CONFERENCE PROGRAM

2020 7th International Conference on Biomedical and Bioinformatics Engineering (ICBBE 2020)

November 06-09, 2020, Kyoto, Japan

Virtual Conference

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Table of Contents

Conference Introduction

2020 7th International Conference on Biomedical and Bioinformatics Engineering (ICBBE 2020) will be held during November 06-09, 2020, Kyoto, Japan. Considering the current COVID-19 situation, ICBBE organizing committee has made the difficult decision to transform the physical conference of ICBBE 2020 into an all-digital conference – ICBBE 2020 will now be held online during November 06-09, 2020.

ICBBE series which is sponsored by Biology and Bioinformatics Society (BBS) under Hong Kong Chemical, Biological & Environmental Engineering Society (HKCBEES) owns the history of 6 years. Previously, ICBBE was successfully held in Shanghai, China in 2019, Okinawa, Japan in 2018, Seoul, South Korea in 2017, Taipei, Taiwan in 2016, Hong Kong in 2015, and Taipei, Taiwan in 2014. ICBBE 2020 is to bring together innovative academics and industrial experts in the field of Biomedical and Bioinformatics Engineering to a common forum. The primary goal of the conference is to promote research and developmental activities in Biomedical and Bioinformatics Engineering. Another goal is to promote scientific information interchange between researchers, developers, engineers, students, and practitioners working in Japan and abroad. The conference will be held every year to make it an ideal platform for people to share views and experiences in Biomedical and Bioinformatics Engineering and related areas.

Papers will be published in the following proceedings or journal:

International Conference Proceedings by ACM (ISBN: 978-1-4503-8822-1), which will be 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).

International Journal of Bioscience, Biochemistry and Bioinformatics (IJBBB, ISSN: 2010-3638) which will be included in the Electronic Journals Library, Chemical Abstracts Services (CAS), Engineering & Technology Digital Library, Google Scholar, ProQuest, etc.

Conference website and email: http://www.icbbe.com; icbbe@cbees.net

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Presentation Guideline

Presentation Requirement

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

Time Zone

- The time shown in this program is **Greenwich Mean Time (GMT+09:00)–Japan Local Time**. Please set up your laptop time in advance.

Equipment Needed

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

Environment Requirement

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

Voice Control Rules during the Presentation

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

Warm Tips for Oral Presentation

- Get your presentation PPT files prepared.
- Keynote Speech: about 40 Minutes of Presentation and 5 minutes of Q&A.
- Regular presentation is 15 minutes including 12 minutes of presentation and 3 minutes of Q&A.
- To effectively control the time and avoid some unexpected situations, it is suggested that you should record your presentation ahead of time, do the live oral presentation online or play the video while it's your turn for presentation.

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

  Step 2: Authors then switch to their slides and provide a voiceover describing images in each slide

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

Presentation Guideline

Best Presentation Award

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

Conference Material

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

Notes

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

Follow us

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

Scanning me:

ZOOM User Guideline

Download the ZOOM:

- https://zoom.us/download
- https://www.zoom.com.cn/download

Learn the ZOOM skills

- Please visit: https://support.zoom.us/hc/en-us/articles/201362033-Getting-Started-on-Windows-and-Mac

How to use ZOOM:

- Sign up an account.
- Set the language.
- Test computer or device audio.
- Join a meeting: Join the meeting with "meeting ID" provided in the program, tap the name as "Paper ID-name", eg. " N0007-Freya Shi", or "Lis-Freya Shi", then click "Join".
- Get familiar with the basic functions: Rename, Chat, Raise Hand, Start Video, Share the Computer Sound and Screen Share, etc.
  The most important function is Share Screen, because you will use it for your online presentation.

On November 06, we will have test session. On that day, we will teach you how to use ZOOM and the functions mentioned above. If you don't know how to use, please do not worry. However, you must download ZOOM, then, you can join the conference.

Test Session

November 6, 2020, Japan Local Time Meeting ID: 64883816688	
Duration	**Event**
10:00-10:10	Opening Remarks: Prof. Yen-Wei Chen
10:10-10:20	Keynote Speaker 1: Prof. Donald Lie
10:20-10:30	Keynote Speaker 2: Prof. Kiyoshi Hoshino
10:30-10:40	Keynote Speaker 3: Dr. Hayao Miyagi
10:40-11:15	Session 1: “Biomedical Electronics and Automation Technology” N2006, N0029-A, N1009, N1016, N0028-A, N0039, N0008
11:15-11:50	Session 2: “Medical Imaging and Medical Image Processing” N3001, N3004, N3010, N3005, N0032, N0030, N3006, N3012
11:50-14:00	Break Time
14:00-14:35	Session 3: “Cell Biology and Immunology” N0018, N1001, N0026, N1021, N0011, N3009, N1018
14:35-15:10	Session 4: “Pharmacy and Clinical Medicine” N0004, N0020-A, N1004, N1002, N1020, N0005, N1005
15:10-15:45	Session 5: “Bioinformatics and Biomedical Signal Analysis” N0027, N1025-A, N2005, N0007, N0010, N0023, N0025, N1015
15:45-16:20	Session 6: “Cancer Therapy and COVID-19” N1003, N1008, N1011, N0038-A, N1007, N1013, N1017, N1010
16:20-16:55	Session 7: “Proteomics and Biochemistry” N0035-A, N1019, N1006, N0036-A, N1012, N1022, N1024-A
16:55-17:30	Session 8: “Machine Learning and Data Processing in Biomedicine” N1014, N0019, N0006, N0003, N3008, N0031, N1023

Formal Session

November 7, 2020, Japan Local Time Meeting ID: 64883816688	
Duration	**Event**
10:00-10:10	Opening Remarks Prof. Yen-Wei Chen, Ritsumeikan University, Japan
10:10-10:55	Keynote Speaker 1 Prof. Donald Lie, Texas Tech University, USA
10:55-11:40	Keynote Speaker 2 Prof. Kiyoshi Hoshino, University of Tsukuba, Japan
11:40-14:00	Break Time
14:00-15:45	Session 1: “Biomedical Electronics and Automation Technology” N2006, N0029-A, N1009, N1016, N0028-A, N0039, N0008
15:45-16:00	Break Time
16:00-18:00	Session 2: “Medical Imaging and Medical Image Processing” N3001, N3004, N3010, N3005, N0032, N0030, N3006, N3012
November 8, 2020, Japan Local Time Meeting ID: 64883816688	
Duration	**Event**
9:30-10:15	Keynote Speaker 3 Dr. Hayao Miyagi, University of the Ryukyus, Japan
10:15-10:30	Break Time
10:30-12:15	Session 3: “Cell Biology and Immunology” N0018, N1001, N0026, N1021, N0011, N3009, N1018
12:15-14:00	Break Time
14:00-15:45	Session 4: “Pharmacy and Clinical Medicine” N0004, N0020-A, N1004, N1002, N1020, N0005, N1005

Program-at-a-Glance

15:45-16:00	Break Time
16:00-18:00	Session 5: “Bioinformatics and Biomedical Signal Analysis” N0027, N1025-A, N2005, N0007, N0010, N0023, N0025, N1015
November 9, 2020, Japan Local Time **Meeting ID: 64883816688**	
Duration	**Event**
9:30-10:15	Keynote Speaker 4 Prof. Yen-Wei Chen, Ritsumeikan University, Japan
10:15-10:30	Break Time
10:30-12:30	Session 6: “Cancer Therapy and COVID-19” N1003, N1008, N1011, N0038-A, N1007, N1013, N1017, N1010
12:30-14:00	Break Time
14:00-15:45	Session 7: “Proteomics and Biochemistry” N0035-A, N1019, N1006, N0036-A, N1012, N1022, N1024-A
15:45-16:00	Break Time
16:00-17:45	Session 8: “Machine Learning and Data Processing in Biomedicine” N1014, N0019, N0006, N0003, N3008, N0031, N1023

Tips: Please log into the meeting room 10 minutes before the session. Should you have any inquiry, please go to the backup room: 69149707871

Opening Remarks

Duration: 10:00-10:10, November 7, 2020
Meeting ID: 64883816688

Prof. Yen-Wei Chen, Conference Chair
Ritsumeikan University, Japan

Prof. Yen-Wei Chen received the B.E. degree in 1985 from Kobe Univ., Kobe, Japan, the M.E. degree in 1987, and the D.E. degree in 1990, both from Osaka Univ., Osaka, Japan. He was a research fellow with the Institute for Laser Technology, Osaka, from 1991 to 1994. From Oct. 1994 to Mar. 2004, he was an associate Professor and a professor with the Department of Electrical and Electronic Engineering, Univ. of the Ryukyus, Okinawa, Japan. He is currently a professor with the college of Information Science and Engineering, Ritsumeikan University, Japan. He is also a visiting professor with the College of Computer Science, Zhejiang University, China. He was a visiting professor with the Oxford University, Oxford, UK in 2003 and a visiting professor with Pennsylvania State University, USA in 2010. His research interests include medical image analysis, computer vision and computational intelligence. He has published more than 300 research papers in a number of leading journals and leading conferences including IEEE Trans. Image Processing, IEEE Trans. SMC, Pattern Recognition. He has received many distinguished awards including ICPR2012 Best Scientific Paper Award, 2014 JAMIT Best Paper Award, Outstanding Chinese Oversea Scholar Fund of Chinese Academy of Science. He is/was a leader of numerous national and industrial research projects.

Keynote Speech I

Duration: 10:10-10:55, November 7, 2020
Meeting ID: 64883816688

Prof. Donald Lie, IEEE Fellow
Texas Tech University, USA

Prof. Donald Y. C. Lie received his B.S.E.E. degree from the National Taiwan University in 1987, and the M.S. and Ph.D. in electrical engineering (minor in applied physics) from Caltech, Pasadena, in 1990 and 1995, respectively. He held technical and managerial positions at companies such as Rockwell International, Silicon-Wave (now Qualcomm), IBM, Microtune, and is currently the Keh-Shew Lu Regents Chair Professor in the Department of Electrical and Computer Engineering, Texas Tech University, and also an Adjunct Professor in the Department of Surgery, Texas Tech University Health Sciences Center. He was a Visiting Lecturer to the ECE Department, University of California, San Diego (UCSD) during 2002-2007 and co-supervised Ph.D. students. He and his students have won 16 Best Paper Awards and authored 220 peer-reviewed technical papers and book chapters with three TOP 100 most downloaded papers in IEEE Xplore™ and he holds seven U.S. patents. Dr. Lie has been awarded with 6 DARPA contracts, and appointed as a Chair Professor, College of Electrical Engineering, National Chiao-Tung University (NCTU), Hsin-Chu, Taiwan, since 2018. He is a Fellow of IEEE. His research interests are: (1) power-efficient 5G/6G mm-Wave/RF/Analog IC design; and (2) interdisciplinary/clinical research on medical electronics, biosensors, oncology, and AI-assisted medicine.

Speech Title: "Prevent the Spread of COVID-19 with Digital Health and Smart Biosensors"

Abstract—The concept of “Digital Health” covers broad areas such as mobile health (mHealth), health information and communication technology (ICT), wearable devices, telehealth and telemedicine, and personalized medicine. Digital health typically involves both software and hardware, utilizing mobile phone or sensor technologies to deliver and/or to improve patient’s healthcare. In 2019, the FDA in the US published a Digital Health Innovation Action Plan, as digital health can empower consumers, healthcare providers and even government agencies to make better-informed decisions during public health crisis, and provide new options for prevention, early diagnosis of life-threatening diseases, and management of chronic conditions. As COVID-19 is highly contagious and the confirmed cases already surpassed 8.8 million with over 230,000 deaths in the US alone, we would like to discuss a real-life example in a country where digital health has been very instrumental to have stopped the spread of COVID-19 without ever needing to lockdown. The COVID-19 death rate in this country is less than 0.3 per million, ranked 192th lowest among 215 countries in the world. We will discuss her digital health strategies on big data analytics, border control and tracking, contact tracing, etc. We will also showcase several novel biosensor technologies our group have developed that might help advance digital health in the post-COVID-19 era. We strongly suggest that there should be urgent efforts for each country to carefully look into the development and deployment of various digital health tools to combat COVID-19.

Keynote Speech II

Duration: 10:55-11:40, November 7, 2020
Meeting ID: 64883816688

Prof. Kiyoshi Hoshino, Conference Chair
University of Tsukuba, Japan

Prof. Kiyoshi Hoshino received two doctor's degrees; one in Medical Science in 1993, and the other in Engineering in 1996, from the University of Tokyo respectively. From 1993 to 1995, he was an assistant professor at Tokyo Medical and Dental University School of Medicine. From 1995 to 2002, he was an associate professor at University of the Ryukyus. From 2002, he was an associate professor at the Biological Cybernetics Lab of University of Tsukuba. He is now a professor. From 1998 to 2001, he was jointly appointed as a senior researcher of the PRESTO "Information and Human Activity" project of the Japan Science and Technology Agency (JST). From 2002 to 2005, he was a project leader of a SORST project of JST. He served as a member of the “cultivation of human resources in the information science field” WG, Special Coordination Funds for the Promotion of Science and Technology, MEXT, a member of “Committee for Comport 3D Fundamental Technology Promotion”, JEITA, and the chairman of the 43rd Annual Meeting of Japanese Society of Biofeedback Research.

Speech Title: "Eye Tracking and Eye Rotation Measurement by a Small Camera Installed almost at the Side of the Eyeball"

Abstract—When a camera for capturing the eyeball is placed almost directly to the side, the pupil center coordinate is distorted and this causes the issue of low accuracy in the conventional eye tracking. In the conventional measurement of eye rotation, the iris pattern is distorted as well and the estimate accuracy decreases. The author will introduce new methods for eye tracking and rotational eye movement measurement, which don’t not reduce the accuracy of estimation even when the pupil camera is almost at the side of the eyeball. They require only a little calibration. In the eye tracking method, the user is asked to look at a minimum of six points of small light that include the corners of a pentagon that is slanted towards the inside corner of the eye and the center of gravity of that pentagon. This is a calibration method that maps the line of sight angles from the pupil center coordinate. In the method to measure rotational eye movement, the system uses the characteristic images of the blood vessels in the whites of the eyeball. There is little interference from reflections of external light sources so that highly accurate measurement of eye rotation is possible, by continuously tracking the area where the degree of similarity in template matching is maximized.

Keynote Speech III

Duration: 09:30-10:15, November 8, 2020
Meeting ID: 64883816688

Dr. Hayao Miyagi, Emeritus Professor
University of the Ryukyus, Japan

Dr. H. Miyagi graduated from Tottori University in 1971, getting B.S. degree. In 1974 and 1978, he graduated from Osaka Prefecture University, getting M.S. degree and Ph.D degree, respectively. He obtained a job with Department of Electrical Engineering, Faculty of Science and Engineering, University of the Ryukyus, in 1977. From 1982 to 1987, he was an Associate Professor, Department of Electronic and Information Engineering, Faculty of Engineering, and was a Professor, Department of information Engineering, from 1987 to 2014. Meanwhile, he studied as a Visiting Research Associate, Department of Electrical Engineering and Computer Sciences, University of California, Berkeley, and worked as a Visiting Specialist (JICA), Jomo Kenyatta University of Agriculture and Technology, Kenya. He was also in the office of University of the Ryukyus, as a Member of the University Council (2002-2003), Dean (2003-2007) of Faculty of Engineering, and Vice President (2007-2010). Now, he is a Professor Emeritus, University of the Ryukyus. Although research areas were Decision Making, Fuzzy Theory, and Systems Theory during his career, his recent interest is in the relation between martial arts and human's unconsciousness. That is, main research he has been studying is how unconsciousness gives the effects on human's behavior.

Speech Title: "Martial Arts "Khudi" and Rykyuan Folk Dance-Strength and Elegance"

Abstract—In this presentation, the relationship between strength and elegance is considered, through the commonalities of martial arts and dances. Usually, strength means the muscle power itself, or the comprehensive power by combining the center of gravity of the body and individual muscles. Besides these physical abilities, another important thing to enhance the power is the consciousness system, especially the work of unconsciousness. In Okinawa, it has been said that martial arts are closely related to Ryukyuan folk dance. There are several types of Ryukyuan dance, and it is interesting that there are types of martial arts in dance. Among the dances, the elegant classical female dance, which is a court dance, is said to be characterized by deep feelings. The deep feeling can bring about a change in cognitive method. Namely, by expanding the actual object into an imaginary space, it becomes possible to make an environment in which human's behavior is not controlled by the normal unconsciousness action. "Ryukyu Khudi" is a martial art that one works on the unconscious layer. Thus, by changing the perception from concentration to expansion, the opponent can be incapacitated. These facts are demonstrated through presentations.

Keynote Speech IV

Duration: 09:30-10:15, November 9, 2020
Meeting ID: 64883816688

Prof. Yen-Wei Chen, Conference Chair
Ritsumeikan University, Japan

Prof. Yen-Wei Chen received the B.E. degree in 1985 from Kobe Univ., Kobe, Japan, the M.E. degree in 1987, and the D.E. degree in 1990, both from Osaka Univ., Osaka, Japan. He was a research fellow with the Institute for Laser Technology, Osaka, from 1991 to 1994. From Oct. 1994 to Mar. 2004, he was an associate Professor and a professor with the Department of Electrical and Electronic Engineering, Univ. of the Ryukyus, Okinawa, Japan. He is currently a professor with the college of Information Science and Engineering, Ritsumeikan University, Japan. He is also a visiting professor with the College of Computer Science, Zhejiang University, China. He was a visiting professor with the Oxford University, Oxford, UK in 2003 and a visiting professor with Pennsylvania State University, USA in 2010. His research interests include medical image analysis, computer vision and computational intelligence. He has published more than 300 research papers in a number of leading journals and leading conferences including IEEE Trans. Image Processing, IEEE Trans. SMC, Pattern Recognition. He has received many distinguished awards including ICPR2012 Best Scientific Paper Award, 2014 JAMIT Best Paper Award, Outstanding Chinese Oversea Scholar Fund of Chinese Academy of Science. He is/was a leader of numerous national and industrial research projects.

Speech Title: "Deep Learning for Computer-aided Diagnosis and Surgery Support"

Abstract—Recently, deep learning (DL) plays important roles in many academic and industrial areas especially in computer vision and image recognition. Deep learning uses a neural network with deep structure to build a high-level feature space. It learns data-driven, highly representative, hierarchical image features, which have proven to be superior to conventional hand-crafted low-level features and mid-level features. In ILSVRC2015 (an Annual competition of image classification at large scale), higher recognition accuracy by deep learning than human has been achieved. Deep learning (DL) has also been applied to medical image analysis. Compared with DL-based natural image analysis, there are several challenges in DL-based medical image analysis due to their high dimensionality and limited number of labeled training samples. We proposed several weakly-supervised and semi-supervised deep learning techniques for computer-aided diagnosis and surgery support including medical image segmentation, medical image detection and medical image recognition. In this talk, I will talk about current progress and futures of computer-aided diagnosis and surgery support with deep learning.

Detailed Program for Oral Session

Session 1: Biomedical Electronics and Automation Technology

Time: 14:00-15:45, November 7, 2020 (Saturday)
Greenwich Mean Time (GMT+09:00) – Japan Local Time
Meeting ID: 64883816688
Session Chair: To be added

S1-1	N2006 14:00-14:15	Introducing Swordsman Robot Defensing **Yoshimasa Ozone**, Chenyang Zhao and Kiyoshi Hoshino University of Tsukuba, Japan *Abstract*—Tankendo is performed by exchanges of strikes with a light and short bamboo sword at a comparatively short distance. Since quick movements and decision-making determine the winner and the loser, without heavily depending on the physical strength and fitness, tankendo can be enjoyed even by elderly persons and females. In this study, an autonomous mobile "tankendo swordsman robot" was developed as a human to robot combat and a training aid machine for health promotion or entertainment. This paper presented this robot.
S1-2	N0029-A 14:15-14:30	Ultrasensitive Point-of-Care Testing of Arsenic based on a Catalytic Reaction of Unmodified Gold Nanoparticles **Deye Liu**, Chengtao Xu and Hong Liu Southeast University, China *Abstract*—Nowadays, there is an urgent demand to develop methods for rapid and onsite determination of toxic arsenic in environmental samples. Herein, we propose a colorimetric method for ultrasensitive point-of-care testing of arsenic using unmodified gold nanoparticles (Au NPs). This system is based on the Au NP catalyzed redox reaction between Rhodamine B (RhB) and sodium borohydride (NaBH4), which leads to a color change of the reaction solution. AsO_2^- significantly inhibits the catalytic activity of Au NPs so that it can be quantified by colorimetric measurements. The method shows high sensitivity with a detection limit of 0.64 ppb, which is below the threshold of arsenic in drinking water recommended by the WHO. It also demonstrates high selectivity among other interfering ions. Samples from daily life are analyzed using this method, and the results agree with those obtained from standard inductively coupled plasma mass spectrometry.
S1-3	N1009 14:30-14:45	Biosensor-based Rapid Detection for Harmful Foodborne Pathogens **Peitong Xu** Shandong Agricultural University, China *Abstract*—With the rapid development of the food industry, food safety has received more and more attention from various countries. There are many factors affecting food safety, among which foodborne pathogens are one of the main factors. Therefore, it is becoming more and more important to develop rapid detection methods for foodborne pathogens. Biosensors have the advantages of simplicity, small size, low cost, high

		sensitivity, strong specificity, strong anti-interference ability, and quick response. To better understand the roles of biosensors in the detection of foodborne pathogens, this review focuses on latest development of pathogens rapid detection with biosensors. We introduced three types biosensors including optical, electrochemical, mass sensitive biosensors and discussed the application of nanobiotechnology in biosensors. We found that the optical and electrochemical biosensors have been studied for quite periods of time, therefore their better performance is accepted and appreciated during commercialization. Beyond that, monitoring viable cells are of great importance for food quality control and people's health supervision. We believe that the potential of various biosensors may shed new light on viable cell measurement and counting in the future.
S1-4	N1016 14:45-15:00	Real-time Social Distancing for Tackling COVID-19 in Workplaces Using Wearable Inertial Sensor **Ahmed M. M. Almassri**, Natsuki Shirasawa and Hiroaki Wagatsuma Kyushu Institute of Technology, Japan *Abstract*—With the unprecedented outbreak of unknown pneumonia in Wuhan, China, in December 2019, a new coronavirus, Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), aroused the attention of the entire world. The World Health Organization (WHO) identified the pneumonia as Coronavirus Disease 2019 (COVID-19) and declared it as a Public Health Emergency of International Concern (PHEIC). Worldwide, several countries have adopted social distancing as the main strategy of limiting the spread of the virus. In this paper, we explored the effectiveness of the indoor positioning system based on Ultra-WideBand (UWB) technology specifically for keeping a social distance for the prevention of the COVID-19 infection in the workplace. In static and dynamic experiments, our verified system demonstrated a real-time 3D millimeter accuracy and simultaneous tracking of multiple wearable tags that successfully visualized in the 3D space, which provide an enough accuracy 3D positioning of around 100-150 mm for the monitoring of the infection process. The results indicated that 3D tracking of multiple tags effectively work in the real-time manner with a high accuracy 3D positioning, which is applicable to further detail analyses of how an infection happen and why a social distancing is important for the prevention.
S1-5	N0028-A 15:00-15:15	High-Resolution Patterning Of Liquid Metal On Hydrogel For Flexible, Stretchable, And Self-Healing Electronics **Chengtao Xu**, Biao Ma, Deye Liu And Hong Liu Southeast University, China *Abstract*—Soft, wet, and biocompatible hydrogels have emerged as promising materials for flexible and stretchable electronics owing to their similar properties with biological tissues. However, most existing conductive materials used for hydrogel-based electronics have drawbacks such as poor biocompatibility, low conductivity, and/or high mechanical

		mismatch with soft hydrogels. In this work, direct patterning of nontoxic and highly conductive liquid metal (LM) on hydrogels is reported for soft and stretchable electronics without mechanical mismatches. The patterning is achieved by coating LM dispersed with magnetic microparticles on the wet hydrogel surface using a magnet. High-resolution LM patterns with microscale linewidths can be created with the assistance of a shadow mask fabricated by in situ digital laser cutting. Mechanical and electrical self-healing are achieved simultaneously by taking advantage of the hydrogen bonds in the polyvinyl alcohol hydrogel network and the merging of LM. A few applications of LM-based hydrogel electronics for wearable sensing, flexible wireless communication, and soft actuating are also demonstrated.
S1-6	N0039 15:15-15:30	3D Measurement of Bow and Postures for Customer Service VR Training System **Tomoya Furuno** and Junichi Hoshino University of Tsukuba, Japan *Abstract*—In many service industries, the focus is on the reception (hospitality) that improves customer satisfaction (CS) by proper understanding of customers' needs and giving good impression. We propose a scenario-based customer service VR training system using multimodal recognition of trainees. We measure the degree of bow and stoops by using bones extracted from RGB-D camera (Kinect). Then the system feedbacks them to trainee with visual aids and comments. We investigated how multiple repeating trainings can change the customer service skills.
S1-7	N0008 15:30-15:45	Gait Stability Analysis with a Two-dimensional Dynamic Parameter **Xing Gao**, Fei Shen, Li Wang, Yingnan Ma, Haijun Niu and Yubo Fan Beijing Research Center of Urban Systems Engineering, China *Abstract*—Objective: To define a two-dimensional (2-D) region of stability derived by center of mass (COM) velocity, and to assess the dynamic walking stability with COM position and velocity. Methods: The 2-D base of support (BOS) was determined by the intersection between the vector of the 2-D COM velocity and the envelope of the foot pressure. The region of stability for velocity (ROSv) in 2-D were determined using normalized COM position and velocity at toe off (TO). In order to exam the utility of this new parameter, fourteen elderly females with and without history of falls participated into a walking experiment. Results: The results showed that the 2-D ROSv could distinguish the coordinates difference between two groups much better than 1-D form in antero-posterior. COM position of elderly fallers demonstrated significant closer to the foot supporting boundary than that of healthy elderly adults at TO. Conclusion: The parameter of 2-D ROSv could differentiate among

		dynamic stability for healthy elderly adults and fallers. The results of walking experiment revealed elderly fallers tend to walk more conservatively compared to healthy subjects, to relieve the pressure of controlling their momentum.

Break Time: 15:45-16:00

Detailed Program for Oral Session

Session 2: Medical Imaging and Medical Image Processing

Time: 16:00-18:00, November 7, 2020 (Saturday)
Greenwich Mean Time (GMT+09:00) – Japan Local Time
Meeting ID: 64883816688
Session Chair: Assoc. Prof. Jie Luo, Shanghai Jiao Tong University, China

S2-1	N3001 16:00-16:15	Automatic Segmentation of the Abdominal Aorta and Stent-Grafts **Bertram Sabrowsky-Hirsch**, Stefan Thumfart, Wolfgang Fenz, Richard Hofer, Pierre Schmit and Franz Fellner RISC Software GmbH, Austria *Abstract*—Understanding and monitoring changes of the treated vessel after Endovascular aneurysm repair is crucial for the prediction of complications and risk assessment to facilitate timely intervention. Due to the complexity of the stent-graft wire frame enveloping the aortic blood lumen and the inherent artifacts caused by the metal wire, segmenting the structures required for simulation and further analysis is a non-trivial task. In this paper we present a fully automatic segmentation architecture combining two 3D U-Nets in a novel patching approach leveraging knowledge of the target anatomy. We evaluated our approach on a real world clini-cal dataset against a competitive baseline, yielding results that surpass the baseline in both accuracy and computation time. On our data we achieve a median Dice similarity coefficient of 0.97 for the blood lumen and 0.88 for the stent-graft segmentation. We point out two common flaws in current segmentation models: undersampling and indiscriminate patching. By addressing them appropriately, our approach gains an advantage that may benefit a multitude of segmentation tasks.
S2-2	N3004 16:15-16:30	Accuracy Comparison Between Learning Method and Signal Processing Method Using Iteration for Severely Blur Images **Masahiro Goto** and Tomio Goto Nagoya Institute of Technology, Japan *Abstract*—Blurring is one of the most common types of image degradation. When the blurring function (PSF) is unknown and a degraded image is to be recovered, the conventional method requires the estimation of two unknowns, which are the PSF and its ideal image, from a single input image. Thus, the method of performing alternating a PSF estimation and an ideal image estimation processing has been successful. On the other hand, blind image restoration using AI has made remarkable progress in recent years, enabling clearer estimation. In this paper, we compare the conventional iterative method with the AI method, and aim to improve the performance of images containing large blurring, which was not expected in conventional test images.
S2-3	N3010 16:30-16:45	EOCNet:Improving Edge Omni-scale Convolution Networks for Skin Lesion Segmentation **Ran Ma**, J. Zhang, Chao Gan and Haifeng Zhao Anhui University, China

		Abstract—In recent years, the number of patients with melanoma and non-melanoma skin cancers has continued to increase [2]. Even the most experienced doctors may misdemeanors skin cancer [3]. What makes medical imaging detection based on artificial intelligence detection, segmentation and classification to help doctors better diagnose skin cancers particularly important. Due to the different shape, size, structure, occluding hair and skin pigmentation of the lesion area, the lesion segmentation of skin cancer is challenging. We introduce a remarkably improving edge segmentation CNN named Edge Omni-scale Convolution Networks (EOCNet), which is represented as an encoder-decoder network. The encoder network is based on ResNet-50 [1]. The feature boundary Omni-scale module fused with the last three layers of Resnet-50 is used for the decoder. Experiments on Skin Lesion segmentation dataset achieve excellent performance.
S2-4	N3005 16:45-17:00	Automatic Joint Part Detection Method for Joint Space Measurement **Kosuke Goto**, Tomio Goto and Koji Funahashi Nagoya Institute of Technology, Japan ***Abstract***—Early detection of rheumatoid arthritis is very important for its treatment. However, it can be difficult to detect changes in medical conditions by visually inspecting medical images. Computer-based applications that can support doctors' diagnoses can be helpful. In this study, we propose a diagnostic application based on computer-based recognition of features in medical images. Specifically, joint learning is performed by using Haar-like features those capture differences in brightness of joints. Furthermore, we aimed to improve detection accuracy by removing false positives based on pixel values and positional relationships of joint detection results. As a case study, we apply it to the detection of third finger joints in X-ray images of hands. The application is able to correctly identify these regions in most cases, thereby aiding doctors in the early detection of rheumatoid arthritis.
S2-5	N0032 17:00-17:15	The Impact of Two Scatter Correction Methods on I-131 AC-SPECT Images using an Anthropomorphic Phantom with Variable Sizes of Thyroid Remnants **Anastasia Hadjiconstanti**, Konstantinos Michael, Theodoros Leontiou, Antonios Lontos, Savvas Frangos, George Demosthenous, Maria Lyra and Yiannis Parpottas Frederick Research Centre, Cyprus *Abstract*—Differentiated thyroid cancer treatment typically involves surgical removal of the whole or the largest part of the thyroid gland and a subsequent radioiodine therapy. It is important in diagnostic postsurgical SPECT/CT imaging to provide information on the actual presence and sizes of thyroid remnants. The aim of this work is to assess the impact of two scatter correction methods, the dual energy window (DEW) and the triple energy window (TEW), on the quality of the I-131 SPECT/CT images. Acquisitions were performed using an anthropomorphic

		neck-thyroid phantom with two thyroid remnants of 1.5 and 3 mL. Activity could be injected in the remnants and the background area. For the first set of acquisitions, the counts in each thyroid remnant from the non-scatter (NSC) and scatter corrected (DEW and TEW) attenuation corrected SPECT (AC-SPECT) images for different administered activity were calculated. For the second set of acquisitions, the image quality in terms of Contrast-to-Noise (CNR), Signal-to-Noise (SNR) ratios and Noise from the NSC, DEW and TEW corrected images were calculated for different remnants-to-background activity ratios. The DEW scatter correction method removed more photons than the TEW one. Even though both scatter correction methods improved image quality, especially for lower background activities and for higher volumes of remnants, this improvement is more profound when applying the TEW method. In addition, two experienced nuclear medicine physicians in a visual evaluation, without having a prior knowledge on any imaging parameters, considered that the TEW scatter corrected AC-SPECT images presented better image quality than the DEW ones. In this study, the qualitative and quantitative comparison of the two scatter correction methods indicated the effectiveness of the TEW method in diagnostic postsurgical thyroid I-131 SPECT/CT imaging.
S2-6	N0030 17:15-17:30	4th Order Tensors for Multi-Fiber Resolution and Segmentation in White Matter **Temesgen Bihonegn**, Avinash Bansal, Jan Slovák and Sumit Kaushik Masaryk University, Czech Republic *Abstract*—Since its inception, DTI modality has become an essential tool in the clinical scenario. In principle, it is rooted in the emergence of symmetric positive definite (SPD) second-order tensors modelling the difusion. The inability of DTI to model regions of white matter with fibers crossing/merging leads to the emergence of higher order tensors. In this work, we compare various approaches how to use 4th order tensors to model such regions. There are three different projections of these 3D 4th order tensors to the 2nd order tensors of dimensions either three or six. Two of these projections are consistent in terms of preserving mean diffusivity and isometry. The images of all three projections are SPD, so they belong to a Riemannian symmetric space. Following previous work of the authors, we use the standard k-means segmentation method after dimension reduction with affinity matrix based on reasonable similarity measures, with the goal to compare the various projections to 2^{nd} order tensors. We are using the natural affine and log-Euclidean (LogE) metrics. The segmentation of curved structures and fiber crossing regions is performed under the presence of several levels of Rician noise. The experiments provide evidence that 3D 2^{nd} order reduction works much better than the 6D one, while diagonal components (DC) projections are able to reveal the maximum diffusion direction.
S2-7	N3006 17:30-17:45	Multimodal Machine Learning for 2D to 3D Mapping in Biomedical Atlases **B. Almogadwy**, N.K. Taylor and A. Burger Heriot-Watt University, UK

Detailed Program for Oral Session

		Abstract—2D to 3D image registration has an important role in medical imaging and remains a significant challenge. This especially relates to the use and analysis of multimodal data. We address the issue by developing a multimodal machine learning algorithm which predicts the position of a 2D slice in a 3D biomedical atlas dataset based on textual annotation and image data. Our algorithm first separately analyses images and textual information using base models, and then combines the outputs of the base models using a Meta-learner model. To evaluate learning models, we have built a custom accuracy function. For image analysis, we tested different variants of Convolutional Neural Network architectures and different transfer learning techniques to build an optimal image base model. To analyse textual information, we used tree-based ensemble models, namely, Random Forest and XGBoost algorithms. We applied the grid search to find optimal hyperparameters for tree-based methods. We have found that the XGBoost model showed the best performance in combining predictions from different base models. Testing of the developed method showed 99.55% accuracy in prediction of 2D slice position in a 3D atlas model.
S2-8	N3012 17:45-18:00	Influence of MRI Modality on Accuracy of Deep Learning Segmentation of Abdominal Organs **Pedro Furtado** University of Coimbra, Portugal *Abstract*—Learning to segment MRI sequences is an exciting current application of deep learning networks. Most recent related work on this issue propose architecture modifications and ensembles with voting to try to improve the quality of the result. One relevant issue that also deserves further investigation is how the MRI modality influences quality of segmentation. In this paper we discuss two well-known MRI modalities (T1-DUAL and T2-SPIR) and compare the quality of segmentation with each. We build and train three segmentation network architectures, then evaluate them with the two modalities to evaluate. We conclude that segmentation of T1-DUAL modality achieves around 6% higher IoU than T2-SPIR for our experimental dataset. Based on the results we conclude that, from the perspective of segmentation performance, T1-DUAL exhibits better contrast to individualize abdominal organs.

Detailed Program for Oral Session

Session 3: Cell Biology and Immunology

Time: 10:30-12:15, November 8, 2020 (Sunday)
Greenwich Mean Time (GMT+08:00) – Japan Local Time
Meeting ID: 64883816688
Session Chair:

S3-1	N0018 10:30-10:45	Ramiprilat Effects on Endothelial Progenitor Cells Migration is Increased by Human Umbilical Cord Blood-Mesenchymal Stem Cells derived Secretome Yudi Her Oktaviono, **Ilma Alfia Isaridha**, Ferry Sandra, Achmad Lefi and Agus Subagjo Universitas Airlangga, Indonesia *Abstract*—Endothelial progenitor cells (EPCs) have a critical role in angiogenesis and vasculogenesis of coronary artery disease (CAD) patients. Secretome of human Umbilical Cord Blood-Mesenchymal Stem Cell (hUCB-MSCs) can promote neovascularization. Ramiprilat is an active metabolite of ramipril that has shown benefit in cardiovascular disease. The effect of hUCB-MSCs-derived secretome alone or combination with ramiprilat on EPCs migration is not yet elucidated. This study aimed to identify the effect of hUCB-MSC derived secretome and its combination with ramiprilat on EPCs migration. EPCs were collected from peripheral blood of CAD patient and cultured in the Stemline II medium. Cultured EPCs were then divided into groups of control, ramiprilat 10 µmol, hUCB-MSCs derived secretome (2%, 10%, and 20%), and its combination. The migration of EPCs was assessed using a Boyden chamber assay. Ramiprilat and hUCB-MSCs-derived secretome at all doses increase EPCs migration in dose-dependent manner. Combination of hUCB-MSCs-derived secretome at dose 10% and 20% and ramiprilat significantly increase migrated cells compared to ramiprilat only and secretome only group ($p<0.001$). In conclusion, hUCB-MSCs-derived secretome and ramiprilat enhance EPCs migration and combination of those two substances furtherly increased the migrated cells. hUCB-MSCs-derived secretome has the potential as regenerative treatment for CAD patients.
S3-2	N1001 10:45-11:00	Factors Affecting the Proliferation Ability of Cardiomyocytes **JiaLiang Tan** University Qiyuan Campus, China *Abstract*—Heart disease is a highly lethal disease that causes a large number of deaths worldwide every year. When heart disease happened, it will cause the death of a large number of cardiomyocytes. Because of the proliferation capacity of mammalian cardiomyocytes is limited, it's unable for cardiomyocytes to compensate the damage through their own proliferation, resulting in severe damage to the heart function, and ultimately leading to death. Therefore, how to improve the proliferation of cardiomyocytes during the occurrence of heart disease has become a key

		issue in the study of heart disease. In this review, we discuss the factors that affect the proliferative ability of cardiomyocytes, namely, oxygen concentration, and transcription factors, so as to contribute to the treatment of heart diseases.
S3-3	N0026 11:00-11:15	Secretome and Ramiprilat Effects on Endothelial Progenitor Cells Proliferation in Chronic Coronary Syndrome Patient Yudi Her Oktaviono, Ferry Sandra, Achmad Lefi and **Christian Pramudita Budianto** Airlangga University, Indonesia *Abstract*—It is known, that patients with chronic coronary syndrome (CCS) have lower endothelial progenitor cells (EPC) levels compared with healthy people. Secretome is a paracrine product from human umbilical cord blood mesenchymal stem cells (hUCB-MSC) that contains growth factors that enhanced the neovascularization and angiogenesis. Ramiprilat is an active form of ramipril which acts as an angiotensisn-converting enzyme inhibitor (ACE-I). Ramipril has been shown to have an effect on EPC proliferation. The effect of secretome alone or combination with ramiprilat is not yet elucidated. This study aimed to identify the effect of secretome compared with ramiprilat on EPC proliferation. The EPC was collected from a CCS person and cultered in stemline II medium for seven days. Cultured EPC were then divided into 8 groups of control, various doses of secretome (2, 10, and 20%), ramiprilat 10 µmol, and combination of various doses of secretome and ramiprilat. Three days after the treatement, the EPC proliferation measured by MTT assay in 96-well plated. The result of this study shown the higher the dose of secretome (2,10, and 20%) increase the proliferation of EPC better than ramiprilat (0.7128; 1.2417; 1.585 OD vs 0.7 OD; $p<0.001$). in conclusion secretome works in dose-dependent manner, the higher the concentration of secretome, the higher the EPC proliferation
S3-4	N1021 11:15-11:30	The Research of Autophagy and Anti-Aging **Baoshu An** Northeastern University, China *Abstract*—Aging is the accumulative process of degenerative changes and metabolic waste products in vivo and the resulting functional failure of body, which can be classified as individual aging and cell aging, while cell aging is the premise of individual aging. Anti-aging is the research topic drilled all the time, and recently the autophagy is proved as a potent mechanism of resisting cell aging. Current studies have concluded that autophagy as a important physiological process of autologous cellular waste degradation help cells maintain a healthy state, resist oxidative stress by clearing damaged mitochondria and proteins, thereby cell aging is suppressed, otherwise, the inhibition of autophagy induces muscle atrophy, neuromuscular junction degeneration, oxidative stress, mitochondria dysfunction, and precocious aging. And autophagy can be induced by spermidine and overexpression of ATG5 and other autophagy-related factors. In this review, we will summarize some studies

		about autophagy and aging, which may provide some information for curing diseases during aging.
S3-5	N0011 11:30-11:45	The Viability Differences on Oocyte Vitrification Surrounded by Cumulus Cells and Oocyte Vitrification not Surrounded by Cumulus Cells after In Vitro Maturation **AA Muhammad Nur Kasman**, Budi Santoso, Widjiati Widjiati, Aucky Hinting, Ni Wajan Tirtaningsih, Reny I'tisom, Budi Utomo and Muhammad Sasmito Djati Universitas Airlangga, Indonesia *Abstract*—This study aims to evaluate the viability differences on oocyte vitrification surrounded by cumulus cells and oocyte vitrification not surrounded by cumulus cells after in vitro maturation. The oocyte collection was through the aspiration technique of puncturing the 10 cc disposable syringe with 18 G needle filled with oocyte medium on follicle 2-6mm. Oocytes with intact cytoplasm were chosen and divided into two treatment groups; oocytes surrounded by cumulus cells and not surrounded by cumulus cells. The oocyte vitrification used hemi-straw into liquid nitrogen for ten days and continued with *warming*. In vitro maturation, each was with 50 µl *drop* for 5-10 oocytes covered with mineral *oil* in incubator for 22 hours under environmental condition of 5% CO2 , temperature of 38 ℃, and humidity of 95-99%. This study resulted in the morphological proportion of normal oocytes was 83.3% in the oocyte group surrounded by cumulus cells and 70% in the oocyte group not surrounded by cumulus cells. The oocyte viability on groups of oocyte surrounded by cumulus cells was insignificantly higher compared to the groups of oocyte not surrounded by cumulus cells after the vitrification and warming followed by in vitro maturation.
S3-6	N3009 11:45-12:00	Validation Methods to Promote Real-world Applicability of Machine Learning in Medicine **Riyad B. Rafiq**, Francois Modave, Shion Guha and Mark V. Albert University of North Texas, USA *Abstract*—The impact of Artificial Intelligence (AI) on health care has been dramatic; however, there is a considerable degree of skepticism among clinicians about the real-world applicability of advanced predictive models; for this reason, it is particularly important to emphasize the need for proper model validation in machine learning. Often model skepticism is well-placed as modelers may overclaim the real-world replicability for their models, understate the known limitations, or simply not be aware of the hidden limits of the modeling approach. Educational approaches limited to rigorous and thorough justification of all model design decisions may not be practical given model complexity. This also becomes more challenging as state-of-the-art models with the highest benchmark accuracy are becoming less interpretable, e.g. ensemble methods or deep learning. However, in the same way that test-driven development has been a successful paradigm to navigate the complex coding landscape through a focus on testable results, we have observed a similar improvement in modeling strategy when the focus of a predictive

		model is driven by validation targets rather than more abstract, theoretical concerns. In this study, we provide an overview of the common limitations of model validation methods in medicine. We then present solutions to address such limitations, with a focus on strengthening the validity of predictive models.
S3-7	N1018 12:00-12:15	A Review for Heart Regeneration **Flora Yong Yu Chen** University of California, USA *Abstract*—Heart disease is one of the diseases with high mortality. When heart disease occurs, a large number of cardiomyocytes die and the heart function is severely damaged. In severe cases, it may lead to death. The research on heart regeneration has become a key issue in the treatment of heart diseases. This review article discusses the factors that influence heart regeneration. Promoters include ERBB2, NRG1, estrogen, and miRNA 19-72 clusters whereas inhibitors consist of innervation, thyroid T4 and miRNA-128. The recognition of factors that influence cardiomyocyte proliferation and heart regeneration may provide reveal new therapeutic possibilities in the treatment of cardiovascular diseases.

Break Time: 12:15-14:00

Detailed Program for Oral Session

Session 4: Pharmacy and Clinical Medicine

Time: 14:00-15:45, November 8, 2020 (Sunday)
Greenwich Mean Time (GMT+09:00) – Japan Local Time
Meeting ID: 64883816688
Session Chair: Assoc. Prof. Muchtaridi, Universitas Padjadjaran, Indonesia

S4-1	N0004 14:00-14:15	Synthesis of Solid Lipid Nanoparticles Containing CoenzymeQ10 and Vitamin E Through Hot Homogenization Process Sirapatsorn Chaiprateep and **Parichart Naruphontjirakul** King Mongkut's University of Technology Thonburi, Thailand *Abstract*—The aim of present work was to develop a new formulation of solid lipid nanoparticles (SLNs) containing coenzyme Q10 (CoQ10) and vitamin E (VitE) for transdermal drug delivery application using hot homogenization process. Three different conditions without drug loading were modified for optimization. The optimum condition was further used to prepare VitE-loaded SLNs and CoQ10&VitE-loaded SLNs. All drug-free and drug-loaded nanoparticles were in a diameter size range of 100 to 200 nm. The mean diameter of drug-free SLNs, SLNs containing VitE, SLNs containing CoQ10&VitE were 135 ± 39, 141 ± 37 and 162 ± 46 nm, respectively. Monodispersed SLNs were successful prepared with polydispersity index (PDI) value (below 0.5). Zeta potential value was around 40 mV for all prepared particles providing a good physical stability. Except that of CoQ10&VitE-loaded particles, their zeta potential was around -60 mV. By UV-vis spectrophotometer, the encapsulation efficiency of VitE-loaded and CoQ10&VitE-loaded SLNs were nearly 100%. XRD analysis results showed amorphousness (broad peak) of the prepared nanoparticles (NPs).
S4-2	N0020-A 14:15-14:30	Computational Screening and *In Vitro* Evaluation of Flavonoids as Cathepsin K Inhibitors: Toward the Potential Treatment for Osteoporosis **Siripat Chaichit**, Motoyuki Itoh, Busaban Sirithunyalug, Piyarat Nimmanpipug and Supat Jiranusornkul Chiang Mai University, Thailand *Abstract*—Cathepsin K becomes an interesting target for osteoporotic treatment due to its ability to degrade type I collagen in the bone matrix**.** Especially, cathepsin K inhibition is not affected by the number of osteoclasts and bone remodeling process**.** Several previous reports indicated that some flavonoids exhibited the therapeutic effect on osteoporosis; however, the mechanisms underlying the decreased rate of bone resorption remain unclear. The purpose of this study is to explore the potential cathepsin K inhibitors obtained from herbal substances by using a variety of *in silico* approaches, including molecular docking and molecular dynamics (MD) simulation**.** These computational studies provide insight into the mechanism of the substances when bound within the cathepsin K active site**.** These candidates were subjected to *in vitro* assay on zebrafish cathepsin K. Our finding indicated that rutin showed

		better effectiveness in inhibiting cathepsin K than other flavonoids, followed by hesperidin and quercetin. Further, the promising substances from this study will be investigated *in vivo* experiments to ensure that these substances possess the ability to decrease bone resorption **rate.**
S4-3	N1004 14:30-14:45	Role of Anti-Müllerian Hormone (AMH) in Regulating Hypothalamus-Pituitary Function **Bin Yan** China Medical University, China *Abstract*—Anti-Müllerian hormone (AMH) is mainly secreted from the ovary and plays a crucial role in sexual differentiation and gonadal functions. AMH plays its role through the receptor AMHR2, which mediates the active function of AMH for a series of reproductive physiology. Although many studies focused the role of AMH and its receptor in the ovary, emerging evidence indicated that AMHR2 were highly expressed in the hypothalamus and/or the pituitary. GnRH neurons express AMHR2 from early fetal development to adulthood and AMH directly stimulates GnRH neuronal activity and hormone secretion, which mainly happens in mature GnRH cells. Additionally, AMH indirectly stimulates GnRH cells through endothelial cells and specialized hypothalamic glia called tanycytes. In this review, we collected the most recent evidence to illustrate the neuroendocrine role of AMH and how AMH participates in the pathogenesis of polycystic ovary syndrome (PCOS).
S4-4	N1002 14:45-15:00	The Heart Failure Treatment of β-Blockers **Su Jiujiu** Nanjing University of Chinese Medicine, China *Abstract*—Heart failure (HF) refers to a syndrome that causes the heart's pumping function to be impaired for a variety of reasons, and the cardiac output cannot meet the basic metabolic needs of systemic tissues. The main symptoms are dyspnea, weariness and fluid retention. HF has plagued patients, greatly reduced their quality of life, and caused a considerable medical burden, so this disease is an urgent problem to be solved. Cardiac adrenergic receptors and their signal transduction mechanisms are closely related to HF. Studies have shown that sympathetic nervous are continuously activated during the process of HF, and the level of circulating catecholamines are relevant to the degree and prognosis of HF, while changes in sympathetic nerve tension directly cause corresponding biological effects mediated by adrenergic receptors, affecting the process of HF. In order to effectively treat HF, many kinds of β-blockers have been studied. β-blockers are a type of drugs that selectively bind to adrenergic receptors, thereby antagonizing the agonistic effects of neurotransmitters and catecholamines on the β-receptors. The present review discusses several different β-blockers and focuses on their selectivity and pharmacokinetics, also some of their common side effects are listed and summarized. β-blockers have been playing a cornerstone role in the treatment of HF, and it can be expected that they will be more widely used in the field of HF treatment. Therefore,

		in order to reduce their side effects and make them better for patients, β-blockers should be further improved based on some of their characteristics. In addition, the use of β-blocker drugs should also be bolder and more personalized to ensure that they exert their maximum effect.
S4-5	N1020 15:00-15:15	BIN1 Isoform 1 has Less Function in Promoting the Stability of TAT System in Adult Rat Cardiomyocytes **Hao-Lin Zheng** Jimei University, China *Abstract*—The process of heart electrical excitation to contraction is called excitation-contraction coupling, which is important for heart to propel blood out. Transverse-axial-tubule (TAT) system in Ventricular myocyte, including classic transverse tubules (TTs) and axial tubules (ATs), is complex tubular structure formed by invaginations of sarcolemma. During many heart diseases, such as arrhythmia, hypertrophy and heart failure, TAT system become disordered which affecting the efficiency of E-C coupling. In heart cell, membrane shape regulation is important for many cellular functions. According to literature report Bin/Amphyiphysin/Rvs (BAR) domain-containing proteins play important role in membrane remodeling during the basic cell life activities such as endocytosis, cell migration, and endosomal sorting. In striated muscle, BIN1 is assumed to be very important palyer in inducing cytomembrane invagination to form the TAT system. BIN1 mutations and misregulation of splicing cause diseases in skeletal muscle and brain, and cardiac isoform of BIN1 (BIN1+13+17 or cBIN1) is known to organize cardiac TT microdomains, but the role of other BIN1 isoforms in heart remains elusive. We are curious about the role of BIN1 isoform 1 and whether it can maintain or promote TAT system stability in cultured adult myocytes. So we transfected adult rat cardiomyocytes with adenovirus of DsRed-BIN1 isoform 1. The results showed that overexpression of BIN1 isoform 1 didn't show a significant positive effect on maintaining or promoting the stability of TAT system in adult cardiomyocytes
S4-6	N0005 15:15-15:30	Modulation of Repetitive Transcranial Magnetic Stimulation on Mood and Cognitive Function in Simulated Weightlessness Rats **Ling Wang**, Jiajia Yang, Xi Xiao, Chenguang Zheng and Dong Ming Tianjin University, China *Abstract*—During spaceflight, microgravity has several negative effects on emotion and cognitive function. However, few effectively preventive methods have been developed yet. Previous studies showed that repetitive transcranial magnetic stimulation (rTMS), as a novel non-invasive technique, alleviated depression and cognitive dysfunctions. In the present study, the hindlimb unloading rat model was used to simulate microgravity conditions. And then, in experiment 1 we investigated whether HU induced anxiety and memory impairment. Behavioral tests including open field test, elevated plus maze test, Y maze

		test, and Morris water maze were performed. In experiment 2, during the simulated microgravity, HU rats were exposed to a two-week rTMS (10Hz). After that, the same behavioral experiments were carried out. The results showed that spontaneous activity of HU rats decreased, reflected in the fewer entries to the central area in open field tests, while rTMS protected against the harmful effect. No difference was observed in the behavioral performance of spatial cognition between control and HU rats. Our data suggests that rTMS-treatment during simulated microgravity plays a role in protecting against anxious emotion induced by microgravity simulation.
S4-7	N1005 15:30-15:45	Overview of Alzheimer's Disease **Wenlu Mao** University of Nottingham, UK *Abstract*—Alzheimer's disease is a neurodegenerative disease that is more widespread worldwide, but there is currently no corresponding drug that can be effectively treated. The clinical phenomena of Alzheimer's disease mainly include memory disorders, cognitive disorders, language disorders and so on. There are many pathogeneses of Alzheimer's disease, such as Aβ toxicity theory, abnormal Tau protein metabolism, cholinergic theory, neuroinflammation theory, etc., but the most important theory is Aβ toxicity theory. In this paper, through the study of galanin, morphine, GABA and VEGF, it was found that the drug protects the brain cells and neurons by protecting Aβ neurotoxicity and reducing the apoptosis rate of cells. Although the above drugs can play a protective role in Aβ neurotoxicity, the treatment of clinical conditions specific to Alzheimer's disease needs further research. This article provides constructive suggestions for the research on the treatment of Alzheimer's disease.

Break Time: 15:45-16:00

Detailed Program for Oral Session

Session 5: Bioinformatics and Biomedical Signal Analysis

Time: 16:00-18:00, November 8, 2020 (Sunday)
Greenwich Mean Time (GMT+09:00) – Japan Local Time
Meeting ID: 64883816688
Session Chair:

S5-1	N0027 16:00-16:15	Expression and Methylation of Tumor Suppressor Gene DKK3 in Nasopharyngeal Carcinoma: A Datamining Study **Zheng Xinyuan** and Cen Dongzhi Guangdong Mechanical and Electrical Polytechnic, China *Abstract*—Objectives: To study the relationship between the expression level of tumor suppressor gene DKK3 in nasopharyngeal carcinoma tissues and the methylation of the promoter region, and to explore the methylation of DKK3 gene promoter as a potential epigenetic intervention target for nasopharyngeal carcinoma. Methods: First, download the nasopharyngeal carcinoma expression profile chip, RNA-Seq sequencing and methylation chip data from the GEO database, use the R software to analyze the difference of DKK3 expression and promoter methylation in nasopharyngeal carcinoma and adjacent tissues and normal control tissues; then, select cancer tissue specimens and corresponding adjacent tissue specimens from 50 patients with nasopharyngeal carcinoma, use RT-PCR to detect the mRNA expression of DKK3 gene and methylation-specific PCR (MSP) to detect the promoter methylation level, and analyze the relationship between the two. Results: The mRNA level of DKK3 gene was found significantly down-regulated (|log2FC|> 1.0) by three different expression profiling platforms of AffymetrixU133 Plus2.0, IlluminaHiSeq 2000 and 4000. Methylation chip analysis found that the methylation status of 4 CpG sites in nasopharyngeal carcinoma tissues was significantly higher than that of normal control tissues. 2 CpG sites in nasopharyngeal carcinoma tissues was significantly higher than that of adjacent tissues (GSE62336). Conclusions: Hypermethylation in the promoter region caused down-regulation of the tumor suppressor gene DKK3 expression in nasopharyngeal carcinoma tissues, which was a potential target for epigenetic intervention.
S5-2	N1025-A 16:15-16:30	Analysis of Human Brain Transcriptomics Data Across the Lifespan using Probabilistic Network Controllability **Eimi Yamaguchi**, Tatsuya Akutsu and Jose C. Nacher Toho University, Japan *Abstract*—Recent studies on network controllability have shown promising results on identifying key life molecules that not only are engaged in biological regulation and control but are also associated to specific diseases and biological functions. In this work, we developed a new network controllability algorithm and techniques that are used to analyze human brain transcriptomics data across the lifespan. We compiled gene expression data from 173 tissue samples associated to four different brain regions and corresponding to individuals ranging from 20

		to 99 years old. By integrating transcriptomics data with human protein network, we constructed a probabilistic protein interaction network. This network was further analysed using a probabilistic controllability model that enabled us to efficiently identify critical proteins governing specific human brain regions across the lifespan. The results showed that the identified critical proteins are significantly associated to well-known aging genes.
S5-3	N2005 16:30-16:45	Voluntary fNIRS Waveform Change to Hot Taste Stimulus by Repeated Experience of Licking A Source of Strong Hot Taste **Yuya Nakai**, Shangshang Nie, Yuto Fukuda, Motomasa Tomida, Hajime Kotani and Kiyoshi Hoshino University of Tsukuba, Japan ***Abstract***—The purpose of this research is to make an fNIRS waveform change occur voluntarily when the user remembers the experience of licking a source of strong hot taste. During the training process of this experiment, a quantity of Tabasco that is sufficient to cause unconditionally and voluntarily a change in the fNIRS waveform was presented as the hot taste stimulus repeatedly at intervals of time to the subject in the test. Particularly in the initial stages of training, several recollection strategies were attempted to cause a waveform change with the subject observing his/her own fNIRS waveform in real time. From about the 4th day after starting the training, a trend was observed of an increase in the frequency of occurrence of a change in the fNIRS waveform in time synchronization with the recollection of the experience of presentation of hot taste stimulus.
S5-4	N0007 16:45-17:00	Using Hidden Markov Model for Identification Based on EEG Signals **Wenxiao Zhong**, Xingwei An, Yang Di, Lixin Zhang and Dong Ming Tianjin University, China *Abstract*—The researches on individual identification approaches based on EEG signals draw lots of attention in recent years. Few of them got time-robust identification performance. In this study, we focused on the time robustness of individual identification using EEG under conditions of resting-state of eye open/closed (REO/REC). Ten subjects participated in this study and each of them conducted three independent runs experiment, with the time intervals between adjacent runs were at least two weeks. There were three sessions within each run, and the time duration of each session is 150 seconds of REO/REC. Two features, auto-regressive (AR) and Mel-frequency cepstrum coefficients (MFCC) were calculated as identity features. Then Support vector machines (SVM) and Hidden Markov model (HMM) were used as classifiers. To access the time-robust performance of our methods, we used one of three runs data as test set and the other two as training set. Results show that the best classification accuracy is 80%. It is believed that under the conditions of REC and REO, the identity features of most subjects are robust across time and can be used for identification. This study will have an important impact on in EEG-based identification system.

Detailed Program for Oral Session

S5-5	N0010 17:00-17:15	Optimization of Acoustic Noise for Single-Shot Echo-Planar Imaging by Varying Echo Spacing **Zhenliang Lin**, Qikang Li, Rui Wang, Guobin Li and Jie Luo Shanghai Jiao Tong University, China *Abstract*—Single-shot echoplanar imaging (EPI) sequence is a commonly-used readout scheme for functional magnetic resonance imaging (fMRI). It acquires signal in a short period of time with loud acoustic noise, which could cause discomfort for patients and even pose risk for sensitive populations, as well as confound auditory fMRI studies. Though a variety of attempts have been made toward quiet EPI scans, none has considered both the noise level and the timbre. In this study, we investigated the effect of varying echo spacing and modified gradient waveform on sound pressure level and noise spectral entropy. We then used genetic algorithm to optimize both sound pressure level and spectral entropy for single-shot EPI sequence by varying the duration of each readout unit with a sinusoidal waveform, changing the timbre significantly with increased entropy and reduced loudness. The resulting image quality were also compared with images obtained by standard EPI sequence.
S5-6	N0023 17:15-17:30	Effective Evaluation of Clustering Algorithms on Single-Cell CNA Data **Marilisa. Montemurro**, GIANVITO URGESE, Elena Grassi, Carmelo Gabriele Pizzino, Andrea Bertotti and ELISA FICARRA Politecnico di Torino, Italy *Abstract*—Clustering methods are increasingly applied to single-cell DNA sequencing (scDNAseq) data to infer the subclonal structure of cancer. However, the complexity of these data exacerbates some data-science issues and affects clustering results. Additionally, determining whether such inferences are accurate and clusters recapitulate the real cell phylogeny is not trivial, mainly because ground truth information is not available for most experimental settings. Here, by exploiting simulated sequencing data representing known phylogenies of cancer cells, we propose a formal and systematic assessment of well-known clustering methods to study their performance and identify the approach providing the most accurate reconstruction of phylogenetic relationships.
S5-7	N0025 17:30-17:45	Orientation and Distance Dependence of Pairwise Correlation in Macaque V1 **Lisha Hu**, Qiyi Hu and Yao Chen Shanghai Jiao Tong University, China *Abstract*—Neuronal responses to sensory stimuli are not independent from each other. For instance, trial-to-trial fluctuations in response strength are shared between neurons. Understanding the mechanisms that underlie these pairwise correlation is critical for determining their role in encoding sensory information. Our goal was to measure the effects of different orientation preferences and electrode recording distances on the correlation of paired neurons under different task difficulty. We simultaneously recorded single-unit activities from V1 neuronal pairs with

		non-overlapping receptive fields separating in different millimeter scales (up to 7.5 mm), while rhesus monkeys performed a detection task under two levels of task difficulty. We found that correlation of distant neurons is dependent on distances, but not sensitive to differences of orientation preference and task difficulty. These findings suggest that correlation of distant neurons likely involves feedback from extra-striate cortex. The circuit mechanism they imply provides new constraints on the functional connectivity that correlation may play in visual processing.
S5-8	N1015 17:45-18:00	Development and Application of CRISPR-mediated Genetic Screening in Oncology **Wanji Li** Beijing National Day School, China *Abstract*—Clustered regularly interspaced short palindromic repeats (CRISPR) is a powerful tool for gene editing. Moreover, it can also be applied to genetic screening to investigate various biological activities for its high efficiency and throughput. The common procedure of CRISPR-mediated genetic screening includes the identification of genes of interest, the construction of sgRNA library, the transduction of sgRNA library on expression vector into target hosts, and the following data analysis. CRISPR-mediated genetic screening would further develop, employing various Cas protein and regulating diverse life process. This review article summarizes the development of CRISPR, the common procedure of CRISPR-mediated genetic screening, and the future applications.

Detailed Program for Oral Session

Session 6: Cancer Therapy and COVID-19

Time: 10:30-12:30, November 9, 2020 (Monday)
Greenwich Mean Time (GMT+09:00) – Japan Local Time
Meeting ID: 64883816688
Session Chair: Assoc. Prof. Tomio Goto, Nagoya Institute of Technology, Japan

S6-1	N1003 10:30-10:45	Overview of Tumor Immunotherapy based on Indoleamine 2,3 Dioxygenase Inhibitors **Xiangyu Hao** China Medical University, China *Abstract*—Tumor immunotherapy is one of the most attractive fields and direction for scientific researchers due to its promising clinical efficacy. While there are still many biomedical obstacles hindering the efficacy of this treatment. Indoleamine 2,3 dioxygenase (IDO) is a key suppressive factor in the tumor microenvironment. Therefore, Inhibition of IDO is strongly effective in some preclinical researches and some IDO inhibitors are in clinical research now. Moreover, IDO-based nano-drug delivery system in anticancer therapy is playing important role. The tumor microenvironment and current research progress of IDO inhibitors and nano-drug delivery systems in tumor immunotherapy are illustrated in this review.
S6-2	N1008 10:45-11:00	The Whole View of Therapies for Breast Cancer **Cui Jie** Yan'an University, China *Abstract*—Breast cancer is a leading cause of death in women, influencing on 1.7 million patients every year in the whole world. So regarding to the treatments of the breast cancer it is very important to summarize and review. Although there are many treatments to the breast cancer, the comparison among these were not addressed. In this review, we did a comprehensive literature research and summarized treatments for breast cancer, especially going through the popular therapy for human breast cancer, analyzing the clinical trial data and the adverse effect of the way. We all know breast cancer contains many subtypes and we summarized the treatments in terms of different cancer subtypes.A deep understanding of human breast cancer could bring a better effect of curing the disease, based on the known therapies we also predicted the future directions of the treatments for human breast cancer, which potentially showed a great achievements in breast cancer treatment.
S6-3	N1011 11:00-11:15	Overview of Cancer Immunotherapy **Zihan Wang** Shenyang Pharmaceutical University, China *Abstract*—Cancer is known as malignant tumor, with a high fatality rate. Early treatment include resection, radiation therapy and chemotherapy, however, due to the severe injure to human, immunotherapy has been

		proposed. Immune checkpoints are one of the major mechanisms of immune escape. Combination of ligands and receptors enables the function of immune checkpoints being available in the pathway. Chimeric antigen receptor (CAR) T-cell therapy is a targeted cellular immunotherapy that uses genetically engineered T cells to specifically eliminate the antigen bearing tumor cells. Currently, the application of immunotherapy in the treatment of cancer has been reported, thus, in this review, we mainly focus on the immunotherapy in solid tumors and leukemia, hoping to provide reference for future cancer treatment.
S6-4	N0038-A 11:15-11:30	A New Tool for CRISPR/Cas13a-based Cancer Gene Therap **Jinliang Gao**, Tao Luo and Na Lin Southeast University, China *Abstract*—Cas13a has already been successfully applied to virus detection. However, as a new gene interference tool, its potential in cancer treatment was not fully explored until now. This study first constructed a new Cas13a expression vector, DMP-Cas13a-U6-gRNA (DCUg), by controlling the Cas13a and guide RNA (gRNA) expression with a NF-κB-specific promoter and U6 promoter, respectively. Then DCUg was used to knock down the expression of target genes in cancer cells and normal cells. Finally, DCUg targeting three oncogenes was packaged into adeno-associated virus (AAV) and treated tumor-bearing mice. The results showed that DCUg could specifically and effectively knock down the expression of reporter genes in the 293T and HepG2 cells. DCUg could also similarly knock down the expression of endogenous oncogenes (TERT, EZH2, and RelA) at both mRNA and protein levels in a human hepatoma cell HepG2, which led to significant apoptosis and growth inhibition. In contrast, the same transfection did not affect the growth of a human normal liver cell HL7702. The recombinant AAV significantly inhibited the growth of the xenografted Hepa1-6 and WEHI-3 tumors in mice. This study therefore developed a new tool for the CRISPR/Cas13a-based cancer gene therapy.
S6-5	N1007 11:30-11:45	Viewing the Development Process of Coronavirus from the Diagnosis and Treatment of COVID-19 **Sarah Wan** Interlake High School, USA *Abstract*—The research progress on the structure and genome of new coronaviruses, epidemiology, disease diagnosis, treatment, and future scenarios were carried out. As of May 23, 2020, there were above 5.38 million cases of new coronavirus (SARS-CoV-2) infection and around 350,000 death tolls. The World Health Organization (WHO) published on March 12, 2020 that the COVID-19 caused by the SARS-CoV-2 virus has characteristics of a global pandemic. It is impossible to produce a vaccine in less than half a year after the outbreak. So, the most effective measure for SARS-CoV-2 is immediate detection, isolation of new sources of infection, and diagnosis and treatment of confirmed patients. But, in order to cope with the outbreak, it is significant to understand the nature and clinical characteristics of the virus in detail.

S6-6	N1013 11:45-12:00	A Molecular View of Coronavirus Disease-2019 (COVID-19) **Chenkai Jiang** Lanzhou University, China *Abstract*—This article reviews the research progress of the spike protein of the virus SARS-CoV-2 that causes COVID-19, including the gene sequence and protein sequence encoding the spike protein, as well as its secondary and tertiary structure through bioinformatics tools. The sequence similarlity comparsion results show that the spike protein has many homologous proteins and the highest similarity is SPIKE_Bat SARS-like CoV, which was also a spike glycoprotein from Bats.Secondary structure prediction shows that the sequence from position 1196 to 1218 occurs across the membrane and the protein has a several secondary domains which are potentially helpful for the virus to infect host cells ; Next, we found that the spike glycoprotein is predicted as a trimer which is extremely useful to bind the ACE2. In addition, this review also summarized the monoclonal antibody drugs targeting the spike protein, as well as several small molecule drugs, and made a comprehensive view for the treatment of COVID-19.
S6-7	N1017 12:00-12:15	Study on Traditional Chinese Medicine for Treating COVID-19 **Jianqiu Wang** Hunan University of Chinese Medicine, China *Abstract*—COVID-19, new coronavirus pneumonia, refers to viral pneumonia caused by new coronavirus (named as 2019-nCoV), with fever, cough, headache, fatigue, difficulty breathing and other symptoms as the main clinical manifestations. The earliest COVID-19 patients in our country were found in Wuhan. The virus is highly infectious and the infection is usually in 14 days from infection to onset. The clinical characteristics of COVID-19 infection is complex and can be roughly classified into mild, moderate, severe and critically ill patients. To get the infection controlled, China has carried out the combination therapy of Chinese and western medicine. In the aspect of traditional Chinese medicine (TCM) therapy, the body has been regarded as a organic whole. In different cases or stages, TCM therapy has been modified according to the details of patients. TCM therapy emphasizes the balance of vital qi and pathogenic factors. In this review, we discussed the effective Chinese medicines included in "New Coronavirus Pneumonia Diagnosis and Treatment Program" and potential mechanisms of TCM therapy when treating COVID-19.
S6-8	N1010 12:15-12:30	View from Public Health to Molecular Biology on Coronavirus Disease 2019 (COVID-19) **Yuru Li** Abington Friends School, USA *Abstract*—The outbreak of the new coronavirus disease (COVID-19) shocked the world and the epidemic was still undergoing. 213 countries were affected and around 10 million people were infected. What's worse, so far, no effective drug has been found to cure patients. SARS-CoV-2

		was the name of the virus and all the things we knew about it was not so much. In this article, we shared a comprehensive view on the COVID-19, from the view of public health and molecular biology.

Break Time: 12:30-14:00

Detailed Program for Oral Session

Session 7: Proteomics and Biochemistry

Time: 14:00-15:45, November 9, 2020 (Monday)
Greenwich Mean Time (GMT+09:00) – Japan Local Time
Meeting ID: 64883816688
Session Chair: Prof. Jose Nacher, Toho University, Japan

S7-1	N0035-A 14:00-14:15	An Investigation into the Allosteric Mechanism of Human Mitochondrial Phenylalanyl-tRNA Synthetase with Molecular Dynamics Simulation and Mutual Information Methods **Zhongjie Han** and Chunhua Li Beijing University of Technology, China *Abstract*—Allostery is one of the most important mechanisms in protein function exertion. Aminoacyl-tRNA synthetase (aaRS), an important class of enzymes, utilizes the allosteric mechanism to catalyze the aminoacylation reaction in genetic code translation. In this work, we explore the structural and dynamical characteristics of human mitochondrial phenylalanyl-tRNA synthetase (hmPheRS) in free and bound states to understand the mechanism for its tRNAPhe recognition with molecular dynamics simulations. The torsional mutual information calculated from molecular dynamics simulation trajectories is used to quantify the correlated motions between residues. Meanwhile, the protein structure network is constructed for the identification of long-range signaling pathways in hmPheRS. Our results validate that there exists the allosteric communication associated with its recognition of tRNAPhe within the bound state of hmPheRS. The conformational changes and the functional motions required for hmPheRS-tRNAPhe recognition are large and highly strong. The communication paths between the anticodon binding region and the aminoacylation region have been identified by our model. Besides, several key residues along the communication paths are identified and demonstrated to be involved in mediating the coordinated coupling between anticodon recognition and activation of amino acids at the active site. This study is helpful for the understanding of the allosteric communication mechanism of hmPheRS and can provide important information for the structure-based drug design of Aminoacyl-tRNA synthetases (aaRSs).
S7-2	N1019 14:15-14:30	The Molecular Dynamics Study on the stability of Elk Prion Protein **Ye Wang** Tianjin University, China *Abstract*—Transmissible spongiform encephalopathies (TSEs), also known as prion diseases, are fatal and highly contagious neurodegenerative diseases, of which the misfolding and aggregation of the prion protein is the only pathogenic factor. After undergoing a specific conformational change. the ubiquitous intracellular prion protein (PrP^{C}) can transform into a pathogenic conformation PrP^{Sc}, and subsequently leads to these devastating diseases. However, the details of the conformational conversion from PrP^{C} to PrP^{Sc} are still undiscovered. In

		this work, molecular dynamics (MD)and steered molecular dynamics (SMD)simulations were combined to study the stability of elk prion protein ($ePrP^{C}$). There is a coiled structure with the helical tendency and the random distortion of the β-sheets in the elk prion protein and these changes can provide a structural basis for the study of the transformation from PrP^{C} to PrP^{Sc}. The elk prion protein, in the meantime, maintains its structural stability through the formation of a rigid mesh structure and the coordination of the loose loop structure, and achieves the purpose of supporting its biological activity. Our results can help to further understanding of the pathogenic mechanism of prion protein and contribute to designing and screening drugs against TSE diseases from a structural perspective.
S7-3	N1006 14:30-14:45	The Molecular dynamics study on the pathogenicity of Cystatin C mutant **Luying Pan** Shanghai Jiao Tong University, China *Abstract*—Cystatin C can inhibit cysteine proteases and performs important physiological functions in cells. This protein is involved in the formation of amyloid fibers, and usually found in patients with Alzheimer's diseases or Down syndromes. Experimental evidence indicates that the mutation of human cystatin C 66th position, named L66Q is more likely to form dimers, which self-assemble subsequently to form amyloid deposits. However, the details about how the L66Q forms amyloid deposits are not clear. Here we used MD simulations and revealed that the single-site mutation in the 68th position of chicken cystatin C will cause changes in structural characteristics. The I68Q mutant has a higher fibro genic tendency than the wt, and the I68Q mutant has a tendency to “open” compared to the wt. The Loop1 region of I68Q has greater flexibility, and are easier to form dimers through domain exchange than wt, followed by further forming amyloid fiber deposits. Our study results are consistent with previous experimental conclusions, and provide a new idea for the future research of similar proteins. Besides, our conclusions also afford a solid theoretical basis for conquering amyloid diseases caused by cystatin C from a structural perspective.
S7-4	N0036-A 14:45-15:00	Systems Biology-Driven Approach to Explore the Comprehensive Protein Interaction Network of Dengue Virus with its Host Homo Sapiens **Qurat ul Ain Farooq** and Chunhua Li Beijing University of Technology, China *Abstract*—Dengue Virus (DENV) infection is a serious threat to human life worldwide and it can cause the most dangerous vector-borne disease leading to thousands of deaths every year. Mapping protein-protein interactions (PPIs) involved in disease pathways is an effective approach to dig into functional constitution of the proteome and to study viral-host relationship. In this study, we constructed a comprehensive PPI network of DENV with its host Homo sapiens. Cytoscape and its various apps were used for the construction, visualization and exploration of the network, and furtherly KEGG pathway and Gene Ontology analysis were

		performed for the gene functional enrichment analysis. We found a total of 1195 interactions between 858 human and 10 DENV proteins. The non-structural protein NS1 in DENV has the maximum number of interactions with host protein, followed by NS5 and NS3. Among the human proteins, HBA1 and UBE2I are associated with 7 viral proteins, and 3 human proteins (CSNK2A1, RRP12 and HSP90AB1) are found to be interacting with 6 viral proteins. For the highly interacting human proteins, we also performed their functional enrichment analysis for exploring the possible disease pathways where they are involved. The insight found in this study reveals that the set of gene products actively involved in Dengue virus infection pathway were not well-studied. The set of proteins we found can be used as potential drug targets for scientists in drug design to fight against dengue virus infection.
S7-5	N1012 15:00-15:15	Recent Insights into Proteomics in Plant Pathology **Shiyu Lin** Ningbo University, China *Abstract*—In this review we examine current proteomic approaches used for studies about plant-pathogen interactions. The proteomic analysis has been greatly developed in recent years, and rapid advances are widely discussed. Proteomic date provides the quantitative and qualitative information about resistance-related proteins during plant-pathogen interaction. By studying these differentially expressed proteins, we can better understand the relationship between these proteins and biological resistance. Proteomic studies provide a strategy for studying plant-pathogen interactions and make significant progress in the study of model plants and major crops. Therefore, the search for resistance-related genes or proteins can provide comprehensive information on the physiological response and regulatory mechanisms, which will in turn provide opportunities to improve plant resistance.
S7-6	N1022 15:15-15:30	The Effect of High Fat Diets on Organic Acids in Mice **Siyang Li** Nankai University, China *Abstract*—The high fat diet (HFD) is the main causes of obesity and can lead to some sever complications associated with metabolic disorder. The content of metabolic intermediates will change caused by HFD. In this review, we will report studies about the change of certain organic acids in high fat diet fed mice. In the researches about HFD's effect on the glycolysis, HFD has great influence on the content of pyruvate lactic acid. Different hypotheses are proposed by researchers for this change. The effect of HFD on citric cycle (TCA cycle) seems not clear needing further studies in related directions. Based on studying the change of organic acid in HFD fed mice, researchers provided some treatments to mitigate the negative impacts of HFD and the sever complications.
S7-7	N1024-A 15:30-15:45	Identification and Analysis of Driven Nodes to Efficiently Control Metabolic Pathways **Yuma Shinzawa**, Tatsuya Akutsu and Jose C. Nacher Toho University, Japan

		Abstract—The maximum matching approach was proposed to control large complex networks by identifying a minimum number of nodes that act as driver nodes. The targets of this set in the network are called driven nodes. Recent results have shown that the driver nodes are underestimated in the context of the maximum matching model. That is, more than one driven node is controlled by a single driver node which is not plausible for biological networks, especially in the context of drug-protein interaction therapies. Moreover, because the solution of a driven set in a complex network is not unique, new algorithms are needed. Here, we present a new algorithm that efficiently identifies unique driven nodes in complex metabolic networks. Our analysis does not only show that the maximum matching approach underestimates the number of driver nodes in many human and plants metabolic pathways but also unveils the importance of the biological functions associated to the identified driven molecules.

Break Time: 15:45-16:00

Detailed Program for Oral Session

Session 8: Machine Learning and Data Processing in Biomedicine

Time: 16:00-17:45, November 9, 2020 (Monday)

Greenwich Mean Time (GMT+09:00) – Japan Local Time

Meeting ID: 64883816688

Session Chair:

S8-1	N1014 16:00-16:15	A Novel Linear B-cell Epitope Prediction Method based on Position Entropy of Amino Acids **Hong-guang Yang**, Bin Cheng and Ling-Yun Liu Hebei Academy of Sciences, China *Abstract*—Epitope prediction plays an important role in diagnosis, treatment of diseases and the development of antibodies. Recently, many machine learning algorithms and new strategies have been used to predict the B-Cell epitopes. However, the performance of epitope prediction is still not satisfactory. We propose the method of Linear B-cell epitope prediction base on the position entropy of amino acids and long and short-term memory (LSTM) network. We design three sets of experiments to verify the effectiveness of the model. The result of experiments indicates that the accuracy of our method can reach to 88.94%. The result also show that the position entropy of amino acids is an effective feature in B-cell epitope prediction.
S8-2	N0019 16:15-16:30	Improved robustness in Water-Fat Separation in MRI using Conditional Adversarial Networks **Chenfei Shen**, Huajun She and Yiping P. Du Shanghai Jiao Tong University, China *Abstract*—Water-fat separation is a post-processing method to obtain water/fat only images and parametric maps from multi-echo magnetic resonance (MR) images. Due to multi-parametric analytic models and optimization algorithm, the water-fat separation problem is complicated and time-consuming to solve. Traditional model-based techniques require a known field map to make the problem becomes “almost linear”, which results in the dependence on the accuracy of field map estimation and the decrease of computing efficiency. In this study, we proposed a deep learning based method to solve the inverse problem and simultaneously obtain the water/fat images, field map and $R2^*$ map without iteration process and field map estimation in advance. Conditional GAN was utilized in this work to preserve the structural details and ground truth was obtained using a graph cut method. The results showed that our method had a more robust performance and higher structural similarity in water-fat separation compared to U-Net based method. The proposed deep learning method is field map free and effective to separate fat/water.
S8-3	N0006 16:30-16:45	Dynamic Functional Connectivity and Graph Convolution Network for Alzheimer’s Disease Classification Xingwei An, **Yutao Zhou**, Yang Di and Dong Ming Tianjin University, China *Abstract*—Alzheimer’s disease (AD) is the most prevalent form of

		dementia. Traditional methods cannot achieve efficient and accurate diagnosis of AD. This paper introduces a novel method based on dynamic functional connectivity (dFC) that can effectively capture changes in the brain. We compare and combine four different types of features including amplitude of low-frequency fluctuation (ALFF), regional homogeneity (ReHo), dFC and the adjacency matrix of different brain structures between subjects. We use graph convolution network (GCN) which consider the similarity of brain structure between patients to solve the classification problem of non-Euclidean domains. The proposed method's accuracy and the area under the receiver operating characteristic curve achieved 91.3% and 98.4%. This result demonstrated that our proposed method can be used for detecting AD.
S8-4	N0003 16:45-17:00	The Study of Voice Pathology Detection based on MFCC and SVM Yipeng Niu, Jiaming Cao, Fei Shen and **Pengling Ren** Beijing Friendship Hospital Capital Medical University, China *Abstract*—Subjective auditory perception evaluation of voice is the most simple and direct method for judgment of the degree of voice lesions and the treatment effect. But it is closely related to the clinical experience of doctors. Recently, some voice automatic diagnosis methods based on voice feature parameters and classification algorithms have been proposed. Mel Frequency Cepstral Coefficient (MFCC) is the most commonly used feature parameter. However, it is not clear the role of MFCC dynamic features in improving diagnosis results. This study adopted the features of MFCC, MFCC + ΔMFCC, and MFCC + ΔMFCC + ΔΔMFCC respectively, combined with the Support Vector Machine (SVM) method to further determine whether adding dynamic MFCC features can improve the accuracy of pathological voice detection. The results showed that no matter whether dynamic features were added or not, the accuracy rate and specificity have not changed significantly. This means the dynamic change of the MFCC characteristic parameters is slight at least for vowel vocalization. This study may provide useful information for pathological voice diagnosis based on vowel vocalization.
S8-5	N3008 17:00-17:15	Mini-DDSM: Mammography-based Automatic Age Estimation Charitha Dissanayake Lekamlage, Fabia Afzal, Erik Westerberg and **Abbas Cheddad** Blekinge Institute of Technology, Sweden *Abstract*—Age estimation has attracted attention for its various medical applications. There are many studies on human age estimation from biomedical images. However, there is no research done on mammograms for age estimation, as far as we know. The purpose of this study is to devise an AI-based model for estimating age from mammogram images. Due to lack of public mammography data sets that have the age attribute, we resort to using a web crawler to download thumbnail mammographic images and their age fields from the public data set; the Digital Database for Screening Mammography. The original images in this data set unfortunately can only be retrieved by a software which is broken. Subsequently, we extracted deep learning features from the collected data

		set, by which we built a model using Random Forests regressor to estimate the age automatically. The performance assessment was measured using the mean absolute error values. The average error value out of 10 tests on random selection of samples was around 8 years. In this paper, we show the merits of this approach to fill up missing age values. We ran logistic and linear regression models on another independent data set to further validate the advantage of our proposed work. This paper also introduces the free-access Mini-DDSM data set.
S8-6	N0031 17:15-17:30	Towards Data-Driven Modelling of SUMOylation Following Heat Shock **Manyu Zhang**, Yifei Zhang, Alice Zhao, Chun Guo and Lingzhong Guo The University of Sheffield, UK *Abstract*—Understanding how cell fate is determined when exposed to extreme stresses such as heat shock is critical in biomedical systems. It has long been understood that exposure of cells to high temperature typically protect themselves with a heat shock response (HSR), where accumulation of denatured or unfolded proteins triggers the synthesis of heat shock proteins (HSPs) through the heat shock transcription factor, *e.g.*, heat shock factor 1 (HSF1). Recent experimental work has also shown that protein posttranslational modifications (PTMs) such as SUMOylation play crucial roles in cellular responses to heat shock. As a complementary approach to the current experimental methodologies, in this study we aim to develop a mathematical model of SUMOylation-development synergism of HSR for the purpose of studying the dynamical behaviour of HSR quantitatively. The structure of our dynamical model is derived mostly from mass action kinetics while the model parameters are optimized by using a genetic algorithm (GA) based data-driven approach. The preliminary results show GA based data-driven approach has potentials for our modelling purpose.
S8-7	N1023 17:30-17:45	Differential Response to the High Doses of Dimethyl Sulfoxide of the Several Human Cancer Cell Lines Cultured in 2D Monolayer, Decellularized Matrix, and 3D Spheroid Cell Culture Systems **Ekaterina Yu Skorova**, Eugenia Y Shabalina, Daria A Chudakova, Vladimir B Anikin, Igor V Reshetov Igor V Reshetov, Ospan A Mynbaev and Elena V Petersen Moscow Institute of Physics and Technology, Russia *Abstract*—When using cell-based models for drug research screening it is of critical importance to validate their applicability and accuracy. Here we report that the patterns of cellular response to high concentrations of DMSO measured with vital dye are cell line-specific and varied in time and type of response for different cell lines and for the same cell line cultures in 2D Monolayer, Decellularized Matrix, or 3D Spheroid cell culture systems. This should be considered at the stage of the experimental design, and for each experiment the more suitable cell culture system should be chosen, based on the characteristics of cellular response to DMSO in this particular system, especially if developing cell-based automated systems for drug screening.

About ICBBE 2021

INTRODUCTION

2021 8th International Conference on Biomedical and Bioinformatics Engineering (ICBBE 2021) is under preparation. ICBBE 2021 will be held during November 12-15, 2021 in Ritsumeikan University, Kyoto, Japan. Welcome to submit papers to ICBBE 2021 to join in the conference. We are looking forward to seeing you in Kyoto, Japan NEXT YEAR!

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Bioelectrical and neural engineering
Biomechanics and bio-transport
Methods and biology effects of NMR/CT/ECG technology
Biomedical devices, sensors, and artificial organs
Biochemical, cellular, molecular and tissue engineering
Biomedical robotics and mechanics
Rehabilitation engineering and clinical engineering
Health monitoring systems and wearable system
Bio-signal processing and analysis
Biometric and bio-measurement
Other topics related to biomedical engineering

Bioinformatics and Computational Biology

Protein structure, function and sequence analysis
Protein interactions, docking and function
Computational proteomics
DNA and RNA structure, function and sequence analysis
Gene regulation, expression, identification and network
Structural, functional and comparative genomics
Gene engineering and protein engineering
Computational evolutionary biology
Drug design and computer aided diagnosis
Data acquisition, normalization, analysis and visualization
Algorithms, models, software, and tools in Bioinformatics
Any novel approaches to bioinformatics problems

Other Related Topics

Biostatics
Biometric
Biomeasurement
Biomechanics
Biophysics
Biochemistry
Biomathematics
Bioengineering
System biology