

# CONFERENCE ABSTRACT

**2019 IEEE 7th International Conference on  
Bioinformatics and Computational Biology (ICBCB 2019)**

**March 21-23, 2019**

**Yuquan Campus, Zhejiang University, Hangzhou, China**

**Co-Sponsored by**



<http://www.icbc.org/>

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## Introduction

Welcome to 2019 IEEE 7th International Conference on Bioinformatics and Computational Biology (ICBCB 2019) which will be held in Zhejiang University, Hangzhou, China during March 21-23, 2019.

Previously, ICBCB 2018 in Chengdu, China, ICBCB 2017 in Hong Kong, ICBCB 2016 in Kuala Lumpur, Malaysia, ICBCB 2015 in Hong Kong, ICBCB 2014 in Beijing, China, ICBCB 2013 in New Delhi, India had been successfully held. The objective of 2019 IEEE 7th International Conference on Bioinformatics and Computational Biology (ICBCB 2019) is to provide an interactive forum for presentation and discussion on Bioinformatics and Computational Biology. The conference welcomes participants from all over the world who are interested in developing professional ties to and/or exploring career opportunities in the region.

We received a large and diverse papers from all corners the world to be considered for presentation and inclusion in the conference proceedings. Finally, the accepted presentations are broadly grouped into areas related to Genetic Engineering, Biosignal Analysis and Data Mining, Medical Image Processing and Application and Bioinformatics and Biomedical Engineering.

### Paper Publication:

After peer review process, all accepted papers after proper registration and presentation, will be published in the following conference proceeding:



further review.

**IEEE ICBCB 2019 conference Proceedings**, which will be reviewed by the IEEE Conference Quality Committees for IEEE Xplore, and submitted to the Ei Compendex and Scopus for

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

# 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 **30** Minutes of Presentation and **5** Minutes of Question and Answer

Plenary Speech: about **30** Minutes of Presentation and **5** Minutes of Question and Answer

Invited Speech: about **15** Minutes of Presentation and **5** Minutes of Question and Answer

Regular 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

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

Poster Presentation: About 5 Minutes of Presentation including Question and Answer Time; Answer Questions Throughout The Session

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

Home-Made Posters: Submit The Poster To The Staff When Signing In

Maximum poster size is A1

Load Capacity: Holds up to 0.5 kg

## Best Presentation Award

One Best Oral and one Best Poster Presentation will be selected from each presentation session, and the Certificate for Best Presentation will be awarded at the end of each session on March 22, 2019.

## Dress Code

Please wear formal clothes or national representative of clothing.

# Keynote Speaker, Plenary Speaker & Invited Speaker Introduction

## Keynote Speaker I



Prof. Bijoy K. Ghosh

Texas Tech University, USA

**Prof. Bijoy K. Ghosh** received the Ph.D. degree in Engineering Sciences from Harvard University, Cambridge, MA, in 1983. From 1983 to 2007 Bijoy was with the Department of Electrical and Systems Engineering, Washington University, St. Louis, MO, USA, where he was a Professor and Director of the Center for BioCybernetics and Intelligent Systems. Currently he is the Dick and Martha Brooks Regents Professor of Mathematics and Statistics at Texas Tech University, Lubbock, TX, USA. He received the Donald P. Eckmann award in 1988 from the American Automatic Control Council, the Japan Society for the Promotion of Sciences Invitation Fellowship in 1997. He became a Fellow of the IEEE in 2000, and a Fellow of the International Federation on Automatic Control in 2014. He was the IEEE Control Systems Society Representative to the IEEE-USA's Medical Technology Policy Committee and currently a member of the IEEE Fellow committee. Bijoy had held visiting positions at Tokyo Institute of Technology, Osaka University and Tokyo Denki University, Japan, University of Padova in Italy, Royal Institute of Technology and Institut Mittag-Leffler, Stockholm, Sweden, Yale University, USA, Technical University of Munich, Germany, Chinese Academy of Sciences, China and Indian Institute of Technology, Kharagpur, India. Bijoy's current research interest is in BioMechanics, Cyberphysical Systems and Control Problems in Rehabilitation Engineering.

*Topic: "Bio-Mimetic Sensing with Multiple Sensors"*

**Abstract**—We revisit the visual sensor pointing control problem as a constrained dynamics on  $SO(3)$  from the point of view of a nonlinear multi input multi output (MIMO) system. The attitude of every sensor is assumed to satisfy a constraint, such as the ones proposed by Donders and Listing for the monocular and binocular eyes and the head rotation problems. While studying the problem of controlling the pointing direction of human head, the constraint, proposed by Donders, is that for every human head rotating away from its primary pointing direction, the rotational vectors are restricted to lie on a surface called the Donders'

surface. In this talk we assume the existence of Donders' surfaces for an array of visual sensors in a flock, tasked with the goal of tracking a point target in the visual space. We assume that the Donders' surfaces are described by a quadratic equation on the coordinates of the rotation vector. The inputs to the MIMO system are three external torque triplet, one for each visual sensor. The three output signals from each sensor are chosen as follows. Two of the signals are coordinates of the frontal pointing direction. The third signal measures deviation of the state vector from the Donders' surface. Thus we have a square system and recent results have shown that this system is feedback linearizable on a suitable neighborhood of the state space. We estimate a lower bound on the size of this neighborhood, by computing distance between the Donders' and the associated Singularity surface. Our results are discussed for the monocular, binocular and the trinocular cases and a comparison is made from the point of view of the observed singularities. Analysis of the feedback linearizing control problem, from the point of view of 'three eyed visual sensing', is new.

## Keynote Speaker II



Prof. Ming Chen

Zhejiang University, China

**Prof. Ming Chen** received his PhD in Bioinformatics from Bielefeld University, Germany, in 2004. Currently he is working as a full Professor in Bioinformatics at College of Life Sciences, Zhejiang University. His group research work mainly focuses on the systems biology, computational and functional analysis of non-coding RNAs, and bioinformatics research and application for life sciences. Prof. Chen is serving as an academic leader in Bioinformatics at Zhejiang University. He chairs the Bioinformatics society of Zhejiang Province, China. He is a committee member of Chinese societies for "Modeling and Simulation of Biological Systems", "Computational Systems Biology", "Functional Genomics & Systems Biology" and "Biomedical Information Technology".

*Topic: "Bioinformatics Studies on Non-Coding RNAs and their Versatile Interactions"*

**Abstract**—One fundamental weakness of microwave imaging is resolution. Good resolution demands a small wavelength and therefore high frequency. Higher frequencies, in the other hand, are attenuated more rapidly, and the adequate depth of penetration dictates a low frequency, no higher than 5 MHz. This is the main problem that plagues almost all microwave systems. The second weakness is small field of view resulting from the non-availability at this time of an efficient miniturised type microwave sensor with large bandwidth. This problem is particularly chronic in organ sensing where at this point and except for specialised area, this type of application requires the size of antenna to be relatively small compared to the field of view. The third drawback is related to the inherent multiple scattering effect. This requires very complicated image reconstruction algorithm and advanced signal processing technique. Currently, most algorithms are based on the beam-forming methods such as the Delay and Sum (DAS) or its variants. The appealing features of this method lies in its simplicity and computational efficiency. However, it only produces approximate solution since the field data is lost due to the linearisation of the inversion procedures. All these problems put the microwave system at a disadvantage. The advent of ultra wide band (UWB) technology and high frequency dielectric resonator antenna (DRA) stimulated new interest in this field as its potential for new applications was recognised. This keynote addresses the development of UWB research at USM, focusing on two potential applications – breast cancer detection and through-the-wall-imaging.

## Keynote Speaker III



Prof. Hesham H. Ali

University of Nebraska at Omaha, USA

**Prof. Hesham H. Ali** is a Professor of Computer Science and Lee and Wilma Seemann Distinguished Dean of the College of Information Science and Technology at the University of Nebraska at Omaha (UNO). He also serves as the director of the UNO Bioinformatics Core Facility that supports a large number of biomedical research projects in Nebraska. He has published numerous articles in various IT areas including scheduling, distributed systems, data analytics, wireless networks, and Bioinformatics. He has also published two books in scheduling and graph algorithms, and several book chapters in Bioinformatics. He has been serving as the PI or Co-PI of several projects funded by NSF, NIH and Nebraska Research Initiative in the areas of data analytics, wireless networks and Bioinformatics. He has also been leading a Research Group that focuses on developing innovative computational approaches to model complex biomedical systems and analyze big bioinformatics data. The research group is currently developing several next generation big data analytics tools for mining various types of large-scale biological and medical data. This includes the development of new graph theoretic models for assembling short reads obtained from high throughput instruments, as well as employing a novel correlation networks approach for analyzing large heterogeneous biological and health data associated with various biomedical research areas, particularly projects associated with infectious diseases, microbiome studies and aging research. He has also been leading two projects for developing secure and energy-aware wireless infrastructure to address tracking and monitoring problems in medical environments, particularly to study mobility profiling for advancing personalized healthcare.

*Topic: "Innovative Graph-Based Tools for Big Data Analytics in Bioinformatics"*

**Abstract**—With continuous advancements of biomedical instruments and the associated ability to collect diverse types of valuable biological data, numerous research studies have been recently focused on how to best extract useful information from the ‘Big Data’ currently available. The currently available data is not only massive in size, but it also exhibits all the features of complex big data systems with a high degree of variability, veracity and velocity. How to leverage this raw data to advance biomedical research, particularly in dealing with outbreaks and infectious diseases, and improve health care, through personalized and targeted medicine, can be considered the most exciting scientific challenge of our generation.

Although many analytical tools have been developed recently to take advantage of this massive raw data, researchers are still scratching the surface regarding what can be mined and utilized to advance biomedical research in general and healthcare in particular. In this talk, we present new big data analytics tools using graph modeling and network analysis along with how to effectively utilize High Performance Computing in implementing such tools. We demonstrate how the proposed tools can be applied to analyze complex data and reveal new useful relationships in various case studies. We illustrate how the graph-based tools led to new biological discoveries by efficiently integrating heterogenous data associated with infectious diseases, aging research and microbiome studies.

## Keynote Speaker IV



Prof. Ashoka Polpitiya

Sri Lanka Technological Campus, Sri Lanka

**Prof. Ashoka Polpitiya**, DSc, is a Professor in Electrical Engineering at Sri Lanka Technological Campus since 2016. Prior to this, he was the Director of Bioinformatics and Biostatistics at Sera Prognostics Inc., in Salt Lake City, Utah where he still works as a consultant. He has also worked in the past as the Lead Bioinformatician for Proteomics at the Translational Genomics Research Institute in Phoenix, Arizona and as a Senior Scientist at the Pacific Northwest National Laboratory (PNNL). He has published articles and developed software tools to address various analytics issues in Genomics and Proteomics experiments. Dr. Polpitiya received his BS in Electrical Engineering from University of Peradeniya, Sri Lanka, an MS and a PhD both from the Washington University in St. Louis in 2000 and in 2004, respectively, in Systems Science and Mathematics. He spends his time in both Sri Lanka and US, working for SLTC and Sera Prognostics.

*Topic: “Biomarker Discovery in Diagnostics: A Case Study on Premature Delivery”*

**Abstract**—Premature delivery or Preterm birth is a major concern across the developing and developed world. It remains as the leading cause of perinatal mortality with a significant strain on healthcare costs. Risk factors and biomarkers used so far have been ineffective in identifying the majority of preterm deliveries. This study focuses on developing and validating a mass spectrometry based protein biomarker test to predict spontaneous preterm delivery in asymptomatic pregnant women. Maternal serum was processed by a proteomic workflow, and proteins were quantified by multiple reaction monitoring mass spectrometry. We evaluated a predictor composed of insulin-like growth factor binding protein 4 (IBP4) and sex hormone binding globulin (SHBG) in a clinical validation study to classify spontaneous preterm delivery cases (<37/7 weeks gestational age). The predictor had an area under the receiver operating characteristic curve value of 0.75. This early detection would guide enhanced levels of care and accelerate development of clinical strategies to prevent preterm delivery.

## Plenary Speaker I



Prof. Ralf Hofest ädt

Bielefeld University, Germany

**Prof. Ralf Hofest ädt** studied Computer Science and Bioinformatics at the University of Bonn. He finished his PhD 1990 (University Bonn) and his Habilitation (Applied Computer Science and Bioinformatics) 1995 at the University of Koblenz. From 1996 to 2001, he was Professor for Applied Computer Science at the University of Magdeburg. Since 2001, he is Professor for Bioinformatics and Medical Informatics at the University Bielefeld. The research topics of the department concentrate on biomedical data management, modeling and simulation of metabolic processes, parallel computing and multimedia implementation of virtual scenarios.

*Topic: “GenCoNet: a Graph Database for the Analysis of Comorbidities by Gene Networks”*

**Abstract**—Based on the medical data and knowledge of the project partner from Tomsk University we could start to identify relevant genes and drugs for asthma and hypertension. Based on lists of genes associated with asthma and hypertension obtained using the HuGENavigator resource and patient drug lists, Bielefeld and Novosibirsk computed and analyzed first relevant metabolic networks. Furthermore, based on the clinical data and semi-automatic data mining approaches a new database was developed and implemented, which presents the positive and negative drug list for asthma and hypertension. A web based implementation of this data base allows the access to this information via internet (<https://genconet.kalis-amts.de>).

## Invited Speaker I



Prof. Zhiwei Qiao

ShanXi University, China

**Prof. Zhiwei Qiao** received his PhD degree in transportation information engineering and control from Beijing Jiaotong University in 2011. He was a Postdoctoral Scholar and Visiting Professor with Department of Radiation and Cellular Oncology, The University of Chicago, Chicago, IL, USA, from August 2012 to August 2014 and from January 2017 to August 2017, respectively. He is currently a professor with School of Computer and Information Technology, Shanxi University, Taiyuan, Shanxi, China. His research interests include electron paramagnetic resonance imaging (EPRI), computed tomography (CT) and magnetic resonance imaging (MRI) etc. He mainly focuses on image reconstruction algorithm, signal processing and high performance computing. He has published a series of papers on CT and EPRI image reconstruction, especially three papers on Journal of Magnetic Resonance. Now, he is constructing the China-USA united lab for medical imaging, supported by Shanxi University and The University of Chicago.

*Topic: “Optimization-Based Image Reconstruction from Fast-Scanned, Noisy Projections in EPR Imaging”*

Abstract—Tumor oxygen concentration image is essential to oxygen-image guided, precise radiation therapy. Electron Paramagnetic Resonance Imaging (EPRI) is an advanced oxygen imaging technique. However, the scanning time is still comparatively long, leading to motion artifacts for static imaging and low time resolution for dynamic imaging. Usually, a projection signal at a specific angle is obtained by averaging thousands of repeatedly collected projections to suppress random noise and achieve a high signal to noise ratio (SNR). Reducing the repetition times of projection collected at a specific angle may effectively speed up the whole scanning process. However, the EPR images reconstructed by the conventional three dimensional filtered backprojection (FBP) algorithm from these fast-scanned, noisy projections are too noisy to be used for further image postprocessing. In the work, we investigate the capability of an optimization-based algorithm in accurate reconstruction from noisy projections. We designed a total variation constrained, data divergence minimization (TVcDM) model, derived its Chambolle-Pock (CP) solving algorithm, and then validated and evaluated the CP algorithm via mathematical and physical phantoms. Studies show that the CP algorithm may accurately reconstruct EPR images from fast-scanned, noisy projections and thus the whole scanning process may be speeded up four times compared with the full scan time demanded by the FBP algorithm.

## Brief Schedule for Conference

<b>Day 1</b>	<b>March 21, 2019 (Thursday)</b> <b>Venue: Room 204 (2nd floor)</b> Arrival Registration 13:00-17:00	
<b>Day 2</b>	<b>March 22, 2019 (Friday)</b> <b>Venue: Lobby of Room 211 (2nd floor)</b> Arrival Registration 08:40-18:50	
	<b>Morning Conference (2nd floor)</b>	
	<b>Venue: Room 211</b>	
	08:40-08:50 <b>Opening Remarks</b> (Prof. Ming Chen)	
	08:50-09:25 <b>Keynote Speech I</b> (Prof. Bijoy K. Ghosh)	
	09:25-10:00 <b>Keynote Speech II</b> (Prof. Ming Chen)	
	10:00-10:30 Coffee Break & Group Photo	
	10:30-11:05 <b>Keynote Speech III</b> (Prof. Hesham H. Ali)	
	11:05-11:40 <b>Keynote Speech IV</b> (Prof. Ashoka Polpitiya)	
	11:40-12:15 <b>Plenary Speech I</b> (Prof. Ralf Hofest ädt)	
12:15-12:35 <b>Invited Speech I</b> (Prof. Zhiwei Qiao)		
<b>12:35-13:45 Lunch (Restaurant)</b>		
<b>Afternoon Conference (2nd floor)</b>		
<b>Session 1</b> 13:45-15:30 <b>Venue: Room 203</b> Topic: “Genetic Engineering” 7 presentations	<b>Session 2</b> 13:45-15:30 <b>Venue: Room 201</b> Topic: “Biosignal Analysis and Data Mining” 7 presentations	
<b>15:30-16:50 Coffee Break</b>		
<b>Session 3</b> 16:50-17:35 <b>Venue: Room 203</b> Topic: “Medical Image Processing and Application” 7 presentations	<b>Session 4</b> 16:50-17:50 <b>Venue: Room 201</b> Topic: “Bioinformatics and Biomedical Engineering” 8 presentations	
<b>Poster Session</b> 17:35-18:50 <b>Venue: Room 203</b> 14 presentations		
<b>18:50-20:30 Dinner (Restaurant)</b>		
<b>Day 3</b>	<b>March 23, 2019 (Saturday)</b> <b>8:30-18:00 Academic Visit</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.

# Detailed Schedule for Conference

**March 21, 2019 (Thursday)**

**Venue: Room 204 (2nd floor)**

<b>13:00-17:00</b>	<b>Arrival Registration</b>
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**March 22, 2019 (Friday)**

<b>Arrival Registration 08:40-18:50</b>	
<b>Venue: Lobby of Room 211 (2nd floor)</b>	
<b>Morning Conference</b>	
<b>Venue: Room 211 (2nd floor)</b>	
<b>08:40-08:50</b>	 <p style="text-align: center;"><b>Opening Remarks</b>                  Prof. Ming Chen                  Zhejiang University, China</p>
<b>08:50-09:25</b>	 <p style="text-align: center;"><b>Keynote Speaker I</b>                  Prof. Bijoy K. Ghosh                  Texas Tech University, USA                  Topic: "Bio-Mimetic Sensing with Multiple Sensors"</p>
<b>09:25-10:00</b>	 <p style="text-align: center;"><b>Keynote Speaker II</b>                  Prof. Ming Chen                  Zhejiang University, China                  Topic: "Bioinformatics Studies on Non-Coding RNAs and their Versatile Interactions"</p>
<b>10:00-10:30</b>	<b>Coffee Break &amp; Group Photo</b>
<b>10:30-11:05</b>	 <p style="text-align: center;"><b>Keynote Speaker III</b>                  Prof. Hesham H. Ali                  University of Nebraska at Omaha, USA                  Topic: "Innovative Graph-Based Tools for Big Data Analytics in Bioinformatics"</p>

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<p>11:05-11:40</p>		<p><b>Keynote Speaker IV</b> Prof. Ashoka Polpitiya Sri Lanka Technological Campus, Sri Lanka Topic: "Biomarker Discovery in Diagnostics: A Case Study on Premature Delivery"</p>
<p>11:40-12:15</p>		<p><b>Plenary Speaker I</b> Prof. Ralf Hofest ädt Bielefeld University, Germany Topic: "GenCoNet: a Graph Database for the Analysis of Comorbidities by Gene Networks"</p>
<p>12:15-12:35</p>		<p><b>Invited Speaker I</b> Prof. Zhiwei Qiao ShanXi University, China Topic: "Optimization-Based Image Reconstruction from Fast-Scanned, Noisy Projections in EPR Imaging"</p>
<p>12:35-13:45</p>	<p><b>Lunch (Restaurant)</b></p>	

- Note:** (1) The registration can also be done at any time during the conference.  
(2) The organizer doesn't provide accommodation, and we suggest you make an early reservation.  
(3) One Best Oral and one Best Poster Presentation will be selected from each presentation session, and the Certificate for Best Presentation will be awarded at the end of each session on March 22, 2019.

**Let's move to the sessions!**

# 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, March 22, 2019 (Friday)**

**Time: 13:45-15:30**

**Venue: Room 203 (2nd floor)**

**Topic: “Genetic Engineering”**

**Session Chair: To be added**

<p>H0030 Session 1 Presentation 1 (13:45~14:00)</p>	<p>The Primary Study for the Integration of Wax-Based Microfluidics on Textile Product <b>Jing Zhang</b>, Xianbo Qiu, Yiqiang Fan, Lulu Zhang and Guijun Miao Beijing University of Chemical Technology, China</p> <p><i>Abstract</i>—This study proposed a novel method for the integration of microfluidic devices on the textile product for the potential applications in wearable sensing and monitoring of human health status. The proposed wearable microfluidic devices enables the controlled fluid flow inside the fiber structure with the capillary force in micro-scale. The structure of microfluidic devices were printed on the surface of a textile product using a commercial wax printer, after thermal treatment, the wax meltdown and permeate through the whole thickness of the textile fiber structure. The hydrophilic textile fiber with hydrophobic wax defined barrier formed a wearable microfluidic device integrated on the textile product. With the proposed protocol, the microfluidics devices could be easily integrated with textile product with a board adaptability with various types of fibers. This primary study for the integration protocols of microfluidics with textile product may have wide potential applications in wearable technology for continues health monitoring and treatment applications.</p>
<p>H0006 Session 1 Presentation 2 (14:00~14:15)</p>	<p>Whole-Genome Sequencing to Determine Origin of Diarrhea in Suckling Piglets in Southern China <b>Jie Li</b>, Jiating Qian, Xuanxuan Mao, Chunyi Xue and Yongchang Cao Changshu Institute of Technology, China</p> <p><i>Abstract</i>—Severe diarrhea in suckling piglets occurred in southern China in 2017 and a new porcine coronavirus, named as porcine enteric alphacoronavirus (PEAV), was identified. Here we reported a detailed process to sequence, assemble and analyze the whole genome of PEAV. GDS04 has 87% amino acid identity comparing to the S proteins of the HKU2 strains without recombination, and their receptor-binding domains in S protein differ at 20 amino acids, suggesting that GDS04 could be a</p>

	<p>new mutant virus from bat-like CoVs and responsible for the most recent diarrhea endemic in pig herds in southern China.</p>
<p>H0004 Session 1 Presentation 3 (14:15~14:30)</p>	<p>Computational Investigations on Target-site Searching and Recognition Mechanism by Thymine DNA Glycosylase during DNA Repair Process <b>Lintai Da</b> Shanghai JiaoTong University, China</p> <p><i>Abstract</i>—DNA glycosylase, as one member of DNA repair machineries, plays an essential role in correcting mismatched/damaged DNA base pair by cleaving the N-glycosidic bond between the sugar and target base through base excision repair (BER) pathways. Efficient corrections of these DNA lesions are critical for maintaining genome integrity and preventing premature aging and cancer. The target-site searching and recognition mechanism by DNA glycosylase, however, remains unknown and experimental characterization of the above process is still challenging due to the limited spatiotemporal resolutions. In this work, by employing high performance computing, combined with markov state model construction based on extensive all-atom molecular dynamics (MD) simulations, we identify the key intermediates of thymine DNA glycosylase (TDG) involved in the target-searching process. In particular, our studies reveal the atomistic-level details of how TDG participates in sculpturing DNA backbone and penetrates into DNA minor groove. Moreover, we also evaluate the substituent effects of various chemical modifications of the pyrimidine rings on the target searching dynamics. More importantly, our model provides the kinetic properties associated with each conformational transition.</p>
<p>H0003 Session 1 Presentation 4 (14:30~15:45)</p>	<p>Gene Regulatory Network Construction and Key Gene Recognition of Diabetic Nephropathy <b>Rao Zheng</b>, Yun Wang, Zhao-lei Lyu and Antonios Armaou Beijing University of Chemical Technology, China</p> <p><i>Abstract</i>—Diabetic nephropathy (DN) is a diabetic complication that seriously endangers human health. Its pathogenesis involves a variety of factors. The purpose of this paper is to determine key genes in the disease progression that will be a potential therapeutic target of DN. Based on gene expression profiles and the databases of interactions of proteins-proteins, transcription factors-genes, transcription factors-miRNAs and miRNAs-genes, the differentially expressed genes of DN were screened. The regulatory network of DN differential genes was established and key genes of DN were identified using the entity grammar system. According to the regulatory interaction between genes, key genes were defined as the ones that could regulate the state of other genes from abnormal towards normal expression. Identified key genes include BMP2 (bone morphogenetic protein 2), VEGFA (vascular endothelial growth factor A), F3 (coagulation factor III/tissue factor),</p>

	<p>EGR2 (early growth response protein 2), CDS1 (CDP- diacylglycerol synthase 1) and PLCE1 (phospholipase C epsilon 1). These findings provide clues for the successful drug development of DN.</p>
<p>H0029 Session 1 Presentation 5 (14:45~15:00)</p>	<p>Predicting RNA Molecular Specific Hybridization via Random Forest <b>Weijun Zhu</b>, Xiaokai Liu, Zhenfei Wang, Yongwen Fan and Jianwei Wang Zhengzhou University, China</p> <p><i>Abstract</i>—RNA hybridization is one of the most important operations in popular RNA simulation software in bioinformatics. However, it is a challenging task to decide whether a specific RNA hybridization is effective within an acceptable time, since this mission has the exponentially computational complexity caused by the combinatorial problem. We hereby introduce a machine learning (ML)-based technique to address this problem. And the Random Forest (RF) algorithm is employed, and many groups of RNA molecular coding and their classification in terms of the results of hybridization are inputted to RF for ML training. The trained ML models are applied to predict the classification of RNA hybridization results. The experiment results show that the average computation efficiency of the RF-based approach is 190690 times higher than that of the existing approach, while the predictive accuracy of the former method is 97.7%, compared with the latter one.</p>
<p>H0009 Session 1 Presentation 6 (15:00~15:15)</p>	<p>Prediction of Linear B-cell Epitopes Based on PCA and RNN Network <b>Ling-yun Liu</b>, Hong-guang Yang and Bin Cheng Hebei Academy of Sciences, China</p> <p><i>Abstract</i>—Epitope prediction plays an important role in production of antibodies and disease treatment. There are mainly two research methods, namely experimental method and calculation method. Experimental method can obtain more accurate experimental results, but it takes a long time and the cost of manpower, material resources are relatively high. So it is not convenient to obtain experimental results more quickly. Calculation method mostly uses computer and machine learning methods for prediction. Calculation method improves prediction speed to some extent, but the result is not satisfactory. In order to further improve the accuracy of epitope prediction, this paper proposes a novel method of processing epitope characteristics. In this paper, we choose six properties to study. The six main physicochemical properties are converted into corresponding digital vectors, resulting in high-dimensional features. Then we use Principal Component Analysis (PCA) method to process them. Finally, dimensionality reduction features are used as input of Recurrent Neural Network (RNN) for epitope prediction, and good prediction results are obtained. PCA method reduces feature dimensions and facilitates the processing of features. At the same time, the prediction</p>

	<p>results obtained with dimensionality reduction features show that dimensionality reduction reduces dimensions, but it retains the main components of original features and improves the rate of successful prediction.</p>
<p>H1024 Session 1 Presentation 7 (15:15~15:30)</p>	<p><b>Clu-RNN: A New RNN Based Approach to Diabetic Blood Glucose Prediction</b>  <b>Yuhan Dong</b>, Rui Wen, Zhide Li, Kai Zhang and Lin Zhang          Graduate School at Shenzhen, Tsinghua University, China</p> <p><i>Abstract</i>—Diabetes is a kind of metabolic disease characterized by increased chronic blood glucose (BG) and may introduce a series of severe complications in a long run. To facilitate health management for diabetic patients, continuous monitoring and prediction of BG concentration are particularly important. Among the popular data driven solutions to BG prediction, machine learning methods, e.g. SVR, RNN and etc., utilize BG data of multiple patients to train the prediction model. However, all the training data sharing the same parameters may not be able to capture the characteristics of BG fluctuation effectively. Motivated by the fact that different subgroups of diabetic patients possess different BG fluctuation patterns, we propose a new BG prediction approach referred to as Clu-RNN based on recurrent neural networks (RNN) by incorporating a pre-process of clustering into the classical RNN. Numerical results suggest that the proposed Clu-RNN approach utilizes more than one cluster for both type I and type II diabetes and has gained improvements compared with support vector regression (SVR) and other RNN methods in terms of BG prediction accuracy.</p>



<p><b>15:30-15:50</b></p>	<p><b>Coffee Break</b></p>
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# 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, March 22, 2019 (Friday)**

**Time: 13:45-15:30**

**Venue: Room 201 (2nd floor)**

**Topic: “Biosignal Analysis and Data Mining”**

**Session Chair: Prof. Qing Li**

<p>H0022 Session 2 Presentation 1 (13:45~14:00)</p>	<p>A Real-Time Algorithm for Sleep Apnea and Hypopnea Detection <b>Yuhan Dong</b>, Jinbo Kang, Rui Wen, Changmin Dai and Xingjun Wang Graduate School at Shenzhen, Tsinghua University, China</p> <p><i>Abstract</i>—In this work, we present a novel rule-based method utilizing single nasal pressure (NP) to diagnose sleep apnea-hypopnea syndrome (SAHS) in real-time. The proposed method has adopted several vital parameters to quantify respiratory patterns and updated all the baselines dynamically. We have investigated thirty-five overnight recordings which are manually annotated by certified physicians and conducted event-by-event comparison and statistical analysis for apnea hypopnea index (AHI). The results are promising with 91.6% accuracy and 91.4% sensitivity for merged apnea-hypopnea detection. Furthermore, calculated AHI obtained by the proposed method highly agrees with manual annotations with Pearson’s correlation coefficient as high as 0.98. It is plausible that the proposed method is viable to be incorporated into polysomnography (PSG) or other portable devices for automatic sleep disorder monitoring since all the events detected are with high time resolution.</p>
<p>H1012 Session 2 Presentation 2 (14:00~14:15)</p>	<p>Research on Localization of sEMG Detection Sites Across Individual Upper Limbs <b>Yun-Long Wang</b>, Xue-Liang Bao, Yu-Xuan Zhou, Xiao-Ying Lü and Zhi-Gong Wang Southeast University, China</p> <p><i>Abstract</i>—In order to recognize upper limb’s motion more accurately, this paper presents a method for locating transcutaneous surface electromyography (sEMG) based on traditional Chinese medicine (TCM) acupoint sites. To get sEMG root mean square (RMS) value distribution, sEMG signals of nine kinds of movements</p>

	<p>of seven healthy individuals were collected under the acupoint coordinate system. Finally, this paper obtains a trans-individual localization map of sEMG detection sites of upper limbs. This method of localization of sEMG detection sites not only can quickly find sites across individual, but also is accepted easily for clinical application.</p>
<p>H0020 Session 2 Presentation 3 (14:15~14:30)</p>	<p>Prediction Model of Chilling Injury Combined with Quadratic-Orthogonal-Rotation-Combination Design Technique for Postharvest Cucumber Fruit during Cold Storage <b>Min Zhang</b>, Jiale Li, Wenting Ai, Yuxuan Zhao and Wei Liu Shanghai Ocean University, China</p> <p><i>Abstract</i>—Cucumber fruit is susceptible to chilling injury (CI) which results in the cellular structure damage of fruit during low temperature storage. However, visual symptoms of chilling injury may not be observed when they were taken out from low temperature. In this study, the critical value of chilling injury for postharvest cucumber fruit during low temperature storage was investigated. The thermal conductivities of cucumber fruit were determined using a specifically designed thermal conductivity probe system. Combined with the quadratic-orthogonal-rotation-combination design technique, a prediction model based on the chilling injury detection indicators from the ratio of thermal conductivity of cucumber fruit was developed and the critical value of chilling injury detection indicator was identified. Verification test was shown that the suggested prediction model was suitable to estimate safe storage temperature and safe storage time by calculating the critical value for preventing chilling injury. Furthermore, it might be beneficial to provide the potential application of method for chilling injury detection in other cold sensitive fruit.</p>
<p>H1015 Session 2 Presentation 4 (14:30~14:45)</p>	<p>Prototype System Design and Experimental Validation of Gait-Oriented EMG Bridge for Volitional Motion Function Rebuilding of Paralyzed Leg <b>Zheng-Yang Bi</b>, Xue-Liang Bao, Hai-Peng Wang, Xiao-Ying Lü and Zhi-Gong Wang Southeast University, China</p> <p><i>Abstract</i>—The voluntary participation of paralyzed patients is crucial for the neuromuscular electrical stimulation (NMES) therapy. In this paper, an NMES technique based on surface electromyogram (sEMG) communication between healthy side and affected side of hemiplegic patients, called gait-oriented EMG bridging (EMGB), is proposed to realize the motion of paralyzed leg under the stimulation of the volitional sEMG signal of healthy leg. The sample entropy</p>

	<p>algorithm is used to detect the onset and offset of agonist sEMG in the healthy side, which triggers or ends the recording of agonist sEMG. The MAV/NSS co-modulation (MNDC) algorithm is used to modulate a various frequency and pulse width of stimulation according to the recording agonist sEMG. The stimulation is triggered by the onset of antagonistic sEMG in healthy side to stimulate the target affected muscles. A prototype gait-oriented EMGB system was developed for real time control of dorsiflexion and plantarflexion in sitting position. The experimental results indicated that alternate ankle motions can be achieved successfully. The angle trajectory of ankle can be reproduced alternately with a latency within 300 ms and a maximum cross-correlation coefficient <math>&gt; 0.82</math>.</p>
<p>H0023 Session 2 Presentation 5 (14:45~15:00)</p>	<p>Rare Association Rules Mining of Diabetic Complications Based on Improved Rarity Algorithm Qiao Pan, <b>Lan Xiang</b> and Yanhong Jin Donghua University, China</p> <p><i>Abstract</i>—Although the frequent pattern mining has attracted widespread attention of scholars, it is undeniable that the rare pattern mining plays a significant role in many fields, such as medical, financial, and scientific fields. And it is more valuable to study the rare pattern mining, because it tends to find some unknown and unexpected associations. There are some previous algorithms of rare itemsets mining, however, Arima spends much time and Rarity wastes much space. So based on the Rarity algorithm, this paper presents an improved top-down approach to efficiently mine all rare itemsets and their association rules, which uses the graph structure to indicate all combinations of existing items in the database, defines a pattern matrix to record all itemsets and the support_count, and combines the hash table to accelerate support calculation to quickly find all rare itemsets, and then generate all patterns to choose useful rules according to their interesting rate. In the experiment, this paper uses the real diabetic clinical data to verify this improved approach and mines some useful rules among the diabetic complications. Moreover, compared with the two methods mentioned above, this method decreases much time and space complexity in the association rules mining.</p>
<p>H1008 Session 2 Presentation 6 (15:00~15:15)</p>	<p>Exploring the Relationship between Neural Mechanism and Detection in Mental Fatigue by Genetic Algorithm and Hierarchical Clustering <b>Yinhe Sheng</b>, Kang Huang, Jiemeng Zou, Liping Wang and Pengfei Wei Shenzhen Institutes of Advanced Technology, China</p>

	<p><b>Abstract</b>—The mental fatigue affects the state of one's daily life easily, therefore, understanding the neural mechanisms of mental fatigue and better detection of it have been the focus of many researchers. Quite a few previous studies have found EEG indicators and high-precision detection methods related to mental fatigue, however, how to combine these EEG indicators with detection methods for better detection remains to be solved. To classify mental fatigue based on EEG features, our previous research, which adopted GA-SVM method, have demonstrated the optimal channels are mainly distributed in the prefrontal, occipital and temporal lobes, and the optimal channel number is 5. Here, we further explored the question by developing a new method combining genetic algorithm and hierarchical clustering to study the mental fatigue caused by visual search. Our results suggest that the optimal EEG features for assessing fatigue state vary from person to person, while the corresponding optimal channel positions are consistent. The channels with the largest changes in EEG features are mainly distributed in the frontal lobe, followed by the temporal lobe and a small area of the occipital lobe, while the corresponding regions of the almost all parietal lobe and part occipital lobe show little changes in EEG features during fatigue. Current study shows that the optimal EEG features of different individuals are different in the mental fatigue detection, and they need to be determined separately, but only a few of the same channels can be used to achieve the better detection.</p>
<p>H0028 Session 2 Presentation 7 (15:15~15:30)</p>	<p>Microarray Data Combining with Molecular Docking Simulation Reveals the Anti-Fibrotic Effect of Yi-Guan-Jian Decoction in Chronic Hepatitis B Patients <b>Guangyao Li</b>, Ging Chan and Yuanjia Hu University of Macau, China</p> <p><b>Abstract</b>—The Yi-Guan-Jian decoction (YGJD) has been widely used in the treatment of liver fibrosis in CHB cases. Although animal studies have reported the anti-fibrotic effects of the decoction, the active ingredients and the mechanisms of action (MOA) remain unknown. In approach, using data mining techniques and a structural clustering analysis, the potential active ingredients were determined. A network analysis of the differentially expressed genes was conducted to identify the potential targets. Selected compounds were docked to the potential targets for the compound-target interaction simulation. As a result, thirty active ingredients of the YGJD and 15 main targets were identified. Literature findings regarding these main targets support YGJD attenuated or even reversed the progression of liver fibrosis among CHB patients by inhibiting hepatic stellate cell activation, preventing excessive extracellular matrix deposition and regulating inflammatory response. All in all, we identified the</p>

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	<p>potential active ingredients of the YGJD and proposed a possible explanation for the MOA in the treatment of CHB patients with liver fibrosis. Moreover, this study provides a methodological reference for the systematic investigation of the bioactive compounds and related MOA of a traditional herbal formula in a clinical context.</p>
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<p><b>15:30-15:50</b></p>	<p><b>Coffee Break</b></p>
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# 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, March 22, 2019 (Friday)**

**Time: 15:50-17:35**

**Venue: Room 203 (2nd floor)**

**Topic: “Medical Image Processing and Application”**

**Session Chair: Prof. Zhiwei Qiao**

<p>H0010 Session 3 Presentation 1 (15:50~16:05)</p>	<p>Dynamic MRI Reconstruction Exploiting Partial Separability and t-SVD <b>Shuli Ma</b>, Huiqian Du, Qiongzhi Wu and Wenbo Mei Beijing Institute of Technology, China</p> <p><i>Abstract</i>—In this paper, we proposed a new method to reconstruct dynamic magnetic imaging (dMRI) data from highly undersampled k-t space measurements. First, we use the partial separability (PS) model to capture the spatiotemporal correlations of dMRI data. Then, we introduce a new tensor decomposition method named as tensor singular value decomposition (t-SVD) to the reconstruction problem. PS and low tensor multi-rank constrains are jointly enforced to reconstruct dynamic MRI data. We develop an efficient algorithm based on the alternating direction method of multipliers (ADMM) to solve the proposed optimization problem. The experimental results demonstrate the superior performance of the proposed method.</p>
<p>H0024 Session 3 Presentation 2 (16:05~16:20)</p>	<p>Applying L-SRC for Non-invasive Disease Detection Using Facial Chromaticity and Texture Features <b>Jianhang Zhou</b>, Qi Zhang and Bob Zhang University of Macau, China</p> <p><i>Abstract</i>—Diseases like hyperuricemia and hystero myoma along with prediabetes (a serious health condition) are causing more suffering and hardship than ever before. Recently, computerized non-invasive diagnostic methods inspired by Traditional Chinese Medicine (TCM) have proved to be reasonable and effective using the face and/or tongue to perform disease detection. These methods no longer require bodily fluids to be extracted (e.g., a blood test), which further relieves the pain of patients and allows doctors to focus on more labor intensive activities. In this paper, we propose a novel classifier based on the fusion of the linear discriminant analysis</p>

	<p>(LDA) and the sparse representation based classifier (SRC) named L-SRC, to perform disease detection. Specifically, we collect facial images using a non-invasive capture device from those suffering from hyperuricemia, hysteryoma and prediabetes, and feed it to the L-SRC classifier to perform classification. The experimental results show that L-SRC can discriminate samples belonging to the three classes with healthy control more effectively, achieving accuracies of 72%, 70.95% and 76.60% respectively. This indicates a promising application prospect in the future.</p>
<p>H0014 Session 3 Presentation 3 (16:20~16:35)</p>	<p>A Novel RNN-Based Blood Glucose Prediction Approach Using Population and Individual Characteristics <b>Yuhan Dong</b>, Rui Wen, Kai Zhang and Lin Zhang Graduate School at Shenzhen, Tsinghua University, China</p> <p><i>Abstract</i>—As a common endocrine disease, diabetes has been plagued the lives of patients. An accurate blood glucose (BG) prediction approach can not only be used in daily BG management to reduce the occurrence of hypoglycemia or hyperglycemia, but also regulate the amount and time of insulin injection combined with insulin pump. Data driven methods have become an effective way for predicting BG. While time series analysis methods only deal with one patient at a time and most machine learning approaches simply use multiple patients' data to capture the population characteristics of BG but ignore the individual characteristics. To overcome these shortcomings, we propose a novel neural network approach based on GRU in which both population and individual characteristics of BG fluctuation are well integrated by pre-training and fine-tune processes. The proposed approach not only overcomes the problem of insufficient data for individual patient, but also makes full use of the population and individual differences of BG fluctuation. Compared with other machine learning or neural network approaches, the numerical results suggest that the proposed approach gains significant improvements on prediction accuracy.</p>
<p>H0007 Session 3 Presentation 4 (16:35~16:50)</p>	<p>Stability of MRI Radiomic Features of the Hippocampus: An Integrated Analysis of Test-Retest Variability <b>Zhuoran Li</b>, Huichuan Duan, Kun Zhao, Yanhui Ding and Yuanjie Zheng Shandong Normal University, China</p> <p><i>Abstract</i>—Radiomic is a quantitative method to extract medical features and it can extend details that are invisible to human eyes. Studies have suggested that the radiomics of the hippocampus is a potential imaging biomarker for several diseases, including Alzheimer disease, mild cognitive impairment and multiple sclerosis. The main aim of the present study is to investigate the test-retest</p>

	<p>reproducibility of the radiomics measures of the hippocampus. For this purpose, the intra-class correlation coefficient (ICC) and overall concordance correlation coefficient (OCCC) of the radiomics properties of the hippocampus were well studied in a dataset including 19 subjects who were scanned two times. The result highlights that most of the hippocampal texture are repeatable, and the possibility that texture may serve as a neuroimaging biomarker for clinical study.</p>
<p>H1020 Session 3 Presentation 5 (16:50~17:05)</p>	<p>Endoscopic Image Colorization Using Convolutional Neural Network <b>HuiPeng Jiang</b>, SongYuan Tang, Yating Li, Danni Ai, Hong Song and Jian Yang Beijing Institute of Technology, China</p> <p><i>Abstract</i>—Colorization of grayscale images is crucial for clinical image-based diagnosis. However, it is an ill-posed problem that requires a comprehensive understanding of image content. The present study proposes a novel convolutional neural network (CNN) for a fully automatic colorization process by first employing the pre-trained residual network to extract high-level image features and then introducing the CNN to analyze the complex nonlinear relationship between the image features and chrominance values. Luminance and the learned chrominance values are then combined to recover the color of the image, and the proposed color-perceptual loss function is used to calculate the recovered and real color image loss. Based on the experiments conducted, the proposed method was proven to be highly effective and robust in restoring endoscopic images to their true colors. The average values of the feature similarity index incorporating chromatic information (FSIMc) and the quaternion structural similarity (QSSIM) for the experimental endoscopic image datasets reached 0.9961 and 0.9739, respectively.</p>
<p>H0017 Session 3 Presentation 6 (17:05~17:20)</p>	<p>Decoding Attention Position Based on Shifted Receptive Field in Visual Cortex <b>Xiaohan Duan</b>, Ziya Yu, Li Tong and Linyuan Wang National Digital Switching System Engineering and Technological Research Center, China</p> <p><i>Abstract</i>—Visual attention is an important issue in the field of neuroscience and computer vision. According to recent research of visual cognitive computation, receptive fields are thought to be shifted with the influence of spatial attention. In the traditional method, researchers decoded various positions of attention based on constant population receptive field (pRF) parameters. Comparing with previous attention decoding researches, recent discovery may help improve the decoding accuracy. In this research, to get a better</p>

	<p>accuracy, a new decoding method is proposed with introducing the shift of pRF parameters. Firstly, we adopted two-dimensional Gaussian receptive field model to characterize the population receptive field(pRF) of each voxel in seven visual areas [V1-V4, inferior occipital gyrus (IOG), posterior fusiform gyrus (pFus), and mid-fusiform gyrus (mFus)]. Then, we introduced a parameter to measure the shift of pRF. With the shifted pRF parameters, the attention position could be decoded by maximum likelihood estimation. With published fMRI dataset, a better decoding accuracy could be obtained in most regions, especially in higher regions. The result also indicated that with the modulation of spatial attention, pRF parameters of voxels in high regions were shifted much more than those in early regions.</p>
<p>H1013 Session 3 Presentation 7 (17:20~17:35)</p>	<p>Feature Engineering in Discrimination of Herbal Medicines from Different Geographical Origins with Electronic Nose <b>Xianghao Zhan</b>, Xiaoqing Guan, Rumeng Wu, Zhan Wang, You Wang and Guang Li Zhejiang University, China</p> <p><i>Abstract</i>—As pharmacists attach great significance to geographical origins of herbal medicines, cheap, nondestructive and convenient methods for discriminating herbal medicines originated from diverse regions are much in need. This work proposes a method of using electronic nose to discriminate herbal medicines from different origins. With 5 categories of herbal medicines and 3 to 4 geographical origins for each category, 8 pattern recognition algorithms prove the feasibility of the classification task and SVM, LDA and BP neural network have shown better classification accuracy. Additionally, feature engineering approaches are used to facilitate classification, showing that normalization based on each feature and each sensor and centralization prove to be better normalization approaches for classifiers; a proper degree of noise addition help classifiers get better generalization ability; finally, feature selection with SNR could lead to more efficient classifiers by selecting the most meaningful features and disregarding unnecessary features. This work provides insights for future herbal medicine evaluation based on electronic nose with better combinations of pattern recognition algorithms and feature engineering approaches for optimal classification performances.</p>

# 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, March 22, 2019 (Friday)**

**Time: 15:50-17:50**

**Venue: Room 201 (2nd floor)**

**Topic: “Bioinformatics and Biomedical Engineering”**

**Session Chair: Prof. Ashoka Polpitiya**

<p>H0011 Session 4 Presentation 1 (15:50~16:05)</p>	<p>A Novel Convolutional Regression Network for Cell Counting <b>Qian Liu</b>, Anna Junker, Kazuhiro Murakami and Pingzhao Hu University of Manitoba, Canada</p> <p><i>Abstract</i>—A stacked deep convolutional neural network (DCNN) model was generated to predict cell density maps and count cells. We treated the cell counting as a regression problem with a preprocessing step to generate cell density maps. We implemented this approach by integrating two trustworthy and state-of-art model architectures (U-net &amp; VGG19). This method combines the advantages from both traditional segmentation-based and density-based methods. It overcomes the limitations such as cell clumping, overlapping, and it can also bypass the fine-tuning step which was necessary for previous density-based methods when applying to different datasets. A publicly available well-labeled dataset was used to train and test the model. An unlabeled real dataset which generated in-house was used to evaluate the performance.</p>
<p>H0015 Session 4 Presentation 2 (16:05~16:20)</p>	<p>PASnet: A Joint Convolutional Neural Network for Noninvasive Renal Ultrasound Pathology Assessment <b>Zhiwei Wu</b>, Kai Qiao, Lijie Zhang, Jinjin Hai, Ningning Liang, Linyuan Wang and Bin Yan National Digital Switching System Engineering &amp; Technological Research Centre, China</p> <p><i>Abstract</i>—Nephropathy is a worldwide clinical and health problem that is getting more and more attention from the public. The gold standard for the diagnosis of nephropathy is still renal puncture biopsy, which is an invasive examination and has many contraindications. We proposed to analyze renal ultrasound images using deep learning method to achieve noninvasive assessment. However, the kidney ultrasound images with accurate pathological diagnosis are relatively difficult to collect, which belongs to the</p>

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	<p>category of few-shot learning. To mitigate the impact of few data on performance, this paper proposed a conceptually simple, flexible, and mixed framework for aided diagnosis of nephropathy. Our method, called the PASnet, consists of pretrained network and siamese network. Pretrained network trained by abundant samples from ImageNet can achieve fast convergence and better performance on a new data set. Siamese network learns to converge or disperse image pairs in distance space according to whether it comes from the same class or not. PASnet combines the advantages of these two methods and obtains a better classification performance on nephropathy classification through joint training. Accuracy of PASnet increases by 5.89% compared to a single network.</p>
<p>H0021 Session 4 Presentation 3 (16:20~16:35)</p>	<p>An Investigation and Analysis of Clinical Trials and Research Centers on Regenerative Medicine Industry—— Case Comparison between China and other Countries <b>Hongshen Pang</b>, Ling Wei, Xiaochu Qin, HaiYun Xu and Hongming Hou Shenzhen University, China</p> <p><b>Abstract</b>—The field of stem cells and regenerative medicine is one of the most attractive foci and research hot spots in the current biology and medicine. The international scientific community has made remarkable breakthroughs in the following issues: 1) The basic regulatory theory of stem cells; 2) iPS cells, targeted reprogramming to functional cells and new types of stem cells; 3) Gene edit technologies; 4) Tissue engineering and translational research, drug development using stem cells, nano-materials research and application in regenerative medicine etc. Scientists in institutes and the biology pharmaceutical industry are actively promoting the clinical translation by discovering new mechanisms, innovating technologies and creating new therapies, leading to a big scale market of the regenerative medicine nowadays. Traditional treatments such as drug therapy and surgery often have little effect on such diseases, and fail to meet the growing medical needs of this age-group. Stem cell-based regenerative medicine is expected to become the third treatment option after drug therapy and surgery. With the increasing financial supports and investments in China recent years, a series of important progress have been made to stem cells and regenerative medicine. In this issue, we investigated the stem cell and regenerative medicine industry in the world and china, such as clinical trial and research institutions distribution.</p>
<p>H0016 Session 4</p>	<p>The Effects of Self-Regulation in Hippocampus Activation Using Different Types of Real-Time Neurofeedback <b>Yashuo Zhu</b>, Hui Gao, Qiang Yan, Zhonglin Li and Li Tong National Digital Switching System Engineering &amp; Technological</p>

<p>Presentation 4  (16:35~16:50)</p>	<p>Research Center, China</p> <p><b>Abstract</b>—Real-time functional magnetic resonance imaging neurofeedback (rtfMRI-NF) is a non-invasive imaging technique which can extract the concurrent brain state and provide neurofeedback to subjects in an online fashion so that subjects can self-regulate their internal brain state accordingly. In this area, most studies give the continuous NF that is obtained upon every fMRI data acquisition. Although the time resolution of NF signal is maximized, the continuous NF may have some drawbacks. Subjects can be dispersed in the condition of emotion regulation because (1) there is an inherent delay between the hemodynamic response which is caused by neuronal activity and associated NF, (2) there is a limit on the cognitive attention available to simultaneously assess NF and keep with the regulation. In this study, we investigated the differences of the capability to up-regulate activity of hippocampus between groups. The three groups were presented with continuous and intermittent NF and a control group receiving sham NF signal using positive autobiographical memories recalling. Compared with the NF groups, there was no remarkable regulating effect in the control group. The performance of hippocampal regulation in the intermittent group was better than it in the continuous neurofeedback group. In general, we not only showed that the NF was a prerequisite to learn self-regulation of hippocampus activity but also showed that intermittent NF was superior to continuous NF presentation. Training with rtfMRI-NF has promising translational value in future therapeutic process of emotionally related mental disorders.</p>
<p>H0026  Session 4  Presentation 5  ((16:50~17:05)</p>	<p>The Automatic Repairing Method addressing Clipping Distortions and Frictional Noises in Electronic Stethoscope Ning Zhou, Jiajun Wang, Bing Sun, Renyu Liu and <b>Nan Hu</b> Soochow University, China</p> <p><b>Abstract</b>—The auscultation signal collected by the electronic stethoscope may be sometimes accompanied by various interferences, including external speech/acoustic interferences, clipping distortions, frictional noises, etc. The external speech/acoustic interferences can be eliminated by adaptive filtering, with the aid of an extra recording sensor. However, clipping distortions and frictional noises cannot be addressed by this methodology, and how to automatically repair them has not been fully discussed in the literatures, which affects the signal quality and further the cardiopulmonary sound automatic diagnosis. In this paper, the repairing method that automatically addresses clipping distortions and frictional noises for electronic stethoscope is developed. A simple signal difference method is introduced to</p>

	<p>automatically detect the clipping distortion regions, and these regions are repaired by the Hermite interpolation. The regions that frictional noises exist are detected by employing Mel-frequency cepstral coefficients (MFCCs) and support vector machine (SVM), and they are repaired by involving the empirical mode decomposition (EMD) as well as correlation coefficients. The proposed method can automatically detect, locate and ultimately repair multiple regions of clipping distortions and frictional noises, and applying it in recorded real auscultation data proves its efficiency.</p>
<p>H0019 Session 4 Presentation 6 (17:05~17:20)</p>	<p>Characterization of Cell Microcapsules and Preparation via Digital Coaxial Injection <b>Qing Li</b>, Rongshuai Liu, Weipeng Zhang and Yuxi Feng Ningbo University of Finance Economics, China</p> <p><i>Abstract</i>—Cell microcapsules are prepared and characterized by digital injection of coaxial micro-fluidics to better control cells number and reduce the redundancy space in microcapsules. The results show that the diameter of the inner and outer nozzles of the micro coaxial nozzle have a significant effect on the particle size of the cell microcapsules, particle size distribution and the number of encapsulated cells. The particle size of the lymphocyte microcapsules increases linearly with the diameter of the outer nozzle, not significantly influenced by the change of the diameter of the inner nozzle. The number of lymphocytes in the microcapsules increases exponentially with the inner nozzle diameter, and is not significantly affected by the diameter of the outer nozzle. So, we can flexibly control the particle size of the microcapsules and the number of encapsulated cell, reduce the redundant space by the ratio between the inner and outer nozzle diameters.</p>
<p>H0008 Session 4 Presentation 7 (17:20~17:35)</p>	<p>Synchronous Optimal Design of Genetic Oscillator Networks Using a Novel VonPSO Algorithm <b>Wei Zhang</b>, Qinqin Yao, Jianming Zhang and Guang Li Zhejiang University, China</p> <p><i>Abstract</i>—As a common phenomenon in biological systems, synchronization plays a vital role in construction of genetic oscillator networks with specific cellular functions. Considering the complexity of connections, optimal synchronous design of oscillator networks become feasible with optimization approaches. In order to improve the efficiency of optimal synchronous design, a novel VonPSO algorithm that applies Von-Neumann topology is proposed to solve the combinational optimization problem involved in optimizing directed interactions within coupled oscillator networks. This VonPSO algorithm applies mutation and crossover operations to</p>

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	<p>generate new candidates that represent the network adjacent matrices. Using order parameter to evaluate the degree of synchronization, this paper applies a twostages optimization framework that adjusts network topologies and coupling parameters at two independent stages. Simulation outcomes indicate that the proposed framework is effective to improve the synchronous indexes between coupled genetic oscillators using the VonPSO algorithm. Experimental outcomes indicate that synchronization of coupled oscillator networks can be significantly enhanced by the two-stages optimization using VonPSO algorithm.</p>
<p>H0025 Session 4 Presentation8 (17:35~17:50)</p>	<p>Application of Deep Learning Models to MicroRNA Transcription Start Site Identification Clayton Barham, Mingyu Cha, <b>Xiaoman Li</b> and <b>Haiyan Hu</b> University of Central Florida, USA</p> <p><b>Abstract</b>—microRNAs (miRNA) are ~22 base pair long RNAs that play important roles in regulating gene expression. Understanding the transcriptional regulation of miRNA is critical to gene regulation. However, it is often difficult to precisely identify miRNA transcription start sites (TSSs) due to miRNA-specific biogenesis. Existing computational methods cannot effectively predict miRNA TSSs. Here, we employed deep learning architectures incorporating Long Short-Term Memory (LSTM) and Convolutional Neural Network (CNN) techniques to detect miRNA TSSs in regions of accessible chromatin. By testing on benchmark experimental data, we demonstrated that deep learning models outperform support vector machine and can accurately distinguish miRNA TSSs from both flanking regions and intergenic regions.</p>

# Poster Session

Afternoon, March 22, 2019 (Friday)

Time: 17:35-18:50

Venue: Room 203 (2nd floor)

<p>H0002 Poster 1</p>	<p>Establishment and Simulation of 3D Gastric Impedance Detection Model Zhangyong Li, <b>Shangzhi Xiang</b> and Zhaoyu Liu Chongqing University of Posts and Telecommunications, China</p> <p><i>Abstract</i>—This paper builds a three-layer electrical impedance imaging (EIT) model. The changes in gastric impedance information in gastric contents and gastric volume of different conductivity were studied in different electrode excitation models. In this paper, the human abdominal cavity model was constructed by using COMSOL MULTIPHYSICS simulation software, and a 48-electrode system was constructed on the outer layer of the model. In the experiment, two models of relative electrode excitation and adjacent electrode excitation were established, and the simulated gastric emptying process was simulated. Secondly, by measuring the voltage and analyzing the data. Finally, the system is evaluated by using the boundary measurement voltage sensitivity <math>\delta</math> and the boundary voltage measurement dynamic range <math>\tilde{U}</math>. The analysis shows that the relative electrode excitation model has lower sensitivity and better signal-to-noise ratio for system detection and stability. At the same time, it is proved that more gastric emptying information can be obtained through the three-layer EIT model, which can effectively reflect different relevant impedance information of gastric contents.</p>
<p>H1007 Poster 2</p>	<p>Exploring the Characteristics of Different Types of RNAs via Topological Analysis of the RNA–RNA Interaction Network <b>Yang Zhang</b>, Lin Ning, Jiayi Yin, Zhixi Yun, Hao Xu and Jian Huang University of Electronic Science and Technology of China , China</p> <p><i>Abstract</i>—Systematic protein–protein interaction network (PPIN) analyses have provided valuable information about the functional organization of cells. However, recent developments have indicated that the RNA–RNA interaction network (RRIN) may play a more extensive role in the cellular regulatory network (CRN). However, to date no study has systematically characterized the RRIN. In this study, we identified a high-confidence RRIN from the RAID v2.0 database (34,874 interactions, 8,438 nodes) and evaluated three of its topological properties (degree, betweenness, k-core). Analysis of the mRNAs, miRNAs, and lncRNAs in this network revealed that miRNAs had the highest degree (<math>p=2.29e-04</math>) and k-core (<math>p=2.45e-02</math>) values, lncRNAs had the highest betweenness value (<math>p=5.09e-03</math>) and the lowest k-core value (<math>p=3.42e-02</math>), and mRNAs had the lowest degree (<math>p=3.75e-02</math>) and betweenness (<math>p=7.71e-03</math>)</p>

	<p>values. The degrees of the mRNAs and miRNAs exhibited a power-law distribution, whereas the lncRNA degrees had a bimodal distribution. In addition, most of the RNAs with high centrality were miRNAs, with the exception of the mRNA MYC, which may indicate that MYC has a special status in the RRIN compared with other mRNAs. In summary, the different characteristics of these three types of RNAs may reflect the different biological roles that they play in the CRN.</p>
<p>H1001 Poster 3</p>	<p>Research on Quantitative Classification of Exercise Fatigue Based on Fuzzy Comprehensive Evaluation Method Wei Wang, <b>Huashan Si</b>, Xiaoni Zhang and Zhangyong Li Chongqing University of Posts and Telecommunication, China</p> <p><i>Abstract</i>—Aiming at the complexity and fuzziness of the connotation, extension and extension of sports fatigue, this paper constructs a quantitative and grading index evaluation model of cycling fatigue based on Kirkpatrick's classical evaluation model. With the help of Ironman tax T2060 virtual intelligent riding platform to obtain real-time riding power and speed, while wearing wearable Zephyr BioHarness physical signs detector, recording the heart rate and respiratory rate of subjects, after 30 subjects during the movement of real-time data collection, analysis and processing of the parameters. Using the multi-level fuzzy comprehensive evaluation method and mathematical matrix method, the fatigue caused by cyclists in sports can be quantitatively classified and evaluated.</p>
<p>H1014 Poster 4</p>	<p>Construction of Reproductive Stage Gene Regulatory Networks Mediated by Stage-Specific Small RNAs in Grapevine <b>Zhihong Yang</b>, Lan Yu, Yeqin Jiang, Xinghuo Yea and Chaogang Shao Huzhou University, China</p> <p><i>Abstract</i>—Grapevine is a widely grown fruit crop playing an important role in the human diet and health. The reproductive stage from inflorescence to berry is critical for fruit setting and quality. But the mechanism of small RNAs (sRNAs) regulating networks were not clear. In hoping to understand the process, regulating networks were constructed by analysis the relationship between small RNAs and the genes expression. The transcript and small RNAs HTS data sets of four development phases (inflorescence, flower, young berry and mature berry) were downloaded from data bases individually. The results demonstrated that most important genes associated with development phases were regulated by these Non-micro-sRNAs in grapevine reproductive stage. In inflorescence phase, 4 phase stage-specific sRNAs and their 10 mRNA target pairs were found. In flower phase, when compared with young berry phase, there were 6 mRNAs found downregulating by 5 stage specific sRNAs. Young berry phase hold the most pairs of 15 mRNAs with 16 sRNAs in the whole reproductive stage. Mature berry stages, 7 mRNAs with 5 sRNAs pairs and 13 mRNAs with 14 sRNAs pairs were existed individually.</p>
<p>H1022</p>	<p>Towards the Recovery of Responsiveness in Disorder of Consciousness via a</p>

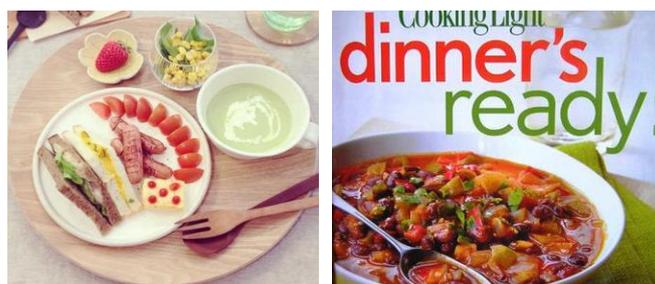
<p>Poster 5</p>	<p>Tactile P300 Brain-Computer Interface  <b>Ren Xu</b>, Nensi Murovec, Alexander Heilinger, Yangyang Miao, Jing Jin, and Christoph Guger  Guger Technologies OG, Austria</p> <p><i>Abstract</i>—Brain-computer interface (BCI) has been emerging as an assessment tool for patients with disorder of consciousness (DOC). With the advantages of high time resolution, low cost and portable design, EEG based BCI systems are especially suitable for bedside measurement. Recent studies have shown the successful application of an EEG based BCI on DOC assessment and communication. In this study, a tactile P300 paradigm was repeated 8 runs for 10 consecutive days on 10 DOC patients. During the 10 sessions every patient achieved at least once an accuracy <math>\geq 60\%</math>. Seven of the ten patients showed an improvement of 1 to 7 points in the Coma Recovery Scale Revised (CRS-R) score after the BCI sessions (mean: 1.8). This study addressed the significance of repeating a tactile BCI on DOC patients, and indicates a promising recovery effect of a tactile BCI on DOC patients.</p>
<p>H1003  Poster 6</p>	<p>Study on the Method of Blood Microscopic Multi-field Image Stitching  Zhangyong Li, <b>Hui Liu</b>, Mengxi Ju, Fuqu Chen and Xinwei Li  Chongqing University of Posts and Telecommunication, China</p> <p><i>Abstract</i>—In the diagnosis of medical blood diseases, there are contradictions between the clear view and the size of view under the microscope. In order to obtain clear blood cell images under a large view, this paper proposes an image stitching method for multi-view blood microscopy images. The method firstly preprocesses the input image sequence, and then uses the SIFT feature and the local LBP feature to extract the feature points of the image sequence, obtains the matching point pairs according to the threshold method, and then uses the improved RANSAC algorithm to calculate the homography matrix between the images. Finally, the weighted average in image fusion is used to realize the seamless stitching of multi-view images. The experimental results show that the improved feature detection algorithm has good performance in the rotary image, blurry image and distorted cell image. The improved RANSAC algorithm effectively improves the computational efficiency of the image, and finally achieves multi-view blood display with high efficiency and seamless stitching of micro images.</p>
<p>H1019  Poster 7</p>	<p>Estimation of the Equilibrium GC Content of Human Genome  <b>Jian-Hong Sun</b>, Shi-Meng Ai, Hong-Jun Luo and Bo Gao  Yunnan University, China</p> <p><i>Abstract</i>—Although the GC content of the human genome is known, it remains undecided whether the base composition is already in equilibrium. This study aimed to examine the equilibrium GC content of the human genome based on 2,504 genomes from the 1000 Genomes Project. By recreating the results of some previous research on genome analysis, we revealed the problems in the</p>

	<p>results of those studies and the causes of the problems. The present results indicate that the GC content of the human genome has not yet reached equilibrium, and it is evolving toward a higher GC content. Furthermore, by analyzing the quantitative changes in CpG dinucleotides before and after mutations, we found that the effect of methylation on the GC content of a genome is very limited, even leading to an increase in the GC content of the genome rather than only a decrease. These findings, therefore, contradict the traditional perception.</p>
<p>H1005 Poster 8</p>	<p>Study on the Characteristics of Blood Agglutination Based on Microscopic Images Zhangyong Li, <b>Qianqian Chen</b>, Fuqu Chen and Chao Ge Chongqing University of Posts and Telecommunication, China</p> <p><i>Abstract</i>—In this paper, we mainly use the ability of lectin molecules to bind specifically to the sugar molecules on the cell surface to study the changes in the associated laws of lectin blood agglutination, so as to widely apply lectin to biology, medicine and other aspects. By collecting the dynamic change information of blood agglutination with lectin under the microscope, we use the image with the information in Gaussian filter to extract I_B component for image enhancement and then get Cr component by obtaining the ycrb image. In the next, we use Or operations with the two components after the top-hat and bottom-hat transformation、 the edge detection of the Canny operator and the Morphological operations separately. Finally, the cell segmentation statistics are performed by Watershed operations. It is obtained from the results of statistical analysis that the addition of lectin will affect the cell grouping rate. Although the cell agglutination is random, the grouping rate tends to be highest when the lectin concentration reaches about 250 ug/mL. We can also get that the fusion rate was positively correlated with the lectin concentration and the speed of cell aggregation is directly related to the lectin concentration and the lectin concentration is more, the reaction time of the cell agglutination process is shorter. The results of this paper fully confirm the agglutinin characteristics and provide a new observation and monitoring method for the study of the action of agglutinin on blood.</p>
<p>H1016 Poster 9</p>	<p>Improved SMQT Algorithm and PCNN Model for Micro-calcification Clusters Detection in Mammograms <b>Lili Zhu</b>, Yonggang Guo, Jianhui Tu, Yide Ma, Ya’nan Guo, Zhen Yang and Deyuan Wang Lanzhou Institute of Physics, China Academy of Space Technology, China</p> <p><i>Abstract</i>—This paper proposes a novel combined method to improve micro-calcification clusters (MCs) detection accuracy in mammograms. The presented method includes three main steps: firstly, exponentiation operation and a new improved successive mean quantization transform (SMQT) algorithm are employed to enhance MCs; secondly, wavelet transform is introduced to obtain the significant MCs information; thirdly, pulse-coupled</p>

	<p>neural network (PCNN) model is used to detect MCs. In the experiment, totally 73 mammograms from MIAS database and 41 mammograms from JSMIT database are chosen to test the algorithm, and experimental results demonstrate that the algorithm presented in this paper is better than the other algorithms by yielding higher specificity of 98.0%, accuracy of 97.26%, and sensitivity of 95.65%. Besides, the method is verified on 20 mammograms from the People's Hospital of Gansu Province, and the detection results indicate that our algorithm can detect MCs correctly. Above all, the proposed method is simple and effective, and it can be considered to assist the radiologist for breast cancer diagnosis.</p>
<p>H1006 Poster 10</p>	<p>A Head Pose Estimation Method Based on Multi-feature Fusion Zhiqiang Zhao, <b>Qiaoli Zheng</b>, Yan Zhang and Xin Shi Chongqing University of Posts and Telecommunications, China</p> <p><i>Abstract</i>—Since head pose estimation is influenced by illumination variation, expression, noise disturbance and other factors, which results in low rate of recognition, a method of head pose estimation based on multi-feature fusion is proposed in this paper. At first, a pose feature combining the second-order histogram of oriented gradient (HOG) and the uniform pattern of local binary pattern (UP-LBP) is proposed, which is used for head pose estimation in single image. Then, an improved random forest algorithm is adopted for classification of head pose and solving the instability problem of the algorithm. Finally, the improved random forest classifier is used for head pose estimation of the novel pose feature. The experimental results show that, the method proposed in this paper is more capable of classification and with better robustness to illumination variation.</p>
<p>H1025 Poster 11</p>	<p>Color Doppler Ultrasound in the Diagnosis of Acute Rejection after Allogeneic Renal Transplantation <b>Yang Bai</b>, Guang-hong Han and Ying Sun the First Hospital of Jilin University, China</p> <p><i>Abstract</i>—The aim of the study was to investigate the role of ultrasound in the diagnosis of acute rejection after allogeneic renal transplantation. Thirty-two renal transplant patients with acute rejection were enrolled in the rejection group, and 32 kidney transplant patients with no acute rejection matched with ageing, gender, and weight were selected to form a non-rejection group for comparative study. Finally, we found Renal volume, cortical echo, resistance index (RI), and end-diastolic velocity (EDV) were significantly different between groups (<math>P &lt; 0.05</math>). There was a significant difference in cortical thickness, resistance index, and perfusion flow between the patients with acute rejection and those with no significant improvement after symptomatic treatment (<math>P &lt; 0.05</math>). So, Color Doppler ultrasound has a high accuracy in the diagnosis of acute rejection after allogeneic renal transplantation, especially for the evaluation of the effect of acute rejection therapy.</p>

<p>H1009 Poster 12</p>	<p>Fast Localization Algorithm of Eye Centers Based on Improved Hough Transform Zhiqiang Zhao, <b>Yan Zhang</b> and Qiaoli Zheng Chongqing University of Posts and Telecommunications, China</p> <p><i>Abstract</i>—Aiming at the problem of localization of eye centers in complex scenes, a method for quickly locating eye center is proposed in this paper. For the collected face images, this paper firstly uses bilateral filtering algorithm to remove the possible noise, and performs histogram equalization operation on the gray image to increase the dynamic range of the image grayscale and improve its distinguishability. Then, constructing cascaded strong classifier based on improved Ada Boost algorithm, and proposed three-layer eye detection. Finally, the method of canny operator edge detection and improved Hough circle detection is used to obtain the pupil center. The experimental results show that the algorithm can acquire the coordinates of the eye center quickly and accurately, and it is robust to eye location under illumination changes.</p>
<p>H1023 Poster 13</p>	<p>Ultrasound Evaluation of Balloon Angioplasty for the Treatment of Autogenous Arteriovenous Fistula Anastomotic Stenosis <b>Yang Bai</b>, Guang-hong Han and Jin-hai Yu the First Hospital of Jilin University, China</p> <p><i>Abstract</i>—The aim of the study was to investigate the effectiveness of ultrasound in the evaluation of percutaneous balloon angioplasty (PTA) for the treatment of autogenous arteriovenous fistula (AVF) stenosis. 40 patients with AVF stenosis participated in the study who were treated with regular hemodialysis in the First Hospital of Jilin University. Among the many indicators, we selected radial blood flow, radial artery resistance index, and anastomotic diameter as monitoring indicators. The results of preoperative, immediate postoperative, postoperative 1 day, 3 days, 7 days, and 14 days were used to find the trend of the indicator and determine the best monitoring time point. Finally, we found morphological indicators and hemodynamic parameters changed significantly after operation; no obvious statistical difference between 1 day postoperative and other postoperative monitoring time points were founded. So, ultrasonography has unique advantages in hemodynamics and morphological examination. It can evaluate the functional status of AVF and the efficacy of PTA accurately, and we believe that the first day after surgery is the best time to monitor.</p>
<p>H0013 Poster 14</p>	<p>Adaptive Deep Brain Stimulation System Based on ADS1292 Dechun Zhao, <b>Li Wang</b> and Shanshan Cheng Chongqing University of Posts and Telecommunications, China</p> <p><i>Abstract</i>—In order to monitor the development of Parkinson's disease for a long time and to study the mechanism of deep brain stimulation for Parkinson's disease, an adaptive deep brain stimulation system based on ADS1292 was</p>

designed for Parkinson's rats. The system consists of a main control unit, an acquisition module, a stimulation module and a wireless communication module, the system uses high-performance, low-power MSP430 as the main control chip. The high resolution, low noise analog to digital conversion chip ADS1292 acquires local field potential (LFP) signals. The stimulus module uses the DAC8532 to output a square wave with adjustable amplitude, frequency, and pulse width. At the same time, the wireless communication module uses the Bluetooth to transmit the LFP signal to the upper computer for processing and receive the control command from the upper computer for achieving adaptive adjustment of the stimulus parameters. Through verification, the system completes the generation of stimulation signals and the acquisition of weak bioelectric signals. The system is light in weight, small in size and low in power consumption, and is very suitable for small animal experiments such as rats.



<b>Dinner</b>	
<b>18:50-20:30</b>	<b>Restaurant</b>

# Listener

Listener 1 <b>Bin Cheng</b> Hebei Academy of Sciences, China
Listener 2 <b>Yeqin Jiang</b> Huzhou University, China
Listener 3 <b>Chaogang Shao</b> Huzhou University, China
Listener 4 <b>Lan Yu</b> Huzhou University, China
Listener 5 <b>Ging Chan</b> University of Macau, China
Listener 6 <b>Meng Li</b> University of Southern California, USA

## Conference Venue

**Shaoyifu Science Building, Yuquan Campus, Zhejiang University,**

**Hangzhou, China**

Add: No. 38, Zheda Road, Xihu District, Hangzhou, China

Tel.: +86-0571-87951547



The Shaoyifu Science Museum of Yuquan Campus was founded in 1985. It was put into use in 1987. In July 2014, the whole building was renovated and reopened in June 2015. There are 10 large and small conference rooms in the hall, of which 117 lecture halls are fixed-seat theater-style venues, which can accommodate 223 people; 211, 212 multi-function halls can accommodate up to 170 people after opening; other small conference rooms and VIP rooms with fixed seats. The Run Run Shaw Science Museum is equipped with a restaurant for 300 people to eat at the same time. After the renovation, the Shao Yifu Science Museum has advanced facilities and beautiful environment to meet the needs of meetings, training, lectures and small exhibitions.

**Hotel Recommendation:**

Union Lingfeng Hotel (圆正-灵峰山庄) Website: <http://hotel.52dingfang.cn/16274/>

Add: NO. 140, Yugu Road, Xihu District, Hangzhou, China

**Tips:** The registration fee does not cover the accommodation. It should be booked by participants themselves.

## Academic Visit

**March 23, 2019 (Friday) 8:30~18:00**

Tip: 1. Please arrive at the Lobby of Union Lingfeng Hotel (圆正-灵峰山庄) before 8:30. The following places are for references, and the final schedule should be adjusted to the actual notice.

2. The quotation covers the ticket of Leifeng Pagoda and lunch. Other paid items should be paid by participants themselves.

### 1. 8:30: Departure at Lobby of Union Lingfeng Hotel (圆正-灵峰山庄)

### 2. Visit Zijingang Campus, Zhejiang University

Zijingang Campus of Zhejiang University is located in the Tangbei block in the west of Hangzhou City, adjacent to the famous and ancient Xixi Scenic Area, it is divided into two parts, with a total plan of 5,856 mu. The overall construction of the Zijingang Campus has always implemented the "people-oriented" thinking, creating a free learning space and communication atmosphere, and improving the overall quality of students. All of them are designed and set around the goal of cultivating creative talents. The Zijingang Campus is the seat of the party and government organs of Zhejiang University. It also has foreign language colleges, life science colleges, medical schools, pharmacy colleges, management colleges, and public administration colleges.



### 3. Lunch

### 4. West Lake Cultural Landscape of Hangzhou

West Lake, located in the west of Hangzhou, Zhejiang Province, is China's main ornamental freshwater lake and the first batch of national key scenic spots in China. The West Lake is surrounded by mountains on three sides, covering an area of 6.39 square kilometers, about 2.8 kilometers wide from east to west, 3.2 kilometers long from north to south, and nearly 15 kilometers around the lake. The lake is separated by Gushan, Baidi, Sudi and Yanggong Dikes. According to the size of the area, there are five water faces, namely, West Lake, Xili Lake, Beili Lake, Xiaonan Lake and Yuehu Lake. Su Di and Bai Dike cross the lake, Xiao Wei Chau The three artificial islands of Huxinting and Gonggongdun stand in the heart of the West Lake.



The Leifeng Pagoda in Xizhao Mountain and the Baoding Tower in the Gem Mountain are separated by the lake, thus forming "One Mountain, Two Towers and Three Islands". The basic pattern of the Three Embankments and the Five Lakes. On June 24, 2011, Hangzhou West Lake was included in the World Heritage List.

### 5. 18:00: Back to Union Lingfeng Hotel



