

CONFERENCE ABSTRACT

**2019 3rd International Conference on Computational
Biology and Bioinformatics (ICCBB 2019)**

October 17-19, 2019

Nagoya City University, Nagoya, Japan



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

Conference Venue

The 4th floor of the Outpatient Facility, Nagoya City University Hospital

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Nagoya City University Hospital (University Hospital) was established in 1931 and was nominated as an advanced treatment hospital in July 1995. It is an education and research institution of Nagoya City University (NCU) that contributes to the development of medical treatment in metropolitan Nagoya by providing a high degree of advanced medical treatment.

How to get there?

Access to NCU

<https://www.nagoya-cu.ac.jp/english/access/index.html>

<https://www.nagoya-cu.ac.jp/english/access/ncu/access.html>

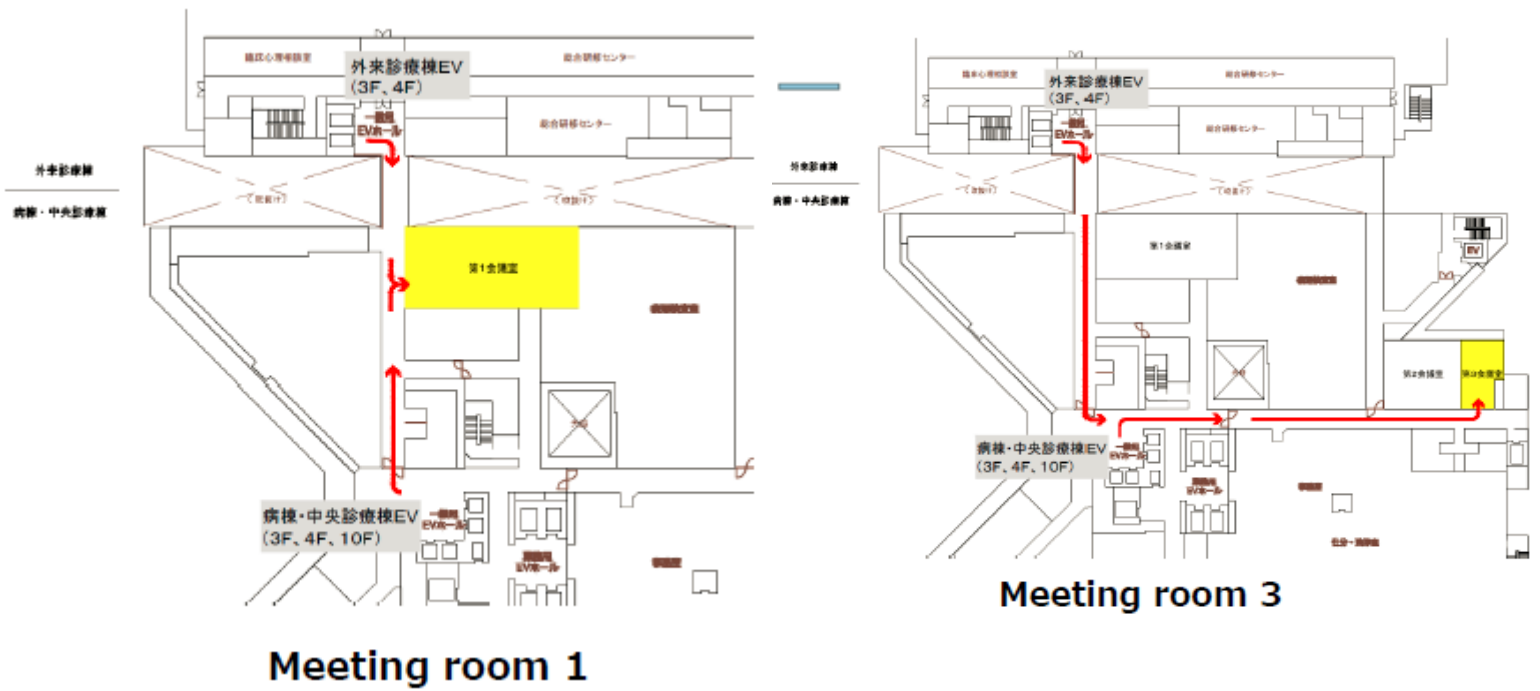
Access to Sakurayama Campus

<https://www.nagoya-cu.ac.jp/english/access/ncu/sakurayama.html>

Sakurayama Campus Map

<https://www.nagoya-cu.ac.jp/english/access/map/sakurayama.html>

4th Floor of Hospital main building



10th Floor of Hospital main building

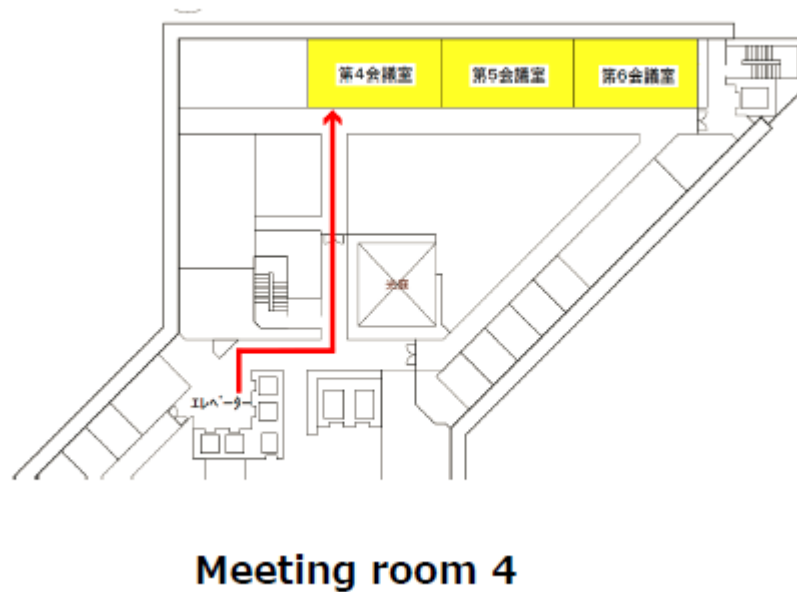


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Introduction

Welcome to 2019 3rd International Conference on Computational Biology and Bioinformatics (ICCBB 2019) which is organized by Biology and Bioinformatics (BBS) under Hong Kong Chemical, Biological & Environmental Engineering Society (CBEEES), and is supported by Nagoya City University, Nagoya, Japan. The objective of 2019 3rd International Conference on Computational Biology and Bioinformatics (ICCBB 2019) is to provide a platform for researchers, engineers, academicians as well as industrial professionals from all over the world to present their research results and development activities in Computational Biology and Bioinformatics.

Papers will be published in the following proceeding:



ACM Conference Proceedings (ISBN: 978-1-4503-7681-5): archived in ACM Digital Library, indexed by EI Compendex and SCOPUS, and submitted to be reviewed by Thomson Reuters Conference Proceedings Citation Index (ISI Web of Science).

Conference website and email: <http://www.iccbb.org/>; iccbb@cbees.net

Presentation Instruction

Instruction for Oral Presentation

Devices Provided by the Conference Organizer:

Laptop Computer (MS Windows Operating System with MS PowerPoint and Adobe Acrobat Reader); Digital Projectors and Screen; Laser Stick

Materials Provided by the Presenters:

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

Duration of each Presentation (Tentatively):

Keynote Speech: about **35** Minutes of Presentation and **5** Minutes of Question and Answer

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

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

Instruction for Poster Presentation

Materials Provided by the Conference Organizer:

The place to put poster

Materials Provided by the Presenters:

Home-Made Posters: Submit the poster to the staff when signing in; Poster Size: A1 (841*594mm) ; Load Capacity: Holds up to 0.5 kg

Best Presentation Award

One Best Oral/Poster Presentation will be selected from each session, and the Certificate for Best Presentation will be awarded at the end of each session on Oct. 17 and Oct. 18, 2019.

Dress Code

Please wear formal clothes or national representative of clothing.

Disclaimer

Along with your registration, you will receive your name badge, which must be worn when attending all conference sessions and activities. Participants without a badge will not be allowed to enter the conference venue. Please do not lend your name badge to the persons who are not involved in the conference and do not bring the irrelevant persons into the conference venue.

The conference organizers cannot accept liability for personal injuries, or for loss or damage of property belonging to conference participants, either during, or as a result of the conference. Please check the validity of your own insurance.

Honored Speaker Introduction

Keynote Speaker I

Prof. Andrey Krylov

Lomonosov Moscow State University, Russia

Andrey Krylov received the M.S., Ph.D., and Dr. Sc. degrees from the Faculty of Computational Mathematics & Cybernetics, Lomonosov Moscow State University (CMC MSU) in 1978, 1982 (supervisor – academician Andrey Tikhonov), and 2009, respectively. He was a member of scientific staff (1981-1988), senior researcher (1988-1998), head scientist (1988-2003), associated professor (2003-2009) CMC MSU and he is currently professor, head of the Laboratory of Mathematical Methods of Image Processing (<http://imaging.cs.msu.ru>). During his career he worked in applied mathematics in areas of nuclear physics, physical chemistry of liquid systems, multimedia and biomedical imaging. In 1989 he received the Leninsky Komsomol Scientific Prize - the highest prize for scholars in the USSR. He has authored or coauthored over 150 published papers. He served as a reviewer for several international journals and conferences; he was in the board of international and national conferences. For a long period of time he is one of the organizers of the GraphiCon conference - the main international computer graphics, computer vision and image processing conference in Russia.

Topic: “Hybrid Method for Biomedical Image Denoising”

Abstract—Many of the state-of-the-art biomedical image denoising methods are based on convolutional neural networks (CNN). They show very good performance and achieve impressive results. Nevertheless we cannot fully rely on CNN-based methods. Their results strongly depend on the used training set and even small differences in the input data can cause output disturbance. Thus new more reliable hybrid denoising methods were suggested. They include combinations of CNN and “classical” algorithms like Non-Local Means, Bilateral, Anisotropic diffusion, Total Variation, etc. Nevertheless hybrid methods need a non-reference automatic parameters estimation for classical algorithms.

In this report we present a hybrid method with automatic choice of the strength parameter for “classical” method. It is based on multiscale method for automatic choice of the parameter. To control biomedical image structures by ridge based approach we calculate image denoising quality using difference between noisy and filtered images. Presence of regular structures in the ridge areas of these difference images is minimized.

Keynote Speaker II

Assoc. Prof. Ahmed Moustafa
Nagoya Institute of Technology, Japan

Dr. Ahmed Moustafa received his PhD from University of Wollongong in Australia. He is an Associate Professor of Department of Computer Science, Graduate School of Engineering, Nagoya Institute of Technology, Japan. He is a member of the Japan Society of Artificial Intelligence, IEEE Computer Society, Australia Computer Society, Service Science Society of Australia. He was a visiting researcher in University of Adelaide, Auckland University of Technology and Data61, Australia. His main research interests include complex automated negotiation, multiagent reinforcement learning, trust and reputation in multiagent societies, deep reinforcement learning, service oriented computing, collective intelligence, intelligent transportation systems and data mining. He served as a PC member in many reputed conferences including ICWS, ICSOC and WWW.

Topic: “Agent that Facilitates Online Crowd Discussions”

Abstract—Since various opinions are openly discussed on the Web and the inherent growing need to facilitate such discussions, discussion-support systems have been attracting attention. In this regard, human facilitator plays an important role for leading constructive discussions on the Web. However, human facilitation for large-scale online discussions is limited in terms of the available resources. For proper facilitation, it is necessary to understand the content of a discussion to effectively lead the discussion and build consensus. Towards this end, we propose an automated facilitator agent for supporting large-scale online discussions. Specifically, the proposed automated facilitator agent structures online discussions using the issue-based information system in order to make these discussions easy to understand for both humans and intelligent agents. In addition, the proposed automated facilitator agent employs several strategies that encourage participants to conduct discussions appropriately. The experimental results demonstrate the efficiency of the proposed automated facilitator in promoting the progress of large-scale online discussions, and thus enabling open and constructive discussions to be conducted.

Keynote Speaker III

Prof. Md. Atiqur Rahman Ahad
University of Dhaka, Bangladesh; Osaka University, Japan

Md Atiqur Rahman Ahad, SMIEEE; Professor, University of Dhaka (DU); Specially Appointed Associate Professor, Osaka University. He did B.Sc.(Honors) & Masters (DU), Masters (University of New South Wales), PhD (Kyushu Institute of Technology), JSPS Postdoctoral Fellow and Visiting Researcher. He has 3 books (in Springer) and 130+ peer-reviewed papers, 60+ keynote/invited talks, 25+ Awards/Recognitions. He is Editorial Board Member of Scientific Reports, Nature; Frontiers in Computer Science; Encyclopedia of Computer Graphics and Games, Springer; Editor-in-Chief, IJCVSP <http://cennser.org/IJCVSP>; General Chair, 9th ICIEV <http://cennser.org/ICIEV>; 4th IVPR; 2nd ABC <https://abc-research.github.io>, Guest-Editor: Pattern Recognition Letters, Elsevier; JMUI, Springer; JHE, Hindawi; IJICIC; Member: OSA, ACM, IAPR. More: <http://AhadVisionLab.com>.

Topic: "Human Action & Activity Recognition"

Abstract—Vision-based human activity recognition and analysis are very important research areas in computer vision and Human Robot/Machine/Computer Interaction. Over a decade, a good number of methodologies have been proposed in the literature to decipher various challenges regarding action and activity. However, due to various complex dimensions, a number of challenges still remain unexplored. In this keynote speech, various important aspects of human activity recognition and analysis will be covered. The keynote speech will emphasize on interesting and challenging research aspects to explore in future.

Keynote Speaker IV

Prof. Kevin Downard
University of New South Wales, Australia

Kevin Downard conducted his postdoctoral studies and held a subsequent academic position at the Massachusetts Institute of Technology after the award of his PhD degree from the University of Adelaide in Australia. For the past 22 years he has held professorial academic positions in the USA and Australia and is currently appointed in the Faculty of Medicine at the University of New South Wales in Sydney. A focus of his research is improving responses to infectious disease causing pathogens using new diagnostic and therapeutic approaches. He has over published over 100 articles as lead author as well as two books. He is internationally recognized in his field of specialty, mass spectrometry, and has received awards from both the American and British Mass Spectrometry Societies as well as the Australian Academy of Science and the Japan Society for the Promotion of Science. He also holds an Honorary Professorship at Yokohama City University.

Topic: “Studies in Evolutionary Biology Using a New Mass-Based Phylonumerics Approach and Algorithm”

Abstract—Molecular based studies in evolutionary biology have almost exclusively used gene sequence data. A new, numerical mass based protein phylogeny approach, known as phylonumerics, has been developed that employs a purpose built algorithm to build phylogenetic-like trees. These trees are constructed from sets of numerical mass map data from the digestion of an expressed protein, without the need for either gene or protein sequences. Such trees have been shown to be highly congruent with sequence based trees and provide a reliable means to study the evolution history of any organism. Furthermore, single point mutations can be determined from the differences in mass of peptide pairs of different mass sets and displayed along branches across the tree. This presentation will describe the basis of the approach and its application to investigate the evolution of the influenza virus. Frequent ancestral and descendant mutations that precede and follow the manifestation of antiviral resistance mutations in influenza neuraminidase have been identified to establish how strains develop resistance to antiviral drugs. Since such mutations usually impart some cost to viral fitness, the approach also allows co-occurring, or consecutive or near consecutive, epistatic and compensatory mutations important to the survival of the virus to be studied.

Invited Speaker I

Prof. Liao Meisong
Chinese Academy of Sciences, China

Liao Meisong, professor, director of the lab of high power laser components, Shanghai Institute of Optics and Fine Mechanics(SIOM), Chinese Academy of Sciences (CAS). He received his Ph.D from SIOM, CAS in 2007. In 2007-2013, he worked at Toyota Technological Institute in Japan. After then he returned to SIOM. He got the support of CAS hundred talents program and Pujiang talent plan in 2014. He has more than 180 publications in international journals and conferences. His research fields cover specialty fibers, supercontinuum lasers and their applications in biomedical imaging, etc.

Topic: “Supercontinuum Lasers and Their Applications in Biological and Medical Imaging”

Abstract—The Supercontinuum laser is a new type of fiber laser developed based on highly nonlinear photonic crystal fibers and ultrashort pulse laser technology. Supercontinuum lasers have a wide spectral width like a xenon lamp and high brightness and directivity like ordinary lasers. Additionally, they are ultrashort pulsed fiber lasers.

Researchers in the Shanghai Institute of Optics and Fine Mechanics of Chinese Academy of Sciences have mastered the key components and integrated machine technology of supercontinuum lasers. They have developed series all-fiber supercontinuum lasers with superior performance. Some of the key technical indicators are world-leading. Their supercontinuum lasers have been successfully applied in the fields of optical waveguide measurement, optical coherence tomography, and fluorescence lifetime imaging, etc.

Invited Speaker II

Assoc. Prof. Dakun Lai

University of Electronic Science and Technology of China, China

Dr. Lai is currently the director of the Biomedical Imaging and Electrophysiology Lab at the University of Electronic Science and Technology of China (UESTC). He received his Ph.D. in Medical Electronics from Fudan University in 2008. Then he completed a three-year Postdoctoral Associate in Biomedical Engineering at the University of Minnesota, USA. From 2012, he has been on the faculty of the School of Electronic Science and Technology, UESTC, China, where he was appointed as an Associate Professor of Electrical Science and Technology. Dr. Lai is members of IEEE and the Engineering in Medicine and Biology Society, and the member of American Heart Associate. He has served as a peer reviewer of IEEE Transction on Biomedical Egnineering, IEEE ACCESS, and related Chinese Journals. He has publised 30 peer-reviewed papers in Circulation, Physics in Medicine and Biology, IEEE Transcation on Information Technology in Biomedicine etc. and holds 20 Chinese Patents. His research interests and main contributions include computational medicine and deep learning, bioelectedromagnetics and medical applications, automated detection and prediction cardiac/neruo electrical disorder.

Topic: “Automated Detection and Prediction of Serious Cardiac Electrical Disorder by Using Machine Learning”

Abstract—Artificial intelligence has transformed key features of human life. Machine learning is a subset of artificial intelligence in which machines autonomously acquire information by extracting patterns from large databases. It has been progressively used in the medical science and clinical diagnosis especially within the domain of cardiac electrical disorders, such as precise detection of cardiac electrical arrhythmias and further earlier prediction of such serious diseases as sudden cardiac death. Compared with manual analysis and diagnosis in past, it shows great superiority under such current mass clinical bio-signal data, which is promoted by the modern fast communication technology and advanced wearable long-term monitoring systems. Modern machine learning models can automatically identify different electrocardiograms (ECG) with high precision; moreover automatically extract all interested features and clinically significant parameters. Several deep learning models have been developed for the high fidelity detection of common rhythm disturbances as in case of atrial fibrillation and complex arrhythmias. Here, we have highlighted numerous applications of machine learning for prediction and early detection of cardiac electrical disorders. Machine learning algorithms try to develop the model by using all the available input. In future it will be used for more healthcare areas to improve the quality of diagnosis.

Detailed Schedule of Conference

<p>Day 1 October 17, 2019 (Thursday)</p>	10:00-17:00	<p>Venue: 研究棟 11 階講義室 B Lecture Room B, Research Building (11th Floor) Arrival Registration</p>
	<p>Afternoon Conference Venue: 研究棟 11 階講義室 B Lecture Room B, Research Building (11th Floor)</p>	
	13:30-13:35	<p>Opening Remarks Prof. Junichiro Hayano, Nagoya City University, Japan</p>
	13:35-14:15	<p>Keynote Speech I Prof. Andrey Krylov Lomonosov Moscow State University, Russia Topic: “Hybrid Method for Biomedical Image Denoising”</p>
	14:15-14:55	<p>Keynote Speech II Assoc. Prof. Ahmed Moustafa Nagoya Institute of Technology, Japan Topic: “Agent that Facilitates Online Crowd Discussions”</p>
	<p>14:55-15:20 Coffee Break & Group Photo</p>	
	<p>Session 1: 15:20-17:05 Venue: 研究棟 11 階講義室 B Lecture Room B, Research Building (11th Floor) Topic: “Computer Vision and Visualization” 7 presentations</p>	
<p>Day 2 October 18, 2019 (Friday)</p>	<p>Morning Conference Venue: 第 1 会議室 (4th Floor) Meeting Room 1 (4th Floor)</p>	
	09:30-09:35	<p>Opening Remarks Prof. Junichiro Hayano, Nagoya City University, Japan</p>
	09:35-10:15	<p>Keynote Speech III Prof. Md. Atiqur Rahman Ahad University of Dhaka, Bangladesh; Osaka University, Japan Topic: “Human Action & Activity Recognition”</p>
	10:15-10:55	<p>Keynote Speech IV Prof. Kevin Downard University of New South Wales, Australia Topic: “Studies in Evolutionary Biology Using a New Mass-Based Phylonumerics Approach and Algorithm”</p>
	<p>10:55-11:20 Coffee Break & Group Photo</p>	

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Day 2 October 18, 2019 (Friday)	11:20-11:40	Invited Speech I Prof. Liao Meisong Chinese Academy of Sciences, China Topic: “Supercontinuum Lasers and Their Applications in Biological and Medical Imaging”		
	11:40-12:00	Invited Speech II Assoc. Prof. Dakun Lai University of Electronic Science and Technology of China, China Topic: “Automated Detection and Prediction of Serious Cardiac Electrical Disorder by Using Machine Learning”		
	12:00-13:30 Lunch (第 4 會議室 10th Floor) Meeting Room 4 (10th Floor)			
	Afternoon Conference			
	Session 2: 13:30-15:45 Venue: 第 3 會議室 (4th Floor) Meeting Room 3 (4th Floor) Topic: “Biosignal Analysis and Processing” 9 presentations		Session 3: 13:30-15:45 Venue: 第 4 會議室 (10th Floor) Meeting Room 4 (10th Floor) Topic: “Medicine and Rehabilitation Engineering” 9 presentations	
	15:45-16:00 Coffee Break			
	Session 4: 16:00-18:00 Venue: 第 3 會議室 (4th Floor) Meeting Room 3 (4th Floor) Topic: “Medical Image Processing Technology and Methods” 8 presentations		Session 5: 16:00-17:45 Venue: 第 4 會議室 (10th Floor) Meeting Room 4 (10th Floor) Topic: “Molecular Biology and Epidemiology” 7 presentations	
	18:00-18:30	Poster Session		
	18:30-20:00 Dinner (Sakra Side Terrace, 1st Floor of West Building)			
	Day 3 October 19, 2019 (Saturday)	8:00-19:00 Academic Visit		

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

Session 1

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

Afternoon, October 17, 2019 (Thursday)

Time: 15:20-17:05

Venue: 研究棟11階講義室B

Lecture Room B, Research Building (11th Floor)

Topic: “Computer Vision and Visualization”

Session Chair: Assoc. Prof. Dakun Lai

<p>N2001 Session 1 Presentation 1 (15:20-15:35)</p>	<p>Assessing the Efficacy of the Dynamic Eye Misalignment Retroversion System (DEMRS) Prototype with Normal and Strabismus Subjects Constantinos M. Glynos, Michael C. Glynos, Olusola O. Aina and Hammadi Nait-Charif Bournemouth University, UK</p> <p><i>Abstract</i>—Strabismus is a medical term used to define eye misalignment conditions that prevent both eyes from focusing on the same target simultaneously. Apart from having an aesthetic impact on the subject, strabismus is a disability that prohibits the correct perception of depth. The purpose of going through treatment is to realign the “bad” (strabismic) eye, so that it fixates on the same target as the “good” (dominant) eye. This paper presents the clinical evaluation of the prototype of a novel system, called Dynamic Eye Misalignment Retroversion System (DEMRS), which adjusts the light rays such that both eyes are stimulated by the correct target, simultaneously at various distances and directions. Clinical evaluation experiments were conducted under lab conditions, using subjects with normal vision and strabismus, between the age of 8 and 98 years. Without using the DEMRS, 50:4% of the test cases, showed successful binocular fusion. When the DEMRS was used, 88:8% of the test cases showed successful binocular fusion. The results indicate that the DEMRS is able to restore successfully the correct perception of depth, through binocular vision, for young children, adults and elders.</p>
	<p>Limited-Angle Low-Dose CT Image Denoising Using Wide Residual Network Li-Sheng Chang, Chia-Jui Hsieh, Siang-Cing Jhang and Jyh-Cheng Chen National Yang-Ming University, Taiwan</p>

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<p>N3001 Session 1 Presentation 2 (15:35-15:50)</p>	<p><i>Abstract</i>—Dose reduction of the computed tomography (CT) has become a serious issue in the recent radiological studies. In dental digital tomosynthesis (DTS), reconstruction from limited-angle scanning would lead to significant noise and artifacts. In this study, we construct and validate an image denoising method for limited-angle low-dose CT or DTS images. For the training process, normal-dose DTS (NDDTS) and low-dose DTS (LDDTS) images of human teeth were acquired. We collected the real data with angular coverage of scanning from -60 to 60 degrees, with a sampling interval of one degree as limited-angle data. We also segmented each slice into small patches for training and modified wide residual network (WRN) for image denoising task. For the streak artifacts reduction, noise reduction, visualization of the tooth structure, our denoising LDDTS images showed significantly better image quality than those of NDDTS images in terms of signal-to-noise ratio (SNR), contrast-to-noise ratio (CNR), and artifact index as quantitative results. In this work, we trained a modified WRN as an image denoising method for limited-angle LDDTS images. The performance evaluation of the results by the visual inspection as well as quantitative measurements shows that our proposed method is comparable to other main stream networks on image denoising.</p>
<p>N2015 Session 1 Presentation 3 (15:50-16:05)</p>	<p>Prediction of 3D Body Parts from Face Shape and Anthropometric Measurements Alessio Gallucci, Dmitry Znamenskiy and Milan Petkovic Eindhoven University of Technology, Netherlands</p> <p><i>Abstract</i>—While 3D body models have been vastly studied in the last decade, acquiring accurate models from the sparse information about the subject and few computational resources is still a main open challenge. In this paper, we propose a methodology for finding the most relevant anthropometric measurements and facial shape features for the prediction of the shape of an arbitrary segmented body part. For the evaluation, we selected 12 features that are easy to obtain or measure including age, gender, weight and height; and augmented them with shape parameters extracted from 3D facial scans. For each subset of features, with and without facial parameters, we predicted the shape of 5 segmented body parts using linear and non-linear regression models. The results show that the modeling approach is effective and giving sub cm reconstruction accuracy. Moreover, adding face shape features always significantly improves the prediction.</p>
	<p>The Development of a Gait Speed Detection System for Older Adults Using Video-Based Processing Teerawat Kamnardsiri, Pattaraporn Khuwuthyakorn and Sirinun Boripuntakul Chiang Mai University, Thailand</p>

<p>N3004 Session 1 Presentation 4 (16:05-16:20)</p>	<p><i>Abstract</i>—This study aimed to develop the gait speed detection system for measuring the instantaneous walking speed of older adults. The proposed system employed a standard camera 60 Hz and fixed on a tripod with 3-way head to collect the body motion. Besides, the proposed system was to assess the validity of instantaneous horizontal speed with the three-dimension motion analysis system. The cross-sectional study was used to design in this study. The proposed system consists of ten steps, which are: (1) Input video, (2) Extraction frames, (3) Calibration of a camera and the capture volume, (4) Colour detection and filling into the body, (5) The human body region detection, (6) Filtering of the foreground regions from image difference, (7) Centroid of the human body detection, (8) Identification of the human body position, (9) Feature tracking of the human speed and (10) Estimation of the human speed. The proposed system employed MATLAB (2015a) with the Computer Vision Toolbox and the Image Processing Toolbox for developing and testing. The fifteen older adults with mean age 67 (SD = 4.19) years performed three walking conditions that comprises: 1) walking at a slow speed, 2) walking at usual speed, and 3) walking at a fast speed. Besides, participants walked along a 10-metre walkway in the motion capture laboratory room. The results demonstrate that the proposed system measures have an excellent correlation with the motion analysis system measures, with correlation coefficients between 0.936 and 0.987. Hence, the proposed system is to be one of the useful tools for assessing instantaneous walking speed among older adults in both clinical and community settings.</p>
<p>N2011 Session 1 Presentation 5 (16:20-16:35)</p>	<p>Automatic Detection of Mediastinal Lymph Nodes Using 3D Convolutional Neural Network May Phu Paing, Chuchart Pintavirooj, Supan Tungjitkusolmun, Kyi Pyar Win, Kazuhiko Hamamoto King Mongkut’s Institute of Technology Ladkrabang, Thailand</p> <p><i>Abstract</i>—Mediastinal lymph nodes are one of the most critical factors to identify the clinical stages of lung cancer. As the lymph nodes are low in attenuation and cluttering with various shapes and sizes, manual detection is usually error-prone and effort-intensive. This paper introduces a method for automatic detection of mediastinal lymph nodes by proposing three significant contributions. First, we constraint the detection area, mediastinal region, using grey-level thresholding. Next, we apply the watershed method and hessian eigenvalues to separate a cluster of lymph nodes. Finally, we build a three-dimensional convolutional neural network (3D CNN) to distinguish the actual lymph nodes from other false lesions. Our experiment is conducted using 70 CT exams containing 314 lymph nodes and achieved a favourable result with 94 % detection rate.</p>
	<p>Gastric Polyp Detection Using Deep Convolutional Neural Network Mayank Laddha, Siddharth Jindal and Jakub Wojciechowski</p>

<p>N2017 Session 1 Presentation 6 (16:35-16:50)</p>	<p>DAIICT, India</p> <p><i>Abstract</i>—Certain types of gastric polyps may increase the risk of stomach cancer. With recent progress in computer vision due to deep learning, it is possible to reduce the gastric polyp miss rate, leading to a better and more accurate endoscopy. Automating the process of gastric polyp detection is a complex task as polyps differ in terms of size, shape and texture. Yolov3 is a fast and accurate object detection algorithm. In this paper, yolov3 is used for polyp detection. The results show that yolov3 used for gastric polyp detection can achieve a mean average precision (mAP) of 0.91. Also, yolov3-tiny, a smaller and faster version achieves a mean average precision (mAP) of 0.82 and gives more than 100 fps on Pascal Titan X GPU. This can help endoscopic physicians increase productivity.</p>
<p>N2004 Session 1 Presentation 7 (16:50-17:05)</p>	<p>Cervical Cancer Detection and Classification from Pap Smear Images Kyi Pyar Win, Yuttana Kitjaidure, May Phyu Paing and Kazuhiko Hamamoto Mongkut's Institute of Technology Ladkrabang, Thailand</p> <p><i>Abstract</i>—In this paper, we propose a framework for detection and classification of cervical cancer from pap smear images. Early detection and accurate diagnosis of cervical cancer can reduce the death rate of cervical cancer patients. Pap smear or pap test is the most popular technique for early detection of cervical cancer. However, the manual analysis is labor intensive and time consuming process which relies on expert cytologist. Hence, it is needed to develop a computer aided diagnosis system to make the pap smear test more accurate and reliable. The objective of this paper is to present an innovative idea of applying random forest algorithm (RF) as a feature selection method using proposed bagging ensemble classifier for improving the predictive performance. The four basic steps of cervical cancer detection and classification system, image enhancement, segmentation, feature extraction and classification were used. K-means clustering combining with morphology operations obtained good segmentation for cell nuclei and cytoplasm. The most important features, shape, color and texture of nuclei and cytoplasm were applied to detect cervical cancer. To improve the accuracy of prediction results, random forest (RF) algorithm was used as a feature selection method. In classification stage, bagging ensemble classifier was applied which aggregated the results of five classifiers, linear discriminant (LD), support vector machine (SVM), weighted k-nearest neighbor (KNN), boosted trees and bagged trees. Herlev data set was used to prove the effectiveness of our proposed method. According to the experimental results, the high classification accuracy was achieved with top10 features using our proposed combined classifier. The accuracy was 97.83% in two class problem and 81.54 % in seven</p>

	<p>class problem. When the results were compared with five classifiers, our proposed method was significantly better in two class and seven class problems.</p>
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Session 2

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

Afternoon, October 18, 2019 (Friday)

Time: 13:30-15:45

Venue: 第3会議室 (4th Floor)

Meeting Room 3 (4th Floor)

Topic: “Biosignal Analysis and Processing”

Session Chair: Prof. Md. Atiqur Rahman Ahad

<p>N2006 Session 2 Presentation 1 (13:30-13:45)</p>	<p>Comparison of Arousal Effect by Beverage Intake in Drowsy Driving Simulation Makoto Murakami, Haruki Kawanaka and Koji Oguri Aichi Prefectural University, Japan</p> <p><i>Abstract</i>—Various studies have been conducted toward the reduction of drowsy driving, which is one of the causes of traffic fatalities. Beverage intake is said to be effective in controlling sleepiness, and general drivers often use a coffee beverage to wake up sleepiness. In this study, we examined the arousal effect of three kinds of beverages (lemon, sugar-free coffee, water) using a driving simulator. As a result of analyzing biological signals and vehicle operation information while driving, it was found that intake of lemon beverage in lowering arousal was equivalent to intake of sugar-free coffee. This suggested the effectiveness of the lemon beverage intake as a measure against drowsy driving.</p>
<p>N2032 Session 2 Presentation 2 (13:45-14:00)</p>	<p>Spatial Mapping and Feature Analysis for Individual Finger Movements Using High Density Electromyography: Preliminary Study Prabhav Mehra, Manya Dave, Ahsan Khan and Raymond Tong The Chinese University of Hong Kong, Hong Kong</p> <p><i>Abstract</i>—The analysis between finger movements has always been an important aspect of biophysics and rehabilitation. In our paper, we aim to study the distinctive muscle activities between finger movements through the help of High-Density Electromyographic (EMG) signals for increased myoelectric control of soft robotic hand. A task of pressing button with each finger for 5 seconds and 15 repetitions was performed by 5 healthy subjects. The signals generated was recorded by 64-channel EMG electrode patch at 2048</p>

	<p>Hz. Raw, single differential and double differential EMG signals across the 2D array was analyzed. Spatial image of these signals for the 4 different finger movement demonstrated multiple distinctive properties, the major distinction for ring finger was top-left array demonstrated higher activity for both raw and differential signal while fourth finger distinctive map showcased very low muscle activity in the left side of the array. Index finger also demonstrated distinctive maps where in raw signals lower half of diagonal across electrode coordinate (1, 8) to (4, 1) had higher activity with respect to other half whereas second finger showed much more equally spread intensity across spatial map from electrodes 1 to 40. A feature set of six distinct feature was also calculated for the array of EMG signals for further quantitative differentiation between movements. Centroid of these feature set acquired different place in the 3D space indicating differences in the finger movements. Analysis of HD-EMG signal during different finger movement indicated that the data thus acquired could be used for differentiating the finger movements and could be used as a method for classification algorithm for increased myoelectric finger control in the future.</p>
<p>N2007 Session 2 Presentation 3 (14:00-14:15)</p>	<p>A New Simple Approach Signal Analysis Suitable for Non-Contact Vital Sensing Using Doppler Sensor Naruya Inagaki, Takahiro Sasaki and Yukihiro Kamiya Aichi Prefectural University, Japan</p> <p><i>Abstract</i>—Recently, health management services by the Internet of things (IoT) has attracted attentions. If it can continuously measure and record respirations and heartbeats in our daily life, it enables us to detect health problems in its early stage. In the implementation of IoT, the sensor nodes often suffer from the limitation of the bandwidth of wireless links. Thus, it is impossible to send all the data captured by the sensor node. In order to avoid this problem, edge computing is applicable to the IoT systems. In this implementation, the data is processed in the sensor node to transmit the result of the data processing so that the data speed is reduced. However, the edge computing causes another problem, the increase of the power consumption at the sensor node. Since it is driven by a battery, the increase of the power consumption results in the shortage of the battery. Eventually, the edge computing with reduced power consumption is required in the realization of IoT. In this paper, we propose a new simple algorithm for data analysis suitable for the edge computing in IoT systems due to its simplicity. The performance is verified through computer simulations.</p>

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<p>N0025 Session 2 Presentation 4 (14:15-14:30)</p>	<p>Effect of Spike-Wave Discharges on Brain Areas of Learning and Memory Using Spatial Learning Task Yu-Hsing Huang and Fu-Zen Shaw National Cheng Kung University Tainan, Taiwan</p> <p><i>Abstract</i>—There is still lacking a systematic study to investigate possible neural network on effect of spike-wave discharge (SWDs) on accuracy of cognitive behavioral paradigm in both learning and retrieval phases. The present study aimed to explore possible networks of the sensation, execution, and learning and memory between SWDs and cognitive performance. This study used T maze with regard to reversal association between the self-referential vibrissae site and food palette as a reversal spatial association task (RSAT). Experiment 1 showed that the rat group under the condition of no SWD reached accuracy of ~100% at the end of 8-day learning phase of a RSAT. Experiment 2 of somatosensory evoked potentials (SEPs) were executed showed extremely different waveforms of somatosensory evoked potential (SEP) in the primary somatosensory cortex under conditions of SWDs or no SWD. According to these results, the present study suggests a possible brain network for cognitive processing under SWDs.</p>
<p>N2008 Session 2 Presentation 5 (14:30-14:45)</p>	<p>A Novel Period Estimation Method for Periodic Signals Suitable for Vital Sensing Ritsuki Kokubo and Yukihiro Kamiya Aichi Prefectural University, Japan</p> <p><i>Abstract</i>—The Internet of Things (IoT) has been widely used in care facilities such as hospitals and nursing homes. These facilities make efficiently health management of its patient or the elderly by monitoring vital signs using the IoT. The non-contact vital sensing is particularly interesting as a measuring method for monitoring since it does not need electrodes. It enables us to release patients from constraints by cables and electrodes. The Doppler sensor is a mean of the non-contact vital sensing. We can detect respirations and heart beats by the electro-magnetic wave. Considering the non-contact vital sensing using the Doppler sensor, there are two problems. First, vital signs obtained by the Doppler sensor is often noisy. Therefore, the signal processing algorithm must be robust against noisy vital signs. Second, the frequency of vital signs is typically very low such like less than 1 Hz. It is well-known that the fast Fourier transform (FFT) suffer from low resolution in such very low frequency band. In this paper, we propose a new signal parameter estimation algorithm which is robust against the noise while it achieves high resolution in the low frequency band. The performance of the proposed method is provided in this paper.</p>

<p>N0023 Session 2 Presentation 6 (14:45-15:00)</p>	<p>Effect of Spike-Wave Discharges on Brain Areas of Learning and Memory Using Spatial Learning Task Yu-Hsing Huang and Fu-Zen Shaw National Cheng Kung University Tainan, Taiwan</p> <p><i>Abstract</i>—There is still lacking a systematic study to investigate possible neural network on effect of spike-wave discharge (SWDs) on accuracy of cognitive behavioral paradigm in both learning and retrieval phases. The present study aimed to explore possible networks of the sensation, execution, and learning and memory between SWDs and cognitive performance. This study used T maze with regard to reversal association between the self-referential vibrissae site and food palette as a reversal spatial association task (RSAT). Experiment 1 showed that the rat group under the condition of no SWD reached accuracy of ~100% at the end of 8-day learning phase of a RSAT. Experiment 2 of somatosensory evoked potentials (SEPs) were executed showed extremely different waveforms of somatosensory evoked potential (SEP) in the primary somatosensory cortex under conditions of SWDs or no SWD. According to these results, the present study suggests a possible brain network for cognitive processing under SWDs.</p>
<p>N2030 Session 2 Presentation 7 (15:00-15:15)</p>	<p>NR-GAN: Noise Reduction GAN for Mice Electroencephalogram Signals Yuki Sumiya, Kazumasa Horie, Hiroaki Shiokawa and Hiroyuki Kitagawa University of Tsukuba, Japan</p> <p><i>Abstract</i>—To support basic sleep research, several automated sleep stage scoring methods for mice have been proposed. Although these methods can score mice sleep stages accurately based on their electroencephalogram (EEG) and electromyogram (EMG) signals, they are fragile against noise, especially in EEG signals. The simplest solution is to reduce or eliminate noise before scoring. However, a method for reducing noise in biological signals does not exist. Because EEG signals contain many types of noise, predicting all of them is difficult, which inhibits the use of hand-engineered methods such as frequency filters. Additionally, noise reduction methods with deep learning models are not applicable as they require records of noise, and the noise considered here cannot be measured separately from biological signals. In this study, we address this problem using adversarial training, which is a method for deep learning models that does not require noise records as training samples. We propose a new noise-reduction model called “NR-GAN.” Its training process requires a set of noisy signals and a set of clear signals. Since these sets can be measured independently, NR-GAN can reduce noise in</p>

	mice EEG signals.
N2033 Session 2 Presentation 8 (15:15-15:30)	<p>Multicollinearity Analysis for Cuffless Blood Pressure Estimation Regression Algorithms Prabhav Mehra, Rajee Gupta, Abhishek Mahajan and Veeky Baths Birla Institute of Technology and Science, India</p> <p><i>Abstract</i>—The estimation of blood pressure in a cuffless manner has been a major study of interest for past decade. Blood Pressure has shown significant correlation with features derived from PPG and ECG signals; this has led to development of multiple regression algorithm for estimating blood pressure using the derived features. The aim of our study is to analyze the existence of multicollinearity in multivariable regression algorithms proposed by earlier studies. Continuous bio-signals constituting Arterial Blood Pressure (ABP), PPG and ECG of 240 minutes length for 250 subjects was collected from MIMIC-III database. Six different features including pulse transit time and heart rate was extracted from the data and subjected to multicollinearity analysis using variation inflation factor and correlation coefficient. Very high multicollinearity was observed for algorithms with more than 2 independent variables indicating that such algorithms suffer from inherent problem and could lead to unstable regression coefficients and algorithm. Principal Component Analysis is proposed in our study to tackle the problem of multicollinearity in blood pressure estimation algorithm. This method would remove the dangers of multicollinearity without any loss of information from features. Further analysis showed that top half of the principal components explained more than 90.0% of the feature variance. Thereby it was concluded that multivariable regression algorithms for blood pressure estimation suffer from multicollinearity and this needs to be addressed before developing an algorithm.</p>
N2034 Session 2 Presentation 9 (15:30-15:45)	<p>Analysis of Needle Electromyography Signal in Neuropathy and Myopathy Conditions Using Tunable-Q Wavelet Transform Lakshmi M. Hari, S. Edward Jero, G. Venugopal and S. Ramakrishnan Indian Institute of Technology Madras, India</p> <p><i>Abstract</i>—Analysis of needle electromyography signal is used for the differentiation of neuropathy and myopathy condition from the normal. Amplitude based features such as root mean square and mean absolute value are used to differentiate between normal and pathological signals. Tunable-Q wavelet transform is used to decompose the frequency bands of the signal. Further, the same set of features are used to analyse each frequency bands. The results show that the proposed approach is able to distinguish between normal and</p>

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	<p>different pathological electromyography signals better than the conventional time domain analysis. It is also observed that myopathy and neuropathy signals are comprised of high frequency components than low frequency components as compared to normal signal. The proposed method yields a higher significance with a p-value <0.05 between normal and each pathological signal such as neuropathy and myopathy.</p>
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Session 3

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

Afternoon, October 18, 2019 (Friday)

Time: 13:30-15:45

Venue: 第4會議室 (10th Floor)

Meeting Room 4 (10th Floor)

Topic: “Medicine and Rehabilitation Engineering”

Session Chair: Prof. Itaru Kaneko

<p>N0005 Session 3 Presentation 1 (13:30-13:45)</p>	<p>Prediction of Hepatic Steatosis (Fatty Liver) Using Machine Learning Ridhi Deo and Suranjan Panigrahi Purdue University, USA</p> <p><i>Abstract</i>—The exact reasons of the incidences of fatty liver disease (Hepatic Steatosis, HS) are not known. Heavy alcohol use leads to alcoholic steatohepatitis (alcoholic fatty liver disease). Contrarily, Non-alcoholic fatty liver disease (NAFLD), is a condition of fat build-up in the liver when alcohol consumption is not the cause. However, certain clinical and demographic factors impact the incidence of HS. We evaluated the predictive capability of fatty liver using a computational model and NHANES-III data. Six predictor variables (age, gender, BMI, triglycerides, HDL, and total cholesterol) and one output variable (HS) were used. The challenge of class imbalanced data was handled using SMOTE algorithm combined with Gower’s distance. Data were divided into training and test in 70:30 ratio with 8,903 and 3,816 observations respectively. Three families of models were trained: SVM (Fine and Medium Gaussian SVM), Bagged Trees, Boosted Tree (Gentle and ADA Boosted Tree). 10-fold cross-validation was used. Of the five models, ‘Gentle Boosted Tree’ model provided the highest average testing accuracy of 79.03% (79%). The average sensitivity, specificity, and AUC of the ‘Gentle Boosted Tree’ model were 75.88%, 81.86% and 0.79 respectively. The novelty of this paper lies in developing and testing algorithms with imbalanced data for prediction of fatty liver condition.</p>
	<p>The Tent-Type Clean Unit System Platform for Air Cleaning and Non-Contact Sleep Assessment Tsung-Hao Hsieh, Sheng-Fu Liang, Akira Ishibashi, Yong Song Liu</p>

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<p>N0022 Session 3 Presentation 2 (13:45-14:00)</p>	<p>and Masahiro Yasutake National Cheng Kung University, Taiwan</p> <p><i>Abstract</i>—Sleep is important to maintain human’s physiological and psychological well-being. The quality is often affected by many environmental factors, such as air dust, temperature and noise. This paper proposes a tent-type clean unit system platform (T-CUSP) to construct a high air quality sleep environment. In this approximate independent-system, the feasibility of non-contact sleep monitoring method based on gas-molecule and air-particle analysis would be evaluated. In this paper, 7 overnight sleep experiments were performed with simultaneous recording of mini PSG (EEG, EOG, and EMG) for sleep staging and actigraph for body movement. The air quality was monitored by the particle counter and fluctuation of air-borne particle. The average concentrations of PM2.5, PM10, and CO2 in the T-CUSP during sleep were $4.85\pm 3.2 \mu\text{g}/\text{m}^3$, $8.43\pm 4.5 \mu\text{g}/\text{m}^3$, and $1122\pm 128 \text{ ppm}$, respectively. The air-quality of T-CUSP conform to the agreed limits in US and EU. Furthermore, the fluctuation of CO2 can reflect the behavior of subjects. 91% of CO2 rising epochs were accompanied by a significant body movement and could be identified as the "wake" stage. The short experimental results demonstrate the feasibility of constructing an air-clean environment with non-contact sleep assessment to support healthy sleep.</p>
<p>N2003 Session 3 Presentation 3 (14:00-14:15)</p>	<p>On the Privacy of Genomic Big Data and HER Standardization and Regulation Itaru Kaneko and Emi Yuda Nagoya City University, Japan</p> <p><i>Abstract</i>—In this paper, we will first summarize recent situations of Genomic Information and Electronic Health Data (EHR). Firstly, we look at the standardization of Genomic information representation. Then summarize regulations in various countries on the privacy of medical and health information. And at the end, we will also discuss the possible technologies and social practices to empower the privacy of genomic information.</p>
	<p>Fluorobenzene Functionalized Lysosome-Retained Probe Design Strategy for Sequential Cell Tracking and Cancer Metastasis Visualization Jinrong Zheng and Haiyan Chen China Pharmaceutical University, China</p> <p><i>Abstract</i>—Precise and efficient strategies for organelle-targeted delivery contribute to the design of subcellular-controlled drugs and probes. This improves the therapeutic efficacy and reflects the</p>

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<p>N2023 Session 3 Presentation 4 (14:15-14:30)</p>	<p>physiopathology state of cells. Therefore, more organelle targeting strategies and their applications need to be explored. In this study, we found fluorobenzene groups could be delivery and retained to lysosomes, hence a molecule design strategy to achieve lysosome targetable and its mechanism are reported. Based on this discovery, a sequential living cell tracking technique has been developed to image cancer metastasis. Confocal imaging showed that the dyes contain a fluorobenzene group could aggregate in lysosomes of various cells and tissues with excellent spatiotemporal resolution. Cellular metabolite analysis of pentafluorobenzene-coupled -hemicyanine (Hcy-5F) by HRMS revealed that Hcy-5F could conjugate with GSH, the targeting ability was attenuated by GSH elimination and restored by supply recovery. Interestingly, confocal imaging showed Hcy-5F process the efficient cellular labeling and tracking ability due to enter lysosomes with steady optical properties and excellent retention toughness (>24h). It was successfully imaging various cancer cells metastasis pathway. Thus fluorobenzene-GSH conjugate based molecular design strategy is a flexible tool for lysosome-specific cargo delivery and will be useful to track cells in vitro and in vivo.</p>
<p>N0024 Session 3 Presentation 5 (14:30-14:45)</p>	<p>Development and Validation of Alpha Neurofeedback Training in Rats Wen-Hsiu Yeh, Sheng-Fu Liang, Yu-Hsuan Shih, Wei-Cheng Lu, Chun-Yu Lin and Fu-Zen Shaw National Cheng Kung University, Taiwan</p> <p><i>Abstract</i>—Neurofeedback training (NFT) of the alpha activity at frontoparietal region is associated with the intelligence or memory of healthy subjects. Alpha NFT has been used for several decades but is still unclear regarding its effects on memory in human. In this study, an alpha NFT system was developed for rat models and then verified the changes of alpha activity of the frontoparietal region during NFT. Ten adult Sprague-Dawley rats were randomly allocated into a group not receiving alpha bandwidth amplitude (Sham) or a group receiving a 9-15 Hz amplitude (Alpha). Three NFT sessions per week were conducted for 4 weeks followed by a frontoparietal region electrocochleography (ECoG) recording. Working memory was assessed by an alternative task. Episodic and recognition memory were assessed by visual discrimination task. The Sham group had no change in all indexes. In a sharp contrast, the Alpha group exhibited significant increase ($p<0.05$) in mean relative alpha amplitude, total alpha duration, 10-11 Hz power spectrum and all memory indexes. The current data provided supporting evidence for rat's alpha trainability by using the developed training system. Further, intracerebroventricular (ICV) will be moved into the rat's brain areas to investigate the mechanism of alpha activity on memory.</p>

<p>N2024 Session 3 Presentation 6 (14:45-15:00)</p>	<p>Mitochondrial Membrane Anchored Photosensitive Nano-Device for Lipid Hydroperoxides Burst and Inducing Ferroptosis to Surmount Therapy-Resistant Cancer Mangmang Sang and Wenyuan Liu China Pharmaceutical University, China</p> <p><i>Abstract</i>—Ferroptosis is a regulated process of cell death caused by iron-dependent accumulation of lipid hydroperoxides (LPO). It is sensitive to epithelial-to-mesenchymal transition (EMT) cells, a well-known therapy-resistant state of cancer. Previous studies on nanomaterials did not investigate the immense value of ferroptosis therapy (FT) in epithelial cell carcinoma during EMT. Herein, the mitochondrial membrane anchored oxidation/reduction response and Fenton-Reaction-Accelerable magnetic nanophotosensitizer complex self-assemblies loading sorafenib (CSO-SS-Cy7-Hex/SPION/Srfn) were constructed in this study for LPO produced to overcome the therapy-resistant state of cancer. The nano-device enriched the tumor sites by magnetic targeting and disassembled by the redox response under high levels of ROS and GSH in FT cells. Superparamagnetic iron oxide nanoparticles (SPION) released Fe²⁺ and Fe³⁺ in the acidic environment of lysosomes, and the NIR photosensitizer Cy7-Hex anchored to the mitochondrial membrane, combined sorafenib (Srfn) leading to LPO burst, which was accumulated ~18-fold of treatment group in breast cancer cells. In vivo pharmacodynamic test results showed that this nanodevice with small particle size and high cytotoxicity increased Srfn circulation and shortened the period of epithelial cancer treatment. Ferroptosis therapy had a successful effect on EMT cells. These findings have great potential in the treatment of therapy-resistant epithelial cell carcinomas.</p>
<p>N2010 Session 3 Presentation 7 (15:00-15:15)</p>	<p>Considerations on Designing on Optical Probe for Endoral 3D Teeth Contouring Carmine Pappalettere, Claudia Barile, Caterina Casavola, Claudia Cianci, Luciano Lamberti, Vincenzo Moramarco and Giovanni Pappalettera Politecnico di Bari, Italy</p> <p><i>Abstract</i>—Study cast is a typical and powerful tool in prosthodontics whose practical realization still relies on uncomfortable and completely manual procedures. In this paper the possibility to use an optical method to perform this task is discussed. Based on this approach, in fact, it would be possible to get 3D reconstruction of the shape of the tooth without contact and without inserting any material inside the mouth of the patients. Different approaches are possible whose specific limitations and point of strength will be discussed</p>

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	<p>based on some experimental evidences. The best approach will be selected as well and it will be developed in order to achieve the required measurement targets. In particular, it will be discussed how to afford the issues of high slopes and how to miniaturize the required optical elements. A procedure to stabilize the phase of the signal will be also proposed. This is necessary because insertion of the probe in the oral cavity changes the refraction index of the fiber optics used inside the probe. The paper will also show a simple calibration procedure and, based on that, final results in terms of final accuracy will be discussed also by comparison with measurement obtained by contact probe machines.</p>
<p>N1005 Session 3 Presentation 8 (15:15-15:30)</p>	<p>Validity of a Speed Detection System for Measuring Gait Speed in Community-Dwelling Older Adults Sirinun Boripuntakul, Kanyapat Panjaroen, Kamolchanok Kormkaew, Prachya Yawisit and Teerawat Kamnardsiri Chiang Mai University, Thailand</p> <p><i>Abstract</i>—The objective of this study was to examine the concurrent validity of a speed detection system for measuring gait speed in healthy community-dwelling older adults. The participants comprised 15 healthy older adults with a mean age 67.00 ± 4.19 years. Participants walked over six-metre walkway at slow, usual, and fast paces. Two trials at each walking speed were performed. The gait speed for all walking conditions was measured concurrently with the motion analysis system. Pearson’s correlation coefficient was used to determine the correlation between the two systems with the significance level at $p < 0.05$. The results show that speed detection system measures have a good correlation with motion analysis system measures, with correlation coefficients between 0.975 and 0.980. Therefore, a speed detection system is proposed to be one of the useful methods to assess gait speed among older adults in both clinical and community settings.</p>
<p>N2005 Session 3 Presentation 9 (15:30-15:45)</p>	<p>Automatic Detection of Calcified Plaques in a OCT Pullback Using Convolutional Neural Network Chunliu He, Yifan Yin and Zhiyong Li Southeast University, China</p> <p><i>Abstract</i>—Coronary artery calcification is a well-known marker of atherosclerotic plaque burden. High-resolution intravascular optical coherence tomography (OCT) imaging has shown the potential to characterize the details of coronary calcification in vivo. In routine clinical practice, it is a time-consuming and laborious task for clinicians to review the over 250 images in a single pullback. Besides, the imbalance label distribution within the entire pullbacks is another problem, which could lead to the failure of the classifier</p>

	<p>model. In this study, we used a customized CNN architecture which differs from those pre-trained network. The implementation of the algorithm needs two steps. First, we initially constructed our training data set so that all labels were equal by random minority oversampling. Then, we used original imbalance training data set to re-train only the output layer of the network and kept the kernels of all the other layers fixed. Area under the receiver operating characteristic curve (ROC AUC) was used as evaluation metric since accuracy was difficult to quantify the result for the imbalance data. The obtained results showed that the algorithm is fast and effective to classify the calcified plaques with imbalance label distribution in each pullback.</p>
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15:45-16:00

Coffee Break

Session 4

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

Afternoon, October 18, 2019 (Friday)

Time: 16:00-18:00

Venue: 第3会議室 (4th Floor)

Meeting Room 3 (4th Floor)

Topic: “Medical Image Processing Technology and Methods”

Session Chair: Prof. Andrey Krylov

<p>N3002 Session 4 Presentation 1 (16:00-16:15)</p>	<p>Detection of Noise in ECG Signals Using Analog Behavioral Modeling for Read-out Circuit Sagar B H, Vishal N Awasthi, Vinay K S and Shashidhar Tantry PES University, India</p> <p><i>Abstract</i>—In VLSI technology, there is a huge demand for low voltage, low noise and high gain readout circuits for biomedical acquisition sensors. As biomedical signals pose problems in processing where a low voltage signal coupled with noise is to be detected, the design of low noise amplifier is critical. Signal processing and data analysis are commonly used methods in a biomedical signal processing engineering. This paper describes development of read-out circuit on electrocardiogram (ECG) signal to detect noise. Designed filters are focused on removing supply network 50 Hz frequency and breathing muscle artifacts. Moreover, this paper contains description of the read-out circuits which are described in Verilog-A which removes most of the noise in ECG and thereby increasing the SNR significantly. By using Verilog-A, we can describe the circuit in terms of its behavioral characteristics. Analog/Behavioural modeling helps designers to capture high-level behavioral descriptions of components in a precise set of mathematical terms. Noise modeling is complex in nature in terms of mathematical expressions, we use Analog Modeling to incorporate that mathematical analysis to circuit simulations.</p>
	<p>A Novel Lesion Segmentation Method Based on Breast Ultrasound Images Xiaoyan Shen, Jiaxin Liu, Hong Li, Hang Sun and He Ma Northeastern University, China</p> <p><i>Abstract</i>—Lesion segmentation is a critical step in computer-aided</p>

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<p>N2002 Session 4 Presentation 2 (16:15-16:30)</p>	<p>diagnostic(CAD) systems based on breast cancer imaging. Accurate segmentation directly affects the final determination of the nature of lesion. However, due to the low quality of ultrasound (US) images, lesion segmentation based on US images of breast is challenging. This paper presents an improved marker watershed algorithm for lesion segmentation of breast US images. It uses the efficient and fast curvature filtering(CF) and Gaussian enhancement method to pre-process the image, then creates the segmentation function through Newton filter based on computing gradient of the image, then compares it with the labeling function obtained by binarizing the image to get the most similar parts of them. The intersection is used as the input of the marked watershed(mw) algorithm, and then the candidate boundary is obtained. Finally, the final boundary is determined by maximizing the average radial derivative(ARD) function. The novel method was tested with 400 sets of US images and quantified by using both area and contour error metrics. The result shows that our method can extract the relatively accurate lesion region effectively and efficiently and solves the problem of over-segmentation of the watershed algorithm to some extent. Especially for the segmentation of tumors with internal calcification points or blurred boundaries, it shows better performance.</p>
<p>N2012 Session 4 Presentation 3 (16:30-16:45)</p>	<p>Enhancement Algorithms for Blinking Fluorescence Imaging Yakov Pchelintsev, Andrey Nasonov, Andrey Krylov, Sawako Enoki and Yasushi Okada Lomonosov Moscow State University, Russia</p> <p><i>Abstract</i>—A probabilistic approach for super-resolution of blinking fluorescence microscopy was suggested. Its performance was compared with modern blinking fluorescence image enhancement algorithms, namely SOFI, MUSICAL and SPARCOM in different conditions. The comparison was performed using both synthetic and real experimental data.</p>
	<p>Suggestions of a Deep Learning Based Automatic Text Annotation System for Agricultural Sites Using GoogLeNet Inception and MS-COCO Shinji Kawakura and Ryosuke Shibasaki The University of Tokyo, Japan</p> <p><i>Abstract</i>—Image recognition methodologies for use by agricultural (agri-) workers, managers, technicians, researchers, and unliving targets (e.g., harvests, agri-tools) have attracted significant interest. Currently, the most common approaches use various real-time visual analyses and recorded data-based analyses at outdoor and indoor agri-sites. However, recent artificial intelligence (AI)-based studies have proposed diverse automatic camera-based awareness systems</p>

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<p>N3003 Session 4 Presentation 4 (16:45-17:00)</p>	<p>with text-annotation. Although some systems have included monitoring and identification tools for the aforementioned agri-fields, their captioning abilities and accuracy levels have been insufficient for practical usage. Thus, further improvements have increased the accuracy by incorporating computing based on recent deep learning methodologies, particularly utilizing recent open services provided by huge IT companies, such as Google or Microsoft. Deep learning based analysis systems sometimes pick up on and highlight hidden, subtle points that a human may fail to notice. Thus, we develop deep learning based auto-annotating systems for Japanese small- to middle-sized indoor and outdoor agri-working sites and workers. We use visual data sets with a variety of real and common Japanese-styled agri-tools. We statistically analyze the obtained data and compare the comments obtained from experienced agri-workers. Our results confirm the systems' utility, validity, and limitations.</p>
<p>N0017 Session 4 Presentation 5 (17:00-17:15)</p>	<p>Research on Recognition Method of Zanthoxylum Armatum Rust Based on Deep Learning Jie Xu, Haoliang Wei, Meng Ye and Wei Wang University of Electronic Science and Technology of China, China</p> <p><i>Abstract</i>—This paper takes zanthoxylum armatum as the research object and studied a recognition method for recognition of the zanthoxylum armatum rust based on computer vision. First, we establish a leaf dataset with 22937 images, consisting of 19 kinds of leaf disease. Then we used deep learning method to analyze the disease of the crop leaf, and conducted 5 sets of experiments with different train set and test set ratio. The experiment results show that as the proportion of train set increases, the recognition accuracy of the model shows an upward trend. When the train set and test set ratio is at 8:2, the recognition accuracy reaching the best and it is 91.0%, which shows that the recognition model has good comprehensive performance and high practicability. The method used in this paper can recognize the rust of zanthoxylum armatum with a good performance, which has a positive effect on guiding agricultural production such as crop protection.</p>
	<p>Basic Phenotypes of Endocytic System Recognized by Independent Phenotypes Analysis of a High-Throughput Genomic Screen Kseniia Nikitina, Sandra Segeletz, Michael Kuhn, Yannis Kalaidzidis and Marino Zerial Max Planck Institute of Molecular Cell Biology and Genetics, Germany</p> <p><i>Abstract</i>—High-content screens (HCS) using chemical and genomic interference based on light microscopy and quantitative image</p>

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<p>N0010 Session 4 Presentation 6 (17:15-17:30)</p>	<p>analysis yielded a large amount of multi-parametric (MP) phenotypic data. Such data-sets hold great promise for the understanding of cellular mechanisms by systems biology. However, extracting functional information from data-sets, such as links between cellular processes and the functions of unknown genes, remains challenging. The limitation of HCS analysis lies in the complexity of cellular organization. Here, we assumed that cellular processes have a modular structure, and deconvolved the MP data into separate signals from different cellular modules by Blind Source Separation. We applied a combination of quantitative MP image analysis (QMPIA) and Independent Component Analysis (ICA) to an image-based HCS of endocytosis, the process whereby cells uptake molecules from the outside and distribute them to different sub-cellular organelles. We named our approach Independent Phenotypes Analysis (IPA). Phenotypic traits revealed by IPA are interpretable in terms of perturbation of specific endosomal populations (e.g. specific cargo, specific molecular markers) and of specific functional modules (early stages of endocytosis, recycling, cell cycle, etc.). The profile of perturbation of each gene in such basic phenotypic coordinates intrinsically suggest its possible mode of action.</p>
<p>N0013 Session 4 Presentation 7 (17:30-17:45)</p>	<p>Characterization of Single Lead Continuous ECG Recording with Various Dry Electrodes Muhammad Faiz ul Hassan, Dakun Lai and Xinshu Zhang University of Electronic Science and Technology of China, China</p> <p><i>Abstract</i>—Atrial fibrillation (AF) is a serious cardiovascular disease with irregular heart beating. It is the main cause of many heart diseases such as myocardial infarction. The current research focus on implementing attachable electrocardiogram (ECG) sensor adhesive patches with low power, cost and relatively small size for continuous monitoring and recording of cardiac events in real time. A single lead home care ECG is recorded when the user wearing the device performs regular activities. The patch is thin and flexible and can be worn comfortably on the human chest to re-encode the ECG for simple self-management. The systems contain batteries, dry electrodes, ECG amplifiers, and microprocessors for long-term recording of events. Different kind of ECG data has been collected from data base and compare the data by using MATLAB. The results of different ECG design systems show that the accuracy of smart T-shirt having printed electrodes, Fiber electrodes, ECG patches with printed electrode and Holter with Ag/Agcl are 99.36%, 100%, 98.80% and 98.52%, respectively. The Heart rate and Signal to artifact Ratio (SAR) also calculated by using the algorithm.</p>
	<p>A Proposal to Differentiate Homogenous and Speckled Shapes in Indirect Immunofluorescence Images Using Neutrosophic Sets</p>

<p>N2031</p> <p>Session 4</p> <p>Presentation 8 (17:45-18:00)</p>	<p>Satyavratan Govindarajan, Neeraj Rajkumar Parmaar and Ramakrishnan Swaminathan Indian Institute of Technology Madras, India</p> <p><i>Abstract</i>—Automated analysis of Indirect Immunofluorescence images is significant in the computerized detection of Autoimmune Diseases (AIDs). The recognition of particular shapes in Indirect Immunofluorescence (IIF) images is clinically associated with specific AIDs. In this work, an attempt to differentiate Homogeneous and Speckled shapes in IIF images using Neutrosophic Sets (NS) segmentation and a neural network-based classification is performed. The characteristics of NS to handle the edge boundary information of the cells is utilized. The IIF specimen images belonging to the two shapes are obtained from the public dataset. The images are subjected to illumination correction using Top-Hat transform, denoising by Split Bregman Anisotropic Total Variation and contrast enhancement with image normalization. Segmentation of cell boundaries is performed using indeterminate subset of NS. Geometric features are extracted from cell edges to assess its morphology. Multilayer Perceptron (MLP) network is employed to classify the two patterns. Results show that the indeterminacy of NS is able to segment cell edges. The geometric features are obtained to be statistically highly significant ($p < 0.001$) between the two patterns. MLP is found to perform better with average Recall, Accuracy, and Area under the Receiver Operating Characteristic measures of 98.6%, 98.7%, and 99.8% respectively. The proposed work is found to provide better results as compared to the existing methods. Hence, this study appears to be clinically significant in the morphological investigation of specimen-level IIF pattern classification for AID detection.</p>
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Session 5

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

Afternoon, October 18, 2019 (Friday)

Time: 16:00-17:45

Venue: 第4會議室 (10th Floor)

Meeting Room 4 (10th Floor)

Topic: “Molecular Biology and Epidemiology”

Session Chair: Assoc. Prof. Dianjing Guo

<p>N0011 Session 5 Presentation 1 (16:00-16:15)</p>	<p>Histone Modifications in Gastric Cancer Yan Zhang and Dianjing Guo The Chinese University of Hong Kong, Hong Kong</p> <p><i>Abstract</i>—Gastric cancer is one of the most common malignant tumors worldwide, and its prognosis is generally poor. Various genetic and epigenetic factors have been indicated in carcinogenesis. In this study, we systematically investigated 5 histone modification marks (H3K4me1, H3K4me3, H3K27ac, H3K27me3, and H3K36me3) in GC. Through chromosome state analysis, a predominant feature of chromatin state change found for GC is a higher frequency of detectable H3K4me1 at bivalent enhancer regions. Interplay of different epigenetic modification, e.g. histone modification and DNA methylation was indicated. By constructing a PPI network, distinct patterns of oncogenic pathways activation in GC were revealed, and key genes in the signaling pathways potentially be used to discriminate between tumor and normal samples were identified. This work may provide important insight into the epigenetic regulation in gastric cancer and other cancers in general.</p>
<p>N0016 Session 5 Presentation 2 (16:15-16:30)</p>	<p>Identification of Heterogeneous Functional Pathways for Single-Cell Rna-Sequencing Data Using Random Forests Hailun Wang, Pak Sham, Tiejun Tong and Herbert Pang The University of Hong Kong, Hong Kong</p> <p><i>Abstract</i>—Advances in single-cell RNA-Sequencing (scRNA-Seq) enable the high-resolution gene expression profiling within individual cells. Numerous studies have applied machine learning algorithms for scRNA-Seq data to identify heterogenous cell populations, however, few of them incorporated functional pathway</p>

	<p>information to the analysis of single-cell gene expression profiles. Since genes work interactively at the pathway level and multiple pathways crosstalk to cooperate the regulation, a pathway-based analytic method utilizing machine learning algorithms can promote a better understanding of heterogeneous functions of different cell populations. In this study, we proposed a pathway-based computational approach for scRNA-Seq data to select heterogeneous functional pathways that are good predictors of different cell populations using Random Forests (RF). Overall, we found that in the setting of pathway-based scRNA-Seq classification, RF has superior performance compared to other state-of-the-art machine learning algorithms including deep neural network. We demonstrated our pathway-based approach could efficiently prioritize important pathways in differentiating multiple cell populations. In conclusion, by addressing the cellular heterogeneity at the pathway level, our machine learning approach can facilitate biomedical researchers to better interpret potential functional alteration among multiple cell populations.</p>
<p>N0021 Session 5 Presentation 3 (16:30-16:45)</p>	<p>In Silico Protein Structure Comparison of Conotoxins with VI/VII Cysteine Framework Marineil C. Gomez, Riggs Anton D. Alvarico, Reiness E. Valbuena, Alisha Marcelle C. Aquino, Andrea R. Matira and Lemmuel L. Tayo Mapúa University, Philippines</p> <p><i>Abstract</i>—Conopeptides are small disulfide-rich peptides isolated from the venom of marine cone snails, and they are amongst the most interesting of the venom species. In this paper, in silico structural models and alignments of ω-conotoxin and different pharmacological family with the same cysteine framework (VI/VII) will be discussed using computational methods – FATCAT and POSA. The results show that with the ω-CTX conopeptide aligned with ω-CTX conopeptide, it would most likely have significantly similar structures with lower RMSD as they both function as blockers of voltage-gated calcium channels, and this conopeptide would be ω-CTX MVIIA 1OMGA aligned with ω-CTX MVIIA 1TTK. On the other hand, having compared different pharmacological with ω-CTX would result to a fewer significantly similar results since their amino acid residues, and ion channels are quite different. Multiple alignment of structures across different pharmacological families show similarities in their polypeptide backbone. Hence, conotoxins sharing the same cysteine framework can be used as models for deducing the polypeptide backbone of a conotoxin with unknown structure.</p>

<p>N0004</p> <p>Session 5</p> <p>Presentation 4</p> <p>(16:45-17:00)</p>	<p>Sequence to Sequence with Attention for Influenza Prevalence Prediction Using Google Trends</p> <p>Kenjiro Kondo, Akihiko Ishikawa and Masashi Kimura</p> <p>University of Tokyo, Japan</p> <p><i>Abstract</i>—Early prediction of the prevalence of influenza reduces its impact. Various studies have been conducted to predict the number of influenza-infected people. However, these studies are not highly accurate especially in the distant future such as over one month. To deal with this problem, we investigate the sequence to sequence (Seq2Seq) with attention model using Google Trends data to assess and predict the number of influenza-infected people over the course of multiple weeks. Google Trends data help to compensate the dark figures including the statistics and improve the prediction accuracy. We demonstrate that the attention mechanism is highly effective to improve prediction accuracy and achieves state-of-the art results, with a Pearson correlation and root-mean-square error of 0.996 and 0.67, respectively. However, the prediction accuracy of the peak of influenza epidemic is not sufficient, and further investigation is needed to overcome this problem.</p>
<p>N0020</p> <p>Session 5</p> <p>Presentation 6</p> <p>(17:15-17:30)</p>	<p>Alpha-Family of Conotoxins: An Analysis of Structural Determinants</p> <p>Marineil C. Gomez, Alisha Marcelle C. Aquino, Andrea R. Matira, Riggs Anton D. Alvarico, Reincess E. Valbuena and Lemmuel L. Tayo</p> <p>Mapúa University, Philippines</p> <p><i>Abstract</i>—Conopeptides are small, disulfide-rich polypeptides that have great potential as sources of possible drug candidates due to their activity against membrane receptors and ion channels. A challenge to the faster high-throughput in silico screening of these potential drug candidates is their diversity in structure and relatively low sequence similarity despite similar functions. In this study, the conopeptides of the α-pharmacological family is studied based on their Cα backbone, surface topology and sequence analysis. Structural alignment using FATCAT shows good alignment of the conopeptides based on their RMSD values. The main factor contributing to the homology of their structures is not only the Cys (Cys) framework forming the disulfide bridges but also the number of intervening amino acids between the Cys residues and the length of the polypeptide. The topological landscape of the conopeptides were influenced by the Cα backbone and the nature of the intervening amino acid, and are predominantly electron-poor regions, allowing them to act as Lewis acids. This may play a role in their ability to interact with ACh receptors.</p>
	<p>Designing an Open-Hardware Remotely Controllable</p>

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<p>N0006 Session 5 Presentation 8 (17:45-18:00)</p>	<p>Phototurbidostat for Studying Algal Growth Gervasi Alain, Cardol Pierre and Meyer Patrick E. University of Liege, Belgium</p> <p><i>Abstract</i>—Keeping an algal culture at a constant turbidity requires expensive and complex devices. We designed a low-cost, user friendly but also highly configurable phototurbidostat using 3D-printing, open-source software and electronics. The device is able to monitor in real time a culture in photobioreactor, and dynamically adjust the conditions to maintain the turbidity at a desired value. It can accommodate to a large set of volumes or laboratory equipments with little effort thanks to its modular and scalable design. Each module (such as light, pumps or sensors) are autonomous and controllable via Wi-Fi. Furthermore, our phototurbidostat is fully open-source and can be remotely controlled by a smartphone or a computer via a web-based graphical user interface. Finally, the device can be reproduced easily for a cost ranging between 1/20th and 1/50th of the price of a classical commercial device.</p>
<p>N1013 Session 5 Presentation 9 (18:00-18:15)</p>	<p>Whole Genome Sequence Analysis of Influenza a Virus from Four Outbreaks Between 1968- 2013 Marineil C. Gomez, Nicole Leigh T. Dasalla, Aniana Sofia M. Espiritu, Rain Allisha M. Lontok, Gabriel Eli A. Santiago, Abigail Hannah B. Torres, Irah Nathanne D. Tiburcio and Lemmuel L. Tayo Mapúa University, Philippines</p> <p><i>Abstract</i>—Influenza A, a rapidly mutating virus that can be easily transmitted in both humans and animals. Influenza A is divided into subtypes based on two glycoproteins in the virus: the hemagglutinin (HA) and the neuraminidase (NA). The virus has been the cause of many epidemics and pandemics throughout history and thus, the utilization of vaccines against the virus is paramount. The study used the program MUSCLE to determine the evolution and mutation of influenza A pathogens. Through this, it was found that the eight segments that make up the influenza A pathogens produced different levels of mutations with some segments being highly conserved and others undergoing major changes. The highly conserved regions in segments 2 and 3 are good targets in developing new vaccines. Genes encoding ofr surface proteins were highly mutated across the strains and prompts vaccine developers to continually update their viral epitope targets. Further studies are encouraged to identify all genes in the highly conserved regions in the hopes of finding a gene product on the surface of the virus that can be locked on to as an epitope target of vaccine development.</p>

Poster Session

October 18, 2019 (Friday)

Time: 18:00-18:30

<p>N2021 Poster 1</p>	<p>A Tumor-Targeting Probe Based on Mitophagy Process for Live Imaging Juanjuan Zhang, Lijuan Gui and Haiyan Chen China Pharmaceutical University, China</p> <p><i>Abstract</i>—A glucosamine modified near-infrared cyanine dye CyT sensitive to pH was synthesized. Due to the different pH of mitochondria and autolysosomes, the probe can simultaneously investigate mitochondria and autolysosomes in living cells. Moreover, due to the introduction of glucosamine groups, this fluorescent probe can be applied for tumor targeting imaging.</p>
<p>N0003 Poster 2</p>	<p>Analysis of Clustering Fragmented Protein Bond Angles Justin S. Diamond Boston University, USA</p> <p><i>Abstract</i>—The desire for accurate protein prediction algorithms has been a hallmark of computational biology achievements. Still, better algorithms and methodologies can achieve even greater success with implication across a diverse range of biological and medicinal fields such as protein function inference. Accurate prediction methods rely heavily on sequence similarity, however structure is more evolutionary conserved, i.e. structure is an alternate characteristic for ancestral relationships between proteins. The premise of this work is that similar structural features will be clustered together, which may show a unique amino acid and secondary structure (SS) distribution, which can be, incorporated into HMMs for SS prediction and protein function inference algorithms. With structural-evolutionary relationship in mind, I propose a methodology for ‘structure’ based SS prediction methods using HMM and k-mean and fuzzy k -means fragmented protein clusters. When fragment distributions were incorporated into HMMs, the average accuracy increased by 1 percent but showed an increase in accuracy of up to 13 percent for particular sequences. The HMM results were not so promising, however the clustering of protein structure fragments by C-alphas bond angles shows to be a useful length-independent metric for inferring functional relationships between proteins.</p>
	<p>Estimation of Virus Host Range Using Receptor Sequence Myeongji Cho, Mikyung Je, Hayeon Kim and Hyeon S. Son Seoul National University, Korea</p> <p><i>Abstract</i>—Although attempts have been made to dealing with emerging and</p>

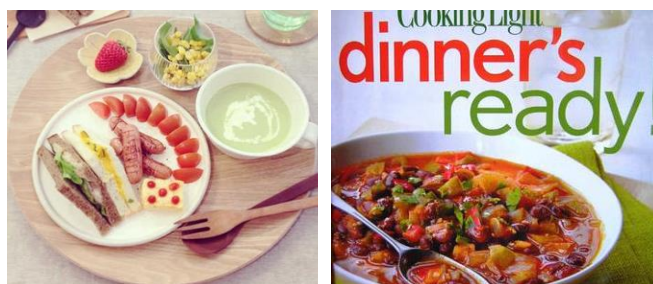
<p>N0007 Poster 3</p>	<p>re-emerging viruses causing infectious diseases for decades, there are still limitations in prediction of the risk of infection or transmission of diverse viral pathogens. In this study, we evaluated the risk of cross-species infection of the virus through evolutionary distance matrix and phylogenetic analysis using receptor sequences. We defined the DI (distance index) to the maximum value of the evolutionary distance for infected hosts, and the host range was estimated using the DI for all taxa on the phylogenetic tree. The reconstructed trees showed that taxa with values less than or equal to DI are primarily assessed as potential hosts by clustering into the host range with regard to the receptor similarity. Interestingly, the distribution of distance values for each tree showed that the host range is more clearly classified in the receptor-based trees than in the mt-based trees, although the classification patterns were highly similar. In conclusion, we have found that the similarity of the receptor proteins, which was measured by evolutionary distance and phylogenetic relationship, can be used as a useful parameter to predict the host range of viruses, and may be more appropriate than using mitochondrial genomes.</p>
<p>N1009 Poster 4</p>	<p>ANGPTL3 Mutations in Unrelated Chinese Han Patients with Familial Hypercholesterolemia Yunyun Yang, Song Yang, Xiaolu Jiao, Juan Li, Miaomiao Zhu, Luya Wang and Yanwen Qin Huazhong University of Science and Technology, China</p> <p><i>Abstract</i>—Background and objective: Familial hypercholesterolemia (FH) is a severe genetic hyperlipidemia characterized by increased levels of low-density lipoprotein cholesterol (LDL-C), leading to premature atherosclerosis. Angiopoietin-like protein (ANGPTL3) is a hepatocyte-specific protein that can be used to lower LDL in FH. However, it was unknown whether ANGPTL3 variants are present in FH patients. This study was performed to identify ANGPTL3 variants in unrelated Chinese Han patients with FH. Methods and results: We screened 80 patients with FH (total cholesterol >7.8mmol/L, LDL-cholesterol >4.9mmol/L) and 77 controls using targeted next-generation sequencing (NGS) of six FH candidate genes (LDLR, ApoB100, PCSK9, ABCG5, ABCG8, and ANGPTL3). Candidate pathogenic variants identified by NGS were validated by Sanger sequencing. Mutant and wild-type plasmids containing the variant sequence were constructed and verified by Sanger sequencing. The gene expression profile was analyzed by an expression profile chip in transfected HepG2 cells using quantitative real-time (qRT)-PCR. We identified 41 variants in 28 FH patients, including two ANGPTL3 mutations: one exonic (c.A956G: p.K319R) and one in the untranslated region (c.*249G>A). Gene ontology analyses found that the cholesterol metabolic process and ANGPTL3 expression were significantly up-regulated in the ANGPTL3 K319R mutation group compared with the wild-type group. qRT-PCR findings were consistent with the expression profile analysis. Conclusion: Rare ANGPTL3 variants were identified in Chinese patients with FH, including ANGPTL3: p.(Lys319Arg) which affected the expression of</p>

	<p>ANGPTL3 and the cholesterol metabolic process as determined by bioinformatics analysis.</p>
<p>N0008 Poster 5</p>	<p>Characterization of Codon Usage Patterns and Evolutionary Relationships in Partitiviruses Mikyung Je, Hayeon Kim, Myeongji Cho and Hyeon S. Son Seoul National University, Korea</p> <p><i>Abstract</i>—This study investigated the overall sequence characteristics and codon usage patterns of Partitiviridae viruses and applied them to viruses that are part of the family Partitiviridae but are unassigned to a genus. In addition, phylogenetic analysis was performed to investigate the evolutionary relationships of viruses belonging to Partitiviridae in relation to their fungal hosts. The sequence data of the CDS region were downloaded from GenBank, including that of the conserved RdRP, capsid protein. The results showed that Botryotinia fuckeliana partitivirus 1, Beauveria bassiana partitivirus 1, Beauveria bassiana partitivirus 2, Penicillium marneffeii partitivirus-1, and Aspergillus fumigatus partitivirus 2 had evolutionary relationships with Gammapartitivirus. Among them, Aspergillus fumigatus partitivirus 2 and Penicillium marneffeii partitivirus-1 preferred U-ended codons similar to Gammapartitivirus in terms of codon usage patterns. In addition, Botryosphaeria dothidea virus 1 showed a different pattern from the viruses belonging to Partitiviridae in all the analysis results. This virus showed a strong bias towards the C-ended codons and the lowest ENC value among the analyzed viruses, forming a separate cluster in the phylogenetic tree. These results may help to understand the genetic diversity and evolutionary relationships of the members and tentative members of the family Partitiviridae.</p>
<p>N2026 Poster 6</p>	<p>Methionine-Decorated Near Infrared Fluorescent Probe for Prolonged Tumor Imaging Ruixi Li and Haiyan Chen China Pharmaceutical University, China</p> <p><i>Abstract</i>—Methionine (Met) is one of the essential amino acids of which the transport system L is overexpressed in various tumor cells. In this study, a near-infrared fluorescent dye (IR-780) and methionine were conjugated through a piperazin–polyamines linker to form Cy-Met. The successful synthesis of Cy-Met was validated by optical characterization, NMR, and MS spectra. The absorption peak of Cy-Met was at 680 nm, and the fluorescence peak was at 790 nm. The cytotoxicity assay and cell imaging studies indicated that Cy-Met had good biocompatibility and specific affinity to tumor cells. The dynamic distribution and clearance investigations showed that Cy-Met was eliminated by the liver–intestine pathway. Notably, Cy-Met displayed tumor-targeting ability in U87, H22, and EAC tumor-bearing mice with an evident long circulation time. The results implied that Cy-Met could act as a promising fluorescence probe specialized for long-term tumor monitoring.</p>

<p>N0012 Poster 7</p>	<p>The Factors that Influence Patients' Use of Telecare System in Taiwan Yi-Horng Lai and Feng-Feng Huang Oriental Institute of Technology, Taiwan</p> <p><i>Abstract</i>—Background: Due to the improvement of medical treatment and healthcare, life expectancy is longer than before. Many chronic diseases have become the threats to contemporary individuals. How to effectively manage chronic diseases becomes an important topic now. Many experts believe that the implementation of information technology is the possible solution to enhance healthcare service efficiency and cost effectiveness. Methods: With 120 Far Eastone Health+ users' responses, partial least squares (PLS) is applied to assess validation and test linkages in the theoretical model. Results: The influence of perceived usefulness and perceived ease of use on behavioral intention to use was significant. The influence of perceived ease of use on perceived usefulness was significant. The influence of computer self-efficacy on perceived ease of use was significant. The influence of subject norm on perceived usefulness and behavioral intention to use was significant. However, the influence of computer anxiety on perceived ease of use was not significant. Conclusions: The finding and implications of this study may contribute to knowledge of health informatics, particularly on the perception and acceptance of the telecare system innovation among elderly patients. Healthcare service provider or hospital can implement proper introduction and advertisement of the telecare system, effective educations and training programs, and select suitable role models to enhance patients' acceptance of the telecare system.</p>
<p>N1010 Poster 8</p>	<p>Transcriptome Sequencing Unravels Potential Biomarkers at Different Stages of Cerebral Ischemic Stroke You Cai, Yufen Zhang, Xiao Ke, Yu Guo, Chengye Yao, Na Tang, Pei Pang, Gangcai Xie, Li Fang, Zhe Zhang, Jincheng Li, Yixian Fan, Ximiao He, Lei Pei and Youming Lu Huazhong University of Science and Technology, China</p> <p><i>Abstract</i>—Ischemic stroke, which accounts for 87% of all strokes, constitutes the leading cause of morbidity and mortality in China. Although the genetics and epigenetics of stroke have been extensively investigated, few studies have examined their relationships at different stages of stroke. This study assessed the characteristics of transcriptome changes at different stages of ischemic stroke using a mouse model of transient middle cerebral artery occlusion (tMCAO) and bioinformatics analyses. Cerebral cortex tissues from tMCAO mice at day 1, 3, 7, 14, and 28 were removed for RNA-Seq and small RNA-Seq library construction, sequencing, and bioinformatics analysis. We identified differentially expressed (DE) genes and miRNAs and revealed an association of the up-regulated or down-regulated DE miRNAs with the correspondingly altered DE gene targets at each time-point. In addition, different biological pathways were activated at different time-points; thus, three groups of miRNAs were verified that may represent potential clinical biomarkers corresponding to</p>

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	<p>day 1, 3, and 7 after ischemic stroke. Notably, this represents the first functional association of some of these miRNAs with stroke; e.g., miR-2137, miR-874-5p, and miR-5099. Together, our findings lay the foundation for the transition from a single-point, single-drug stroke treatment approach to multiple time-point multi-drug combination therapies.</p>
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Dinner	
18:30-20:00	Sakra Side Terrace

Academic Visit

08:00-19:00, October 19, 2019 (Saturday)

Day Trip to Shirakawago and Hida Takayama from Nagoya

8:00	Depart from Esca (Underground Shopping Mall), JR Nagoya Taikodoriguchi Exit(West Exit), 6-9 Tsubakichō, Nakamura Ward, Nagoya, Aichi 453-0015, Japan
10:00	Arrive at Takayama, tour and lunch
13:00	Depart from Takayama
14:00	Shirakawago tour
16:00	Depart from Shirakawago
19:00	Arrive at Nagoya Station



Brief Introduction of the Itinerary

Meet in the morning at ESCA, an underground shopping in Nagoya, to begin your excursion to the town of Hida Takayama. Spend time on your own wandering through the charming streets of this traditional-style Japanese town, an urban area known to many Japanese as “Little Kyoto” for its architectural similarities to the famous ancient capital. Following your Hida Takayama visit, you’ll head to an included lunch. Depending on the season, the lunch menu will be different: • For departures in April and May, lunch will be a set meal of Japanese-style hot pot called "Shabu-shabu" made with local ingredients like the Hida-Beef. • From June to 15 October, lunch will be Hida-Beef Sukiyaki set meal. • From 21 October to

the end of March, lunch will be "Shabu-shabu" set meal with Keichan chicken marinated in miso and soy sauce, grilled with cabbage, onions and other vegetables. Continue after lunch by coach to Shirakawago, a UNESCO World Heritage site that's known for its traditional Japanese architecture. You'll have time to admire the area's collection of historic Japanese-style farmhouses built using the "Gassho-zukuri" method, a roof technique that looks like two hands placed together in prayer. You'll then transfer back to the JR Nagoya station to finish your excursion.

NOTICE:

Due to traffic conditions, the bus arrival may be delayed and the order of the itinerary may change. Autumn leaves are expected from mid-October to late November in Shirakawago. (The best time to view autumn leaves might change depending on the weather conditions.) Wearing comfortable shoes and clothes is strongly recommended. Lunch may be served slightly earlier at 11:00 or later at 13:00 depending on the congestion of the restaurant on the tour day.



Feedback Information

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

Personal Information					
Conference Name and Paper ID					
Full Name					
E-mail Address					
Area of Research					
Affiliation					
Please indicate your overall satisfaction with this conference with “√”					
	Very Satisfied	Somewhat Satisfied	Neutral	Somewhat Dissatisfied	Very Dissatisfied
Conference Content					
Presentation and Paper Value					
Registration Process					
Venue					
Food and Beverage					
Are You A Member of CBEES	Yes <input type="checkbox"/> No <input type="checkbox"/> (If “No”, you may apply membership from http://www.cbees.org/member.htm)				
Do You Willing to Receive CBEES Future Conferences Information Via E-mail	Yes <input type="checkbox"/> No <input type="checkbox"/>				
Where did you get the conference information?					
Would you please specify the main reason for attending this conference?					
Did the conference fulfill your reason for attending?	Yes– Absolutely <input type="checkbox"/> Yes- But not to my full extent <input type="checkbox"/> No <input type="checkbox"/> (If “No”, please tell us the main reason)				

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<p>Would you please list the top 3 to 5 universities in your city?</p>	
<p>Other Field of Interest</p>	
<p>Any Other Suggestions/Comments</p>	

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