

# 2017 CBEES-BBS SEOUL, SOUTH KOREA CONFERENCE ABSTRACT

**November 12-14, 2017**

**Seoul National University, Hoam Faculty House,**

**South Korea**



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# 2017 CBEES-BBS Seoul, South Korea Conference Introduction

Welcome to 2017 Seoul, South Korea conference which is sponsored by Hong Kong Chemical, Biological & Environmental Engineering Society (CBEES) and Biology and Bioinformatics (BBS). The objective of Seoul, South Korea conference is to provide a platform for researchers, engineers, academicians as well as industrial professionals from all over the world to present their research results and development activities in Biomedical and Bioinformatics Engineering, and Biometric Engineering and Forensics.

## 2017 4th International Conference on Biomedical and Bioinformatics Engineering (ICBBE 2017)

Papers will be published in one of the following conference proceedings or journal:



**International Conference Proceedings Series by ACM.** Archived in the ACM Digital Library, and indexed by Ei Compendex and submitted to be reviewed by Scopus and Thomson Reuters Conference Proceedings Citation Index (ISI Web of Science).



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

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

## 2017 International Conference on Biometric Engineering and Forensics (ICBEF 2017)

Papers will be published in one of the following conference proceedings or journal:



**International Conference Proceedings Series by ACM.** Archived in the ACM Digital Library, and indexed by Ei Compendex and submitted to be reviewed by Scopus and Thomson Reuters Conference Proceedings Citation Index (ISI Web of Science).



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

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

# Presentation Instruction

## Instruction for Oral Presentation

### Devices Provided by the Conference Organizer:

Laptop Computer (MS Windows Operating System with MS PowerPoint and Adobe Acrobat Reader)

Digital Projectors and Screen

Laser Stick

### Materials Provided by the Presenters:

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

### Duration of each Presentation (Tentatively):

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

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

Plenary Speech: about **25** Minutes of Presentation and **5** 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

Maximum poster size is A1

Load Capacity: Holds up to 0.5 kg

## Best Presentation Award

One Best Oral Presentation will be selected from each presentation session, and the Certificate for Best Oral Presentation will be awarded at the end of each session on November 12-13, 2017.

## Dress code

Please wear formal clothes or national representative of clothing.

# Keynote Speaker Introduction

## Keynote Speaker I



Prof. Yasushi Yagi  
Osaka University, Japan

**Yasushi Yagi** is the Executive Vice President of Osaka University in 2015. He received his Ph.D. degree from Osaka University in 1991. In 1985, he joined the Product Development Laboratory, Mitsubishi Electric Corporation, where he worked on robotics and inspections. He became a research associate at Osaka University in 1990, a lecturer in 1993, an associate professor in 1996, and a professor in 2003. He was the director of the Institute of Scientific and Industrial Research at Osaka University from 2012 to 2015. The studies in his laboratory focus on computer vision and media processing including basic technologies such as sensor design, and applications such as an intelligent system with visual processing functions. Some of our major research projects are: the development of a novel vision sensors such as an omnidirectional catadioptric system; biomedical image processing such as endoscope and microscope images; person authentication, intention, and emotion estimation from human gait, and its applications to forensic and medical fields; photometry analysis and its application to computer graphics; an anticrime system using a wearable camera; and 3D shape and human measurement using infrared light. He is a member of the Editorial Board of the International Journal of Computer Vision and the Vice-President of the Asian Federation of Computer Vision Societies. He is a fellow of IPSJ and a member of IEICE, RSJ, and IEEE.

Topic: “*Gait Analysis for Person Authentication*”

**Abstract**—We have been studying human gait analysis for more than 10 years. Because everyone's walking style is unique, human gait is a prime candidate for person authentication tasks. Our gait analysis technologies are now being used in real criminal investigations. We have constructed a large-scale gait database, and proposed several methods of gait analysis. The appearances of gait patterns are influenced by changes in viewpoint, walking direction, speed, clothes, and shoes. To overcome these problems, we have proposed several approaches using a part-based method, an appearance-based view transformation model, a periodic temporal super resolution method, a manifold-based method and score-level fusion. In this talk, I briefly introduce an overview of our gait analysis technologies and show the efficiency of our approaches by evaluating them with our large gait database.

## Keynote Speaker II



Prof. Kar-Ann Toh  
Yonsei University, South Korea

**Kar-Ann Toh** is a Professor in the School of Electrical and Electronic Engineering at Yonsei University, South Korea. He received the PhD degree from Nanyang Technological University (NTU), Singapore. He worked for two years in the aerospace industry prior to his post-doctoral appointments at research centers in NTU from 1998 to 2002. He was affiliated with Institute for Infocomm Research in Singapore from 2002 to 2005 prior to his current appointment in Korea. His research interests include biometrics, machine learning, pattern classification, and neural networks. He is a co-inventor of two US patents and has made several PCT filings related to biometric applications. Besides being active in publications, Dr. Toh has served as an advisor/co-chair/member of technical program committee for international conferences related to biometrics and artificial intelligence. He has served as an Associate Editor of IEEE Transactions on Information Forensics and Security, Pattern Recognition Letters and IET Biometrics. He is a senior member of the IEEE.

Topic: “*Multi-biometrics and Machine Learning*”

**Abstract**—We shall begin this talk with a brief introduction to biometrics and multi-biometrics. Then several modes for fusing a multiple number of biometrics will be discussed. Since the method for fusion under these modes can be viewed as a classification problem, a brief overview of related literature in classifier design is subsequently provided. With these backgrounds in place, we shall introduce several learning methods where their learning objective functions fit the needs of biometrics and have a deterministic solution. Particularly the minimization of the classification counting error goal and the maximization of the receiver operating characteristic curve will be presented with deterministic solution. Finally, we shall walk through several experimental case studies before concluding the talk.



## Keynote Speaker III



Assoc. Prof. Kuo-Yuan Hwa

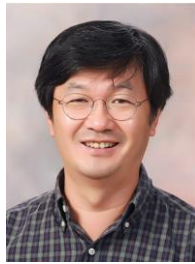
National Taipei University of Technology, Taiwan

**Dr. Kuo-Yuan Hwa** is an associate professor and the director of the Center for Biomedical Industries at the National Taipei University of Technology. Dr. Hwa graduated and received her PhD from the School of Medicine, the Johns Hopkins University. She is the president of the Medical Association for Indigenous Peoples of Taiwan (MAIPT). Dr. Hwa's scientific interests are: 1) nanotechnology and biosensor, 2) new drug discovery for human diseases by proteomics and genomics approaches and 3) glycobiology, especially on enzymes kinetics. She has published 85 conference and journal articles and 10 patents. She has served in many national and international committees. Dr. Hwa has been invited as a speaker for many academic research institutes and universities in China, Korea, Japan and USA. She has been invited as a reviewer, a judge and an editor for international meetings and journals. In addition, one of her current works is on developing culturally inclusive health science educational program, with both indigenous and western science knowledge for indigenous children.

Topic: *“Anti-Cancer Drug Discovery in the Era Precision Medicine- from Compounds to SNPs”*

**Abstract**—According to the World Health Organization, cancer is the second leading cause of death globally. Globally, nearly 1 in 6 deaths is due to cancer, about 8.8 million deaths in 2015. Cancer is a group of diseases which begin with abnormal and uncontrollable cell division and growth. Neoplastic cells can convert into malignant tumors. Although many anticancer drugs have been developed over the past 50 years such as 5-Fluorouracil, there are still limitations. It is because when chemotherapy is carried out, normal cells in the body are also killed, that results in many adverse effects. To develop more effective anticancer treatments i.e. targeted-based drugs is needed. Moreover, the majority of the first-in-class drugs approved by the FDA between 2009 and 2013 have been discovered through target-based approaches. We have previously isolated a series of anti-cancer compounds with defined mechanisms of actions via a comparative genomics approach. To further develop these compounds, here we have taken in silico approaches to find the specific SNPs in association with the efficacy of compounds by developing an analysis workflow. The identified SNPs can be further developed as complementary screening tools for designing pre-clinical and clinical studies. The SNPs found in this study can be used to recruit the correct patients for the drug development that would accelerate the drug discovery in the era of precision medicine.

## Plenary Speaker I



Prof. Taesung Park  
Seoul National University, South Korea

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

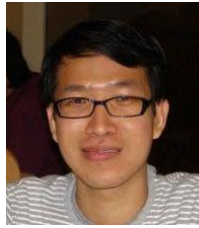
Topic: *“Hierarchical Structural Component Analysis of Gene-Gene Interactions”*

Sungkyoung Choi, Sungyoung Lee, Yongkang Kim, Heungsun Hwang, and **Taesung Park**

**Abstract**—While many statistical approaches have been proposed to detect gene-gene interactions (GGI), most of these focus primarily on SNP-to-SNP interactions. While there are many advantages of gene-based GGI analyses, such as reducing the burden of multiple-testing correction, and increasing power by aggregating multiple causal signals across SNPs in specific genes, only a few methods are available. In this study, we proposed a new statistical approach for gene-based GGI analysis, “Hierarchical structural CoMponent analysis of Gene-Gene Interactions” (HisCoM-GGI). HisCoM-GGI is based on generalized structured component analysis (GSCA), and can consider hierarchical structural relationships between genes and SNPs. For a pair of genes, HisCoM-GGI first effectively summarizes all possible pairwise SNP-SNP interactions into a latent variable, from which it then performs GGI analysis. HisCoM-GGI can evaluate both gene-level and SNP-level interactions. Through

simulation studies, HisCoM-GGI demonstrated higher statistical power than existing gene-based GGI methods, in analyzing a GWAS of a Korean population for identifying GGI associated with body mass index.

## Plenary Speaker II



Assoc. Prof. Andrew Teoh  
Yonsei University, South Korea

**Andrew Beng Jin Teoh** obtained his BEng (Electronic) in 1999 and Ph.D degree in 2003 from National University of Malaysia. He is currently an associate professor in Electrical and Electronic Engineering Department, College Engineering of Yonsei University, South Korea. His research, for which he has received funding, focuses on biometric applications and biometric security. His current research interests are Machine Learning and Information Security. He has published more than 250 international refereed journal papers, conference articles, edited several book chapters and edited book volumes. He served and is serving as a guest editor of IEEE Signal Processing Magazine, TPC member of Information Forensic and Security in IEEE Signal Processing Society, associate editor of IEEE Biometrics Compendium and editor-in-chief of IEEE Biometrics Council Newsletter. He was a program co-chair of ICONIP 2014, area chair of ICPR 2016 and ICIP 2017, track chair and TPC for several conferences related to computer vision, pattern recognition and biometrics.

Topic: *“Cancelable Biometrics for Template Protection: Recent Advancements and Challenges”*

**Abstract**—Although biometrics is a powerful means against repudiation and has been widely deployed in various security systems, the biometric characteristics are largely immutable, resulting in permanent biometric compromise. Cancellable biometrics was proposed by storing a transformed version of the biometric template and provides higher privacy level by allowing multiple templates to be associated with the same biometric data. This helps to promote non-linkability of user’s data stored across various databases and revocation can be done when template is compromised. This talk will present the advancement and the challenges of cancellable biometrics.

## Plenary Speaker III



Prof. Jose Nacher  
Toho University, Japan

**Prof. Jose Nacher** received his Ph.D. in Theoretical Physics from Valencia University. From 2003-2007 he was a postdoctoral research fellow at the Bioinformatics Center, Institute for Chemical Research (ICR), Kyoto University. He was awarded with a JSPS Research Fellowship at the ICR, Kyoto University (2005-2007). From 2007-2012, he was a Lecturer and an Associate Professor at the Department of Complex and Intelligent Systems, Future University, concurrently with a visiting Associate Professor appointment at the Bioinformatics Center, ICR, Kyoto University (2011-2102) and Future University (2012-2013), respectively. From 2012, he was an Associate Professor at the Department of Information Science, Toho University. Since 2016, he is a Professor at the Department of Information Science, Faculty of Science, Toho University. He is a reviewer of more than 30 international journals in his field, serves as an Editorial Review Board of the International Journal of Knowledge Discovery in Bioinformatics (IJKDB) since 2009, as an Editorial Board of the Computational Biology Journal since 2012 and as an Editorial Board Member of Scientific Reports NPG since 2015. Prof. Nacher Lab's bioinformatics research interests include the development and application of novel mathematical methods and algorithms in systems biology and complex biological networks.

Topic: “*Recent Progress on Controllability Models for Analysing Biological Networks*”

**Abstract**—The increasing availability of biological data has allowed us to represent biological systems as networks, in which nodes are life molecules and edges denote biochemical interactions, from protein-protein interaction (PPI) networks to metabolic pathways. Recent developments on network analysis are shifting the focus on controllability features of complex systems. In particular, controllability of complex networks is aiming at integrating concepts from control theory and network science with the purpose of understanding and ultimately control large-scale networks. Several frameworks have been proposed to control complex networks and among them, the Maximum Matching (MM) and the Minimum Dominating Set (MDS) models have recently gained popularity and have been used in several biological network analyses. In this talk, we first present the MM and MDS frameworks and the main theoretical grounds on which the models are built. Then, we review the controllability analysis results of several biological networks, from protein-protein interactions networks to metabolic pathways and ncRNA-protein networks.

## Plenary Speaker IV



Assoc. Prof. Naomichi Yamamoto  
Seoul National University, South Korea

**Dr. Naomichi Yamamoto** is an Associate Professor in the Department of Environmental Health Sciences at Seoul National University. His current research interests include applications of molecular biology-based techniques to study risks and transports of indoor and atmospheric fungal bioaerosols. His primary research expertise is: i) aerosol science; ii) aerobiology; and iii) molecular fungal biology. His research team applies cutting-edged technologies such as next-generation sequencing (NGS) and RNA-Seq to study human health risks of pathogenic and allergenic fungal bioaerosols. Before joining to SNU faculty in 2012, Dr. Yamamoto worked at Yale School of Engineering as a postdoctoral scientist supported by the Japan Society for the Promotion of Science (JSPS). He received his B.Eng. degree in applied physics from Waseda University, M.S. degree in environmental health sciences from UCLA, and Ph.D. degree in environmental studies from the University of Tokyo.

Topic: *“High-throughput Sequencing as a Tool to Analyze Medically Important Fungal Pathogens and Diversities”*

**Abstract**—The kingdom Fungi is a diverse group of eukaryotic organisms with an estimated 1.5 million constituent species. Fungi discharge microscopic spores into air, and inhalation of fungal spores may cause respiratory illnesses such as allergies and opportunistic infections in human. Development of allergic diseases such as asthma is thought to be associated with the early-life exposures to environmental microbes and their diversities. Inhalation of pathogenic fungal spores may cause invasive fungal infections in immunocompromised individuals. To assess the risks of diseases caused by and associated with fungal pathogens and diversities, it is essential to correctly identify fungal pathogens down to the species level and accurately characterize diverse fungal communities in the environment. In this presentation, I introduce how high-throughput sequencing technologies and bioinformatics techniques are useful for accurately characterizing diverse fungal communities and correctly identifying fungal pathogens down to the species level, which are thought to be important when assessing the risks of fungal allergies and infections.

## Plenary Speaker V



Prof. Sun Kim

Seoul National University, South Korea

**Sun Kim** is Professor in the School of Computer Science and Engineering, Director of Bioinformatics Institute, and an affiliated faculty for the Interdisciplinary Program in Bioinformatics at Seoul National University. Before joining SNU, he was Chair of Faculty Division C; Director of Center for Bioinformatics Research, an Associate Professor in School of Informatics and Computing; and an Adjunct Associate Professor of Cellular and Integrative Physiology, Medical Sciences Program at Indiana University (IU) Bloomington. Prior to joining IU in 2001, he worked at DuPont Central Research from 1998 to 2001, and at the University of Illinois at Urbana-Champaign from 1997 to 1998. Sun Kim received B.S and M.S and Ph.D in Computer Science from Seoul National University, KAIST and the University of Iowa, respectively.

Sun Kim is a recipient of Outstanding Junior Faculty Award at Indiana University 2004, US NSF CAREER Award DBI-0237901 from 2003 to 2008, and Achievement Award at DuPont Central Research in 2000. He is actively contributing to the bioinformatics community, serving on the editorial board for journals including editors for the METHODS journal and International Journal of Data Mining and Bioinformatics, having served on a board of directors for ACM SIG Bioinformatics and for education for the IEEE Computer Society Technical Committee on Bioinformatics. He has been co-organizing many scientific meetings including ACM BCB 2011 as a program co-chair, IEEE International Conference on Bioinformatics and Biomedicine (BIBM) 2008 as a program co-chair and 2009 as a conference co-chair. In Korea, he is currently President of Korea Artificial Intelligence Society and Vice President of Korea Society of Bioinformatics and Systems Biology.

Topic: *“Analysis of Omics Data: To Use Domain Knowledge or Not”*

**Abstract**—Domain knowledge can be very helpful in analyzing genome-wide molecular data or omics data. However, incorporating domain knowledge into the computational framework is not straightforward. One popular and successful approach is to utilize curated biological networks for the analysis of omics data. These networks are constructed by utilizing literature and experimental data. A condition specific omics data measured under a specific condition can be mapped to biological networks and then various computational methods such as clustering and composition methods are used for the analysis of the condition specific data. We introduce some of the network-based analysis methods developed in my lab. Another

important domain knowledge is the literature information on genes and biological pathways. The typical use of these literature information is for the interpretation of the omics data analysis results, but not for the analysis per se. Our group developed computational frameworks that can perform integrated analysis of experimental and literature data. While domain knowledge is important and useful, a typical situation is that we do not have enough domain knowledge since we as human did not create living organisms. In this case, we found that the popular deep learning technologies are very effective. In this talk, we will introduce some of the deep learning based analysis methods from my lab for the protein function prediction and breast cancer subtype classification.



## Brief Schedule for Conference


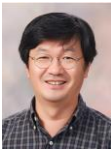



Nov. 12, 2017 (Sunday)	10:00~17:45    Arrival Registration	
	13:30~17:45	Opening Remarks, Keynote, Plenary Speech and Session 1
	Venue: G-Tulip (G-tulip) Room (First Floor)	
	13:30-13:35	Opening Remarks (Prof. Kar-Ann Toh)
	13:35-14:05	Plenary Speech I (Prof. Taesung Park)
	14:05-14:45	Keynote Speech I (Prof. Yasushi Yagi)
	14:45-15:15	Plenary Speech II (Assoc. Prof. Andrew Beng Jin Teoh)
	15:15-15:35	Coffee Break & Group Photo
	15:35-16:15	Keynote Speech II (Prof. Kar-Ann Toh)
	16:15-17:45	Session 1: Signal Analysis and Image Processing
Nov. 13, 2017 (Monday) Morning	09:00~12:10	Opening Remarks, Keynote Speech, Plenary Speech and Session 2
	Venue: G-ROSE (G-로즈) Room (First Floor)	
	09:00-09:05	Opening Remarks (Assoc. Prof. Kuo-yuan Hwa )
	09:05-09:45	Keynote Speech III(Assoc. Prof. Kuo-yuan Hwa)
	09:45-10:10	Coffee Break & Group Photo
	10:10-10:40	Plenary Speech III (Prof. Jose Nacher)
	10:40-12:10	Session 2: Bioinformation Technology and Engineering
	12:10~13:30	Lunch (In front of the building B1 crystal hall)
Nov. 13, 2017 (Monday) Afternoon	Venue: G-ROSE (G-로즈) Room (First Floor)	
	13:30-14:00	Plenary Speech IV (Assoc. Prof. Naomichi Yamamoto)
	14:00-15:30	Session 3: Development of Medical Equipment and Device
	15:30-15:50	Coffee Break
	15:50-16:20	Plenary Speech V (Prof. Sun Kim)
	16:20-17:50	Session 4: Clinical Diagnosis and Rehabilitation Therapy
	18:00~20:00	Dinner (In front of the building B1 crystal hall)
Nov. 14, 2017 (Tuesday)	9:30~17:30	One Day Visit and Tour

**Tips:** Please arrive at the Conference Room 10 minutes before the session begins to upload PPT into the laptop.

# Detailed Schedule for Conference

November 12, 2017 (Sunday)

Venue: G-Tulip (G-tulip) Room (First Floor)

10:00~17:45		<b>Arrival and Registration</b>
13:30-13:35		<b>Opening Remarks</b> Prof. Kar-Ann Toh Yonsei University, South Korea
13:35-14:05		<b>Plenary Speech I</b> Prof. Taesung Park Seoul National University, South Korea Topic: <i>"Hierarchical Structural Component Analysis of Gene-Gene Interactions"</i>
14:05-14:45		<b>Keynote Speech I</b> Prof. Yasushi Yagi Osaka University, Japan Topic: <i>"Gait Analysis for Person Authentication"</i>
14:45-15:15		<b>Plenary Speech II</b> Assoc. Prof. Andrew Beng Jin Teoh Yonsei University, South Korea Topic: <i>"Cancelable Biometrics for Template Protection: Recent Advancements and Challenges"</i>
15:15-15:35		<b>Coffee Break &amp; Group Photo</b>
15:35-16:15		<b>Keynote Speech II</b> Prof. Kar-Ann Toh Yonsei University, South Korea Topic: <i>"Multi-biometrics and Machine Learning"</i>
16:15-17:45		<b>Session 1 (Signal Analysis and Image Processing)</b>

**November 13, 2017 (Monday)**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

09:00-09:05		<b>Opening Remarks</b> Assoc. Prof. Kuo-yuan Hwa National Taipei University of Technology, Taiwan
09:05-09:45		<b>Keynote Speech III</b> Assoc. Prof. Kuo-yuan Hwa National Taipei University of Technology, Taiwan Topic: <i>"Anti-Cancer Drug Discovery in the Era Precision Medicine- from Compounds to SNPs"</i>
09:45-10:10		<b>Coffee Break &amp; Group Photo</b>
10:10-10:40		<b>Plenary Speech III</b> Prof. Jose Nacher Toho University, Japan Topic: <i>"Recent Progress on Controllability Models for Analysing Biological Networks"</i>
10:40-12:10		<b>Session 2 (Bioinformation Technology and Engineering)</b>
12:10-13:30		<b>Lunch (In front of the building B1 crystal hall)</b>
13:30-14:00		<b>Plenary Speech IV</b> Assoc. Prof. Naomichi Yamamoto Seoul National University, South Korea Topic: <i>"High-throughput Sequencing as a Tool to Analyze Medically Important Fungal Pathogens and Diversities"</i>
14:00-15:30		<b>Session 3 (Development of Medical Equipment and Device)</b>
15:30-15:50		<b>Coffee Break</b>
15:50-16:20		<b>Plenary Speech V</b> Prof. Sun Kim Seoul National University, South Korea Topic: <i>"Analysis of Omics Data: To Use Domain Knowledge or Not"</i>
16:20-17:50		<b>Session 4 (Clinical Diagnosis and Rehabilitation Therapy)</b>
18:00~20:00		<b>Dinner (In front of the building B1 crystal hall)</b>

**Note: (1) The registration can also be done at any time during the conference.**

**(2) The organizer doesn't provide accommodation, and we suggest you make an early reservation.**

**(3) One Best Oral Presentation will be selected from each oral presentation session, and the Certificate for Presentation will be awarded at the end of each session on November 12-13, 2017.**

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

# 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, November 12, 2017 (Sunday)**

**Time: 16:15-17:45**

**Venue: G-Tulip (G-tulip) Room (First Floor)**

**Session 1: Topic: “Signal Analysis and Image Processing”**

**Session Chair: Assoc. Prof. Kuo-Yuan Hwa**

E0019 Presentation 1 (16:15~16:30)

Classification of Movement Direction from EEG Signals before Movement

**Hyeonseok Kim** and Yasuharu Koike

Tokyo Institute of Technology, Japan

*Abstract*—Understanding intention of human is important in brain-machine interface. Many efforts to understand human intention have been tried through EEG signals. Especially, reaching task, which is basic movement in brain-machine interface, has been analyzed. Previous researches about reaching task have been conducted in direct reaching. However, we used EEG signals before movement to understand human intention for more general use in brain-machine interface. In this study, 5 Subjects were instructed they move the cursor to certain direction which is one of up, down, left, right directions determined randomly on screen through touch pad. EEG signals were separated through independent component analysis. Two independent components were selected to classify direction (left vs right and up vs down) through support vector machine. Cross-validation was conducted to estimate classification performance. Two selected independent components were mostly good for classification with more than 80% accuracy. We found that two primary independent components for high accuracy in left vs right classification differ from two primary independent components for high accuracy in up vs down classification. In further study for practical application, optimal independents should be investigated through calibration before the movement. We confirmed feasibility of two primary independent components for prediction of movement direction.

**Afternoon, November 12, 2017 (Sunday)**

**Time: 16:15-17:45**

**Venue: G-Tulip (G-톨립) Room (First Floor)**

**Session 1: Topic: “Signal Analysis and Image Processing”**

**Session Chair: Assoc. Prof. Kuo-Yuan Hwa**

E0030 Presentation 2 (16:30~16:45)

Detection of the Top Anemic Diseases in Blood Smear Images Using Image Quantization Followed by Ensemble of Classifiers

**Bakht Azam**, Samiur Rahman, Sehat Ullah and Fazal Hanan

University of Malakand, Pakistan

*Abstract*—Anemia is a condition caused due to the deficiency of Red Blood Cells (RBCs) and hemoglobin in blood. It is an indication to a specific disorder in the human body. Different types of anemic diseases infect the shapes of Red Blood Cells in different ways and the infected cells form various geometric shapes, such as elongated ellipse, triangular shapes, cut circles, boundary interruption in ellipse or circle etc. Leveraging these shapes the type of anemia can easily be identified. We have used various boundary based shape descriptors like shape signatures and color profiles as features for the infected RBCs recognition. The algorithm is followed by preprocessing steps like color channel separation, segmentation through quantization, feature extraction and finally classification of Red Blood Cells and the diseases associated with them. We have achieved 92 % accuracy and the proposed method is cost effective and easy to use.

**Afternoon, November 12, 2017 (Sunday)**

**Time: 16:15-17:45**

**Venue: G-Tulip (G-톨립) Room (First Floor)**

**Session 1: Topic: “Signal Analysis and Image Processing”**

**Session Chair: Assoc. Prof. Kuo-Yuan Hwa**

E0031 Presentation 3 (16:45~17:00)

Spectral Characteristics of Microcirculatory Signals Response to Muscle Stretching among Diabetic Smokers

**Jian-Guo Bau**, Yue-Der Lin and Bo-Wen Huang

Hungkuang University, Taiwan

*Abstract*—Cigarette smoking is reported to be the major risk factor for endothelial dysfunction. The variations of the spectral compositions of microcirculatory perfusion signal could provide the information related to the regulatory function of microvasculature. The aim of the present study was to compare the spectral characteristics response to muscle stretching between diabetic smokers and non-smokers, and investigate the influence of cigarette smoking on microvascular function. Twenty four diabetic patients (12 smokers v.s. 12 non-smokers) and twelve normal non-smoking subjects were recruited. We observed that the diabetic smokers had a significantly reduced endothelial activity. The mechanisms for the reduction of the endothelial activity remain to be elucidated. The spectral analysis might be used to evaluate endothelial function for research, for diagnostic purposes, and maybe also to assess effects of therapy in cardiovascular diseases.

**Afternoon, November 12, 2017 (Sunday)**

**Time: 16:15-17:45**

**Venue: G-Tulip (G-톨립) Room (First Floor)**

**Session 1: Topic: “Signal Analysis and Image Processing”**

**Session Chair: Assoc. Prof. Kuo-Yuan Hwa**

W0004 Presentation 4 (17:00~17:15)

Automated Diagnosis of Lung Cancer with the Use of Deep Convolutional Neural Networks on Chest CT

**Joongwon Kim**, Hojun Lee and Taeseon Yoon

Hankuk Academy of Foreign Studies, Korea

*Abstract*—For the past several decades, machine learning has greatly enhanced the process of image analysis. With the development of deep learning technologies in the 21st century, image recognition has gained applicability to various technologies such as automated driving system, face recognition and medical data processing. This research attempts to diagnose lung cancer using chest CT of patients and non-patients. A modified form of Deep Convolutional Neural Network is introduced, which involves using multiple 2D convolutional neural networks on individual slices and combining the results to diagnose patients and non-patients. Each patient/non-patient’s chest CT data were first segmented for the lung features and stored into three-dimensional arrays. The preprocessed three-dimensional arrays were fed into the CNN framework, and the parameters of the network were trained. Many iterations of the process with enough data modified network parameters in a way that the network was able to diagnose CT scans of patients with accuracy between 70~80%.

**Afternoon, November 12, 2017 (Sunday)**

**Time: 16:15-17:45**

**Venue: G-Tulip (G-톨립) Room (First Floor)**

**Session 1: Topic: “Signal Analysis and Image Processing”**

**Session Chair: Assoc. Prof. Kuo-Yuan Hwa**

W2001 Presentation 5 (17:15~17:30)

A Multi-Finger Touchless Fingerprinting System: Mobile Fingerphoto and Legacy Database Interoperability

Lewis A. Carney, Josiah Kane, Jonathan F. Mather, Asem Othman, Andrew G. Simpson, **Aryana Tavanai**, Richard A. Tyson and Yiqun Xue

VERIDIUM, UK

*Abstract*—We have developed a Multi-Finger Touchless fingerprinting system that can be deployed on most smartphones, capturing prints with only the rear camera and the LED flash. These prints are interoperable with conventional touch-based print databases. This allows fingerprint identification to be rolled out to the general population as a software only solution. This system features an automatic image capture system where we automatically detect each finger and enhance each finger’s corresponding image to resemble a touch-based print. From start to finish the capture time is approximately 6 seconds with a favourable deployment footprint of under 10MB. On an initial test database of 1400 touchless fingerprints and 6600 touch-based fingerprints, we achieved a touchless-touch match rate of 98.6% with a 0.0% false accept rate.



**Afternoon, November 12, 2017 (Sunday)**

**Time: 16:15-17:45**

**Venue: G-Tulip (G-톨립) Room (First Floor)**

**Session 1: Topic: “Signal Analysis and Image Processing”**

**Session Chair: Assoc. Prof. Kuo-Yuan Hwa**

W0005 Presentation 6 (17:30~17:45)

An In-Air Signature Verification System Using Wi-Fi Signals

Han-Cheol Moon, Se-In Jang, Kangrok Oh and **Kar-Ann Toh**

Yonsei University, Korea

*Abstract*—This paper presents a Wi-Fi based system for in-air signature verification. The proposed system is able to authenticate in-air signatures which are captured through Wi-Fi signals. The system consists of four main stages namely, data acquisition, preprocessing, feature extraction and matching. The proposed system shows an average equal error rate of 4.31% on an in-house dataset which consists of 1040 samples collected from 13 subjects. This experiment shows that the Wi-Fi signals can be applied to in-air signature verification effectively.

# 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.

**Morning, November 13, 2017 (Monday)**

**Time: 10:40-12:10**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 2: Topic: “Bioinformation Technology and Engineering”**

**Session Chair: Prof. Jose Nacher**

E0009 Presentation 1 (10:40~10:55)

Minimum Dominating Set-Based Analysis and Its Applications to Biological Networks

**Masayuki Ishitsuka**, Tatsuya Akutsu and Jose Nacher

Toho University, Japan

*Abstract*—Recent progress on controllability has made it possible to combine complex networks features and techniques with control theory concepts. The theoretical developments in controllability have been applied to various biological networks. By performing controllability analysis, we are not only focusing on determining potential driver nodes that can eventually control the entire network, but also aim to identify life molecules associated to specific biological functions or disease states. In fact, the Minimum Dominating Set (MDS) approach has shown that proteins in the MDS tend to be significantly enriched with oncogenes. In this talk, we first introduce the MDS approach to control complex networks. We then present our recent results on critical controllability of undirected biological networks. In particular, we explain the algorithm that allows us to investigate critical controllability in proteome-wide protein interaction networks. Second, we present new preliminary results on our analysis of directed biological networks such as metabolic networks. The fast algorithmic approach as well as the details of data analysis will be discussed.

**Morning, November 13, 2017 (Monday)**

**Time: 10:40-12:10**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 2: Topic: “Bioinformation Technology and Engineering”**

**Session Chair: Prof. Jose Nacher**

E0015 Presentation 2 (10:55~11:10)

Heat Transfer Enhancement with Microscale-flow Systems for Vitrification of Cells/Tissues

**Xiaoming Zhou**

University of Electronic Science and Technology of China, China

*Abstract*—Vitreous cryopreservation, which utilizes the principle of vitrification to avoid ice formation, has displayed significant advantages to the conventional methods. In our study, several kinds of microscale-flow systems were designed to accomplish ultra-rapid cooling and rewarming desired in vitrification. Theoretically evaluation was perform with a microchannel system first. It was indicated the cooling and the rewarming rate were as high as 105 °C/min. Accordingly, prototype devices were fabricated, and their performance were examined with an operation/measurement platform. It was demonstrated that the microchannel devices were able to deliver ultra-high cooling/rewarming rate ( $2 \times 10^4 \sim 1 \times 10^5$  °C/min) for flexible sizes of samples (10~600  $\mu$ l). With a similar platform, several other microscale-flow systems were also tested. Among those, a microjet impingement system was found to be able to produce cooling or re-warming rates over 104 °C/min for milliliters of samples. The temperature distribution was quite uniform, while the overall heat transfer efficiency was a little lower than that of the microchannel systems. A hybrid system, which combines microchannel flow and microjet impingement, would be the best solution. With significant breakthrough in obtaining both desired cooling/warming rate and uncompromised sample size, the presented approach provide a promising solution for high throughput vitreous cryopreservation.

**Morning, November 13, 2017 (Monday)**

**Time: 10:40-12:10**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 2: Topic: “Bioinformation Technology and Engineering”**

**Session Chair: Prof. Jose Nacher**

E0027 Presentation 3 (11:10~11:25)

The Activity of Salsolinol Synthase in Models of Parkinson’s Disease Induced by 6-Hydroxydopamine

**Xiaotong Zheng**, Xuechai Chen and Rugang Zhong

Beijing University of Technology, China

*Abstract*—Salsolinol (Sal) is an endogenous neurotoxin derived from dopamine. It has been proved to cause the apoptosis of the dopaminergic neurons and involved in the pathogenesis of Parkinson’s disease (PD). Sal synthase is the key enzyme of the biosynthesis of Sal, which is first detected and isolated from the urine of PD patients. Our previous work had confirmed the existence of this enzyme in normal rat brains. To investigate the relationship between the activity of Sal synthase and PD in animal level, a series of experiments were performed. The results showed the Salsolinol synthase was one of the most important factor of PD.

**Morning, November 13, 2017 (Monday)**

**Time: 10:40-12:10**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 2: Topic: “Bioinformation Technology and Engineering”**

**Session Chair: Prof. Jose Nacher**

E0029 Presentation 4 (11:25~11:40)

Association of Serum miR-145 with Vascular Endothelial Growth Factor (VEGF) in Patients with Non-Small Cell Lung Cancer

**Pichitpon Chaniad**, Paramee Thongsuksai and Pritsana Raungrut

Prince of Songkla University, Thailand

*Abstract*—Non-small cell lung cancer (NSCLC) accounts for approximately 85% of all lung cancers and it is the leading cause of cancer death globally. Vascular endothelial growth factor (VEGF) plays an important role in cancer progression, including lung cancer. Therefore, it would be interesting to determine key modulators that can suppress VEGF production. This study aimed to identify miRNAs regulating VEGF using systematic reviews and bioinformatics tools. We further validated miRNA expression and VEGF level using qRT-PCR and ELISA, respectively. A total 17 studies were selected using systematic review. 97 miRNAs were found to be up-regulated in serum of NSCLC compared to controls. miR-145 was selected to further validate in clinical samples. Serum miR-145 expression in NSCLC ( $10.77 \pm 3.40$ ) was lower than patient with other lung diseases ( $25.10 \pm 7.90$ ) with p-value of 0.019. The VEGF level in serum of NSCLC was significantly higher than other lung diseases and healthy persons with p-value of 0.003 and 0.002, respectively. However, a weak negative correlation of miR-145 and VEGF in serum of NSCLC was observed without significant difference. In conclusion, the expression of miR-145 and VEGF in NSCLC patients may be involved with lung tumorigenesis; however, the VEGF is not regulated by miR-145 in lung cancer.

**Morning, November 13, 2017 (Monday)**

**Time: 10:40-12:10**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 2: Topic: “Bioinformation Technology and Engineering”**

**Session Chair: Prof. Jose Nacher**

W0001 Presentation 5 (11:40~11:55)

Analysis of Mycobacterium Tuberculosis, Mycobacterium Bovis, and Mycobacterium africanum that Cause Tuberculosis Using Apriori and Decision Tree Algorithm

**Juhyun Lee, Seoyoung Yoon and Taeseon Yoon**

Hankuk Academy of Foreign Studies, South Korea

*Abstract*—About two million people die from Tuberculosis(TB) each year, and the high death rate of the disease has persisted for decades. TB infection, which is caused by bacteria that belong to genus Mycobacterium, can significantly affect normal functions of lungs and other body parts such as brain and spine. Although tuberculosis patients have been treated with medicines, it took much time to detect visible effects. To further enhance the vaccines and treatment of TB, people should conduct more comprehensive research about the TB infection. Therefore, in this research, we aim to analyze genomes of three bacteria in Mycobacterium genus: Mycobacterium tuberculosis, Mycobacterium bovis, and Mycobacterium africanum. We adopted mainly two algorithms, apriori and decision tree, in order to proceed analysis. Before we undertook an experiment, we established a hypothesis: M. tuberculosis and M. bovis would exhibit a stronger correlation because they are the most common cause of tuberculosis for a long time. By analyzing their DNA sequences and amino acid frequency, we examined relationships between those three bacteria, especially similarities and differences. Furthermore, we tried to prove the hypothesis. We expect that our research will give a chance to improve potent vaccines and medicines by adopting these relationships we found in our research.

**Morning, November 13, 2017 (Monday)**

**Time: 10:40-12:10**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 2: Topic: “Bioinformation Technology and Engineering”**

**Session Chair: Prof. Jose Nacher**

W0007 Presentation 6 (11:55~12:10)

Electroformation of Giant Unilamellar Vesicles in Saline Solution

**Qingchuan Li** and Xiaojun Han

Harbin Institute of Technology, China

*Abstract*—Giant unilamellar vesicle (GUV) is an excellent model for bioanalysis, cellular membrane activity study and artificial cell fabrication. Electroformation method is commonly used to form GUVs with high quality and yields, while it has proven to be difficult for GUV formation in saline solution and from charged lipids. We present a way to overcome this problem by using plasma cleaned ITO electrodes. GUVs from zwitterionic lipids, lipid mixtures and even pure charged lipids could be electroformed under physiological conditions and even higher concentrations of NaCl. Finite element analysis simulating the effect of the electric field on GUV formation in saline solution could well explain the experimental results. Frequencies in the kHz-range favored for GUVs formation in saline solution, as they suppress the formation of electric double layer, while higher frequencies could again impair the effect of electric field and impede GUV formation. The diameters of the GUVs increased gradually with NaCl concentration from 0 mM to 200 mM and subsequently decreased from 200 mM to 2 M. This method is a promising way to prepare GUVs for bioanalysis and cellular activity study on a large scale in physiological relevant conditions.

Lunch	
12:10	In front of the building B1 crystal hall

# 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, November 13, 2017 (Monday)**

**Time: 14:00~15:30**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 3: Topic: “Development of Medical Equipment and Device”**

**Session Chair: Assoc. Prof. Naomichi Yamamoto**

E0008 Presentation 1 (14:00~14:15)

Effect of N-Vinyl-Pyrrolidone on the Properties of Silicone-Based Hydrogel Contact Lens

**Nguyen-Phuong-Dung Tran**, Huynh-Quang-Dieu Nguyen and Ming-Chien Yang

National Taiwan University of Science and Technology, Taiwan

*Abstract*—Silicone hydrogel contact lens was prepared from copolymerization of tris-(trimethyl-silyl-propyl-methacrylate) (TRIS), dimethylacrylamide (DMA), and N-vinylpyrrolidone (NVP). The properties of these polymers were characterized including equilibrium water content, oxygen permeability, optical transparency, and protein adsorption. The results showed that the increase of NVP concentration could increase the equilibrium water content of silicone hydrogel lens. Nevertheless, higher NVP ratio led to the decrease of oxygen permeability of polymers. The silicone hydrogel samples attained minimum oxygen permeability of 46 barrers with 25 wt% NVP. In addition, all lenses exhibited excellent optical transparency and resisted protein deposition. The highest protein adsorption was at 25 wt% NVP. The results demonstrated that by varying NVP content, the ophthalmic properties of TRIS-DMA-NVP can be controlled.



**Afternoon, November 13, 2017 (Monday)**

**Time: 14:00~15:30**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 3: Topic: “Development of Medical Equipment and Device”**

**Session Chair: Assoc. Prof. Naomichi Yamamoto**

E0005 Presentation 2 (14:15~14:30)

Optimizing Gait Parameters and Insole Sensor Positioning for Parkinson’s Disease Assessment

**Jiaxin Ma**, Kenichi Kameyama and Makoto Nakagawa

Teijin Pharma Ltd., Japan

*Abstract*—Gait abnormality is a characteristic symptom of Parkinson’s disease (PD) and could be exploited to assess PD progression. In this study, we examined various gait parameters and insole sensor positioning for evaluating PD. We first verified the results from several published papers in which gait parameters exhibited significant differences between PD patients and healthy controls. Then, we investigated additional gait parameters derived from individual sensors in 8 positions across the sole. The result demonstrated that the balls, heels, and center of arches are valuable positions for PD gait assessment. Furthermore, a random forests method showed the most important gait parameters to predict PD include swing time on the balls and medial arches, double support time on the balls and medial arches, and ground reaction forces on the heels. The optimization of sensor positioning and gait parameters suggests a low-cost and effective way identify Parkinsonian gait characteristics.

**Afternoon, November 13, 2017 (Monday)**

**Time: 14:00~15:30**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 3: Topic: “Development of Medical Equipment and Device”**

**Session Chair: Assoc. Prof. Naomichi Yamamoto**

E0017 Presentation 3 (14:30~14:45)

Bio-based Active Agent Encapsulated Intelligent Micro and Nanoparticles: Tuning the Size, Morphology and Property

**Nirmala Devi**, Parineeta Das, Dilip K. Kakati and Tarun K. Maji

National Institute of Technology Nagaland, India

*Abstract*—Natural polymer-based intelligent micro and nanoparticles have been exploited as carriers for bio-based active agent delivery. Spherical and needle like carrier particles with varied sizes (nano/micro), shapes (spherical/needle like) and morphology (porous/nonporous) were synthesized by using natural polymers from renewable resource. Micro/nanoparticles with encapsulated bio-based active agents (neem and olive oil, curcumin) were prepared by using polyelectrolyte complexation of natural polymers gelatin and sodium carboxymethyl cellulose/sodium alginate/carrageenan/rosin. %yield, viscosity and turbidity measurements were carried out to evaluate the pH and ratio of the two polymers that produced highest yield. The encapsulation efficiency of active agents was dependent on the amount of crosslinker, active agent loading and polymer concentration. Scanning electron micrographs showed the formation of free flowing spherical micro/nanoparticles in case of isoniazid loading and a bit agglomerated in case of oil loading. The particles were found to be pH responsive. The size, morphology and property of the micro and nanoparticles were tuned. TGA showed the improvement of thermal stability with crosslinking. FTIR study showed no significant interaction between oil/drug and polymer complex. Active agent encapsulated biopolymer based nanorod carriers revealed needle-like morphology on TEM analysis. The particles were further characterized by NMR, XRD and DSC studies. The natural polymeric micro and nano carriers showed immense potential for versatile active agent delivery applications.

**Afternoon, November 13, 2017 (Monday)**

**Time: 14:00~15:30**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 3: Topic: “Development of Medical Equipment and Device”**

**Session Chair: Assoc. Prof. Naomichi Yamamoto**

E3001 Presentation 4 (14:45~15:00)

Optimal Placement of Multi-Channels sEMG Electrode for Finger Movement Classification

**Direk Sueaseenak**, Thunchanok Uburi and Paphawarin Tirasuwannarat

Srinakharinwirot University, Thailand

*Abstract*—This research aims to propose the optimal electrode positions for surface EMG by using a modern gesture control device called MYO armband. Seven healthy volunteers participated in this research. The sEMG signal was collected from three different electrode positions in the superficial forearm muscles positions such as Extensor digitorum muscle, Flexor digitorum superficialis muscle, Palmaris longus muscle during finger movements 5 gesture including flexion thumb, index, middle, ring and little. Waveform length(WL) is a feature extraction method, EMG features were represented in scatter diagrams to explain their behaviors. The well-known quantitative parameters used to evaluate the performance of EMG feature included scattering criterion. The result showed optimal position to obtain the best quality surface EMG recording by MYO armband for finger movement classification. The position is a middle of forearm length area.

**Afternoon, November 13, 2017 (Monday)**

**Time: 14:00~15:30**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 3: Topic: “Development of Medical Equipment and Device”**

**Session Chair: Assoc. Prof. Naomichi Yamamoto**

E0007 Presentation 5 (15:00~15:15)

Application of Organosolv Pretreatment on *Pennisetum Purpureum* for Lignin Removal and Cellulose Recovery

Danny Chin Wei-Kit, **Steven Lim**, Pang Yean Ling and Wong Kam-Huei

Universiti Tunku Abdul Rahman, Malaysia

*Abstract*—*Pennisetum Purpureum* or Napier Grass, a native to African grass happened to be one of the most promising candidates for bioethanol production. However, literature studies on the organosolv pretreatment process for *P. Purpureum* were relatively rare. Therefore, in this research, organosolv pretreatment on *P. Purpureum* was studied and compared with different types of solvent (1-pentanol and ethylene glycol) and homogeneous catalysts (sodium hydroxide and sulfuric acid) in order to provide the feasibility study and filling the current research gap. The chemical composition of *P. Purpureum* was found to comprise of 21.50% lignin, 54.67% alpha cellulose and 23.83% of beta cellulose and hemicellulose. The substantial composition of cellulose and hemicellulose in *P. Purpureum* proved its promising potential as a raw material for bioethanol production. Ethylene glycol with concentration of 50.0 v/v% with addition of 2.0 v/v% of sodium hydroxide had proven to be the most effective organosolv pretreatment combination in removal of lignin (83.4%). In terms of lignocellulosic component recovery, this pretreatment solvent achieved up to 70.10% alpha cellulose recovery and 97.90% beta cellulose and hemicellulose recovery.

**Afternoon, November 13, 2017 (Monday)**

**Time: 14:00~15:30**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 3: Topic: “Development of Medical Equipment and Device”**

**Session Chair: Assoc. Prof. Naomichi Yamamoto**

E0024 Presentation 6 (15:15~15:30)

Study the Heart Valve Elasticity and Optimal of Vortex Formation for Blood Circulation Measurement on the Left Ventricle Using the Heart Simulator (Heart-S) Apparatus

**Mohd Azrul Hisham Mohd Adib** and Nur Hazreen Mohd Hasni

Universiti Malaysia Pahang, Malaysia

*Abstract*—Modeling of heart simulator gives a better understanding of blood circulation and the figure of the heart valve’s movement as well as the fluid flow movement in the heart chamber. In this study, the relationship between heart valve elasticity and the angle of the heart valve position to the heart valve opening width were investigated. Also, the optimal of vortex formation was observed by using the heart simulator (Heart-S) apparatus on the left ventricle during the cardiac cycle. The result shows good relation on heart valve elasticity and the angle of the heart valve position to the valve opening. The optimal of vortex formation in the heart chamber also clearly observed.



# 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, November 13, 2017 (Monday)**

**Time: 16:20~17:50**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 4: Topic: “Clinical Diagnosis and Rehabilitation Therapy”**

**Session Chair: Prof. Sun Kim**

E0013 Presentation 1 (16:20~16:35)

The Optimal Algorithm of Sub-Symptom Threshold Exercise Training for Aural Habilitation/Rehabilitation

**Direk Sueaseenak**, Pavarisa Sangsai, and Piyamas Detyong

Srinakharinwirot University, Thailand

*Abstract*—This paper presents the comparison study of the speech recognition system for the Thai language in the noise of the different environment. The well-known algorithms, such as MLP, SVM, GMM, HMM, VQ, DTW, DNN and End to End were used in this research. A test was conducted with 50 men and 50 women subjects during 5-60 years old. The proposed method consists of several parts which are (i) the feature extraction by Mel-frequency cepstral coefficients (MFCC) algorithm, (ii) The learning and decision process. The performance testing of the systems by the Ling’s six sounds, such as ah, mm, oo, ee, sh and ss. The experiment results of our proposed method show that the accuracy of the system more than 80 percent.

**Afternoon, November 13, 2017 (Monday)**

**Time: 16:20~17:50**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 4: Topic: “Clinical Diagnosis and Rehabilitation Therapy”**

**Session Chair: Prof. Sun Kim**

E0022 Presentation 2 (16:35~16:50)

Prediction of Parkinson Disease Using Nonlinear Classifiers with Decision Tree Using Gait Dynamics

**Satyabrata Aich**, Kiwon Choi, Hee-Cheol Kim and Jinse Park

Inje University, South Korea

*Abstract*—In the last decade, the second most common neurodegenerative disorder among the old people is the Parkinson’s disease (PD). PD affects 2-3% of the population over the age of 65 years. Since the aging population rate is increasing at a faster rate all over the world, so many advanced techniques such as artificial intelligence and machine learning algorithms have been used to detect the progression of disease at early stage in short time. Few past research has been made to classify the PD from the healthy older peoples. They have used linear classification techniques for classification as well as linear dimensionality algorithm for feature selection. In this paper an attempt has been made to classify the PD group from the healthy control group by using nonlinear based classifier with decision tree and also nonlinear feature selection algorithm called Recursive Feature Elimination for selection of features. Finally, a performance comparison has been made between the original set of features as well as the reduced features. Our result does not able to find any significance difference in the performance metrics of the two feature sets, but achieved the classification accuracies ranging from 81.7% to 85.31%.

**Afternoon, November 13, 2017 (Monday)**

**Time: 16:20~17:50**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 4: Topic: “Clinical Diagnosis and Rehabilitation Therapy”**

**Session Chair: Prof. Sun Kim**

E0018 Presentation 3 (16:50~17:05)

Effectiveness of Fitting Pressure Garments for Minor and Moderate Burn Patients: A Literature Review

**Pi-Wen Huang** and Chih-Wei Lu

Chung Yuan Christian University, Taoyuan, Taiwan

*Abstract*—Aim: Burn reconstruction and rehabilitation are difficult and time-consuming processes; a burn patient must endure a long rehabilitation process to treat burn scars. The continued proliferation of scars and anxiety engender considerable difficulties for patients. A burn scar contracture is like a burned rubber band; the skin is never restored to its original flexibility.

Wearing pressure garments (PGs) is uncomfortable and challenging for patients, but constant adherence is necessary. To improve adherence, precise knowledge about the advantages and disadvantages of PG therapy (PGT) is necessary.

Methods: This review examined experimental studies that have applied PGT on patients with varicose veins and burns, as well as healthy human controls. The participants answered questionnaires to determine the best or “ideal” pressure. All scars were treated under a scar management program and followed up by the treating hospital and scanned by ultrasound. Scars were assessed using the Tissue Ultrasound Palpation System (TUPS), as well as the Vancouver Scar Scale (VSS) for rating scar thickness, pliability, pigmentation, and vascularity. Scar thickness and color were objectively measured using the Plance X system and Laser Doppler Imaging (LDI).

Results: In general, the application of 15–25 mmHg pressure is most commonly used in clinical practice. Minor and moderate burn patients could wear PGs in the very beginning of the recovery process. According to guidelines, closed scars should always be reevaluated 6 months after the burn to determine whether additional scar management interventions are required or whether preventive therapy can be terminated.



**Afternoon, November 13, 2017 (Monday)**

**Time: 16:20~17:50**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 4: Topic: “Clinical Diagnosis and Rehabilitation Therapy”**

**Session Chair: Prof. Sun Kim**

E0025 Presentation 4 (17:05~17:20)

Therapeutic Potential of Molecular Hydrogen for Ovarian Teratoma

**Lei Shang**, Fei Xie, Jia-la Li, Ya-ting Zhang and Xue-mei Ma

Beijing University of Technology, China

*Abstract*—Ovarian teratoma (OT) are common ovarian germ cell tumors. Mature cystic teratomas are the most common type of ovarian neoplasm and are usually benign. Molecular hydrogen has been reported to function as a novel antioxidant and exert protective effects in a wide range of disease models and human diseases. The present study was designed to investigate the effect of molecular hydrogen and sorafenib combined with molecular hydrogen on OT. The in vivo study was performed by using a mouse model of OT. The in vitro study was performed by using PA-1 and Hs38.T cells of OT. The results showed that hydrogen molecules can inhibit the growth of ovarian teratoma in animals hydrogen molecules can improve the therapeutic effect of sorafenib and reduce the growth of tumor after stopping.

**Afternoon, November 13, 2017 (Monday)**

**Time: 16:20~17:50**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 4: Topic: “Clinical Diagnosis and Rehabilitation Therapy”**

**Session Chair: Prof. Sun Kim**

E1003 Presentation 5 (17:20~17:35)

Study on Repositioning of Comminuted Fractured Bones for Computer-Aided Preoperative Planning

**Irwansyah Idram**, Jiing-Yih Lai, Terence Essomba and Pei-Yuan Lee

National Central University, Taiwan

*Abstract*—The objective of this study is to provide a 3D medical imaging system for the preoperative planning and simulation for orthopedic surgery. This study also emphasizes to investigate several repositioning algorithms for recovering the orientation and position of comminuted bone fragments. General concept and application program for 3D simulation based on personal computer is presented, enabling surgeons to relocate fracture fragments onto their original position. The laboratory default software, called PhysiGuide, was employed to deal with the repositioning of comminuted fracture fragments. To explore appropriate repositioning methods respect to registration of bone fragments, contralateral, landmarks and fracture line constraints are analyzed. The clinical case of patient's proximal femur fragments generated from CT scans used for evaluating the performance of the proposed system. The displacements of fracture fragments after repositioning are calculated and compared to ground truth as a standard. The experimental results show that acceptable displacement presented by point to point registration based. The root mean square is  $\pm 1.9$  mm.

**Afternoon, November 13, 2017 (Monday)**

**Time: 16:20~17:50**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Session 4: Topic: “Clinical Diagnosis and Rehabilitation Therapy”**

**Session Chair: Prof. Sun Kim**

E0026 Presentation 6 (17:35~17:50)

Identification of Anticancer peptides using optimal feature space of Chou’s Split Amino acid composition and Support Vector Machine

**Fazlullah Khan**, Shahid Akbar, Abdul Basit, Hamza Akhlaq, Inamullah Khan and Nasir Khan  
Abdul Wali Khan University Mardan, Pakistan

*Abstract*—Cancer is a serious disease and occurs the cause of death around the world. Various traditional methods i.e. targeted therapy chemotherapy and radiation based therapies have been extensively used by the investigators but still it is considered ineffective due to its high cost, side effects and Vulnerability towards finding errors. Therefore; an automatic and efficient model highly desirable to identify anticancer peptides. In this paper, the peptides sequences are formulated using three numerical descriptors namely; Split amino acid composition, dipeptide composition and Pseudo amino acid composition. The predicted outcomes of the proposed method is evaluated using two different nature classification learners, i.e., instance based k-nearest neighbor and Support vector machine. Our proposed model achieved the an accuracy of 93.31% sensitivity of 86.23% and specificity of 98.06% and MCC of 0.86, the success rate shows the remarkable improvement in performance matrices in comparison with existing techniques in the literature. It is observed that our proposed method will be useful for the investigators in the area of drugs design and proteomics.

# Poster Session

**November 13, 2017 (Monday)**

**Time: 09:00~17:50**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Poster session: 4 presentations**

E0002 Poster 1

BreastCancerMine: a Comprehensive Biological Database for Breast Cancer

Zhang Yang, **Jiannan Chen** and Yi Zhao

Harbin Institute of Technology (Shenzhen), China

*Abstract*—BreastCancerMine is an integrated breast cancer database and analysis platform developed for large and complex biological and clinical data sets. It can help researchers to analysis data from multiple databases quickly and easily, and then, free them from the annoying and time-consuming data management. Designed for integrative analysis, it can be accessed through a user-friendly web interface. This central data warehousing system retrieves biological and clinical data from multiple databases and presents them in an interactive and uniformed way. BreastCancerMine will enable users to access, visualize and analysis multiple types of data and to generate new ideas intuitively for breast cancer research.

**November 13, 2017 (Monday)**

**Time: 09:00~17:50**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Poster session: 4 presentations**

E0004 Poster 2

Modeling the Uncertainty in Finger-Vein Authentication by the Gaussian Mixture Model

Hongyu Ren, **Da Xu** and Wenxin Li

Peking University, China

*Abstract*—The robustness and uniqueness of finger-vein makes it an ideal biometric feature for personal authentication. General finger-vein authentication methods consist of two parts, feature extraction and feature matching. Finger-vein images captured by infrared device are subject to uncertainties caused by various temperature, irregular illumination and finger posture deformation. Uncertainties cause severe artifacts, which make the extracted features unsatisfying and hard to match.

We try to alleviate the problem during matching by modeling the extracted features as Gaussian Mixture Model (GMM). In the proposed method, given two feature maps of finger-vein, we first model inputs as GMM using the normal distribution transform, and then minimize the distance between two GMMs based on gradient descent, lastly we output the possibility that two feature maps belong to one person.

To show its superiority, we replace conventional feature matching schemes with proposed method and test the performance gain based on two kinds of finger-vein features: finger-vein trajectory and finger-vein skeleton. Experimental results on the RATE dataset show that the proposed method is superior to the conventional methods in precision.

**November 13, 2017 (Monday)**

**Time: 09:00~17:50**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Poster session: 4 presentations**

E0010 Poster 3

Engineering Glycerol Dehydratase via A Semi-Rational Approach for Application to the Production of Biochemicals from Glycerol

**Abdul Nasir**, Choi Sang Jin and Yoo Tae Hyeon

Ajou University Suwon South Korea, South Korea

*Abstract*—The production of biodiesel has become an important strategy to address the fading petroleum reservoirs and environmental issues, and the rapid growth of biodiesel production has considerably reduced the price of crude glycerol. Recently biological processes to produce high-value products from glycerol have drawn much attention. The first step of such processes is the dehydration from glycerol to form 3-hydroxypropanal (3-HPA), which can be catalyzed by glycerol dehydratase (GdHt), and the intermediate can be converted into 1,3-propandiol or 3-hydroxypropionic acid. In this presentation, we will describe our effort to engineer coenzyme B12-dependent GdHt from *Klebsiella pneumonia*. In particular, the binding site for coenzyme B12 was targeted to address the inactivation problem of the enzyme, which results from unwanted modification of coenzyme B12. Computations methods were used to investigate the coenzyme B12-binding site, and rationally designed libraries were generated. In addition, a screening method was established based on detection of 3-HPA. We expect that the information about GdHt and the engineering method will valuable sources to engineer GdHt and to develop biological processes to covert glycerol into valuable products.

**November 13, 2017 (Monday)**

**Time: 09:00~17:50**

**Venue: G-ROSE (G-로즈) Room (First Floor)**

**Poster session: 4 presentations**

E0016 Poster 4

Correlation between Cobb Angle and Spinous Process Angle Measured from Ultrasound Data

**Junhua Zhang**, Hongjian Li and Bo Yu

Yunnan University, China

*Abstract*—The correlation between the Cobb angle and spinous process angle (SPA) measured from ultrasound data was analyzed in this study. The three-dimensional (3D) spine model was reconstructed by using a freehand 3D ultrasound imaging system. With non-planar volume rendering, the Cobb angle and SPA were measured by manually detecting anatomical landmarks of the spine. A thoracic spinal phantom set in 24 different poses was used in the experiment. For each spinal curve, the Cobb angle and SPA were measured twice by three observers, respectively. Results showed that the correlation coefficients between these two measurements were 0.92 and 0.78 for the curves with two-dimensional (2D) and 3D deformity, respectively. Results indicate that the SPA has high correlation with the Cobb angle measured from ultrasound data, especially for the curves with 2D deformity. Therefore, SPA may be used as an alternative parameter to the Cobb angle for scoliosis assessment in an ultrasound imaging system.



Dinner	
18:00	In front of the building B1 crystal hall

# One Day Visit & Tour

**November 14, 2017 (Tuesday) 9:30~17:30**

*(Tip: Please arrive at Seoul National University, Hoam Faculty House --the place for registration before 9:30 a.m. The following places are for references, and the final schedule should be adjusted to the actual notice.)*

1. (9:30) Assemble at Seoul National University, Hoam Faculty House
2. (10:00-12:00) Visit Seoul National University



## Seoul National University

Seoul National University (SNU; Korean, 서울대학교, Seoul Daehakgyo, colloquially Seouldae) is a national research university located in Seoul, South Korea.

Founded in 1946, Seoul National University is the most prestigious university in the country. It is located on three campuses: the main campus is in Gwanak and two additional campuses in Daehangno and Pyeongchang. The university comprises sixteen colleges, one graduate school and nine professional schools. The student body consists of nearly 17,000 undergraduate and 11,000 graduate students. According to data compiled by KEDI, the university spends more on its students per capita than any other university in the country that enrolls at least 10,000 students.

Seoul National University holds a memorandum of understanding with over 700 academic institutions in 40 countries, the World Bank and a general academic exchange program with the University of Pennsylvania. The Graduate School of Business offers dual master's degrees with Duke University, ESSEC Business School and Peking University, double-degrees with the MIT Sloan School of Management and Yale School of Management and MBA-, MS- and PhD-candidate exchange programs with universities in ten countries on four continents. Following a government mandate to globalize Korean universities, the university's international faculty head count peaked at 242 or 4% of the total in 2010, but subsequently declined.

3. (12:00-13:00) Lunch time
4. (13:00-17:30) Visit Seoul



## Myeongdong Cathedral

The Cathedral Church of the Virgin Mary of the Immaculate Conception, also known as Myeongdong Cathedral, is cathedral of the Roman Catholic Archdiocese of Seoul. Located in the Myeongdong neighborhood of Jung-gu, Seoul, South Korea, it is the cathedra, or seat, of the Latin Rite Archbishop of

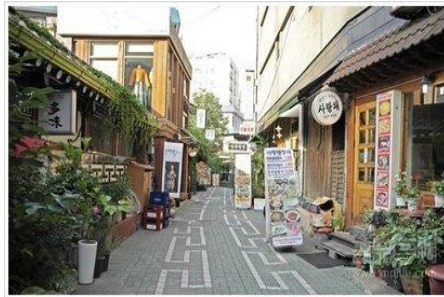


Seoul Cardinal Andrew Yeom Soo-jung, the highest Roman Catholic prelate within Roman Catholicism in South Korea. Dedicated to Our Lady of the Immaculate Conception, the principal patron saint of Korea and the Korean people, the cathedral is a community landmark and a notable symbol of Catholicism in Korea. The cathedral church is one of the earliest and most notable examples of Gothic Revival architecture in Korea.



### Gyeongbokgung

Gyeongbokgung, also known as Gyeongbokgung Palace or Gyeongbok Palace, was the main royal palace of the Joseon dynasty. Built in 1395, it is located in northern Seoul, South Korea. The largest of the Five Grand Palaces built by the Joseon dynasty, Gyeongbokgung served as the home of Kings of the Joseon dynasty, the Kings' households, as well as the government of Joseon. Gyeongbokgung continued to serve as the main palace of the Joseon dynasty until the premises were destroyed by fire during the Imjin War and abandoned for two centuries. However, in the 19th century, all of the palace's 7,700 rooms were later restored under the leadership of Prince Regent Heungseon during the reign of King Gojong. Some 500 buildings were restored on a site of over 40 hectares. The architectural principles of ancient Korea were incorporated into the tradition and appearance of the Joseon royal court. In the early 20th century, much of the palace was systematically destroyed by Imperial Japan. Since then, the walled palace complex is gradually being reconstructed to its original form. Today, the palace is arguably regarded as being the most beautiful and grandest of all five palaces. It also houses the National Palace Museum of Korea and the National Folk Museum within the premises of the complex.



### Insa-dong

Insa-dong is a dong, or neighborhood of the Jongno-gu district of the South Korean city of Seoul. The main street is Insa-dong-gil, which is connected to a multitude of alleys that lead deeper into the district, with modern galleries and tea shops. At one time it was the largest market for antiques and artworks in Korea.

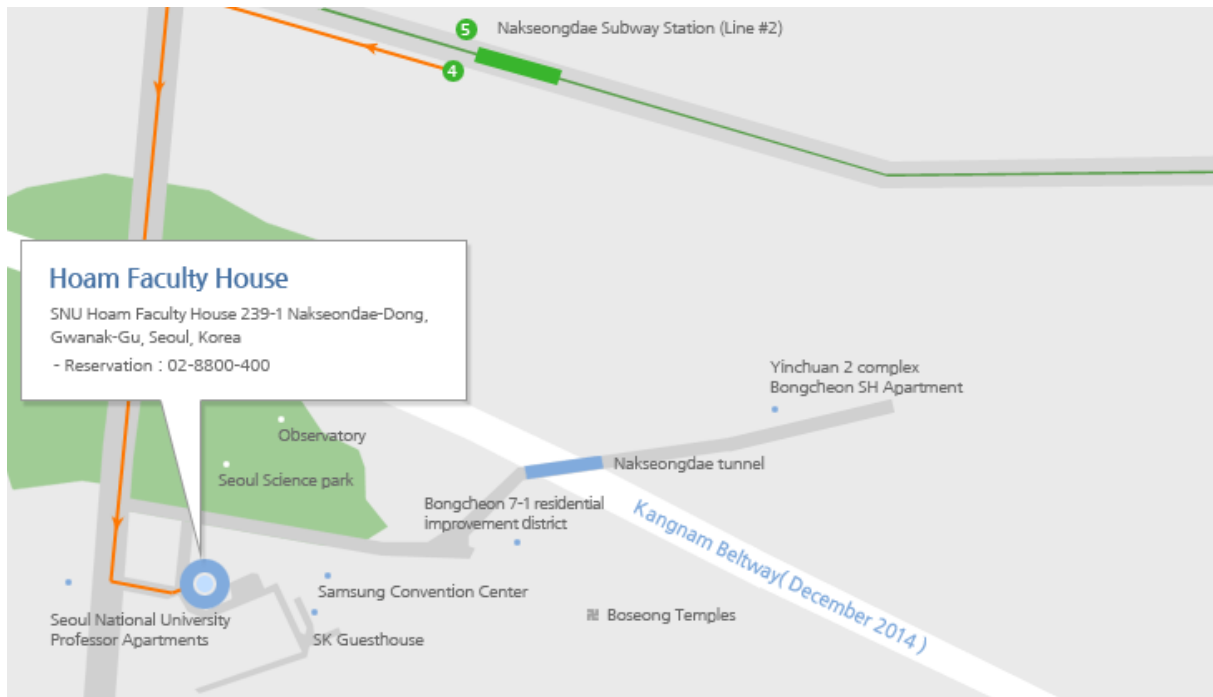
In area, 12.7 hectares (or 31.4 acres), the district is bordered by Gwanhun-dong to the north, Nagwon-dong to the east, and Jongno 2-ga and Jeokseon-dong to the south, and Gongpyeong-dong to the west.

5. (17:30) Back to Seoul National University.

# Conference Venue

## Seoul National University, Hoam Faculty House, Seoul, South Korea

<http://www.hoam.ac.kr/eng/>  
Tel.: 82-2-871-4053 / Fax. 82-2-871-4056  
Email: [front@hoam.ac.kr](mailto:front@hoam.ac.kr)



### How to Get Here?

#### Way #1 From Incheon airport to Hoam



1. Take the "#6017 Airport limousine bus" at the GATE 6B or 13B. (Check the Bus time table)
2. Get off at the last stop "Hoam Faculty House"

The other way can be found from: [http://www.hoam.ac.kr/eng/hoamHotel/contact\\_us.php](http://www.hoam.ac.kr/eng/hoamHotel/contact_us.php)

**Tips:** The registration fee is not included the accommodation. It is suggested that an early reservation be made.

### Note

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### Note

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## Feedback Information

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

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## 2017 CBEES-BBS SEOUL, SOUTH KOREA CONFERENCE

Would you please list the top 3 to 5 universities in your city?	
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Thank you for taking time to participate in this conference evaluation. Your comments will enable us to execute future conferences better and tailor them to your needs!