chen, Ziyuan Zhou, and Le Zhang
<b>10:30-10:50</b>	<b>Coffee Break</b>	
	<b>Session 2</b> Session Chair: Xingming Zhao Co-chair: Kang Ning	
<b>11:00-12:00</b>	Characteristic Gene Selection via L2,1-norm Sparse Principal Component Analysis	Yao Lu, Ying-Lian Gao, Jin-Xing Liu, Chang-Gang Wen, Ya-Xuan Wang, and Jiguo Yu
	Detecting Protein Complexes from DPINs by OPTICS Based on Particle Swarm Optimization	Xiujuan Lei, Huan Li, and Fang-Xiang Wu
	Protein Expression Data Improves Gene Function Prediction	Huadong Yang, Xiaofeng Song, and Xuejiang Guo
<b>12:00-13:30</b>	<b>Lunch</b>	
	<b>Session 3</b> Session Chair: Kang Ning Co-chair: Xingming Zhao	
<b>13:30-15:30</b>	The exploration of functional divergence between human and macaque brains based on gene networks	Xing-Ming Zhao and Peipei Xiao
	Toward Optimization-Oriented NGS Peak Alignment Within the Context of Precision Medicine Initiative	Binhua Tang
	Machine Learning for Classification of RNA Expression Profiles to Predict QT Prolongation Liability and Potential Drug Repositioning	Dennis Bergau, Cong Liu, and Hui Lu
	Profiling of the viruses and bacteria in the microbial community: a network perspective	Wang Xi, Pengshuo Yang, and Kang Ning
	More accurate models for detecting gene-gene interactions from public expression compendia	Lu Zhang, Jia Xing Chen, and Shuai Cheng Li
	A High-Precision Shallow Convolutional Neural Network based Strategy for the Detection of Genomic Deletions	Wang Jing, Ling Cheng, and Gao Jingyang
<b>15:30-15:50</b>	<b>Coffee Break</b>	
	<b>Session 4</b> Session Chair: Kang Ning Co-chair: Xingming Zhao	
<b>15:50-16:50</b>	A Disease Module Detection Algorithm for Lung Adenocarcinoma Tumor Network with Significance of Connections and Network Controllability Methodology	Guimin Qin, Yibo Hou, Baoguo Yu, and Xiyang Liu
	A Graph-Laplacian PCA Based on L1/2-Norm Constraint for Characteristic Gene Selection	Chun-Mei Feng, Jin-Xing Liu, Ying-Lian Gao, Juan Wang, Dong-Qin Wang, and Yong Du
	Dynamic evolutions of HIV infection on treatment with combinatorial drugs	Lu Xiaojing, Liu Yanwei, Jiao Jianfeng, and Wang Ruiqi
<b>16:50</b>	<b>Closing Remarks</b>	

## Data Mining in Translational Biomedical Informatics & 2016 Workshop on Accelerator-Enabled Algorithms and Applications in Bioinformatics

*Session Chairs: Qian Zhu*

Time	Title	Presenter/Author
<b>08:00-09:15</b>	<b>Session I: Data Mining in Translational Biomedical Informatics (TBI)</b>	
08:00-08:25	Analyzing and Retrieving Illicit Drug-Related Posts from Social Media	Tao Ding, Arpita Roy, Zhiyuan Chen, Qian Zhu, and Shimei Pan
08:25-08:50	Multiple Confounders Correction with Regularized Linear Mixed Effect Models, with Application in Biological Processes	Haohan Wang and Jingkang Yang
08:50-09:15	C. elegans Search Behavior Analysis Using Multivariate Dynamic Time Warping	YIYANG WANG, CARLETON SMITH, MINGFEI SHAO, LI HUANG, JACOB FURST, HONGKYUN KIM, and DANIELA RAICU
<b>09:15-11:40</b>	<b>Session II: 2016 Workshop on Accelerator-Enabled Algorithms and Applications in Bioinformatics (WACEBI 2016)</b>	
09:15-09:40	The need of accelerators in analyzing biological networks	Jian-Yu Shi
09:40-10:05	A comparison of seed-and-extend techniques in modern DNA read alignment algorithms	Nauman Ahmed, Koen Bertels, and Zaid Al-Ars
10:05-10:30	Multiple sequence alignment and reconstructing phylogenetic trees with Hadoop	Quan Zhou
<b>10:30-10:50</b>	<b>Coffee Break</b>	
10:50-11:15	GBOOST 2.0: a GPU-based tool for detecting gene-gene interactions with covariates adjustment in genome-wide association studies	Meng Wang, Wei Jiang, Ronald Ching Wan Ma, and Weichuan Yu
11:15-11:40	DNA mapping using processor-in-memory architecture	Dominique Lavenier, Jean-Francois Roy, and David Furodet
<b>12:00-13:30</b>	<b>Lunch</b>	

## International Workshop on Biological Ontologies and Knowledge Bases (BiOK-2016)

*Session Chair: Jiajie Peng and Jin Chen*

Time	Title	Presenter/Author
<b>14:00 – 15:40</b>	<b>Session 1 (15 minutes for talk and 5 minutes for Q and A)</b> <i>Session Chair: Jiajie Peng and Jin Chen</i>	
	Opening Remarks	
	Constructing an integrated gene similarity network for the identification of disease genes	Zhen Tian, Maozu Guo, Chunyu Wang, Linlin Xing, Lei Wang, and Yin Zhang

	Biological Entity Relationship Extraction Method Based on Multiple Kernel Learning	Dongliang Xu, Jingchang Pan, Bailing Wang, Fei Yang, and Xinyi Zou
	Revealing protein functions based on relationships of interacting proteins and GO terms	Teng Zhixia, Guo Maozu, Liu Xiaoyan, Tian Zhen, and Kai Che
	DisSetSim: an online system for calculating similarity between disease sets	Yang Hu, Lingling Zhao, Zhiyan Liu, Hong Ju, Hongbo Shi, Peigang Xu, Yadong Wang, and Cheng Liang
<b>15:40-16:00</b>	<b>Coffee Break – perhaps poster session</b>	
<b>16:00-17:40</b>	<b>Session 2(15 minutes for talk and 5 minutes for Q and A)</b> <i>Session Chair: Jiajie Peng and Jin Chen</i>	
	Dynamic Analysis of Cell interactions in Biological Environments under Multiagent Social Learning Framework	Chengwei Zhang, Xiaohong Li, Shuxin Li, and Jianye Hao
	A Novel Method to Identify Pre-microRNA in Various Species Knowledge Base	Tianyi Zhao, Ningyi Zhang, Jun Ren, Peigang Xu, Zhiyan Liu, Liang Cheng, and Yang Hu
	Analyzing factors involved in the HPO-based semantic similarity calculation	Jiajie Peng, Qianqian Li, Bolin Chen, Jialu Hu, and Xuequn Shang
	An Automatic Approach for Constructing a Knowledge Base of Symptoms in Chinese	Tong Ruan, Mengjie Wang, Jian Sun, Ting Wang, Lu Zeng, Yichao Yin, and Ju Gao
<b>17:40</b>	<b>Closing</b>	

<b>2016 Workshop on Computational Structural Bioinformatics</b> <i>Sunday, December 18, 2016</i> <i>Co-chairs: Jing He, Kamal Al Nasr, Weitao Sun</i>	
<b>Opening Remarks</b>	
Paper 1 (remote presentation)	S19206 “An Efficient Method for Validating Protein Models Using Electron Microscopy Data” Kamal Al Nasr, Christopher Jones, Bashar Aboona, and Abdulrahman Alanazi
Paper 2 (remote presentation)	S19203 “Uncertainty Quantified Computational Analysis of the Energetics of Virus Capsid Assembly” Nathan Clement, Muhibur Rasheed, and Chandrajit Bajaj
Paper 3 (remote presentation)	S19207 “Identifying Amino Acids Sensitive to Mutations Using High-Throughput Rigidity Analysis” Michael Siderius and Filip Jagodzinski
Paper 4	B378 “RNAimage: A Method for Comparison of RNA Secondary Structures using Grayscale Image” Ying Li, Ye He, and Wei Du
Paper 5	S19205 “Community structure partition and key residue interaction pair detection in residue networks” Weitao Sun and Yukun Fan
Paper 6	

S19201 “Mining Structure Patterns on the Protein-DNA Interfaces” Qing Sun and Changhui Yan
Paper 7 S19202 “Selecting Near-native Structures From Decoys Using Maximal Cliques” Jinyang Yan, Yonggang Lu, and Jing He
Paper 8 S19208 “CHALLENGES IN MATCHING SECONDARY STRUCTURES IN CRYO-EM: AN EXPLORATION” DEVIN HASLAM, MOHAMMAD ZUBAIR, DESH RANJAN, Abhishek Biswas, and JING HE
Paper 9 B447 “Non-sequential Protein Structure Alignment Based on Variable Length AFPs Using the Maximal Clique” Xingmei Liu, Yonggang Lu, and Hu Cao

## 2016 Workshop on Health Informatics and Data Science (HI-DS)

*Session Chairs: Xiong Liu, Rong Liu, Chunhui Hou*

Time	Title	Author/Presenter
09:00 – 10:30	<b>Session 1 (20 minutes for each talk)</b>	
	<b>Opening</b>	
	Finding group structures in "Big Data" in healthcare research using mixture models	Shu-Kay Ng and Geoffrey McLachlan
	Healthcare Monitoring based on Digital Transactions at Pharmacies: Malaria in Kigali	Danny Habamwabo and Patrick McSharry
	Assisting humans to achieve optimal sleep by changing ambient temperature	Vivek Gupta, Siddhant Mittal, Sandip Bhaumik, and Raj Roy
	Automatic fall detection of human in video using combination of features	Kun Wang, Guitao Cao, Dan Meng, Weiting Chen, and Wenming Cao
<b>10:30 – 10:50</b>	<b>Coffee Break</b>	
<b>10:50 – 12:10</b>	<b>Session 2(20 minutes for each talk)</b>	
	Space-efficient k - mer search algorithm for the Generalized Suffix Tree	Freeson Kaniwa, Venu Madhav Kuthadi, Otlhapile Dinakennyane, and Heiko Schroeder
	Benchmarking Platform for Ligand-Based Virtual Screening	Petr Škoda and David Hoksza
	Setup and Integrate I2B2 Software Architecture to Implement CLIPPS Research for Electronic Health Record	Jinlei Guo, Tongbin Zhang, Jake Chen, and Lin Ma



	Multidimensional Visual Tool for Analysis of a Complex Program in Clinical & Translational Research	Chunlei Liu, Lemin Xiao, Roger Xu, Olga Brazhnik, Pan Gao, and Ken Samuel
<b>12:10-13:30</b>	<b>Lunch (on your own)</b>	
<b>13:30-15:30</b>	<b>Session 3(20 minutes for each talk)</b>	
	Using the Machine Learning Approach to Predict Patient Survival from High-Dimensional Survival Data	Wenbin Zhang, Jian Tang, and Nuo Wang
	Factorial Analysis of Error Correction Performance Using Simulated Next-Generation Sequencing Data	Isaac Akogwu, Hwanseok Choi, Huixiao Hong, Nan Wang, Chaoyang Zhang, and Ping Gong
	Assessing the Public Image of the NIH Clinical and Translational Science Awards (CTSA) Program through Analysis of Publications	Chunlei Liu, Lemin Xiao, Roger Xu, and Olga Brazhnik
	Classification of Tongue Images Based on Color Space Dictionary and Doublet	Guitao Cao, Jie Ding, Ye Duan, Liping Tu, Jiatuso Xu, and Dong Xu
	Assessing Stress Levels via Speech using Three Reading Patterns	Zhenyu Liu, Lihua Yan, Tianyang Wang, Bin Hu, and Fei Liu
	Community Outlier Based Fraudster Detection	Chenfei Sun
<b>15:30-15:50</b>	<b>Coffee Break</b>	
<b>15:50-16:50</b>	<b>Session 4(20 minutes for each talk)</b>	
	Identification of Discriminative Genes for Predicting Breast Cancer Subtypes	Roohollah Etemadi, Abedalrhman Alkhateeb, Iman Rezaeian, and Luis Rueda
	Adding Security to OpenEMR and GNU Health	Subrata Acharya and Thomas Hurd
	End Point Security Using AppLocker	Subrata Acharya and Kyle Di Giorgio

**7th International Workshop on High Performance Bioinformatics and Biomedicine (HiBB-2016)** *Session Chair: To Be Decided - Location: ZIYUN Hall 1 (2nd floor)*

Time	Title	Presenter/Authors
<b>1:30 – 3:30</b>	<b>Session 1 (15 minutes for talk and 5 minutes for Q and A)</b> <i>Session Chair: To Be Decided</i>	
	Opening Remarks	
	Immune Based Prognostic Biomarkers for Multiple Anticancer Therapies in Lung Adenocarcinoma	Kritika Karri and Dhundy Bastola

	Compression-Based Distance Methods as an Alternative to Statistical Methods for Constructing Phylogenetic Trees	Mohamed El-Dirany, Forrest Wang, Jacob Furst, John Rogers and Daniela Raicu
	MTBGD: Multi Type Biclustering for Genomic Data	Syeda Bintul Huda and Nighat Noureen
	On the identification of long non-coding RNAs from RNA-seq	Francesca Cristiano, Giuseppe Tradigo, Mattia Prosperi and Pierangelo Veltri
<b>3:30-3:50</b>	<b>Coffee Break</b>	
<b>3:50-6:30</b>	<b>Session 2 (15 minutes for talk and 5 minutes for Q and A)</b> <i>Session Chair: To Be Decided</i>	
	K2: Efficient Alignment-free Sequence Similarity Measurement using the Kendall Statistic	Jie Lin, Don Adjeroh, Bing-Hua Jiang and Yue Jiang
	IMDBfs: Bridging the Gap between In-Memory Database Technology and File-based Tools for Life Sciences	Matthieu-P. Schapranow, Milena Kraus, Marius Danner and Hasso Plattner
	A Global Approach for Determining Protein Function	Kamal Tahr
	Experiences on Quantitative Cardiac PET Analysis	Patrizia Vizza, Annalisa Papa, Giuseppe Lucio Cascini, Pietro Hiram Guzzi, Pierangelo Veltri, Giorgio Sesti and Elena Succurro,
	<b>Concluding Remarks</b>	

<b>7<sup>th</sup> Workshop Integrative Data Analysis in Systems Biology (IDASB) and International Workshop on Biological Network Driven Analysis (BNDA)</b> <i>Session Chairs: Huiru Zheng, Rui Jiang, Zhongming Zhao and Fiona Browne</i> <i>Saturday 17<sup>th</sup> December, Room: 一楼杜鹃厅 1<sup>st</sup> floor DUJUAN Hall</i>		
Time	Title	Presenter/Author
<b>14:00 – 14:05</b>	<b>Opening Remarks</b>	
<b>14:05 – 15:40</b>	<b>Session 1 (25minutes for each talk, including Q and A)</b>	
	(B232) A Method of Removing Ocular Artifacts from EEG using Discrete Wavelet Transform and Kalman Filtering	Yan Chen, Qinglin Zhao, Bin Hu, Jianpeng Li, Hua Jiang, Wenhua Lin, Yang Li, Shuangshuang Zhou, and Hong Peng
	(B254) Effects of propafenone on KCNH2-linked short QT syndrome: a modelling study	Cunjin Luo, Kuanquan Wang, and Henggui Zhang
	(S18201) Development of a Computer-Aided System for an Effective Brain Connectivity Network	Yaoxin Nie, Linlin Zhu, Yipeng Su, Xudong Li, and Zhendong Niu
	(I) Methods Medical Concepts Embedding and Visualization	Xu Min, Rui Jiang
<b>15:40 – 16:10</b>	<b>Coffee Break – perhaps poster session</b>	
<b>16:10 – 17:50</b>	<b>Session 2 (25minutes for each talk, including Q and A)</b>	
	(B364) Schizophrenia Genes Discovery by Mining the Minimum Spanning Trees from Multi-dimensional Imaging Genomic Data Integration	Su-Ping Deng, Dongdong Lin, Vince D. Calhoun, and Yu-Ping Wang
	(B419) A Network Analysis of Methane and Feed Conversion Genes in the Rumen Microbial Community	Fiona Browne, Haiying Wang, Huiru Zheng, Rainer Roche, Richard Dewhurst, and Paul Walsh
	(S18202) GLAlign: Using Global Graph Alignment to Improve Local Graph Alignment	Marianna Milano, Mario Cannataro, and Pietro hiram Guzzi
	(B283) Study on Performance of Non-negative Matrix Factorization	Mi-Xiao Hou, Jin-Xing Liu, Ying-Lian Gao, Xiang-Zhen Kong, and Chun-Hou Zheng
<b>17:50</b>	<b>Closing Remarks</b>	

**The Third International Workshop on High Performance Computing on Bioinformatics (HPCB 2016)** *Session Chairs: Che-Lun Hung, Huiru Zheng, Chuan Yi Tang, Chun-Yuan Lin*

<b>Time</b>	<b>Title</b>	<b>Presenter/Author</b>
09:00-10:30	<b>Session 1 (15mins for each talk)</b> <i>Session Chair: Che-Lun Hung</i>	
	<b>Opening Remarks</b>	
	Constructing a GPU Cluster Platform based on Multiple NVIDIA Jetson TK1	Kuan-Yu Yeh, Hui-Jun Cheng, Jin Ye, Jyh-Da Wei, and Chun-Yuan Lin
	The Role of High Performance, Grid and Cloud Computing in High-Throughput Sequencing	Gaye Lightbody, Valeriia Haberland, Fiona Browne, Jaine Blayney, and Huiru Zheng
	Efficient Parallel UPGMA algorithm based on Multiple GPUs	Che-Lun Hung, Chun-Yuan Lin, Fu-Che Wu, and Yu-Wei Chan
	Feature Study of Conversion Blindness on Functional Network with Aggregation of Local Key Information	Keling Fei, Wei Wang, Shusen Tang, Qiaoli Yang, Xu Wang, and Qi Xu
	Large Scale Extraction of Perfect and Imperfect DNA Palindromes Using In-Memory Computing	William Baskett, Matt Spencer, and Chi-Ren Shyu
	An Evaluation of Data Replication for Bioinformatics Workflows on NoSQL Systems	Iasmini Lima, Matheus Oliveira, Waldeyr Mendes Cordeiro da Silva, Diego Kieckbusch, Maristela Holanda, Maria Emília Walter, Aletéia Araújo, Márcio Victorino, and Sergio Lifschitz
<b>10:30-10:50</b>	<b>Coffee Break</b>	
<b>10:50-12:05</b>	<b>Session 2 (15mins for each talk)</b> <i>Session Chair: Che-Lun Hung</i>	
	K-mer Mapping and De Bruijn Graphs: the case for Velvet Fragment Assembly	Sergio Lifschitz, Elvismery Molina de Armas, Edward Hermann Haeusler, Maristela Torto de Holanda, Waldeyr Mendes Cordeiro da Silva, and Paulo Cavalcanti Gomes Ferreira
	Exploration of Alternative GPU Implementations of the Pair-HMMs Forward Algorithm	Shanshan Ren, Koen Bertels, and Zaid Al-Ars
	Mining sequential patterns from uncertain big DNA data in the Spark framework	Fan Jiang, Carson Leung, Oluwafemi Abimbola Sarumi, and Christine Zhang
	LCTD: a Lossless Compression Tool of FASTQ File Based on Transformation of Original File Distribution	Jiabing Fu, Yacong Ma, Bixin Ke, and Shoubin Dong,
	aWGRS: Automates Paired-end Whole Genome Re-sequencing Data Analysis Framework	Xiujuan Sun, Xiaohua Wan, Fa Zhang, and Jinzhi Zhang
<b>12:05</b>	<b>Closing Remarks</b>	

# Poster Program

Paper ID	Accepted Paper
P201	<p><i>A Clustering Approach for DeNovo Assembly using Next Generation Sequencing Data</i>  Mehdi Kchouk and Mourad Elloumi,  <b>Author Email(s):</b> mehdi.kchouk@gmail.com, mourad.elloumi@gmail.com  <b>Contact Person:</b> mehdi kchouk &lt;mehdi.kchouk@gmail.com&gt;</p>
P202	<p><i>Enhancing protein homology batch search algorithm with sequence compression and clustering</i>  Hongwei Ge, Liang Sun, and Jinghong Yu  <b>Author Email(s):</b> hwge@dlut.edu.cn, liangsun@dlut.edu.cn  <b>Contact Person:</b> Hongwei Ge &lt;hwge@dlut.edu.cn&gt;</p>
P203	<p><i>Splicing Isoform Expression Provides Insights into Neurodevelopmental Disorders</i>  Guan Ning Lin, Jorge Urresti, Megha Amar, and Roser Coronimas,  <b>Author Email(s):</b> nickgnlin@sjtu.edu.cn, jurresti@ucsd.edu, mamar@ucsd.edu, roser.corominas@upf.edu  <b>Contact Person:</b> Guan Ning Lin &lt;nickgnlin@sjtu.edu.cn&gt;</p>
P204	<p><i>Traditional Chinese Medicine Clinical Records Classification using Knowledge-Powered Document Embedding</i>  Liang Yao, Yin Zhang, Baogang Wei, Zherong Li, and Xiangzhou Huang  <b>Author Email(s):</b> yaoliang@zju.edu.cn, Yinzh@zju.edu.cn, wbg@zju.edu.cn, rsmile_lzr@zju.edu.cn, 690003374@qq.com  <b>Contact Person:</b> Liang Yao &lt;yaoliang@zju.edu.cn&gt;</p>
P205	<p><i>Differential Co-Expression Networks using RNA-seq and microarrays in Alzheimer's disease</i>  Hyojin Kang, Junehawk Lee, and Seokjong Yu  <b>Author Email(s):</b> hjkang@kisti.re.kr, juneh@kisti.re.kr, codegen@kisti.re.kr  <b>Contact Person:</b> Hyojin Kang &lt;hjkang@kisti.re.kr&gt;</p>
P206	<p><i>Template-based prediction of RNA tertiary structure</i>  Rastislav Galvnek, David Hoksza, and Josef Pnek  <b>Author Email(s):</b> david.hoksza@mff.cuni.cz, r.galvanek@outlook.sk, panek@biomed.cas.cz  <b>Contact Person:</b> David Hoksza &lt;david.hoksza@mff.cuni.cz&gt;</p>
P207	<p><i>Enlarging Drug Dictionary with Semi-Supervised Learning for Drug Entity Recognition</i>  Donghuo Zeng, Chengjie Sun, Lei Lin, and Bingquan Liu  <b>Author Email(s):</b> dhzeng@insun.hit.edu.cn, cjsun@insun.hit.edu.cn, linl@insun.hit.edu.cn, liubqg@insun.hit.edu.cn  <b>Contact Person:</b> Donghuo Zeng &lt;dhzeng@insun.hit.edu.cn&gt;</p>
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P213	<p><b><i>Semantic Analysis Based on Human Thought Pattern</i></b>  Libo Zhang, Tiejian Luo, Yihan Sun, and Lin Yang,  <b>Author Email(s):</b> zsmj@hotmail.com  <b>Contact Person:</b> Libo Zhang &lt;zsmj@hotmail.com&gt;</p>
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# BIBM 2017 Call for Papers

# BIBM2017

Kansas City, MO, USA  
Middle November, 2017

2017 IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2017)

We are soliciting high quality original research papers (including significant work-in-progress) in any aspect of bioinformatics and biomedicine. New computational techniques and methods in machine learning; data mining; text analysis; pattern recognition; knowledge representation; databases; data modeling; combinatorics; stochastic modeling; string and graph algorithms; linguistic methods; robotics; constraint satisfaction; data visualization; parallel computation; reverse engineering molecular biological systems, data integration; medical informatics, healthcare informatics, modeling and simulation and their application in life science domain are especially encouraged. Relevant topics included, but are not limited to:

## 1. Genomics and Molecular Structure, Function and Evolution

- a) Next-Gen Sequencing and Metagenomics
- b) Evolution, Phylogeny, Comparative Genomics
- c) SNPs and haplotype analysis, GWAS
- d) Protein/RNA Structure, Function and Interactions
- f) Personal Genome Analysis

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- a) Transcriptomics – RNA-Seq and Microarray Data Analysis
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- c) Proteomics, PTMs, Metabolomics
- d) Epigenomics, non-coding RNA analysis, DNA methylation analysis

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- a) Biomedical Intelligence, Clinical Data Analysis, and Electronic Health Record
- b) Biomedical Signal/Image Analysis
- c) Genome-Phenome Analysis
- d) Biomarker Discovery

## 4. Cross-Cutting Computational Methods and Bioinformatics Infrastructure

- a) Biomedical Text Mining and Ontologies
- b) Biological Data Mining and Visualization
- c) Computational Modeling and Data Integration
- d) High Performance Computing

## 5. Healthcare Informatics

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## 6. Industry and Government Program

implementations of Bioinformatics and Biomedicine solutions relevant to industrial settings. The focus of industry track is on papers that address the practical, applied, or pragmatic or new research challenge issues related to the use of bioinformatics and biomedicine technologies in industry

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