

# CONFERENCE ABSTRACT

**2019 7th International Conference on Biological and  
Medical Sciences (ICBMS 2019)**

**Chengdu, China**

**August 13-15, 2019**



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# Table of Contents

ICBMS 2019 Conference Introduction	6
Presentation Instruction	7
Keynote Speaker Introduction	8
Brief Schedule of Conference	13
<b>Session 1: Biomedicine</b>	
C3006: OTUB2 Inhibits Ovarian Cancer Initiation and Progression via TLR10-mediated Suppression of NF/ $\kappa$ B Signaling <i>Wan Chang, Qingyu Luo, Xiaowei Wu and Zhihua Liu</i>	15
C2003: Study of the Interaction between Fluorescent Probes and Their Targets using Molecular Docking <i>Yueqing Li, Jianli Fan and Xiaojun Peng</i>	15
C3007: Parthenolide Provides a Second Hit to ARID1A Epigenetic Silencing in Squamous Cell Carcinoma <i>Qingyu Luo, Xiaowei Wu and Zhihua Liu</i>	16
C0024: A Review of Antibiotic Resistance in Developing Countries and Suggested Solutions to Tackle It <i>Xuan Zuo</i>	16
C2005: OTUD1 Promotes AIF Nuclear Translocation and Activates Caspase-independent Apoptosis Signaling in Squamous Cell Carcinoma <i>Pengfei Zhao, Xiaowei Wu, Qingyu Luo and Zhihua Liu</i>	17
C3013: Effect of Refined-deep Sea Water on Serum Lipid Profile in Hypercholesterolemia: A Randomized, Double-blind, Placebo-controlled, Clinical Trial <i>Hojun Kim</i>	17
C2007: USP11 Promotes the Chemotherapy Resistance in Ovarian Cancer <i>Xiaolin Zhu, Hongyan Chen and Zhihua Liu</i>	18
C3005: JOSD1 Deubiquitinates MCL1 to Drive Acquired Chemoresistance in Gynaecological Cancer <i>Xiaowei Wu, Qingyu Luo and Zhihua Liu</i>	19
<b>Session 2: Medical Image Processing</b>	
C0006: Minimal Path based Particle Tracking in Low SNR Fluorescence Microscopy Images <i>Sheng Lu, Tong Chen, Fan Yang, Chenglei Peng, Sidan Du and Yang Li</i>	20

C0008: Application of Euler Elastica Regularized Logistic Regression on Resting-state fMRI for Identification of Alzheimer's Disease	20
<i>Weiping Guo, Li Yao and Zhiying Long</i>	
C0022: Computer Aided Annotation of Early Esophageal Cancer in Gastroscopic Images based on Deeplabv3+ Network	21
<i>Ding-Yun Liu, Hong-Xiu Jiang, Ni-Ni Rao, Cheng-Si Luo, Wen-Ju Du, Zheng-Wen Li and Tao Gan</i>	
C0017: Facial Spot Contour Extraction based on Color Image Processing	21
<i>Xiaojin Liu, Jiukai Sun and Xiong Wang</i>	
C0016: Multi-organ Segmentation from Abdominal CT with Random Forest based Statistical Shape Model	22
<i>Jiaqi Wu, Guangxu Li, Huimin Lu and Hyoungeop Kim</i>	
C1011: Three-dimensional Reconstruction of Optical Coherence Tomography Images of Esophagus	22
<i>Sihan Nao, Miao Zhang, Lirong Wang, Yongjin Xu and Xiaohe Chen</i>	
C1002: Detection of Abnormal Regions on Temporal Subtraction Images based on CNN	22
<i>Mitsuaki Nagao, Huimin Lu, Hyoungeop Kim, Takatoshi Aoki and Shoji Kido</i>	
C0010: Computer-aided Cervical Cancer Screening Method based on Multi-spectral Narrow-band Imaging	23
<i>Zihan Yang, Dirong Yi and Jiahao Shen</i>	
<b>Session 3: Computer-aided Medicine</b>	
C2008: TNF $\alpha$ -FOXO2 Axis Drive ESCC Metastasis through FA2H Mediated Lipid Metabolic Reprogramming	25
<i>Xuantong Zhou, Furong Huang, Gang Ma and Zhihua Liu</i>	
C0015: Muscle Artifacts Cancellation Framework for ECG Signals Combining Convolution Auto-encoder and Average Beat Subtraction	25
<i>Yongfeng Huang, Zijian Ding and Guijin Wang</i>	
C1007: Design of Cleaning Module based on CAN	26
<i>Feifei Sun, Wenliang Zhu, Gang Ma, Kongpeng Xing and Lirong Wang</i>	
C3011: Dynamic Functional Connectivity Analysis of Seafarer's Brain Functional Networks	27
<i>Yuhu Shi</i>	
C1009: Fall Guard: Fall Monitoring Application for the Elderly based on Android Platform	27
<i>Jenny Ni, Wenliang Zhu, Jinfu Huang, Longfei Niu and Lirong Wang</i>	
C1001: Forecasting of Ventricular Tachyarrhythmia based on Multi-scale Entropy of Short-term Heart Rate Variability	28
<i>Liu Qing, Dong Hong-Sheng and Ma Yin-Yuan</i>	

C1006: An Automatic Detection Algorithm for T Wave Position based on T Wave Morphology 28

*Wanyue Li, Lishen Qiu, Jie Zhang, Wenliang Zhu and Lirong Wang*

#### **Session 4: Pattern Recognition and Classification**

C0001: Application of Granger Causality in Decoding Covert Selective Attention with Human EEG 30

*Weikun Niu, Yuying Jiang, Yujin Zhang, Xin Zhang and Shan Yu*

C0014: Relationships of Cohen's Kappa, Sensitivity, and Specificity for Unbiased Annotations 30

*Juan Wang and Bin Xia*

C1010: Practical Fall Detection Algorithm based on Adaboost 31

*Wenqiang Cai, Lishen Qiu, Wanyue Li, Jie Yu and Lirong Wang*

C0020: Different Goal-driven CNNs Affect Performance of Visual Encoding Models based on Deep Learning 31

*Ziya Yu, Chi Zhang, Linyuan Wang, Li Tong and Bin Yan*

C1008: Epileptic Seizure Classification based on the Combined Features 32

*Jie Yu, Lirong Wang and Xueqin Chen*

C0018: RGB-D-based Hand Gesture Recognition for Letters Expression 32

*Jin Li, Jishuo Yan, Guangxu Li, Liyuan Wang and Fan Yang*

C1005: Region-based High-resolution Siamese Network for Robust Visual Tracking 33

*Chunbao Li and Bo Yang*

#### **Poster Session**

C1003: Retinal Artery/Vein Classification via Rotation Augmentation and Deeply Supervised U-Net Segmentation 34

*Zhaolei Wang, Junbin Lin, Ruixuan Wang and Weishi Zheng*

C3010: Discovery of Novel HDAC Inhibitor from Traditional Chinese Medicine 34

*Chia-Min Chen, Chang-Sheng Chiang, Yung-Jen Yang, Zhi-Lin Wang, Cheng-Fang Tsai and Pei-Chun Chang*

C3014: Anti-obesity Effect of Fermented *Panax Notoginseng* via Modulating Gut Microbiota 35

*Na Rae Shin, Soo-Kyoung Lim, Hyunsuk Song and Hojun Kim*

C0004: Kinematic Characteristics of Backhand Block in Table Tennis 35

*Yi Ren, Zhipei Huang, Yiming Guo, Jiankang Wu and Yingfei Sun*

C0013: An Approach for Recognition of Enhancer-promoter Associations based on Random Forest 36

*Tianjiao Zhang and Yadong Wang*

C0011: Control of Upper Limb Motions by Combinations of Basic Muscle Synergies 36

<i><b>Bingyu Pan, Yingfei Sun, Licai Sun, Zhipei Huang and Jiankang Wu</b></i>	
C0025: AWGI: An Auto-weighted Framework Integrating Heterogeneous Networks for Gene Interaction Prediction	36
<i><b>Han Luo, Zhenfeng Lei and Hanping Ke</b></i>	
C3015: The Effect of <i>Crataegus Pinnatifida</i> in High-fat Diet Induced Mice via Gut Microbiota	37
<i><b>Meng Yang, Yura Choi, Na Rae Shin, Soo-Kyoung Lim and Hojun Kim</b></i>	
C0003: Automatic Sleep Staging based on Curriculum Learning Approach	38
<i><b>Xingjun Wang and Ziyao Xu</b></i>	
Listener	39
Conference Venue	40
Academic Visit	41
One Day Tour	42
Note	44
Feedback Information	47

## Introduction

Welcome to 2019 7th International Conference on Biological and Medical Sciences (ICBMS 2019) which is organized and supported by Hong Kong Chemical, Biological & Environmental Engineering Society (CBEEES), Biology and Bioinformatics (BBS). Previously, ICBMS series has been held successfully in 2018 in Seoul, South Korea; 2017 in Kitakyushu, Japan; 2016 in Budapest, Hungary; 2015 in Shanghai, China; 2014 in Bali, Indonesia and 2013 in Phuket, Thailand. The aim of ICBMS is to provide opportunities for the researchers, engineers, academicians as well as industrial professionals from all over the world to exchange new ideas and application experiences face to face, to establish business or research relations and to find global partners for future collaboration. In addition to the high-profile keynotes, the conference program will feature invited speeches, oral and poster sessions for participants related to Biological and Medical Sciences from all over the world. It is welcomed authors to submit papers for publication and presentation, abstracts for presentation and listener to participate in ICBMS 2019.

**Papers will be published in the following journal:**



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

**Conference website and email:** <http://www.icbms.org>; [icbms@cbees.org](mailto:icbms@cbees.org)

# Presentation Instruction

## Instruction for Oral Presentation

### **Devices Provided by the Conference Organizer:**

Laptop Computer (MS Windows Operating System with MS PowerPoint and Adobe Acrobat Reader)

Digital Projectors and Screen

Laser Stick

### **Materials Provided by the Presenters:**

PowerPoint or PDF Files (Files should be copied to the Conference laptop at the beginning of each Session.)

### **Duration of each Presentation (Tentatively):**

Keynote Speech: about **40** Minutes of Presentation and **5** Minutes of Question and Answer

Oral Presentation: about **12** Minutes of Presentation and **3** Minutes of Question and Answer

## Instruction for Poster Presentation

### **Materials Provided by the Conference Organizer:**

The place to put poster

### **Materials Provided by the Presenters:**

Home-Made Posters: Submit the poster to the staff when signing in

Poster Size: A1 (841\*594mm)

Load Capacity: Holds up to 0.5 kg

## Best Presentation Award

One Best Presentation will be selected from each session, and the Certificate for Best Presentation will be awarded at the end of each session on August 14, 2019.

## Dress Code

Please wear formal clothes or national representative of clothing.

# Keynote Speaker Introduction

## Keynote Speaker I



Prof. Bairong Shen  
Sichuan University, China

**Bairong Shen** is Professor & Executive Director General in Institutes for Systems Genetics, West China Hospital, Sichuan University. He received his Ph.D. in Chemistry from Fudan University in 1997. Dr. Shen was appointed as associate professor of Physical Chemistry at Fudan University in 1999, for his accomplishments in theoretical and computational surface chemistry focused on chemical reactions catalyzed by metals and alloys by ab initio and semi-empirical quantum mechanical methods. In the early 2000s, Dr. Shen started his new exploration into biomedical informatics and related computational biology in his postdoctoral research in the University of Tampere, Finland. His success in the new paradigm of biological research won him a competitive faculty position in the European university as an assistant professor of Bioinformatics since 2004. He joined the Soochow University by founding the University's Center for Systems Biology in 2008. In Finland and China, Dr. Shen has taught more than ten different courses in biomedical informatics and systems biology and published more than 100 peer-reviewed articles in competitive journals which covered the medical genetic areas including cancer-marker development and medical informatics and the basic exploration in physics, chemistry, biology and computational science. His recent researches focus on Biomedical informatics and Systems Biology of complex diseases. He has been actively involving in initiating and organizing international and national scientific collaborations, conferences and publication in his area.

***Topic:** "Ontologies for Biomedical Data Sharing and Mining in the Era of Personalized Healthcare"*

**Abstract**—The developing of 5G wireless network will further promote the biomedical big data paradigm and make the personalized and active healthcare practical. But the sharing and mining of big data still has lots of challenges. I will talk about the state-of-the-art of biomedical ontology and discuss the future integrative ontologies based data analysis and applications, introduce theories, models for the understanding of these diverse biomedical big data including genomic and phenotype data, lifestyle data and complex diseases by our researches and discuss the future developing of modern biomedical informatics, emphasizing the biomedical ontologies development and participatory medicine; evolutionary medicine



and network robustness or vulnerability; physiological and sensor informatics; N-of-1 studies and systems health, *etc.*

## Keynote Speaker II



Prof. Hiroshi Fujita  
Gifu University, Japan

**Prof. Hiroshi Fujita** received the B.S. and M.S. degrees in electrical engineering from Gifu University, Japan, in 1976 and 1978, respectively, and Ph.D. degree from Nagoya University in 1983. He became a research associate in 1978 and an associate professor in 1986 at Gifu National College of Technology. He was a visiting researcher at the K. Rossmann Radiologic Image Laboratory, University of Chicago, in 1983-1986. He became an associate professor in 1991 and a professor in 1995 in the Faculty of Engineering, Gifu University. He has been a professor and chair of intelligent image information since 2002 at the Graduate School of Medicine, Gifu University. He is now a Research Professor of Gifu University. He is a member of the Society for Medical Image Information (Honorary President), the Institute of Electronics, Information and Communication Engineers (Fellow), its Technical Groups on Medical Image (Adviser), the Japan Society for Medical Image Engineering (Director), and some other societies such as SPIE. He has been also served as scientific committee or program committee members, such as in International Workshop on Digital Mammography (Breast Imaging), SPIE Medical Imaging, and Computer Assisted Radiology and Surgery (CARS). He was worked as a General co-chair of Asian Forum on Medical Imaging 2007 held in Cheju National University, Korea, and as a General Chair of International Workshop for Breast Imaging (IWDM2014, Gifu). He has also worked as a Guest Editor-in-Chief in Special Section Editorial Committee for Medical Imaging, issued in April, 2013, from IEICE Society in Japan, and also as a Guest Editor-in-Chief in the Special Issue on Advanced Image Technologies in Diagnostic Imaging in 2018 in the Journal of Medical Imaging and Health Informatics. His research interests include computer-aided diagnosis system, image analysis and processing, and image evaluation in medicine. He has published over 1000 papers in Journals, Proceedings, Book chapters and Scientific Magazines.

**Topic:** *"The State-of-the-art of AI-aided Diagnosis in Medical Imaging"*

**Abstract**—Computer-aided detection/diagnosis, so-called CAD, is rapidly entering the radiology mainstream. It has already become a part of the routine clinical work especially for the detection of breast cancer with mammograms, in which the computer output is used as a "second opinion" in assisting radiologists' image interpretations. Recent powerful artificial intelligence (AI) technology including deep learning advances the development and improving performance of CAD to the next stage, sometimes called as AI-CAD. In this talk, the state-of-the-art of AI-CAD and issues to be solved will be reviewed and discussed.

## Keynote Speaker III



Prof. Peidu Jiang

University of Electronic Science and Technology of China, China

**Peidu Jiang** received MD degree in Oncology from West China School of Medicine, Sichuan University (China) in 2011. Later, he received his second doctoral degree from Tokyo Medical and Dental University (Japan) where he studied Cell Biology. Following his doctorate, Dr. Jiang completed post-doctoral studies at the University of Tokyo (Japan) in the laboratory of Dr. Noboru Mizushima where he studied autophagy. Currently, Dr. Jiang is a Professor of Pharmacology at School of Medicine, University of Electronic Science and Technology of China. His research focuses on autophagic degradation of proteins and organelles, pathogenesis and therapeutic strategy of intracellular turnover-related diseases.

*Topic: "Molecular Mechanism of Autophagy and Development of its Potent Modulators"*

**Abstract**—Autophagy is a self-degradative process by which cytosolic components and organelles are delivered to the lysosome for degradation. Although over 38 autophagy-related (*Atg*) genes have been identified in yeast and mammalian cells, the mechanism how autophagosomes fuse with lysosomes still needs to be further elucidated. Here, we identified YKT6 as a novel autophagosomal SNARE (soluble *N*-ethylmaleimide-sensitive factor attachment protein receptor) protein. Depletion of YKT6 inhibited autophagosome–lysosome fusion partially in wild-type and completely in syntaxin 17 (a known autophagosomal SNARE) KO cells, suggesting that YKT6 and syntaxin 17 are independently required for autophagosome–lysosome fusion. Autophagy plays important roles in cellular homeostasis and disease pathogenesis. For example, downregulation of autophagy is involved in numerous diseases including neurodegenerative diseases, cancer, aging, metabolic disorders, and infectious diseases. Therefore, small chemical molecules that can modulate autophagy activity may have pharmacological value for treating these autophagy-related diseases. Using a GFP-LC3-based high content screening assay, we identified a novel chemical that is able to activate autophagy at initiation stage. This molecule, termed as CPC, increases the numbers of autophagosomes and reduces the autophagy substrate p62/SQSTM1 levels by inhibiting mTOR signaling pathway.

## Keynote Speaker IV



Prof. Hyoungseop Kim  
Kyushu Institute of Technology, Japan

**Prof. Hyoungseop Kim** received his B.A. degree in electrical engineering from Kyushu Institute of Technology in 1994, the Masters and Ph.D. degree from Kyushu Institute of Technology in 1996 and 2001, respectively. He is a professor in the department of control engineering at Kyushu Institute of Technology. His research interests are focused on medical application of image analysis.

***Topic:** "A Computer Aided Diagnosis Method for Identification of Rheumatoid Arthritis on CR Images"*

**Abstract**—With the aging of the population in Japan, patients with osteoporosis are increasing year by year. Because there is a prediction that the number of patients will increase due to the progress of aging society in the future, counterplan is socially important. On the other hand, although diagnostic imaging is effective for osteoporosis, many symptoms similar to osteoporosis are also present. In visual screening on osteoporosis, since it is very difficult to read an enormous number of images and interpret the affected part of osteoporosis accurately from each image, much screening time are required and the burden on interpreting doctors is concerned. To solve this problem, we are working on a computer-aided diagnosis (CAD) system for osteoporosis. In this study, we propose some segmentation methods of the phalange region from the phalange CR images and classification of osteoporosis based on machine techniques. In this talk, I will introduce a CAD system and its usefulness with some experimental results.

## Brief Schedule of Conference

<b>Day 1</b> <b>August 13,</b> <b>2019</b> <b>(Tuesday)</b>	10:00-17:00	<b>Venue: Hotel Lobby(1<sup>st</sup> Floor)</b> <b>Arrival Registration</b>
	14:00-16:00	<b>Academic Visit in Institutes for Systems Genetics,</b> <b>West China Hospital, Sichuan University</b>
<b>Day 2</b> <b>August 14,</b> <b>2019</b> <b>(Wednesday)</b>	<b>Venue: Tanggula Hall</b> <b>(唐古拉厅, 17<sup>th</sup> Floor)</b>	
	09:00-09:05	<b>Opening Remarks</b> Prof. Hyoungseop Kim Kyushu Institute of Technology, Japan
	09:05-09:50	<b>Keynote Speech I</b> Prof. Bairong Shen Sichuan University, China Topic: "Ontologies for Biomedical Data Sharing and Mining in the Era of Personalized Healthcare"
	09:50-10:35	<b>Keynote Speech II</b> Prof. Hiroshi Fujita Gifu University, Japan Topic: "The State-of-the-art of AI-aided Diagnosis in Medical Imaging"
	10:35-11:00	<b>Coffee Break &amp; Group Photo</b>
	11:00-11:45	<b>Keynote Speech III</b> Prof. Peidu Jiang University of Electronic Science and Technology of China, China Topic: "Molecular Mechanism of Autophagy and Development of its Potent Modulators"
	11:45-12:30	<b>Keynote Speech IV</b> Prof. Hyoungseop Kim Kyushu Institute of Technology, Japan Topic: "A Computer Aided Diagnosis Method for Identification of Rheumatoid Arthritis on CR Images"
	<b>12:30-13:45 Lunch</b> <b>Tibetan Auspicious Restaurant(藏宴厅, 2<sup>nd</sup> Floor)</b>	

ICBMS 2019 CONFERENCE ABSTRACT

<b>Day 2</b> <b>August 14,</b> <b>2019</b> <b>(Wednesday)</b>	<b>Session 1: 13:45-15:45</b> <b>Venue: Tangula Hall</b> <b>(唐古拉厅, 17<sup>th</sup> Floor)</b> Topic: “Biomedicine” 8 presentations	<b>Session 2: 13:45-15:45</b> <b>Venue: Red Mountain Hall</b> <b>(红山厅, 17<sup>th</sup> Floor)</b> Topic: “Medical Image Processing” 8 presentations
	<b>15:45-16:15 Coffee Break and Poster Session</b> <b>(Tangula Hall, 17<sup>th</sup> Floor)</b>	
	<b>Session 3: 16:15-18:00</b> <b>Venue: Tangula Hall</b> <b>(唐古拉厅, 17<sup>th</sup> Floor)</b> Topic: “Computer-aided Medicine” 7 presentations	<b>Session 4: 16:15-18:00</b> <b>Venue: Red Mountain Hall</b> <b>(红山厅, 17<sup>th</sup> Floor)</b> Topic: “Pattern Recognition and Classification” 7 presentations
	<b>18:30-20:30 Dinner</b> <b>Yak Caf é(亚克咖啡厅, 2<sup>nd</sup> Floor)</b>	
<b>Day 3</b> <b>August 15,</b> <b>2019</b> <b>(Thursday)</b>	<b>9:00-17:30</b>	<b>One Day Tour</b>

**Tips:** Please arrive at the Conference Room 10 minutes before the session begins to upload PPT into the laptop; submit the poster to the staff when signing in.

# Session 1

**Tips:** The schedule for each presentation is for reference only. In order not to miss your presentation, we strongly suggest that you attend the whole session.

**Afternoon, August 14, 2019 (Wednesday)**

**Time: 13:45-15:45**

**Venue: Tanggula Hall(唐古拉厅, 17<sup>th</sup> Floor)**

**Topic: “Biomedicine”**

**Session Chair: Prof. Peidu Jiang**

<p>C3006 Session 1 Presentation 1 (13:45-14:00)</p>	<p>OTUB2 Inhibits Ovarian Cancer Initiation and Progression via TLR10-mediated Suppression of NF/κB Signaling <b>Wan Chang</b>, Qingyu Luo, Xiaowei Wu and Zhihua Liu Chinese Academy of Medical Sciences and Peking Union Medical College, China</p> <p><i>Abstract</i>—Ovarian cancer has been recognized as a silent killer for its lowest five-year survival rate among all female cancers. Difficulty in the early diagnosis and the chemoresistance in the late-chemotherapy are main reasons for the poor prognosis of ovarian cancer patients. The ubiquitin system regulates diverse biological processes involved in cancer pathogenesis by altering the stability, activity, localization and interactions of protein substrates through adding or removing ubiquitin from substrates. However, the role of many DUBs in ovarian cancer remains largely unknown. In this study, we showed that deubiquitinase OTUB2 is epigenetically silenced in ovarian cancer. OTUB2 knockout mice showed increased ovarian cancer tumorigenesis following DMBA treatment. Overexpression of OTUB2 inhibits proliferation and promotes apoptosis and chemosensitivity of ovarian cancer cells. Mechanistically, OTUB2 stabilizes and cooperates with SNX29P2 to recruit HCE, which then activates TLR10 expression and inhibits NF/κB signaling. Our study for the first revealed the tumor-suppressive role of OTUB2 in ovarian cancer.</p>
<p>C2003 Session 1 Presentation 2 (14:00-14:15)</p>	<p>Study of the Interaction between Fluorescent Probes and Their Targets using Molecular Docking <b>Yueqing Li</b>, Jianli Fan and Xiaojun Peng Dalian University of Technology, China</p> <p><i>Abstract</i>—There are a kind of “off-on” fluorescent probes, designed for medical labeling and imaging based on photoinduced electron transfer (PET) principle, which target overexpressed enzymes in cancer cells and tissues. The “off-on” mechanism of the fluorescence is related to the</p>

ICBMS 2019 CONFERENCE ABSTRACT

	<p>conformations of the probe. When they are in folded state, the fluorescence of the probe is quenched by PET between the fluorophore and the enzyme inhibitor part. When the enzyme inhibitor part of the probe interacts with the active site of the enzyme, intramolecular PET is blocked and the fluorescence is restored. We used molecular docking to imitate the detail interaction between three probes (NB-BF, NBFMeI, DCM-APN) and their corresponding enzymes (Pim-1, aminopeptidase N), respectively. The docking result showed NB-BF could be in an unfolded state when the targeting part was embedded in the groove of Pim-1 kinase and the long hexanediamine linker between NB fluorophore and BF inhibitor could lie along the cranny and fit well. The docking targeting aminopeptidase N also indicated the probes could coordinate with the catalytic zinc ion. In the experiments, NBFMeI and DCM-APN could be hydrolyzed by APN and liberate strong fluorescence. Thereby, molecular docking can be an effective method to shed light on the interaction between the probes and their targets.</p>
<p>C3007 Session 1 Presentation 3 (14:15-14:30)</p>	<p>Parthenolide Provides a Second Hit to ARID1A Epigenetic Silencing in Squamous Cell Carcinoma <b>Qingyu Luo</b>, Xiaowei Wu and Zhihua Liu Chinese Academy of Medical Sciences and Peking Union Medical College, China</p> <p><i>Abstract</i>—SWI/SNF chromatin remodeling complexes feature a mutation rate of nearly 20% in human cancer, and ARID1A is the most frequently mutated component. However, some components of SWI/SNF complexes, including ARID1A, exhibit a very low mutation rate in squamous cell carcinoma (SCC), illustrating that mechanisms other than mutation might contribute to their inactivation. Here, we demonstrated that promoter hypermethylation contributes to low ARID1A expression in SCC and leads to poor prognosis. We showed that ARID1A maintains transcriptional homeostasis by both direct and indirect chromatin remodeling mechanisms. ARID1A depletion activates an oncogenic transcriptome that drives SCC initiation and progression. Moreover, we found that parthenolide synthetically targets SCC cells with low ARID1A expression via a second hit to both HDAC1 and oncogenic signaling. Our results identified a novel inactivation mechanism of ARID1A in SCC despite its high mutation rate in other cancer types. Additionally, we revealed a switch from a tumor-suppressive to an oncogenic transcriptome following ARID1A depletion and demonstrated that parthenolide effectively interfered with this switch.</p>
<p>C0024 Session 1 Presentation 4</p>	<p>A Review of Antibiotic Resistance in Developing Countries and Suggested Solutions to Tackle It <b>Xuan Zuo</b> Kaohsiung American School, Taiwan</p>



ICBMS 2019 CONFERENCE ABSTRACT

<p>(14:30-14:45)</p>	<p><i>Abstract</i>—Antibiotic resistance is a global healthcare issue that is a major factor in mortality worldwide. The development and spreading of resistance are facilitated by the misuse and overuse of antibiotics. This treat is especially severe in developing countries for many factors like lack of education, lack of government regulation, poverty, and lack of trained healthcare workers. In this systematic review, the current situation of the antibiotic resistance issue is discussed by comparing the strategies implemented in developing and developed countries. Following the Global Action Plan by the World Health Organization (WTO) and national strategies of UK, USA, and Australia, some recommendations are given on the basis of national conditions of developing countries. In addition, this journal is composed to remind people of innovative strategy such as educational games or mobile phone applications to tackle the antibiotic resistance.</p>
<p>C2005 Session 1 Presentation 5 (14:45-15:00)</p>	<p>OTUD1 Promotes AIF Nuclear Translocation and Activates Caspase-independent Apoptosis Signaling in Squamous Cell Carcinoma <b>Pengfei Zhao</b>, Xiaowei Wu, Qingyu Luo and Zhihua Liu Chinese Academy of Medical Sciences and Peking Union Medical College, China</p> <p><i>Abstract</i>—Squamous cell carcinoma (SCC) includes a range of different types of tumors, usually occurring in organs or tissues with squamous epithelium, including skin, mouth, esophagus, etc. As a traditional treatment, chemotherapy has been widely used in the clinical treatment of squamous cell carcinoma. However, the intrinsic/acquired chemoresistance has become one of the most severe clinical problems. As one of the most crucial post-transcriptional modification, deubiquitylation plays an important role in the development of various tumors. After an in vivo screening of 45 deubiquitinases, we found OTUD1 depletion significantly inhibited cisplatin-induced apoptosis. Moreover, ectopic expression of OTUD1 in SCC cell lines dramatically increased the sensitivity to cisplatin treatment. We further showed that OTUD1 promotes apoptosis through promoting nuclear translocation of apoptosis inducing factor (AIF). IHC analysis of 122 ESCC samples showed that low OTUD1 expression correlates with poor prognosis of SCC patients. Collectively, these results suggest that OTUD1 is a bona fide tumor suppressor and low OTUD1 expression contributes to chemoresistance in squamous cell carcinoma.</p>
<p>C3013 Session 1 Presentation 6 (15:00-15:15)</p>	<p>Effect of Refined-deep Sea Water on Serum Lipid Profile in Hypercholesterolemia: A Randomized, Double-blind, Placebo-controlled, Clinical Trial <b>Hojun Kim</b> Dongguk University, Republic of Korea</p> <p><i>Abstract</i>—Background: Deep sea water (DSW), which is rich in minerals,</p>

ICBMS 2019 CONFERENCE ABSTRACT

	<p>has been investigated for its lipid-lowering effects, but clinical evidence is still far from conclusive. Therefore, this study was conducted to examine the effects of refined-DSW on hypercholesterolemia as well as lipid metabolic parameters. <b>Materials and Methods:</b> In this randomized, double-blind, placebo-controlled trial, a total of 78 participants were randomized to either a refined-DSW group (n=39) that drank 440 ml refined-DSW twice a day for eight weeks or a placebo group (n=39). Clinical laboratory information was collected from all subjects at 0, 4, and 8 weeks and telephone follow up was conducted at 2 and 6 weeks to check for adverse events (AE). <b>Results:</b> Although both groups showed reduced total cholesterol (TC) and low-density lipoprotein cholesterol (LDL-C) (p&lt;0.05), only the DSW group showed a consistent decline of TC and LDL-C relative to the time of administration. Moreover, stratified analysis of the poor healthy group and disease group demonstrated a greater change in TC and LDL-C than when comparing the entire population. In addition, lipoprotein(a) (Lp(a)) decreased significantly in the DSW group (p&lt;0.05). However, refined-DSW did not affect other lipid profiles, including high-density lipoprotein cholesterol (HDL-C), triglyceride (TG), free fatty acid (FFA), apolipoproteins (Apo), inflammation marker, hematology parameters, blood chemistry, urine parameters, or vital signs. <b>Conclusion:</b> Refined-DSW improved lipid profiles as it reduced TC and LDL-C while maintaining HDL-C levels in people with hypercholesterolemia.</p>
<p>C2007 Session 1 Presentation 7 (15:15-15:30)</p>	<p><b>USP11 Promotes the Chemotherapy Resistance in Ovarian Cancer</b> <b>Xiaolin Zhu</b>, Hongyan Chen and Zhihua Liu Chinese Academy of Medical Sciences and Peking Union Medical College, China</p> <p><i>Abstract</i>—Ovarian cancer is a common type of malignant tumors in the female reproductive system. Treatment of ovarian cancer comprises a combination of surgery and chemotherapy, but patients typically experience disease relapse within 2 years after the initial treatment. Ubiquitin-proteasome system is a widespread protein regulatory system in eukaryotic cells. As a reversible process, deubiquitinases(DUBs) exert important functions in the regulation of protein stability. In the present study, we aimed to identify DUBs contributing to the chemotherapy resistance in ovarian cancer. By functional screening using DUBs siRNA library, we found that USP11 exerted the most obvious effect on chemotherapy resistance of ovarian cancer cells. Further study of tissue microarrays of ovarian cancer samples showed that USP11 was upregulated in chemoresistant cases and was correlated with poor prognosis. We next validated that overexpression of USP11 in ovarian cancer cells promoted cell growth and inhibited cell apoptosis under CBP treatment, while USP11 depletion significantly improved the sensitivity of ovarian cancer cells to CBP. In consist, in vivo xenograft assay also</p>

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	<p>confirmed the above results. Our study revealed that USP11 can promote the chemotherapy resistance in ovarian cancer and targeting USP11 could be a potential strategy for the clinical treatment of ovarian cancer.</p>
<p>C3005 Session 1 Presentation 8 (15:30-15:45)</p>	<p>JOSD1 Deubiquitinates MCL1 to Drive Acquired Chemoresistance in Gynaecological Cancer <b>Xiaowei Wu</b>, Qingyu Luo and Zhihua Liu Chinese Academy of Medical Sciences and Peking Union Medical College, China</p> <p><i>Abstract</i>—Gynaecological cancer is a main subtype of cancer in women, and acquired chemoresistance is a major contributor to the poor prognosis of gynaecological cancer, but its underlying mechanism remains ill-defined. JOSD1 has been recognized as a deubiquitinase, but its biological functions remain largely unknown, especially in the context of cancer. Here, we established a chemoresistant xenograft model and acquired chemoresistant cell lines to mimic the establishment of acquired chemoresistance. We identified that JOSD1 is the most significantly upregulated DUB during the development of chemoresistance. JOSD1 depletion led to severe apoptosis in gynaecological cancer cells both in vivo and in vitro. Mechanistically, we showed that JOSD1 deubiquitinated and stabilized MCL1 to suppress mitochondrial apoptotic signalling. JOSD1 overexpression caused chemoresistance in gynaecological cancer by upregulating the MCL1 protein. Importantly, high JOSD1 expression was correlated with poor prognosis among ovarian cancer patients, and serum JOSD1 levels could be a marker for clinical diagnosis. Our study showed that JOSD1 is a novel and critical oncogene that contributes to the acquisition of chemoresistance by inhibiting mitochondrial apoptotic signalling via MCL1 stabilization. We also suggest that JOSD1 is an ideal therapeutic target and a promising diagnostic marker.</p>

# Session 2

**Tips:** The schedule for each presentation is for reference only. In order not to miss your presentation, we strongly suggest that you attend the whole session.

**Afternoon, August 14, 2019 (Wednesday)**

**Time: 13:45-15:45**

**Venue: Red Mountain Hall(红山厅, 17<sup>th</sup> Floor)**

**Topic: “Medical Image Processing”**

**Session Chair: Prof. Hyoungseop Kim**

<p>C0006</p> <p>Session 2</p> <p>Presentation 1</p> <p>(13:45-14:00)</p>	<p>Minimal Path based Particle Tracking in Low SNR Fluorescence Microscopy Images</p> <p>Sheng Lu, <b>Tong Chen</b>, Fan Yang, Chenglei Peng, Sidan Du and Yang Li Nanjing University, China</p> <p><i>Abstract</i>—Single Particle Tracking (SPT) in fluorescence microscopy image is of great importance in the field of computational biology. Automatic or slightly interactive tracking algorithms are essential for the motional analysis of micro particles. Even with prior knowledge, conventional methods may fail when the signal-to-noise ratio (SNR) is too low because they highly depend on the quality of the image and the results of detection. To reliably track particles in the low SNR images, we proposed a novel method based on minimal path theory and attempted to extract complete trajectories between two points. Our method was evaluated on several simulated image sequences and showed its accuracy and robustness in the task of particle tracking.</p>
<p>C0008</p> <p>Session 2</p> <p>Presentation 2</p> <p>(14:00-14:15)</p>	<p>Application of Euler Elastica Regularized Logistic Regression on Resting-state fMRI for Identification of Alzheimer’s Disease</p> <p>Weiping Guo, Li Yao and <b>Zhiying Long</b> Beijing Normal University, China</p> <p><i>Abstract</i>—Many machine-learning methods have been widely applied to predict Alzheimer’s disease based on functional magnetic resonance imaging (fMRI) data. In our previous study, we proposed the Euler Elastica Regularized Logistic Regression (EELR) method and demonstrated its advantages over the other classifiers. In this study, we applied EELR to resting-state fMRI (RS-fMRI) data of 24 healthy aged subjects and 22 Alzheimer’s disease (AD) patients for the identification of Alzheimer’s disease. Moreover, in order to reveal the neural discriminative pattern, permutation test was performed to test the differences of EELR weight between AD and healthy aged subject. The results showed that EELR classifier could successfully classify AD and</p>

	<p>healthy aged subject. Moreover, EELR revealed that the amplitude of low-frequency fluctuations (ALFF) of posterior cingulate cortex, prefrontal cortex and hippocampus are the important biomarkers for distinguishing AD and healthy aged subject.</p>
<p>C0022 Session 2 Presentation 3 (14:15-14:30)</p>	<p>Computer Aided Annotation of Early Esophageal Cancer in Gastroscopic Images based on Deeplabv3+ Network <b>Ding-Yun Liu</b>, Hong-Xiu Jiang, Ni-Ni Rao, Cheng-Si Luo, Wen-Ju Du, Zheng-Wen Li and Tao Gan University of Electronic Science and Technology of China, China</p> <p><i>Abstract</i>—The diagnoses of Early Esophageal Cancer (EEC) based on gastroscopic images is a challenging task in clinic, which relies heavily on subjective artificial detection and annotation. As a result, computer aided diagnosis (CAD) methods that support the clinicians become highly attractive. In this paper, we proposed a CAD method which realized the automatic detection and annotation of EEC lesions in gastroscopic images. The proposed method initially utilized an advanced Deep Learning (DL) network Deeplabv3+ to obtain a preliminary prediction of EEC regions. Then, a post-processing step which referenced the clinical requirements was designed and applied to get the final annotation results. Totally 3190 gastroscopic images of 732 patients were used in this work. The final experimental results show that the EEC detection rate of our method was 97.07%, and the mean Dice Similarity Coefficient (DSC) was 74.01%, which are higher than those of other state-of-the-art DL-based methods. In addition, the false positive output of our method is fewer. Therefore, the proposed method offers a good potential to aid the clinical diagnoses of EEC.</p>
<p>C0017 Session 2 Presentation 4 (14:30-14:45)</p>	<p>Facial Spot Contour Extraction based on Color Image Processing <b>Xiaojin Liu</b>, Jiuai Sun and Xiong Wang University of Shanghai for Science and Technology, China</p> <p><i>Abstract</i>—In this paper we discuss the problem of automatic contour extraction of facial spot based on RGB images. Prior similar work has been frequently used for processing those hyperpigmentation skin conditions such as melasma and melanoma, where the separation between pigmented area and normal skin is easy to define. However the melanin under facial spots is normally deposited in a scatter way and distributed superficially, this makes the contrast between the area of spots and that of normal skin become small. As such it is difficult to directly extract the contour of the spots. After analyzing the individual three color channels of facial spot RGB skin image, we found that the blue channel provides the clearest edge of the spots, while the edge presents a certain amount of blur in the red channel. Therefore, this study proposed a new image processing strategy for facial spots analysis, i.e. to firstly separate the RGB channels to obtain the blue channel, then, the maximum entropy threshold</p>

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	<p>segmentation and the Snake method are used to extract the contour of color spots. The experiments verified that the separated color channel and Snake-based method can help to reliably extract edge contours and preserve the color information of the spot.</p>
<p>C0016 Session 2 Presentation 5 (14:45-15:00)</p>	<p>Multi-organ Segmentation from Abdominal CT with Random Forest based Statistical Shape Model <b>Jiaqi Wu</b>, Guangxu Li, Huimin Lu and Hyoungseop Kim Kyushu Institute of Technology, Japan</p> <p><i>Abstract</i>—An automatic multi-organ segmentation method from upper abdominal CT image is proposed in this paper. A group of statistical shape models for multiple organs are generated by learning the statistical distribution of organs' shapes and intensity profiles. Then, a random forest regression model is trained to find the candidate position to initialize the statistical shape model. The proposed method is evaluated at segmentation of four abdomen organs (spleen, right kidney, left kidney and liver) from training set of 26 cases of upper abdominal CT images. The accuracy shows that the initialization improves the accuracy for statistical shape model-based segmentation.</p>
<p>C1011 Session 2 Presentation 6 (15:00-15:15)</p>	<p>Three-dimensional Reconstruction of Optical Coherence Tomography Images of Esophagus <b>Sihan Nao</b>, Miao Zhang, Lirong Wang, Yongjin Xu and Xiaohe Chen Shanghai University, China</p> <p><i>Abstract</i>—The combination of optical coherence tomography (OCT) and endoscope can take images of the body tissues for clinical diagnosis. OCT images are difficult to photograph with regular imaging devices, such as the esophagus and gastrointestinal tract. Three-dimensional reconstruction of the two-dimensional sequence images can help the doctor understand the clinical situation of the body tissue, therefore improve the accuracy of diagnosis. In this paper, Ray Casting method is used to reconstruct three-dimensional image of OCT cross-section images of guinea pig esophagus. Preprocessing including image segmentation, coordinate transformation, angle correction is used to achieve a better result in three-dimensional reconstruction. The performance of the algorithm is discussed and can achieve the same effect as what of commercial software.</p>
<p>C1002 Session 2 Presentation 7 (15:15-15:30)</p>	<p>Detection of Abnormal Regions on Temporal Subtraction Images based on CNN Mitsuaki Nagao, Huimin Lu, <b>Hyoungseop Kim</b>, Takatoshi Aoki and Shoji Kido Kyushu Institute of Technology, Japan</p> <p><i>Abstract</i>—Recently, visual screening based on CT images becomes the useful tool in the medical diagnosis. However, due to the increasing data</p>

	<p>volumes and the computational complexity of the algorithms, image processing technique for the high quality visual screening is still required. To this end, some computer aided diagnosis (CAD) algorithms are proposed. Meanwhile, cancer is a leading cause of death in the world. Detection of cancer region in CT images is the most important task to early detection and early treatment. We design and develop a framework combining convolutional neural networks (CNN) with temporal subtraction techniques-based non-rigid image registration algorithm. However, conventional CNN has the issue that as the layers deeper, global information close to input images is lost. Therefore, we add a skip connection to conventional CNN. By adding a new skip connection, the proposed CNN network maintains the global information without loss of important features of input image. All in all, our proposed method can be built into three main steps; i) pre-processing for image segmentation, ii) image matching for registration, and iii) classification of abnormal regions based on machine learning algorithms. We perform our proposed technique to 25 thoracic MDCT sets and obtain the AUC score of 0.951.</p>
<p>C0010 Session 2 Presentation 8 (15:30-15:45)</p>	<p>Computer-aided Cervical Cancer Screening Method based on Multi-spectral Narrow-band Imaging <b>Zihan Yang</b>, Dirong Yi and Jiahao Shen Huaqiao University, China</p> <p><i>Abstract</i>—The contrast of white colposcopy images is low, which is not conducive to the computer assisted identification of different degrees of diseased tissue. In order to improve the sampling accuracy under the image guidance of colposcopy, in this paper, we propose a Computer-aided cervical cancer screening method based on Multi-spectral Narrow-Band Imaging(CMNBI). We sequentially get images of cervical tissue under different illumination sources including white light, narrow-band blue light at a center wavelength of 415nm, and narrow-band green light at a center wavelength of 540nm. The multi-spectral pathology diagnosis methods consist of two stages: the first one is image preprocessing and the other is tissue classification. The image preprocessing algorithm consists of the following steps: First, we perform filtering process on three modes of images to remove noises. Secondly, the sequentially obtained images are spatially co-registered. Thirdly, the multiple narrow-band spectral images are fused. In the stage of tissue classification, a two-class K-means clustering algorithm is used, using clinics manually identified diseased region as the seed points. To eliminate strong specular reflection points of cervical tissue, we then applied improved K-means clustering algorithm combined with contour coefficient method to improve robustness of the proposed computer-aided cervical cancer screening method. To evaluate the proposed method, we apply the method to both the fused narrow-band multispectral images as well as the conventional white light images. As a result, the sensitivity,</p>

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specificity and accuracy of CMNBI are all improved with the fused narrow-band multispectral images over that of the conventional white light images.



**15:45-16:15**

**Coffee Break and Poster Session**



# Session 3

**Tips:** The schedule for each presentation is for reference only. In order not to miss your presentation, we strongly suggest that you attend the whole session.

**Afternoon, August 14, 2019 (Wednesday)**

**Time: 16:15-18:00**

**Venue: Tanggula Hall(唐古拉厅, 17<sup>th</sup> Floor)**

**Topic: “Computer-aided Medicine”**

**Session Chair: Prof. Xuejun Zhang**

<p>C2008 Session 3 Presentation 1 (16:15-16:30)</p>	<p>TNF<math>\alpha</math>-FOXC2 Axis Drive ESCC Metastasis through FA2H Mediated Lipid Metabolic Reprogramming <b>Xuantong Zhou</b>, Furong Huang, Gang Ma and Zhihua Liu Chinese Academy of Medical Sciences and Peking Union Medical College, China</p> <p><i>Abstract</i>—Dysregulated metabolism has been linked to multi-cancer development. Yet metabolic reprogramming involving cancer metastasis remains less understood. In this study, we firstly established lung highly metastatic esophageal squamous cell carcinoma (ESCC) sublines (LM cells) with experimental metastasis mouse model, which possessed stronger metastatic potency both in vivo and in vitro. Through transcriptomic profiling, we identified both FOXC2 and FA2H were co-upregulated in lung metastatic sublines compared to parental cells. FOXC2 promoted ESCC cells metastasis and proliferation through modulating FA2H expression both in vivo and in vitro. Mechanistically, FOXC2 upregulated FA2H expression transcriptionally by directly binding to its promoter regions. Furthermore, TNF<math>\alpha</math> activated FOXC2-FA2H signaling in ESCC metastasis by upregulating FOXC2 and thus increasing FA2H level in time dependent manner. Importantly, FA2H functioned as one of the key regulators in lipid metabolism which catalyzed the synthesis of 2-hydroxysphingolipids. By functional lipidomics analysis, we identified several differentially expressed lipid species in FA2H silencing LM cells, which may act as metastasis suppressor in ESCC. Taken together, our findings uncovered the TNF<math>\alpha</math>-FOXC2-FA2H axis mediated dysregulated lipid metabolic programs in ESCC metastasis, suggesting that TNF<math>\alpha</math> blockade or lipid-based regimen could be a promising therapeutics for metastatic ESCC.</p>
<p>C0015 Session 3</p>	<p>Muscle Artifacts Cancellation Framework for ECG Signals Combining Convolution Auto-encoder and Average Beat Subtraction <b>Yongfeng Huang</b>, Zijian Ding and Guijin Wang</p>

<p>Presentation 2 (16:30-16:45)</p>	<p>Tsinghua University, China</p> <p><i>Abstract</i>—As the basic tool for the diagnosis of cardiac diseases, electrocardiogram (ECG) is often contaminated by muscle artifacts, which can cause unreliable interpretation and measurement for ECG. To adequately remove muscle artifacts which contaminates ECG signals, we propose a novel computation framework combining the convolution auto-encoder (CAE) and average beat subtraction in this paper. Firstly, the framework subtracts from the original ECG signal based on an initial average beat, which preserves the characteristics of an heart beat; the average beat is updated according to the original ECG signal to incorporate inter-beat variations. Then, the framework filters the residual ECG signal by a convolution auto-encoder (CAE), which filters out the contaminated parts and keeps the specific information related to the ECG signal. Finally, we combine the filtered residual ECG signal and updated average beat to obtain an enhanced ECG signal. Our framework is evaluated on ECG records from the MIT-BIH Arrhythmia Database, and results show that our framework outperforms existing methods in muscle artifacts removal.</p>
<p>C1007 Session 3 Presentation 3 (16:45-17:00)</p>	<p>Design of Cleaning Module based on CAN</p> <p><b>Feifei Sun</b>, Wenliang Zhu, Gang Ma, KongPeng Xing and Lirong Wang Soochow University, China</p> <p><i>Abstract</i>—In order to promote the automation of medical devices, we designed a test and analysis instrument which we call it as automatic liquid chip system. Based on the fully automatic liquid chip system, we designed various modules, including sample needle module, reagent bin module, reaction plate module, cleaning module, waste bin module and system liquid module. It includes the design of mechanical structure and electronic control system. The control chip of each module is STM32F103RET6. The main control part includes stepping motor, optocoupler sensor and AD converter. The whole communication is carried out through CAN (Controller Area Network) protocol. The serial instructions are sent to the upper computer, and the conversion from serial instructions to CAN instructions is completed in the transfer station. Each module receives CAN instructions, performs FIFO caching, and then performs corresponding operations. Considering the stability of each module, the universality of debugging and the stability of the whole system, this experiment designs the common parts of the module, including the design of stepping motor driver, the generation of software PWM and the configuration of CAN communication protocol. Then we take the cleaning module as an example to design its circuit and workflow.</p>

<p>C3011 Session 3 Presentation 4 (17:00-17:15)</p>	<p>Dynamic Functional Connectivity Analysis of Seafarer’s Brain Functional Networks <b>Yuhu Shi</b> Shanghai Maritime University, China</p> <p><i>Abstract</i>—As a special occupation, Seafarers often face different working and living conditions compared to the terrestrial environment, so it is very important to explore the influence of maritime environment on seafarers' brain function. Based on the eight typical resting-state brain functional networks obtained by group independent component analysis, this paper adopt sliding temporal window and affine propagation clustering methods to deeply analyze the differences of dynamic functional connectivity between seafarers before and after sailing with those between seafarers and non-seafarers corresponding to these networks. The results show that the dynamic change among the eight brain functional networks between seafarers before and after sailing has obvious differences with those between non-seafarers and seafarers, which mean that the impact of marine environment on the seafarers' brain functional networks has certain timeliness. Some changes of the brain functional connectivity networks can be recovered within a certain period of time, while others may have long-term effects on the connections between brain functional networks, so as to reorganize the topological relationship between brain functional networks and form the unique brain network biomarkers of seafarers, which has a great significance to explore the plasticity of seafarer's brain functional networks and the neural rules of sea-farer's brain functional activities.</p>
<p>C1009 Session 3 Presentation 5 (17:15-17:30)</p>	<p>Fall Guard: Fall Monitoring Application for the Elderly based on Android Platform <b>Jenny Ni, Wenliang Zhu, Jinfu Huang, Longfei Niu and Lirong Wang</b> Soochow University, China</p> <p><i>Abstract</i>—In order to solve the situation that the elderly can't get timely assistance when they fall down, this paper designs and implements an Android-based fall monitoring application for the elderly (Fall Guard). Combined with existing fall detection devices and cloud server, Fall Guard uses Model-View-Control (MVC) structure and OkHttp network request framework. In this paper, OkHttp is used to send network requests to the cloud server and the fall detection device is bound to the mobile client to obtain user and device information. After successfully obtaining data, the obtained information is displayed on the user interface through JSON parsing, including device positioning, electronic fence, fall alarm information and motion track. One login account can be bound to multiple devices. The login account is set to the emergency contact number of the elderly by default. When the elderly fall, Fall Guard can receive many</p>

	<p>types of fall alarm prompts, including alarm information list, notification bar reminder, SMS notification, device user status bar information and other prompt functions. Test results show that Fall Guard has good monitoring accuracy and terminal compatibility. On the one hand, it can adapt to different models and brands of Android mobile terminals to achieve accurate positioning and alarm functions. On the other hand, due to its one-to-many management mode, it can be applied to deployment of different application scenarios such as home, community and nursing home.</p>
<p>C1001 Session 3 Presentation 6 (17:30-17:45)</p>	<p>Forecasting of Ventricular Tachyarrhythmia based on Multi-scale Entropy of Short-term Heart Rate Variability Liu Qing, <b>Dong Hong-Sheng</b> and Ma Yin-Yuan Lanzhou Institute of Technology, China</p> <p><i>Abstract</i>—The weighted integrated multi-scale entropy(WIMSE) is analyzed for the 135 about ten minutes RR interval series preceding the onset of ventricular tachycardia and ventricular fibrillation(called VT/VF series),and the change of WIMSE is discussed for the data samples of significant increase of heart rate (called SI_HR group) and no significant change of heart rate (called nSI_HR group) preceding the onset of VT/VF events. Results show that the WIMSE of VT/VF series has significantly reduction compared with normal sinus rhythm (scale:1-30, <math>p&lt;0.05</math>),and the reduction of WIMSE is more significant for the VT/VF series of SI_HR group, the extracted complexity index (scale:1-10,<math>p&lt;10^{-6}</math>). Therefore the WIMSE may be an effective nonlinear predictive parameters for forecasting VT/VF events.</p>
<p>C1006 Session 3 Presentation 7 (17:45-18:00)</p>	<p>An Automatic Detection Algorithm for T Wave Position based on T Wave Morphology <b>Wanyue Li</b>, Lishen Qiu, Jie Zhang, Wenliang Zhu and Lirong Wang Soochow University, China</p> <p><i>Abstract</i>—ECG signals are the most commonly used signals in heart disease detection. It contains many waveforms that are directly related to cardiac activity, where the T wave contains much important physiological information. The T wave position detection algorithm is based on the differential threshold method, and the T wave morphological judgment is used before the T wave position detection. The algorithm includes three parts: preprocessing, T wave morphological judgment, T wave position detection. Firstly, the signal is preprocessed to eliminate the effects of noise and other waves. Secondly, a detection window is defined to realize the T wave morphological judgment. Finally, based on the T wave morphology, the T wave position is obtained by a differential threshold method in the detection window. The algorithm was tested on the QT</p>

	<p>database. By comparing with the manual annotation of the expert in the database, the standard deviation between the algorithm positioning results and the manual labeling results in the database is 30.55 ms at the peak of T wave, and the standard deviation is 47.46 ms at the end of T wave.</p>
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# Session 4

**Tips:** The schedule for each presentation is for reference only. In order not to miss your presentation, we strongly suggest that you attend the whole session.

**Afternoon, August 14, 2019 (Wednesday)**

**Time: 16:15-18:00**

**Venue: Red Mountain Hall(红山厅, 17<sup>th</sup> Floor)**

**Topic: “Pattern Recognition and Classification”**

**Session Chair: Prof. Hojun Kim**

<p>C0001 Session 4 Presentation 1 (16:15-16:30)</p>	<p>Application of Granger Causality in Decoding Covert Selective Attention with Human EEG <b>Weikun Niu</b>, Yuying Jiang, Yujin Zhang, Xin Zhang and Shan Yu University of Chinese Academy of Sciences, China</p> <p><i>Abstract</i>—Electroencephalography (EEG)-based BCIs have experienced a significant growth in recent years, especially the passive Brain Computer Interfaces (BCIs) with a wide application in the detection of cognitive and emotional states. But it is still unclear whether more subtle states, e.g., covert selective attention can be decoded with EEG signals. Here we used a behavioral paradigm to introduce the shift of selective attention between the visual and auditory domain. With EEG signals, we extracted features based on Grange Causality (GC) and successfully decoded the attentional shift through a support vector machine (SVM) based classifier. The decoding accuracy was significantly above the chance level for all 8 subjects tested. The features based on GC were further analyzed with tree-based feature importance analysis and recursive feature elimination (RFE) method to search for the optimal features for classification. Our work demonstrate that specific patterns of brain activities reflected by GC can be used to decode subtle state changes of the brain related to cross-modal selective attention, which opens new possibility of using passive BCIs in sophisticated perceptual and cognitive tasks.</p>
<p>C0014 Session 4 Presentation 2 (16:30-16:45)</p>	<p>Relationships of Cohen’s Kappa, Sensitivity, and Specificity for Unbiased Annotations <b>Juan Wang</b> and Bin Xia Delta Micro Technology Inc., USA</p> <p><i>Abstract</i>—For the binary classification tasks in supervised learning, the labels of data have to be available for classifier development. Cohen's kappa is usually employed as a quality measure for data annotation, which is inconsistent with its true functionality of assessing the inter-annotator consistency. However, the derived relationship functions of Cohen's</p>

	<p>kappa, sensitivity, and specificity in the literature are complicated, thus are unable to be employed to interpret classification performance from kappa values. In this study, based on an annotation generation model, we develop simple relationships of kappa, sensitivity, and specificity when there is no bias in the annotations. A relationship between kappa and Youden's J statistic, a performance metric for binary classification, is further obtained. The derived relationships are evaluated on a synthetic dataset using linear regression analysis. The results demonstrate the accuracy of the derived relationships. It suggests the potential of estimating classification performance from kappa values when bias is absent in the annotations.</p>
<p>C1010 Session 4 Presentation 3 (16:45-17:00)</p>	<p>Practical Fall Detection Algorithm based on Adaboost <b>Wenqiang Cai</b>, Lishen Qiu, Wanyue Li, Jie Yu and Lirong Wang Soochow University, China</p> <p><i>Abstract</i>—In order to improve the accuracy and efficiency of the fall detection, we proposed a fall detection algorithm based on Adaboost with single-layer decision tree under six-axis acceleration (three-axis acceleration, three-axis angular acceleration) time features. We set two thresholds for the resultant linear acceleration. When the value of the resultant linear acceleration is within these two thresholds, the algorithm of fall detection classifier is triggered. The fixed window is used to intercept the time waveform of the six-axis acceleration and extract the time features. We selected seven features with less computational complexity, and finally used these seven features to construct a fall detection model based on Adaboost with single-layer decision tree. Our algorithm can achieve 99.08% accuracy in the data set collected by ourselves, and has high specificity and sensitivity. The most critical point is that the algorithm proposed in this paper has a small computational cost and can be transplanted onto the embedded system, which is a practical and reliability fall detection method.</p>
<p>C0020 Session 4 Presentation 4 (17:00-17:15)</p>	<p>Different Goal-driven CNNs Affect Performance of Visual Encoding Models based on Deep Learning <b>Ziya Yu</b>, Chi Zhang, Linyuan Wang, Li Tong and Bin Yan National Digital Switching System Engineering and Technological Research Centre, China</p> <p><i>Abstract</i>—A convolutional neural network with outstanding performance in computer vision can be used to construct an encoding model that simulates the process of human visual information processing. However, training goal of the network may have impacted the performance of encoding model. Most neural networks used to establish encoding models in the past were performed image classification task, the task of which is single. While in the process of human's visual perception, multiple tasks are performed simultaneously. Thus, the existing encoding model does not</p>

	<p>well satisfy the diversity and complexity of the human visual mechanism. In this paper, we first established a feature extraction model based on Fully Convolutional Network (FCN) and Visual Geometry Group (VGG) with similar network structure but different training goal, and employed Regularize Orthogonal Matching Pursuit (ROMP) to establish the response model, which can predict the stimuli-evoked responses measured by functional magnetic resonance imaging (fMRI). The results revealed that the convolutional neural networks trained by different visual tasks had significant difference in the performance of visual encoding with almost the same network structure. The VGG-based encoding model can achieve a higher performance in most voxels of ROIs. We concluded that classification task in computer vision can better fit the visual mechanism of human compared to visual segmentation task.</p>
<p>C1008 Session 4 Presentation 5 (17:15-17:30)</p>	<p>Epileptic Seizure Classification based on the Combined Features <b>Jie Yu</b>, Lirong Wang and Xueqin Chen Soochow University, China</p> <p><i>Abstract</i>—Electroencephalography(EEG) can provide a wealth of valuable information to help understand the mechanism of seizures. The automatic classification of EEG signals can help clinicians make effective judgments on whether seizures occur. In this work, a method based on combined features is proposed to classify epilepsy seizures. Firstly, discrete wavelet transform is applied to the signal, and the line length features, energy distribution proportion and approximate entropy of each sub-band signal are extracted. Then the statistical features of the raw signal are extracted, including mean, standard deviation, coefficient of variation, median absolute deviation (MAD) and interquartile range (IQR). All the features are combined and the dimension of the combined feature vector is reduced by the principal component analysis(PCA). Finally, the support vector machine (SVM) is used to classify the epileptic seizure. The dataset is from the epilepsy laboratory of the University of Bonn, Germany. The accuracy of 98.40% proves the validity of this method.</p>
<p>C0018 Session 4 Presentation 6 (17:30-17:45)</p>	<p>RGB-D-based Hand Gesture Recognition for Letters Expression Jin Li, Jishuo Yan, <b>Guangxu Li</b>, Liyuan Wang and Fan Yang Tiangong University, China</p> <p><i>Abstract</i>—Hand Gesture Recognition (HGR) is a system to translate the hand gestures express to literature, which is a natural way of communication between deaf-mutes and non-disabled people. However, due to the complexity of relative positions of fingers, hands sizes, and environmental illumination, the hand gesture recognition is difficult. In this paper, a Fully Connected Neural Network (FCNN) algorithm for RGB-D sensor based HGR is proposed. We firstly build datasets of fingers joints and the center coordinates of hands in 3 dimensions. Then</p>



	<p>we normalize the samples to eliminate the natural difference of hands. Finally, the data are classified using a 3 layers FCNN. Totally 13,000 data of 26 hand gestures are collected. We randomly select 80% of these data for training and 20% of them for testing. According to the experiments, the average recognition accuracy is 94.73%.</p>
<p>C1005 Session 4 Presentation 7 (17:45-18:00)</p>	<p>Region-based High-resolution Siamese Network for Robust Visual Tracking <b>Chunbao Li</b> and Bo Yang University of Electronic Science and Technology of China, China</p> <p><i>Abstract</i>—Visual tracking is an active and challenging research topic in computer vision, as objects often undergo significant appearance variations caused by occlusion, deformation and background clutter. In recent years, many convolutional neural network based trackers have achieved impressive performance by integrating multi-layer features. However, in order to conduct multi-scale feature fusion, most of these trackers recover high-resolution presentations from low-resolution representations produced by a high-to-low resolution network, which tend to result in inaccurate feature maps or lose of details of the target object. In this paper, we propose an end-to-end region-based high-resolution fully convolutional Siamese network for tracking. In the tracker, we propose to extract the spatial information and semantic information of the target object using a high-resolution network that maintains rich high-resolution representations of the target object through the whole process. Furthermore, a set of position-sensitive score maps are obtained for all regions of the target template, and an adaptive weighting method is proposed to fuse score maps of multiple regions. Experimental results on the OTB50 and OTB100 benchmark datasets demonstrate that our tracker performs better than several state-of-the-art trackers while running in real-time.</p>

# Poster Session

**August 14, 2019 (Wednesday)**

**Time: 15:45-16:15**

**Venue: Tanggula Hall(唐古拉厅, 17<sup>th</sup> Floor)**

<p>C1003 Poster 1</p>	<p>Retinal Artery/Vein Classification via Rotation Augmentation and Deeply Supervised U-Net Segmentation <b>Zhaolei Wang</b>, Junbin Lin, Ruixuan Wang and Weishi Zheng Sun Yat-sen University, China</p> <p><i>Abstract</i>—Automatic classification of artery and vein vessels in retinal images is still a challenging task. Recent work mainly focuses on the graph analysis of retinal vessels or intensity based feature extraction. In this study, we use one stage multiclass segmentation without any graph-based or vote-based post processing to solve the artery/vein classification problem directly and effectively. We experimentally showed that with limited training data, data augmentation may be at least as crucial as designing complicated deep model architectures in improving the performance of artery/vein classification. In particular, simply with rotation augmentation, the popular deeply supervised U-Net (DS-UNet) is already comparable to or even outperforms the state-of-the-art methods on DRIVE dataset. Our experiments on two datasets show that artery-vein-background segmentation based on deep learning can be used as a promising method for arteriovenous classification and can be combined with conventional methods for better results.</p>
<p>C3010 Poster 2</p>	<p>Discovery of Novel HDAC Inhibitor from Traditional Chinese Medicine Chia-Min Chen, <b>Chang-Sheng Chiang</b>, Yung-Jen Yang, Zhi-Lin Wang, Cheng-Fang Tsai and Pei-Chun Chang Asia University, Taiwan</p> <p><i>Abstract</i>—Cancer is a fatal disease. The abnormal proliferation of cancer cells may invade other parts of the body and cause lethal. Human histone deacetylases (HDAC) have been proven to be a useful target in various types of cancer. In the past few years, we have continued to research for more effective inhibitors. Recently, the components in traditional Chinese medicine as a lead compound is getting more and more attention. Under such a trend, we performed ligand-based QSAR modeling to select potential TCM candidate compounds for HDAC inhibition. The results show that 5-O-caffeoyl quinic acid butyl ester, agaritine, gammg-L-glutamyl-L-glutamic acid, glutathione, hemerocallin, salvianolic acid C, and stypanrol might have the potential for HDAC inhibition.</p>

<p>C3014 Poster 3</p>	<p>Anti-obesity Effect of Fermented <i>Panax Notoginseng</i> via Modulating Gut Microbiota  <b>Na Rae Shin</b>, Soo-Kyoung Lim, Hyunsuk Song and Hojun Kim  Dongguk University, Republic of Korea</p> <p><b>Abstract</b>—<i>Panax notoginseng</i> (PN), a traditional herbal medicine, has several active compounds such as saponins and ginsenosides. Fermented herbal medicine increase bioavailability, and fermentation using lactic acid bacteria has potential to metabolize ginsenosides. Therefore, this study investigated whether fermented PN (FNP) showed the synergistic effect on anti-obesity model via modulation of gut microbiota. For this, PN was fermented with a <math>\beta</math>-glucosidase active <i>Lb. plantarum</i> and then administered to a high fat diet (HFD) induced mice. The treatment of FPN highly reduced body and fat weight as well as food intake. The relative mRNA level of LPL, leptin and LBP in adipose tissue synergistically reduced in treatment of FPN compared to PN. The treatment of FPN also modulated the gut microbiota composition. The population of gut microbiota was clearly distinguished between PN and FPN treatment group. The relative abundance of Bacteroidetes highly increased in FPN group than other groups while the relative abundance of <i>Akkermansia</i> enhanced high in FPN group compared with PN group. In conclusion, this results support that FPN exerts synergistic effect on anti-obesity via modulation of gut microbiota.</p>
<p>C0004 Poster 4</p>	<p>Kinematic Characteristics of Backhand Block in Table Tennis  <b>Yi Ren</b>, Zhipei Huang, Yiming Guo, Jiankang Wu and Yingfei Sun  University of Chinese Academy of Sciences, China</p> <p><b>Abstract</b>—Kinematic characteristics have been playing a crucial role in assessing the quality of movements and improving training plans. We design five characteristic parameters of table tennis technical movements in these papers, i.e., the normalized path, joint angle, phase duration, root mean square and velocity entropy. Based on the motion data obtained from immersive motion capture system, the validity of these characteristic parameters was verified by analyzing backhand block movement. Twenty subjects with two different skill levels were involved in this test to perform backhand block against the ball. The statistical analysis results revealed that there were significant differences between the parameters of the professional group and those of the novice group, including normalized path, velocity entropy, root mean square and joint angle. Meanwhile, phase duration and joint angle showed practical significance biomechanically. These characteristic parameters could serve as indicators for movement quality assessment and could be extended to other table tennis technical movements as well as further biomechanics research.</p>

<p>C0013 Poster 5</p>	<p>An Approach for Recognition of Enhancer-promoter Associations based on Random Forest <b>Tianjiao Zhang</b> and Yadong Wang Harbin Institute of Technology, Harbin, China</p> <p><i>Abstract</i>—Enhancers are sequences in the genome that regulate gene expression and are usually located far from transcription start sites. Enhancers regulate gene expression by interacting with promoters. Therefore, the recognition of the association between enhancers and promoters is an important issue in the study of enhancer regulation. At present, computational methods to recognize the association between enhancers and promoters are mainly realized by designing machine learning methods based on the biological signals on the genome sequence. These recognition methods ignore evaluating the classification power of features, resulting in limited recognition performance. In this paper, the classification power of the feature signals near enhancers and promoters in the genome sequence was evaluated, and the features with strong classification power were picked up. This was conducive to improving the recognition accuracy. The correlation between enhancers and promoters was recognized by the random forest method. Compared with the five main recognition methods, the accuracy of the recognition method in this paper is higher.</p>
<p>C0011 Poster 6</p>	<p>Control of Upper Limb Motions by Combinations of Basic Muscle Synergies <b>Bingyu Pan</b>, Yingfei Sun, Licai Sun, Zhipei Huang and Jiankang Wu University of Chinese Academy of Sciences, China</p> <p><i>Abstract</i>—Motor system relies on the recruitment of motor modules to perform various movements. Muscle synergies are the modules used by the central nervous system to simplify the control of complex motor tasks. In this paper, we verified the hypothesis that the control of upper limb motions can be realized by combinations of basic muscle synergies extracted from electromyography signals of simple upper limb motions. Muscle synergies and corresponding activation coefficients were extracted via non-negative matrix factorization from three basic and five complex motions. Similarities across basic synergies and complex synergies were compared. We found that the structure of muscle synergies from complex tasks was similar to the corresponding basic synergies and muscle synergies from basic tasks can be used to reconstruct muscle patterns of the complex tasks. This study demonstrates that different kinds of upper limb motions can be accomplished by the combinations of basic muscle synergies modulated by different activation coefficients.</p>
<p>C0025 Poster 7</p>	<p>AWGI: An Auto-weighted Framework Integrating Heterogeneous Networks for Gene Interaction Prediction <b>Han Luo</b>, Zhenfeng Lei and Hanping Ke</p>

	<p>Xiamen University, China</p> <p><i>Abstract</i>—Gene networks (GNs) capture the knowledge of diverse interactions among genes, which are conducive to discovering disease gene sets and locate the target of the drug. Discovering gene interactions via biological experiments is always exhaustive and expensive. The application of combining gene networks with integrated computing for effectively guiding experiments is widely used in gene interaction prediction. Some of work has been designed to integrate the neighbor information of Heterogeneous Data (HD) to predict gene interaction, but ignored the difference among gene networks and interaction types. Here, we proposed an auto-weighted framework integrating heterogeneous networks for gene interaction prediction (called AWGI), which evaluates and aggregates the neighbor information of five GNs to infer the associations among genes. In this paper, we compared the prediction ability of our method with other state-of-the-art methods. The experimental results show that AWGI can learn more informative gene representations from the HD and achieved a significant improvement in terms of the accuracy of interaction prediction.</p>
<p>C3015 Poster 8</p>	<p>The Effect of <i>Crataegus Pinnatifida</i> in High-fat Diet Induced Mice via Gut Microbiota <b>Meng Yang</b>, Yura Choi, Na Rae Shin, Soo-Kyoung Lim and Hojun Kim Dongguk University, Republic of Korea</p> <p><i>Abstract</i>—Gut microbiota plays a key role in the pathophysiology of obesity. Indeed, low-grade inflammation and specific changes in gut microbiota composition exacerbate obesity and metabolic dysfunction in high-fat diet (HFD) induced model. <i>Crataegus pinnatifida</i> (CP), traditional herbal medicine, has effect on anti-oxidant and anti-cancer. However, the effect of anti-obesity of CP via gut microbiota is unclear. In order to explore the activities of CP on high-fat diet mice, CP extract was administrated to the HFD induced mice for 10 weeks. We measured the food intake, body weight, visceral fat, total fat, serum total cholesterol (TC), triglyceride (TG), glutamic oxaloacetate transaminase (GOT) and glutamic pyruvic transaminase (GPT) levels. The body weight, visceral fat and total fat of CP group were significantly lower than HFD group. Also, serum TG levels in the CP group were significantly decreased. Glucose tolerance was improved by CP supplementation compared with the HFD group. Moreover, MCP-1, IL-1<math>\beta</math>, TNF-<math>\alpha</math> and PPAR<math>\gamma</math> were decreased in CP group. Taken together, insulin sensitivity and inflammation were ameliorated in CP group. In addition, RFLP result from feces showed that CP might modulate the composition of gut microbiota. In conclusion, these results showed that CP extract has effect on anti-obesity, anti-inflammation via modulation of gut microbiota.</p>

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<p>C0003 Poster 9</p>	<p><b>Automatic Sleep Staging based on Curriculum Learning Approach</b>  <b>Xingjun Wang and Ziyao Xu</b>                  Tsinghua University, Shenzhen, China</p> <p><i>Abstract</i>—Automatic sleep staging is helpful to improve diagnosis efficiency of sleep-related diseases. This work introduces the many-to-many formulation for automatic sleep staging, which means using a many-to-many mapping to convert the contextual input to the corresponding contextual output. We use convolutional neural networks (CNNs) to perform the many-to-many mapping, and use multilayer perceptron (MLP) to merge the contextual output into the final prediction for a particular epoch. In order to avoid the influence of unobvious characteristic waves and wrong labels on the training process, this work leverages the technology of curriculum learning. By clustering algorithm based on local density, the training set is divided into several subsets according to the signal quality. We design a learning strategy by successively leveraging these subsets. To the best of our current knowledge, this is the first work using curriculum learning for automatic sleep staging. It is showed by experiments that our scheme yields an accuracy comparable to the state-of-the-art on the public dataset Sleep-EDF.</p>
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<b>Dinner</b>	
<b>18:30-20:30</b>	<b>Yak Café(亚克咖啡厅, 2<sup>nd</sup> Floor)</b>

## Listener

<b>Name</b>	<b>Affiliation</b>
Qing Liu	Lanzhou Institute of Technology, China
Zijian Ding	Tsinghua University, China
Dacheng Liang	Yangtze University, China
Wei Zheng	Henan Institute of Technology, China
Hao Sun	Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, China
Yuan Li	Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, China
Fuhui Wang	Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, China
Changpeng Li	Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, China
Tingting Yang	Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, China
Fei Meng	Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, China
Qian Li	Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, China
Xiaowei Lai	Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, China
Mei Liu	Cancer Hospital Chinese Academy of Medical Sciences, China
Lixin Sun	Cancer Hospital Chinese Academy of Medical Sciences, China
Bin Xia	Shenzhen SiBionics Co., LTD., China
Zhigang Hu	Shenzhen SiBionics Co., LTD., China
Jin Deng	Shanghai Maritime University, China
Ying Li	Shanghai Maritime University, China
Jiatong Cai	Shanghai Maritime University, China
Yong Guo	National Research Institute for Family Planning, China
Hongfei Xia	National Research Institute for Family Planning, China

## Conference Venue

### Tibet Hotel Chengdu | 成都西藏饭店

<http://www.tibethotelchengdu.cn/index.html>

Addr.: No.10, North Renmin Road, Chengdu, China | 成都人民北路一段10号



Tibet Hotel Chengdu is located at No.10, North Renmin Road, Chengdu. It is near Manjusri Square, Living Water Park. It may just take you 5 minutes from the hotel to Chengdu North Railway Station(2 km), and 30 minutes to Chengdu Shuangliu International Airport(27 km).

Hotel in 1988 by the Tibet Autonomous Region People's Government invest in the construction, in February 2002 by the American teacher, Mr. Katz designed a new reconstruction is completed, with 300 rooms, an area of 45 square meters standard. Exquisite luxury room furniture, all rooms equipped with broadband INTERNET interface, free Internet access, take good care of fine design, business rooms and convenient amenities. Hotel Non-smoking floors, ladies and floors, commercial floors, can meet different customers needs. Elegant International Conference Hall, the conference, lectures, display the best choice. At the same time, all rooms free broadband Internet access.



**Note:** 1. The registration fee does not cover the accommodation. It is suggest that an early reservation be done because of peak season.

2. The hotel will not contact any participants for hotel booking, and please be careful when anyone asks you to provide your credit card information to reserve room for you.



# Academic Visit

**14:00-16:00, August 13, 2019**

**Institutes for Systems Genetics, West China Hospital, Sichuan University**

(四川大学华西医院系统遗传研究院)

**Web:** <http://www.sysbio.org.cn/index.php>

**Address:** Jitaian Center, 17 Gaopeng Avenue, Wuhou District, Chengdu (地址: 成都市武侯区高朋大道17号吉泰安中心)

Institutes for Systems Genetics, West China Hospital, Sichuan University was established in 2018 and is one of the interdisciplinary research institutes of Sichuan University (affiliated with West China Hospital of Sichuan University).

It is located in Jitaian Center, 17 Gaopeng Avenue, Wuhou District, Chengdu.

The task of the Institute is to integrate data, information and knowledge at different levels of histology, integrate multi-disciplinary methods, and analyze and solve problems at the system level. Specific research objectives are as follows, but not limited to this:

1. Improve the arithmetic to determine different forms of cancer at specific stages by meta-analysis.
2. Study the difference in system dynamics between health and cancer

# One Day Tour

9:00-17:30, August 15, 2019

Chengdu is a starting point for the national historical and cultural city, the best tourist city in China and the southern Silk Road. It is one of the 'Top 10 Ancient Capital Cities', and it was built around the 5th century BC. In the Western Han Dynasty, it became one of the six major cities in China. During the Northern Song Dynasty, Chengdu people jointly issued the earliest banknotes in the world, and the government set up the world's earliest managed savings bank in Chengdu. More than 2,600 years of history of the city gave birth to Dujiangyan, Wuhou Temple, Du Fu Thatched Cottage, Jinsha sites and many other places of interest.

## Travel Schedule

**Morning: Chengdu Research Base of Giant Panda (熊猫基地) Jinli (锦里)**

**Afternoon: Temple of Marquis (武侯祠) Kuan & Zhai Ally (宽窄巷子)**

### Chengdu Research Base of Giant Panda Breeding(熊猫基地)

Chengdu Research Base of Giant Panda Breeding, or simply Chengdu Panda Base, is a non-profit research and breeding facility for giant pandas and other rare animals. It is located in Chengdu, Sichuan, China. Chengdu Panda Base was founded in 1987. It started with 6 giant pandas that were rescued from the wild. By 2008, it had 124 panda births, and the captive panda population has grown to 83. Its stated goal is to "be a world-class research facility, conservation education center, and international educational tourism destination."



### Jinli (锦里)

Jinli is a street about 550 meters long. There are many bars, inns, snack stores and souvenir shops. The street was renovated in 2004. In 2005, Jinli was named as "National Top Ten City Commercial Pedestrian Street". In 2006, Jinli was named as "National Demonstration Base of the Cultural Industry" by the Ministry of Culture.



## Temple of Marquis (武侯祠)

Wuhou Temple (Memorial Temple of Marquis Wu) is dedicated to Zhuge Liang, the Marquis Wu (Wuhou) of Kingdom of Shu in the Three Kingdoms Period (220 - 280). Zhuge Liang was the personification of noble character and intelligence. Memorial architectures erected in many places after his death include a famous one in Chendu. Located in the south suburb of Chengdu, the temple covers 37,000 square meters. It was combined with the Temple of Liu Bei at the beginning of the Ming Dynasty; consequently, the entrance plaque reads 'Zhaolie Temple of Han Dynasty' (Zhaolie is the posthumous title of Liu Bei). The current temple was rebuilt in 1672. Surrounded by old cypresses and classical red walls, it evokes nostalgia.



## Kuan & Zhai Alley (宽窄巷子)

Kuan Alley is a relatively large-scale ancient Qing Dynasty street left in Chengdu. Together with Daci Temple and Wenshu Monastery, it is also known as the Three Preservation Historical and Cultural Cities Block in Chengdu. Kuan & Zhai Alley is a long history card of Chengdu, where you can touch the traces of history, but also appreciate the original taste of Chengdu leisure lifestyle, into the width of the alley, walked into the most Chengdu, the world, the oldest and most fashionable old Chengdu business card. Kuan & Zhai alley is a microcosm of the ancient and young city in Chengdu, a symbol of memory. Chengdu people's generalization is more refined: Wide Alley: Chengdu's 'free life'; Narrow Alley: Old Chengdu's 'slow life'; Alley: Chengdu's 'new life.'



## Note:

- Pick up at Tibet Hotel Chengdu at 8:50 a.m.
- Guests are responsible for their belongings.
- The above places are for references, and the final schedule should be adjusted to the actual notice.









## Feedback Information

(Please fill this form and return it to conference specialist during the conference days.)

<b>Personal Information</b>					
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Are You A Member of CBEES	Yes <input type="checkbox"/> No <input type="checkbox"/> (If “No”, you may apply membership from <a href="http://www.cbees.org/member.htm">http://www.cbees.org/member.htm</a> )				
Do You Willing to Receive CBEES Future Conferences Information Via E-mail	Yes <input type="checkbox"/> No <input type="checkbox"/>				
Where did you get the conference information?					
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<p>Other Field of Interest</p>	
<p>Any Other Suggestions/Comments</p>	

Thank you for taking time to participate in this conference evaluation. Your comments will enable us to execute future conferences better and tailor them to your needs!