CONFERENCE ABSTRACT

2020 6th International Conference on Environment and Bio-Engineering (ICEBE 2020)

January 19-22, 2020

Uji Obaku Plaza, Uji Campus, Kyoto University, Kyoto, Japan

Organized by

Supported by

Published and Indexed by

http://www.icebe.org/

Conference Venue

Uji Obaku Plaza, Uji Campus, Kyoto University
Website: http://www.uji.kyoto-u.ac.jp/campus/obaku.html
Address: Gokasho, Uji, Kyoto 611-0011
Tel: 0774-38-3021
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1. How to Get Here?

The access/map is available from: https://www.kuicr.kyoto-u.ac.jp/sites/icr/about/access/.

2. Hotel Recommendation

Tips: The registration fee does not cover the accommodation. It should be booked by participants themselves. The follows are some hotels for recommendation. It is suggested an early booking should be done.

A. New Miyako Hotel
https://www.miyakohotels.ne.jp/newmiyako/english/index.html

B. Kyoto Century Hotel
https://www.keihanhotels-resorts.co.jp/kyoto-centuryhotel/english/

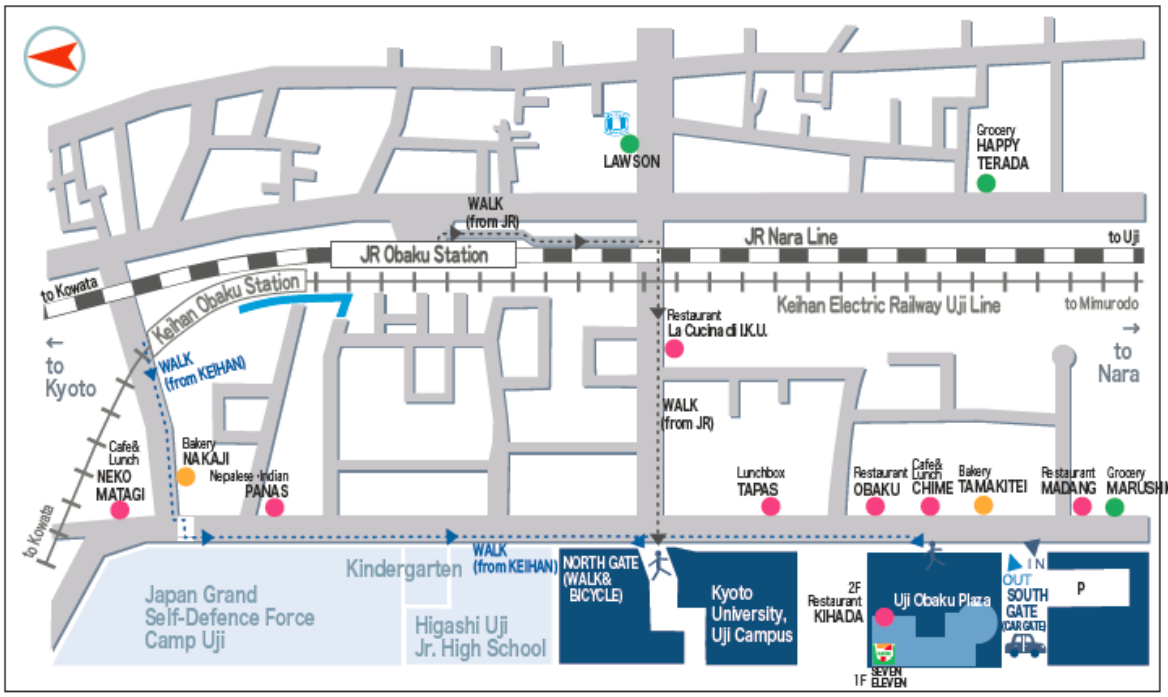
C. APA Hotel Kyoto-Ekimae
https://www.apahotel.com/hotel/kansai/01_kyoto-ekimae/

D. El Inn Kyoto
https://www.elinn-kyoto.com/en/

E. Uji Dai-ichi Hotel
http://ujidai1.jp/ (Japanese page only)

Map

NEAR THE UJI CAMPUS



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Introduction

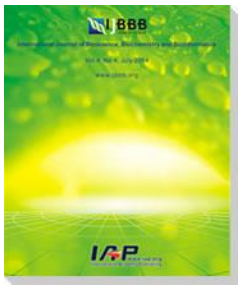
Welcome to 2020 6th International Conference on Environment and Bio-Engineering (ICEBE 2020). It is organized by Biology and Bioinformatics Society (BBS) under Hong Kong Chemical, Biological & Environmental Engineering Society (CBEES) and supported by Kaohsiung Medical University and Kyoto Convention & Visitors Bureau.

ICEBE is an interdisciplinary international conference that invites academics and independent scholars and researchers from around the world to meet and exchange the latest ideas and views in a forum encouraging respectful dialogue. ICEBE serves as an outstanding platform that gathers all the relevant communities and domains together, an international forum for researchers and industry practitioners to exchange the latest fundamental advances in the state of the art and practice of Environment and Bio-Engineering.

Papers will be published in the following journals:

Journal of Environmental Science and Development (IJESD, ISSN:2010-0264): indexed by **Scopus** (Since 2019), **Chemical Abstracts Services (CAS)**, CABI, Ulrich Periodicals Directory, Electronic Journals Library, Crossref, ProQuest.

Or



International Journal of Bioscience, Biochemistry and Bioinformatics (IJBBB, ISSN: 2010-3638), and will be included in the Engineering & Technology Digital Library, and indexed by **WorldCat, Google Scholar**, Cross ref, **ProQuest**.

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

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Prof. Ahmad Zuhairi Abdullah, Universiti Sains Malaysia, Malaysia
Assist. Prof. Narong Touch, Tokyo University of Agriculture, Japan

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	11:20-11:40	**Invited Speech II** Prof. Sung Wing Kin, Ken, National University of Singapore, Singapore Topic: "Improving CNV Calling from High-Throughput Sequencing Data through Statistical Testing"	
	11:40-12:00	**Invited Speech III** Prof. Ryoji Nagai, Tokai University, Japan Topic: "Protein Modification by Metabolic Intermediates and its Involvement with Life-Style Related Diseases"	
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Tips: Please arrive at the Conference Room 10 minutes before the session begins to upload PPT into the laptop; submit the poster to the staff when signing in.

Presentation Instruction

Instruction for Oral Presentation

Devices Provided by the Conference Organizer:

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

Materials Provided by the Presenters:

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

Duration of each Presentation (Tentatively):

Keynote Speech: about **35** Minutes of Presentation and **5** Minutes of Question and Answer
Invited Speech: about **15** Minutes of Presentation and **5** Minutes of Question and Answer
Oral Presentation: about **12** Minutes of Presentation and **3** Minutes of Question and Answer
Poster Presentation: about **3** Minutes of Presentation and **2** Minutes of Question and Answer

Instruction for Poster Presentation

Materials Provided by the Conference Organizer:

The place to put poster

Materials Provided by the Presenters:

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

Best Presentation Award

One Best Oral or Poster Presentation will be selected from each session, and the Certificate for Best Presentation will be awarded at the end of the session on January 20-21, 2020.

Dress Code

Please wear formal clothes or national representative of clothing.

Disclaimer

Along with your registration, you will receive your name badge, which must be worn when attending all conference sessions and activities. Participants without a badge will not be allowed to enter the conference venue. Please do not lend your name badge to the persons who are not involved in the conference and do not bring the irrelevant persons into the conference venue.
The conference organizers cannot accept liability for personal injuries, or for loss or damage of property belonging to conference participants, either during, or as a result of the conference. Please check the validity of your own insurance.

Keynote Speaker Introduction

Keynote Speaker I

Prof. TSUI Kwok-Wing Stephen
The Chinese University of Hong Kong, Hong Kong

TSUI Kwok-Wing Stephen is currently a Professor in the School of Biomedical Sciences, the Head of Division of Genomics and Bioinformatics and the Director of Hong Kong Bioinformatics Centre in the Chinese University of Hong Kong (CUHK). In 1995, he received his PhD degree in Biochemistry at CUHK. He was then appointed as an Assistant Professor in the Biochemistry Department in 1997 and promoted to the professorship in 2004. He was also a former member of the International HapMap Consortium and worked on the single nucleotide polymorphisms of human chromosome 3p. During the SARS outbreak in 2003, his team was one of the earliest teams that cracked the complete genome of the SARS-coronavirus. Totally, he has published more than 220 scientific papers in international journals, including Nature, NEJM, Lancet, PNAS, Circulation, JACI and Genome Biology. His major research interests are next generation sequencing, bioinformatics, human genetic diseases and molecular microbiology.

Topic: "The Genomes and Microbiomes of Dermatophagoides Farinae and Dermatophagoides Pteronyssinus Reveal a Broad Spectrum of Dust Mite Allergens"

Abstract—It is well known that house dust mites (HDMs) are predominant sources of inhalant allergens associated with allergic disease. Therefore, sequenced house dust mite (HDM) genomes would certainly advance our understanding of HDM allergens, a common cause of human allergies. To produce annotated Dermatophagoides (D.) farinae and D. pteronyssinus genomes, we developed a combined genomic-transcriptomic-proteomic approach for the elucidation of HDM allergens. High quality D. farinae and D. pteronyssinus genomes and transcriptomes were assembled with high-throughput DNA sequencing platforms including PacBio, Illumina HiSeq and ion torrent. The mite's microbiome composition was at the same time determined and the predominant genus was validated immunohistochemically. Putative allergens were then evaluated with immunoblotting, immunosorbent assays, and skin prick tests. In this study, 79.79-Mb and 66.85-Mb genomes of D. farinae and D. pteronyssinus, respectively, was constructed. Moreover, the full gene structures of canonical allergens and non-canonical allergen homologues were produced. Using mass spectrometry analysis of D. farinae protein spots reactive to pooled sera from HDM-allergic patients, novel major allergens were found. In D. farinae, the predominant bacterial genus among 100 identified

species was Enterobacter (63.4%), among them Enterobacter cloacae and Enterobacter hormaechei were most predominant. KEGG pathway analysis revealed a phototransduction pathway in D. farinae as well as thiamine and amino acid synthesis pathways suggestive of an endosymbiotic relationship between D. farinae and its microbiome. In summary, high quality HDM genomes produced from genomic, transcriptomic, and proteomic experiments revealed allergen genes and a diverse endosymbiotic microbiome, providing a tool for further identification and characterization of HDM allergens and development of diagnostics and immunotherapeutic vaccines.

Keynote Speaker II

Prof. Jean-Philippe Vert
Google Brain, France and MINES ParisTech, France

Jean-Philippe Vert is a research scientist at Google Brain, and adjunct researcher at MINES ParisTech. After a PhD in mathematics at ENS Paris in 2001 and a post-doc at Kyoto University, he held various academic positions at MINES ParisTech, Institut Curie, UC Berkeley and ENS Paris. His main research contributions are in machine learning and computational biology, in particular in cancer genomics and precisions medicine.

Topic: "Learning from Single-cell Genomics Data"

Abstract—Single-cell genomics allows capture the diversity of individual cells at the molecular level, and has revolutionized our understanding of development processes or tumor heterogeneity. It also raises numerous modeling and computational challenges. In this talk I will present some approaches we developed for data normalization, gene network inference and integration of heterogeneous views from single-cell genomics data.

Keynote Speaker III

Prof. Kuo-Sheng Cheng
National Cheng Kung University, Taiwan

Prof. Kuo-Sheng Cheng received his B.Sc, M.Sc, and Ph.D degrees from Department of Electrical Engineering, National Cheng Kung University, Tainan, TAIWAN. He also received his M.Sc degree from Department of Biomedical Engineering, Rensselaer Polytechnic Institute, USA. Currently, he is a professor with the Department of Biomedical Engineering, National Cheng Kung University. He also is the Director of Department of Maintenance and Engineering, National Cheng Kung University Hospital and the Director of Engineering and Technology Promotion Center, which is financial supported by Ministry of Science and Technology, TAIWAN. He was the past President of the Biomedical Engineering Society of TAIWAN. His research interests includes medical image processing, electrical impedance imaging and biomedical instrumentation.

Topic: "An Integrated Analysis System for Cephalometric Applications"

Abstract—With the rapid advance of information and communication technologies, to develop the digital as well as smart dentistry becomes an important issue in oral medicine. In the procedures of conventional cephalometry, many steps rely on the manual processing such as the landmarking and superimposition. The automation of landmarking and superimposition are the first step in cephalometric analysis. Those points in cephalograms representing the anatomical structures of the skull are called landmarks, which are routinely analyzed for diagnosis and treatment planning. In this integrated analysis system, the image processing module was developed for locating the landmarks of X-ray cephalogram automatically. The image was divided into eight rectangular subimages that containing all the useful landmarks. A genetic algorithm combined with perceptron was proposed for feature subimage extraction. All the sugimages were enhanced in the preprocessing stage. The pyramid method was applied to reduce the resolution of image, and the edges were detected by the appropriate edge detectors or the best orientation edge detector. The curve of each edge was adjusted elastically with the pre-stored models. Positions of landmarks could be then located immediately and the associated parameters could also be computed for diagnosis. Secondly, the analysis of the spatial changes of the craniofacial structures for orthodontic treatment or surgery always relies on the superimposition of pre- and post-treatment cephalometric tracings. A computerized superimposition module was also developed for solving this problem. The feature curves were detected and traced for the cranial base using the best oriental edge detector and Hough transform, and for the mandibular using the Laplacian of Gaussian and

grouping methods. The superimposition was automated following the clinically available procedures. From the experimental results, it was shown that the cephalometric analysis may be improved with its accuracy and processing time using this proposed integrated analysis syste.

Keynote Speaker IV

Prof. Hans-Uwe Dahms
Kaohsiung Medical University, Taiwan

Dr. Hans-Uwe Dahms is a professor at Kaohsiung Medical University. He is interested in stress responses in general and within aquatic systems in particular. He, his colleagues and students integratively study pollution and the toxicology of stressors from physical, chemical, and biological sources. He is equally interested in climate change, the spread of diseases, antibiotic-resistance, food and drink safety from water sources, and integra-tive approaches in environmental and public health monitoring, risk assessment and management. He advised more than 25 Ph.D. students in their research and published more than 275 papers in scientific journals. He served as a reviewer for more than 70 SCI journals, as editorial board member of 12 reputed scientific journals, academic editor of PLosONE, and as editor in chief of FRONTIERS in Marine Pollution.

Topic: "Which Toxicity Evaluations Provide Better Risk Assessments–in situ, in vivo, in vitro, or in silico?"

Abstract—Describing the toxicological profile of a substance is the first step required for risk assessments. Among a wide range of approaches are in vitro methods widely used to characterise toxicological properties including toxicokinetics with regulatory acceptance mainly confined to in vitro tests which investigate genotoxic endpoints. Chemoinformatics refers to in silico approaches that make use of computer applications or computer simulations. In silico predictive models generally provide fast and economic screening tools for compound properties. They allow a high throughput and a constant optimization. They are less expensive, less time consuming, have a high reproducibility, and reduce experimental efforts. Computational approaches can also prioritize chemicals for their toxicological evaluation in order to reduce the amount of costly in vitro and ethically problematic in vivo toxicological screenings, and provide early alerts for newly developed substances. Limitations include that ADME aspects (absorption, distribution, metabolism, and excretion – which are basic pharmacokinetic descriptors) are difficult to consider. The programs, descriptors, and applicabilities are sometimes not clear. In addition are carcinogenicity predictions only possible when genotoxic compounds are considered. An approach is developed here that selects appropriate methods in a multiple weight of evidence.

Keynote Speaker V

Prof. Jiann-Shing Shieh
Yuan Ze University, Taiwan

Jiann-Shing Shieh received the B.S. and M.S. degrees in chemical engineering from National Cheng Kung University, Taiwan, in 1983 and 1986, respectively, and the Ph.D degree in automatic control and systems engineering from The University of Sheffield, U.K. in 1995. He is currently a Professor with the Department of Mechanical Engineering, also a Joint Professor with the Graduate School of Biotechnology and Bioengineering, and also serves as the Dean of the College of Engineering, Yuan Ze University, Taiwan. His research interests are focused on biomedical engineering, particularly in bio-signal processing, intelligent analysis and control, medical automation, pain model and control, critical care medicine monitoring and control, dynamic cerebral autoregulation research, and brain death index research.

Topic: "Intelligent Signal Processing in Autonomous Systems for Healthcare Monitoring and Control"

Abstract—Recently, significant developments have been achieved in the field of artificial intelligence (AI), in particularly the introduction of deep learning technology that has improved the learning and prediction accuracy to unpresented levels, especially when dealing with big data and high-resolution images. Significant developments have occurred in the area of medical signal processing and healthcare monitoring such as vital biological signs for biomedical systems which are carried out by instruments that generate large data sets, in addition to the growth in population that has resulted in big data sets that require artificial intelligence techniques to analyse and model. Hence, we propose an autonomous system (including not only monitoring sensors from patients, but also modelling, critic, fault detection, and specification algorithms for patients) which will be the key driving factor of future healthcare concepts, and together with internet of things (IoT), AI, big data analysis, edge computing, fog computing, and cloud computing. Definitely, it will open a new era of intelligent signal processing in autonomous systems for healthcare monitoring and control.

Invited Speaker Introduction

Invited Speaker I

Assoc. Prof. Jiangning Song
Monash University, Australia

Dr. Song is an Associate Professor and Group Leader in the Cancer and Infection and Immunity Programs in School of Biomedical Sciences, Faculty of Medicine, Nursing and Health Sciences, Monash University, Melbourne, Australia. Trained as a bioinformatician and data-savvy scientist, he has a very strong specialty in Artificial Intelligence, Bioinformatics, Comparative Genomics, Cancer Genomics, Computational Biomedicine, Data Mining, Infection and Immunity, Machine Learning, Proteomics, and 'Biomedical Big Data', which are highly sought-after expertise and skill sets in the data-driven biomedical sciences. He was awarded a four-year NHMRC Peter Doherty Biomedical Fellowship. He also received both the JSPS Long-term and Short-term Fellowships and did his postdoctoral research at the Bioinformatics Center, Kyoto University, Japan. He is a member of the Monash Centre for Data Science and also Associate Investigator of the ARC Centre of Excellence in Advanced Molecular Imaging at Monash University. He is an Associate Editor of BMC Bioinformatics and Protein & Peptide Letters and serves as an Advisory Board member of Current Protein & Peptide Science.

Topic: "Leveraging the Power of Data-driven Machine Learning Techniques to Address Significant Biomedical Classification Problems"

Abstract—Recent advances in high-throughput sequencing have significantly contributed to an ever-increasing gap between the number of gene products ('proteins') whose function is well characterized and those for which there is no functional annotation at all. Experimental techniques to determine the protein function are often expensive and time-consuming. Recently, machine-learning (ML) techniques based on statistical learning have provided efficient solutions to challenging problems of sequence classification or functional annotation that were previously considered difficult to address. In this talk, by combining our recent research progress, I will highlight some important developments in the prediction of two representative sequence labeling problems in computational biology based on the high-dimensional, noisy and redundant information derived from sequences and the 3D structure. I will illustrate how ML methods can extract the predictive power from a variety of features that are derived from different aspects of the data and useful strategies that help to contribute to the predictive performance of ML approaches.

Invited Speaker II

Prof. Sung Wing Kin, Ken
National University of Singapore, Singapore

Prof. Dr. Wing-Kin Sung received both the B.Sc. and the Ph.D. degree in the Department of Computer Science from the University of Hong Kong in 1993, 1998, respectively. He is a professor in the Department of Computer Science, School of Computing, NUS. Also, he is a senior group leader in Genome Institute of Singapore. He has over 20 years experience in Algorithm and Bioinformatics research. He also teaches courses on bioinformatics for both undergraduate and postgraduate. He was conferred the 2003 FIT paper award (Japan), the 2006 National Science Award (Singapore), and the 2008 Young Researcher Award (NUS) for his research contribution in algorithm and bioinformatics.

Topic: "Improving CNV Calling from High-throughput Sequencing Data through Statistical Testing"

Abstract—Structural variations (SV) are large scale mutations in a genome; although less frequent than point mutations, due to their large size they are responsible for more heritable differences between individuals. Two prominent classes of SVs are deletions and tandem duplications. They play important roles in many devastating genetic diseases, such as Smith-Magenis syndrome, Potocki-Lupski syndrome and Williams-Beuren syndrome. Since paired-end whole genome sequencing data has become widespread and affordable, reliably calling deletions and tandem duplications has been a major target in bioinformatics; unfortunately, the problem is far from being solved, since existing solutions often offer poor results when applied to real data. In this talk, we will focuses on detecting deletions and tandem duplications from paired next-generation sequencing data. We will discuss why deletions and tandem duplications are difficult to call. Then, we will propose a statistical method SurVIndel that outperforms existing methods on both simulated and real biological datasets

Invited Speaker III

Prof. Ryoji Nagai
Tokai University, Japan

Dr. Ryoji Nagai received his Bachelor of Science in Teikyo University Science & Engineering, Master degree in University of Shizuoka and Ph. D degree in Kumamoto University. He is a Professor in the Laboratory of Food and Regulation Biology, Graduate School of Agriculture, Tokai University. His research fields are investigation of pathways of advanced glycation end-products (AGEs) and its inhibitors to prevent lifestyle-related diseases.

Topic: "Goodness of Fit Test at Extreme of Disease Risk Distribution"

Abstract—The number of diabetic patients in the world is continuously increasing. A measurement of Hemoglobin A1c (HbA1c), which is formed by the reaction between hemoglobin and blood sugar through the Maillard reaction, is generally adopted as a clinical marker of blood glucose control in patients with diabetes. In the end, advanced glycation end products (AGEs) are formed through oxidation, dehydration and condensation. This reaction progresses not only in processing foods but also in physiological conditions. Detection of AGEs in samples is still difficult and many studies overestimate AGEs levels in physiological samples. Furthermore, many pathways have been reported to be involved in the generation of AGEs in vivo, it is difficult to clarify the relationship between pathology and glycation by measuring only a single AGE structure. Therefore, monitoring for multiple AGEs in biological samples by instrumental analyses, such as liquid chromatography tandem mass spectrometry (LC-MS/MS), is widely done to assess the biological significance of AGEs. Therefore, in this talk, we would like to explain the advantages of the multiple analysis of AGEs to demonstrate the protein modification in vivo and its involvement with lifestyle-related diseases

Session 1

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

Afternoon, January 20, 2020 (Monday)
Time: 13:30-15:00
Venue: Room 1 (1F)
Topic: "Computational Biology"
Session Chair: Prof. Sung Wing Kin, Ken

K0016 Session 1 Presentation 1 (13:30-13:45)	LTR-TCP-FR: Protein Fold Recognition based on Learning to Rank Yulin Zhu and **Bin Liu** Harbin Institute of Technology, Shenzhen, China *Abstract*—Fold type reflects the topological patterns of protein core structures, and fold recognition is one of the most important tasks in the field of protein structure and function prediction. Previous studies have shown that Learning to Rank algorithm combined with different features extracted by different methods is an effective strategy for protein classification and detection, and protein similarity network can further improve the performance of the algorithm. In this study, we added the profile-based features, alignment score features and protein structure features into the Learning to Rank model, and then constructed a protein similarity network to transform fold recognition from low similarity problem to high similarity problem. Finally, a predictor called LTR-TCP-FR was proposed. The rigorous test on LE benchmark dataset shows that the LTR-TCP-FR predictor achieved an accuracy of 73.2%. It outperformed all the other existing computational predictors. Therefore, LTR-TCP-FR is an effective method for protein fold recognition, and it will become a useful tool for protein sequence analysis.
K0069 Session 1 Presentation 2 (13:45-14:00)	A Mono-bidomain Electrophysiological Simulation Method for Electrical Defibrillation Research **Jianfei Wang**, Lian Jin, Weiqi Wang and Xiaomei Wu Fudan University, China *Abstract*—Computational simulation is highly useful to study the mechanisms and methods of electrical defibrillation. However, current simulation methods have considerable limitations, such as inability to obtain the virtual electrode polarization and tremendous computational load. In order to solve these problems, we proposed a Mono-Bidomain simulation method that synthesizes the characteristics of the passive bidomain model and the active monodomain model to simulate the effect of active bidomain

	simulation. The distribution of virtual electrodes is obtained on the passive bidomain model by applying an electrical shock on the defibrillation electrodes at the moment of defibrillation, and the transmembrane potential of every myocardial node is converted into a transmembrane stimulus current; then the current is applied to the active monodomain model to get the propagation of ventricular electrical activity after defibrillation. Using this method, we simulated the changes of electrical activity of point and plate stimuli schemes on the ideal 2D and 3D tissue models, respectively. It shows that the simulation result of this method is very close to that of the active bidomain simulation, and the maximum average error of upstroke time is less than 2.5 ms, which verifies the effectiveness of the proposed method. This method can improve the simulation efficiency by greatly reducing the computational time and flexibly adjusting the electrode configurations, and provides a new means for the simulation study of arrhythmia electrotherapy.
K0042 Session 1 Presentation 3 (14:00-14:15)	Using Gene-level to Generalize Transcript-level Classification Performance on Multiple Colorectal Cancer Microarray Studies **Hendrick Gao-Min Lim** and Yuan-Chii Gladys Lee Taipei Medical University, Taiwan *Abstract*—Several classification algorithms have been applied into microarray studies for colorectal cancer identification. Algorithms such as naïve bayes, random forest, logistic regression, support vector machine, and deep learning have been successfully used in previous studies. The accuracy of these algorithms shown promising result through n-fold validation. However, most of studies are limited to transcript-level that will implicate to biased interpretation of classification result due to different microarray platform entanglement. Therefore, we applied gene-level classification to generalize transcript-level classification result on multiple colorectal cancer microarray studies through different classification algorithms including: naïve Bayes, random forest, logistic regression, support vector machine, and deep learning. We evaluated classification performance using several parameters including: accuracy, area under ROC curve, recall and precision. As the result, we found biased classification result in transcript-level from multiple microarray studies can be solved through gene-level classification by applying annotation and merging. In addition, applying batch effect removal method can make gene-level classification performance slightly improved. Furthermore, annotation and merging also can be used to solve another biased result of feature selection in transcript-level.
K0048 Session 1 Presentation 4 (14:15-14:30)	Efficient GPU Acceleration for Computing Maximal Exact Matches in Long DNA Reads **Nauman Ahmed**, Koen Bertels and Zaid Al-Ars Delft University of Technology, Netherlands *Abstract*—The seeding heuristic is widely used in many DNA analysis

	applications to speed up the analysis time. In many applications, seeding takes a substantial amount of the total execution time. In this paper, we present an efficient GPU implementation for computing maximal exact matching (MEM) seeds in long DNA reads. We applied various optimizations to reduce the number of GPU global memory accesses and to avoid redundant computation. Our implementation also extracts maximum parallelism from the MEM computation tasks. We tested our implementation using data from the state-ofthe-art third generation Pacbio DNA sequencers, which produces DNA reads that are tens of kilobases long. Our implementation is up to 9x faster for computing MEM seeds as compared to the fastest CPU implementation running on a server-grade machine with 24 threads. Computing suffix array intervals (first part of MEM computation) is up to 3x faster whereas calculating the location of the match (second part) is up to 9x faster. The implementation is publicly available at https://github.com/nahmedraja/GPUseed.
K2034 Session 1 Presentation 5 (14:30-14:45)	Spectral Structure and Nonlinear Dynamics Properties of Long-term Interstitial Fluid Glucose **Junichiro Hayano**, Atsushi Yamada, Yutaka Yoshida, Norihiro Ueda and Emi Yuda Nagoya City University, Japan *Abstract*—The spread of continuous indwelling sensors in the subcutaneous tissue has enabled continuous monitoring of interstitial fluid glucose concentration (ISFG) under daily activities. This technology is considered to enable the development of a method for evaluating glycemic control function by analyzing not only the detailed state of diabetes and other pathological conditions but also the characteristics of glycemic dynamics. To clarify the basic fluctuation characteristics of long-term ISFG, the spectral structure and nonlinear dynamics properties of ISFG obtained by continuous monitoring for 11 days were analyzed in healthy and diabetic subjects.
K0039 Session 1 Presentation 6 (14:45-15:00)	Assessing Information Quality and Distinguishing Feature Subsets for Molecular Classification **Hung-Yi Lin** and Da-Yi Yen National Taichung University of Science and Technology, Taiwan *Abstract*—A feature reduction scheme is developed in this study. The proposed scheme is a hybrid of unsupervised and supervised methods. The unsupervised process is designed to exclude the irrelevant and useless information before executing feature selection. Fuzzy clustering algorithm will categorize all features into different groups. Then, the supervised process using the target class information will purify the relevant and informative factors from the approved feature clusters. This purifying procedure is particularly suitable for high dimensional datasets with erroneous information. This proposed strategy is to retain the advantage of

	simplicity and lower selecting time consumption in filter methods while the disadvantage of high computational cost due to the exponential quantity of feature subsets in wrapper methods is completely avoided.

Session 2

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

Afternoon, January 20, 2020 (Monday)
Time: 13:30-15:00
Venue: Room 2 (1F)
Topic: "Pharmaceutical Science"
Session Chair: Prof. Max Leong

K0014 Session 2 Presentation 1 (13:30-13:45)	Docking Simulation of Chemerin-9 and ChemR23 Receptor **Keiichi Nobuoka**, Hironao Yamada, Takeshi Miyakawa, Ryota Morikawa, Takuya Watanabe and Masako Takasu Tokyo University of Pharmacy and Life Sciences, Japan *Abstract*—Chemerin-9 is a nonapeptide that corresponds to the YFPGQFAFS sequence on the C-terminus of Chemerin protein. Recent clinical and animal studies using mice, it has been recently reported that Chemerin-9 binds to the ChemR23 receptor and can suppress the inflammation-related diseases such as arteriosclerosis. In this study, molecular dynamics simulations were performed with the Chemerin-9 peptide to identify structures with high and low free energy. Docking simulations of these structures of Chemerin-9 and ChemR23 receptor were performed, and the docking model with the lowest free energy and binding energy of Chemerin was identified. For this model, the binding sites and binding forces were evaluated. Based on these findings, we aim to provide insights into the development of new drugs that suppress arteriosclerosis.
K0021 Session 2 Presentation 2 (13:45-14:00)	Drug Discovery for Kidney Chromophobe using Molecular Docking **Aysegul Caliskan** and Kazim Yalcin Arga Istinye University / Marmara University, Turkey *Abstract*—Chromophobe renal cell carcinoma (KICH) is one of renal cell carcinoma types and effective drugs are not available for treatment of this disease. With the development of technology, computer-based drug development studies have started to gain importance in order to shed light on experimental studies. The aim of this study is to discover new drug candidates for treatment of KICH by using computer-based drug repositioning and docking analysis techniques. For this purposes, DPP4, one of the hub and over-expressed proteins of KICH, was chosen for drug repositioning by taking account its position and function on cell. Crystal

	structure of DPP4 was fetched from Protein Data Bank. Zinc15 database was used to determine appropriate drugs which have the potential to bind DPP4 protein. 12 molecules that have best binding affinity to DPP4 were determined among 3786 substances taken from Zinc15 database after molecular docking studies. These molecules are open to experimental studies for treatment of KICH. Besides Saxagliptin and Dutogliptin are already commercially available drugs that are used for treatment of type 2 diabetes by selectively inhibiting DPP4. We recommend that these two drugs should be investigated also for kidney chromophobe.
K0036 Session 2 Presentation 3 (14:15-14:30)	Docking Small Molecules Belonging *Laserpitium* sp. into LCK Protein Upregulated in Rheumatoid Arthritis **Meltem Gulec**, Aysegul Caliskan and Ahmet Cenk Andac Istinye University / Istanbul University, Turkey *Abstract*—Docking is a increasingly frequent method and developing technology in pharmaceutical studies assuring the researchers the chance to dock small-molecule libraries to a macromolecule in order to find proper compounds with certain biological functions. At the same time a great number of pharmacognosy studies has given rise to a database in which active ingredients isolated from a variety of plants are available. Although some studies have been carried out to determine biological activities of the active ingredients, there is still much to discover biological activities for the rest of the molecules in the database. In-vitro determination of biological activites for each of the molecules is an exhaustive process and the required expenses are very high. In-silico docking experiments are very helpful in studying binding interactions between receptors and ligands, reducing the exhaustive-time required for in-vitro activity studies. In traditional medicine, some *Laserpitium* species have been used in the treatment of rheumatoid arthritis. The main objective of this study is to determine binding affinities of the active ingredients of the plant genus *Laserpitium* toward LCK proto-oncogene, a Src Family Tyrosine Kinase that is upregulated in rheumatoid artirititis. The active small molecules of *Laserpitum*, obtained from the online database Sci-Finder, docked into the binding site of LCK protein and yielded high binding affinities with some small molecules. This is a unique study due to resulting a computer-based docking data for the isolated active compounds obtained by plant isolation studies which has not conducted. However, the small molecues with high binding affinites should be further tested in-vitro.
K2033 Session 2 Presentation 4 (14:30-14:45)	Antimicrobial Property and Mechanism of Action of Mangiferin from *Curcuma Amada* **Sayanti Dey**, Abhishek Raj, Hari Om and Debjani Dutta National Institute of Technology Durgapur, India *Abstract*—Food spoilage is a process where a food product becomes unsuitable to ingest by the consumer. Globally, spoilage caused by food

	borne microorganisms still widely affects all types of food and causes food waste and loss, even in developed countries. Bacteria, yeast and molds are the common types of microbes that are responsible for the spoilage of a considerable amount of food products. Traditionally, the crude extracts of different parts of medical plants including root, stem, flowers, leaves are widely used for the treatment of many diseases. These plants contain bioactive compounds such as flavonoids, poly phenol, alkaloids that possess antimicrobial, antioxidant and antimutagenic activity. Mangiferin is one such bioactive compound having putative chemo preventive and antioxidant properties and has the potential of being used as nutraceutical. It is a poly-phenol compound derived from Anacardiaceae and Gentianaceae families and primarily found in Mangifera indica. In this study we have used Curcuma amada (Mango ginger) to extract mangiferin and found the concentration to be as high as 206 micrograms/ml. Various antimicrobial assays have been done using crude Curcuma amada against gram (-) ve and gram (+) ve bacteria like Escherichia coli, Bacillus subtilis and Staphylococcus aureus. It has been observed that mangiferin has inhibited the growth of gram (-) ve bacteria and has selective inhibitory effect on gram (+) ve bacteria. It can be concluded that mangiferin from Curcuma amada is a potential nurtaceutical and can be used as antimicrobial, antioxidative agent.
K2021 Session 2 Presentation 5 (14:45-15:00)	In *situ* Transfection through Wound Dressing to Promote Tissue Regeneration **Wei-Wen Hu** and Yu-Ting Lin National Central University, Taiwan *Abstract*—Chronic wounds may retard the healing process to cause many risks. Therefore, it is essential to develop a multifunctional wound dressing to promote tissue regeneration. To fabricate a versatile composite nanofibrous matrix, sodium alginate and poly (ε-caprolactone) (PCL) were coelectrospun as composite nanofibers using a dual jet system. Hydrophilic alginate fibers may provide a moist environment in wound sites. In addition, PCL were applied to increase mechanical strength and cell adhesion. Silver nanoparticles were embedded in PCL fibers for long-term release to inhibit the growth of microorganism. Plasmid DNA encoding platelet-derived growth factor B (PDGFB) was delivered from composite fibers because this growth factor is a chemoattractant for neutrophils and can induce the proliferation and differentiation of fibroblasts. These PDGFB plasmids were complexed with polyethylenimine (PEI) to form cationic nanoparticles which may thus be adsorbed onto anionic alginate fibers through electrostatic interaction. As wound cells adhered to composite fibers, they can be in situtransfected to continuously express PDGFB. Moreover, calcium ions in alginate fibers were released to wound sites through ion exchange to accelerate hemostasis. This comprehensive dressing provides an ideal solution to heal chronic wounds.

K0029 Session 2 Presentation 6 (14:00-14:15)	Theoretical Prediction of Parallel Artificial Membrane Permeability Assay Permeability using a Two-QSAR Approach **Max K. Leong** National Dong Hwa University, Taiwan *Abstract*—Drug absorption is one of pivotal drug metabolism and pharmacokinetics (DM/PK) properties that should be taken into account in the process of drug discovery and development. The *in vitro* parallel artificial membrane permeability assay (PAMPA) has been adopted as the preliminary screening to estimate the passive diffusion of compounds in the practical applications. A classical quantitative structure–activity relationship (QSAR) model and a machine learning (ML)-based QSAR model were derived using the partial least square (PLS) scheme and hierarchical support vector regression (HSVR) scheme to elucidate the underlying passive diffusion mechanism and to estimate the PAMPA effective permeability (*P*e), respectively, in this investigation. It was observed that HSVR performed better than PLS as indicated by the predictions of the molecules in the training set, test set, and outlier set as well as various statistical assessments. When applied to the mock test, HSVR also demonstrated better predictive performance. PLS, conversely, can render some relationships between descriptors and permeability. Thus, the synergy of predictive HSVR and interpretable PLS models can be greatly useful in facilitating drug discovery and development by predicting passive diffusion.


15:00-16:00	**Coffee Break & Poster Session**

Session 3

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

Afternoon, January 20, 2020 (Monday)
Time: 16:00-17:45
Venue: Room 1 (1F)
Topic: "Biological Science and Information Technology"
Session Chair: Prof. Kuo-Sheng Cheng

K1007 Session 3 Presentation 1 (16:00-16:15)	Effects of 2, 3', 4, 4', 5-pentachlorobiphenyl Exposure during Pregnancy dn Germ Cell Development and Epigenetic Modification of F1 Mice **Qi-Long He**, Xu-Yu Wei, Qian Zhou, Hai-Quan Wang and Shu-Zhen Liu Shandong Normal University, China *Abstract*—2, 3', 4, 4', 5-pentachlorobiphenyl (PCB118) is an important dioxin-like polychlorinated biphenyls compound with strong toxicity. PCB118 can accumulate in adipose tissue, serum and milk in mammals, and it is highly enriched in the follicular fluid. In this study, pregnant mice were exposed to 0, 20 and 100 μg/kg/day of PCB118 during pregnancy at the fetal primordial germ cell migration stage. The methylation patterns of some imprinted genes as well as the expression levels of *Dnmts*, *Uhrf1* and *Tets* in fully grown oocytes, sperm or testes and the methylation level in oocytes or testes were measured in offspring. The rates of *in vitro* maturation, *in vitro* fertilization, oocyte spindle and chromosomal abnormalities were also calculated. The results showed that prenatal exposure to PCB118 altered the DNA methylation status of differentially methylated regions in some imprinted genes, the methylation levels in oocytes and testes also reduced. The expression levels of *Dnmts*, *Uhrf1* and *Tet3* were changed by prenatal exposure of PCB118 in oocytes or testes. In addition, PCB118 disturbed the development process of progeny mouse germ cells in a dose-dependent manner. Therefore, attention should be paid to the potential impacts of PCB118-contaminated dietary intake during pregnancy on the offspring's reproductive health.
K2027 Session 3 Presentation 2 (16:15-16:30)	Morphological Variation and Systematic Value of Indumentum in Philippine Vavaea Bentham (Meliaceae) Species **Dhiocel A. Celadiña** and Edwino S. Fernando Western Philippines University, Philippines *Abstract*—There is only one recognized species of *Vavaea* in the Philippines, *Vavaea amicorum*. *Vavaea amicorum* is widespread and

	polymorphic in nature having a very broad circumscription. However, recent collections in Surigao, Philippines from two populations discovered that this species can hyperaccumulate nickel while others cannot. Thus, the very broad circumscription of the widespread *Vavaea amicorum* in the taxonomic revision of Pennington (1969) needs a closer re-examination. Leaf morphological variations and indumentum characters of the eight Philippine *Vavaea* species previously recognized were studied. Description of each taxon is presented, and dichotomous key is provided for quick reference. Principal component and cluster analyses of all species was performed, using 25 morphological characters, to test their morphological distinctiveness. The Principal Component Analysis generated five axes explaining 85.73% of the total variance among the species. The most important morphological characters differentiating Philippine *Vavaea* are the indumentum type on branchlet, branchlet tips, petiole, leaf surfaces, midrib and lateral veins. Three species may be resurrected, namely: *Vavaea pilosa*, *Vavaea pachyphylla* and *Vavaea surigaoense* based from cluster analysis. These three distinct morphological entities may be assigned back to its previous taxonomic rank. Correct taxonomic position of Philippine *Vavaea* is essential in crafting their conservation measures.
K0043 Session 3 Presentation 3 (16:30-16:45)	Deep Learning based System to Extract Agricultural Workers' Physical Timeline Data for Acceleration and Angular Velocity **Shinji Kawakura** and Ryosuke Shibasaki The University of Tokyo, Japan *Abstract*—Several physical characteristics of workers can be extracted from physical timeline data to understand acceleration and angular velocity. Although various approaches have been implemented globally for indoor and outdoor agricultural (agri-) working sites, there is room for improvement. In this study, we aim to adapt these approaches particularly for real agri-directors, leaders and managers to improve the quality of tasks and their security levels. Thus, we apply a deep learning-based method and qualitatively demonstrate the classification of physical timeline datasets. To create our dataset, our subjects were six experienced agri-manual workers and six completely inexperienced men. The targeted task was cultivating the semi-crunching position using a simple, Japanese-style hoe. We captured the subjects' acceleration and angular velocity data from an integrated multi-sensor module mounted on a wood lilt 15 cm from the gripping position of the dominant hand. We used Python code and recent distributed libraries for computation. For data classification, we successively executed a Recurrent Neural Network (RNN), which we evaluated using wavelet analyses such as the Fast Fourier Transform (FFT). These methods of analyzing digital data could be of practical use for providing key suggestions to improve daily tasks.
K0013	A Method for the Inverse QSAR/QSPR based on Artificial Neural Networks and Mixed Integer Linear Programming

Session 3 Presentation 4 (16:45-17:00)	**Rachaya Chiewvanichakorn**, Chenxi Wang, Zhe Zhang, Aleksandar Shurbevski, Hiroshi Nagamochi and Tatsuya Akutsu Kyoto University, Japan *Abstract*—In this study,we propose a novel method for the inverse QSAR/QSPR. Given a set of chemical compounds G and their values a(G) of a chemical property, we define a feature vector f (G) of each chemical compound G. By using a set of feature vectors as training data, the first phase of our method constructs a prediction function ψ with an artificial neural network (ANN) so that ψ(f (G)) takes a value nearly equal to a(G) for many chemical compounds G in the set. Given a target value a∗ of the chemical property, the second phase infers a chemical structure G∗ such that a(G∗) = a∗ in the following way. We compute a vector f ∗ such that ψ(f ∗) = a∗, where finding such a vector f ∗ is formulated as a mixed integer linear programming problem (MILP). Finally we generate a chemical structure G∗ such that f (G∗) = f ∗. For acyclic chemical compounds and some chemical properties such as heat of formation, boiling point, and retention time, we conducted some computational experiments with our method.
K2014 Session 3 Presentation 5 (17:00-17:15)	An Investigation of Factors Influencing Performance of RFID-based Vehicle Detection Li-Fei Chen, Ruei-Shiuan Tsai, Yuan-Jui Chang and **Chao-Ton Su** National Tsing Hua University, Taiwan *Abstract*—Electronic toll collection (ETC) is an automatic charge system. The driver can pass through the toll booth without needing to stop via this ETC system. The ETC system can help to lower the cost of charging and reducing the travel time. In this presentation, we provide a real case study to investigate the performance of the highway ETC system. The system uses sensors to transmit radio waves and detect radio frequency identification (RFID) tags that are attached to the car. Five machine learning techniques, random forest, XG-boost, gradient boost, support vector machine, and neural network, are applied to analyze ETC data for vehicle detection in order to identify key features that affect RFID tag detection and increase RFID tag detection accuracy rate. After implementation, several valuable insights are collected to enhance RFID tag detection rate; therefore, company's operating costs can be greatly reduced.
K2020 Session 3 Presentation 6 (17:15-17:30)	Energy Monitoring and Management System Design Based on Embedded Structure **Horng-Lin Shieh**, Cheng-Chien Kuo and Sheng-Bo Gao St. John's University, Taiwan *Abstract*—Due to the huge amount of energy demanded by humans, it causes serious damage to the environment, for example, the destruction of the ozone layer by the exhaust gas generated by thermal power plants. In order to reduce energy waste, this study designed a smart energy monitoring

	system that combines ARM embedded system, wireless transmission and database technologies. In the designed system, ARM Cortex-M4 was adopted as the system core. The customer's power consumption data can be transmitted to the back-end database via wire or wireless, and the power consumption information can be instantly displayed in a graphical interface. In order to save and reduce wasted energy, this study uses a sorting algorithm to automatically unload loads according to the urgency of energy demand to avoid unnecessary energy waste.
K0046 Session 3 Presentation 7 (17:30-17:45)	GpemDB: A Scalable Database Architecture with the Multi-omics Entity-relationship Model for Integrating Heterogeneous Big-data in Precise Crop Breeding **Liang Gong**, Shengzhe Fan and Wei Wu Shanghai Jiao Tong University, China *Abstract*—With the development of high-throughput genome sequencing and phenotype screening techniques, there is a possibility of leveraging multi-omics to speed up the breeding process. However, heterogenous big data complicate the progress and the lack of database supported end-to-end association analysis impedes the efficient use of these data. In response to this problem, a scalable entity relationship model and a database architecture are proposed in this paper to manage the cross-platform data sets and explore the relationship among multi-omics. First, the targeted omics regarding to precise breeding of crops are clarified from the engineering viewpoint of cultivars. Meanwhile, a typical breeding data content and structure is demonstrated with the case study of rice (Oryza sativa L.) where the agronomic phenotype traits are highlighted. Second, the breeding multi-omics data structure, patterns and hierarchy are described with entity-relationship modeling technique. Third, a general-purpose scalable database, called GpemDB (integrating Genomics, Phenomics, Enviromics, and management), is developed. The developed GpemDB, involving Gpem metadata-level layer and informative-level layer, provides a visualized scheme to display the content of the database and facilitates users to manage, analyze and share the breeding data. GpemDB with application to rice breeding demonstrates that the proposed database architecture and models are feasible to serve as the foundation for precise breeding of crops.

Session 4

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

Afternoon, January 20, 2020 (Monday)
Time: 16:00-17:45
Venue: Room 2 (1F)
Topic: "Environmental Chemistry and Materials"
Session Chair: Prof. Manuel Garcia Roig

K3002 Session 4 Presentation 1 (16:00-16:15)	Methotrexate Degradation by UV-C and UV-C/TiO2 Processes with and without H2O2 Addition on Pilot Reactors L. A. González-Burciaga, J. C. García-Prieto, C. M. Núñez-Núñez, **M. García-Roig**, J. B. Proal-Nájera University of Salamanca, Spain *Abstract*—Methotrexate (MTX) is an anti-cancer drug that can be excreted up to 90% after administration due to its low biodegradability. Advanced Oxidation Processes (AOPs) are a feasible alternative for the elimination of MTX in the environment. In this research, AOPs were performed in specialized patented reactors (UBE Photocatalytic systems and BrightWater Titanium Advanced Oxidation Process) under experimental pilot conditions. Photolysis and heterogeneous photocatalysis (UV and UV/TiO2) experiments were performed with and without addition of H2O2 and at different initial pHs. Best degradation percentage was achieved by photolysis when initial Ph was 3.5 and added H2O2 was 3 Mm, reaching a MTX degradation of 82% after 120 min of reaction. HPLC-MS analysis of the resulting samples showed four possible byproducts of MTX degradation, which presented a higher ecotoxicity than the starting compound.
K2015 Session 4 Presentation 2 (16:15-16:30)	Empirical Approach for Modeling of Partition Coefficient on Lead Concentrations in Riverine Sediment **Saadia Bouragba**, Katsuaki Komai, and Keisuke Nakayama Kitami Institute of Technology, Japan *Abstract*—Since a large part of heavy metals input in aquatic system accumulates in sediment, their concentrations in sediment are regarded as an important indicator of the heavy metal pollution of aquatic environment. The partition coefficient (K_d) is an empirical parameter that can represent the interaction of heavy metals at the sediment-water interface in aquatic system, however, it is not always stable with environmental conditions. Therefore, the introduction of K_d model with dominant physicochemical parameters would facilitate and improve the simulation of heavy metals

	concentrations in riverine sediment. The present study aims to develop a K_d model considering four physicochemical properties in stream water in order to simulate heavy metal concentrations in sediment of severely polluted urban rivers. Lead (Pb) concentrations in sediment of Harrach River, Algeria, were simulated using one-dimensional distributed hydrological model incorporating with presented K_d model. Multivariable equation of K_d model with physicochemical parameters (pH, suspended solid concentration (SS), chemical oxygen demand (COD) and biological oxygen demand (BOD)) was obtained from multiple regression analysis with observation data in various environmental condition. Hydrological simulations were tested with K_d model comparing to giving constant K_d. The numerical results agreed better with K_d model than with constant K_d, where the results accuracy increased from R^2 0.05 for constant K_d to R^2 0.67 for K_d model.
K2023 Session 4 Presentation 3 (16:30-16:45)	Potassium Fluoride-doped CaMgAl Layered Double Hydroxides for HCl Adsorption in the Presence of CO2 at Medium-high Temperature **Wei Wu**, Tongwei Wang, Decheng Wang and Baosheng Jin Southeast University, China *Abstract*—In the present work, the potassium fluoride-doped CaMgAl layered double hydroxides (CaMgAl-LDHs) were synthesized by co-precipitation method, which were used as adsorbents for HCl adsorption in a quartz reactor under medium-high temperature (400-800 ℃). In addition, the influence of CO_2 to the HCl removal capacity of Ca-Mg-Al layered double oxides (CaMgAl-LDOs) was also investigated. The results showed that the KF/CaMgAl-LDOs loading with 25wt.% KF was the optimal adsorbent for HCl removal. The microstructure of the adsorbents after reaction revealed that the adsorbents were encapsulated by dense chloride, and the adsorption process was mainly dominated by chemical adsorption, strong acid-base properties, specific surface area and mesopore number. Furthermore, the moderate CO_2 concentration (0~6%) in the flue gas of the municipal solid-waste incinerators could lessen the HCl removal capacity of the CaMgAl-LDOs. However, the reduction of the HCl removal capacity was less than 9% when the CO_2 concentration was below 10%. Moreover, the most suitable reaction temperature was optimized as 600 ℃ for the CaMgAl-LDOs. It can be drawn that employing some anti-sintering support was efficient to improve the absorption capacity of the CaMgAl-LDOs.
K2025 Session 4 Presentation 4 (16:45-17:00)	Quantum Chemical Research on Mechanism of Hydrogen Chloride Removal by Calcium Carbonate **Jie Zhu**, Wei Wu and Dejian Shen Hohai University, China *Abstract*—A detailed quantum chemical calculation was performed to explore the mechanism of hydrogen chloride removal by calcium carbonate. The possible pathways of the reaction between hydrogen chloride and

	calcium carbonate were studied by using gaussian software. The nature of bonding evolution based on the main reaction pathway was studied by using both electron localization function and atoms in molecules analysis. Moreover, the reaction equilibrium constant and the reaction rate constant were calculated between 298 K and 1100 K based on the rate-determining step of the main reaction pathway. The results showed that: (1) the main pathway of the reaction between hydrogen chloride and calcium carbonate was $CaCO_3$+HCl→$CaClCO_2OH$, $CaClCO_2OH$+HCl→$CaCl_2$ H_2O CO_2, $CaCl_2$ H_2O CO_2→$CaCl_2$+H_2O+CO_2; (2) the activation energy barrier of the main pathway was 61.00 kJ mol^{-1}; (3) the reaction equilibrium constant or the reaction rate constant decreased or increased with the increase of the temperature, respectively. The present study may provide useful information for understanding the reaction mechanism of calcium-based adsorbent.
K2024 Session 4 Presentation 5 (17:00-17:15)	Bifunctional MOFs as Efficient Catalysts for Catalytic Conversion of Carbon Dioxide into Cyclic Carbonates and DFT Studies **Yuanfeng Wu** and Guomin Xiao Southeast University, China *Abstract*—The metal organic framework materials of [(CH_3NH_3][$Mn(COOH)_3$] (MA-MnF), [($CH_3CH_2NH_3$][$Mn(COOH)_3$] (EA-MnF), and [$C_3H_5N_2$][$Mn(COOH)_3$] (Im-MnF) were easily prepared under room temperature, and further employed as the highly-efficient catalysts for catalytic conversion of carbon dioxide into cyclic carbonates. The metal organic frameworks including MA-MnF, EA-MnF, Im-MnF were studied via several characterizations such as XRD, FT-IR, XPS, N_2-adsorption, TG-DSC, CO_2-adsorption and NH_3-TPD. Interestingly, Im-MnF compound was observed to possess the highest catalytic activity among the studied compounds, which is associated not only with the amounts of basic sites, but also related to the nitrogen-containing species. Various reaction parameters including reaction temperature, reaction time, catalyst loading, reaction pressure as well as recyclability and coupling scope were explored. 97.27% conversion of allyl-glycidyl ether (AGE, TOF: 36.78 h^{-1}) and 97.66% selectivity to allyl-glycidyl carbonate (AGC) were obtained under the explored optimized conditions (100 ^oC, 15bar, 6h, 1.0 wt.% of AGE). In addition, only a slight downward in catalytic activity was found when the sample was reused twice. Furthermore, coupling reactions of CO_2 with various epoxides were also performed, of which, the yield of the cyclic carbonates followed the order: Epichlorohydrin > Allyl glycidyl ether > Styrene oxide > Cyclohexene oxide> Propylene oxide. Finally, a mechanism was proposed for explaining carbon dioxide insertion into epoxide. Besides density functional theory (DFT) calculations were also performed on Gaussian 09 Packages (M06 method//6-31g(d, p) for main-group element, ECP-Lanl2DZ for Mn element). The calculated results were in good agreement with the DFT calculation.
K1013	A Novel Deep-blue Thermally Activated Delayed Fluorescence Emitter

Session 4 Presentation 6 (17:15-17:30)	Dimethylacridine/Thioxanthene-S,S-Dioxide for Highly-efficient Organic Light-emitting Devices **Young Pyo Jeon** Hanyang University, South Korea *Abstract*—Even though the development of organic light-emitting devices (OLEDs) as a potential sustainable future display technology has made great progress, a study on materials with deep-blue emission for use in thermally activated delayed fluorescence (TADF) OLEDs is still an important challenge in this field of scientific research. Hence, a novel deep-blue emissive dopant material, 2,7-bis(9,9-dimethylacridine-10(9H)-yl)-9,9-diphenyl-9H-thioxanthene 10-,10-dioxide (DMA-ThX), is synthesized for highly-efficient thermally activated delayed fluorescence organic light-emitting devices (TADF OLEDs). The molecular design of DMA-ThX retains the overlap between the lowest singlet excited state (S_1) and the lowest triplet excited state (T_1) because of its twisted molecular structure. From photoluminescence emission measurements at low temperature, the difference between of the S_1 and T_1 energy levels of 3.14 and 3.07 eV is found to be 0.07 eV. Furthermore, the external quantum efficiency of the deep-blue-emitting TADF OLEDs with DMA-ThX-doped bis[2-(diphenylphosphino)phenyl] ether oxide is 18.4%, which is significant, and the Commission Internationale de l'Eclairage coordinates are (0.14, 0.14), indicative of very pure deep-blue emission.
K2036 Session 4 Presentation 7 (17:30-17:45)	Environmental Sustainability: Management Perception in Oil and Gas Industry in Libya **Nahg A. Alawi**, Khairi Ahmed Masaud and Samer A. Bamansoor Aden University, Yemen & Geomatika University, Malaysia *Abstract*—This study aims to examine the environmental sustainability perceptions of corporate managers in oil and gas industry in Libya and the factors that effect this perception. Based on primary data collected via a self-administered survey sent to 274 managerial and executive level and analysed using descriptive means and regression. The result shows that managers have high level of environmental sustainability perception. The results also show that only educational level have a positive and significant impact on managers' environmental sustainability perceptions. Limitation of this study is noted including the generalizability of the findings within organisation in Libya. The study has bridged the literature gaps in such that it offers empirical evidence and new insights on environmental sustainability body of knowledge which could be used to further improvement of the environmental sustainability perception in oil and gas companies in Libya.

Session 5

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

Afternoon, January 21, 2020 (Tuesday)
Time: 13:30-15:15
Venue: Room 1 (1F)
Topic: "Bioinformatics"
Session Chair: Prof. Tomohiro Araki

K0077 Session 5 Presentation 1 (13:30-13:45)	A Sparse Bayesian Approach to Combinatorial Feature Selection and Its Applications to Biological Data **Ryoichiro Yafune**, Daisuke Sakuma, Yasuo Tabei, Noritaka Saito, Einoshin Suzuki and Hiroto Saigo Kyushu University, Japan *Abstract*—With the rapid increase in the availability of large amount of data, prediction is becoming increasingly popular, and has widespread through our daily life. However, powerful non-linear prediction methods such as neural networks and SVM suffer from interpretability problem, making it hard to use in domains where the reason for decision making is required. In this presentation, we present a prediction model that consider variable interactions, in which salient variables are selected based on a Bayesian sparse prior. We demonstrate its usefulness in bioinformatics applications, such as detecting interactions among biomarkers.
K0017 Session 5 Presentation 2 (13:45-14:00)	Analyses of Interaction between Platinum Bonded LARFH and Gold Surface by Molecular Dynamics Simulation Mao Watabe, Keiichi Nobuoka, Hironao Yamada, Takeshi Miyakawa, Ryota Morikawa, **Masako Takasu**, Tatsuya Uchida and Akihiko Yamagishi Tokyo University of Pharmacy and Life Sciences, Japan *Abstract*—Proteins that specifically bind to metals have been used for research on development of new organic-inorganic hybrid materials. Several peptides and proteins that bind to metals have been reported; this property can be attributed to their structures. In this paper, we assessed the binding of a sequence of the protein called LARFH to a metal surface. We performed simulation with several models of LARFH protein with different loop sequences binding to the metal surface. It was found that the angle between the LARFH protein and the metal surface varied for different loop sequences. We also performed simulations of the detachment process of LARFH. It was concluded that the stronger binding to metal is established by two gold-binding loops of the LARFH sequences.

K0038 Session 5 Presentation 3 (14:00-14:15)	Identification of Redox-sensitive Cysteines using Sequence Profile Information **Md. Mehedi Hasan** and Hiroyuki Kurata Kyushu Institute of Technology, Japan *Abstract*—Redox-sensitive cysteine (RSC) thiol contributes to many biological processes. The identification of RSC plays an important role in clarifying the mechanism of redox-sensitive factors; nonetheless, experimental investigation of RSCs through traditional methods is expensive and time-consuming. Therefore, the computational approaches that potentially predict candidate RSCs using the sequence information are critically needed. Herein, a sophisticated computational predictor IRC (Identification of Redox-sensitive Cysteine) was developed to identify the RSC using sequence profile information with a non-parametric feature selection approach. Then, a machine learning algorithm called "random forest" was trained with these features to build the predictor. The resultant IRC achieved an AUC score of 0.803 on the training dataset. The IRC performed better than other existing computational models on both the training and independent datasets. The IRC is a helpful computational predictor for the prediction of RSCs..
K0019 Session 5 Presentation 4 (14:15-14:30)	Relationship between Dynamics of Structures and Dynamics of Hydrogen Bonds in Hras-GTP/GDP Complex **Takeshi Miyakawa**, Kimikazu Sugimori, Kazutomo Kawaguchi, Masako Takasu, Hidemi Nagao and Ryota Morikawa Tokyo University of Pharmacy and Life Sciences, Japan *Abstract*—Hras protein is an intermediate for signals of cell proliferation and cell differentiation when Hras combines with guanosine triphosphate (GTP). In ordinary cells, GTP combined with Hras is hydrolyzed to guanosine diphosphate (GDP), and the structures of the protein-ligand complex strongly depend on hydrogen bonds. In such a system, hydrogen bonds exist between protein and ligand, between protein and water, and between ligand and water. In this study, we applied a relaxation mode analysis (RMA) to the trajectories of MD simulations for Hras-GTP/GDP to investigate the relationship between the dynamics of structures and those of hydrogen bonds. Different relaxation time of relaxation modes of Hras structures and Hras-solvent water hydrogen bonds were evident between Hras-GTP and Hras-GDP, and the results imply that the structure of Hras in Hras-GTP is stiffer than that in Hras-GDP. The method devised here and its interpretation can be applied to other systems focusing on objects with different stiffnesses.
K0079 Session 5	Bayesian Optimization for Sequence Data Kohei Oyamada and **Hiroto Saigo** Kyushu University, Japan

Presentation 5 (14:30-14:45)	*Abstract*—Directed evolution is a method used in protein engineering that mimics the process of natural selection to steer proteins or nucleic acids toward a user-defined goal. It iteratively introduce randomness in sequence, and choose members with desired functionalities. In order to decrease the number of experimental rounds, we consider introducing a strategy known as a Bayesian optimization. It requires similarity measure among sequences, so we employ vectorization methods such as k-mers and seq2seq as well as alignment scores. We validate the effectiveness of our approach in four benchmark datasets. In the two tasks where consideration of evolutionary distance is deemed to be important, alignment scores showed better performance than vectorization methods. We also demonstrate the usefulness of introducing batch processing for accelerating the computation.
K0020 Session 5 Presentation 6 (14:45-15:00)	Microorganism Hydrolysate Reduced Lipo-oxidation in Regulated High-fructose Induced Nonalcoholic Fatty Liver Disease in A Murine Model **Chang-Chi Hsieh** and Li-Jia Huang Tunghai University, Taichung, Taiwan *Abstract*—Pet suffered from metabolic syndrome were change in eating habits in diet. In Taiwan, Sixty percent of pets have obesity problems, and the obese pets are at higher risk of nonalcoholic fatty liver disease (NAFLD). Pig kidney is a large amount of slaughter by-products. We developed the pig kidney by-products were recycled and applied to healthy food for pets. The purpose of a study, we will use *Lactobacillus Plantarum* hydrolyzed pig kidney by-products, and explored the effects of hydrolysate on NAFLD in murine model. In this study, male C57BL/6JNarl mice were divided into five groups, normal group, control group (administered with the distilled water), treatment group (administered with pig kidney by-products microorganism hydrolysate 50 and 200 mg/kg/day) and microorganism control group. And mice induced NAFLD by 30% high-fructose corn syrup solution for 8 weeks. Finally, we measured serum aspartate aminotransferase (sAST), alanine aminotransferase (sALT), triglyceride (sTG), total cholesterol (sTC) and cytokines (IL-6, MCP-1, adiponectin). Pathology of liver staining sections were determinate by H&E staining and immunohistochemical staining for 4 Hydroxynonenal (4-HNE), thymic stromal lymphopoietin (TSLP). The results indicate the microorganism hydrolysate decreased sTG, sTC, IL-6, MCP-1 and increased adiponectin. The inhibition of lipo-oxidation might be the results of the improve in NASLD by reduced the lipo-oxidation related indicators.
K0045 Session 5 Presentation 7 (15:00-15:15)	Improvement of Protein Stability Prediction by Integrated Computational Approach **Chi-Wei Chen**, Meng-Han Lin, Hsung-Pin Chang and Yen-Wei Chu National Chung-Hsing University, Taiwan *Abstract*—Mutation of a single amino acid residue may change protein

	structure which affect protein function and diseases. Increasing protein stability or maintaining its stability while changing protein properties is often a goal in protein engineering, drug design or industrial optimization. A variety of methods and features have been proposed to predict the stability of protein mutations, the conflicting prediction results from different tools could cause confusion to users. Therefore, this study integrates structure and sequence-based prediction tools with machine learning and adds information of protein sequences. The best model is selected through feature selection methods to improve accuracy and reduce the time complexity of the training model. The PCC (Pearson correlation coefficient) of the integrated model can be increased from 0.669 to 0.702. Not only successfully integrates predictors, but also improves the accuracy of integration tools.

Session 6

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

Afternoon, January 21, 2020 (Tuesday)
Time: 13:30-15:15
Venue: Room 2 (1F)
Topic: "Biomedicine"
Session Chair: Prof. Hongmin Cai

K0034 Session 6 Presentation 1 (13:30-13:45)	Expression of TLR4 Signaling in Acute Appendicitis and Experimental Peritonitis **Han-Ping Wu** China Medical University Children's Hospital, Taiwan *Abstract*—Background: Simple appendicitis can progress to perforation, which may carry septic peritonitissepsis, and mortality. Toll-like receptors (TLRs) and myeloid differentiation factor 88 (MyD88) are essential for pathogen recognition and protective immunity. Methods: From 2015 to 2016, 126 pediatric patients with suspected appendicitis were enrolled. The protein expressions in excised appendices were analyzed by immunohistochemistry (IHC) staining. An animal study was investigated in rats with septic peritonitis induced by cecal ligation and puncture (CLP). The expressions of MyD88-dependent pathway biomarkers, including MyD88, nuclear factor-κB (NF-κB) and serum tumor necrosis factor-α (TNF-α) were analyzed and compared to the sham controls at the different time points after CLP surgery. Results: MyD88 expression highly increased in early-stage simple appendices. In our animal model, CLP-induced sepsis increased liver MyD88 mRNA and protein expressions at 2 hours after surgery. MyD88 protein expressions in rats with CLP-induced sepsis marked increased at 4 and 6 hours, and their NF-κB activities and serum TNF-α levels also increased at 4 hours after CLP surgery (both $p<0.05$). Conclusion: This study showed different expressions of proinflammatory markers in pediatric appendicitis. The different serial expression of MyD88-dependent pathway during sepsis may serve as biomarkers during sepsis.
K0049 Session 6 Presentation 2 (13:45-14:00)	Mapping the Humoral Immune Response of Patients with American Trypanosomiasis using Phage Display Technology André A. R. Teixeira, **Luis A. Rodriguez-Carnero**, Edécio Cunha-Neto, Walter Colli and Ricardo J. Giordano University of São Paulo, Brazil

	Abstract—Trypanosomiasis is a neglected disease caused by Trypanosoma cruzi. It is known that the immune system plays important roles in the disease, but its molecular mechanisms are still unresolved. Besides, it is unknown why just 30% of patients eventually develop cardiomyopathy, while most remain asymptomatic. We need better molecular markers for diagnosis, for following disease progression, and for cure. Considering all this, we produced a comprehensive T. cruzi Genomic Shotgun phage display library and used it to select epitopes recognized by IgG from patients in different clinical stages of the disease. The library we built had coverage of at least 120 times the T. cruzi genome and allowed us to identify more than 400 epitopes. Many of them had never been associated with the disease and are still considered hypothetical proteins with unknown functions. ELISA assay was used to validate 8 epitopes identified in our study, confirming our findings. It also revealed that individual patient response is very heterogeneous, adding another layer of complexity to the disease. In sum, our findings might be important to identify new markers for disease progression and cure. Also, it may work as blueprint for antigenic profiling of patients with other neglected diseases.
K1009 Session 6 Presentation 3 (14:00-14:15)	External Harmful Substances Induced Sensitization and Its Association Assessments of Inflammation Mechanisms in Epithelial Cell and Animal Model Zhi-Yao Ke, Thung-Shen Lai and **En-Chih Liao** Mackay Medical College, Taiwan *Abstract*—Environmental pollutants are compounds introduced in the natural environment causing adverse changes, for example, adversely affecting health or causing other types of damage. The house dust mites are the most important sources of indoor allergens responsible for the development of asthma. Staphylococcal enterotoxin B (SEB), is an enterotoxin produced by the *Staphylococcus aureu*s, common cause of food poisoning. Incense burning is an integral part of daily lives in large parts of Asia. To build a cell and animal model of multi-environmental factors(House dust mites, staphylococcal enterotoxin B and incense smoke) induced inflammation, we can proof its feasibility by study the correlation between monocyte associated inflammasome activation and the production of inflammatory cytokines. IgE and IgG1 in sera were increased significantly when compared with those of the normal saline group after sensitization. Splenocyte were collected and cultured with PMA and ionomycin for 5 hours before CD4+ cells producing the TH1-type cytokine IFN-a and TH2-type cytokine IL-4 were analyzed the percentage of CD4 cells producing IL-4 in HDM-sensitized mice was higher than the normal saline group. Lung tissue was acquired for polymerase chain reaction assay to investigate gene expression, including T-bet, GATA-3, IL33, the proinflammatory gene IL6. The results of polymerase chain reaction revealed significant upregulation of the gene expression after sensitization in

	lung. The cytokine productions (IL4, IL6, and TNF-α) were significantly increased compared with the normal saline group after sensitization. The findings indicated that sensitization with external harmful substances led to significant expression of lung tissue inflammation, tracheal thickening, and tracheal rupture. In conclusion, the effects of different environmental factors(House dust mites, staphylococcal enterotoxin B and incense smoke) may have a synergistic effect in the inflammation reactions.
K2017 Session 6 Presentation 4 (14:15-14:30)	The Molecular Mechanism and Drug Therapy of Heart Failure **Yifan Su** SUNY-ESF, USA *Abstract*—Heart failure (HF) is a complex clinical syndrome that results from left ventricular myocardial dysfunction and contributes to dyspnea, fatigue and fluid retention. It's essential to characterize disease progression and symptoms to optimize therapy selection. Also, understanding the mechanisms of HF to guide therapy selection is of vital importance. This review focuses on the demonstrating mechanisms of HF and points out the possible pathways involved in the process. Drug therapies of HF with different effects on specific targets are analyzed. Finally, we conclude the features of the now going drugs and depict the future perspectives of drug therapy of HF, including potential new targets and new drug therapies.
K2003 Session 6 Presentation 5 (14:30-14:45)	Rapid Dysphagia Diagnostic Test based on Voice Features Hsin-Yu Chou, **Li-Ya Lin**, Li-Chun Hsieh, Pei-Yi Wang and Shih-Tsang Tang Ming Chuan University, Taiwan *Abstract*—The diagnosis of dysphagia is quite time consuming and uncomfortable. Most patients usually do not seek medical treatment until the situation deteriorates, which results in missing the golden treatment period. Because the organs involved in swallowing and vocalization are almost overlapping, both of their function may decline simultaneously. Therefore, the aim of this study is to develop the rapid dysphagia diagnostic test based on voice features. In the clinical trial, the subject was firstly evaluated by the swallowing questionnaire scales, and then their voices were recorded. After extraction of the voice features, the correlation between swallowing scales and voice features were analyzed finally. A total of 40 subjects had completed the trial. The results showed that the dysphagia severity was highly correlated with jitter, shimmer, HNR and speech rate significantly. For the patient, the voice features analysis is easily carried out, which only requires vocalization. The record of voice is almost unrestricted by time and place. Hence rapid dysphagia diagnostic test would be clinically feasible, and it prompts early diagnosis and early treatment.
K0059 Session 6	Corpus Construction of Precision Medicine **Xuejing Ren**, Xinying An and Shaoping Fan Chinese Academy of Medical Sciences, China

Presentation 6 (14:45-15:00)	*Abstract*—[Background] For advancing biomedical text-mining research, formal evaluations and manually annotated text corpus are critically important. In terms of biomedical corpus construction, in order to meet different needs, many scholars have built different biomedical corpus with different emphasis. Through horizontal observation and vertical comparison of existing biomedical corpus, it is found that most of the entities of biomedical corpus are roughly classified and have narrow coverage. Most of the classification and sub-classification of entities only includes genes, proteins, drugs, diseases and other entities, while the classification of pathways, mutations and other entities is rarely involved. The exploration of the relationship between entities is not enough in depth and the relationship type is uncomprehensive. Therefore, we have developed our own precise medical corpus to store more comprehensive medical knowledge and enrich the biomedical corpus.[Methods]Through repeated iteration the process of article selection, systematic evaluation, manual annotation, formulating consensus of annotation, cross validation, submission assessment to form a more comprehensive and authoritative text corpus, which is also of great significance to promote biomedical text mining research.[Results]At present, a total of 6000 articles have been auto and manual annotated. Each 1000 PubMed English articles of cardiovascular diseases (circulatory system) intestinal neoplasm and liver neoplasm (digestive system) metabolic diseases; 1500 articles of lung neoplasm (respiratory system) and 500 articles of neurological diseases. (but in this issue, we only had a detailed illustration of the lung neoplasm.[Conclusion]A high-quality precise medical corpus was constructed, which promotes the research process of biomedical data mining. At present, some resources of the corpus have been opened to the public, welcome scholars to use and put forward valuable suggestions.
K0040 Session 6 Presentation 7 (15:00-15:15)	Computational Drug-target Interaction Prediction based on Graph Embedding and Graph Mining **Maha A. Thafar**, Somayah Albaradie, Rawan S. Olayan, Haitham Ashoor, Magbubah Essack and Vladimir B. Bajic King Abdullah University of Science and Technology (KAUST), Saudi Arabia *Abstract*—Identification of interactions of drugs and proteins is an essential step in the early stages of drug discovery and in finding new drug uses. Traditional experimental identification and validation of these interactions are still time-consuming, expensive, and do not have a high success rate. To improve this identification process, development of computational methods to predict and rank likely drug-target interactions (DTI) with minimum error rate would be of great help. In this work, we propose a computational method for (Drug-Target interaction prediction using Graph Embedding and graph Mining), DTiGEM. DTiGEM models identify novel DTIs as a link prediction problem in a heterogeneous graph constructed by integrating

	three networks, namely: drug-drug similarity, target-target similarity, and known DTIs. DTiGEM combines different techniques, including graph embeddings (e.g., node2vec), graph mining (e.g., path scores between drugs and targets), and machine learning (e.g., different classifiers). DTiGEM achieves improvement in the prediction performance compared to other state-of-the-art methods for computational prediction of DTIs on four benchmark datasets in terms of area under precision-recall curve (AUPR). Specifically, we demonstrate that based on the average AUPR score across all benchmark datasets, DTiGEM achieves the highest average AUPR value (0.831), thus reducing the prediction error by 22.4% relative to the second-best performing method in the comparison.

15:15-16:15	**Coffee Break & Poster Session**

Session 7

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

Afternoon, January 21, 2020 (Tuesday)
Time: 16:15-18:15
Venue: Room 1 (1F)
Topic: "Medical Informatics"
Session Chair: Prof. Chang-Chi Hsieh & Prof. Jiann-Shing Shieh

K0012 Session 7 Presentation 1 (16:15-16:30)	Rapid Detection and Prediction of Influenza A Subtype using Deep Convolutional Neural Network based Ensemble Learning **Yu Wang**, Junpeng Bao, Jianqiang Du and YongFeng Li Xi'an Jiaotong University, China *Abstract*—Seasonal pandemics of influenza A viruses bring enormous threaten to human healthy. Different subtypes of influenza A viruses disseminated in human have variable susceptibilities to antiviral drug, so rapid subtyping of influenza A viruses has been increasingly important. Traditional biochemical methods for subtyping these viruses are expensive and time-consuming. Various sequencing techniques and deep learning methods bring an opportunity to analyse and gain information of those biont more conveniently and accurately. This paper proposes a deep convolutional neural network based ensemble learning model to precisely detect all subtypes of influenza A viruses. The experiments show that the proposed method can achieve the state-of-art performance for subtyping influenza A viruses and detecting a fire-new subtypes according to sequence data.
K0015 Session 7 Presentation 2 (16:30-16:45)	Predicting lncRNA-disease Association based on Extreme Gradient Boosting **Xi Tang**, Menglu Li, Wei Zhang and Junfeng Xia Anhui University, China *Abstract*—There is increasing evidence that long non-coding RNAs (lncRNAs) play an important role in many significant biological processes. Associations' detection between lncRNAs and human diseases by computational models is beneficial to the identification of biomarkers and the discovery of drugs for the diagnosis, treatment, and prognosis of human diseases. In this study, we propose a method called PrLDA (Predicting LncRNA-Disease Association based on extreme gradient boosting) for predicting potential lncRNA-disease associations based on eXtreme Gradient Boosting (XGBoost). Firstly, we compute semantic similarity of diseases and lncRNA sequence similarity. Then, we extracte feature vectors

	by concatenating these similarities horizontally. At last, the feature matrix after dimension reduction is used as the input for XGBoost and we get the score about the lncRNA association with a specific disease. Computational results indicate that our method can predict lncRNA-disease associations with higher accuracy compared with previous methods. Furthermore, case study shows that our method can effectively predict candidate lncRNAs for breast cancer, with 80% of the top 10 predictions are confirmed by experiments. Therefore, PrLDA is a useful computational method for lncRNA-disease association prediction.
K0041 Session 7 Presentation 3 (16:45-17:00)	Breast Cancer Subtype by Imbalanced Omics Data through A Deep Learning Fusion Model **Jingwen Zeng, Hongmin Cai** and Tatsuya Akutsu South China University of Technology, China *Abstract*—Breast cancer is a highly heterogeneous disease that consists of subtypes with distinct genetic features and clinical symptoms. The patients with different subtypes react to different therapies, thus identifying molecular subtypes greatly contributes to precision diagnosis and personalized cancer treatment. PAM50 subtype is a widely accepted standard in breast cancer classification. The large amount of multi-omics data in public database like TCGA greatly contribute to the study of breast cancer subtype identification. However, the imbalance of sample subtypes in the existing database results in a large difficulty in correctly identifying subtypes with small sample size. In this paper, we proposed a novel method to accurately identify the PAM50 subtypes by utilizing the patients' omics profiles in TCGA database. Based on the integrated expression profiles of RNA-seq and Copy Number Alteration (CNA), the proposed method identifies subtype-related patterns by a multi-layer Convolutional Neural Network (CNN). A weighted loss function was applied to alleviate the effects of imbalanced samples, thus contributing to the accurate identification. We demonstrated that our method could identify PAM50 subtypes of patients with high precision (90.02%) and outperformed two benchmark methods.
K2006 Session 7 Presentation 4 (17:00-17:15)	Design and Implementation of NoSQL-based Medical Image Archive Underlaying FHIR **Chien-Hua Chu**, Shih-Tsang Tang and Chung-Yueh Lien Ming Chuan University, Taiwan *Abstract*—In this study, we proposed the architecture of the NoSQL-based medical image archive underlying Fast Healthcare Interoperability Resources (FHIR) to provide several web services for medical image retrieval applications. The Node.js framework is used to create an HTTP server providing web services for medical image retrieval including CRUD operations (create, read, update and delete) to manage the DICOM (Digital Imaging and Communications in Medicine) objects via HTTP protocol. A

	set of DICOM objects, uploaded to the server, are processed and converted to JSON formatted documents stored in a NoSQL database with MongoDB. To maintain the consistency of the hierarchical relationship among the DICOM objects, the schema of patient-based architecture combined with FHIR ImagingStudy was determined according to DICOM hierarchical data structure, i.e. patient/study/series/objects. The development of the NoSQL-based method does not only improve the shortcomings of traditional SQL-based image archive but also supports the FHIR standard that effectively improves the efficiency of web-based medical retrieval.
K0066 Session 7 Presentation 5 (17:15-17:30)	A Novel Feature Selection and Classification Method of Alzheimer's Disease based on Multi-features in MRI **Peiqi Luo**, Guixia Kang and Xin Xu Beijing University of Posts and Telecommunications, China *Abstract*—In this paper, we describe a novel machine learning method for classifying Alzheimer's disease (AD), Mild cognitive impairment (MCI) and Normal Control (NC) subjects based on structural MRI. We first extracted features from MRI scans, including cortical volumes, cortical thicknesses, subcortical volumes, and hippocampal subfields volumes. Then a new feature selection method combining the support vector machine-recursive feature elimination (SVM-RFE), maximal-relevance-minimal-redundancy (mRMR) and random forest (RF) was proposed to select the optimal subsets among all these features. Finally, the SVM classifier was used for AD/MCI/NC classification by 10-fold cross-validation. We applied the proposed method to the Alzheimer's Disease Neuroimaging Initiative (ADNI) dataset, and the experimental results show a high degree of accuracy, sensitivity and specificity, which are superior to some other state-of-the-art approaches
K0071 Session 7 Presentation 6 (17:30-17:45)	Tracking and Analysis of FUCCI-labeled Cells based on Particle Filters and Time-to-event Analysis **Kenji Fujimoto**, Shigeto Seno, Hironori Shigeta, Tomohiro Mashita, Junichi Kikuta, Masaru Ishii and Hideo Matsuda Osaka University, Japan *Abstract*—FUCCI (fluorescent ubiquitination-based cell cycle indicator) is a fluorescent probe used to visualize the cell cycle progression of individual cells using fluorescent proteins of different colors. Because the cell cycle is related to biological processes such as proliferation of cancer cells, analysis of imaging data visualized using FUCCI is extremely important. This paper proposes a method for spatiotemporal tracking and analysis of FUCCI-labeled cells from time-lapse videos. To address the color transition of the FUCCI-labeled cell with the cell cycle progression, the proposed method simultaneously estimates the location and the cell cycle phase of the target cell. Furthermore, to analyze the cell phase transition, this paper proposes to apply multistate time-to-event analysis to the information

	obtained through our tracking method. This paper demonstrates the usefulness of our method with application to FUCCI-labeled HuH7 cells (human hepatocellular carcinoma cell line).
K2004 Session 7 Presentation 7 (17:45-18:00)	Home Wound Dressing Photo Management Cloud System **Meng-Jie Su**, Yu-Tong Liu, Szu-Hsien Wu, Ming-Liang Hisiao and Shih-Tsang Tang Ming Chuan University, Taiwan *Abstract*—Many patients with chronic trauma often need wound dressings by themselves. The wound dressing affect directly the wound's healing. Therefore the quality of home wound dressing becomes very important. This study developed a home wound dressing photo management cloud system, which is to collect home wound dressing photos, and then evaluate the wound condition. The system would assist physicians in clinical evaluation and patient's care recommendations. The proposed system developed a series of interactive web forms basing on Windows operating system, Apache web server and MySQL database engine. The wound dressing photos are stored and managed by a cloud system. Patient could upload wound dressing photos on a daily basis, which includes the photos before the wound dressing and after the dressing. The system is further developing AI functions, which would provide the trend forecasting in the wound healing.
K0076 Session 7 Presentation 8 (18:00-18:15)	Development of Photo-activatable Insulin Receptor for Insulin Signalling Pathway Control **Bryan John J. Subong**, Mizuki Endo and Takeaki Ozawa The University of Tokyo, Japan *Abstract*—The insulin signaling pathway is one of the most crucial biochemical pathways which controls energy functions such as glucose and lipid metabolism. Impairment of the said signaling pathway has been implicated in various diseases such as diabetes mellitus and cancer. Current approaches in studying the said pathway uses mass-spectrometry driven phosphoproteomics. However, this technique is destructive and does not allow a spatio-temporal analysis of the said signaling cascade. In our present study, we develop an optogenetic probe which can be used to study the insulin signaling pathway spatio-temporally. The probe utilizes light for dimerization of the insulin receptor beta-subunit instead of insulin. Upon 10-minute light irradiation, activation of various insulin signaling downstream proteins such as phopho-irs1, phospho-Akt and phospho-Erk were confirmed using western blotting. Further, glucose uptake assay using luminescence technology to measure uptake of 2-deoxyglucose-6-phosphate showed statistically significant (at alpha = 0.05) increased glucose uptake response for cells transiently expressing the said probe. Further, the steady-state localization of the probe expressing enhanced green fluorescent protein was determined to be at the plasma membrane. Moreover, cell

	viability assay showed no cytotoxic effect between light irradiated and non-light irradiated cells. Thus, the developed optogenetic tool can be safely used to interrogate living systems. This study highlights the use of emerging tools such as optogenetics in controlling various intracellular processes at a spatio-temporal level. In particular, the development of the said probe will allow better understanding of the effects of regulating and controlling spatio-temporally the insulin signaling pathway in living systems.

Session 8

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

Afternoon, January 21, 2020 (Tuesday)
Time: 16:15-18:15
Venue: Room 2 (1F)
Topic: "Preventive Medicine and Rehabilitation Medicine"
Session Chair: Prof. Han-Ping Wu

K3003 Session 8 Presentation 1 (16:15-16:30)	Variability of Local Weather as Early Warning for Dengue Hemorrhagic Fever Outbreak in Indonesia **Khaidar Ali**, Isa Ma'rufi, Wiranto and Anis Fuad Universitas Gadjah Mada, Indonesia *Abstract*—The incidence of Dengue Hemorrhagic Fever (DHF) is related to the alternation of environment condition, particularly weather, in which global warming may elevate the DHF case. The objective of study is to analyses the relationship between local weather and DHF, and to create prediction model by using big data in Surabaya Municipally. Employing quantitative method, monthly time series data was used during 2012-2016. Univariate, bivariate and multivariate analysis was performed in Stata 13. Local weather (mean humidity, maximum humidity, minimum humidity, rainy days and rainfall) correlates to the incidence of DHF ($p < 0.05$), in which minimum humidity lag 1 month and rainy days lag 2 month had strong correlation ($r > 0.7$). In addition, prediction model in the study recognize the occurrence of four peak epidemic of DHF cases in Surabaya Municipally. Therefore, utilizing local weather to create prediction model may contribute as early warning for DHF incident in order to handle the disease in Surabaya Municipally.
K2035 Session 8 Presentation 2 (16:30-16:45)	Associations Between Seasonal Variation of Heart Rate Variability and Healthy Life Expectancy in Japan **Emi Yuda,** Masaya Kisohara, Yutaka Yoshida, Norihiro Ueda and Junichiro Hayano Tohoku University & Nagoya City University, Japan *Abstract*—Although both summer heat and winter cold increase the risk of health problems, the effects could be modified by living environment and clothes. We investigated the relationship between regional differences in healthy life span (HALE) and seasonal variations in heart rate variability (HRV) that may reflect biological burden caused by heat and cold weather. Using the Allostatic State Mapping by Ambulatory ECG Repository

	(ALLSTAR) database, we analyzed the 24-h standard deviation of sinus-rhythm R-R intervals (SDNN) among 86,712 men and 108,771 women across Japan as a measure of HRV. Then, SDNN data were divided into 47 prefectures, averaged over 4 seasons, and associated with the prefectural averages of HALE reported by Japanese government. As the results, in both sexes, prefectural age-adjusted HALE negatively correlated with seasonal variation of prefectural age-adjusted SDNN, while it did not corelated significantly with prefectural age-adjusted SDNN of any seasons. Additionally, there was no significant correlation between prefectural age-adjusted average life expectancy and the seasonal variation of prefectural age-adjusted SDNN. Our observations support the hypothesis that the magnitude of the seasonal variation in biological burden might be a shortening factor for HALE.
K0063 Session 8 Presentation 3 (16:45-17:00)	Exploring Elders' Willingness and Needs for Adopting an Interactive Somatosensory Game into Muscle Rehabilitation Systems **Yu-Ling Chu**, Chien-Hsiang Chang, Yi-Wen Wang, Chien-Hsu Chen and Yang-Cheng Lin National Cheng Kung University, Taiwan *Abstract*—Disease of the lower limb musculoskeletal system is one of the most common diseases in elders. The use of interactive somatosensory games (ISGs) in rehabilitation has been widely used. Most relevant studies have focused on efficacy, while only a few have investigated the difficulties, willingness, and requirements of elderly people in playing the game. Therefore, this study is to design an ISG that is focused on lower-limb rehabilitation and to explore whether the designed ISG can enhance the willingness and motivation of elders to undergo rehabilitation. In this study, 15 elders (5 males and 10 females with average age of 78 years) with degenerative joint disease were recruited to participate in our pretest-posttest design experiments. First, the subjects completed a five-minute pre-test questionnaire after a one-minute traditional rehabilitation (TR). Second, they completed a five-minute post-test questionnaire after a one-minute interactive somatosensory game rehabilitation (ISGR). The average experiment time for each subject was 25 min. We used a t-test to analyze the data. According to the result, there are significant differences in four factors (i.e., interest ($t=-6.89$, $p<0.05$), self-affirmation ($t=-3.17$, $p<0.05$), understanding of rehabilitation states ($t=-3.31$, $p<0.05$), and fatigue ($t=2.49$, $p<0.05$)). The results show that (1) for the same treatment arrangement, ISGR can make the elderly people more interested in and reduce their fatigue while undertaking the long-term rehabilitation; (2) using ISGR can increase their understanding of, and their confidence in, their rehabilitation states; and (3) elders generally have positive attitudes toward the ISGR. The results and analysis of willingness and needs in this study can be as a reference for future studies of rehabilitation game development, and the development of rehabilitation to improve the health of the elders.

K2005 Session 8 Presentation 4 (17:00-17:15)	The Smartphone-based Rehabilitation Assistant for Stroke Patient **Pei-Yu Lin**, Chieh-Min Lin, Chih-Liang Wu, Kuo-Feng Chou and Shih-Tsang Tang Ming Chuan University, Taiwan *Abstract*—In addition to surgery and medicine, the rehabilitation is also an important part for stroke treatment. However, it's a time-consuming and tedious task. The physician usually ask patient for home rehabilitation. Because the physician can not effectively realize patient's home condition, the prognosis is poor. Therefore, this study developed a smartphone based system for home rehabilitation assistant, which can record and store the rehabilitation data, and then evaluate the outcome. This study used the accelerometer module and MATLAB® to develop the prototype system, which was for feasibility evaluation. And then the prototype system was migrated to the smartphone. In the trial process, the subject was first to wear the accelerometer module on the waist, and then walked in straight line and went back. Next, the acceleration data were imported to MATLAB® for gait analysis. After the prototype phase, the analysis algorithm was migrated to the smartphone, and directly used the embedded accelerometer of smartphone. In the aging society, the necessity of home rehabilitation is increasing. Although this study is focusing on the stroke patient, but the system structure and concept could also be a valuable reference in developing the home rehabilitation system for other diseases.
K0060 Session 8 Presentation 5 (17:15-17:30)	Dynamically Colour Changing Actuator for Cyanosis Baby Manikin Application with the Philips Hue LED Kit **Azmi Nur Fatihah**, Frank Delbressine and Loe Feijs Eindhoven University of Technology, Netherlands *Abstract*—Medical simulation training is an important approach contributing to medical safety. In the field of neonatology, serious efforts have been devoted to construct manikins, which are realistic in shape and improve the haptic experience. As central cyanosis is a severe pathological sign in infants, new medical trainees or clinicians need to have professional-level skills in assessing central cyanosis. In this paper, we are trying out a new type of actuator, the Philips Hue LED bulb, to dynamically generate a changing colour of cyanosis in a baby manikin. Philips Hue smart lighting is widely used to remotely illuminate home and office. It is also famous because of the wide range of white and coloured-LED bulbs, light strips, and lamps which are used for changing the ambience and switching on and off lights in response to the user input. In this paper, we describe a dynamically colour changing actuator as the application of central cyanosis in a newborn baby using Philip's Hue LED Kit. Herein, we demonstrated a colourimetry analysis based on real cyanosis and non-cyanosis colour changes on a 3D- printed baby's head. The colour change of the baby's head was measured using the Spectraval 1501 spectroradiometer. In this study,

	the Hue lamp could be turned into a useful actuator to simulate cyanosis on a baby. We measure the combined effects of the subtractive and additive colour mixing which occur when adding an observation lamp. We believe that these measurements will pave the way for a future implementation step, in which the 3D printed head can be turned into a practical cyanosis simulator to be used in real training.
K2007 Session 8 Presentation 6 (17:30-17:45)	A Deep Image based Proposal for Posture Classification **Wan-Chun Liao**, Jing Wang, Yi-Shu Zhou, Ying-Hui Lai, Wai-Keung Lee and Shih-Tsang Tang Ming Chuan University, Taiwan *Abstract*—Motion tracking is widely applied in military, entertainment, sports, medical rehabilitation, computer vision, robotics, etc. The posture classification is the basis technology for motion tracking. General posture classification is implemented by wearable inertial device or RGB camera. The inertial method need to be wore device in advanced, which is inconvenient. The camera method is as well concerned in privacy. Our study proposed an innovated method for posture classification. The ToF camera is used to capture the deep image, which just acquires the distances data of the reflected points on the object. As a result, there are no issues on the wearing inconvenient and privacy. The artificial intelligent technology is then applied for classification. In the trial, the subject is asked to pose before the ToF camera. Then the deep image data are used to train the model for posture classification. In the current status, we have successful discriminated the postures of sitting, standing, and lying. Because of the proposed method is convenient and private, which also shows a great potential in developing the home rehabilitation assistant.
K0002 Session 8 Presentation 7 (17:45-18:00)	Rational Discovery of Human Superoxide Dismutase I (hSOD1) Modulators: A Potential Therapeutic Target for Amyotrophic Lateral Sclerosis (ALS) **Balasundaram Padmanabhan** National Institute of Mental Health and Neuro Sciences (NIMHANS), India *Abstract*—Human Superoxide Dismutase I (hSOD1) is a cytoplasmic homodimer enzyme involved in metabolizing superoxide radicals, protecting cells from oxidative damage. The mutations in the SOD1 gene have been linked to the neurodegenerative disease, familial amyotrophic lateral sclerosis (fALS). The SOD1 toxic gain-of-function is caused by the mutations in SOD1 which leads to get aggregation. Since both aggregation propensity and protein stability strongly influence patient survival time after onset of symptoms, working on protein stability is one of the better strategies to improve the patient survival rate. The toxic-gain-of-function can be prevented by stabilizing the hSOD1 dimer and/or by protecting the Trp32 residue from oxidation. Hence, identifying and developing potential library compounds to tackle the above-mentioned features are in need for

	the treatment of ALS. In this aspect, we have identified the ligands by virtual screening using NCI-Diversity Set III and in-house library. The SOD1-ligand complexes were crystallized, collected the X-ray diffraction data on the beamline BM14 at ESRF, Grenoble, France. The structures of an apo-form and protein-ligand complexes of hSOD1 refined to 1.9Å resolution and their binding studies would be discussed.
K0031 Session 8 Presentation 8 (18:00-18:15)	Orai3 Contributes to the Migration Capacity in Lobular Liver Cancer **Jing Yan**, Xiuliang Zhao, Xia Liu, Zhaodi Gao and Ting Wei Jining Medical University, China *Abstract*—Store-operated calcium channels are known to be involved in tumorigenesis, and one major component, calcium release-activated calcium channel protein1 (Orai1), has already been extensively explored, whereas the contribution of Orai3 to cancer remains unclear. The present study investigated the role of Orai3 in lobular liver cancer. Western blot and RT-PCR were utilized to assess Orai1/3 in patients and murine xenograft models of liver cancer. Ca2+ imaging and whole-cell patch clamp were used to examine store-operated Ca2+ entry (SOCE) activity. Transwell assays and colony forming experiments were used to determine tumor characteristics. We found that patients with lobular liver cancer displayed high Orai1/3 levels, similar to that of murine xenograft models of lobular liver cancer. Decreased Orai1/3 expression inhibited cancer volume in vivo and suppressed colony formation and migration in vitro. However, only Orai3-knockdown inhibited cancer metastasis in nude mice. Orai3 overexpression facilitated to the expression of E-cadherin in HepG2 and SMMC7721 cells. Our findings suggest that liver cancer metastasis requires Orai3 expression.

Poster Session 1

Afternoon, January 20, 2020 (Monday)
Time: 15:00-16:00
Topic: "Biochemistry and Chemical Engineering"
Venue: Lobby of Room 3 (1F)
Session Chair: Prof. Ryoji Nagai

K0009 Poster 1	Mutation of Microbial Glycosyltransferase for Efficient and Regioselective Biosynthesis of Rare Ginsenoside Rh1 **Lu Zhao**, Jianlin Chu and Bingfang He Nanjing Tech University, China *Abstract*—Ginsenoside Rh1 isolated from plant *ginseng* receives much attention for its potential anticancer drug discovery. Enzymatic synthesis has been developed as an alternative strategy to plant extraction and traditional chemical synthesis of rare ginsenoside Rh1. Herein, we demonstrated the glycosyltransferase UGTBL1 from *Bacillus licheniformis* which could synthesize Rh1. Protopanaxatriol and UDP-glucose were docked into active site of UGTBL1, and structure-based mutagenesis was carried out to explore "hotspot" amino acids involved in substrate binding for regioselective glycosylation of protopanaxatriol. Compared with wild type UGTBL1, the mutants I62Y and I62H obtained by alanine scanning and saturation mutations exhibited 12.89 and 13.31-fold regiospecificity towards glycosylated product (Rh1), respectively. Moreover, mutants I62Y, I62H also showed 1.51 and 1.44-fold conversion compared to wild type UGTBL1, respectively. The exploratory mutational experiments of UGTBL1 indicated that I62 is a key residue to efficient and regioselective glycosylation of protopanaxatriol for ginsenoside Rh1 product. The mutants of UGTBL1 acquired in this study proved that the regioselectivity and glycosylation activity of the enzyme for ginsenoside Rh1 synthesis could both be enhanced. This may provide a new strategy for efficient biosynthesis of ginsenoside Rh1.
K0061 Poster 2	The Biological Effects of Haematococcus Pluvialis Extracts on Fibroblasts **Lin Jun-Yan**, Liu Wei-Chung adn Keng Nien-Tzu Tzu Chi University of Science and Technology, Taiwan *Abstract*—Aastaxanthin is a kind of antioxidant extracted from haematococcus pluvialis. Research has indicated Aastaxanthin has the function of anti-oxidation and would healing. The high level of reactive oxygen species (ROS) will inhibit cell proliferation and reduce wound healing; however, the bioeffects of Aastaxanthin on would healing are still

	unknown. This study focused on the ability of Aastaxanthin extracted from Haematococcus pluvialis to promote would healing after cell damage. The cytotoxicity of Astaxanthin extracts was evaluated by MTT assay. The safety dose of extracts was added into the culture medium to investigate the effects of ROS expression and cell migration rate in NIH 3T3 (mouse embryonic fibroblast). The results showed that Astaxanthin extracts can increase cells migration and proliferation. In addition, the ROS expression in NIH 3T3 cells was inhibited. The present results indicated that Astaxanthin extracts can stimulate wound healing rate possibly via increasing the level of cells migration and proliferation.
K0010 Poster 3	An Efficient Synthesis of Nucleoside Analogues Catalyzed by A Novel Thermostable Purine Nucleoside Phosphorylase from *Aneurinibacillus Migulanus* AM007 **Gaofei Liu**, Tiantong Cheng, Jianlin Chu, Sui Li and Bingfang He Nanjing Tech University, China *Abstract*—A novel purine nucleoside phosphorylase from *Aneurinibacillus migulanus* AM007 (*Am*PNP) was cloned and heterologously expressed in *Escherichia coli BL21*(DE3). The microbial *Am*PNP was identified as a trimer and displayed low phosphorolysis activity toward adenosine. The enzyme was thermostable at 55 ℃ for 12 h (retaining nearly 100% activity), and efficiently biosynthesized adenosine analogs. A one-pot, two-enzyme mode of trans-glycosylation was successfully constructed by combining pyrimidine nucleoside phosphorylase derived from *Brevibacillus borstelensis* LK01 (*Bb*PyNP) and *Am*PNP for the production of purine nucleoside analogs. The ratio of *Am*PNP and *Bb*PyNP greatly influenced the yield of purine nucleoside synthesis. The two-enzyme synthesis of 2-amino-6-chloropurine ribonucleoside catalyzed by *Bb*PyNP and *Am*PNP resulted in 95.1% conversion (20 mM sugar donor: 10 mM base acceptor; 1:1000 enzyme ratio). The conversions of 2,6-diaminopurine ribonucleoside and 6-thioguanine ribonucleoside reached 98.3% and 92.3%, respectively. The reaction of *Am*PNP coupled with *Bb*PyNP could also efficiently biosynthesize 2'-deoxyribonucleosides with the conversion of 96.5% 2,6-diaminopurine, 74.0% 2-amino-6-chloropurine, and 89.3% 6-thioguanine.
K3001 Poster 4	Repeated-batch Lactic Acid Fermentation using a Novel Bacterial Immobilization Technique based on a Microtube Array Membrane Chien-Chung Chen, Chuan-Chi Lan and **Hong-Ting Victor Lin** National Taiwan Ocean University, Taiwan *Abstract*—Lactic acid has received considerable attention for its various applications. Although lactic acid is usually produced by batch fermentation using free microbes, repeated-batch fermentation using immobilized cells could offer several advantages over this method. In the present study, a novel bacteria immobilization technique using a renewable poly-L-lactic

	acid (PLLA) microtube array membrane (MTAM) was thoroughly evaluated in terms of its suitability for lactic acid fermentation. A bacteria encapsulation efficiency of 85–90% was obtained using a siphon approach, and bacteria in MTAMs with greater porosity showed greater lactic acid productivity. MTAM-immobilized *Lactobacillus acidophilus* were evaluated in eight cycles of repeated-batch lactic acid fermentation of commercial medium MRS (4% glucose) and red seaweed *Gracilaria* hydrolysate. The MTAM exhibited physical stability during lactic acid fermentation and improved glucose consumption and lactic acid production were achieved by immobilized cells. The immobilized bacteria showed a maximum C_{LA} of 37.39 g/L, r P_{LA} of 0.79 g/L ħ, and $Y_{L/S}$ of 0.94 g/g in MRS fermentation, and a maximum C_{LA} of 27.76 g/L, r P_{LA} of 0.58 g/L ħ, and $Y_{L/S}$ of 0.92 g/g in seaweed hydrolysate fermentation. Our data indicate that PLLA-MTAM is a novel, promising immobilization technology for lactic acid fermentation.
K0011 Poster 5	A Simple Enhancer for Efficient Extracellular Expression of Human Epidermal Growth Factor Secreted by *E. Coli* **Lupeng Cui**, Yumeng Qiu and Bingfang He Nanjing Tech University, China *Abstract*—Human epidermal growth factor (hEGF) is a polypeptide (6.2 kDa) composed of 53 amino acids, and plays an important role to stimulate the proliferation of various epidermal and epithelial tissues and is widely used in clinical practices. However, the extracellular secretion strategy for recombined hEGF expression by *E. coli* has rarely been successfully achieved. In our previous study, we reported that a recombinant β-fructofuranosidase (β-FFase) from *Arthrobacter arilaitensis* NJEM01 can be efficiently secreted to culture medium with fused signal peptide by *E. coli*. In present study, we exploited a simple enhancer which the truncated N-terminal of signal peptide from β-FFase was fused to the N-terminal of OmpA, and then the simple enhancer was further fused to the N-terminal of hEGF to facilitate the expression of hEGF in *E.coli*. Interestingly, the recombinant hEGF product was not only secreted to the periplasmic place but also to the culture media by tricine-glycerin-SDS-PAGE analysis. The biological activity of the extracellular expressed hEGF with simple purification on cell proliferation was fully bioactive in vitro. These results suggested that the simple enhancers introduced herein displayed the secretary ability with signal peptide function and the hEGF protein was successfully excreted to the culture medium by *E. coli*. As a result, the novel enhancer was proved to be practically useful tool for the expressed production of hEGF secretion.
K0065 Poster 6	Retinoic Acid Receptor α- and Retinoid X Receptor α-specific Agonists are Hemodynamics-based Therapeutic Components for Vascular Disorders **Ting-Yu Lee** China University of Science and Technology, Taiwan

	Abstract—MicroRNA (miR)-10a has been found to be induced by RAR and RXR to drive anti- inflammatory signaling in endothelial cells (ECs) in response to atheroprotective pulsatile flow (PS). The aim of this study is to identify whether RAR - and RXR -specific agonists can mimic the effect of PS to induce miR-10a to repress inflammatory signaling and vascular disorder. Our in vitro flow results showed that co-addition of RAR - and RXR -specific agonists has synergistic effect on rescuing OS-inhibited EC miR-10a expression to repress inflammatory GATA6/VCAM-1 signaling. Moreover, administration of ApoE$^{-/-}$ mice with RAR - and RXR -specific agonists induced the expression of endothelial miR-10a to repress GATA6/VCAM-1 signaling and inflammatory cell infiltration in the vascular wall. In vivo inhibition of endothelial miR-10a by antagomiR abolished the protective effect of RAR - and RXR -specific agonists. Our findings suggest that RAR /RXR -specific agonists induce EC miR-10a to inhibit the pro-inflammatory GATA6/VCAM-1 signaling and inflammatory cell infiltration in the vessel wall and protect blood vessel from vascular disorder.
K0044 Poster 7	The Mechanical Behaviors of Polyethylene/Silver Nanoparticle Composites: An Insight from Molecular Dynamics Study **Chuan Chen** and Shin-Pon Ju Meiho University, Taiwan *Abstract*—The mechanical properties of pristine polyethylene (PE) and its composites with silver nanoparticles (PE/Ag NPs) at two Ag NP weight fractions of 1.05 wt% and 3.10 wt% were studied by molecular dynamics simulation (MD). It can be seen from the stress-strain distribution of the tensile process that the embedded Ag NPs can significantly improve the Young's modulus and tensile strength of the pristine PE, which is due to the improve of the local density and strength of the PE near the Ag NP surface in the range of 12 A□ . Regarding the effect of temperature on the mechanical properties of pristine PE and PE/Ag NP composites, the Young's modulus and the strength of the pristine PE and PE/Ag NP composites decreased significantly to 350 K and 450 K, consistent with predicted melting temperature of pristine PE, which lies at around 360 K. At such temperatures as these, PE material has stronger ductility and a higher mobility of Ag NPs in the PE matrix than those at 300 K. With the increase of tensile strain, Ag NPs tend to be close, and the fracture of PE leads to a similarity between both the Young's modulus and ultimate strength found for the pristine PE and those found for the PE/Ag NP composites at 350 K and 450 K.
K2010 Poster 8	Characteristics of Hydrocarbons and Carbonyl Compounds Emitted from the Oil Fume of Restaurant Oil Trap **Chia-Hsiang Lai**, Yao-Kai Xiang and Zhen-Hong Zhu Central Taiwan University of Science and Technology, Taiwan

	Abstract—The study investigated the emissions of the oil trap to hydrocarbons, aldehydes and ketones at a university restaurant in central Taiwan. Gaseous pollutions were collected over 15 working days in 2019. The results found the highest levels of all restaurant oil fume was Methane (19.35±2.43 ppm). The most abundant compounds of aldehydes were 2-Methylbutyaldehyde (7.92±0.09 ppm), followed by Formaldehyde, Propionaldehyde and o-Tolualdehyde, with concentrations of 4.97±0.21, 2.29±3.22, and 2.11±0.13 ppm, respectively. The 9 compounds of ketones were identified from the restaurant oil fume. The most abundant ketone species were Methyl Ethyl Ketone (10.37±4.11 ppm) and Diethyl ketone (2.08±1.32 ppm). The levels of the others ranged from 0.07–0.86ppm. The total aldehydes concentration was approximately 2.6 times higher than that for all ketones. The characteristics of hydrocarbons and carbonyl compounds from restaurant oil fume might be affected by food, cooking temperature and oil types. Comparison of emission levels of hydrocarbons, aldehydes and ketones suggests that the most abundant contributions of aldehydes from kitchen fume give priority to develop control devices.
K3004 Poster 9	Research on the Coordinated Development of Energy-environment System **Zhang Song** Research Institute of Petroluem Exploration& Development, China *Abstract*—Energy-environment system is an open complex adaptive system far from thermodynamic equilibrium. Based on the analysis of the features of dissipative structure and key factors of entropy change in energy-environment system, the coordinated development of energy-environment system is studied in this paper. Furthermore, the dissipative structure model is constructed to explore the operating and evolutionary mechanism of energy-environment system. It also explores the way to predict evolutionary trend of energy-environment system combined with prediction theory. In the end, some strategic suggestions for developing the energy-environment system are put forward. First, we should grasp the evolution rule of energy-environment system. Second, we should construct the innovation mechanism of energy-environment system and make full use of the nonlinear function between elements to promote the formation of self-organizing system. At last, it is important to further increase the openness of the energy-environment system and promote the exchange of material, energy, information and technology between internal and external environment. The energy-environment system would accordingly become more orderly and efficient.
K0018 Poster 10	Optimization of Cold-aDapted α-amylase Production in *Escherichia Coli* by Regulation of Induction Conditions and Supplement with Osmolytes **Xiaofei Wang**, Guangfeng Kan, Xiulian Ren, Cuijuan Shi and Ruiqi Wang Harbin Institute of Technology at Weihai, China

	Abstract—In this study, the induction expression conditions of cold-adapted α-amylase (Amy175) from *Pseudoalteromonas* sp. M175 in *E. coli* were investigated. The optimal induction conditions were as follows：20 mM L-proline was added into the culture medium at the initial inoculation time point, the concentration of the inducer IPTG was 0.04 mM, the induction point was 0.6 of OD_{600}, the induction temperature was 15 ℃, and the induction time was 12 h, and the rotation speed was 120 rpm. The maximum amylase activity could reach 141.1 U/ml at the optimal induction conditions. Thus, the yield of the active and soluble α-amylase was found to be increased in the lower induction temperature, lower IPTG concentration, and the supplement of the proper amount of L-proline into the culture medium.
K0037 Poster 11	Using Multiple Machine Learning Algorithms for Cancer Prognosis in Lung Adenocarcinoma **Le Wei**, Wanning Wen and Zhou Fang The First Affiliated Hospital of Zhengzhou University, China *Abstract*—Lung cancer is the most prevailing source of death due to cancer, accounting for over 25% of death in the United States. Being able to predict the survival time for patients will provide valuable information for the choice of their treatment plans and benefit patient management. With the advancement of next-generation sequencing, many high-throughput sequencing data for DNA and RNA becomes available for cancer patients. Here we present the results for using multiple machine learning algorithms in predicting the survivorship of patients with Lung cancer adenocarcinoma. Using the publicly available datasets in TCGA with the overall survival length, and transcriptomic information, we evaluated our ability to predict prognosis. We found that using the expression level of a few candidate genes alone generates significant statistical power from a very limited number of patients, suggesting more future studies to be conducted on collecting such data to facilitate personalized medicine.
K1004 Poster 12	Identification of the Association between Hepatitis B Virus and Liver Cancer using Machine Learning Approaches based on Amino Acid **Zhaoyang Cao** University of British Columbia, Canada *Abstract*—Primary liver cancer has been a common reason for death from cancer globally. The most common type of primary liver cancer is the hepatocellular carcinoma (HCC). The major cause of HCC is chronic infections with hepatitis B virus (HBV). In this research, we used next generation sequencing (NGS), which has been very widely used to produce deep, efficient, and high-quality sequence data. NGS was used to sequence the pre-S region of the HBV genome of total 139 patients, which contain 94 HCC patients and 45 chronic HBV (CHB) patients. We generated two types of datasets. Firstly, for the data of amino acid occurrence frequency, we used

	basic local alignment search tool (BLAST) to map each NGS short read and translated each alignment into amino acid by DNA codon table. The input features are the occurrence frequencies of 20 basic amino acids using Shannon entropy. We picked 40 patients with 27 HCC and 13 CHB as the independent testing set. Then we used machine learning methods including logistic regression, random forest and support vector machine (SVM) to construct the classification models and make the prediction. The AUC values on the independent testing set for those machine learning methods (logistic regression, random forest and SVM) are 0.946, 0.923 and 0.960 respectively. Secondly, for the data of word pattern frequency of amino acids, we calculated word pattern frequencies of amino acids of all individuals and compared them using Euclidean distance. The input features are the frequencies of amino acid word of length 2, which is normalized by dividing the total occurrence number of all words. What's more, word pattern frequencies of amino acids were used to construct the classification models for HCC status using machine learning methods. Principal coordinate analysis (PCoA) was also used to visualize the associations between patient clusters, the HCC disease status of patients, and the fraction of HBV genotypes. We found that word patterns are powerful for the analysis of the HBV sequences from the aspect of amino acids because the AUC values of the classification models for machine learning methods are all above 0.9. Hence, our study showed that word pattern frequencies of amino acids is powerful for revealing the underlying principles of the occurrence of HCC triggered by HBV. Our essential findings consist of three parts. Firstly, all machine learning methods can generate classification models with high AUC values. Then, we can find some certain positions of amino acids or word patterns of amino acids that the mutation occurred on those positions will induce the HCC. Last, PcoA is associated with the disease status (HCC or CHB) and the fraction of genotype B (or C).
K0070 Poster 13	Computational Modeling of Myocardial Thermal Lesion Induced by Multi-source Frequency Control RF ablation Method **Shengjie Yan**, Kaihao Gu, Weiqi Wang and Xiaomei Wu Fudan University, China *Abstract*—In minimally invasive surgery for atrial fibrillation, radiofrequency (RF) voltage is usually used to ablate cardiac tissue. In this study, a computational modeling of multi-source frequency control RF ablation mode (FcM) was constructed to analyze the characteristics of thermal field and electric field in myocardium. To highlight the relationship between frequency difference and lesion size of ablation, the amplitude and phase angle of voltage in the simulation were fixed at 20 V peak and 0 degree, respectively. Furthermore, the thermal lesion depth, width and continuity produced by FcM and multi-source bipolar ablation mode(BiM) were also compared in this paper. At the electrical boundary condition for creating continuous lesion, the transmural and continuous lesion (long or

	short) was generated by FcM, whereas BiM did not create transmural lesion. At the electrical boundary condition for creating discrete lesion, FcM was able to create two or one transmural discrete lesion, whereas BiM did not create transmural lesion. Simulation results show that a kind of transmural, continuous, symmetrical lesion shape was generated in atrial tissue using multi-source frequency control RF ablation and the lesion size was larger than BiM at identical ablation condition.

Poster Session 2

Afternoon, January 21, 2020 (Tuesday)
Time: 15:15-16:15
Topic: "Systematic Biology"
Venue: Lobby of Room 3 (1F)
Session Chair: Prof. Masako Takasu

K0083 Poster 1	CitAB Two-component System-regulated Citrate Utilization Contributes to Vibrio Cholerae Competitiveness with the Gut Microbiota **Ming Liu** NanJing Agricultural University, China *Abstract*—Citrate is a ubiquitous compound and can be utilized by many bacterial species, including enteric pathogens, as a carbon and energy source. Genes involved in citrate utilization have been extensively studied in some enteric bacteria, such as Klebsiella pneumoniae, however, their role in pathogenesis is still not clear. In this study, we investigated citrate utilization and regulation in Vibrio cholerae, the causative agent of cholera. The putative anaerobic citrate fermentation genes in V. cholerae, consisting of citCDEFXG, citS-oadGAB, and two-component system (TCS) genes citAB, are highly homologous to those in K. pneumoniae. Deletion analysis shows that these cit genes are essential for V. cholerae growth when citrate is the sole carbon source. The expression of citC and citS operons was dependent on citrate and CitAB, whose transcription was autorepressed and regulated by another TCS regulator ArcA. In addition, citrate fermentation was under the control of catabolite repression. Mouse colonization experiments showed that V. cholerae can utilize citrate in vivo using the citrate fermentation pathway and that V. cholerae likely needs to compete with other members of the gut microbiota to access citrate in the gut.
K2002 Poster 2	Preparation and Application of Chitosan-phytic Acid Complex Gel Beads **Shao-Jung Wu**, Zhi-Run Chen and **Chi-Chen Kuo** Ming Chi University of Technology, Taiwan *Abstract*—A novel and straightforward synthetic technique for the preparation of chitosan beads with less cytotoxicity is desirable. Chitosan can form gels with the nontoxic and multivalent inositol hexakisphosphate counter ion. The polycationic chitosan and polyanionic phytic acid via an ionotropic gelation process to form gels. Crosslinking characteristics of the chitosan-polyanions beads were improved by the modification of in-liquid curing mechanism of the beads. The present study aims to explore the adsorption capacities and kinetics of Cu(II) ions from aqueous solution onto

	fabricated gel beads. The influence of initial pH of the metal ions solution and initial concentration of metal ions solution on the uptake of metal ions were also studied. The equilibrium adsorption data of Cu(II) ions on the gel beads were correlated well with Langmuir isotherm model with a maximum adsorption capacity of 188.68 mg/g. The adsorption of Cu(II) ions on the gel beads exhibited pseudo-second order kinetics. The adsorption thermodynamic parameters indicated that the involved process should be spontaneous and endothermic. This study includes a comparative study on the adsorption capacity of chitosan-based adsorbent, and the results for the application of chitosan-polyanions beads are evaluated in future wastewater treatments.
K0084 Poster3	The 58th Cysteine of TcpP is Essential for Vibrio Cholerae Virulence Factor Production and Pathogenesis **Mengting Shi** NanJing agricultural university, China *Abstract*—Vibrio cholerae, the causative agent of the severe diarrheal disease cholera, has evolved signal transduction systems to control the expression of virulence determinants. It was previously shown that two cysteine residues in the periplasmic domain of TcpP are important for TcpP dimerization and activation of virulence gene expression by responding to environmental signals in the small intestine such as bile salts. In this study, the functions of cysteine residues in TcpP cytoplasmic domain were investigated and we found that only C58 is essential for TcpP dimerization and for activating virulence gene expression. To better characterize this cysteine residue, site-directed mutagenesis was performed to assess the effects on TcpP homodimerization and virulence gene activation. A TcpPC58S mutant was unable to form homodimers and activate virulence gene expression, and did not colonize infant mice. However, a TcpPC19/51/124S mutant was not attenuated for virulence. These results suggest that C58 of TcpP is indispensable for TcpP function and is essential for Vibrio cholerae virulence factor production and pathogenesis.
K0053 Poster 4	Laboratory Solution Service using ExTOPE® IoT Portal **Kazuyuki Kato**, Zentaro Kadota, Shoichi Uemura, Masataka Okayama, Hiroshi Yamaguchi and Tomohiro Araki Hitachi High-Tech Fielding Corporation, Japan *Abstract*—We are developing a protein identification system by amino acid composition analysis. This system identifies a protein automatically by comparing the amino acid analysis results with Uni-Prot array data. This protein identification method is unique as using the total amino acid composition information not the amino acid sequence information such as mass analysis or classical protein sequencer analysis. For the data processing using such a protein identification system, we focused on improving the data treatments. To improve the data accessibility, ExTOPE

	system enables to worldwide data processing and data sharing. Namely, ExTOPE® served by cloud computing has 3 useful functions; automatic data gathering by measurement the results and error logs, operating by remote control, and connecting with other applications by application interfaces. Therefore, ExTOPE® could be a component for automatic system which identified proteins after upload amino acid composition analysis data into cloud computing. Besides, we could use remote control and increase stable quality of machines. As a result, we suggest serviceable laboratory solution to increase useful value of amino acid analyzers with ExTOPE®. We propose ExTOPE® as a laboratory solution system that maximize the utility value of the equipment.
K1012 Poster 5	Procleave: A Bioinformatic Approach for Protease-specific Substrate Cleavage Site Prediction by Combining Sequence and Structural Information **Fuyi Li**, Tatsuya Akutsu, Jian Li and Jiangning Song Monash University, Australia *Abstract*—Proteases are enzymes that cleave and hydrolyse the peptide bonds between two specific amino acids of target substrate proteins. Protease-controlled proteolysis plays a key role in the degradation and recycling of proteins, which is essential for various physiological processes. Thus, solving the substrate identification problem will have important implications for the precise understanding of protease functions and their physiological roles, as well as for therapeutic target identification and pharmaceutical applicability. Consequently, there is a great demand for bioinformatics methods that can predict novel substrate cleavage events with high accuracy by utilizing both sequence and structural information. In this study, we present Procleave, a novel bioinformatics approach for predicting protease-specific substrates and specific cleavage sites by taking into account both sequence and 3D structural information. Structural features of known cleavage sites were represented by discrete values using a LOWESS data-smoothing optimization method, which turned out to be critical for the performance of Procleave. The optimal approximations of all structural parameter values were encoded in a conditional random field (CRF) computational framework, alongside sequence and chemical-group-based features. Here, we demonstrate the outstanding performance of Procleave through extensive benchmarking and independent tests. Procleave is capable of correctly identifying most cleavage sites in case study proteins. Importantly, when applied to the human structural proteome encompassing 17,628 protein structures, Procleave suggests a number of potential novel target substrates and their corresponding cleavage sites of different proteases. Procleave has been implemented as a webserver and is freely accessible at http://procleave.erc.monash.edu/.
K1005	BnMTP3, An Intracellular Transporter from Brassica Napus Confer Zn and Mn Tolerance in Arabidopsis Thaliana

Poster 6	**Dongfang Gu**, Xueli Zhou, Xi Chen and Wei Zhang Nanjing Agricultural University, China *Abstract*—The micronutrient elements Zn and Mn are required for plant growth and development. As an important oil crop in the world, the yield and quality of rapeseed are affected by Zn or Mn toxicity. The CDF family plays an important role in maintaining intracellular ionic homeostasis and tolerance in model plants, but it has rarely been reported in rapeseed. In this study, the functional characterisation of a Brassica napus cation diffusion facilitator (CDF/MTP) protein BnMTP3, homologous to AtMTP3, is investigated. The heterologous expression of BnMTP3 in yeast enhances tolerance and intracellular sequestration to Zn and Mn. The MTP3-dependent increase in metal tolerance was more pronounced for Zn than for Mn. Expression of BnMTP3 increased Zn and Mn tolerance in Arabidopsis thaliana, but also markedly increased Zn accumulation in roots. This is consistent with the results of expression analysis that BnMTP3 was primarily expressed in roots. Subcellular localisation suggested that BnMTP3 was localised to TGN and PVC, and fluorescent signals were observed on vacuolar membranes after treatment with Zn and Mn. These findings indicated that BnMTP3 is a member of Zn-CDFs that may sequester excess Zn and/or Mn into vacuoles.
K0055 Poster7	Comparing Dissimilarity Metrics for Clustering Gene into Functional Modules using Machine Learning **Xin Yan** and Dantong Lyu Sun Yat-Sen University, China *Abstract*—Clustering is widely used in biological analyses for clustering genes into functional modules. For any clustering mechanism, we need to define some measurements for dissimilarity. The two most commonly used dissimilarity metrics are the Manhattan distance and Euclidean distance. Moreover, the 1-correlation coefficient is also commonly used for defining similarity. Here, we use the transcriptomic data across multiple environments in yeast for gene clustering and evaluate the performance of using these four dissimilarity metrics. We designed two metrics that use 1-abs(correlation) for Pearson and Spearman correlation. We found that 1-abs(Pearson correlation) works the best in two test cases for identifying genes involved in ethanol metabolism and galactose metabolism and build a clustering model based on the metric. We propose that this dissimilarity metric be used for future studies of clustering of genes based on expression level. Such information, combined with more gathering of transcriptomic information across environments, will boost our understanding of gene clustering and modularity in exploring unknown species.
K1006 Poster 8	OsGCT1, A Novel Gene Related to Cadmium, Copper Tolerance and Accumulation in Rice **Ending Xu**, Xi Chen and Wei Zhang

	Nanjing Agricultural University, China *Abstract*—Copper (Cu) is an essential micronutrient for plants and humans. Cadmium (Cd) is a Cu analog and one of the most toxic heavy metals to humans. Here we investigated the role of the Cu/Cd transporter OsGCT1. OsGCT1:GFP fusion protein localized to the Golgi in rice protoplast. The growth of yeast expressing OsGCT1 was impaired in the presence of Cd and Cu compared with yeast transformed with an empty vector. Moreover, the Cd and Cu content of OsGCT1-expressing yeast exceeded that of the vector control. The expression of OsGCT1 in rice was observed mainly in the leaves where OsGCT1 transcripts were abundant in vascular bundles. Knockdown of OsGCT1 resulted in growth inhibition in the presence of high concentrations of Cd and Cu, and also led to increased accumulation of Cd and Cu in the shoots and new leaves. The overexpression of OsGCT1 was found to enhance Cd and Cu tolerance in rice. These findings suggest that OsGCT1 is a Golgi-localized Cd and Cu transporter that is required for Cd and Cu homeostasis and contributes towards Cd and Cu tolerance in rice.
K1001 Poster 9	Rectal Methods of Delivery of Medical Drugs of the Protein Nature **J.K. Ukibayev**, U.M. Datkhayev, A.P. Frantsev and D.A. Myrzakozha Kazakh National Medical University named after S.D. Asfendiyarov, Kazakhstan *Abstract*—Intravenous injection of protein drugs causes many negative side effects known as infusion reactions and serious consequences, such as serum sickness. This article shows the possibility of intake into the body of recipients of drug preparations of protein nature in the form of rectal suppositories. The use of rectal forms of protein preparations has a number of significant advantages compared with injectable forms. They are more effective than injectable forms, since their active molecules are less exposed to the destructive action of liver enzymes. Rectal forms of protein preparations are easy to use for children and elderly patients, they are absolutely safe for nosocomial infections - syphilis, hepatitis, HIV, etc. Moreover, they are simpler in the technology of their manufacture.
K2018 Poster 10	The Application of Designated Manager System on Protection Forest Management at Saga Prefecture, Japan - from the Public-Private Partnership and Policy Implementation Approaches Ching Li, **Chiachi Cheng** and Yi-Chine Chu Industrial Technology Research Institute, Taiwan *Abstract*—In 2003, Japanese government pointed out the Deigned Manager System to emphasize the importance of combining national and private ability to raise the public benefits and increase citizen participation rates. In addition, Forest Agency hopes to make use private ability to realize the diversified management of forest business, those are the backgrounds of public-private partnerships of forest management in Japan. The purpose of

	this study was to discuss the application of the Designated Manager System on protection forest management at Saga Prefecture, Japan. The study took Nijinomatsubara Pine Forest and Saga 21 Century Kenminnomori Forest Learning Center as the examples, attempted to define the roles of each organization, the public values, and the co-governors on the policy implication processes. This study applied document analysis and interview with government officers and NPO managers. This study found, the governments played different roles to integrate process for different public value, in Nijinomatsubara, local government plays the role as a communication person between government and locals; in the case of Kenminnomori Forest Learning Center, local government plays the role as a provider, provides the wellness place to NPO and citizens for learning forest related knowledge. Also, vary with issue initiation, each NPO niche abilities for co-governers, Nijinomatsubara's NPO have basically ecological environment knowledge and activity integration ability, the NPO of Saga Forest Learning Center have professional forest related knowledge and woodworking ability. Both of these 2 cases aim to widen range of public participation. Therefore, PPP not only the idea for taking advantage of private organization or the NPO only want to get benefits from governments, but share the value within government, NPO and citizens, and widen the range of public participation.
K0067 Poster 11	Automatic Brain Mask Segmentation for Mono-modal MRI **Yanwu Yang**, Chenfei Ye, Xutao Guo, Chushu Yang and Heather T. Ma Harbin Institute of Technology, Shenzhen, China *Abstract*—In recent years, deep learning methods have gained promising results in different kinds of image processing tasks, such as image classification, semantic segmentation, image generation and so on. This paper focuses on the research of brain masking for mono-modal MRI, structural MRI, which is the most commonly used by the clinic and research. The brain mask is a basic and essential tool for brain function analysis and voxel-based structural analysis. In this paper, we present an automatic method for brain masking which would match the brain atlas for the origin image and also extract the regions of interest (ROI), like Hippocampus. Our network is developed from the U-net and a coarse mask is added into the network, which is generated by the method of region seeds growing. The combination of coarse mask and origin input speeds up the localization of the network and also increases the segmentation accuracy. In this work, two groups of experiments have been carried out, the one to do the brain mask automatically for the whole brain and the other for the region of Hippocampus extraction. Finally we have gained 0.893 dice coefficient for Hippocampus and 0.865 for the whole brain regions in average
K0056 Poster 12	The Application and Comparison of Confocal and SIM Imaging System **Yiran Liu** University of California, USA

	Abstract—Optical imaging is a popular method for biology research, and now there lots of optical imaging system. Confocal imaging is a wide used one which was introduced the pinhole and subsequently is not affected by the out-of-focus signal, making the method be better than widefield microscopy. It is acceptable that confocal microscopy has its own limits in resolution. Researchers struggled to push the resolution to another limit during the process many fancy optical imaging methods were invented, such as structured illumination microscopy (SIM). We are here to apply the two optical imaging methods in RyR2 labelled heart cells to compare the two methods, and we found that confocal imaging does show the disadvantages such as photobleaching and limited resolution, while SIM imaging has a higher resolution to observe much more details of the RyR2 location.
K0082 Poster 13	Colon Cancer Inhibition Capacity Evaluation and Mechanism Study of A Novel Biopolymer Conjugated Gold Nanoparticle System as Chemo-reagent Carrier Wei-Hung Hung, Kuen-Chan Lee and **Er-Chieh Cho** Taipei Medical University, Taiwan *Abstract*— Colon cancer is a common leading cause of death around the world, especially in western countries. Even though great progress has been made for colon cancer therapeutic development, there are still clinical challenges in treating late staged or metastatic patients. Nanomaterials have been intensively applied in biomedical studies. Gold nanoparticles have been demonstrated as a promising drug carrier with great cellular biocompatibility, yet little studies examined the capacity of biopolymer conjugated gold nanoparticle in colon cancer. In this study, we assembled and investigated the system with chemo-reagent in both cancer cell model and mice model. The system was evaluated by UV spectrum and transmission electron microscope, etc. first, and then the cancer suppression capacity of the system and regulatory mechanisms have been studied by different molecular biological assays. In conclusion, our results showed that our novel drug carrier system is powerful in treating colon cancer, and that this system can potentially contribute to other diseases in the future.

Academic Visit
9:30-17:30, January 22, 2020 (Wednesday)

Tip: 1. Gather at 京都駅八条口 日本〒601-8003 Kyoto, Minami Ward, Higashikujo Nishisannocho. (In front of 7-ELEVEN Convenience Store.) before 9:30 a.m.

2. The quotation only includes lunch, admission tickets of Kinkaku-ji Temple and Kiyomizu Temple.

3. The following places are for references, and the final schedule should be adjusted to the actual notice.

Time	Specific Arrangement
9:30-10:00	Depart at 京都駅八条口
10:30-12:00	Enjoy the breathtaking *Kinkaku-ji Temple* - the golden pavilion
12:00-15:30	Lunch
	Discover the amazing *Kiyomizu Temple*
	Appreciate handicrafts at *Ninen-zaka and Sannen-zaka*
	Photograph at *Ishibe Alley*
	Stroll around *Gion (The Geiko/Geisha District)*
	Visit *Yasaka Shrine*
15:30-17:00	Walk among vermillion gates at *Fushimi Inari*
17:00-17:30	Return

Kinkakuji is a Zen temple in northern Kyoto whose top two floors are completely covered in gold leaf. Kinkakuji is an impressive structure built overlooking a large pond, and is the only building left of Yoshimitsu's former retirement complex. It has burned down numerous times throughout its history including twice during the Onin War, a civil war that destroyed much of Kyoto; and once again more recently in 1950 when it was set on fire by a fanatic monk. The present structure was rebuilt in 1955.

Kiyomizu (literally "Pure Water Temple") is one of the most celebrated temples of Japan. It was founded in 780 on the site of the Otowa Waterfall in the wooded hills east of Kyoto, and derives its name from the fall's pure waters. The temple was originally associated with the Hosso sect, one of the oldest schools within Japanese Buddhism, but formed its own Kita Hosso sect in 1965. In 1994, the temple was added to the list of UNESCO world heritage sites.

Ninen-zaka and Sannen-zaka Two of Kyoto's most attractive streets are Sannen-zaka and Ninen-zaka, a pair of gently sloping lanes that lead down from Kiyomizu-dera Temple toward Nene-no-Michi Lane. Lined with beautifully restored traditional shophouses and blissfully free of the overhead power lines that mar the rest of Kyoto, Sannen-zaka and Ninen-zaka are a pair of pedestrian-only lanes that make for some of the most atmospheric strolling in the whole city.

Ishibe Alley is a must-see in Kyoto. As you walk through the alleyways you feel like you've stepped into a movie set, only it's real, because the establishments in Ishibe are not just for display.

Gion is Kyoto's most famous geisha district, located around Shijo Avenue between Yasaka Shrine in the east and the Kamo River in the west. It is filled with shops, restaurants and ochaya (teahouses), where geiko (Kyoto dialect for geisha) and maiko (geiko apprentices) entertain.Gion attracts tourists with its high concentration of traditional wooden machiya merchant houses.

Yasaka Shrine, also known as Gion Shrine, is one of the most famous shrines in Kyoto.

Founded over 1350 years ago, the shrine is located between the popular Gion District and Higashiyama District, and is often visited by tourists walking between the two districts.The shrine's main hall combines the honden (inner sanctuary) and haiden (offering hall) into a single building. In front of it stands a dance stage with hundreds of lanterns that get lit in the evenings. Each lantern bears the name of a local business in return for a donation.

Fushimi Inari Shrine is an important Shinto shrine in southern Kyoto. It is famous for its thousands of vermilion torii gates, which straddle a network of trails behind its main buildings. The trails lead into the wooded forest of the sacred Mount Inari, which stands at 233 meters and belongs to the shrine grounds. Fushimi Inari is the most important of several thousands of shrines dedicated to Inari, the Shinto god of rice. Foxes are thought to be Inari's messengers, resulting in many fox statues across the shrine grounds. Fushimi Inari Shrine has ancient origins, predating the capital's move to Kyoto in 794.

Note

Note