CONFERENCE PROGRAM

2020 12th International Conference on Bioinformatics and Biomedical Technology (ICBBT 2020)

May 16-18, 2020

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Conference Introduction

Welcome to 2020 12th International Conference on Bioinformatics and Biomedical Technology (ICBBT 2020). ICBBT 2020 will be held during May 16-18, 2020. Previously, ICBBT series had been successfully held in Chengdu, China in 2010, Sanya, China in 2011, Singapore in 2012, Macau in 2013, Gdansk, Poland in 2014, Singapore in 2015, Barcelona, Spain in 2016, Lisbon, Portugal in 2017, Amsterdam, The Netherlands in 2018, Stockholm, Sweden in 2019.

ICBBT 2020 is to bring together innovative academics and industrial experts in the field of Bioinformatics and Biomedical Technology to a common forum. The primary goal of the conference is to promote research and developmental activities in Bioinformatics and Biomedical Technology. Another goal is to promote scientific information interchange between researchers, developers, engineers, students, and practitioners working in China and abroad. The conference will be held every year to make it an ideal platform for people to share views and experiences in Bioinformatics and Biomedical Technology and related areas.

Papers will be published in the following proceedings:

ACM International Conference Proceedings (ISBN: 978-1-4503-7571-9), which will be archived in the ACM Digital Library, indexed by Ei Compendex and Scopus, and submitted to be reviewed by Thomson Reuters Conference Proceedings Citation Index (ISI Web of Science).

Conference website and email: http://www.icbbt.org; icbbt@cbees.org

Presentation Guideline

Presentation Requirement

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

Time Zone

- The time shown in this program is **Greenwich Mean Time (GMT+08:00)–China Local Time**. Please set up your laptop time in advance.

Equipment Needed

- A computer with an internet connection (wired connection recommended).
- USB plug-in headset with a microphone (recommended for optimal audio quality).
- Webcam (optional): built-in or USB plug-in.

Environment Requirement

- Quiet Location.
- Stable Internet Connection.
- Proper lighting.

Voice Control Rules during the Presentation

- The host will mute all participants while entering the meeting.
- The host will unmute the speakers' microphone when it is turn for his or her presentation.
- Q&A goes after each speaker, the participant can raise hand for questions, and the host will unmute the questioner.
- After Q&A, the host will mute all participants and welcome next speaker.

Warm Tips for Oral Presentation

- Get your presentation PPT files prepared.
- Regular presentation is 15 minutes including 12 minutes of presentation and 3 minutes of Q&A.
- To effectively control the time and avoid some unexpected situations, it is suggested that you should record your presentation ahead of time, do the live oral presentation online or play the video while it's your turn for presentation.

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

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

  Step 3: Authors need to be able to upload these presentations to a location specified by YOU in advance. Send the video to the staff in advance.

Presentation Guideline

Best Presentation Award

- One Best Presentation will be selected from each session, and the result will be announced at the end of the session.

Conference Material

- All presented papers will be issued with soft copy of conference materials: Receipt, Participation and presentation certificate, etc.

Notes

- Log in the meeting room 10 minutes ahead of the session.
- Learn the zoom skills.
- Please kindly keep your Paper ID in mind so that the staff can quickly locate your registration information.
- Your punctual arrival and active involvement in each session will be highly appreciated.
- The conference will be recorded; we will appreciate your proper behavior.

Follow us

- Add the Wechat of ICBBT for more detailed and updated conference news.

Scanning me:

ZOOM User Guideline

Download the ZOOM: https://zoom.us/download

Learn the ZOOM skills

- Please visit: https://support.zoom.us/hc/en-us/articles/201362033-Getting-Started-on-Windows-and-Mac
- GIF guideline: http://icbbt.org/zoom.htm

How to use ZOOM:

- Sign up an account.
- Set the language.
- Test computer or device audio.
- Join a meeting: Join the meeting with "meeting ID" provided in the program, tap the name as "Session number-paper ID-name", eg. "S1-T0007-Freya Shi" or "Lis-Freya Shi", then click "Join".
- Get familiar with the basic functions: Rename, Chat, Raise Hand, Start Video, and Screen Share, etc.
  The most important function is Share Screen, because you will use it for your online presentation.
- On May 16, we will have test session. On that day, we will teach you how to use ZOOM and the functions mentioned above. If you don't know how to use, please do not worry. However, you must download ZOOM, then, you can join the conference.

Program-at-a-Glance

Test Session Schedule—May 16, 2020 (Saturday)

Meeting ID: 630-4619-2506		**Time**
Keynote Speaker I--Prof. Ying Xu, University of Georgia, USA		10:00-10:10
Keynote Speaker VI--Prof. Taesung Park, Seoul National University, South Korea		10:10-10:20
Keynote Speaker VII--Prof. Hongbing Lu, Fourth Military Medical University, China		10:20-10:30
Keynote Speaker III--Prof. Guoying Zhao, University of Oulu, Finland		10:30-10:40
Keynote Speaker II--Prof. Ashoka Polpitiya, Sera Prognostics Inc, USA		10:40-10:50
Keynote Speaker IV--Prof. Bijoy K. Ghosh, Texas Tech University, USA		10:50-11:00
Keynote Speaker V--Prof. Y-h Taguchi, Chuo University, Japan		11:00-11:10
Break		11:10-13:30
Meeting ID: 630-4619-2506	**Meeting ID: 630-4619-2506**	**Time**
Test-Session 1 Topic: “Health Medicine and Wearable System” T0043, X0005, T0044, X1002, X0017, T0033	Test-Session 2 Topic: “Medical Bioinformatics” T0021, T0037, X0022, X0011, X0020, T1006	13:30-14:10
Test-Session 3 Topic: “Bioelectric Signal” X0009-A, T1005, X3001, X0024, T0004, T0047	Test-Session 4 Topic: “Genomics” T0020, T0027, T0018-A, T0029, T0010, T0039, T1002-A	14:10-14:50
Break		14:50-15:00
Meeting ID: 630-4619-2506	**Meeting ID: 630-4619-2506**	**Time**
Test-Session 5 Topic: “Biomedical Imaging” T0030, X0019, T0046, X0030, X1003, T0005, T0006	Test-Session 6 Topic: “Computational Biology” T0049, T0003, X0018, T0012-A, X0007, X1005, T0036-A	15:00-15:40
Test-Session 7 Topic: “Biophysics and Image Processing” X0025, X0027, T0007, X0026, T0011, T0022, X1006	Test-Session 8 Topic: “Systems Biology” T0015, T0009, X1004, X0001, X1008, T0038	15:40-16:20
Meeting ID: 630-4619-2506 **Back up Room for Q&A**		10:00-16:20

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

Program-at-a-Glance

Formal Session Schedule—May 17, 2020 (Sunday)

Morning Conference **Meeting ID: 630-4619-2506**		**Time**
Join in the Meeting Room		08:40-09:00
Opening Remarks--Prof. Ming Chen, Zhejiang University, China		09:00-09:10
Keynote Speech I--Prof. Ying Xu, University of Georgia, USA		09:10-09:50
Keynote Speech II--Prof. Ashoka Polpitiya, Sera Prognostics Inc, USA		09:50-10:30
Break		10:30-10:40
Panel Topic: Advances in Bioinformatics and their Impact on Healthcare		10:40-11:40
Break		11:40-13:30
Afternoon Conference		
Keynote Speech III--Prof. Guoying Zhao, University of Oulu, Finland		13:30-14:10
Join in the meeting room		14:10-14:25
Meeting ID: 630-4619-2506	**Meeting ID: 630-4619-2506**	Time
Session 1 Topic: “Health Medicine and Wearable System” T0043, X0005, T0044, X1002, X0017, T0033	Session 2 Topic: “Medical Bioinformatics” T0021, T0037, X0022, X0011, X0020, T1006	14:25-15:55
Break		15:55-16:15
Session 3 Topic: “Bioelectric Signal” X0009-A, T1005, X3001, X0024, T0004, T0047	Session 4 Topic: “Genomics” T0020, T0027, T0018-A, T0029, T0010, T0039, T1002-A	16:15-18:00
Meeting ID: 630-4619-2506 **Back up Room for Q&A**		09:00-18:00

Program-at-a-Glance

Formal Session Schedule—May 18, 2020 (Monday)

Morning Conference **Meeting ID: 630-4619-2506**		
Opening Remarks--Prof. Ming Chen, Zhejiang University, China		09:00-09:10
Keynote Speech IV--Prof. Bijoy K. Ghosh, Texas Tech University, USA		09:10-09:50
Keynote Speech V—Prof. Y-h Taguchi, Chuo University, Japan		09:50-10:30
Break		10:30-10:40
Keynote Speech VI—Prof. Taesung Park, Seoul National University, South Korea		10:40-11:20
Keynote Speech VII--Prof. Hongbing Lu, Fourth Military Medical University, China		11:20-12:00
Break		12:00-13:30
Afternoon Conference		
Meeting ID: 630-4619-2506	**Meeting ID: 630-4619-2506**	Time
Session 5 Topic: “Biomedical Imaging” T0030, X0019, T0046, X0030, X1003, T0005, T0006	Session 6 Topic: “Computational Biology” T0049, T0003, X0018, T0012-A, X0007, X1005, T0036-A	13:30-15:15
Break		15:15-15:40
Session 7 Topic: “Biophysics and Image Processing” X0025, X0027, T0007, X0026, T0011, T0022, X1006	Session 8 Topic: “Systems Biology” T0015, T0009, X1004, X0001, X1008, T0038	15:40-17:25
Meeting ID: 630-4619-2506 **Back up Room for Q&A**		09:00-17:00

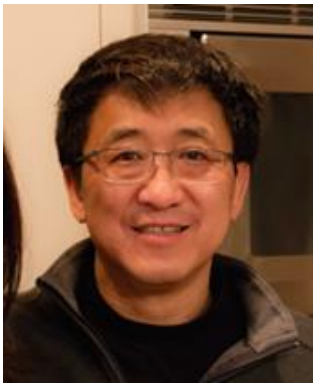
Panel Introduction

Panel Topic: Advances in Bioinformatics and their Impact on Healthcare

Time: 10:40am-11:40am, May 17, 2020
Venue: Meeting ID: 630-4619-2506
Moderator: Prof. Hesham Ali, University of Nebraska Omaha, USA
Panelists:
Prof. Y-h Taguchi, Chuo University, Japan
Prof. Bijoy K. Ghosh, Texas Tech University, USA
Prof. Ashoka Polpitiya, Sera Prognostics Inc, USA
Prof. Hesham Ali, University of Nebraska Omaha, USA

Introduction: With strong roots in computational biology, as well as various computational and biological sciences, Bioinformatics emerged in the mid 1990s as an exciting new scientific discipline. With the energy and enthusiasm associated with the human genome project, Bioinformatics promised to play a significant role in advancing biomedical research and healthcare. Today, over 25 years later, there are mixed views about the realization of this role. On the one hand, many developments and advances in Bioinformatics have touched many aspects of biomedical research and have exhibited a certain level of impact on practices associated with healthcare. On the other hand, we may have expected Bioinformatics as a discipline to be further along in 2020, and it can be argued that the impact of Bioinformatics on the clinical aspects of healthcare remains limited. While many biomedical domains enjoy more available data and many useful computational tools, that does not always transfer into impactful knowledge. Healthcare still struggles with infectious diseases and chronic conditions, and cancer remains an unsolved mystery for the most part. This panel addresses some of the key advances in Bioinformatics and addresses the challenges we need to overcome in order to allow Bioinformatics reach its maximum potential.

Keynote Speaker I



Prof. Ying Xu
University of Georgia, USA

Ying Xu has been the "Regents and Georgia Research Alliance Eminent Scholar" Chair of bioinformatics and computational biology and Professor in Biochemistry and Molecular Biology Department since 2003, and was the Founding Director of the Institute of Bioinformatics, the University of Georgia (UGA). He received his Ph.D. degree in theoretical computer science from the University of Colorado at Boulder in 1991. He started his bioinformatics career in 1993 when he joined Oak Ridge National Lab. His current research interests are mainly in cancer bioinformatics and systems biology. He has over 300 publications, including five books, with total citations more than 14,000 and H-Index = 62; and has given over 250 invited/contributed talks at conferences, research organizations and universities.

Topic: "Metabolic Reprogramming in Cancer: the Bridge that Connects Intracellular pH Stress and Cancer Behaviors"

Abstract—Cancer has been considered as a genomic disease, which has served as the guiding principle in cancer research and the basis for cancer diagnosis and treatment. However, increasingly more researchers have challenged this viewpoint in the past decade since it could not answer too many cancer related questions! We have been developing a cancer evolutionary theory in the past few years. The key idea is: persistent inflammation of certain types will lead to increased local H_2O_2 and iron concentrations, which together will give rise to Fenton reaction: $Fe^{2+} + H_2O_2 \rightarrow Fe^{3+} + \cdot OH + OH^-$. If the environment is also rich in O2·-, which is predominantly released from neutrophils in cancer tissues, O2·- can reduce Fe^{3+} back to Fe^{2+}, hence driving the reaction to go on as long as O2·- is available. We have discovered that (1) all cancer tissues in TCGA have persistent Fenton reactions in their cytosol and mitochondria, and (2) the rates of cytosolic Fenton reactions will saturate the pH buffer quickly, hence driving the cytosolic pH up if not neutralized. Our next key finding is that the affected cells utilize a wide range of metabolic reprogramming (MR) to produce more protons to keep the Fenton reaction-produced OH- neutralized. We have studied some 50 MRs in 14 cancer types, which each produce more protons compared to the original metabolism. Further analyses suggest that the affected cells use cell division as way to rid of the persistently produced nucleotides. I will explain how other clinical behaviors of cancer may be driven by other reprogrammed metabolisms, mainly to remove their end- or intermediate products so the proton-producing MRs can continue and keep the affected cell alive.

Keynote Speaker II

Prof. Ashoka Polpitiya
Sera Prognostics Inc, USA

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: "Scale-Free Genetic Interaction Networks in Heliothis virescens Challenged with Bacillus thuringiensis"

Abstract—Large scale genomic experiments allow analysis of regulatory pathways used by biological systems to transmit signals and coordinate multiple processes. These networking mechanisms allow the systems to respond and adapt to ever changing environments. It has been observed that transcription networks exhibit an approximately scale-free distribution, signifying the potential of transcription factors to regulate a multitude of target genes. These signaling networks are poorly understood in many organisms. In this project, we focus on the tobacco budworm (TBW, *Heliothis virescens*), which is a model insect for studying insecticide resistance, to quantitatively describe a network of hundreds or thousands of interacting genes that will give us clues about the dynamic response of this pest to insecticidal proteins from *Bacillus thuringiensis* (Bt) toxins. Early fourth instar larvae of TBW were exposed to a sub-lethal dose of Cry1Ac and Illumina short reads were obtained from three pools of midguts harvested at 0, 120, and 480 min after exposure. Approximately 20 million reads from each replicate were mapped to 18,728 TBW genes and weighted co-expression networks that exhibit a scale-free topology were identified. The highly interactive modules obtained from this analysis identified some of the genes associated with Bt mode of action/resistance being co-regulated with those that may be directly or indirectly involved in the response to Bt toxins in TBW.

Keynote Speaker III

Prof. Guoying Zhao
University of Oulu, Finland

Guoying Zhao is currently a Professor with the Center for Machine Vision and Signal Analysis, University of Oulu, Finland, where she has been a senior researcher since 2005 and an Associate Professor since 2014. She received the Ph.D. degree in computer science from the Chinese Academy of Sciences, Beijing, China, in 2005. She has authored or co-authored more than 220 papers in journals and conferences. Her papers have currently over 12200 citations in Google Scholar (h-index 51). She is co-program chair for ACM International Conference on Multimodal Interaction (ICMI 2021), was co-publicity chair for FG2018, General chair of 3rd International Conference on Biometric Engineering and Applications (ICBEA 2019), and Late Breaking Results Co-Chairs of 21st ACM International Conference on Multimodal Interaction (ICMI 2019), has served as area chairs for several conferences and is associate editor for Pattern Recognition, IEEE Transactions on Circuits and Systems for Video Technology, and Image and Vision Computing Journals. She has lectured tutorials at ICPR 2006, ICCV 2009, SCIA 2013 and FG 2018, authored/edited three books and eight special issues in journals. Dr. Zhao was a Co-Chair of many International Workshops at ICCV, CVPR, ECCV, ACCV and BMVC. Her current research interests include image and video descriptors, facial-expression and micro-expression recognition, emotional gesture analysis, affective computing, and biometrics. Her research has been reported by Finnish TV programs, newspapers and MIT Technology Review.

Topic: "Remote Heart Rate Measure from Videos: Methods and Application in Atrial Fibrillation Detection"

Abstract—Physiological signals, including heart rate (HR), heart rate variability (HRV), and respiratory frequency (RF) are important indicators of our health, which are usually measured in clinical examinations. Traditional physiological signal measurement often involves contact sensors, which may be inconvenient or cause discomfort in long-term monitoring sessions. Recently, there were studies exploring remote HR measurement from facial videos, and many methods have been proposed. This talk first introduces this new emerging research topic and recent methods in heart rate measuring from remote face video analysis. Then the application to atrial fibrillation (AF) with the video-extracted HRV features is presented, together with a new Oulu Bio-Face (OBF) database as a benchmark set.

Keynote Speaker IV

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: "Computational Biology and Control Problems arising from Pandemic Models"

Abstract—The local spread and control of a virus is important in our understanding of a pandemic and how it spreads over a community. Using epidemiological models, we shall focus on how a disease is spread and how use of drug together with human interaction pattern would help. In this talk I focus application of control and AI.

Keynote Speaker V

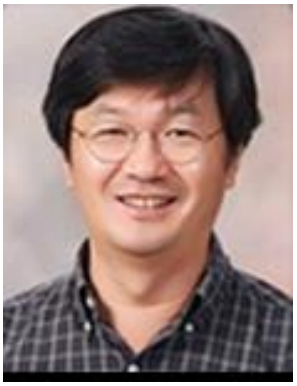
Prof. Y-h Taguchi
Chuo University, Japan

Prof. Taguchi is currently a Professor at Department of Physics, Chuo University. Prof. Taguchi received a master degree in Statistical Physics from Tokyo Institute of Technology, Japan in 1986, and PhD degree in Non-linear Physics from Tokyo Institute of Technology, Tokyo, Japan in 1988. He worked at Tokyo Institute of Technology and Chuo University. He is with Chuo University (Tokyo, Japan) since 1997. He currently holds the Professor position at this university. His main research interests are in the area of Bioinformatics, especially, multi-omics data analysis using linear algebra. Dr. Taguchi has published a book on bioinformatics entitled "Unsupervised Feature Extraction Applied to Bioinformatics: A PCA Based and TD Based Approach" from Springer at September 2019 and more than 100 journal papers, book chapters and papers in conference proceedings. He is also serving as Academic editors of various journals including PLoS ONE, BMC Medical Genomics and Non-coding RNA (published from MDPI) as well as guest editors of nine special issues in Cells and International Journal of Molecular Sciences published also from MDPI.

Topic: "Application of Tensor Decomposition based Unsupervised Feature Extraction to Single Cell RNA-seq Data Analysis"

Abstract—Recently, single cell RNA-seq (scRNA-seq) has become the most advanced and popular methods to measure transcriptome in genomic science. However, generally, scRNA-seq does not have enough amount of labeling information to annotate in contrast to the standard RNA-seq, which is usually measured in well-defined samples, e.g., specific tissues or patients with specific disease. Thus, more unsupervised oriented methods are desired. In this keynote, I will introduce some or tensor decomposition (TD) methods based methods that are applicable to scRNA-seq data analysis. Compared with traditional methods developed for the scRNA-seq, TD based methods turn out to have more capability to select genes with more biologically reliable annotations. Since more single-cell based methods will be developed, tensor based methods are promising ones that can be applicable to these forthcoming single-cell oriented measurements.

Keynote Speaker VI



Prof. Taesung Park
Seoul National University, South Korea

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

Topic: "Hierarchical Structural Component Models for Pathway Analysis"

Abstract—Genome-wide association studies (GWAS) have been widely used to identify phenotype-related genetic variants using many statistical methods, such as logistic and linear regression. However, GWAS-identified SNPs, as identified with stringent statistical significance, explain just a small portion of the overall estimated genetic heritability. To address this 'missing heritability' issue, gene- and pathway-based analysis, and biological mechanisms, have been used for many GWAS studies. However, many of these methods often neglect the correlation between genes and between pathways. We constructed a hierarchical component model that considers correlations both between genes and between pathways. We propose a novel pathway analysis method for GWAS datasets, Hierarchical structural Component Model for Pathway analysis. HisCoM first summarizes the variants of each gene, first at the gene-level, and then analyzes all pathways simultaneously by ridge-type penalization of both the gene and pathway effects on the phenotype. Statistical significance of the gene and pathway coefficients can be examined by permutation tests. Through simulation studies and real data application, we showed that HisCoM well-controlled type I error, and had a higher empirical power compared to other existing methods. Our approach has the advantage of providing an intuitive biological interpretation for associations between common variants and phenotypes, via pathway information, potentially addressing the missing heritability conundrum.

Keynote Speaker VII

Prof. Hongbing Lu
Fourth Military Medical University, China

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

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

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

Detailed Program for Oral Session

Session 1: Health Medicine and Wearable System

Time: 14:25-15:55, May 17, 2020 (Sunday)
Greenwich Mean Time (GMT+08:00) – China Local Time
Meeting ID: 630-4619-2506
Session Chair: Prof. Aoqun Jian, Taiyuan University of Technology, China

S1-1	T0043 14:25-14:40	Conformal Wearable and Wireless System for the Machine Learning Classification of Diadochokinesia for Hemiparesis **Robert LeMoyne** and Timothy Mastroianni Northern Arizona University, USA *Abstract*—The observation of diadochokinesia is a standard component for neurological evaluation. Diadochokinesia pertains to the oscillation between agonist and antagonist muscle groups, such as with respect to pronation and supination of the forearm. With respect to hemiparesis the disparity of diadochokinesia is visibly perceptible, for which a skilled clinician may apply an expert although subjective perspective through an ordinal scale. Using the gyroscope signal of a conformal wearable and wireless inertial sensor mounted about the dorsum of the hand, diadochokinesia with respect to pronation and supination of the forearm can be objectively quantified. The research objective is to apply machine learning through a multilayer perceptron neural network to differentiate between a hemiplegic affected and unaffected upper limb pair through diadochokinesia regarding pronation and supination of the forearm. The gyroscope signal data from the conformal wearable and wireless inertial sensor provides the basis for a machine learning feature set. Considerable classification accuracy is attained with respect to diadochokinesia regarding pronation and supination of the forearm for a hemiplegic arm pair based on the quantified data provided by the gyroscope signal of a conformal wearable and wireless inertial sensor.
S1-2	X0005 14:40-14:55	Associations between Obesity Indicators and Cardiovascular Disease Risk **Yao Ding,** Xiaoyu Zhang, Yang Xu, Lisheng Gao, Yining Sun and Zuchang Ma Institute of Intelligent Machines Chinese Academy of Sciences, China *Abstract*—The discriminatory capability of multiple obesity indicators for cardiovascular disease (CVD) risk remains uncertain. The purpose of this study was to find the best indicator(s) of obesity among these anthropometric parameters for assessing cardiovascular risk. This study included 1497 residents (864 males and 633 females) of China. Participants were required to carry out questionnaires, general physical examinations, body composition measurements, and laboratory measurements. The Framingham CVD risk assessment tool was used to evaluate individual CVD risk. High CVD risk was defined as a 10-year incidence probability ≥10%. The subjects were divided into normal or obese group according to the threshold of indices for determining.

		Logistic regression was used to compare the performance of the indicators for the assessment of CVD risk. The results showed waist-to-height ratio (WHtR) was most associated to CVD risk. The odds ratios (ORs) of the high WHtR group in men and women were 5.36 and 3.84, respectively. The combination of obesity index was superior to single index in assessing high CVD risk. The ORs of males and females with high WHtR and BMI were 6.12 and 6.68, respectively. WHtR had the best correlation with CVD risk; and its combination with BMI was the best to assess CVD risk.
S1-3	T0044 14:55-15:10	Conformal Wearable and Wireless Inertial Sensor System for the Machine Learning Classification of Hemiplegic Gait using a Multilayer Perceptron Neural Network **Robert LeMoyne** and Timothy Mastroianni Northern Arizona University, USA *Abstract*—The conformal wearable and wireless inertial sensor system, such as the BioStamp nPoint, uniquely enables the quantification of gait status with a profile on the order of a bandage. In particular, the conformal wearable and wireless inertial sensor system is well suited for the quantification of hemiplegic gait, respective of the hemiplegic affected leg and unaffected leg. The acquired inertial sensor data, such as the gyroscope signal, obtained through the conformal wearable and wireless system can be transmitted wirelessly to a secure Cloud computing environment. Subsequent post-processing of the inertial sensor signal data through software automation using Python can develop a feature set appropriate for machine learning classification. Using the multilayer perceptron neural network through the Waikato Environment for Knowledge Analysis (WEKA) considerable classification accuracy is achieved for distinguishing between a hemiplegic affected leg and unaffected leg. The research findings establish a pathway for the amalgamated role of conformal wearable and wireless inertial sensor systems and machine learning algorithms for the classification distinction of hemiplegic gait.
S1-4	X1002 15:10-15:25	Influence of Fat Distribution on Arterial Stiffness in Middle-aged and Elderly People: Cross-Sectional Study from a Community-based Cohort **Ting Sun**, Hui Xie and Zuchang Ma Bengbu Medical College, China *Abstract*—Finding a tool to diagnose the correlation of obesity with arteriosclerosis is very important. We analyzed the relationship between different anthropometric and body-composition parameters with arterial stiffness (AS) in middle-aged and elderly people. Data were from a community-based cohort. Anthropometric, biochemical and lifestyle data were collected each year from 2018. We surveyed 1410 participants, aged 45–91 (mean = 64.8) years. Body-composition parameters were measured by electrical impedance. AS was assessed by measurement of brachial–ankle pulse wave velocity (baPWV). Bivariate correlations and stepwise linear regression models were used for analyses. Among male

		participants, only one parameter (i.e., ratio of fat-free mass (FFM) of the trunk) had a negative correlation with baPWV ($P < 0.01$). The waist–hip ratio, waist–height ratio (WHtR), total fat mass, total body water and percentage body fat (%BF) correlated positively with baPWV, whereas the ratio of arm muscle mass, ratio of arm/leg/trunk muscle mass, and ratio of arm and leg FFM were correlated negatively in women ($P < 0.05$ for all). Age, systolic blood pressure (SBP), heart rate (model 1: $R^2 = 0.67$) and age, SBP, heart rate, WHtR, ratio of trunk muscle mass (RTMM) and percentage body fat (FP%) (model 2: $R^2 = 0.69$) were significant predictors of AS in women. These data suggested that, in middle-aged and elderly women, WHtR, RTMM and FP% had a strong association with baPWV.
S1-5	X0017 15:25-15:40	Smartphone Based Early Detection of Epileptic Seizures Using Machine Learning **Shweta Gupta** Jain University, India *Abstract*—This research paper proposes early detection of epileptic signal using wearable sensor and signal is transmitted to smartphone. In smartphone, by using machine learning algorithm which works on EEG signal and after processing, it with machine learning model there is detection of preictal state and immediately emergency SMS is sent to nurse/doctor mobile so that drug can be injected in the body of the patient before the actual attack happens .Tremors of brain diseases like Epilepsy, Parkinson's and depression can be identified and diagnosed using machine learning methods. Due to deficiency of dopamine chemical in Substantia Nigra region of the brain, it results in epileptic seizures, which if predicted before the onset can be controlled through medication. Thus, Computational methods and machine learning methods involves prediction of epileptic seizures from Electroencephalograms (EEG) signals. But removal of noise and extracting features are two major challenges for prediction of epileptic seizures. Thus, in the upcoming research paper we propose a model which helps in epileptic seizures prediction sufficient time before seizures start. Support Vector Machine algorithm has been proposed as suitable machine learning model which finds it's application in preprocessing and train the model by extracting frequency and time domain features. Preictal state is detected through proposed model, which starts couple of minutes before the seizure onset, and accuracy is 92.2% and average time taken for prediction is 92.23 minutes by taking samples from 22 subjects using wearable sensors.
S1-6	T0033 15:40-15:55	Study on Pathological Mechanism of Pneumonia Infected by Coronavirus based on Time-series Gene Co-expression Network Analysis **XingCheng Yi**, Yan Zhang, Tong Xu, Xiaoyun Su and Cong Fu Jilin University, China *Abstract*—Recently, the epidemic of COVID-19 infection broke out in Wuhan, China. To explore the pathological mechanism of pneumonia infected by coronavirus, we built a bioinformatics pipeline based on time-series gene co-expression network analysis to analyze the gene

		expression profile of lung cells in mice infected by SARS-Cov (GSE19137). In this study, Pearson correlation analysis was performed to construct a gene co-expression network. Time-ordered gene network modules were digged out by BFS algorithm . PageRank algorithm was used to explore HUB genes related to pneumonia infected by coronavirus. Based on the information we got, we think that cell lines infected by coronavirus might go through 5 stages, and 10 HUB genes(AKT1, CD68, CTSS, FCGR3A, HSPA8, PTPRC, UBC, VCP, PRPF31, ITPKB) might play a key role in coronavirus infection. This might provide some hints for coronavirus related research.

Detailed Program for Oral Session

Session 2: Medical Bioinformatics

Time: 14:25-15:55, May 17, 2020 (Sunday)
Greenwich Mean Time (GMT+08:00) – China Local Time
Meeting ID: 630-4619-2506
Session Chair: Prof. Y-h Taguchi, Chuo University, Japan

S2-1	T0021 14:25-14:40	Identification of Potentially Therapeutic Target Genes in Ovarian Cancer via Bioinformatic Approach **Li Chengzhang** and Xu Jiucheng Henan Normal University, China *Abstract*—Objective: To identify potentially therapeutic target genes in ovarian cancer involved in the pathogenesis of ovarian cancer using bioinformatic approach. Methods: The online GEO2R tool was employed to analyze the gene expression profiles of ovarian cancer. GO and KEGG enrichment analysis was utilized to annotate differentially expressed genes (DEGs). STRING database was employed to construct a protein-protein interaction (PPI) network with the DEGs. The PPI network interaction information was then visualized using Cytoscape software and ovarian cancer hub genes were identified based on Maximal Clique Centrality (MCC) algorithm. The identified hub genes were then analyzed with Kaplan Meier plotter to measure their role on survival time of ovarian cancer patients. Results: Differentially expressed analysis resulted in 332 DEGs, of which 340 were down-regulated and 92 were up-regulated. Gene Ontology (GO) enrichment analysis indicated that the DEGs were significantly enriched in some tumor-associated biological processes, molecular functions, and cellular components. Kyoto Encyclopedia Genes and Genomes (KEGG) pathway enrichment analysis resulted in 5 cancer related pathways. A total of 10 hub genes were identified based on the topology analysis of PPI network. Survival analysis showed 7 of the hub genes were associated with significantly decreased survival time of the ovarian cancer patients ($P<0.05$). Conclusion: Our study resulted in identification of 7 hub genes contributing to the development of ovarian cancer. These hub genes may be potentially therapeutic target genes for treatment of ovarian cancer.
S2-2	T0037 14:40-14:55	ITGAX: A Potential Biomarker of Acute Myeloid Leukemia (AML) through Bioinformatic Analysis **Heng-Yi Yang** and Tian-Ni Mao Dalian Maritime University, China *Abstract*—Acute Myeloid Leukemia (AML) constitutes nearly eighty percent of total adult leukemias, which also is almost all common origin cause of leukemia death. Consequently, Understanding the molecular mechanisms of AML and identifying potential biomarkers are significant for clinical treatment. To identify the differentially expressed genes (DEGs), microarray datasets GSE114868, GSE67936 and GSE65409 were downloaded from Gene Expression Omnibus (GEO) database.

		Function enrichment analysis was performed and protein-protein interaction network (PPI) was constructed.62 DEGs were identified, made up of 15 downregulated genes and 47 upregulated genes. The module analysis was performed using STRING and Cytoscape. The enriched functions and pathways of the DEGs include leukocyte degranulation, cytokine production, Th1 and Th2 cell differentiation, chromatin remodeling at centromere, somatic diversification of immune receptors and Renin-angiotensin system. Ten hub genes were identified through degrees calculated by CytoHubba and KEGG analysis indicated that hub genes were particularly enriched in Th1 and Th2 cell differentiation, Natural killer cell mediated cytotoxicity and Cytokine-cytokine receptor interaction. Supplementary analysis showed that only ITGAX gene had a big potential as higher expression and considerably worse survival in AML compared with normal. In a word, our study drew a conclusion that ITGAX could be a potential prognostic factor and beneficial target for AML therapy. And we should do further experimentations to verify the result.
S2-3	X0022 14:55-15:10	Identification of Important Biological Pathways for Ischemic Stroke Prediction through a Mathematical Programming Optimisation Model —DIGS **Yongnan Chen**, Konstantinos Theofilatos, Lazaros G Papageorgiou and Sophia Tsoka King's College London, UK *Abstract*—Stroke ranks second after heart disease as a cause of disability in high-income countries and as a cause of death worldwide. Identifying the biomarkers of ischemic stroke is possible to help diagnose stroke cases from non-stroke cases, as well as advancing the understanding of the underlying theory of the disease. In this study, a mathematical programming optimisation framework called DIGS is applied to build a phenotype classification and significant pathway inference model using stroke gene expression profile data. DIGS model is specifically designed for pathway activity inference towards supervised multi-class disease classification and is proved has great performance among the mainstream pathway activity inference methods. The highest accuracy of the prediction on determining stroke or non-stroke samples reaches 84.4% in this work, which is much better than the prediction accuracy produced by currently found stroke gene biomarkers. Also, stroke-related significant pathways are inferred from the outputs of DIGS model in this work. Taken together, the combination of DIGS model and expression profiles of stroke has better performance on the discriminate power of sample phenotypes and is capable of effective in-depth analysis on the identification of biomarkers.
S2-3	X0011 15:10-15:25	Mining of Gene Modules and Identification of Key Genes in Hepatocellular Carcinoma Based on Gene Co-expression Network Analysis **Zhao Qian**, Zhang Yan and Lin Zhengkui Dalian Maritime University, China

		Abstract—About 80% of liver cancer cases were hepatocellular carcinoma. To explore the pathogenesis of hepatocellular carcinoma, a bioinformatics algorithm based on gene co-expression network analysis was used to study the gene expression data of hepatocellular carcinoma in this paper. The Pearson correlation analysis was used to construct the 2538 genes into a gene co-expression network, and the eigenvector algorithms was used to divide genes into 9 modules. The correlation analysis between gene modules and clinical indicators results showed that the RNA localization (GO: 0006403) related genes changed in four modules. The cell cycle and mitosis processes were related to event module, tRNA transport and multi-organism transport processes were related to T module, Organic biosynthetic process was related to N module and viral transcription process was related to M module. Furthermore, the Disgenet database results showed that 6 key genes was related to liver cancer, such as CASP2, HCFC1, ILF3, NAA40, NCOA6 and SENP1. Among them, the expression of CASP2, ILF3, NAA40 and NCOA6 were negatively correlated with the survival prognosis. Thus, these identified genes may play important roles in the progression of hepatocellular carcinoma and sever as potential biomarker for future diagnosis. Dalian Maritime University, China
S2-5	X0020 15:25-15:40	An Exploration of Possible Association between m6A Methylation Regulators and Chronic Obstructive Pulmonary Disease by a Bioinformatics Analysis **Lin Hua**, Hong Xia and Li An Capital Medical University, China *Abstract*—Chronic obstructive pulmonary disease (COPD) is a chronic respiratory system disease with high mortality rates. COPD has a tendency of family aggregation, and is often caused by the accumulation of multiple genes interaction and environmental factors. Currently, N6-methyladenosine (m6A) has been found to affect mRNA processing in multiple stages in some cancers related studies. However, the related studies about the modification of m6A by regulatory factors are related to cell death and cell proliferation, leading to COPD disease were not addressed. Therefore, in this study, we aimed to explore the potential relationships among m6A RNA methylation regulators and COPD based on the COPD expression profiles. We constructed m6A regulators related sub-networks and network motifs using STRING database and performed Gene Set Variation Analysis (GSVA) for each sub-network. Our results found that a high correlation among writers, erasers and readers. Specially, the obvious difference was observed between COPD patients from normal controls in activation of YTHDF2-related network. This study may provide new perspective for explore pathology of the occurrence and development of COPD.
S2-6	T1006 15:40-15:55	Deep and Confident Image Analysis for Disease Detection **Stephen Wambura**, Jianbing Huang and He Li Xidian University, China

		Abstract—This paper proposes an efficient deep learning classifier built on Bayesian deep neural network framework for general probabilistic disease detection along with reliable principled uncertainty estimation. Specifically we harness the expressiveness and temporal nature of Sequence-to-Sequence Convolutional neural networks (CNNs) to model explicitly disease detection problem via image processing. The work in this paper shows that the uncertainty informed decision making can improve the diagnostic performance considerably. Furthermore, we deploy a Memory Network in order to memorize infected cells in historical records. We demonstrate and validate empirically the effectiveness of the proposed framework via extensive experimental and rigorous evaluation on large-scale real world data sets. Experiments across different tasks and datasets show robust generalization, accurate and superior performance of proposed method compared to the well-known state-of-the-art diseases detector.

Break Time: 15:55-16:15

Detailed Program for Oral Session

Session 3: Bioelectric Signal

Time: 16:15-17:45, May 17, 2020 (Sunday)
Greenwich Mean Time (GMT+08:00) – China Local Time
Meeting ID: 630-4619-2506
Session Chair: Assoc. Prof. Shweta Gupta, Jain University, India

S3-1	X0009-A 16:15-16:30	Neural Spike Train Reconstruction from Calcium Imaging via a Signal-Shape Composition Model **Yu Shen**, Tingwei Quan and Shaoqun Zeng Huazhong University of Science and Technology, China *Abstract*—Calcium imaging can simultaneously record calcium signals of several hundreds of neurons. Due to the close relationship be- tween neuronal firing and intracellular Ca2+ concentration change, calcium imaging has been a powerful tool to measure the functional activities of neuronal population. Reconstruction AP train from calcium signals, as a key step in this measurement, is still challenging. Most of reconstruction methods neglect some important shape features of real AP train and calcium signal, and thus finely setting threshold is required for transforming the reconstructed signals to AP train. Here, we propose a recon- struction model with signal-shape composition (SSC) in which the smooth of calcium baseline and all-or-none nature of AP are introduced. The SSC method can directly output the AP train from its corresponding calcium signal without the threshold- ing of the reconstructed signal. In addition, because it can accurately estimate the signal baseline, the SSC method is robust to calcium baseline fluctuation. We demonstrated these two merits on the synthetic and experimental calcium signals. The results indicate that even when optimal thresholds are set and baselines fluctuate wildly, the SSC method can accurately reconstruct the action potential and is superior to the sparsity model and the OASIS method in the reconstruction.
S3-2	T1005 16:30-16:45	Study on Recent Developments from Aquilaria Sinensis and Future Perspectives **Arif Hussain Kaleri**, Xi-Qiang Song, Hao Fu Dai, Anum Mehmood, Uzair Aslam Bhatti and Mir Muhammad. Nizamani Hainan University, China *Abstract*—Latest development in agarwood creates better use in different fields of life sciences. With the development of social economy, China's agarwood industry has developed rapidly in recent years and has gradually become a characteristic industry of local pillar industries. Due to the particularity of agarwood and its precious rarity, it is the most treasured treasure of collection. The agarwood collection is a fashion and the best way to preserve value, both ancient and modern. New advancement was discussed in advance use of chemical constituents of Aquilaria siwasis mainly include flavonoids, benzophenones, lignans, phenyl propanoids, terpenoids, alkaloids, steroids, phenolic compounds.

		Some of them have anti-tumor, anti-bacterial, anti-inflammatory, analgesic, and laxative activities antibacterial constituents isolated from Aquilaria sinensis were reviewed, the latest uses of agarwood for religious as well as medical treatment and the biological activities of some compounds were also introduced. These would provide scientific basis for development and utilization of A.
S3-3	X3001 16:45-17:00	Discriminative Color Space Learning for Face Anti-Spoofing via Convolutional Neural Networks **Dong Huang,** Yifeng Ren, Lei Sun, Zhe Liu and Qingyan Li Northwestern Polytechnical University *Abstract*—Face spoofing detection is gaining an increasing attention in the biometric research. Various approaches have been proposed in the literatures. In these methods, the color variation of facial regions, caused by the defect of medium of fake face, is a vitally important clue. The traditional color spaces (e.g. RGB, HSV and YCbCr) are used in many spoofing detection approaches, however, it is not very discriminative to distinguish real and fake faces in these existing color spaces. So, in this paper, we propose a novel method to learn a new color space, which is suitable for face anti-spoofing and can be discriminative between real and fake faces. Different from other color learning methods, our novel method is based on convolutional neural networks and can nonlinearly project the real and fake face images into a distinguishable color space. Extensive experiments are conducted on two publicly available databases, showing very interesting performance compared to other existing color spaces and stateof-the-art
S3-4	X0024 17:00-17:15	A Preliminary Analysis of the Various Reaching Pattern Classifications **Kunkun Zhao**, Zhisheng Zhang, Chuan Guo and Jiankang Wu Southeast University, China *Abstract*—Surface electromyographic (sEMG) signals contain rich motion information, which could be used for motion recognition and activities of daily living detection. The study analyzed the possibility of classifying the various reaching patterns in a horizontal plane based on the sEMG signals. Three tasks, classifying directions and distances simultaneously (Task I), recognizing the directions (Task II), and distances (Task III) respectively, were designed for the purpose. The sEMG signals were recorded from nine muscles of the upper limb. Two time-domain features and three classification algorithms were applied to recognize different reaching patterns. The influence of different feature combinations and muscle groups was compared. The result showed that the classification rate for three tasks is lower than 90% based on the extracted time-domain features, and Task III achieved the highest classification rate among three tasks comparing the other two tasks whichever algorithms or feature combinations were used. Besides, the results demonstrated that the classification rate was sensitive to algorithms and muscle groups. The findings illustrated the complexity of reaching movement, and a personalized procedure should be designed to subtly control assist devices for patient rehabilitation.

Detailed Program for Oral Session

S3-5	T0004 17:15-17:30	Investigating Oscillatory Activity in Cerebral Cortex during Affective Picture Processing **Ning Zhuang**, Kai Yang, Bin Yan, Li Tong, Jun Shu, Ying Zeng and Ying Zeng PLA Strategy Support Force Information Engineering University, China *Abstract*—Emotion plays an important role in people's life. Previous studies have revealed that the characteristics of high frequency bands of Electroencephalogram (EEG) have shown good performance in emotion recognition. However, there is a lack of clear and unified conclusions about which brain regions to select for feature extraction. In this study, pleasant, neutral, unpleasant and scrambled pictures selected from international affective picture system (IAPS) were presented to subjects. In order to improve the spatial resolution, source estimation algorithm was used to reconstruct the cortical response in the processing of affective pictures. Oscillation activities of different frequency bands in the key brain regions were studied in cerebral cortex. The results showed that the activation of the brain was the weakest under scrambled condition. Referring to neutral condition, the energy of Alpha, Beta and Gamma bands under pleasant condition increased significantly in the bilateral middle temporal gyrus, middle frontal gyrus and prefrontal gyrus, while the energy of Alpha and Beta bands under unpleasant condition decreased significantly in the left middle occipital gyrus and bilateral middle temporal gyrus. These results provide a scientific basis for the selection of electrodes and frequency bands in emotion recognition based on EEG signals.
S3-6	T0047 17:30-17:45	Short-term Impact of Polarity Therapy on Physiological Signals in Chronic Anxiety Patients **Joaquim Comas**, Decky Aspandi, Manel Ballester, Francesc Carreas, Lluis Ballester and Xavier Binefa Universitat Pompeu Fabra, Spain *Abstract*—Increasing interest in complementary therapies prompts analysis of the objective impact on human physiology. Polarity Therapy (PT) is a branch of complementary medicine that relates to energy field therapies. Although previous clinical work has provided evidence of the impact on patients, the present work analyzes, for the first time, a short-term systematic investigation of such therapy. Several physiological signals were collected from 25 consecutive chronic anxiety patients seen in an outpatient clinic before and after PT, which included electrocardiographic analysis (ECG), galvanic skin response (GSR), blood volume pulse (BVP), and temperature. Also included was the analysis of facial expressions using state of the art deep learning-based models for automatic valence and arousal estimations. Using the recorded samples, we proceeded to calculate heart rate variability (HRV) analysis in a temporal, frequency and non-linear domain, which proves assessment of the autonomous nervous system. Fine analysis of the ECG was developed using wavelet-based techniques. The area under the T wave, recently described to correlate with electromagnetic ventricular activity, was also

		calculated. A psychological questionnaire assessed the clinical therapeutic impact before and after the session. Results revealed a positive impact of 30-minute therapy on blood pressure and heart rate reduction, direct evidence of down-regulation of sympathetic activity and up-regulation of parasympathetic activity, an inverse correlation of T-wave and BVP, which suggests improved cardiac coherence, and changes in facial expression which correlated with subjective perceptions of wellbeing. The combination of physiological variables, facial expression and self-assessment of wellbeing before and after a PT session revealed parallelism between the observed changes in physiological data and subjective feelings.

Detailed Program for Oral Session

Session 4: Genomics

Time: 16:15-18:00, May 17, 2020 (Sunday)
Greenwich Mean Time (GMT+08:00) – China Local Time
Meeting ID: 630-4619-2506
Session Chair: Dr. Takoua Jendoubi, Imperial College London, UK

S4-1	T0020 16:15-16:30	Genetic Epidemiology of Porcine Transmissible Gastroenteritis Virus Based on Whole Genome and S gene Sequences Yifan Feng, Jiating Qian, Jiefei Yu, Wenjuan Li and **Jie Li** Changshu Institute of Technology, China *Abstract*—Porcine transmissible gastroenteritis virus (TGEV) is a pathogenic agent responsible for high diarrhea-associated morbidity and mortality in suckling piglets. To understand the genomic characteristics and evolutionary trend of TGEV during nearly 70 years, we reanalyzed published TGEV whole genome sequences. The genomic sequences of 40 strains from different sources were downloaded from National Center for Biotechnology Information. The phylogenetic analysis was performed using both whole genome sequences and S gene sequences. The regional distribution of TGEV virus was obvious while the time distribution was relatively scattered. In the whole genome sequences, 2505 variable sites were found and 56% of them occurred more than once. In S gene sequences, 505 variable sites were detected, which generated 191 amino acid mutations.
S4-2	T0027 16:30-16:45	Codon Effect on the Entire Genome Based upon Genome-wide Recoded Escherichia coli **Yi Huang** Sichuan Agricultural University, China *Abstract*—Synonymous codon mutation can influence transcription and translation through gene expression. Researchers have studied how altering codons is linked to expression. However, they did not investigate the correlations at a whole genome level. We classified 1090 genes encoding proteins and analyzed their sequence properties in both strains of Escherichia coli with the entire genome recoded before and after codon alterations. It was observed that expression levels of the genes associated with cell membrane almost increase, while those related to protein production nearly decrease. Regarding to cytosolic metabolism, the overall expression of TCA cycle goes up, while glycolysis holds most genes with lessened expressions. The different values of A+T content, global and local codon usage, and stability of mRNA structure impacts expression ratios in an ambiguous degree, suggesting us take more parameters at cell level into account.
S4-3	T0018-A 16:45-17:00	aPRBind: Protein-RNA Interface Prediction by Combining Sequence and I-TASSER Based Structural Features Learned with Convolutional Neural Networks **Yang Liu** and Chunhua Li

		Beijing University of Technology, China *Abstract*—Protein-RNA interactions play a critical role in various biological processes. The accurate prediction of RNA-binding residues in proteins has been one of the most challenging and intriguing problems. The existing prediction methods still have a relatively low accuracy especially for the ab-initio methods. In this work, we propose an approach aPRBind, a convolutional neural networks (CNN)-based ab-initio method that can in high-throughput predict RNA-binding residues. aPRBind is trained with sequence features and structural ones (particularly including residue dynamic information and the residue-nucleotide propensity developed by us) that are extracted from the predicted structures by I-TASSER. The analysis of feature contribution indicates that besides SNB-PSSM (spatial neighbor based position-specific scoring matrix) proposed by us, the features such as solvent accessibility, charge type, residue dynamic information and interface preference of residues play important roles in the prediction of binding sites. Experimental results show that aPRBind consistently outperforms other state-of-the-art ab-initio methods. It should be pointed out that aPRBind can give a better prediction for the modeled structures with TM-score ≥ 0.5. Additionally, our method does not have a high requirement for the predicted structures, since the structural features used by us are not very sensitive to the subtle secondary structures.
S4-4	T0029 17:00-17:15	iPRIns: A Tool with the Improved Precision and Recall for Insertion Detection in the Human Genome **Sakkayaphab Piwluang** and Duangdao Wichadakul Chulalongkorn University, Thailand *Abstract*—An insertion is a specific type of the structural variations. The identification of insertions in a human genome is essential for the study of diseases or their functional effects. There are many tools available for identifying the insertion type with different methods and strategies. However, most of them could not deliver both good recall and precision, especially for the real datasets sequenced with the paired-end short reads. In this paper, we propose iPRIns, a new computational method for detecting insertions aiming to improve both precision and recall. The proposed method with discovering and filtering processes outperformed all other three tools for 5 out of 10 real datasets, the variations of NA12878, for both precision and recall. iPRIns is released under the open-source GPLv3 license. The source code and documentation are available at https://github.com/cucpbioinfo/iPRIns.
S4-5	T0010 17:15-17:30	A Polynomial Algorithm for a Class of Contig-based Two-sided Scaffold Filling **Li Chunliang**, Xu Qinye, Jia Handong, Song Weixing and Liu Nan Shandong Jianzhu University, China *Abstract*—Recently, the genomic scaffold filling problem has attracted a lot of attention at home and abroad. However, almost current studies assume that the scaffold is given as an incomplete sequence (i.e., missing

		genes can be inserted anywhere in the incomplete sequence). This differs significantly from most of the real genomic dataset (where a scaffold is given as a list of contigs). In this paper, we review the genomic scaffold filling problem by considering this important case when two scaffolds R and S is given, the missing genes can only be inserted in between the contigs, and the objective is to maximize the number of common adjacencies between the filled genome R' and S'. For this problem, a polynomial time algorithm is designed by using greedy search strategy, which proves the correctness of the algorithm, analyzes the time complexity of the algorithm, and completes the development of a visual program based on python, which further validates the effectiveness of the algorithm.
S4-6	T0039 17:30-17:45	Phenotype Anomaly Detection in Early C. Elegans Embryos by Variational Auto-encoder **Takumi Oibayashi**, Takaya Ueda, Yuki Kimura, Yukako Tohsato and **Ikuko Nishikawa** Ritsumeikan University, Japan *Abstract*—Variational auto encoder (VAE) is used to detect and quantify the phenotype anomaly in the nuclear division of the early embryo of C. elegans. The latent space of VAE, on which the normal data distribution is obtained through the training, is used to characterize not only the morphological anomaly, but also the temporal anomaly of the time series data, based on the position in the latent space. The proposed method is applied to the time series of three dimensional DIC data of nuclear division process during two-cell stage of C. elegans. Wild type data is used as the normal data for the training, and then an anomaly is evaluated on an embryo, for which one of the lethal genes is silenced by RNAi. First, Morphological anomaly is quantified by the reconstruction error. Then, for the well-reconstructed data, the trajectory in the latent space corresponding to the input time series is used to characterize the time development of the division process. Anomaly score is defined based on the normal time distribution in the latent space, and the proposed method successfully obtains a list of lethal genes, which cause the temporal anomaly by the knocking down.
S4-7	T1002-A 17:45-18:00	Evaluating Pairwise Associations for in Multi-omics Data **Takoua Jendoubi** and Korbinian Strimmer Imperial College London, UK *Abstract*—Nasopharyngeal carcinoma (NPC) is a subtype of head and neck cancer. NPC is of high prevalence in southern China, including Hong Kong, it is cancer closely associated with Epstein-Barr virus (EBV) infection. Lake of EBV positive cancer cell model hampers the development of NPC drugs. Recently, the new established EBV positive cell lines offer us a unique opportunity to study the virus response during the drug treatment. Three EBV positive NPC cell lines have been treated with single drug of palbociclib, single drug of Vorinostat and two drugs in combination for 24 hours. RNA sequence had been applied to these cells, and then both human and virus genome pattern has been analyzed. The

		Venn diagrams analyzed the differentially expressed genes (DEG) of treatment and un-treatment cells after normalization revealing 513 downregulated genes and 915 upregulated genes. Enrichment analysis of these DEGs based on the KEGG database was further performed, and a large population of genes was observed to be involved in autophagy. This finding had been further verified by western blot and QPCR. Heatmap of RNA sequence data indicated a change in the expression profile of the EBV virus genome in NPC cells after drug treatment.

Detailed Program for Oral Session

Session 5: Biomedical Imaging

Time: 13:30-15:15, May 18, 2020 (Monday)
Greenwich Mean Time (GMT+08:00) – China Local Time
Meeting ID: 630-4619-2506
Session Chair: Prof. Daishun Ling, Zhejiang University, China

S5-1	T0030 13:30-13:45	AI Auxiliary Labeling and Classification of Breast Ultrasound Images **Lei Wang**, Biao Liu, Shaohua Xu, Pan Ji and Qi Zhou Suzhou Mitxieser Artificial Intelligence CO., LTD, China *Abstract*—In this paper we developed a deep learning (DL) method to assistant radiologists quickly and accurately labeling and classifying the lesions of the breast ultrasound images. A faster R-CNN detector was trained to label and classify the lesions with the Breast Imaging Reporting and Data System (BI-RADS). The initial trained model used 2000 labeled images. From the testing results with 6000 images, we got poor accuracy. Therefore, we developed the second DL model with 4294-image set in which the images of BI-RADS 4 were removed. Then the second DL model was tested by 1000 images and used to classify 1836 images of BI-RADS 4. The results show that the classification accuracy, sensitivity and specificity are achieved as 92.37%, 98.34%, and 82.46%, respectively when it used to classify the BI-DADS 4 images into 4A and 4B, and 98.10%, 97.78% and 98.13%, respectively when it is used for breast cancer screening. Clinical Relevance—This DL labeling and classification method for breast ultrasound images is an efficient way to help the radiologists to annotate the lesions of the ultrasound breast images and relieve them of the heavy workload when they annotate a lot of images for DL model training.
S5-2	X0019 13:45-14:00	Fusion of 3D Medical ROIs Based on Transfer Functions **Jingfei Fu**, Wenyao Zhang and Yuanzhao Cao Beijing Institute of Technology, China *Abstract*—Volume rendering is a key visualization technology in the medical field. It is often used to observe medical volumes such as CTs and MRIs, but the rendering results may not present multiple regions of interest (ROIs) well. In order to solve this problem, a method of fusing ROIs based on transfer functions is proposed in this paper. The entire process is divided into three steps. Firstly, two pairs of one-dimensional color transfer function (1D-CTF) and one-dimensional opacity transfer function (1D-OTF) are designed to separate different target structures. Secondly, a fusion method is taken to combine the 1D-CTFs and 1D-OTFs to get a new pair of transfer functions. Finally, the original volume is rendered again with the new transfer functions to get the fusion image of ROIs. Experiments show that the resulting images not only integrate the ROIs appearing in the two different cases, but also present

		their spatial relationships clearly. Besides, both visual perception and information entropy evaluation confirm that this kind of fusion is better than image-level fusion and accumulation-level fusion. On the whole, this method facilitates the analysis of medical volumes and the diagnosis of diseases.
S5-3	T0046 14:00-14:15	A Computer-aided Diagnosis System of Breast Lesion Classification based on Multi-angle Fusion Strategy in Ultrasound Images **Yijun Zhao**, Igbe Tobore and Dashun Que Wuhan University of Technology, China *Abstract*—Ultrasound is one of the most widely applied imaging modalities for breast lesion assessment. The accurate breast lesion diagnosis can improve patients' survival rate. The purpose of this study is to develop a computer-aided diagnosis (CAD) system that can acquire information from grayscale and elastic ultrasound images to classify benign and malignant breast tumors. The U-Net was used for automatic segmentation of grayscale ultrasound images. After reconstructing elastic ultrasound images, 218 breast features (morphological, gray, calcification, texture and elastic features) were extracted. We proposed a feature selection method based on multi-angle fusion strategy (MAFS) to select important breast features. In this method, least absolute shrinkage and selection operator (LASSO), mutual information (MI) and random forest (RF) feature selectors were fused to establish a robust and accurate feature selector. A support vector machine (SVM) classifier was used for breast lesion classification. The ultrasound images in our study contained 77 malignant cases out of 199 breast lesion cases, in which the results of core biopsy or fine-needle aspiration were regarded as the golden standard. The area under the receiver operating characteristic curve (AUC) of the combined breast set based on MAFS, LASSO, MI and RF was 0.897, 0.871, 0.880 and 0.869, respectively. The accuracy, sensitivity and specificity of the breast lesion classification performance based on MAFS were 91.0%, 84.0% and 95.4%, respectively. Our results demonstrate the feasibility that the CAD system based on MAFS can be applied in breast lesion diagnosis. Also, the CAD system based on MAFS performed well in grayscale and elastic ultrasound image sets, showing it had robust and generalization ability in ultrasound images.
S5-4	X0030 14:15-14:30	Development of Rapid Circulating Tumor Cells Detection Instrument based on Large Field of View Optical Imaging Technology with High Resolution **Yang Zhang**, WeiWei Fu and Hailong Zhu Suzhou Institute of Biomedical Engineering Technology, Chinese Academy of Sciences, China *Abstract*—Circulating tumor cell (CTC) detection is used to identify malignant tumor cells that are disseminated in the patient's circulating blood. It has been widely used in early tumor classification, prognosis judgment and efficacy evaluation. It also plays an important role in finding new tumor markers and developing new anti-tumor drugs. The existing methods to detect CTCs can only be combined with cells

		enrichment and fluorescence imaging, which is called separation and identification of CTCs. Cell enrichment leads to cell omission, and small fluorescence imaging field leads to long detection time, which affects clinical application. In this paper, 7.5ml whole-blood large-size slices were used to avoid cell selection. The two-step imaging method was adopted. The first step is the large-size slices fast imaging based on the large field of view (LFOV) and high resolution optical system, which is used to initially locate target CTCs. The second step is target CTCs accurately identifying by fluorescence imaging. Through this method, the detection time is greatly reduced, the detection efficiency is greatly improved, accuracy is higher because of the avoidance of cells misdetection. A new solution for clinical detection of CTC cells is provided, which is conducive to promoting the CTCs count as a routine blood test item.
S5-5	X1003 14:30-14:45	Influence of Transducer Aperture on Magnetoacoustic Tomography Resolution **Lili Wang**, Hui Xia and Guoqiang Liu University of Chinese Academy of Sciences, China *Abstract*—The magnetoacoustic tomography with magnetic induction (MAT-MI) is a noninvasive imaging method which can reflect the conductivity distribution of the imaging target, and has broad application in early diseases diagnosis. Most previous studies of MAT-MI ignored the transducer aperture. However, the collected signal waveform is directly determined by the transducer acquisition mode, which affects the reconstruction images. In this paper, we use the finite element simulation software COMSOL Multiphysics to build magnetoacoustic tomography models, the signal is firstly collected by the a finite aperture transducer, and the sound sources distribution images based on measurements are constructed with time reversal method.Then, we study the relationship between transducer aperture and reconstructed image resolution. The results show that the transducer location should be far away from the detected sample under the premise of acceptable sensitivity to reduce the influence of the transducer aperture on the image resolution, which can obtain high quality reconstructed images. Our study provides guidance for the construction of MAT-MI detection systems.
S5-6	T0005 14:45-15:00	Construction and Simulation Analysis of 3D Model based on Bladder **Jiewen Deng**, Peng Ran, Yalan Mao and Jingwen Wang Chongqing University of Posts and Telecommunications, China *Abstract*—For people with urinary incontinence who cannot control bladder urination freely, the principle of electrical impedance imaging was used to simulate the bladder state to select the electrode array method and excitation method suitable for bladder filling detection. In this paper , a three-dimensional human abdominal model including pelvis and bladder was constructed. The bladder filling degree is simulated by setting different bladder radii separately, and the electrodes are arranged on the surface of the model. The model designed in this paper is a common hierarchical array model and a rectangular array model based on bladder

		position design. The excitation, current of 5 mA is used to simulate the relative, interphase and adjacent excitation of two different electrode array models. Through the analysis of parameter voltage sensitivity and dynamic range, the evaluation of two-electrode array mode and three-electrode excitation was finally realized. The experimental results show that the rectangular array method and interphase excitation have more application value in bladder filling detection, which can more effectively obtain the voltage change caused by bladder volume change, which provides a basis for the design of bladder filling detection system.
S5-7	T0006 15:00-15:15	Investigating Spatio-temporal Interactions in Embryonic Morphogenesis by 4D Cell-Nucleus Imaging and System-level Comparative Analysis Taking Eutelic Nematodes C .elegans and C. briggsae as Examples **Guoye Guan**, Lu-Yan Chan, Xiaomeng An, Vincy Wing Sze Ho, Zhongying Zhao and Chao Tang Peking University, China *Abstract*—Metazoan Embryonic morphogenesis is involved with spatio-temporal interactions between cells during embryogenesis from zygote to larva. These regulatory interactions (e.g. active and passive cytomechanics) contribute to accurate, robust and stereotypic embryo pattern among individuals of a species. To in-depth decipher the underlying mechanism and biological function of these interactions, in this work, we used two closely related species Caenorhabditis elegans and Caenorhabditis briggsae as examples and provided a general framework for system-level comparative analysis. We cultured and imaged 11 wild-type embryos in vivo using 3-dimensional time-lapse confocal microscope for each species, with following automatic cell tracing and lineaging. We quantitatively reconstructed their normalized and comparable 4D cell-position atlas in silico, including information of each cell (e.g. division timing and migration trajectory) during embryogenesis from 4- to 350-cell stage. With highly similar cell lineages in both C. elegans and C. briggsae, we compared their division-timing program and cell-packing pattern globally and locally, which revealed a turning point of regulation on positional variation among individuals, within a species as well as between the two species. Moreover, this down regulation could rescue some cellular positional variation caused by division-order chaos between C. elegans and C. briggsae. Last but not least, asynchrony of division between sister cells (i.e. ADS) were found to be functional for local positioning of newborn cells. Our information-rich dataset as well as computational analytic methods could facilitate related research in developmental biology, evolutionary biology and comparative biology.

Detailed Program for Oral Session

Session 6: Computational Biology

Time: 13:30-15:15, May 18, 2020 (Monday)
Greenwich Mean Time (GMT+08:00) – China Local Time
Meeting ID: 630-4619-2506
Session Chair: Prof. Ikuko Nishikawa, Ritsumeikan University, Japan

S6-1	T0049 13:30-13:45	Antimicrobial Peptide Prediction Using Ensemble Learning Algorithm **Neda Zarayeneh** and Zahra Hanifeloo Washington State University, USA *Abstract*—Recently, Antimicrobial peptides (AMPs) have been area of interest in the researches, as the first line of defense against the bacteria. They are raising attention as an efficient way in fighting multi drug resistance. Discovering and identification of AMPs in the wet labs are challenging, expensive, and time consuming. Therefore, using computational methods for AMP predictions have grown attention as they are more efficient approaches. In this paper, we developed a promising ensemble learning algorithm that integrates well-known learning models to predict AMPs. First, we extracted the optimal features from the physicochemical, evolutionary and secondary structure properties of the peptide sequences. Our ensemble algorithm, then trains the data using conventional algorithms. Finally, the proposed ensemble algorithm has improved the performance of the prediction about 10% comparing to the traditional learning algorithms.
S6-2	T0003 13:45-14:00	Analyzing Genomic Features with Predictive Chromatin Interaction Models: A Comprehensive Evaluation Yi Kou and **Daniel Zhao** California Institute of Technology, USA *Abstract*—Enhancer-Promoter (EP) interactions reflected by Hi-C technology are crucial to understanding genomic functions. Particularly, identifying 'unique' genomic features that are characteristically important in a specific cell line can further our current understanding of the mechanisms that drive cell differentiation, tissue development, and disease progression. However, classic prediction models such as TargetFinder provide little valuable insight towards the large disparity between important genomic features across different cell lines. To comprehensively approach this question, herein we first evaluated seven classifiers to predict EP interactions using high-resolution Hi-C maps of genome loci across six classic cell lines, surpassing TargetFinder in all benchmark metrics. We then evaluated the model's predictive performance with features provided by seven feature selection methods from the embedded, wrapper and filter categories. Moreover, groups of features were aggregated from the results of two or more feature methods and analyzed based on the model's performance. Finally, we examined the distinguishing features across six cell lines. Our study suggests the existence of 'unique' genomic features that are especially predictive of EP

		interactions only in specific cell lines.
S6-3	X0018 14:00-14:15	Study of Data Imbalanced Problem in Protein-peptide Binding Prediction **Lu Gao** and Shirley Weng In Siu University of Macau, Macau *Abstract*—Peptide-binding proteins are excessive in living cells and protein-peptide interactions mediate a wide range of cellular functions. Prediction of protein-peptide binding residues has been vital and popular in the past decades and machine learning methods have gained more attention in recent years. However, the data imbalance problem has not been dealt with effectively. On this matter, we study the effects of sampling methods and degrees of imbalance on data classes on construction of prediction model. We first developed the NearMiss under-sampling method (NMUS) as a way to screen out a given number of quality data samples from majority class to balance the data sets. The remarkable sensitivity (SEN) with 0.818 shows the advantage of NMUS in handling class imbalance problem. This research carried on valuable analysis on data imbalance problem and achieved a better prediction of protein-peptide binding interaction.
S6-4	T0012-A 14:15-14:30	Use of RNA Sequence to Identify Drug Mechanism on Preclinical Cancer Models **Zhichao Xue**, Anna Chi Man Tsang and George Sai Wah Tsao The University of Hong Kong, Hong Kong *Abstract*—Nasopharyngeal carcinoma (NPC) is a subtype of head and neck cancer. NPC is of high prevalence in southern China, including Hong Kong, it is cancer closely associated with Epstein-Barr virus (EBV) infection. Lake of EBV positive cancer cell model hampers the development of NPC drugs. Recently, the new established EBV positive cell lines offer us a unique opportunity to study the virus response during the drug treatment. Three EBV positive NPC cell lines have been treated with single drug of palbociclib, single drug of Vorinostat and two drugs in combination for 24 hours. RNA sequence had been applied to these cells, and then both human and virus genome pattern has been analyzed. The Venn diagrams analyzed the differentially expressed genes (DEG) of treatment and un-treatment cells after normalization revealing 513 downregulated genes and 915 upregulated genes. Enrichment analysis of these DEGs based on the KEGG database was further performed, and a large population of genes was observed to be involved in autophagy. This finding had been further verified by western blot and QPCR. Heatmap of RNA sequence data indicated a change in the expression profile of the EBV virus genome in NPC cells after drug treatment.
S6-5	X0007 14:30-14:45	Evaluating Variants of Firefly Algorithm for Ligand Pose Prediction in Protein-Ligand Docking Program **Meng Chi Ao** and Shirley W. I. Siu University of Macau, Macau *Abstract*—Protein-ligand docking is an important and effective

		structure-based drug design method widely used for large-scale screening of drug candidates. The core of a protein-ligand docking program consists of a sampling algorithm and a scoring function, which produce different poses of a ligand and estimate a score for the pose with respect to how good it reproduces the native conformation of the ligand at the protein binding site, respectively. Nature-inspired algorithms such as particle swarm optimization (PSO) and firefly algorithm (FA) are emerging optimization techniques for simulating social behavior of creatures and the nature-based law of the survival of the fittest. In this study, we investigated the application of FA in ligand pose prediction using a protein-ligand docking program PSOVina. Importantly, we tested four strategies on the classical FA to enhance the protein-ligand docking performance, namely application of the logistic map to diversify the search, Mantegna's method for simulating Lévy flight to generate random walk, elite selection to inherit better solutions across iteration, and k-mean clustering to find more than one optimum solutions. We performed parametric analysis of FA and benchmark tests using two datasets, PDBbind database (version 2014) and Astex Diverse set. The results show that although the average relative mean standard deviation (RMSD) of predicted poses is not always the best, our FA variants are better than those of PSOVina in average success rate, suggesting that FA has potential usefulness for performing robust searches in the ligand conformational space.
S6-6	X1005 14:45-15:00	Nanopore based Programmable DNA Structure Detection to Solve the Shortest Path Problem **Nan Zhao**, Xinxin Zhang, Yuan Liang, Jing Yang and Cheng Zhang North China Electric Power University, China *Abstract*—The shortest path problem in graphs is a famous NP-complete problem, and the traditional use of computer algorithms to solve this problem has great limitations. Based on the nanopore detections of parallelism and programmable DNA assembly strategy, this paper proposes an algorithm that uses a programmable DNA self-assembly model to solve the shortest path of the graph. In according to the set graph, the algorithm first plans a specific molecular hybridization path by inducing the start and end of the self-assembly chain reactions. Using different DNA inputs referring to the start and end points in the graph, thereby a specific DNA structure can be constructed. Through nanopore detection technology , all paths that satisfy the conditions can be found. Therefore, the nanopore signal analysis is performed to obtain the shortest path of the graph. Considering the biocomputing algorithm can be implemented automatically in the search process, and the nanopore results has high reliability, the established method can be applied to solving more complex NP-complete problem.
S6-7	T0036-A 15:00-15:15	Alternating EM Algorithm for a Bilinear Model in Isoform Quantification from RNA-seq Data **Wenjiang Deng**, Tian Mou, Yudi Pawitan and Trung Nghia Vu Karolinska Institutet, Sweden

		Abstract—Motivation: Estimation of isoform-level gene expression from RNA-seq data depends on simplifying assumptions, such as uniform read distribution, that are easily violated in real data. Results: We have developed a novel method called XAEM based on a more flexible and robust statistical model. Existing methods are essentially based on a linear model Xβ, where the design matrix X is known and is computed based on the simplifying assumptions. In contrast, XAEM considers Xβ as a bilinear model with both X and β unknown. Joint estimation of X and β is made possible by a simultaneous analysis of multi-sample RNA-seq data. Compared to existing methods, XAEM automatically performs empirical correction of potentially unknown biases. We use an alternating expectation-maximization (AEM) algorithm, alternating between the estimation of X and β. For speed XAEM utilizes quasi-mapping for read alignment, thus leading to a fast algorithm. Overall XAEM performs favorably compared to recent advanced methods. For simulated datasets, XAEM obtains higher accuracy for multiple-isoform genes. In a differential-expression analysis of a real single-cell RNA-seq dataset, XAEM achieves substantially better rediscovery rates in independent validation sets.

Break Time: 15:15-15:40

Detailed Program for Oral Session

Session 7: Biophysics and Image Processing

Time: 15:40-17:25, May 18, 2020 (Monday)
Greenwich Mean Time (GMT+08:00) – China Local Time
Meeting ID: 630-4619-2506
Session Chair: Assoc. Prof. Xiaoyue Jiang, Northwestern Polytechnical University, China

S7-1	X0025 15:40-15:55	Optical System Design of Corneal Crosslinker based on Digital Light Modulation **Tianli Zheng**, Hailong Zhu and Weiwei Fu Suzhou Institute of Biomedical Engineering Technology, Chinese Academy of Sciences, China *Abstract*—In this paper, according to the treatment status of keratoconus and the principle of projection optical system, the corneal crosslinker optical system was designed to cover the single eye with uniform and variable shape. Firstly, this paper presents the scheme of the system and its working principle. Then, DMD uniform light path is designed based on the principle of compound eye lens, and the spot uniformity reaches 92%. Finally, according to the specific practical requirements in the use of corneal crosslinker, an ultraviolet projection lens with a working distance of 150mm and a magnification of β=-0.345 was designed, with a resolution of 45LP/mm in the full field of view far greater than 0.3.
S7-2	X0027 15:55-16:10	Predicting COVID-19 Evolution during Mid-March Crisis **Pedro Furtado** University of Coimbra, Portugal *Abstract*—The corona virus responsible for COVID-19 has come into our lives with huge stampede. Every human activity has been seriously hurt and millions were confined to their homes. As of March, people in Europe wonder whether the confinement, closures and no-flights policies are effective or how effective they are, in spite of the positive previous example of China. In this paper we present our analysis specifically focused at detecting whether the new daily cases curves are in a stabilization route or exploding. This required a set of steps for data processing and analysis that we describe in detail. The conclusion is that, as of 22 March, the curves were in a trajectory of stabilization and possible decrease soon. We show why, also finding a most probable correlation with confinement and other government policies.
S7-3	T0007 16:10-16:25	Development of Intra-aortic Balloon Pump with Vascular Stent and Vitro Simulation Verification **Yao Xie**, Honglong Yu, Dong Yang, Kun Wang and Qilian Xie University of Science and Technology of China, China *Abstract*—Intra-aortic balloon pump(IABP) has been widely used in the rescue and treatment of patients with cardiac insufficiency and heart

		failure, but IABP is not effective in increasing cardiac output. In this study, an aortic balloon pump with a vascular stent was developed, and an experimental bench for simulating heart failure in vitro was built to study the effect of a balloon pump with a vascular stent on hemodynamic changes. Experiments have shown that compared with the traditional balloon pump, a balloon pump with a stent has higher cardiac output and counterpulsation pressure, lower systolic and diastolic blood pressure, and therefore has better performance in heart failure treatment.
S7-4	X0026 16:25-16:40	Testing Deep Segmentation of Computer Tomography Scans **Pedro Furtado** University of Coimbra, Portugal *Abstract*—Given the current relevance of deep learning approaches, their use in segmentation tasks and the fact that they can learn to segment from examples, it is important to assess the quality of the result. In this work we do an assessment of the quality of segmentation of Computer Tomography (CT) sequences of the upper abdomen, testing two popular deep learning networks on the liver. The shape of the liver evolves along the slices of the sequence, it is interesting to test how well the networks may be able to learn the varying shapes. We build two networks, evaluate segmenting the organ from CT scans and draw conclusions regarding merits and limitations. Future work involves more evaluation with larger datasets and considering how to improve the results further.
S7-5	T0011 16:40-16:55	A Bi-directional Hierarchical Clustering (Bhc) for Peak Matching of Large Mass Spectrometry Data Sets **Nazanin z Kermani**, Xian Yang, Yike Guo, James S McKenzie and Zoltan Takats Imperial College Lodnon, UK *Abstract*—The preprocessing of mass spectrometry (MS) data is a crucial step in every MS study, which not only makes data comparable and manageable but also makes the study more reproducible. However, an essential part of this process, which is often overlooked, is peak matching. Although existing clustering methods have been applied for peak matching, the use of these methods have been limited. For example, the use of hierarchical agglomerative clustering (HAC) for matching of mass/charge signals has been constrained to small-scale MS data sets due to the computational complexity of HAC. In this paper, we reintroduce a bi-directional hierarchical agglomerative clustering (BHC) as a scalable and accurate peak matching technique. As a result, the computational complexity of hierarchical agglomerative clustering for peak matching was optimized by BHC to O(RlogR). BHC was benchmarked against existing peak matching techniques. Finally, we propose a parallelization framework that significantly reduces the peak matching method's computation time.
S7-6	T0022 16:55-17:10	Exploring the Adaptation of Recurrent Neural Network Approaches for Extracting Drug–drug Interactions from Biomedical Text Wen-Juan Hou and **Bamfa Ceesay** National Taiwan Normal University, Taiwan

		Abstract—Information extraction (IE) is the process of automatically identifying structured information from unstructured or partially structured text. IE processes can involve several activities, such as named entity recognition, event extraction, relationship discovery, and document classification, with the overall goal of translating text into a more structured form. Information on the changes in the effect of a drug, when taken in combination with a second drug, is known as drug–drug interaction (DDI). DDIs can delay, decrease, or enhance absorption of drugs and thus decrease or increase their efficacy or cause adverse effects. Recent research trends have shown several adaptation of recurrent neural networks (RNNs) from text. In this study, we highlight significant challenges of using RNNs in biomedical text processing and propose automatic extraction of DDIs aiming at overcoming some challenges. Our results show that the system is competitive against other systems for the task of extracting DDIs.
S7-7	X1006 17:10-17:25	Real-time Differentiation of Monocotyledons and Dicotyledons Leaves by Using Haar-like Features **Josué L. M. Dantas** and André R. Hirakawa University of São Paulo, Brazil *Abstract*—This paper proposes a method to differentiate accurately and rapidly Ipomoea spp, a weed, from sugar cane plantation. Weeds compete for water and nutrients with sugar cane thus Ipomoea spp causes losses to production. Ipomoea spp is dicotyledon and sugar cane is a monocotyledon. Because of this, there are differences between them, such as, the venation patterns of leaves. Ipomoea spp has vesiculate venation and sugar cane has parallel venation. Leaves have usually been used for plant identification. This research proposed the Haar-like features to differentiate monocotyledons and dicotyledons. In this method, some templates have been used to identify the venation pattern of plants. Experiments were realized to find the size of the template that correlate a high value between accuracy and a low time of processing. Besides, an Integral image was applied to reduce the processing time of those templates. Other experiments were conducted to analyze the accuracy with leaves in the different rotations because in a real environment the leaves are in many positions. The proposed method has shown a low processing time and satisfactory accuracy comparing to others.

Detailed Program for Oral Session

Session 8: Systems Biology

Time: 15:40-17:10, May 18, 2020 (Monday)
Greenwich Mean Time (GMT+08:00) – China Local Time
Meeting ID: 630-4619-2506
Session Chair: Prof. Tao Yang, Shanxi Medical University, China

S8-1	T0015 15:40-15:55	HilbertEPIs: Enhancer-promoter Interactions Prediction with Hilbert Curve and CNN Model **Yujia Hu**, Chunlin Long, Ruichen Peng and Min Zhu Sichuan University, China *Abstract*—Enhancers are DNA cis-regulatory sequences that control the transcriptional activities of many gene regulation elements. Due to enhancers always get close to promoters by complex spatial structures, accurately identifying Enhancer-Promoter Interactions will help us understand mechanisms of gene regulations, recognize specific genes associated with diseases, as well as offer help with disease diagnosis and treatment. In this article, we develop a model named HilbertEPIs to predict the interactions between enhancers and promoters. We first transfer 1D sequence into 3D picture representations with Hilbert Curve to preserve the spatial structure of this sequence. Then extract features by CNN model. Finally, using two strategies to deal with unbalanced data. Experimental results have proved that HilbertEPIs has perfect performance compared to existed methods, as well as to show that Hilbert Curve is qualified to represent spatial relationships among different genetic regulatory elements. We train model in two ways and learn from six cell lines, finally achieve the data in 0.908~0.983 of AUROC, 0.926~0.988 of AUPR.
S8-2	T0009 15:55-16:10	Achieving Optimal Tradeoff Adaptation Functionality for the Minimal Gene Regulatory Network **Xiaona Huang**, Jiaqi Li and Zhirong Zhang Hexi University, China *Abstract*—Adaptation functionality is an essential property for gene regulatory network (GRN). Understanding the relationship between optimal tradeoff adaptation performance and GRN parameters remains an open question. In this paper, a minimal three-node GRN with 12 parameters is modeled by the Michaelis-Menten rate equations. The NSGA-III algorithm is used to find the 'best' parameter sets as many as possible, which make GRN achieve optimal tradeoff adaptation: high sensitivity, high precision, short peak time and short settle down time. Further statistical analysis is performed to obtain reliable rules of the 'best' parameter sets. The results show that 11 out of 12 GRN parameters have preferred value. The proposed methodology can provide the guidance to design GRN with optimal tradeoff adaptation, or with other biological functionalities.

S8-3	X1004 16:10-16:25	Study on the Recombinant expression and Purification of a Fusion Protein ACTH-TPAST-IGFI in E. coli Wang Dayong, Anum Mehmood, Mir Mohammad Nizamani, Arif Hussain Kaleri, Saqib Ali Nawaz and **Uzair Aslam Bhatti** Hainan University, China *Abstract*—Whenever there is a tension hypothalamus got activated and release CRH (corticotropin releasing hormone) and this works on anterior pituitary gland which is located below hypothalamus to release Adrenocorticotropic Hormone (ACTH), than ACTH works on adrenal cortex to release both glucocorticoid and androgens.Secondry Adrenal Insufficiency is a disease in which there is deficiency of ACTH .the main cause of this disease is pituitary tumor..when there is no ACTH it will not effect on adrenal cortex to release glucocorticoid and androgen.Acth have fast metabolism as compose of just 39 aminoacids. ACTH which is used in clinical medicine is extracted from animal tissues which poses a potential risk for infection from animal diseases and is also expensive. Moreover, their half life is only 15 minutes and so requires prolonged drug infusion time with high costs. Hence, it is crucial and relevant to have a recombinant human ACTH hormone that has increased half life and enhanced activity. Producing large scale biological drugs by gene engineering is a new trend in pharmaceutical industry. This study can help to produce high purity, low cost, large scale ACTH. To express a recombinant fusion protein of ACTH fused to Tissue Plasminogen Activator (TPAST) fused to Insulin Like Growth Factor (IGF1) (HisTag-Linker-ACTH-TPAST-IGFI-PET21) in E. coli and purify using Ni-NTA agarose beads. The reason IGF1 is fused to ACTH through a TPAST substrate linker is because in the blood, there is the Tissue Plasminogen Activator (TPAST) that will act on TPAST substrate linker and cleave the site to release the ACTH and IGF1. IGFI can enhance the effects of ACTH twenty times more. The recombinant plasmids were transformed into E. coli strain BL21-DE3 for protein expression. After analysing if the expression of the ACTH-TPAst-IGF1 fused recombinant protein was in the Supernatant or pellet fraction, it was further purified using Ni-NTA agarose beads. Since the protein was expressed in the pellet fraction of E. coli they are denatured and particulate due to formation of Inclusion Bodies. Hence, they need to be renatured and solubilized to refold them to increase activity. The next steps are to test the functionality of this protein both in-vitro cell-based assays and in-vivo assays. The fused gene product was created by Overlap PCR and then subcloned into pET21a vector. Plasmids of wild type (WT) ACTH-TPAST-IGFI, were constructed and thereafter validated by DNA sequencing: All the above were expressed and purified from E. coli strain BL21-DE3. Coomassie brilliant blue staining was done on the SDS-PAGE gel showing the expression of the 14kd fusion protein in the pellet fraction of the IPTG induced culture and in the elute fraction after protein purification fractions.
S8-4	X0001 16:25-16:40	Chemical Reactivation of Resin-embedded Multicolor Fluorescent Proteins Imaging

		Yurong Liu, Xiaojun Wang and Shaoqun Zeng Huazhong University of Science and Technology, China *Abstract*—Resin-embedding of fluorescent proteins (FPs) has been widely used with optical and electron microscopy in neural circuit studies. However, current available chemical reactivation (CR) strategy was limited to specific kinds of FPs, e.g., enhanced green fluorescent protein (EGFP) and enhanced yellow fluorescent protein (EYFP) after resin-embedding. Here, we studied the effects of various factors during resin-embedding, such as the organism and pKa value of the FPs, the pH and the type of resin. We found that high pKa values and acidic hydrophobic environment were key determinants for resin-embedding, which could greatly improve fluorescence during CR-based imaging. We found out several FPs suitable for CR-based resin-embedding from library of FPs, including mClover3, mKate, mMaroon1, mOrange2, mApple, pHTomato, td-Orange2 and pHOran4. Combined with whole-brain imaging systems, we demonstrated fine structures of long-range projections within a dual-color mouse brain sample labeled with mClover3 and pHOran4. Therefore, resin-embedding of FPs for multicolor imaging offers a powerful tool to elucidate organizations of neural circuits.
S8-5	X1008 16:40-16:55	Correlation of Macrophage Migration Inhibitory Factor (MIF) Expression and Asymmetric Dimethylarginine (ADMA) Levels in *Helicobacter pylori* Infection **OK. Yulizal**, Aznan Lelo, Syafruddin Ilyas and R. Lia Kusumawati Universitas Sumatera Utara, Indonesia *Abstract—Helicobacter pylori* induces inflammation and gastric mucosal injury. Inflammation is characterized by increased activity of proinflammatory cytokines, those are controlled and stimulated by macrophage migration inhibitory factor (MIF). Gastric injury, proinflammatory factors and oxidative stress in *H. pylori* infection produce asymmetric dimethylarginine (ADMA) which inhibits the activity of nitric oxide synthase (NOS), an enzyme in nitric oxide (NO) production. Over production of ADMA generates gastric mucosal disintegrity and severe inflammation. The aim of this study was to investigate the correlation between MIF expression and ADMA levels in rats induced by *H. pylori* infection. Twenty four male Wistar rats were randomly divided into two groups equally. Group-1 as control group, group-2 as *H. pylori* infected group. MIF expression was determined by immunoreactive score (IRS). Serum ADMA levels was analyzed using ELISA technique. Group-2 had a higher IRS compared to group-1 ($P = 0.000$). Serum ADMA levels in group-2 was higher compared to control group ($P = 0.000$). There was a significant positive correlation between MIF expression and ADMA levels ($r = 0.876$, $P < 0.05$). There was a significant increase in MIF expression, ADMA levels and a significant positive correlation between MIF expression and ADMA levels in *H. pylori* infection.

Detailed Program for Oral Session

S8-6	T0038 16:55-17:10	Analyzing Phenotype Microarray Data for Escherichia coli Using an Infinite Relational Model **Yukako Tohsato**, Tadahiro Taniguchi, Hirotada Mori and Masahiro Ito Ritsumeikan University, Japan *Abstract*—To elucidate the dependence of gene function on the environmental conditions, we focused on quantitative data from a phenotype microarray (PM) of the wild type and ca. 300 single-gene knockout mutants of Escherichia coli K-12 cultured under various medium conditions. We developed an infinite relational model (IRM) applicable to three-valued relational data and applied it to the PM data. The results of gene ontology (GO) analysis showed that mutants with deletion of the genes that encode the enzymes threonine synthase and methionine synthase exhibited reduced cell growth in medium containing amino acids as a nutrient source. By comparing the number and degree of overlap of clusters enriched in certain GO terms obtained by IRM and other biclustering methods, we confirmed the effectiveness of our IRM for omics data analysis.