The 3rd EITA-Bio Conference

(the EITA-Bio 2015) or (the EITA-EITC 2015)

"Recent Advances in Biomedical Research"

Conference Proceedings

Barry Lam Hall, College of EECS
National Taiwan University
Taipei, Republic of China (Taiwan)

Saturday-Sunday, October 24-25, 2015

<Draft: 10/30/15>

Table of Contents

Welcome Message

Conference Themes

"Recent Advances in Biomedical Research"

The EITA-Bio 2015 (or **the EITA-EITC 2015**) conference consists of five parallel workshops:

- **Workshop 1 (W1)**: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics
- **Workshop 2 (W2):** Medicine and Life Sciences, Biological and Biomedical Sciences
- **Workshop 3 (W3):** Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems
- **Workshop 4 (W4):** Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health
- **Workshop 5 (W5):** Student Poster Competition

Planning Committee

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Hsueh-Fen Juan	(阮雪芬)	National Taiwan University

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Project Manager

Hsiang-Ying (Sherry) Lee	(李湘盈)	Massachusetts Institute of Technology

Program Steering Committee

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Program Committee

Workshop Track Co-Chairs

Workshop 1 (W1): Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Aichi Chien	(簡艾琪)	University of California at Los Angeles

Workshop 2 (W2): Medicine and Life Sciences, Biological and Biomedical Sciences

Nei-Li Chan	(詹迺立)	National Taiwan University

Workshop 3 (W3): Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Chihchen Chen	(陳致真)	National Tsing Hua University

Workshop 4 (W4): Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Ai-Chun Pang	(逄愛君)	National Taiwan University

Workshop 5 (W5): Student Poster Competition

Hsueh-Fen Juan	(阮雪芬)	National Taiwan University
Chia-Lang Hsu	(許家郎)	National Taiwan University

Conference Manager

Chia-Lang Hsu	(許家郎)	National Taiwan University

Publication

Conference Programs:

Hsiang-Ying (Sherry) Lee	(李湘盈)	Massachusetts Institute of Technology

Conference Proceedings:

Woei-Jyh (Adam) Lee	(李偉智)	University of Maryland, College Park

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Min-Chun Chen	National Taiwan University
Xiang-Jun Chen	National Taiwan University
Yun-Peng Chen	National Taiwan University
Yun-Ru Chen	National Yang-Ming University
Norton Cheng	National Taiwan University

Hoi Yin Cheung	National Taiwan University
Yun-Hsien Chung	National Taiwan University
Chun-Li Hou	National Taiwan University
Chiao-Hui Hsieh	National Taiwan University
Chen-Tsung Huang	National Taiwan University
Ding-Yu Huang	National Taiwan University
Ruey-Lin Jeremy Jahn	National Taiwan University
Kuei-Yueh Ko	National Taiwan University
Tsai-Yu Lin	National Taiwan University
Pei-Chun Lu	National Yang-Ming University
Divya Sahu	National Yang-Ming University
Ching-Yu Tsai	National Yang-Ming University
Yeuh-Hua Tu	National Yang-Ming University
Wei-Hsuan Wang	National Taiwan University
Chang-Hsun Wu	National Taiwan University
Chih-Hsun Wu	National Yang-Ming University
Tz-Wen Yang	National Taiwan University
Chieh Fan Yin	National Taiwan University

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Organizing Associations

- Emerging Information and Technology Association (新興資訊科技協會)
- College of Electrical Engineering and Computer Science, National Taiwan University (國立臺灣大學電機資訊學院)
- Graduate Institute of Biomedical Electronics and Bioinformatics, National Taiwan University (國立臺灣大學生醫電子與資訊學研究所)
- Department of Life Science, National Taiwan University (國立臺灣大學生命科學系)

Co-Organizing Associations

- Ministry of Science and Technology, R.O.C. (Taiwan) (中華民國科技部)
- Ministry of Economic Affairs, R.O.C. (Taiwan) (中華民國經濟部)
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- National Yang Ming University (國立陽明大學)
- Science and Technology Division, Taipei Economic & Cultural Representative Office in the U.S. (駐美台北經濟文化代表處科技組)

- Investment & Trade Office, Taipei Economic & Cultural Representative Office in the U.S. (駐美投資貿易服務處)

Co-Sponsors

- The Ministry of Science and Technology, R.O.C. (Taiwan) (中華民國科技部)

Conference Program

Day 1 (Saturday, October 24, 2015)

10/24 (Sat) 8:00 am - 4:00 pm: Registration

Room: **Barry Lam Hall: BL-101**

10/24 (Sat) 9:30 am - 10:00 am: Opening Session

Chair: **Dr. Chyung-Ru Wang**, Professor, Department of Microbiology and Immunology, Feinberg School of Medicine, Northwestern University (西北大學醫學院王瓊如教授)

Chair: **Dr. Hsueh-Fen Juan**, Professor, Institute of Biomedical Electronics and Bioinformatics, Institute of Molecular and Cellular Biology, and Department of Life Science, Center for Systems Biology and Bioinformatics National Taiwan University (台灣大學分子細胞生物學研究所阮雪芬教授)

Room: **Barry Lam Hall: BL-101**

Opening Remarks:

Dr. Eric Y. Chuang
Professor, Department of Electrical Engineering, National Taiwan University
Director and Professor, Graduate Institute of Biomedical Electronics and Bioinformatics
Professor, Department of Electrical Engineering & Department of Life Science & Graduate Institute of Epidemiology and Preventive Medicine & Institute of Zoology & Genome and Systems Biology Degree Program, College of Life Science & Graduate Institute of Oncology
Director, Yong Lin Biomedical Engineering Center
Deputy Director, Research and Development Center for Medical Devices
Principal Investigator, Bioinformatics and Biostatistics Core Lab, NTU Center of Genomic Medicine
National Taiwan University
(臺灣大學電機工程學系與生醫電子與資訊學研究所所長莊曜宇教授)

Plenary Sessions:

10/24 (Sat) 10:00 am - 11:00 am: Plenary Session (I):

Chair: **Dr. Hsueh-Fen Juan**, Professor, Institute of Biomedical Electronics and Bioinformatics, Institute of Molecular and Cellular Biology, and Department of Life Science, Center for Systems Biology and Bioinformatics National Taiwan University (台灣大學分子細胞生物學研究所阮雪芬教授)

Room: **Barry Lam Hall: BL-101**

Plenary Speaker:

"Big Challenges of Big Data: What are the Prospects for the Future of Precision Medicine?"
Dr. Yu Shyr
Harold L. Moses Chair in Cancer Research
Director, Vanderbilt Center for Quantitative Sciences
Director, Vanderbilt Technologies for Advanced Genomics Analysis and Research Design
Professor of Biostatistics, Biomedical Informatics, Cancer Biology, and Health Policy
Vanderbilt University School of Medicine
(范德堡大學定量科學中心主任石瑜教授)

10/24 (Sat) 11:00 am - 11:15 am: Coffee Break

10/24 (Sat) 11:15 am – 12:15 pm: Plenary Session (II)

Chair: **Dr. Chyung-Ru Wang**, Professor, Department of Microbiology and Immunology, Feinberg School of Medicine, Northwestern University (西北大學醫學院王瓊如教授)
Room: **Barry Lam Hall: BL-101**

Plenary Speaker:

"Big data in E. coli science"
Dr. Hirotada Mori
Professor, Department of Biological Sciences
Nara Institute of Science and Technology
(奈良先端科學技術大學院大學生物科技學院森浩禎教授)

10/24 (Sat) 11:35 pm – 12:55 pm: Student Poster Competition

Chair: **Dr. Hsueh-Fen Juan**, Professor, Institute of Biomedical Electronics and Bioinformatics, Institute of Molecular and Cellular Biology, and Department of Life Science, Center for Systems Biology and Bioinformatics National Taiwan University (台灣大學分子細胞生物學研究所阮雪芬教授)

Co-Chair: **Dr. Chia-Lang Hsu**, Postdoctoral Fellow, Institute of Molecular and Cellular Biology, and Department of Life Science, National Taiwan University (台灣大學分子細胞生物學研究所許家郎博士)

Room: **Barry Lam Hall: B1 博理藝廊**

10/24 (Sat) 12:55 pm - 2:15 pm: Lunch Break

Parallel Sessions:

10/24 (Sat) 2:15 pm – 3:35 pm: Technical Session D1-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Chair: **Dr. Aichi Chien**, Associate Professor, Division of Interventional Neuroradiology, Department of Radiological Sciences, Biomedical Physics IDP, David Geffen School of Medicine at UCLA, Ronald Reagan UCLA Medical Center (加州大學洛杉磯分校大衛格芬醫學院簡艾琪教授)
Room: **Barry Lam Hall: BL-113**

"A Bioinformatics Approach to the Infection of Hepatitis C Virus Using Human Protein-Protein Interaction Data"
Dr. Ming-Jing Hwang
Research Fellow, Institute of Biomedical Sciences
Academia Sinica
(中央研究院生物醫學科學研究所黃明經博士)

"Genetic Association Studies on Alzheimer's Disease in Taiwan Elderly"

Dr. Karen Yen-Ching Chen
Associate Professor, Institute of Epidemiology and Preventive Medicine, Department of Public Health
Research Center for Gene, Environment and Human Health, College of Public Health
National Taiwan University
(台灣大學流行病學與預防醫學研究所程蘊菁教授)

"Two-Stage Modified Toxicity Probability Interval Design for Low Target Toxicity Rate"
Dr. Sheau-Chiann Chen
Research Fellow, Center for Quantitative Sciences
Vanderbilt University School of Medicine
(范德堡大學定量科學中心陳曉倩博士)

"Translating genomic sequences into neutralization activities and off-target effects of antibodies against influenza toward clinical trial outcomes"
Dr. Hsih-Te Yang
Assistant Professor, Institute of Medical Informatics
Department of Computer Science and Information Engineering
National Cheng Kung University
(成功大學資訊工程學系楊士德教授)

10/24 (Sat) 2:15 pm – 3:35 pm: Technical Session D1-W2-T1: Medicine and Life Sciences, Biological and Biomedical Sciences

Chair: **Dr. Nei-Li Chan,** Professor, Institute of Biochemistry and Molecular Biology, National Taiwan University (台灣大學醫學院生物化學暨分子生物學研究所詹迺立教授)
Room: **Barry Lam Hall: BL-112**

"Role of a tumor-associated NADH oxidase (tNOX) in stress-mediated cell death"
Dr. Pin-Ju Chueh
Professor, Institute of Biomedical Sciences
Director, Division of Academic Exchange, Office of International Affairs
National Chung Hsing University
(中興大學生物醫學研究所闕斌如教授)

"Expression and Homeostasis of Stemness Properties in Cancer Disease"
Dr. Rita Yen-Hua Huang
Professor and Director, Department of Biochemistry and Molecular Cell Biology, College of Medicine
Director, Center for Cell Therapy and Regeneration Medicine
Taipei Medical University
(臺北醫學大學醫學科學研究所生物化學暨細胞分子生物學科主任黃彥華教授)

"Toward complete understanding of metabolic network of E. coli K-12: exploration of missing pathways by the genetic interaction analysis"
Dr. Ai Muto
Assistant Professor, Department of Biological Sciences
Nara Institute of Science and Technology
(奈良先端科學技術大學院大學生物科技學院武藤愛教授)

"Introduction of Micro-Western Array Platform and Biomedical Applications"

Dr. Chih-Pin Chuu
Associate Investigator, Institute of Cellular and System Medicine
National Health Research Institutes
(國家衛生研究院細胞及系統醫學研究所褚志斌博士)

10/24 (Sat) 2:15 pm – 3:35 pm: Technical Session D1-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Chair: **Dr. Chihchen Chen,** Associate Professor, Institute of NanoEngineering and MicroSystems (NEMS), National Tsing Hua University
(清華大學奈米工程與微系統研究所陳致真教授)
Room: **Barry Lam Hall: BL-114**

"Nano/Micro Fluidic Systems for Circulating Tumor Cells (CTCs) Rapid Detection and Diagnosis"
Dr. Fan-Gang Tseng
Distinguished Professor, Department of Engineering and System Science
Deputy Director, Biomedical Technology Research Center
National Tsing-Hua University
(清華大學工程與系統科學系曾繁根教授)

Dr. Chih-Ting Lin
Associate Professor, Department of Electrical Engineering
National Taiwan University
(台灣大學電機工程學系林致廷教授)

"Effects of Cold Plasma on Human Dental Pulp Stem Cells"
Dr. Yun-Chien Cheng
Assistant Professor, Department of Medical Engineering
National Chiao-Tung University
(交通大學機械工程學系鄭雲謙教授)

"A Bead-Based Quantification Technique for Microorganisms using Optical Diffusometry"
Dr. Oswald Han-Sheng Chuang
Associate Professor, Department of Biomedical Engineering
National Cheng Kung University
(成功大學生物醫學工程學系莊漢聲教授)

10/24 (Sat) 2:15 pm – 3:35 pm: Technical Session D1-W4-T1: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Chair: **Dr. Ai-Chun Pang,** Director and Professor, Graduate Institute of Networking and Multimedia and Professor, Department of Computer Science and Information Engineering
National Taiwan University (臺灣大學資訊工程學系兼資訊網路與多媒體研究所所長逄愛君教授)
Room: **Barry Lam Hall: BL-103**

Dr. Feipei Lai
Professor, Graduate Institute of Biomedical Electronics and Bioimformatics

Department of Electrical Engineering
National Taiwan University
(台灣大學電機工程學系生醫電子與資訊學研究所賴飛羆教授)

"Nationwide Integrated Electronic Health Records: Opportunities and Challenges"
Dr. Chien-Tsai Liu
Professor and Chair, Graduate Institute of Biomedical Informatics
Taipei Medical University
(臺北醫學大學醫學資訊研究所所長劉建財教授兼所長)

"Wireless Healthcare and Related Life Style Applications"
Dr. Hsi-Pin Ma
Associate Professor, Institute of Communications Engineering and
Department of Electrical Engineering
National Tsing Hua University
(清華大學電機工程學系馬席彬教授)

"Multiuser MIMO Systems: From Rate Adaptation to User Selection"
Dr. Kate Ching-Ju Lin
Associate Research Fellow, Research Center for Information Technology Innovation
Academia Sinica
(中央研究院資訊科技創新研究中心林靖茹博士)

10/24 (Sat) 3:35 pm – 3:50 pm: Coffee Break

Parallel Sessions:

10/24 (Sat) 3:50 pm – 5:10 pm : Technical Session D1-W1-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Chair: **Dr. Hsuan-Cheng Huang**, Director and Professor, Institute of BioMedical Informatics, National Yang Ming University (陽明大學生物醫學資訊研究所長黃宣誠教授)
Room: **Barry Lam Hall: BL-113**

Dr. Von-Wen Soo
Professor, Department of Computer Science
National Tsing Hua University
(清華大學資訊系統與應用研究所蘇豐文教授)

"Next-generation Sequencing Data Analysis in Biomedical Applications"
Dr. Chien-Yu Chen
Professor, Department of Bio-Industrial Mechatronics Engineering
National Taiwan University
(臺灣大學生物產業機電工程學系陳倩瑜教授)

"A regulatory similarity measure using the location information of transcription factor binding sites in Saccharomyces cerevisiae"
Dr. Darby Tien-Hao Chang
Professor, Department of Electric Engineering

National Cheng Kung University
(成功大學電機工程學系張天豪教授)

"Monotonic Feature Selector (MFSelector)"
Dr. I-Fang Chung
Professor, Institute of BioMedical Informatics
National Yang Ming University
(陽明大學生物醫學資訊研究所鍾翊方教授)

10/24 (Sat) 3:50 pm – 5:10 pm: Technical Session D1-W2-T2: Medicine and Life Sciences, Biological and Biomedical Sciences

Chair: **Dr. Hsueh-Fen Juan**, Professor, Institute of Biomedical Electronics and Bioinformatics, Institute of Molecular and Cellular Biology, and Department of Life Science, Center for Systems Biology and Bioinformatics National Taiwan University (台灣大學分子細胞生物學研究所阮雪芬教授)
Room: **Barry Lam Hall: BL-112**

"The roles of androgens and androgen receptor in stem and progenitor cells for skeletal regeneration"
Dr. Hong-Yo Kang
Professor, Graduate Institute of Clinical Medical Sciences
College of Medicine, Chang Gung University
(長庚大學臨床醫學研究所康宏佑教授)

"Prc contributes to Escherichia coli evasion of classical complement-mediated serum killing"
Dr. Ching-Hao Teng
Associate Professor, Institute of Basic Medical Sciences
National Cheng Kung University Medical College
(成功大學基礎醫學研究所鄧景浩教授)

"Superresolution Mapping Reveals the Molecular Architecture of Primary Cilia"
Dr. Jung-Chi Liao
Associate Research Fellow, Institute of Atomic and Molecular Sciences
Academia Sinica
(中央研究院原子與分子科學研究所廖仲麒博士)

Dr. Chih-Hong Wang
Assistant Professor, Department of Biological Science and Technology
National Chiao Tung University
(交通大學生物科技學系王志宏教授)

10/24 (Sat) 3:50 pm – 5:10 pm : Technical Session D1-W3-T2: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Chair: **Dr. Fan-Gang Tseng,** Distinguished Professor, Department of Engineering and System Science, Deputy Director, Biomedical Technology Research Center, National Tsing-Hua University (清華大學工程與系統科學系曾繁根教授)
Room: **Barry Lam Hall: BL-114**

"Diffuse Optical Tomographic System"
Dr. Min-Chun Pan
Professor, Graduate Institute of Biomedical Engineering
Department of Mechanical Engineering
National Central University
(中央大學生物醫學工程研究所潘敏俊教授)

"A label-free electrochemical impedimetry-based affinity biochip integrated with the AC electrokinetic mixer"
Dr. Ching-Chou Wu
Professor, Department of Bio-industrial Mechatronics Engineering
National Chung Hsing University
(中興大學生物產業機電工程學系吳靖宙教授)

"Bioinspired Conducting Polymers to Selectively Couple PC12 Cells"
Dr. Shyh-Chyang Luo
Assistant Professor, Department of Materials Science and Engineering
National Taiwan University
(臺灣大學材料科學及工程學系羅世強教授)

Dr. Ling Chao
Assistant Professor, Department of Chemical Engineering
National Taiwan University
(臺灣大學化學工程學系趙玲教授)

10/24 (Sat) 3:50 pm – 5:10 pm : Technical Session D1-W4-T2: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Chair: **Dr. Feipei Lai,** Professor, Graduate Institute of Biomedical Electronics and Bioimformatics, Department of Electrical Engineering National Taiwan University
(台灣大學電機工程學系生醫電子與資訊學研究所賴飛羆教授)
Room: **Barry Lam Hall: BL-103**

"Convex Geometric Analysis for Non-negative Blind Source Separation"
Dr. Chong-Yung Chi
Professor, Institute of Communications Engineering and
Department of Electrical Engineering
National Tsing Hua University
(清華大學電機工程學系祁忠勇教授)

"Design and Implementation of Physical Sensing and Fuzzy Control for Dynamic Shuttle Walking Exercise"
Dr. Chih-Yu Wen
Professor, Department of Electrical Engineering
Director, Center for Research and Development of Engineering Technology
National Chung Hsing University
(中興大學電機工程學系溫志煜教授)

"Next Generation Mission-Critical Machine-to-Machine Communications: Opportunities and Challenges"

Dr. Hung-Yu Wei
Professor, Department of Electrical Engineering
National Taiwan University
(台灣大學電機工程學系魏宏宇教授)

"Design and Implementation of a Low-Complexity O-QPSK Transceiver with Spatial Modulation for Wireless Sensor Networks"

Dr. Pei-Yun Tsai
Associate Professor, Department of Electrical Engineering
National Central University
(中央大學電機工程學系蔡佩芸教授)

Day 2 (Sunday, October 25, 2015)

10/25 (Sun) 8:00 am - 4:00 pm: Registration

Room: **Barry Lam Hall: BL-101**

10/25 (Sun) 8:45 am - 10:00 am: Panel Discussions - Big Data Analytics, Data Science and Machine Learning: Challenges and Opportunities

Moderator and Panelist: **Dr. Hsuan-Cheng Huang**, Director and Professor, Institute of BioMedical Informatics, National Yang Ming University (陽明大學生物醫學資訊研究所長黃宣誠教授)
Room: **Barry Lam Hall: BL-113**

Panelists:

Dr. Yu Shyr
Harold L. Moses Chair in Cancer Research
Director, Vanderbilt Center for Quantitative Sciences
Director, Vanderbilt Technologies for Advanced Genomics Analysis and Research Design
Professor of Biostatistics, Biomedical Informatics, Cancer Biology, and Health Policy
Vanderbilt University School of Medicine
(范德堡大學定量科學中心主任石瑜教授)

Dr. Hirotada Mori
Professor, Department of Biological Sciences
Nara Institute of Science and Technology
(奈良先端科學技術大學院大學生物科技學院森浩禎教授)

Dr. Chien-Yu Chen
Professor, Department of Bio-lndustrial Mechatronics Engineering
National Taiwan University
(臺灣大學生物產業機電工程學系陳倩瑜教授)

Dr. Aichi Chien
Associate Professor, Division of Interventional Neuroradiology, Department of Radiological Sciences, Biomedical Physics IDP, David Geffen School of Medicine at UCLA, Ronald Reagan UCLA Medical Center
(加州大學洛杉磯分校大衛格芬醫學院簡艾琪教授)

Parallel Sessions:

10/25 (Sun) 10:00 am – 11:20 am: Technical Session D2-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Chair: **Dr. Aichi Chien**, Associate Professor, Division of Interventional Neuroradiology, Department of Radiological Sciences, Biomedical Physics IDP, David Geffen School of Medicine at UCLA, Ronald Reagan UCLA Medical Center (加州大學洛杉磯分校大衛格芬醫學院簡艾琪教授)
Room: **Barry Lam Hall: BL-113**

"Identifying simple sequence repeats (SSRs) for personal genomes"

Dr. Tun-Wen Pai
Professor, Department of Computer Science and Engineering
National Taiwan Ocean University
(臺灣海洋大學資訊工程學系白敦文教授)

"Contribution of Sequence Motif, Chromatin State and DNA Structure Features to Predictive Models of Transcription Factor Binding in Yeast"
Dr. Huai-Kuang Tsai
Associate Research Fellow, Institute of Information Science
Academia Sinica
(中央研究院資訊科學研究所蔡懷寬博士)

"Combination of Genomic Technologies and Bioinformatics for Exploring New Toxicogenomics Biomarkers"
Dr. Sher Singh
Associate Professor, Department of Life Science
National Taiwan Normal University
(臺灣師範大學生命科學系沈林琥教授)

"Identification of B-cell Epitopes Based on Immunoinformatics Approaches"
Dr. Emily Chia-Yu Su
Assistant Professor, Graduate Institute of Biomedical Informatics
Taipei Medical University
(臺北醫學大學醫學資訊研究所蘇家玉教授)

"Biomarker discovery—Issues in ranking, model selection, and p-value calculation"
Dr. Torbjörn E. M. Nordling
Assistant Professor, Department of Mechanical Engineering
National Cheng Kung University

10/25 (Sun) 10:00 am – 11:20 am: Technical Session D2-W2-T1: Medicine and Life Sciences, Biological and Biomedical Sciences

Chair: **Dr. Nei-Li Chan,** Professor, Institute of Biochemistry and Molecular Biology, National Taiwan University (台灣大學醫學院生物化學暨分子生物學研究所詹迺立教授)
Room: **Barry Lam Hall: BL-112**

"The interaction between metabolism to immunity"
Dr. Chia-Lin Hsu
Assistant Professor, Institute of Microbiology and Immunology
National Yang-Ming University
(陽明大學微生物及免疫學研究所徐嘉琳教授)

Dr. Helene Minyi Liu
Assistant Professor, Department of Clinical Laboratory Sciences and Medical Biotechnology
National Taiwan University
(臺灣大學醫學院醫學檢驗暨生物技術學系劉旻禕教授)

"Application of dendritic cell platform in medical research"
Dr. Ching-Liang Chu
Associate Professor, Graduate Institute of Immunology

College of Medicine, National Taiwan University
(臺灣大學醫學院免疫學研究所朱清良教授)

"Recombinant lipoimmunogen-based therapeutic HPV vaccine"
Dr. Shih-Jen Liu
Associate Investigator
National Institute of Infectious Diseases and Vaccinology
National Health Research Institutes
(國家衛生研究院感染症與疫苗研究所劉士任博士)

10/25 (Sun) 10:00 am – 11:20 am: Technical Session D2-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Chair: **Dr. Chihchen Chen,** Associate Professor, Institute of NanoEngineering and MicroSystems (NEMS), National Tsing Hua University
(清華大學奈米工程與微系統研究所陳致真教授)
Room: **Barry Lam Hall: BL-114**

"Three-dimensional refractive-index microscopy for live-cell imaging"
Dr. Kung-Bin Sung
Associate Professor, Graduate Institute of Biomedical Electronics and Bioimformatics
Department of Electrical Engineering
National Taiwan University
(台灣大學電機工程學系生醫電子與資訊學研究所宋孔彬教授)

"Fiber-needle optical coherence tomography image-guided system to assist epidural anesthesia"
Dr. Wen-Chuan Kuo
Professor, Institute of Biophotonics
National Yang-Ming University
(陽明大學生醫光電研究所郭文娟教授)

Dr. Meng-Tsan Tsai
Associate professor, Graduate Institute of Electro-Optical Engineering
Chang Gung University
(長庚大學光電工程研究所蔡孟燦教授)

"High-Speed Direct Visualization of Dynamics at the Nanoscale in Biological Systems"
Dr. Chia-Lung Hsieh
Assistant Research Fellow, Institute of Atomic and Molecular Science
Academia Sinica
(中央研究院原子與分子科學研究所謝佳龍博士)

"Bilirubin Molecular Imaging for the Diagnosis of Cancers"
Dr. Tzu-Ming Liu
Associate Professor, Institute of Biomedical Engineering
National Taiwan University
(台灣大學醫學工程學研究所劉子銘教授)

10/25 (Sun) 10:00 am – 11:20 am: Technical Session D2-W4-T1: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Chair: **Dr. Ai-Chun Pang,** Director and Professor, Graduate Institute of Networking and Multimedia and Professor, Department of Computer Science and Information Engineering National Taiwan University (臺灣大學資訊工程學系兼資訊網路與多媒體研究所所長逄愛君教授)
Room: **Barry Lam Hall: BL-103**

"Interactive Technologies in Arts"
Dr. Shih-Wei Sun
Assistant Professor, Department of New Media Art
Director, Ultra-Communication Vision Laboratory
Taipei National University of the Arts
(臺北藝術大學新媒體藝術學系孫士韋教授)

"Mental Disorder Detection and Measurement using Latent Dirichlet Allocation and SentiWordNet"
Dr. Hana Chih-Hua Tai
Assistant Professor, Department of Computer Science and Information Engineering
National Taipei University
(台北大學資訊工程學系戴志華教授)

"A state-of-the art overview of computer-aided diagnosis in breast cancer"
Dr. Chung-Ming Lo
Assistant Professor, Graduate Institute of Biomedical Informatics
Taipei Medical University
(臺北醫學大學醫學資訊研究所羅崇銘教授)

10/25 (Sun) 11:20 am – 11:35 am: Coffee Break

Parallel Sessions:

10/25 (Sun) 11:35 am – 12:55 pm: Technical Session D2-W1-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Chair: **Dr. Tun-Wen Pai,** Professor, Department of Computer Science and Engineering National Taiwan Ocean University (臺灣海洋大學資訊工程學系白敦文教授)
Room: **Barry Lam Hall: BL-113**

"Phylostratification of Human Cellular Networks"
Dr. Hsuan-Cheng Huang
Director and Professor, Institute of BioMedical Informatics
National Yang Ming University
(陽明大學生物醫學資訊研究所長黃宣誠教授)

"Extracting Functional Information from Dynamics of Biomolecular Systems in Extremely High Dimension"
Dr. Jung-Hsin Lin
Research Fellow, Research Center for Applied Sciences & Institute of Biomedical Sciences

Academia Sinica
(中央研究院應用科學研究中心及生物醫學科學研究所林榮信博士)

"Development of TOP-PCR (T Oligo-primed Polymerase Chain Reaction) for Efficient Amplification of Trace Amount of DNA in Body Fluids"
Dr. Kuo-Ping Chiu
Associate Research Fellow, Genomics Research Center
Academia Sinica
(中央研究院基因體研究中心邱國平博士)

"Simple and efficient k-ordered FM-index construction for biological sequences"
Dr. Jui-Hung Hung
Assistant Professor, Institute of Bioinformatics and Systems Biology
National Chiao-Tung University
(交通大學生物資訊及系統生物研究所洪瑞鴻教授)

10/25 (Sun) 11:35 am – 12:55 pm: Technical Session D2-W2-T2: Medicine and Life Sciences, Biological and Biomedical Sciences

Chair: **Dr. Shih-Jen Liu,** Associate Investigator, National Institute of Infectious Diseases and Vaccinology, National Health Research Institutes (國家衛生研究院感染症與疫苗研究所劉士任博士)
Room: **Barry Lam Hall: BL-112**

Dr. Che Alex Ma
The Taiwan Bio-Development Foundation (TBF) Chair in Biotechnology
Associate Research Fellow, Genomics Research Center
Academia Sinica
(中央研究院基因體研究中心馬徹博士)

"The effects of microRNAs in MAPK/ERK signaling pathway in Melanoma"
Dr. Nianhan Ma
Associate Professor, Institute of Systems Biology and Bioinformatics
National Central University
(中央大學系統生物與生物資訊研究所馬念涵教授)

"Identifying simple sequence repeats (SSRs) for personal genomes"
Dr. Yi-Chao Hsu
Assistant Professor, Institute of Biomedical Sciences
Mackay Medical College
(馬偕醫學院生物醫學研究所許益超教授)

"Low-dose resveratrol ameliorates lupus nephritis by restoration of FcγRIIB expression on autoreactive B lymphocytes to induce apoptosis"
Dr. Shiang-Jong Tzeng
Assistant Professor, Department of Pharmacology
National Taiwan University
(臺灣大學醫學院藥理學研究所曾賢忠教授)

10/25 (Sun) 11:35 am – 12:55 pm: Technical Session D2-W3-T2: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and

Biomedical Engineering and Systems

Chair: **Dr. Kung-Bin Sung,** Associate Professor, Graduate Institute of Biomedical Electronics and Bioimformatics, Department of Electrical Engineering, National Taiwan University (台灣大學電機工程學系生醫電子與資訊學研究所宋孔彬教授)
Room: **Barry Lam Hall: BL-114**

"Hybrid Nano-constructs for Cancer Therapy"
Dr. Ja-An Annie Ho
Professor, Department of Biochemical Science and Technology
National Taiwan University
(台灣大學生化科技學系何佳安教授)

"Polypeptide Multilayer-Coated Electrodes for Monitoring Differentiation of Human Mesenchymal Stem Cells into Cardiomyocytes"
Dr. Chun-Min Lo
Associate Professor, Department of Biomedical Engineering
National Yang-Ming University
(陽明大學生物醫學工程學系羅俊民教授)

"Microfluidic chip-approach for dissociating neurosphere cell aggregates"
Dr. Chia-Hsien Hsu
Assistant Investigator, Institute of Biomedical Engineering and Nanomedicine
National Health Research Institutes
(國家衛生研究院生醫工程與奈米醫學研究所許佳賢博士)

"Development and Application of Functional Nanogenerators"
Dr. Zong-Hong Lin
Assistant Professor, Institute of Biomedical Engineering
National Tsing Hua University
(清華大學生物醫學工程研究所林宗宏教授)

10/25 (Sun) 11:35 am – 12:55 pm: Technical Session D2-W4-T2: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Chair: **Dr. Hung-Yu Wei,** Professor, Department of Electrical Engineering, National Taiwan University (台灣大學電機工程學系魏宏宇教授)
Room: **Barry Lam Hall: BL-103**

"3D Liver Vessel Reconstruction from CT Images"
Dr. Shang-Hong Lai
Professor and Chairman, Department of Computer Science
National Tsing Hua University
(清華大學資訊工程系系主任賴尚宏教授)

Dr. Chii-Wann Lin
Professor, Institute of Biomedical Engineering, Institute of Bioelectronics and Bioinformatics, and Institute of Applied Mechanics

National Taiwan University
(台灣大學醫學工程學研究所林啟萬教授)

"Neuromarkers for predicting the rehabilitation outcome after stroke"
Dr. Chun-Chuan Chen
Associate Professor, Graduate Institute of Biomedical Engineering
National Central University
(中央大學生物醫學工程研究所陳純娟教授)

Dr. Shih-Ching Yeh
Associate Professor, School of Mobile Information Engineering
Sun Yat-Sen University
(中山大學移動信息工程學院葉士青教授)

10/25 (Sun) 11:35 am – 12:55 pm: Student Poster Competition

Chair: **Dr. Hsueh-Fen Juan**, Professor, Institute of Biomedical Electronics and Bioinformatics, Institute of Molecular and Cellular Biology, and Department of Life Science, Center for Systems Biology and Bioinformatics National Taiwan University (台灣大學分子細胞生物學研究所阮雪芬教授)

Co-Chair: **Dr. Chia-Lang Hsu**, Postdoctoral Fellow, Institute of Molecular and Cellular Biology, and Department of Life Science, National Taiwan University (台灣大學分子細胞生物學研究所許家郎博士)

Room: **Barry Lam Hall: B1 博理藝廊**

10/25 (Sun) 12:55 pm – 2:15 pm: Lunch Break

Parallel Sessions:

10/25 (Sun) 2:15 pm – 3:35 pm: Technical Session D2-W1-T3: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Chair: **Dr. Jung-Hsin Lin,** Research Fellow, Research Center for Applied Sciences & Institute of Biomedical Sciences, Academia Sinica (中央研究院應用科學研究中心及生物醫學科學研究所林榮信博士)
Room: **Barry Lam Hall: BL-113**

Dr. Yen-Wei Chu
Associate Professor, Institute of Genomics and Bioinformatics
National Chung Hsing University
(中興大學基因體暨生物資訊學研究所朱彥煒教授)

"Next-generation sequencing identifies novel, rare variants associated with human genetic diseases"
Dr. Peng-Chieh Jessica Chen
Assistant Professor, Institute of Clinical Medicine, College of Medicine
National Cheng Kung University
(成功大學-臨床醫學研究所陳芃潔教授)

"The relationship between protein function and local structural conservation"
Dr. Chih-Hao Lu
Assistant Professor, Graduate Institute of Basic Medical Sciences
China Medical University
(中國醫藥大學基礎醫學研究所陸志豪教授)

"Ensembl@YM: Tools for automating the build of virtualized genome annotation database, browser, and a light-weighted online editor of gene structures"
Dr. Yen-Hua Huang
Assistant Professor, Institute of Biomedical Informatics
Center for Systems and Synthetic Biology
National Yang-Ming University
(陽明大學生物醫學資訊研究所黃彥華教授)

10/25 (Sun) 2:15 pm – 3:35 pm: Technical Session D2-W2-T3: Medicine and Life Sciences, Biological and Biomedical Sciences

Chair: **Dr. Che Alex Ma,** The Taiwan Bio-Development Foundation (TBF) Chair in Biotechnology, Associate Research Fellow, Genomics Research Center, Academia Sinica (中央研究院基因體研究中心馬徹博士)
Room: **Barry Lam Hall: BL-112**

"EZH2-mediated epigenetic regulation of cancer/stem cells"
Dr. Long-Yuan Li
Associate Professor, Graduate Institute of Cancer Biology
China Medical University
(中國醫藥大學癌症生物學研究所李龍緣教授)

"Immuno-Targeting ENO1 as A Novel Strategy for Cancer Therapy"
Dr. Neng-Yao Shih
Associate Investigator, National Institute of Cancer Research
National Health Research Institutes
(國家衛生研究院癌症研究所施能耀博士)

"Oncogene MCT-1 promotes aneuploidy and tumor metastasis"
Dr. Hsin-Ling Hsu
Associate Investigator, Institute of Molecular and Genomic Medicine
National Health Research Institutes
(國家衛生研究院分子與基因醫學研究所徐欣伶博士)

"Peering into Neural Stem Cells in Live Brain: Multidisciplinary Approaches to Investigating Neural Development and Disorder"
Dr. Jin-Wu Tsai
Assistant Professor, Institute of Brain Science
School of Medicine, National Yang-Ming University
(陽明大學醫學院腦科學研究所蔡金吾教授)

10/25 (Sun) 2:15 pm – 3:35 pm: Technical Session D2-W3-T3: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Chair: **Dr. Ja-An Annie Ho,** Professor, Department of Biochemical Science and Technology National Taiwan University (台灣大學生化科技學系何佳安教授)
Room: **Barry Lam Hall: BL-114**

Dr. Her-Ming Chiueh
Associate Professor, Institute of Biomedical Engineering
National Chiao-Tung University
(交通大學生醫工程研究所闕河鳴教授)

"Novel Biodegradable Emulsions for Vaccine Adjuvant Development"
Dr. Ming-Hsi Huang
Associate Investigator, National Institute of Infectious Diseases and Vaccinology
National Health Research Institutes
(國家衛生研究院感染症與疫苗研究所黃明熙博士)

"An Innovative Bio-Sensing Scheme and Platform Embedded in a Dental Implant Fixture for Painless and Long-Term Bio-Medical Analysis"
Dr. Chih-Cheng Lu
Associate Professor, Institute of Mechatronic Engineering
National Taipei University of Technology
(台北科技大學機電整合研究所呂志誠教授)

"Fabrication and applications of proteome microarrays"
Dr. Chien-Sheng Chen
Associate Professor, Graduate Institute of Systems Biology and Bioinformatics
National Central University
(中央大學系統生物與生物資訊研究所陳健生教授)

10/25 (Sun) 2:15 pm – 3:35 pm: Technical Session D2-W4-T3: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Chair: **Dr. Sao-Jie Chen,** Professor, Graduate Institute of Electronics Engineering and Electrical Engineering Department, National Taiwan University (台灣大學電機工程學系陳少傑教授)
Room: **Barry Lam Hall: BL-103**

"Low Power Wireless ECG Acquisition Circuits and Systems for Body Sensor Networks"
Dr. Shuenn-Yuh Lee
Professor, Department of Electrical Engineering
National Cheng Kung University
(成功大學電機工程學系李順裕教授)

"Microelectronic Contact Lens for Healthcare"
Dr. Yu-Te Liao
Assistant Professor, Department of Electrical and Computer Engineering

National Chiao-Tung University
(交通大學電機工程學系廖育德教授)

"Development of Wireless Sensing Devices for Diagnosis and Rehabilitation Application"
Dr. Chao-Min Wu
Assistant Professor, Department of Electrical Engineering
National Central University
(中央大學電機工程學系吳炤民教授)

"EEG-based Functional Brain Network and its Clinical Applications"
Dr. Yi-Li Tseng
Assistant Professor, Department of Electrical Engineering
Fu Jen Catholic University
(天主教輔仁大學電機工程學系曾乙立教授)

10/25 (Sun) 3:35 pm – 3:50 pm: Coffee Break

Parallel Sessions:

10/25 (Sun) 3:50 pm – 5:10 pm: Technical Session D2-W1-T4: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Chair: **Dr. Peng-Chieh Jessica Chen,** Assistant Professor, Institute of Clinical Medicine, College of Medicine, National Cheng Kung University (成功大學-臨床醫學研究所陳芃潔教授)
Room: **Barry Lam Hall: BL-113**

"A dynamics database housing ~ 11,000 PDB structures whereby mined data reveal dynamics prerequisites for protein functions and interactions"
Dr. Lee-Wei Yang
Associate Professor, Institute of Bioinformatics and Structural Biology
National Tsing-Hua University
(清華大學生物資訊與結構生物研究所楊立威教授)

"Applications of Satellite Remote Sensing Technology for Disease Prediction"
Dr. Ting-Wu Chuang
Assistant Professor, Department of Molecular Parasitology and Tropical Diseases
Taipei Medical University
(臺北醫學大學醫學系分子寄生蟲暨熱帶疾病學科莊定武教授)

"Identification of prognostic and predictive biomarkers for lung adenocarcinoma"
Dr. Tzu-Pin Lu
Assistant Professor, Graduate Institute of Epidemiology and Preventive Medicine
College of Public Health, National Taiwan University
(臺灣大學公共衛生學院流行病學與預防醫學研究所盧子彬教授)

"Stroke Risk Analysis for Early Detection and Aneurysm Assessment"
Dr. Aichi Chien
Associate Professor, Division of Interventional Neuroradiology, Department of Radiological Sciences, Biomedical Physics IDP, David Geffen School of Medicine at UCLA, Ronald Reagan

UCLA Medical Center
(加州大學洛杉磯分校大衛格芬醫學院簡艾琪教授)

10/25 (Sun) 3:50 pm – 5:10 pm: Technical Session D2-W2-T4: Medicine and Life Sciences, Biological and Biomedical Sciences

Chair: **Dr. Hsin-Ling Hsu,** Associate Investigator, Institute of Molecular and Genomic Medicine National Health Research Institutes (國家衛生研究院分子與基因醫學研究所徐欣伶博士)
Room: **Barry Lam Hall: BL-112**

"p53 negative regulators induce hepatic steatosis in zebrafish"
Dr. Guor Mour Her
Professor, Department of Bioscience and Biotechnology
National Taiwan Ocean University
(臺灣海洋大學生命科學暨生物科技學系何國牟教授)

"Translational bioinformatics: from information integration to in silico discovery"
Dr. Ueng-Cheng Yang
Associate Professor, Institute of Biomedical Informatics
National Yang-Ming University
(陽明大學生物醫學資訊研究所楊永正教授)

"Roles of RBFOX3/NeuN in Epilepsy and Cognitive Impairments"
Dr. Hsien-Sung Huang
Assistant Professor, Graduate Institute of Brain and Mind Sciences
National Taiwan University
(台灣大學腦與心智科學研究所黃憲松教授)

"Integrated systems and synthetic biology for cancer research"
Dr. Hsueh-Fen Juan
Professor, Institute of Biomedical Electronics and Bioinformatics, Institute of Molecular and Cellular Biology, and
Department of Life Science, Center for Systems Biology and Bioinformatics
National Taiwan University
(台灣大學分子細胞生物學研究所阮雪芬教授)

10/25 (Sun) 3:50 pm – 5:10 pm: Technical Session D2-W3-T4: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Chair: **Dr. Her-Ming Chiueh,** Associate Professor, Institute of Biomedical Engineering National Chiao-Tung University (交通大學生醫工程研究所闕河鳴教授)
Room: **Barry Lam Hall: BL-114**

Dr. Wen-Yih Chen
Distinguished Professor, Department of Chemical and Materials Engineering
Institute of Systems Biology and Bioinformatics
National Central University
(中央大學化材系及生物與生物資訊研究所陳文逸特聘教授)

Dr. Yen-Wen Lu
Associate Professor, Department of Bio-lndustrial Mechatronics Engineering
National Taiwan University
(臺灣大學生物產業機電工程系盧彥文教授)

"Impedimetric Monitoring of Cellular Activities in Microfluidic Systems"
Dr. Thomas Kin Fong Lei
Associate Professor, Graduate Institute of Medical Mechatronics
Chang Gung University
(長庚大學醫療機電工程研究所李健峰教授)

Dr. Chihchen Chen
Associate Professor, Institute of NanoEngineering and MicroSystems (NEMS)
National Tsing Hua University
(清華大學奈米工程與微系統研究所陳致真教授)

10/25 (Sun) 3:50 pm – 5:10 pm: Technical Session D2-W4-T4: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Chair: **Dr. Shuenn-Yuh Lee,** Professor, Department of Electrical Engineering, National Cheng Kung University (成功大學電機工程學系李順裕教授)
Room: **Barry Lam Hall: BL-103**

"Intelligent Cloud Computing for Biotechnology via Deep Learning using Algorithm/Architecture Co-Design"
Dr. Gwo Giun (Chris) Lee
Professor, Department of Electrical Engineering
National Cheng Kung University
(成功大學電機工程學系李國君教授)

"Facial Status Recognition for Baby Vomit and Drowsy Driver Detections"
Dr. Chih-Peng Fan
Professor, Department of Electrical Engineering
National Chung Hsing University
(中興大學電機工程學系范志鵬教授)

"Opportunities and Challenges for Smartphone-based Audiometric Tests and Hearing Aids"
Dr. Pei-Chun Li
Assistant Professor, Department of Audiology and Speech Language Pathology
Mackay Medical College
(馬偕醫學院聽力暨語言治療學系李沛群教授)

Dr. Sao-Jie Chen
Professor, Graduate Institute of Electronics Engineering and
Electrical Engineering Department
National Taiwan University
(台灣大學電機工程學系陳少傑教授)

Abstracts and Biographies

Day 1 (October 24, 2015)

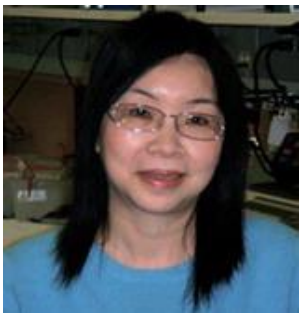
Opening Session

Opening Speech and General Conference Chair

Chyung-Ru Wang

Professor, Department of Microbiology and Immunology
Feinberg School of Medicine, Northwestern University
(西北大學醫學院王瓊如教授)

BIOGRAPHY



Opening Session

Opening Speech and General Conference Chair

Hsueh-Fen Juan

Professor, Institute of Biomedical Electronics and Bioinformatics, Institute of Molecular and Cellular Biology, Department of Life Science, Center for Systems Biology and Bioinformatics, National Taiwan University, Taipei, Taiwan
No. 1, Sec. 4, Roosevelt Road, Taipei, 10617 Taiwan
Tel: +886-2-33664536, Fax: +886-2-23673374
Email: yukijuan@ntu.edu.tw
(台灣大學分子細胞生物學研究所阮雪芬教授)

BIOGRAPHY

Hsueh-Fen Juan was born in 1969, Miao-Li, Taiwan. She received her BS and MS degree in Botany and PhD in Biochemical Sciences from National Taiwan University (NTU) in 1999. She worked as a research scientist in the Japan International Research Center for Agricultural Sciences (Tsukuba, Japan) during 2000-2001 and a postdoctoral research fellow in the Institute of Biological Chemistry, Academia Sinica (Taipei, Taiwan) during 2001-2002.

She started her academic career in the Department of Chemical Engineering, National Taipei University of Technology as an assistant professor and in the Department of Computer Science and Information Engineering at NTU as an adjunct assistant professor in 2002. She moved to NTU in 2004 as an assistant professor in the Department of Life Science and the Institute of Molecular and Cellular Biology. She was promoted to be an associate professor in 2006 and full professor in 2009. Dr. Juan is currently working on cancer systems biology, integrating transcriptomics, proteomics and bioinformatics for biomarker and drug discovery.

Prof. Juan has developed a number of novel methods to advance systems-biology research and applied such approach for drug discovery and elucidating molecular mechanism of drug responses in cancer cells. She has published more than 85 journal papers including prestigious journals such as Briefings in Bioinformatics, Proc. Natl. Acad. Sci. USA, Cancer Research, Nucleic Acids Research, Oncogene, Bioinformatics. She is now the editor of Scientific Reports (Nature Publishing Group), Computational and Mathematical Methods in Medicine (Hindawi Publishing Corporation), PeerJ, PeerJ Computer Science and Stem Cell Treatments (Publisher Frontiers, joining Nature Publishing Group). She also serves as a reviewer of various journals like Molecular and Cellular Proteomics (ASBMB), Proteomics (Wiley-VCH), BMC Bioinformatics, and has organized several international systems biology and bioinformatics symposiums. She is one of the founders of Center for Systems Biology (NTU), and currently the Board Member in The Taiwan Society for Biochemistry and Molecular Biology, Taiwan Proteomics Society, and Taiwan Bioinformatics and System Biology Society. Since Dr. Juan made significant contributions through systems biology approach to development of methodology and cancer therapy; she received the awards “Taiwan's Ten Outstanding Young Persons” (2008), FY2011 JSPS Invitation Fellowship Program for Research in Japan (2011), K. T. Li Breakthrough Award by Institute of Information and Computing Machinery (2012), and National Science Council (NSC) Award for Special Talents of the Colleges (2010-2015).

Opening Session

Welcome Remarks

Eric Y. Chuang

Professor, Department of Electrical Engineering, National Taiwan University
Director and Professor, Graduate Institute of Biomedical Electronics and Bioinformatics
Professor, Department of Electrical Engineering
Professor, Department of Life Science
Professor, Graduate Institute of Epidemiology and Preventive Medicine
Professor, Institute of Zoology
Professor, Genome and Systems Biology Degree Program, College of Life Science
Professor, Graduate Institute of Oncology
Director, Yong Lin Biomedical Engineering Center
Deputy Director, Research and Development Center for Medical Devices
Principal Investigator, Bioinformatics and Biostatistics Core Lab, NTU Center of Genomic Medicine
National Taiwan University
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BIOGRAPHY

Plenary Session (I)

Session Chair

Hsueh-Fen Juan

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BIOGRAPHY

Hsueh-Fen Juan was born in 1969, Miao-Li, Taiwan. She received her BS and MS degree in Botany and PhD in Biochemical Sciences from National Taiwan University (NTU) in 1999. She worked as a research scientist in the Japan International Research Center for Agricultural Sciences (Tsukuba, Japan) during 2000-2001 and a postdoctoral research fellow in the Institute of Biological Chemistry, Academia Sinica (Taipei, Taiwan) during 2001-2002.

She started her academic career in the Department of Chemical Engineering, National Taipei University of Technology as an assistant professor and in the Department of Computer Science and Information Engineering at NTU as an adjunct assistant professor in 2002. She moved to NTU in 2004 as an assistant professor in the Department of Life Science and the Institute of Molecular and Cellular Biology. She was promoted to be an associate professor in 2006 and full professor in 2009. Dr. Juan is currently working on cancer systems biology, integrating transcriptomics, proteomics and bioinformatics for biomarker and drug discovery.

Prof. Juan has developed a number of novel methods to advance systems-biology research and applied such approach for drug discovery and elucidating molecular mechanism of drug responses in cancer cells. She has published more than 85 journal papers including prestigious journals such as Briefings in Bioinformatics, Proc. Natl. Acad. Sci. USA, Cancer Research, Nucleic Acids Research, Oncogene, Bioinformatics. She is now the editor of Scientific Reports (Nature Publishing Group), Computational and Mathematical Methods in Medicine (Hindawi Publishing Corporation), PeerJ, PeerJ Computer Science and Stem Cell Treatments (Publisher Frontiers, joining Nature Publishing Group). She also serves as a reviewer of various journals like Molecular and Cellular Proteomics (ASBMB), Proteomics (Wiley-VCH), BMC Bioinformatics, and has organized several international systems biology and bioinformatics symposiums. She is one of the founders of Center for Systems Biology (NTU), and currently the Board Member in The Taiwan Society for Biochemistry and Molecular Biology, Taiwan Proteomics Society, and Taiwan Bioinformatics and System Biology Society. Since Dr. Juan made significant contributions through systems biology approach to development of methodology and cancer therapy; she received the awards “Taiwan's Ten Outstanding Young Persons” (2008), FY2011 JSPS Invitation Fellowship Program for Research in Japan (2011), K. T. Li Breakthrough Award by Institute of Information and Computing Machinery (2012), and National Science Council (NSC) Award for Special Talents of the Colleges (2010-2015).

Plenary Session (I)

Big Challenges of Big Data: What are the Prospects for the Future of Precision Medicine?

Plenary Speaker

Yu Shyr

Harold L. Moses Chair in Cancer Research
Director, Vanderbilt Center for Quantitative Sciences
Director, Vanderbilt Technologies for Advanced Genomics Analysis and Research Design
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ABSTRACT

The key concepts of precision medicine are prevention and treatment strategies that take individual molecular profiles and clinical information into account. Next-generation sequencing technologies (NGS) and other types of high-throughput assays have recently exploded in popularity thanks to their ability to quickly produce an enormous volume of data at a relatively low cost. The emergence of these big data has advanced the goal of precision medicine, but in consideration of the entire scope of capture and utilization, from the electronic health records (HER) and big data analysis on high-throughput biomarkers to the ultimate goal of clinical usage based on a patient's genome, many challenges still persist. In this talk, I will introduce several initiatives on precision medicine in the United States, including Vanderbilt University's BioVU initiative and the U.S.'s new initiative on precision medicine. Finally, I will discuss some potential pathways of seamlessly integrating molecular, cellular and genomic data with clinical, physiological, behavioral, and environmental parameters.

BIOGRAPHY

Yu Shyr received his bachelor's degree in statistics from Tamkang University in Taiwan in 1985 and received his master's degree in statistics from Michigan State University, East Lansing, Michigan, USA, in 1989. He then received his Ph.D. in biostatistics from the University of Michigan, Ann Arbor, Michigan, USA, in 1994. He subsequently joined the faculty at Vanderbilt University School of Medicine in Nashville, Tennessee, USA.

At Vanderbilt, he has collaborated on numerous research projects; assisted investigators in developing clinical research protocols; collaborated on multiple grants funded through external peer-reviewed mechanisms; and developed biostatistical and bioinformatic methodologies for clinical trial design, high-dimensional data preprocessing, estimating relative potency in a parallel line bioassay, and other statistical and bioinformatic approaches, published in journals such as Nature, NEJM, JAMA, Cell, Lancet, Nature Medicine, Nature Protocol, Statistics in Medicine, Bioinformatics, Clinical Trials, Computational Statistics and Data Analysis, and BMC

Bioinformatics. He is currently the Harold L. Moses Chair in Cancer Research, Director of the Vanderbilt Center for Quantitative Sciences (CQS), and the Director of the Vanderbilt Technologies for Advanced Genomics Analysis and Research Design (VANGARD). He serves as a professor of biostatistics, biomedical informatics, cancer biology, and health policy. His current research interests focus on developing statistical bioinformatics methods for analyzing next-generation sequencing data, including a series of papers on estimating the sample size requirements for studies conducting RNA sequencing analysis.

Dr. Shyr is a Fellow of the American Statistical Association and the US Food and Drug Administration advisory committee voting member. He has served as a member of the US National Cancer Institute (NCI) Developmental Therapeutics Study Section and the Population and Patient-oriented Training subcommittee; he also has served on numerous NIH/NCI SPORE, P01, and CCSG review panels/committees, as well as the epidemiology section of the U.S. Army Medical Research and Materiel Command Breast Cancer Research Program (BCRP). Dr. Shyr has presented as an invited faculty member in the ASCO Educational Section on Advanced Concepts in Clinical Trial Design and Methodology and he is the co-course director for the AACR/ASCO Methods in Clinical Cancer Research Vail Workshop. In addition to this, he has prepared statistical workshops worldwide and presented them in countries, such as, Belgium, The Netherlands, Germany, Austria, Taiwan, Japan, China, Saudi Arabia and Malaysia. He currently serves on 13 external advisory boards for university and medical center institutions and is a member of the editorial board for the Journal of Clinical Oncology, Clinical Cancer Research, Cancer and Cancer Prevention Research Journal, the ASCO's Cancer Research Committee, and he is the associate editor for JAMA Oncology. He directs the biostatistics and bioinformatics cores for the NCI-funded Vanderbilt University Breast Cancer SPORE, GI Cancer SPORE, and other program projects, and he is the principle investigator of the NCI U01 grant of Barrett's esophagus translational research network coordinating center (BETRNetCC). To date, he has delivered more than 200 abstracts at professional meetings and has published more than 375 peer-reviewed papers in a variety of high-impact journals.

Plenary Session (II)

Session Chair

Chyung-Ru Wang

Professor, Department of Microbiology and Immunology
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BIOGRAPHY

Plenary Session (II)

Plenary Speaker

Big data in E. coli science

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ABSTRACT

I was one of the members of launching the E. coli genome project in Japan in 1989. Since then, I started to prepare the database for accelerating the sequencing project, named GenoBase (http://ecoli.naist.jp). In total seven years had been required to complete the E. coli W3110 genome, but finally in the beginning of 1997 the project itself had was finished and moved on the post-genomic functional project. To perform this, we started to construct the comprehensive E. coli experimental resources, such as ORF clones(1), deletions strains libraries(2). Once these resources were established, we had moved in the fields of so-called OMICs by constructing E. coli full-length microarray PCR amplified ORF fragments using plasmid clone library(3). During these period, our research interests were shifted to physiological interactions in the network of genes, proteins, metabolites, etc. Then we had analyzed comprehensive protein-protein interactions(4), perturbation analysis in the metabolic network(5), etc. And now we are focussing on the genetic interaction in a cell by double gene knockout method.

E. coli has about 4000 protein coding genes and we developed the method to construct double gene deletion strains combining two single deletion strains by conjugation(6, 7). We also developed the efficient and accurate quantitative measurement system using commercially available scanners(8). Currently we are accumulating the genetic interaction data in LB and M9 minimal medium with four different carbon sources.

And finally to make integrative analysis of those comprehensively generated data, we decided to start text mining from the literature as one of the big data issues. Currently roughly 300,000 papers related the term of “Escherichia coli” have been registered in PubMed. From these literature data, the text mining by natural language processing and machine learning method will be performed as a collaborative work with Prof. Matsumoto, NAIST, to mine biological information by combination our comprehensive biological data.

I would introduce our current situation and discuss about the perspectives Escherichia coli sciences in the systems and synthetic biology fields.

1. M. Kitagawa et al., DNA Res 12, 291-299 (2005).
2. T. Baba et al., Mol Syst Biol 2, 2006 0008 (2006).
3. T. Oshima et al., Mol Microbiol 45, 673-695 (2002).
4. M. Arifuzzaman et al., Genome Res 16, 686-691 (2006).

5. N. Ishii et al., Science 316, 593-597 (2007).
6. A. Typas et al., Nat Methods 5, 781-787 (2008).
7. G. Butland et al., Nat Methods 5, 789-795 (2008).
8. R. Takeuchi et al., BMC microbiology 14, 171-181 (2014)

BIOGRAPHY

Name: Hirotada Mori
Birth: Kyoto, Japan 1956. Feb. 5

Education and degrees:

Dept. Agriculture, Kyoto Univ. Kyoto, Japan	BS	1980	ecology
Dept. Science, Kyoto Univ. Kyoto, Japan	MS	1985	biophysics
Dept. Science, Kyoto Univ. Kyoto, Japan	PhD	1989	biophysics

Job Career:
1. Assistant Researcher, 1985/4-1985/10, Shiga Medical University
2. Assistant Researcher, 1985/11-1989/9, Medical Department, Kumamoto University
3. Assistant Researcher, 1989/10 – 1993/4, Research Center for Virus, Kyoto University
4. Associate Professor, 1993/5 – 1996/3, Bioinformatics, Research and Education Center for Genetic Information, Nara Institute of Science and Technology
5. Professor, 1996/4- present, Systems Microbiology, Graduate School of Biological Sciences, Nara Institute of Science and Technology
6. Professor, 2001/4- 2011/3, Institute for Advanced Biosciences, Keio University

Research interest:

My major research interest is to elucidation of relationships between genes so-called "network biology" in the field of systems biology. Research direction is focusing more fundamental biology using *Escherichia coli K-12*. My research career in this field started in 1989, when the Japanese E. coli genome project launched, and since then I have always been focusing on the biology on global aspect. After completion of genome sequencing, we started to construct comprehensive experimental resources, such as ORF plasmid clone library and single gene deletion library for making systematic and comprehensive analyses possible for this well studied bacterium. Using such comprehensive resources, our first target was the construction of DNA microarray and transcriptome analysis using those. Our research activities were expanding variety of omics approaches, such as proteomics for comprehensive protein-protein interaction, metabolomics to measure and analyze central metabolic pathway quantitatively and currently focusing on genetic interaction by synthetic lethal/sickness analysis using double knockout strains.

Honors:
1. 2009 Jan. Fellow, American Academy for Microbiology, USA
2. 2010 Mar. Fellow, The Royal Society of Chemistry, UK

Memberships in professional societies:
1. The Molecular Biology Society of Japan
2. The Biophysical Society of Japan
3. Society of Genome Microbiology, Japan
4. American Society for Microbiology
5. Editor for BMC Microbiology

Publication (Major 10 papers):
1. Otsuka, Y., Muto, A., Takeuchi, R., Okada, C., Ishikawa, M., Nakamura, K., Yamamoto, N., Dose, H., Nakahigashi, K., Tanishima, S., Suharnan, S., Nomura, W., Nakayashiki, T., Aref,

W.G., Bochner, B.R., Conway, T., Gribskov, M., Kihara, D., Rudd, K.E., Tohsato, Y., Wanner, B.L. & Mori, H. GenoBase: comprehensive resource database of Escherichia coli K-12. Nucleic Acids Res 43, D606-17 (2015).

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7. Baba, T., Ara, T., Hasegawa, M., Takai, Y., Okumura, Y., Baba, M., Datsenko, K.A., Tomita, M., Wanner, B.L. & Mori, H. Construction of Escherichia coli K-12 in-frame, single-gene knockout mutants: the Keio collection. Mol Syst Biol 2, 2006 0008 (2006).
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Student Poster Competition

Session Chair

Hsueh-Fen Juan

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BIOGRAPHY

Hsueh-Fen Juan was born in 1969, Miao-Li, Taiwan. She received her BS and MS degree in Botany and PhD in Biochemical Sciences from National Taiwan University (NTU) in 1999. She worked as a research scientist in the Japan International Research Center for Agricultural Sciences (Tsukuba, Japan) during 2000-2001 and a postdoctoral research fellow in the Institute of Biological Chemistry, Academia Sinica (Taipei, Taiwan) during 2001-2002.

She started her academic career in the Department of Chemical Engineering, National Taipei University of Technology as an assistant professor and in the Department of Computer Science and Information Engineering at NTU as an adjunct assistant professor in 2002. She moved to NTU in 2004 as an assistant professor in the Department of Life Science and the Institute of Molecular and Cellular Biology. She was promoted to be an associate professor in 2006 and full professor in 2009. Dr. Juan is currently working on cancer systems biology, integrating transcriptomics, proteomics and bioinformatics for biomarker and drug discovery.

Prof. Juan has developed a number of novel methods to advance systems-biology research and applied such approach for drug discovery and elucidating molecular mechanism of drug responses in cancer cells. She has published more than 85 journal papers including prestigious journals such as Briefings in Bioinformatics, Proc. Natl. Acad. Sci. USA, Cancer Research, Nucleic Acids Research, Oncogene, Bioinformatics. She is now the editor of Scientific Reports (Nature Publishing Group), Computational and Mathematical Methods in Medicine (Hindawi Publishing Corporation), PeerJ, PeerJ Computer Science and Stem Cell Treatments (Publisher Frontiers, joining Nature Publishing Group). She also serves as a reviewer of various journals like Molecular and Cellular Proteomics (ASBMB), Proteomics (Wiley-VCH), BMC Bioinformatics, and has organized several international systems biology and bioinformatics symposiums. She is one of the founders of Center for Systems Biology (NTU), and currently the Board Member in The Taiwan Society for Biochemistry and Molecular Biology, Taiwan Proteomics Society, and Taiwan Bioinformatics and System Biology Society. Since Dr. Juan made significant contributions through systems biology approach to development of methodology and cancer therapy; she received the awards “Taiwan's Ten Outstanding Young Persons” (2008), FY2011 JSPS Invitation Fellowship Program for Research in Japan (2011), K. T. Li Breakthrough Award by Institute of Information and Computing Machinery (2012), and National Science Council (NSC) Award for Special Talents of the Colleges (2010-2015).

Student Poster Competition

Session Co-Chair

Chia-Lang Hsu

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National Taiwan University
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BIOGRAPHY

Technical Session D1-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Session Chair

Aichi Chien

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BIOGRAPHY

Aichi Chien, Ph.D. is an Associate Professor in the Department of Radiological Sciences and the Biomedical Physics IDP Graduate Program in the UCLA Medical School since 2009; a faculty member of Medical School Short Term Training Program (SSTP) and Cross-disciplinary Scholars in Science and Technology (CSST) program since 2010, and faculty in the UCLA Center for Domain Specific Computing (CDSC) since 2011.

Dr. Chien received her Bachelor's Degree from National Taiwan University, Dept. of Agricultural Machinery Engineering in 1999, Taipei, Taiwan. She then completed her Master's Degree on the subject of Micro/Nano Resonators in the Dept. of Mechanical and Aerospace Engineering, Cornell University, Ithaca, NY; and her PhD Degree in Biomedical Engineering at the University of California, Los Angeles, CA on the topic of MEMS/NEMS implantable devices for cardiovascular disease. She went on to complete Postdoctoral Fellowship training in endovascular treatment in the Division of Interventional Neuroradiology in the UCLA David Geffen School of Medicine.

Dr. Chien's research interests include cerebral vascular disease and treatment effectiveness analysis, and encompass the integration of science and engineering for clinical decision-making and individualized medicine. Her research broadly impacts the medical community and medical device industry. Her research has been featured in various news, including Fierce Medical Devices, Interventional News, Endovascular Today, and Neuro News. She has published more than 70 peer-reviewed publications of original research in high impact factor medical journals such as Stroke, Journal of Vascular and Interventional Radiology, Neurosurgery, Journal of Neurosurgery, and American Journal of Neuroradiology, including 22 papers as first author. She has received many awards, including the Brain Aneurysm Foundation Research Grant Award, the SIR Ring Career Development Award, the Cerebrovascular Research Award from The Aneurysm and AVM Foundation, the Bee Foundation Medical Research Award, the American Heart Association Outreach Award, Heart Failure Society of America Award, and Young Investigator Award from the Cardiovascular System Dynamics Society. She is also the lead inventor on more than five US Patents and International Patents; Principle Investigator in a Philips Healthcare research grant and Radiology Exploratory grants. She is currently a Co-Investigator on two NIH R01 projects and one NSF (CCF) multi-disciplinary program. She regularly gives lectures in universities and medical centers in the US and internationally.

Technical Session D1-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

A Bioinformatics Approach to the Infection of Hepatitis C Virus Using Human Protein-Protein Interaction Data

Ming-Jing Hwang

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ABSTRACT

Hepatitis C virus infection is a serious public health concern as it could lead to severe liver diseases including hepatocellular carcinoma. Although much has been known about the life cycle of HCV, much remains to be elucidated especially pertaining to the precise mechanism of its entry. We have carried out a comprehensive Bioinformatics investigation aiming to identify the host factors that facilitate HCV's entry. The premise of our bioinformatics sleuthing is that these entry factors interact with the envelope surface proteins of the virus. Analysis of protein-protein interaction, protein complex and signal transduction pathway data revealed two distinct network modules comprising, respectively, proteins that appear to involve directly in viral entry and proteins that are associated with inflammation responses. Our bioinformatics strategies and results will be presented and discussed in the meeting.

BIOGRAPHY

Ming-Jing Hwang was born in 1957 in a small southern town of Taiwan. He grew up there until he went to Taipei to study at National Taiwan University in 1976. After receiving a BS degree in chemical engineering from NTU in 1980 and completing a two-year military service in the army, he went to the United States of America for graduate studies in 1982. He received his Master degree from West Virginia University (Morgantown, WV) in 1984 and Ph.D. degree from University of Pittsburgh (Pittsburgh, PA) in 1989, both in chemical engineering.

Upon graduation, he went to work for Biosym Technologies Inc. (San Diego, CA) as a Research Scientist. At Biosym, he helped lead a team funded by a consortium of pharmaceutical and chemical companies to develop a suite of new-generation molecular energy functions for the simulation and modeling of biological and chemical molecules. In 1994, He returned to Taiwan after 5 years of employment at Biosym. He was recruited by the Institute of Biomedical Sciences at Academia Sinica, located in the Nankang district of Taipei, to be the Principal Investigator for the Laboratory for Bioinformatics and Biomolecule Modeling. He became a tenured Research Fellow of the institute in 2005, which remains his position title to date. The main focus of his research has been to develop fast computational algorithms for analysis, especially on large-scales, of biological sequences, structures, and other biological data. His recent research topics include network-based approaches for protein docking and binding site

prediction, and for studying patterns of the expression of human genes. He is also interested in understanding the design principles of biological circuits, and has developed a computational pipeline to mathematically model and simulate them.

Dr. Hwang received the Distinguished Alumni Award from Kang-Ming High School, Tainan County, in 2003. He was a recipient of the 2004 Academia Sinica Research Award for Junior Research Investigators. He has published over 70 research articles in international journals in the field of computational chemistry, bioinformatics, and computational biology.

Technical Session D1-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Genetic Association Studies on Alzheimer's Disease in Taiwan Elderly

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ABSTRACT

Taiwan's aging rate ranks the 2nd in the world, and thus dementia becomes an important health issue in the old age. A national survey (2011–2012) in Taiwan showed that 4.97% of the elderly had dementia. Alzheimer's disease (AD) is the most common type of dementia and is characterized by accumulation of extracellular senile plaques intracellular, neurofibrillary tangles, and degenerating neurons. In US elderlies, AD was the sixth leading cause of death in 2013. However, AD is not one of the top 10 leading cause of death probably due to under-diagnosis and under-reported.

Previous genetic association studies, including genome-wide association studies (GWASs), focused on White populations. However, genetic profiles tend to vary across races. In Taiwan, AD genetic research have been restricted to candidate genes and GWAS data are limited. Therefore, my lab put effort on AD genetic association studies in Taiwanese. In this talk, studies of candidate genes and GWAS on AD in Taiwanese elders will be present to compare with studies on other races.

BIOGRAPHY

Yen-Ching Chen received her Sc.D. (2001) from Harvard School of Public Health. After graduation, she became a postdoctoral fellow of Channing Laboratory, Brigham and Women's Hospital, Harvard Medical School. Her training was mainly at genetic epidemiology, environmental epidemiology and analytical chemistry, and prostate cancer research.

Currently, she is an Associate Professor of Institute of Epidemiology and Preventive Medicine, and Associate Director of Program of Master of Public Health, College of Public Health, National Taiwan University (NTU), Taipei, Taiwan. She is also the Joint Appointment Associate Professor of Master Program in Statistics, Research Fellow of Genetic Epidemiology Core Laboratory, and faculty of Research Center for Genes, Environment and Human Health, NTU. Dr. Chen research interest includes geriatric epidemiology (dementia, cognition), human genome epidemiology (dementia and prostate cancer), and environmental epidemiology with extensive collaboration with clinicians and scientists from multidiscipline. She has published over fifty peer-reviewed book chapters and journals on related topics.

Prof. Chen has served as academic committee of various workshops and conferences and

editorial board member of Scientific Reports (Nature Publishing Group). She is the member of the Alzheimer's Association International Society to Advance Research and Treatment (ISTAART) and European Society for Translational Medicine (EUSTM) Expert Panel Member. She also won the Academic Achievement Award of NTU since 2009. She is the now Principal Investigator (PI) and Co-PI of two 3-year projects on cognitive function funded by the Ministry of Science and Technology, Taiwan.

Technical Session D1-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Two-Stage Modified Toxicity Probability Interval Design for Low Target Toxicity Rate

Sheau-Chiann Chen

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ABSTRACT

In recent phase I oncology trials, the modified toxicity probability interval (mTPI) design for a binary response has been increasingly used to find the maximum tolerated dose (MTD). The dose-finding decision table of the mTPI design includes escalation, staying, de-escalation and unacceptable toxicity actions. But, when the target toxicity rate is 0.1 or less, there is no staying action for a small cohort size at each dose. This problem may reduce the accuracy of the identified MTD.

Our aim is to improve the operating characteristics of the mTPI design by incorporating lower grade toxicity information into dose finding designs. A Dirichlet/multinomial model is used to develop a two-stage mTPI design for a polytomous response (no toxicity, mild/moderate toxicity and severe toxicity). For the first stage, the dose-finding action is based on the marginal beta distribution of the mild/moderate probability. After half of the patients are treated, the dose-finding action for the second stage is based on the marginal beta distribution of the severe probability.

The simulation results show that the two-stage mTPI design performs better than, or non-inferior to, the mTPI design. Our proposed design performs well when all doses are too toxic. The outcome of mild/moderate toxicity provides useful information for finding MTD. Thus, the two-stage mTPI design is recommended for use with a target toxicity rate of 0.1 or less. This study is a joint-collaboration with Dr. Yu Shyr.

BIOGRAPHY

Sheau-Chiann Chen received her bachelor's degree (2001) and master's degree (2003) in statistics from Tamkang University, Taipei, Taiwan. She received her Ph.D. degree (2010) in statistics from the National Cheng Kung University, Tainan, Taiwan. She was a Research Fellow at National Cheng Kung University between October 2010 and January 2011. She was an Assistant Professor at National Chiayi University between February 2011 and July 2013. Currently she is a Research Fellow in the Center for Quantitative Sciences at Vanderbilt University School of Medicine, USA. Her research interests include industrial statistics, quality control, pattern detection and clinical trials. Dr. Chen has authored fourteen peer-reviewed journals on these topics.

Technical Session D1-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Translating genomic sequences into neutralization activities and off-target effects of antibodies against influenza toward clinical trial outcomes

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ABSTRACT

The antibodies, known as immunoglobulins and elicited from influenza infections or vaccines, demonstrate an explicit mode of defensive action by blocking the attachment of antigenic strains of influenza viruses to sialic acid receptor of epithelium cells. Beside vaccination to the public, antibodies are regarded as a newly emerging therapeutics to provide passive border protections against influenza. Although the applications of genomic and high-through technologies to clinics have been overwhelming, the number of therapeutics to untreated diseases is still unmet, and the cost for a new drug to be approved is unceasingly increasing yearly. To effectively translate genomic information into regulatory approval therapeutics, we initially established a computational pipeline to reconstruct 3D structures of Hemagglutinin (HA) and antibody (Ab) based on protein sequences, and subsequently modeled Ab - HA (antigen) interactions. This platform is capable of testing bioinformatics against experimental data sets, indicating a clear correlation (R2 = 0.60 – 0.86) between the docking scores and the neutralization titers of 4 experimental antibodies (CH65, CR8020, C05, and 5J8). Beyond predicting these Abs' efficacy, their off-target effects were considered as well to prospectively identify CR8020, which was only the potentially successful candidate in the process of human clinical trial. Our computational approach may be applied to increase productivity as well as reduce attrition rate for biologics discovery and development against infectious diseases.

BIOGRAPHY

Hsih-Te Yang, Ph.D., graduated from National Yang-Ming University with a bachelor's degree in Medical Technology and thereafter with a doctoral degree in Biochemistry and molecular biology. Now, he is currently an assistant professor at Institute of Medical Informatics, Department of Computer Science and information engineering, National Cheng Kung University (NCKU), and a visiting assistant professor at School of Medicine, Keio University, Japan. Prof. Yang has been leading an innovative lab and team by conducting the research of system medicine. Our goal is to computationally discover and develop novel therapeutics toward improving human health using modern state-of-the-art technologies as well as Biomedical "Big" data.

From 2005 to 2011, his research interests involve the construction of mathematical models, and their application to biological data. He had been extensively trained in the techniques

relevant to systems and theoretical biology, such as gene network inference from microarray data, and the construction of kinetics models for biological pathways (The Journal of Biochemistry, 2007; BMC Bioinformatics, 2007; BBRC, 2007). In 2008 he earned NIH fellowship scholar to work with Minoru. Ko., MD, Ph.D. who has been one of the top investigators in the field of stem cell biology using high-throughput genomics. His role in Dr. Ko's group was to develop computational systems biology approaches for modeling genomic regulatory networks on mouse embryonic stem cells (Cell Stem Cell, 2009; Nature, 2010; PLoS One, 2012; Scientific Report, 2013). In 2012, he was awarded with ORISE fellowship of CBER in FDA and began the brand-new research journey to translate basic discoveries into clinical practices using regulatory science. After coming back to Taiwan, he worked as a research specialist of Taiwan FDA to oversee the premarket reviews of class III medical devices.

Prof. Yang is now not only engaged in developing research and teaching of translational biomedical informatics in NCKU, but also serve as a member of Health & Medical Device STD & Tech. Committee in the Bureau of Standards, Metrology & Inspection, M.O.E.A. Thus, he envision his career to be heavily focused on "Regulatory science" facilitates the discovery of biotechnology and genomic medicine for marketability as well as public health. It would be a privilege to be able to collaborate with the relevant research groups in conducting this effort.

Technical Session D1-W2-T1: Medicine and Life Sciences, Biological and Biomedical Sciences

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BIOGRAPHY

Nei-Li Chan received a BSc degree in Chemistry in 1991 from National Taiwan University, Taiwan. After two years of compulsory military service as a Second Lieutenant in the Taiwanese Army, he enrolled in the Biochemistry doctoral program offered by the University of Iowa (USA) and completed his PhD degree in 1998. From 1999 to 2001, he conducted post-doctoral training with Prof. Chris Hill (University of Utah, USA). He then returned to Taiwan and joined the faculty of National Chung Hsing University. He moved to National Taiwan University in 2007, where he is currently appointed as a Professor of Biochemistry and Molecular Biology.

He uses various biochemical and biophysical techniques, including X-ray crystallography, to study the structure and function of proteins. In recent years, he has been actively engaged in the "structural-based design of type II topoisomerase isozyme-specific anticancer agents" and the elucidation of "structural basis of antizyme-mediated proteosomal degradation pathway".

Selected Publications

1) Wu, H.-Y., Chen, S.-F., Hsieh, J.-Y., Chou, F., Wang, Y.-H., Lin, W.-T., Lee, P.-Y., Yu, Y.-J., Lin, L.-Y., Lin, T.-S., Lin, C.-L., Liu, G.-Y., Tzeng, S.-R.*, Hung, H.-C.*, & **Chan, N.-L.*** (2015) Structural Basis of Antizyme-Mediated Regulation of Polyamine Homeostasis. Proc. Natl. Acad. Sci. U.S.A. (published ahead of print August 24, 2015, doi:10.1073/pnas.1508187112)

2) Chang, C.-C., Lin, L.-Y., Zou, X.-W., Huang, C.-C.*, & **Chan, N.-L.*** (2015) Structural Basis of the Mercury(II)-Mediated Conformational Switching of the Dual-Function Transcriptional Regulator MerR. Nucleic Acids Res (Epub ahead of print, PMID: 26150423)

3) Wu, C.-C., Li, Y.-C., Wang, Y.-R., Li, T.-K.*, & **Chan, N.-L.*** (2013) On the structural basis and design guidelines for type II topoisomerase-targeting anticancer drugs. Nucleic Acids Res, 41:10630-40.

4) Wu, C.-C., Li, T.-K., Farh, L., Lin, L.-Y., Lin, T.-S., Yu, Y.-J., Yen, T.-J., Chiang, C.-W., & **Chan, N.-L.*** (2011) Structural basis of type II topoisomerase inhibition by the anticancer drug etoposide. Science, 333:459-62

Technical Session D1-W2-T1: Medicine and Life Sciences, Biological and Biomedical Sciences

Role of a tumor-associated NADH oxidase (tNOX) in stress-mediated cell death

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ABSTRACT

tNOX activity, originally isolated from rat hepatoma cells, is a tumor-associated member of a family of growth-related NADH (or hydroquinone) oxidases. Subsequent studies have demonstrated that tNOX is expressed in numerous lines of cancer/transformed cells and is also detected in the sera of cancer patients, but not in those of healthy volunteers. More importantly, inhibition of tNOX by anticancer agents is correlated with attenuated cancer cell growth. One such agent is capsaicin, an active component of chili peppers that is shown to possess anti-growth activity against various cancer cell lines. We examined the effect of capsaicin on SNU-1 and TMC-1 gastric cancer cells and found differing outcomes between the two cell lines. Our results show that capsaicin induced significant cytotoxicity with increases in oxidative stress, PARP cleavage, and apoptosis in sensitive SNU-1 cells. Capsaicin-induced apoptosis in SNU-1 cells was associated with tNOX down-regulation at both transcriptional and translational levels. On the other hand, TMC-1 cells were much less sensitive to capsaicin, exhibiting low cytotoxicity and very little apoptosis, which were also accompanied by little changes in tNOX expression in response to capsaicin treatments. We further showed that tNOX-knockdown sensitized TMC-1 cells to capsaicin-induced apoptosis and G1 phase accumulation, and led to decreased cell growth, demonstrating that tNOX is essential for cancer cell growth.

Interestingly, capsaicin is also considered as a chemopreventive agent by virtue of its selective anti-growth activity against cancer cells, whereas non-cancerous cells possess relatively higher tolerance to capsaicin. Capsaicin preferentially inhibits tNOX activity in cancer cells, which normally oxidizes hydroquinones and NADH, converting the latter to the oxidized NAD+ form. Thus, it is of interest to study whether tNOX and NAD+/NADH ratio is involved in the differential effect of capsaicin. We used MRC-5 normal human lung tissue fibroblast and A549 human lung adenocarcinoma epithelial cell lines to investigate the differential effects of capsaicin and the underlying mechanisms for this difference. We demonstrated that capsaicin decreased the intracellular NAD+/NADH ratio through tNOX inhibition and diminished SIRT1 expression, a NAD+-dependant deacetylase, which led to enhanced p53 acetylation and apoptosis. In comparison, capsaicin augmented SIRT1 deacetylase activity and the intracellular NAD+/NADH ratio, which decreased acetylation of p53 and induced autophagy in MRC-5 cells. Moreover, targeting tNOX in A549 cells with siRNA decreased the NAD+/NADH ratio compared to A549 cells expressing control (scrambled) siRNA. We also noticed that tNOX-depleted A549 cells exhibited reduced SIRT1expression; whereas p53 acetylation and JNK phosphorylation were increased and cyclin D was attenuated, conforming a tumor-promoting role of tNOX in

cancer cells. Collectively, these data not only explain the differential cytotoxicity of capsaicin but also shed light on the molecular mechanisms of tNOX action.

BIOGRAPHY

Dr. Chueh was born and grew up in Chia-Yi, Taiwan. For her educational background, she received her Bachelor's and Master's degrees from the Department of Chemistry at National Chung Hsing University in Taichung, Taiwan, where she worked on the synthesis and determination of crystal structures of new phosphate compounds. It was always her dream to study abroad, and she was admitted to the Interdepartmental Nutrition Program in Purdue University, West Lafayette, Indiana, USA in 1994. She was awarded PhD degree from Purdue University in 1997.

After a few years of post-doctoral training, she later obtained a position as a Research Associate in the Department of Medicinal Chemistry and Molecular Pharmacology at Purdue University. In 2003, she and her family decided to return to Taiwan and to set up her own laboratory. She began her academic career as an Assistant Professor in the Department of Life Sciences at Chung Shan Medical University in Taichung. In 2005, she transferred to the Institute of Biomedical Sciences at National Chung Hsing University in Taichung as an Assistant Professor. She was promoted to Associated Professor in 2009 and Professor in 2013. Her research interests focus on the understanding biological function of a tumor-associated NADH oxidase (tNOX, ENOX2) that is universally expressed in many cancers. Gain-of-function and loss-of-function support that tNOX is important for cancer cell phenotypes and could potentially serve as a cancer biomarker. Additionally, the molecular mechanisms underlying nanomaterial-mediated cytotoxicity are also a major focus of her research interests.

Professor Chueh has published one book chapter and more than 40 manuscripts.

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Technical Session D1-W2-T1: Medicine and Life Sciences, Biological and Biomedical Sciences

Expression and Homeostasis of Stemness Properties in Cancer Disease

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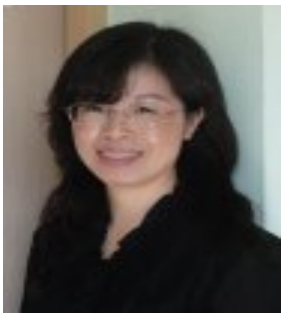
ABSTRACT

The expression levels of pluripotency-related genes in cells, like pluripotent transcription factor OCT4, are linked to drug susceptibility which challenges the current cancer therapy. Niche environment apparently plays a critical role in cell stemness regulation either of somatic- or embryonic stage. In this talk, two human cancer disease of somatic hepatocellular carcinomas (HCC) and embryonic pluripotent germ cell tumor seminoma and embryonic carcinoma will be discussed to address the potential homeostasis mechanism of pluripotent transcription factor OCT4 in cancer disease, and its impacts on drug susceptibility and poor prognosis in cancer therapy.

Hepatocellular carcinoma (HCC) is an inflammation-associated cancer which is commonly associated with chronic virus infection. In a large cohort of frozen HCC samples, we found the niche inflammatory cytokine IL-6 is critical for the re-expression of OCT4 in patient tissues. The underlying mechanism involves that IL-6-induced IGF/IGF-IR signal activation particularly for hepatitis B virus (HBV)-related HCC (HBV-HCC), and is associated with tumor aggressiveness and recurrence. Niche IL-6 stimulated the expression of autocrine IGF-I and IGF-IR in a STAT-dependent manner, which stimulated the stemness-related properties in both the cell lines and the xenograft mouse tumors. The inhibition of the IGF-IR activation by RNA interference and molecular inhibitor significantly suppressed the IL-6-induced stemness-related properties in vitro and in vivo. These findings suggest that the IL-6-induced IGF-IR signaling is a potential strategy targeting on cancer stemness for individualized adjuvant therapy against HBV-HCC.

Human seminoma and embryonal carcinoma (EC) are cancer stem cells transformed from the embryonic pluripotent primordial germ cells. This human disease provides an excellent cell model to study the OCT4 homeostasis as the tumor express high OCT4 levels in cells. We found niche hypoxia is able to down-regulate the OCT4 level and results in chemoresistance and poor prognosis by regulating the SUMO1 peptidase SENP1. Overexpression of SENP1 reduced the Su-OCT4 level induced by SUMO1gg overexpression, thereby maintaining OCT4 levels and enhancing chemosensitivity. Mechanistic investigations revealed that OCT4 sumoylation occurred at K123, as overexpression of an OCT4-K123R mutant effectively reduced the level of Su-OCT4 under hypoxic conditions. These results demonstrated that hypoxia reduces OCT4 expression levels in pluripotent germ cell tumors to increase drug resistance, and these effects could be countered to ablate the suppressive effects of hypoxia on chemosensitivity.

BIOGRAPHY



Yen-Hua Huang received her B.S. in Chemistry (1989) from National Taiwan Normal University, Taipei, Taiwan. She received her M.S. (1993) and Ph.D. (1997) from National Taiwan University both in Biochemistry, and was a postdoctoral fellow in Stem Cell Biology at Academia Sinica from 1997 to 2002. She was recruited as an Assistant Professor by Taipei Medical University at 2002, and currently she is a Professor and Director of Department of Biochemistry and Molecular Cell Biology, Graduate Institute of Medical Sciences (since 2013).

Dr. Huang's research interests are focusing on pluripotent embryonic germ cells, therapeutic potential human placenta stem cells, and somatic cancer stemness. She is the Deputy Director of Center for Teeth Bank and Dental Stem Cell Biotechnology (since 2010), and Director of TMU Center for Cell Therapy and Regeneration Medicine, Taipei, Taiwan (since 2015). She was Secretary General (2011-2013) and now is the Member of Director Board (2014-now) both of the Taiwan Society for Stem Cell Research (TSSCR) and Taiwan Association for Cell Therapy (TACT), Taiwan. She now is the Committee Member of Regeneration Medicine Board, Food and Drug Administration, Taiwan (TFDA).

Selected publications: * Corresponding author

1. Chang TS, Wu YC, Tsai YH, and **Huang YH***. (2015) Hepatocellular carcinoma surveillance: A Strategy that merits moving forward. **Am J Gastroenterol**. In press (2014 SCI) Impact factor: 10.755; Ranking: 7.9%. (6/76) GASTROENTEROLOGY & HEPATOLOGY

2. Chang TS, Wu YC, Tung SY, Wei KL, Hsieh YY, Huang HC, Chen WM, Shen CH, Lu CH, Wu CS, Tsai YH, and **Huang YH***. (2015) Alpha-fetoprotein measurement benefits hepatocellular carcinoma surveillance in patients with cirrhosis. **Am J Gastroenterol**. 110(6):836-44. (2014 SCI) Impact factor: 10.755; Ranking: 7.9%. (6/76) GASTROENTEROLOGY & HEPATOLOGY

3. Chang TS, Wu YC, Su WC, Chi CC, Chang PJ, Lee KF, Liu JJ, Tung SY, Kuo LM, Ho HN, Ling TY, and **Huang YH***. (2015) Activation of IL6/IGF-IR confers poor prognosis of HBV-related hepatocellular carcinoma through induction of OCT4/NANOG expression. **Clin Cancer Res.** 21(1):201-10. (2014 SCI) Impact factor: 8.722; Ranking: 5.7 %. (12/211) ONCOLOGY.

4. Liao HF, Chen SC, Chen YH, Kao TH, Lee CY, Chiu YC, Lin QY, Tseng YZ, Ching YH, Hata K, Cheng TK, Tsai MH, Sasaki H, Ho HN, Wu SC, **Huang YH**, Yen P and Lin SP. (2014) DNMT3L quiescent the postnatal spermatogonial progenitor cells. **Development.** 141(12):2402-13. (2014 SCI) Impact factor: 6.462; Ranking: 9.8 %. (4/41) DEVELOPMENT BIOLOGY.

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5.1 %. (4/79) OBSTETRICS & GYNECOLOGY

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Technical Session D1-W2-T1: Medicine and Life Sciences, Biological and Biomedical Sciences

Toward complete understanding of metabolic network of E. coli K-12: exploration of missing pathways by the genetic interaction analysis

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ABSTRACT

A goal of systems biology is to construct models that enable us to interpret genotype-phenotype relationships. A possible target of such relationships is metabolism; the network of chemical transformation reactions catalyzed by enzymes within the cells. Since there are direct relationships between genotypes and metabolism, metabolic network modeling has been a good target for many systems biologists. Genome-scale reconstructions of Escherichia coli metabolic networks, such as iJO1366 [1], have been performed systematically using omics data, genome annotation and biological knowledge from literatures. These systems allow computational predictions as a useful tool for designing metabolisms and sharing new hypotheses of metabolic functions. Currently, iJO1366 showed more than 80% accuracy for computational prediction of single-knockout (SKO) mutants' viability. However, it still shows 2.0% false negative (model had predicted no-growth but colonies of a gene knockout showed normal growth) and 5.3% false positive (model had predicted growth but colonies of a gene knockout showed no-growth). These discrepancies between predicted and observed cell growth may due to existence of unknown enzymes or unknown pathways. For complete model of metabolic network, comprehensive double knockout (DKO) experiment can provide us clues to identify the genes that are relevant to those unknown pathways. Our group previously established two comprehensive collections of single-gene deletion mutant of E.coli (Keio-Collection and Aska deletion library) and double-knockout method via conjugating single-knockout strains [2]. We have also established a growth monitoring system (Colony-live) to monitor the growth of colonies on agar plates [3]. I would like to talk about our current achievements.

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BIOGRAPHY

Ai Muto received her B.S. (2004) in Molecular Biology from Shinshu University. She received her M.S. (2006) in Bioinformatics. She was a research scholar at Boston University in 2008. She received her Ph.D. (2013) from Kyoto University in Bioinformatics. Currently she is an assistant professor of Nara Institute of Science and Technology. Dr. Muto's research integrates bioinformatics and genomics to study metabolic networks in bacteria, especially E.coli.

Technical Session D1-W2-T1: Medicine and Life Sciences, Biological and Biomedical Sciences

Introduction of Micro-Western Array Platform and Biomedical Applications

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ABSTRACT

Micro-Western Array (MWA), a recently developed high-throughput antibody-based proteomics system, is a modified reverse phase array composes of a GeSim Nanoplotter arrayer, a GE multiphor, and a Licor Odyssey infra-red scanner. MWA allows detecting protein expression level or phosphorylation status change of 96-384 different antibodies in 6-15 samples simultaneously with very little amount of samples and antibodies. MWA is very powerful for signaling transduction network or protein profiling study. We have implied MWA system to research on cancer biology, drug mechanism study, protein interaction, development and differentiation, as well as gene and protein signaling study.

BIOGRAPHY

Dr. Chih-Pin Chuu was born in Taipei, Taiwan on April 9th, 1976. Dr. Chuu graduated from Physics Department of National Tsing Hua University (Hsinchu, Taiwan) in 1997 with physics major. Dr. Chuu earned Ph.D. degree from Committee on Cancer Research, The University of Chicago (Chicago, Illinois, U.S.A.) in 2005 focus on prostate cancer and androgen receptor research.

He served in Taiwanese (R.O.C.) Army as Instructor in Army Tank and Armed Forced Academy as reserved Second Lieutenant from 1997-1999. After receiving his Ph.D. degree, he worked as Postdoc Scholar in Ben May Department of Cancer Research, The University of Chicago from 2005-2007 and as Postdoc Fellow in Institute of Genomics and Systems Biology, The University of Chicago from 2007-2009. He became Assistant Investigator in Institute of Cellular and System Medicine, National Health Research Institutes (NHRI, Miaoli, Taiwan) in Taiwan since September in 2009 and got promotes to Associate Investigator from July, 2015. He also holds joint Assistant Professorship in National Chung Hsing University (Taichung, Taiwan), China Medicine University (Taichung, Taiwan), and Kaohsiung Medical University (Kaohsiung, Taiwan). He is the Supervising PI of Micro-Western Array Core in NHRI since 2009.

Dr. Chih-Pin Chuu is member of American Association of Cancer Research (AACR), Japanese Cancer Association (JCA), Molecular Biology Society of Japan (MBSJ), and Taiwan Proteomics Society (TPS). Dr. Chuu was selected for 2011 Edition Marquis Who's Who and 011-2012 Edition Marquis Who is Who in Medicine and Healthcare. He is Academic Editor of PLOS One since 2013 and served as reviewer for several scientific journals, including Cancer Research, Cancer Letters, International Journal of Cancer, Gastroenterology, British Journal of Cancer,

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Chieh Liu, Jong-Ming Hsu, Li-Kuo Kuo, **Chih-Pin Chuu***. Med Hypotheses. 2013 May; 80(5):617-619. *corresponding author

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Technical Session D1-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Session Chair

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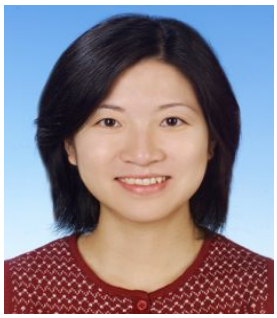
BIOGRAPHY



Chihchen Chen was born in Taipei, Taiwan. She received her B.S. (1995) and M.S. (1997) in Electrical Engineering from the National Taiwan University. She was an R&D engineer at ASUS Computer Inc., Taiwan from 1997 to 1999. She received her Ph.D. (2006) from the University of Washington at Seattle, WA, with dual degrees in Bioengineering and Nanotechnology. She was a postdoctoral associate at the Massachusetts General Hospital between 2006 and 2009.

Currently she is an Associate Professor of the Institute of NanoEngineering and MicroSystems, Department of Power Mechanical Engineering at the National Tsing Hua University, Hsinchu, Taiwan, where she started her own research group in the summer of 2010. Her areas of expertise and research interests are micro- and nano-fluidic technologies for applications in biology and medicine, with a focus on the isolation and characterization of the cellular and sub-cellular components.

Dr. Chen is a member of the International Society for Extracellular Vesicles, and a member on the Product Advisory Board of Journal of Visualized Experiments (JoVE).

Technical Session D1-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Nano/Micro Fluidic Systems for Circulating Tumor Cells (CTCs) Rapid Detection and Diagnosis

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ABSTRACT

Despite the recent advancement of biotechnology and pharmaceutical research, cancers remain the leading cause of human mortality. It is vital to diagnose cancers at an early stage when treatment can dramatically improve prognosis. So far, low-cost and easy to operate devices, which allow efficient isolation and sensitive detection of circulating tumor cells (CTCs) for routine blood screening, remain lacking. This talk will introduce a novel micro fluidic platform which can isolate CTCs from the real blood sample in 30 minutes: this system includes a high throughput blood cell separation chip which can separate white blood cells with CTCs from red blood cells and platelets by inertial and suction actions; a nano structured surface which can allow higher retention rate of CTCs on the surface for sample enrichment by 100 folds from 1/107 up to 1/105 CTCs/WBCs, and the enriched sample will go through a final cells self-assembly process into a dense monolayer on a cell assembly chip for in parallel inspection at high speed. Isolated CTCs will still be in vital and can be further characterized and cultivated for the identification of cancer stem cells for prognosis.

BIOGRAPHY

Dr. Fan-Gang Tseng received the B.S. degree in Power Mechanical Engineering from National Tsing Hua University at Taiwan in 1989, and the M.S. degree from the Institute of Applied Mechanics in National Taiwan University at Taiwan, in 1991. In 1998, he received his Ph.D. degree in mechanical engineering from the University of California at Los Angeles, USA (UCLA), under the supervision of Prof. C.-M. Ho and C.-J. Kim. He jointed Engineering and System Science Department of National Tsing-Hua University at Taiwan as an Assistant Professor in August 1999, and was advanced to Associate Professor in August 2002, Professor in August 2006, as well as Distinguished Professor in August 2015. He served as the ESS department chairman from 2010 to 2013 and Associate Vice President of NTHU in global affair from 2013 to 2014, and has been the Deputy Director of the Biomedical Technology Research Center of NTHU since 2009. He has been elected a fellow of ASME in March 2014. His research interests are in the fields of Nano-Biosensors, Bio-MEMS, Micro Fuel Cells, and Nano/Micro-Fluidic Systems. He received 40 patents, wrote 7 book chapters, published more than 150 SCI Journal papers and 330 conference technical papers in Biosensors, Bio-N/MEMS, Micro Fuel Cells, and Micro/Nano Fluidics related fields, and co-organized or co-chaired many conferences including IEEE MEMS, IEEE NEMS, IEEE Transducers, Micro TAS, ISMM, IEEE Nano, and IEEE Nanomed. He received several awards,

including Outstanding in Research Awards (2010, 2014) and Mr. Wu, Da-Yo Memorial Award (2005) from MOST Taiwan, two National Innovation Awards (2010, 2014), ten Best Paper/Poster awards (1991, 2003, 2004, 2005, 2008, 2010, 2012, 2013, 2014), and others.

Technical Session D1-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

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ABSTRACT

BIOGRAPHY

Technical Session D1-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Effects of Cold Plasma on Human Dental Pulp Stem Cells

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ABSTRACT

In recent years, low-temperature atmospheric-pressure plasma becomes a new tool in medical treatment because of its portability, treatment versatility, ingredient adjustability, and penetrative gaseity. Latest papers report that plasma induces cell differentiation, proliferation and transfection, which paves a new direction for tissue regeneration engineering. In addition, previous study shows that the reactive oxygen/nitrogen species (RONS) produced by cold plasma would influence the inter- and intracellular networks on mammalian cells, and other study indicates that latent transforming growth factor-β 1 can be induced by reactive oxygen species (ROS) to direct dental stem cells differentiation. The purpose of this work is to investigate the efficacy of plasma on human dental pulp stem cells (DPSCs), and measure the ROS in plasma treated cell culture medium (DMEM). The plasma treated medium in different time period (10 s to 300 s) and then the ROS (H2O2 and OH radical) concentration in medium were measured with FTIR, OES, and colorimetry. The same plasma jet was applied to the Human DPSCs, and the cell differentiation, proliferation, and viability were analyzed (5 mins, 2 hrs, 24 hrs after treatment) with ALP, cell counting, and MTT, respectively. As a result, about 1-3 ppm H2O2 was measured in medium treated by plasma. Besides, data regarding the interaction of plasma with DPSCs demonstrated that 60 s plasma treatment did not inhibit the viability at early stage (5 mins and 2 hrs after treatment). The feasibility and mechanism of plasma to enhance DPSCs proliferation was discussed at first step. Further examinations including other ROS concentration and cell differentiation will be evaluated in following study.

BIOGRAPHY

Dr. Yun-Chien Cheng received his B.S. (2004) and M.S. (2006) in Electrical Engineering from the National Taiwan University. From 2008 on, he worked jointly in German Cancer Research Center, Darmstadt University of Technology, and Karlsruhe Institute of Technology, Germany, and received Dr. Ing. in 2012. Currently he is an Assistant Professor of Mechanical Engineering Department and Institute of Biomedical Engineering, National Chiao Tung University. Dr. Cheng's research interests include high-density peptide array manufacture and medical application of low-temperature atmospheric-pressure plasma.

Technical Session D1-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

A Bead-Based Quantification Technique for Microorganisms using Optical Diffusometry

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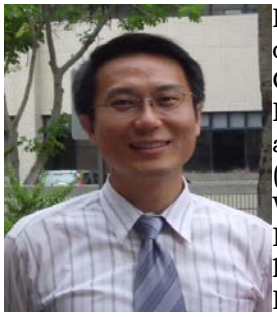
ABSTRACT

Optical diffusometry is used to detect the quantity of microorganisms in this study. By binding a target bacterium, P. aeruginosa, with functionalized particles, the Brownian motion of the particles can be altered accordingly. The corresponding particle diffusivity can then serve as an indicator in relation to the concentration of the microorganisms. The technique requires neither sophisticated fabrication nor intricate instruments. A high sensitivity detection as low as one cell was achieved. A comparison of the bacterium, P. aeruginosa, treated with and without the antibiotic, gentimicin, was complete within 120 min. The result suggests that antimicrobial susceptibility testing can potentially be improved from days to hours based on the proposed technique.

BIOGRAPHY



Han-Sheng Chuang is currently an associate professor in the Department of Biomedical Engineering at National Cheng Kung University, Taiwan. Dr. Chuang received his bachelor and master degrees in the Department of Mechanical Engineering from National Cheng Kung University in 1998 and 2000, respectively. He joined Industrial Technology Research Institute (ITRI) as a R&D engineer in 2001. After then, he worked with Prof. Steve Wereley for advanced microfluidics and received his Ph.D. in the School of Mechanical Engineering from Purdue University in 2010. After graduation, he received an appointment as a postdoctoral researcher at University of Pennsylvania and worked with Prof. Haim H. Bau on cell sorting and Caenorhabditis elegan manipulation. In 2005, he was awarded a competitive fellowship from Ministry of Education, Taiwan. He and his research fellows were the finalists of the prestigious Burton D. Morgan Business Competition in 2008 and 2009, respectively. Lately, he was awarded the 2014 Young Researcher Career Grant from the Ministry of Science and Technology. In addition, he is also a cofounder of a US-based technical start-up, Microfluidic Innovations, since 2009. Dr. Chuang has dedicated to the fields of optoelectromechanical microfluidics for more than 10 years. His research interests are focused on nano-/microfluidics, Bio-MEMS/NEMS, optical diagnostics, and biomechanics of C. elegans.

Technical Session D1-W4-T1: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Session Chair

Ai-Chun Pang

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BIOGRAPHY

Technical Session D1-W4-T1: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

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ABSTRACT

BIOGRAPHY

Technical Session D1-W4-T1: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Nationwide Integrated Electronic Health Records: Opportunities and Challenges

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ABSTRACT

Evidence shows that patients who receive medical care more frequently from multiple health care providers, particularly from different hospitals, are more likely to receive duplicate medications and suffer adverse drug reactions. The main reason is lack of infrastructure for sharing health information and medication history among the primary care offices (clinics) or hospitals. To tackle this problem the National Health Insurance Administration (NHIA), a single payer in Taiwan, has established a PharmaCloud web-based systems since 2013. The system allows physicians to access their patients' medication records of past 3 months with the patients' authorization. As such, when prescribing for a patient the physician can avoid the occurrence of the ADRs.

However, a physician usually uses a computerized physician ordering (CPOE) system to order prescriptions. Due to lack of semantic interoperability between the CPOE and PharmaCloud systems, the physician has to operate two systems back and forth to find out potential ADRs when prescribing. In our study, we enhanced the semantic interoperability by adopting the Anatomical Therapeutic Chemical (ATC) classification system as a common model for cross-mapping the drugs represented in the PharmaCloud and the ones represented in the CPOE system. We also extended the functionality of the CPOE system with alerts when detecting potential ADR events automatically. Thus, our approach can effectively reduce physician's workload and prevent from prescribing duplicated medications and the drugs with DDIs.

Since the NHIA collect the medical records covered by the NHI program only. To extend the scope of medical records, the NHIA has further developed an integrated electronic Health Records (EHR) system, called My Health Bank. It provides a patient's medical visit records of past one year at any clinic/hospital in Taiwan. With the integrated EHRs, combining with other self-collected health data, such as those generated by wearable devices, self-paid gene test results, vital signs measured on daily basis, and so on, it increases the data complexity in terms of care domains. Despite our past studies that could be extended to cope with the complex health data, we are still facing challenges that require better interoperable semantic models and decision making tools for different care purposes.

BIOGRAPHY

Dr. Chien-Tsai Liu received his BS degree in Electronic Engineering from Tamkang University in 1982, MS degree in Electronic Engineering from National Taiwan University of Science and

Technology in 1986, and Ph.D. degree in Computer Science from University of Pittsburgh, Pennsylvania, USA in 1994. His research interests focus on medical data modeling and sharing, electronic health records and the standards for health data exchange. Dr. Liu has joined the Graduate Institute of Biomedical Informatics at Taipei Medical University in Feb 1998. He currently serves as Professor and Director at the Institute. Dr. Liu served as the Chair of HL7 Taiwan, an affiliate of HL7 International, a standards development organization, from 2001 to 2005 and 2007 to 2009.

Dr. Liu is a senior member of HL7 International, and a founding executive council member of HL7 Asia. He has been leading the Project Management Office for Electronic Health Record Projects in Taiwan since 2010. He is one of key persons who have engaged in the infrastructure development for exchanging electronic health records in Taiwan.

Technical Session D1-W4-T1: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Wireless Healthcare and Related Life Style Applications

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ABSTRACT

With the capability of low power, highly integration, and miniaturization, the ICT industry can contribute more and more to the biomedical applications. We will present a wireless health system (collaborated with National Taiwan University Hospital) in this talk. We have finished an energy efficient prototype, energy-efficient chip, and flexible cloud for diagnostic grade mobile ECG monitoring. The prototype uses a mobile phone as a gateway to transmit the measured ECG data back to the medical cloud. Therefore, the patients are not tied to the hospital or home, and can go outside for common life. We can obtain the ECG features both on mobile phone and in the cloud (more accurate). The platform can also analyze the linear and non-linear analysis of heart rate variability in patients with multi-scale entropy. With the possibilities of wearable sensing techniques, we can also extend the techniques to the life style applications or interdisciplinary collaborations. Some demos will be presented within the talk.

BIOGRAPHY

Hsi-Pin Ma received the B.S. and Ph.D. degrees in electrical engineering from the National Taiwan University, Taiwan, in 1995 and 2002. At the summer of 2000, he interned at Siemens Telecommunication Systems Limited, for feasibility study and establishment of a dual-mode base station for WCDMA and cdma2000. Since 2003, he has been with the Department of Electrical Engineering and Institute of Communications Engineering, National Tsing Hua University, Hsinchu, Taiwan, where he is currently as an Associate Professor.

Dr. Ma's research interests include biomedical electronics and signal processing, telemedicine, wearable and implantable technologies, and health informatics. For communications, he continues to focus on the system design, signal processing, and SoC implementation for advanced MIMO and cognitive radios. He has published 14 journal and 55 conference papers, and 8 international patents. He has got 3 times outstanding publication awards from NTHU and 1 excellent project award from National SoC Program, National Science Council. He has also four cases of technology transfer to the industries.

Technical Session D1-W4-T1: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Multiuser MIMO Systems: From Rate Adaptation to User Selection

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ABSTRACT

Multi-user multiple input and multiple output (MU-MIMO) is one predominate approach to improve the wireless capacity. However, the aggregate capacity of MU-MIMO heavily depends on the channel correlations among the mobile users served concurrently. This means that the optimal bit rate of a user will be highly dynamic and change from one packet to the next. This breaks traditional bit rate adaptation algorithms, which rely on recent history to predict the best bit rate for the next packet. We introduce a rate adaptation scheme customized for MU-MIMO LANs. Our design allows clients in a MU-MIMO LAN to adapt their bit rate on a per-packet basis by simply passively learning two variables: its SNR when it transmits alone to the access point, and the direction along which its signal is received at the AP. Another important issue is how to select a proper set of concurrent clients to maximally realize the MU-MIMO gain. The fundamental challenge for user selection is the large searching space, and hence there exists a tradeoff between search complexity and achievable capacity. Previous works have proposed several low complexity heuristic algorithms, but they suffer a significant capacity loss. To remedy this inefficiency, we propose an adaptive user selection scheme that leverages a knob to control the aggressiveness in searching the best beamforming group. Our design keeps tracking the channel and the coherence time for each mobile user, and largely avoids unnecessary computing with a progressive update strategy. A prototype implementation in USRP-N200 shows that our rate adaptation improves the throughput gain by 1.7x and 2.3x for 2-antenna and 3-antenna APs, respectively. By further enabling adaptive user selection, we can achieve around 90% of the capacity compared to exhaustive search.

BIOGRAPHY

Kate Ching-Ju Lin received the BS degree from the Department of Computer Science, National Tsing Hua University in 2003, and the PhD degree from Graduate Institute of Networking and Multimedia, National Taiwan University in 2009. She was a visiting scholar at CSAIL, MIT, from March 2007 to March 2008 and from October 2010 to March 2011.

After her graduation, she joined Research Center for Information Technology Innovation at Academia Sinica, Taiwan. She is currently an associate research fellow. Her current research interests include wireless systems, wireless multimedia networking and visible light communications.

Dr. Lin received the Exploration Research Award from Pan Wen Yuan Foundation in 2012, the

Research Project for Excellent Young Scholars from Taiwan's Ministry of Science and Technology in 2013, the K. T. Li Young Researcher Award from ACM Taipei/Taiwan in 2014, and the 23rd Ten Outstanding Young Women Award in 2015. She is now the Editor of Wireless Networks, and has served as the TPC member of several major conferences, including IEEE INFOCOM, ACM MOBICOM, USENIX NSDI, IEEE ICC. She is a member of the IEEE and ACM.

Technical Session D1-W1-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Session Chair

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BIOGRAPHY

Hsuan-Cheng Huang received his B.A., M.A., and Ph.D. degrees in physics from National Taiwan University in 1992, 1994 and 1998, respectively. He was engaged in experimental high-energy physics research at Taiwan and at High Energy Accelerator Research Organization, Japan, and awarded NSC Distinguished Postdoctoral Fellowship in 2003. Encouraged by the emerging of systems biology, Dr. Huang joined National Yang-Ming University in 2004 and is currently a Professor and the Director of the Institute of Biomedical Informatics, also affiliated with the Center for Systems and Synthetic Biology. In 2007, he received the NSC Wu Ta-You Memorial Award, an honor for excellent young investigators in Taiwan. Now he serves as an Editorial Board Member of Scientific Reports, an Associate Editor and Deputy Section Editor of BMC Systems Biology, and an Executive Board Member in Taiwan Society of Evolution and Computational Biology. His research interests include bioinformatics, computational and systems biology, and network biology. Currently, Dr. Huang endeavors his research efforts to computational analysis and modeling of biological networks, and applies them to unravel molecular mechanisms of cancer cell response, non-coding RNA regulation, as well as other biological processes..

Technical Session D1-W1-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

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ABSTRACT

BIOGRAPHY

Technical Session D1-W1-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Next-generation Sequencing Data Analysis in Biomedical Applications

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ABSTRACT

In the past five years, next-generation sequencing (NGS) has significantly changed the ways of doing biomedical research. As sequencing technology matured and the data quality gradually improved, bottlenecks of doing good NGS research turned to whether innovative bioinformatics methods can be developed in time and employed correctly. In this talk, I am going to share some good examples of applying NGS computational pipelines on solving biomedical problems. The data adopted included DNA-seq for genome assembly, RNA-seq for transcriptome exploration, and ChIP-seq for studying protein-DNA interactions. In 2010, we sequenced and assembled the transcriptome of oriental fruit flies (Bactrocera dorsalis) for the studies of insecticide resistance. Later, a similar RNA-seq pipeline was applied on sweet potatos (Ipomoea batatas) for investigating the differential sporamin expression in response to abiotic mechanical wounding and biotic herbivore attack. Meanwhile, RNA-seq analysis was also applied on axolotl blastema (Ambystoma mexicanum) for identification of differentially expressed genes during limb regeneration. In 2012, we initiated a genome sequencing project on agarwood (Aquilaria agallocha) for identification of cucurbitacins, and later more RNA-seq data was performed to study the effect of red light and far-red light conditions on secondary metabolisms in agarwood. One year later, the de novo genome assembly pipeline developed in the agarwood project was applied on mungbean (Vigna radiata [L.] R. Wilczek) studies to complete a draft genome of a bruchid-resistant recombinant inbreeding line, and then comparative genomics was conducted on this resistant line against a previously published draft genome of a bruchid-susceptible mungbean line (Vigna radiata var. radiata VC1973A) for discovering critical bruchid resistance-related genomic regions. More successful examples of applying de novo gnome assembly and comparative genomics on strains or lines with different phenotypes included Vibrio parahaemolyticus, a bacterium that caused diseases in shrimp in China and Thailand. Some RNA-seq and ChIP-seq experiments were further performed on the model organism, fruit fly (Drosophila melanogaster) for studying human diseases, while ChIP-seq pipeline was also demonstrated to be useful in studying differentially regulated pathways associated with the development of regional specificity in chicken skins. In summary, many experiences of using NGS technology in biomedical applications were accumulated on the NTU campus, and the developed computational pipelines can be easily found on the Galaxy Bioinformatics platform we built for the local researchers.

BIOGRAPHY

Dr. Chien-Yu Chen (1974 ~) is currently a professor of department of Bio-Industrial Mechatronics Engineering, National Taiwan University. She holds a B.S. degree of Electrical

Engineering from National Taiwan University (1996), a M.S. degree of Electrical Engineering from Stanford University (1998), and a Ph.D degree of Computer Science and Information Engineering from National Taiwan University (2003). During the Ph.D program, she initiated the research of Bioinformatics, and has mainly focused on developing algorithms for studying molecular biology. She has been an Assistant Professor of Graduate School of Biotechnology and Bioinformatics in Yuan Ze University from Feb. 2004 to July 2005, where she began her academic career.

As a computational biologist, her research centers on two problems: sequence analysis and expression data analysis. On sequence analysis, the research topics span several effective sequence-based methods for predicting protein functional sites associated with protein-DNA interactions, protein-ligand interactions, and protein-protein interactions. The basic idea behind those prediction methods is exploiting pattern mining technology in finding concurrent conserved regions among protein families. For another research topic, expression data analysis, she utilizes the state of the art clustering and classification techniques on microarray or RNA-seq datasets for patient outcome prediction, time-course data analysis, and association discovery. Moreover, she applies pattern mining skills to identifying transcription factor binding sites directly from ChIP-chip or ChIP-seq data and combines expression data for constructing regulatory networks.

Technical Session D1-W1-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

A regulatory similarity measure using the location information of transcription factor binding sites in Saccharomyces cerevisiae

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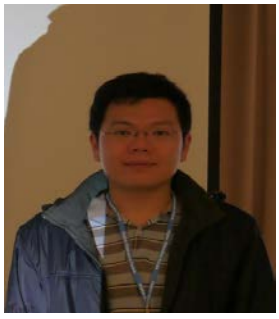
ABSTRACT

Defining a measure for regulatory similarity (RS) of two genes is an important step toward identifying co-regulated genes. To date, transcription factor binding sites (TFBSs) have been widely used to measure the RS of two genes because transcription factors (TFs) binding to TFBSs in promoters is the most crucial and well understood step in gene regulation. However, existing TFBS-based RS measures consider the relation of a TFBS to a gene as a Boolean without utilizing the information of TFBS locations in promoters. Functional TFBSs of many TFs in yeast are known to have a strong positional preference to occur in a small region in the promoters. This biological knowledge prompts us to develop a novel RS measure that exploits the TFBS location information. The performances of different RS measures are evaluated by the fraction of gene pairs that are co-regulated (validated by literature evidence) by at least one common TF under different RS scores. The experimental results show that the proposed RS measure is the best co-regulation indicator among the six compared RS measures. In addition, the co-regulated genes identified by the proposed RS measure are also shown to be able to benefit three co-regulation-based applications: detecting gene co-function, gene co-expression and protein-protein interactions.

BIOGRAPHY



Tien-Hao Chang received his B.S. (2002), M.S. (2004) and Ph.D. (2006) in Computer Science and Information Engineering from National Taiwan University. Currently he is a Professor of Department of Electrical Engineering, National Cheng Kung University. Dr. Chang focuses on machine learning and Systems Biology and has developed many analytical algorithms for protein/DNA sequences, structures, binding sites and interactions. He has co-worked with researchers in various fields such as computer science, life science, pharmacy and medicine and executed many cross-filed researches. Recently, he has expanded his interest and started to collaborate with specialists of industrial design, business, finance, data science and social science.

Technical Session D1-W1-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Monotonic Feature Selector (MFSelector)

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ABSTRACT

Identification of genes with ascending or descending monotonic expression patterns over time or stages of stem cells is an important issue in time-series microarray data analysis. We propose a method named Monotonic Feature Selector (MFSelector) based on a concept of total discriminating error (DEtotal) to identify monotonic genes. MFSelector considers various time stages in stage order (i.e., Stage One vs. other stages, Stages One and Two vs. remaining stages and so on) and computes DEtotal of each gene. MFSelector can successfully identify genes with monotonic characteristics.

We have demonstrated the effectiveness of MFSelector on two synthetic data sets and two stem cell differentiation data sets: embryonic stem cell neurogenesis (ESCN) and embryonic stem cell vasculogenesis (ESCV) data sets. We have also performed extensive quantitative comparisons of the three monotonic gene selection approaches. Some of the monotonic marker genes such as OCT4, NANOG, BLBP, discovered from the ESCN dataset exhibit consistent behavior with that reported in other studies. The role of monotonic genes found by MFSelector in either stemness or differentiation is validated using information obtained from Gene Ontology analysis and other literature. We justify and demonstrate that descending genes are involved in the proliferation or self-renewal activity of stem cells, while ascending genes are involved in differentiation of stem cells into variant cell lineages.

We have developed a novel system, easy to use even with no pre-existing knowledge, to identify gene sets with monotonic expression patterns in multi-stage as well as in time-series genomics matrices. The case studies on ESCN and ESCV have helped to get a better understanding of stemness and differentiation. The novel monotonic marker genes discovered from a data set are found to exhibit consistent behavior in another independent data set, demonstrating the utility of the proposed method. The MFSelector R function and data sets can be downloaded from: http://microarray.ym.edu.tw/tools/MFSelector/.

BIOGRAPHY

I-Fang Chung received the B. S. and M. S. degrees in control engineering from the National Chiao-Tung University (NCTU), Taiwan, in 1993 and 1995, respectively. He received the Ph.D. degree in Electrical and Control Engineering from NCTU in 2000. From 2000 to 2003, he was a Research Assistant Professor in Electrical and Control Engineering, NCTU. During 2003 to 2004, he worked as a Postdoctoral Fellow in the Institute of Medical Science, the laboratory of DNA Information Analysis of Human Genome Center of Tokyo University in Japan. In 2004, he

joined the Institute of Biomedical Informatics, National Yang-Ming University, Taipei, Taiwan, where, since 2015, he has been a Professor. He is also with the Center for Systems and Synthetic Biology, National Yang-Ming University. His current research interests include bioinformatics, computational intelligence, biomedical engineering, and biomedical signal processing.

Technical Session D1-W2-T2: Medicine and Life Sciences, Biological and Biomedical Sciences

Session Chair

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BIOGRAPHY

Hsueh-Fen Juan was born in 1969, Miao-Li, Taiwan. She received her BS and MS degree in Botany and PhD in Biochemical Sciences from National Taiwan University (NTU) in 1999. She worked as a research scientist in the Japan International Research Center for Agricultural Sciences (Tsukuba, Japan) during 2000-2001 and a postdoctoral research fellow in the Institute of Biological Chemistry, Academia Sinica (Taipei, Taiwan) during 2001-2002.

She started her academic career in the Department of Chemical Engineering, National Taipei University of Technology as an assistant professor and in the Department of Computer Science and Information Engineering at NTU as an adjunct assistant professor in 2002. She moved to NTU in 2004 as an assistant professor in the Department of Life Science and the Institute of Molecular and Cellular Biology. She was promoted to be an associate professor in 2006 and full professor in 2009. Dr. Juan is currently working on cancer systems biology, integrating transcriptomics, proteomics and bioinformatics for biomarker and drug discovery.

Prof. Juan has developed a number of novel methods to advance systems-biology research and applied such approach for drug discovery and elucidating molecular mechanism of drug responses in cancer cells. She has published more than 85 journal papers including prestigious journals such as Briefings in Bioinformatics, Proc. Natl. Acad. Sci. USA, Cancer Research, Nucleic Acids Research, Oncogene, Bioinformatics. She is now the editor of Scientific Reports (Nature Publishing Group), Computational and Mathematical Methods in Medicine (Hindawi Publishing Corporation), PeerJ, PeerJ Computer Science and Stem Cell Treatments (Publisher Frontiers, joining Nature Publishing Group). She also serves as a reviewer of various journals like Molecular and Cellular Proteomics (ASBMB), Proteomics (Wiley-VCH), BMC Bioinformatics, and has organized several international systems biology and bioinformatics symposiums. She is one of the founders of Center for Systems Biology (NTU), and currently the Board Member in The Taiwan Society for Biochemistry and Molecular Biology, Taiwan Proteomics Society, and Taiwan Bioinformatics and System Biology Society. Since Dr. Juan made significant contributions through systems biology approach to development of methodology and cancer therapy; she received the awards “Taiwan's Ten Outstanding Young Persons” (2008), FY2011 JSPS Invitation Fellowship Program for Research in Japan (2011), K. T. Li Breakthrough Award by Institute of Information and Computing Machinery (2012), and National Science Council (NSC) Award for Special Talents of the Colleges (2010-2015).

Technical Session D1-W2-T2: Medicine and Life Sciences, Biological and Biomedical Sciences

The roles of androgens and androgen receptor in stem and progenitor cells for skeletal regeneration

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ABSTRACT

Androgens are required for skeletal growth and development as well as the protection of bone health throughout adult life, and androgen deficiency is a major contributed factor in the development of osteoporosis in patients with male hypogonadism, androgen-insensitive syndromes and castration resistance prostate cancer. There have been considerable advances in our knowledge of how androgens and androgen receptor (AR) signaling, influences bone modeling and remodeling in health and disease. New insights into the function of AR, learned from human genetic mutations and gene targeting mouse models have all contributed to increased understanding of the androgenic effects on bone biology and disease, both in males and females. Studies of untreated and treated osteoporosis in patients with androgen deficiency have also contributed to this knowledge and have provided unequivocal evidence for the potential of androgen therapy to have anabolic effects on skeletal regeneration. Here we summarize and discuss recent findings from the osteoporotic fractures related to androgens status and elucidate the molecular mechanisms of AR signaling in stem/progenitor cells by which the androgenic steroids act as skeletal hormones on bone repair and regeneration. In conclusion, there is compelling evidence that androgens accelerate bone fracture repair thus has the potential to improve the clinical management. Consequently, androgens should not exclusively be regarded as the 'male sex hormones' but as skeletogenic steroids that is required for regeneration in bone defect. The development of selective androgen receptor modulators may has implications for the therapeutic use in bone regeneration and provide a new approach to the prevention of not only osteoporotic fractures, but also a number of other bone diseases related to androgens status.

BIOGRAPHY

Hong-Yo Kang received his B.S. (1991) in Pharmacy and M.S. (1993) in Microbiology from the National Taiwan University. He received his Ph.D. (1999) from the University of Wisconsin, Madison in Endocrinology and Reproductive Physiology, and was a postdoctoral fellow at the University of Rochester till 2000.

He is currently a Professor of the Graduate Institute of Clinical Medical Sciences, Chang Gung University and the Director of the Center for Menopausal and Reproductive Research, Chang Gung Memorial Hospital at Kaohsiung Medical Center. He also serves as an Adjunct Professor in the Department of Biological Sciences, National Sun Yat-Sen University in Taiwan.

His primary research interests are focusing on studying the roles of sex steroid hormones such as androgens in both normal and abnormal development of androgen targeted organs by combining molecular biology and genomics tools, gene targeting mouse models and advanced in vivo imaging technologies. Currently, he has conducted several translational research projects in androgen-related diseases such as male infertility, menopause, osteoporosis, rheumatoid arthritis, prostate cancer and androgenic alopecia by analyzing human sample biopsies. He has published more than sixty (60) papers with a series of editorial and commentary papers presented at international conferences and symposia. He currently served as the primary investigator (PI) of distinguished grant for the potential and outstanding scholars from ministry of science and technology in Taiwan .

Dr. Kang's exceptional achievements have been recognized by many prestigious awards in the world, including the 84th Endocrine Society Young Investigator Award (2002), the Young Investigator Award for 11th International Congress on Hormone steroids and 7th International Congress on Hormones and Cancer (2002), the Young Investigator Award for 1st joint meeting of the International Bone and Mineral Society and Japanese Society for Bone and Mineral Research (2003), the Young Scientist Award for 2nd Scientific Meeting of the Asia Pacific Menopause Federation (2004), the Young Investigator Award for International Osteoporosis Foundation of World Congress on Osteoporosis (2006) and Special Talent Reward in Ministry of Science and Technology (2010-2015).

Technical Session D1-W2-T2: Medicine and Life Sciences, Biological and Biomedical Sciences

Prc contributes to Escherichia coli evasion of classical complement-mediated serum killing

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ABSTRACT

Escherichia coli is a common Gram-negative organism that causes bacteremia. Prc, a bacterial periplasmic protease, and its homologues are known to be involved in the pathogenesis of Gram-negative bacterial infection. The present study examined the role of Prc in E. coli bacteremia, and characterized the ability of the prc mutant of the pathogenic E. coli strain RS218 to cause bacteremia and survive in human serum. The prc mutant of RS218 exhibited a decreased ability to cause a high level of bacteremia and was more sensitive to serum killing compared to strain RS218. This sensitivity was due to the mutant's decreased ability to avoid activation of the antibody-dependent and -independent classical complement cascades, as well as its decreased resistance to killing mediated by the membrane attack complex, the end product of complement system activation. The demonstration of Prc in pathogenic E. coli evasion of classical complement-mediated serum killing makes this factor a potential target for developing therapeutic and preventive measures against E. coli bacteremia

BIOGRAPHY

Dr. Ching-Hao Teng received his bachelor degree from the Department of Veterinary Medicine, National Taiwan University, Taiwan, in 1992. He earned a Ph. D degree in the field of Comparative Biomedical Science, Cornell University, USA, in 2002. After his Ph.D. study, he spent about one year (2002) at the Division of Infectious Diseases, School of Medicine, University of Maryland, as a postdoctoral fellow. Then, he transferred to the Division of Infectious Diseases of the School of Medicine in Johns Hopkins University as a postdoctoral fellow (2002-2005). Dr. Teng has joined the Institute of Molecular Medicine of the National Cheng Kung University medical college, Taiwan, as a faulty since 2005. Currently, he is an associate professor in this institute. Dr. Teng's research interest is to understand the pathogenic mechanisms of bacterial pathogens. He mainly focuses on the neonatal meningitis pathogenic E. coli (NMEC) and uropathogenic E. coli (UPEC).

Technical Session D1-W2-T2: Medicine and Life Sciences, Biological and Biomedical Sciences

Superresolution Mapping Reveals the Molecular Architecture of Primary Cilia

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ABSTRACT

Primary cilia are cellular sensors associated with important signaling pathways including hedgehog signaling and Wnt signaling. Intraflagellar transport is actively regulated to deliver precursors and other molecules in primary cilia. Despite the importance, our knowledge of the ciliary architecture is limited, hindering a structure-based understanding of ciliary functions. Here we reveal the molecular architecture at the base of primary cilia using superresolution microscopy. We found that there are multiple levels of trafficking rests for intraflagellar transport proteins and transmembrane proteins, suggesting the gating regulation at the ciliary base is performed at different resting sites upon the architecture of primary cilia.

BIOGRAPHY

Dr. Liao is an associate research fellow at the Institute of Atomic and Molecular Sciences, Academia Sinica since 2014. Before joining Academia Sinica, he was an assistant professor at Columbia University from 2008 to 2013. Dr. Liao received his PhD degree from MIT. He did his postdoctoral research at University of California, Berkeley and served as a research associate at Stanford University before being a faculty member at Columbia University. His lab focuses on primary cilium studies and superresolution microscopy. Dr. Liao has been invited to serve as a leading coordinator of the Biomolecular Motors Theme in the First Thematic Conference on Multiscale Methods and Validation in Medicine and Biology, a leading organizer of the Multiscale Modeling and Simulation Meeting in the Pacific Symposium of Biocomputing, a chair in the Protein Structure and Allosteric Communication Platform of the Biophysical Society Meeting, and a guest editor of the Special Issue: Biomolecular Motors and Motor Assemblies of the Cellular and Molecular Bioengineering journal. Recently, he has been recognized as one of the leading young investigators in superresolution imaging and primary cilium studies, serving as a chair of the Optical Microscopy & Super Resolution Imaging Platform in the Biophysical Society 2014 Annual Meeting, a session chair of the FASEB Science Research Conference on Biology of Cilia and Flagella in 2013, a chair of the Cell and Bacterial Mechanics & Motility Platform of the Biophysical Society 2012 Annual Meeting, and a chair of the Cellular and Subcellular Imaging Platform of the Biomedical Engineering Society Meeting in 2011.

Technical Session D1-W2-T2: Medicine and Life Sciences, Biological and Biomedical Sciences

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ABSTRACT

Diabetic nephropathy (DN) is the leading cause of end-stage renal disease in many countries. The animal models that recapitulate human DN undoubtedly facilitate our understanding of this disease and promote the development of new diagnostic markers and therapeutic interventions. Based on the clinical evidence showing the association of eNOS dysfunction with advanced DN, we have created diabetic mice that lack eNOS expression in Akita mice and streptozotocin-induced type 1 diabetic mice and shown that eNOS-deficient diabetic mice exhibit advanced nephropathic changes with distinct features of progressive DN, including pronounced albuminuria, nodular glomerulosclerosis, mesangiolysis, and arteriolar hyalinosis. These studies clearly defined a critical role of eNOS in DN and developed a robust animal model of this disease, which enables us to study the pathogenic mechanisms of progressive DN. Further, we found that miR-200a plays a key role in the regulation of eNOS expression. Increased miR-200a resulted in decrease of eNOS expression. Thus, the findings that the novel mechanisms by which eNOS deficiency causes advanced DN and provided the new insight into the pathogenesis of DN.

BIOGRAPHY

Chih-Hong Wang received his B.S. (1996) and M.S. (2000) in Biochemistry from the National Chung-Hsin University. He received his Ph.D. (2010) from the University of North Carolina at Chapel Hill (UNC), in Department of Molecular and Pathology, and was a postdoctoral fellow at the University California, San Diego (UCSD) between 2010 and 2012. Currently he is an Assistant Professor of Department of Biological Science of Technology at National Chiao Tung University.

Dr. Wang's research focuses on MicroRNAs in diabetes and obesity-induced gastrointestinal cancer because diabetes and obesity have been known to increase hepatocellular carcinoma (HCC) risk by up to 4.5-fold, and pancreatic ductal adenocarcinoma (PDAC) by 2.6 fold. The importance of microRNAs in cancer and metabolic syndrome have been underlined by the identification of alterations in microRNA target binding sites. Dr. Wang have identified Let-7 which plays an important for inhibition of IL-6 and miR-200a in diabetic nephropathy. He has authored eleven publications on these topics.

Technical Session D1-W3-T2: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Session Chair

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BIOGRAPHY

Dr. Fan-Gang Tseng received the B.S. degree in Power Mechanical Engineering from National Tsing Hua University at Taiwan in 1989, and the M.S. degree from the Institute of Applied Mechanics in National Taiwan University at Taiwan, in 1991. In 1998, he received his Ph.D. degree in mechanical engineering from the University of California at Los Angeles, USA (UCLA), under the supervision of Prof. C.-M. Ho and C.-J. Kim. He jointed Engineering and System Science Department of National Tsing-Hua University at Taiwan as an Assistant Professor in August 1999, and was advanced to Associate Professor in August 2002, Professor in August 2006, as well as Distinguished Professor in August 2015. He served as the ESS department chairman from 2010 to 2013 and Associate Vice President of NTHU in global affair from 2013 to 2014, and has been the Deputy Director of the Biomedical Technology Research Center of NTHU since 2009. He has been elected a fellow of ASME in March 2014. His research interests are in the fields of Nano-Biosensors, Bio-MEMS, Micro Fuel Cells, and Nano/Micro-Fluidic Systems. He received 40 patents, wrote 7 book chapters, published more than 150 SCI Journal papers and 330 conference technical papers in Biosensors, Bio-N/MEMS, Micro Fuel Cells, and Micro/Nano Fluidics related fields, and co-organized or co-chaired many conferences including IEEE MEMS, IEEE NEMS, IEEE Transducers, Micro TAS, ISMM, IEEE Nano, and IEEE Nanomed. He received several awards, including Outstanding in Research Awards (2010, 2014) and Mr. Wu, Da-Yo Memorial Award (2005) from MOST Taiwan, two National Innovation Awards (2010, 2014), ten Best Paper/Poster awards (1991, 2003, 2004, 2005, 2008, 2010, 2012, 2013, 2014), and others.

Technical Session D1-W3-T2: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Diffuse Optical Tomographic System

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ABSTRACT

Interest has been growing rapidly in various imaging modalities of optical tomography (OT) since computed tomography (CT) apparatus was first introduced in the 1970s. OT systems using non-radioactive sources can be built at relatively low cost. Diffuse optical tomography (DOT) providing functional information related to tissues has drawn great attention for the last two decades. Developed techniques include mainly estimating in the near-infrared (NIR, wavelength 650-950 nm) the distribution of optical properties and their changes within a tissue volume, and then relate to spatial variations of physiological parameters such as hemoglobin concentration and oxygen saturation. A wide range of applications has been explored, such as brain, breast, forearm, and hand joint, etc.

This session "Diffuse Optical Tomographic System" aims to briefly present the basic principles of optical property image reconstruction through inverse problems based on diffusion equation. In order to obtain real computed absorption (ma) and scattering (ms') coefficients, system calibration issues are addressed including the calibration tasks on opto-electrical measuring components, measurement-to-computation, and numerical quantities in computation. Multi-wave length NIR data acquiring to deliver functional images of hemoglobin concentration and oxygen saturation is discussed. Two scanning architectures, parallel scanning (compression type) and ring scanning (prostrate type), for DOT imaging are presented in the talk; besides, the clinical trials of parallel scanning module associated with a GE mammographic system are shown.

BIOGRAPHY

Dr. Min-Chun Pan was born in Kaohsiung, Taiwan. He received his Ph.D. degree in mechanical engineering from the Katholieke Universiteit Leuven, Belgium, in May 1996. The major field of study focused on signal analysis and machine condition monitoring / fault diagnostics.

In 1996, he worked as a Senior Researcher at the Sanyang Industry Corporation, and meanwhile, a Junction Associate Professor at the Department of Forensic Science, Central Police University, Taiwan. After a two-and-half-year career in the industry, in 1999 he joined the Department of Mechanical Engineering (ME Department) at the National Central University (NCU), Taoyuan Taiwan, as an Assistant

Professor. He has been an Associate Professor and full Professor with both the ME Department and the Graduate Institute of Biomedical Engineering (GIBE), NCU, since 2003 and 2007, respectively. From 2010/8 to 2013/7, he served as the director of GIBE, NCU.

Dr. Pan has been the member of professional societies ASME, IEEE, OSA and SPIE. He was the recipient of 2010 the 7th National Innovation Award "Diffuse Optical Tomographic Imaging Technology," the recipient of silver medal "Order Tracking Technology of Rotary Machinery" in 2012 Taipei Int'l Invention Show & Technomart, and the recipient of gold medal "Apparatus and Method of Irregular Bone Defect Detection of Dental Implant" and silver medal "Highly-Efficient Ultrasonic Ink-jet Head and Fabrication Method for the Same" in 2010 Taipei Int'l Invention Show & Technomart. He has published 59 peer-reviewed journal papers and over 120 international and domestic conference papers so far. His research interests are in the areas of diffuse optical tomographic system, medical devices design, biomedical/mechanical signal processing, sensing technology, and machine fault diagnostics, etc.

Technical Session D1-W3-T2: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

A label-free electrochemical impedimetry-based affinity biochip integrated with the AC electrokinetic mixer

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ABSTRACT

Using immunoreaction or DNA hybridization to specifically detect important biomarkers, hazardous chemicals, toxics and pathogens is a cost-effective and inexpensive method, compared with conventional analytical instruments. For example, the determination of specific nucleic acid sequences originating from organisms has attracted widespread interest for use in diagnostic applications, including the detection of food contamination, the identification of pathogenic species and the recognition of genetic diseases. In order to quantify the analyzed concentration, different sensing methodologies, such as optics, radiology and electrochemistry, are developed by using optical, isotopic or electroactive labels. In contrast, label-free methods, such as quartz crystal microbalance, surface plasmon resonance spectroscopy, mass-sensitive cantilever [3] and electrochemical impedance spectroscopy (EIS), promise easy, fast and cost-effective detection. Among the label-free methods, EIS-based biosensors exhibit several advantages, including good compatibility with electrical instruments and ease of large-scale production, making them well-suited for use in miniature diagnostic systems. In the presentation, the design and performance of label-free EIS-based immunosensors will be introduced and the detection of drug residue, such as enrofloxacin, salbutamol and FK506, was taken as an example.

Although label-free affinity biosensors can significantly simplify the detecting procedures, the hybridization process still takes one or more hours in stationary solutions. The long hybridization time is mainly due to the Brownian motion of nanometer-scale agents, moving stochastically toward the antibodies or probe DNA (pDNA) immobilized on the sensor surface. Furthermore, the lower the analyte concentration is, the smaller the diffusive flux of analytes toward the immobilized affinity receptors becomes, thus resulting in longer hybridization times and lower binding densities when detecting lower analyte concentrations.

In our studies, an DC-biased AC electrokinetic vortex was integrated with the label-free EIS-based biosensing chip to enhance and fasten the immunoreaction and DNA hybridization. The DC-biased AC electroosmotic (ACEO) stirring using concentric double ring-single disk electrodes was proved to greatly promote the hybridization efficiency of 20-base target DNA (tDNA) fragments. The +0.7 V-biased ACEO flow of 3 Vpp and 380 Hz applied at the outer ring electrode (ORE) and inner ring electrode (IRE) can drive the tDNA-containing 1 mM Tris solution from the ORE to the pDNA-modified central disk electrode (DE) to achieve 90% saturation hybridization within 141 s. The DNA biosensor, respectively using Pd-deposited ORE and IRE as the pseudo-reference electrode and the counter electrode for on-chip-type three-

electrode EIS measurement, presented good linearity and repeatability in the range of 1 aM–10 pM and exhibited an ultrasensitive detection limit of 0.5 aM. The label-free EIS-based DNA sensing chips with integrated DC-biased ACEO vortex can achieve rapid hybridization, high selectivity and ultrasensitive detection for different tDNA samples.

BIOGRAPHY

Ching-Chou Wu was born in Tainan prefecture, Taiwan, R.O.C on September 03 1972. He obtained a Bachelor degree of Biomedical Engineer in bioelectronics division, the Department of Biomedical Engineering, Chung-Yuan Christian University, Taiwan in June 1994, a master degree of Biomedical Engineer in neuroscience division, the Institute of Biomedical Engineering, Chung-Yuan Christian University, Taiwan in July 1996, and a Ph.D. degree of Biomedical Engineer in the division of electrochemical biosensors, the Institute of Biomedical Engineering, National Cheng Kung University, Taiwan, in July 2003.

After finishing Ph.D. program, he worked as a post-doctoral fellow in Prof. Matsue's laboratory, Graduate School of Science, Tohoku University, Japan from November 2003 to January 2015. Afterwards, he returned to Taiwan to be an assistant professor in the Department of Bio-industrial Mechatronics Engineering, National Chung Hsing University, Taiwan, in February 2005. He promoted the academic position to associate professor in August 2010 and to professor in February 2014. He published more than 36 regular papers, three books (3 chapters) and eight patents. His current interest is the fabrication and integration of electrochemical microsensor with an electrokinetic microfluidic system in biomedical applications, such as cell-based chips, capillary electrophoresis microchip and affinity-based lab-on-a-chip.

Prof. Wu obtained a Distinguished Lectureship Award of Chemical Society of Japan (2008), Distinguished Paper Award of Association of Chemical Sensors in Taiwan (2012, 2013), Young Scholar Innovative Competition Award of Taiwan Comprehensive University System (2013) and a Best Poster Award Winner in 65th Annual Meeting of International Society of Electrochemistry (2014). Moreover, Prof. Wu is the senior member of Association of Chemical Sensors in Taiwan (ACST), Taiwanese Society of Biomedical Engineering (TSBME) and International Society of Electrochemistry (ISE). He is also the executive committee and vice executive director of ACST and responsible for the Biosensor and Chemical Sensor Technology Consortium.

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3. M-Y Lee , S-J Ding, C-C Wu*, J Peng*, C-T Jiang, C-C Chou, (2015) Fabrication of nanostructured copper phosphate electrodes for the detection of α-amino acids, Sensors & Actuators: B. Chemical 206, 584-591.

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6. L-C Chen, C-C Wu*, R-G Wu, H-C Chang, (2012) Electroosmotic Flow Control in Microfluidic Chips Using a Self-Assembled Monolayer as the Insulator of a Flow Field-Effect Transistor, Langmuir, 28, 11281–11285.

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Technical Session D1-W3-T2: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Bioinspired Conducting Polymers to Selectively Couple PC12 Cells

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ABSTRACT

Interfacing materials with cells through specific ligand/receptor interactions, matching mechanical properties, and matching nanostructures are very critical in biomedical technologies. Recently, conducting polymers have emerged for various related applications, ranging from biosensing to medical bionics. Many features of conducting polymers, including simplicity for nanostructure fabrication, tailored functional groups for bioconjugation, intrinsic electrical conductivity, and soft mechanical properties, provide advantages as biomaterials for cell-related diagnostic and therapeutic platforms as well as cell engineering. These features are especially valuably for electro-active cells, such as neurons. In this talk, I would like to introduce our research on developing functionalized poly(3,4-ethylenedioxythiophenes) (PEDOTs), which specifically target neural engineering.

Nerve injury and disorder can cause significant losses of mobility and physical function. Several neuroprosthetics have been developed to replace damaged motor, sensory, or cognitive modality, thereby to recover body functions. Although certain success has been achieved, the application of such platforms faces many challenges, including invasiveness, implant and re-implant induced injury, host–interface response occurring upon implanting. For this purpose, we developed a series of biomimetic conducting polymers with zwitterionic and cell targeting groups, which allows us to specifically interact with PC12 cells without non-specific adsorption of proteins. The introduction of stimuli-responsive bio-conjugation linkage enables a stimuli-responsive platform. The function of controlled cell attachment/release could be used for building noninvasively removable bioelectronics or for tissue engineering applications. Besides, the polymers displayed low impedance at low frequency range, which is ideal for providing electrical communication and stimulation on attached cells. As a result, the controlled cell attachment/release function and electrical communication with cells are achieved cooperatively from our biomimetic conducting polymers.

BIOGRAPHY

is a native Taiwanese. He received his B.S. (in Chemistry) and M.S. (in Materials Science and Engineering) from National Taiwan University in 1996 and 1998, respectively. He then went to United States in 2001 and received his Ph.D. degree (in Materials Science and Engineering) from the University of Florida in 2005. His current research interests include organic conducting systems, such as biointerfaces, bioelectronics, biosensors, and stimuli-responsive materials.

He did his postdoctoral research at Institute of Bioengineering and Nanotechnology in Singapore starting from 2006 to 2009. He then joined RIKEN in Japan as a research scientist from 2009 to 2013. In August of 2013, he received an offer National Cheng Kung University to join the Department of Materials Science and Engineering as an assistant professor. In 2015, he decided to move back his hometown and contribute to his alma mater-- National Taiwan University. He is currently an assistant professor in the Department of Materials Science and Engineering.

Dr. Luo has published more than 30 papers. Because of his achievement in the field of conductive biointerfaces, in 2013, he was invited to be as a guest editor of a top journal in polymer science, Polymer Reviews, to organize a special issue “conducting polymers as biomaterials and biointerfaces”.

Technical Session D1-W3-T2: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

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ABSTRACT

BIOGRAPHY

Technical Session D1-W4-T2: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Session Chair

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BIOGRAPHY

Technical Session D1-W4-T2: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Convex Geometric Analysis for Non-negative Blind Source Separation

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ABSTRACT

Despite the tremendous advances made in imaging methodologies and equipment, often most of the real world observations are mixtures of the true sources. Blind Source Separation (BSS) is a signal processing methodology to extract the source signals from the mixed observations, devoid of (or with very limited) prior knowledge about the source natures and mechanisms of how those source signals are mixed in the observations. Inherently, many of the real world source signals and their mixtures are non-negative in nature (e.g., imaging applications such as biomedical imaging and hyperspectral imaging, micro-array data etc.), thereby naturally leading to a specific class of BSS, namely non-negative BSS (nBSS). Till date, many useful nBSS algorithms, centered around non-negative independent component analysis (nICA) and non-negative matrix factorization (NMF), have been reported. Originated from philosophies that are different from successfully developed nICA and NMF algorithms, there is a branch of nBSS methods exploiting intrinsic exquisite structural features of the mixtures characterized by convex geometry (CG). In this talk, we intend to give a historical review of nBSS methods, and present some representative and state-of-the-art CG-based nBSS algorithms in a unified perspective manner, together with experimental results for some practical applications. Finally, we conclude with the research trend of nBSS for solving hidden challenges and bottlenecks in related science and engineering applications.

BIOGRAPHY

Chong-Yung Chi received the Ph.D. degree in Electrical Engineering from the University of Southern California, Los Angeles, California, in 1983. From 1983 to 1988, he was with the Jet Propulsion Laboratory, Pasadena, California. He has been a Professor with the Department of Electrical Engineering since 1989 and the Institute of Communications Engineering (ICE) since 1999 (also the Chairman of ICE during 2002-2005), National Tsing Hua University, Hsinchu, Taiwan. He has published more than 200 technical papers, including more than 75 journal papers (mostly in IEEE Trans. Signal Processing), 4 book chapters and more than 130 peer-reviewed conference papers, as well as a graduate-level textbook, Blind Equalization and System Identification, Springer-Verlag, 2006. His current research interests include signal processing for wireless communications, convex analysis and optimization for blind source separation, biomedical and hyperspectral image analysis.

Dr. Chi is a senior member of IEEE. He has been a Technical Program Committee member for

many IEEE sponsored and co-sponsored workshops, symposiums and conferences on signal processing and wireless communications, including Co-organizer and General Co-chairman of 2001 IEEE Workshop on Signal Processing Advances in Wireless Communications (SPAWC), and Co-Chair of Signal Processing for Communications (SPC) Symposium, ChinaCOM 2008 & Lead Co-Chair of SPC Symposium, ChinaCOM 2009. He was an Associate Editor (AE) of IEEE Trans. Signal Processing (5/2001~4/2006), IEEE Trans. Circuits and Systems II (1/2006-12/2007), IEEE Trans. Circuits and Systems I (1/2008-12/2009), AE of IEEE Signal Processing Letters (6/2006~5/2010), and a member of Editorial Board of Signal Processing (6/2005~5/2008), and an editor (7/2003~12/2005) as well as a Guest Editor (2006) of EURASIP Journal on Applied Signal Processing. He was a member of Signal Processing Theory and Methods Technical Committee (SPTM-TC) (2005-2010), IEEE Signal Processing Society. Currently, he is a member of Signal Processing for Communications and Networking Technical Committee (SPCOM-TC) and a member of Sensor Array and Multichannel Technical Committee (SAM-TC), IEEE Signal Processing Society, and an AE of IEEE Trans. Signal Processing.

Technical Session D1-W4-T2: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Design and Implementation of Physical Sensing and Fuzzy Control for Dynamic Shuttle Walking Exercise

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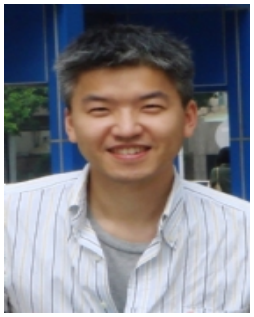
ABSTRACT

Chronic obstructive pulmonary disease (COPD) is a chronic inflammatory disease of the airways characterized by progressive downhill of the lung functions and frequent systemic involvement. The most recent international treatment guideline suggests that early introducing of pulmonary rehabilitation (PR) and pharmacological management may help improve the quality of life and reduce the frequency of acute exacerbation. PR includes exercise training and breathing training for patients with COPD. Since exercise training is a crucial component of PR, we develop an approach with calibration, rehabilitation, artifact/safety monitoring, and endpoint decision to perform adaptive subject exercise training and monitoring with fuzzy logic control and wireless sensor networking. This talk will introduce an exercise training model with overload principle and safety concern. To show the correctness and effectiveness of the proposed protocol, the system performance is examined through case studies prototype implementation. The experimental results show that the proposed scheme has better capability to adjust the exercise training level and is promising to efficiently put exercise training into practice for home-based rehabilitation.

BIOGRAPHY



Chih-Yu Wen (S'03–M'05–SM'15) received the B.S.E.E. and M.S.E.E. degrees in electrical engineering from National Cheng Kung University, Tainan, Taiwan in 1995 and 1997, respectively. He also received the M.S.E.E. degree and the Ph.D. degree in electrical engineering from the University of Wisconsin-Madison, USA, in 2002 and 2005, respectively.

He served in the R.O.C. Marine Corps at the rank of second lieutenant from 1997 to 1999. He joined the Department of Electrical Engineering at National Chung Hsing University, Taichung, Taiwan in 2006, where he is now a Professor. His current research interests include wireless communications, biomedical signal processing for health monitoring, software-defined radio, and distributed networked sensing and control. He has held eight Taiwanese invention patents in pervasive healthcare.

Prof. Wen is a senior member of IEEE Communication Society, a senior member of IEEE Signal Processing Society, and a member of Chinese Institute of Engineers. He received the Excellent Teaching Award – Department of Electrical Engineering in 2012, the Outstanding Mentor

Award – College of Engineering in 2013, and the Outstanding Young Investigator Award – National Chung Hsing University in 2014.

Technical Session D1-W4-T2: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Next Generation Mission-Critical Machine-to-Machine Communications: Opportunities and Challenges

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ABSTRACT

There are explosive growth in the number of IoT (Internet of Things) devices. Long Term Evolution(LTE) is prospering as one of the promising mobile communication systems. LTE-based M2M communications have become an important research topic. There are several advantages using cellular wireless M2M (machine-to-machine) connectivity to serve IoT devices. In the next generation cellular wireless networks (also know as 5G wireless), machine-to-machine communications will play a key role. Based on ITU study, 5G wireless is aimed to enable three types of services: enhanced mobile broadband communications, massive machine type communications (or massive M2M) , and ultra-reliable and low latency communications (mission-critical M2M). In this talk, opportunities and design challenges of mission-critical M2M communications will be discussed. Mission-critical M2M communications will play a key role for the future medical IoT services, and low-latency smart city applications.

BIOGRAPHY

Hung-Yu Wei is a Professor in Department of Electrical Engineering and Graduate Institute of Communications Engineering, National Taiwan University. He received the B.S. degree in electrical engineering from National Taiwan University in 1999. He received the M.S. and the Ph.D. degree in electrical engineering from Columbia University in 2001 and 2005 respectively. He was a summer intern at Telcordia Applied Research in 2000 and 2001. He was with NEC Labs America from 2003 to 2005. He joined Department of Electrical Engineering at the National Taiwan University in July 2005. His research interests include wireless mesh networks, mobility management in mobile Internet, sensor networks, cross-layer design and optimization in wireless multimedia communications, and game theoretical models for communications networks.

Dr. Wei received NTU Excellent Teaching Award in 2008. He also received "Recruiting Outstanding Young Scholar Award" from the Foundation for the Advancement of Outstanding Scholarship in 2006, K. T. Li Young Researcher Award from ACM Taipei/Taiwan Chapter and The Institute of Information and Computing Machinery in 2012, Ministry of Science and Technology Research Project for Excellent Young Scholars in 2014, Excellent Young Engineer Award from the Chinese Institute of Electrical Engineering in 2014, and Wu Ta You Memorial

Award from MOST in 2015.He has been actively participating in NGMN, IEEE 802.16 and 3GPP standardization, and was a voting member of the IEEE 802.16 working group.

Technical Session D1-W4-T2: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Design and Implementation of a Low-Complexity O-QPSK Transceiver with Spatial Modulation for Wireless Sensor Networks

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ABSTRACT

Since the design of sensor nodes is energy-limited, how to prolong the lifetime of a wireless sensor network is an important issue. Extended from the specifications of IEEE 802.15.4, a low-complexity transceiver that is capable of offering various data rates is designed and developed. 2x2 Spatial modulation is also incorporated in one of the operation modes. The proposed communication system then supports data rates from 250Kbps to 3Mbps, covering the majority of applications in wireless sensor networks. To be operated in low-cost and low signal-to-noise ratio (SNR) scenarios, robust symbol timing detection and carrier frequency offset (CFO) tracking mechanisms are designed. In addition, the start-of-frame delimiter (SFD) field of the packet format is revised so that the receiver can realize if the maximum likelihood detection of the spatial modulation should be activated or not. Finally, the architecture of the transmitter and receiver is designed to achieve low complexity. Simulation results are also provided to demonstrate the system performance.

BIOGRAPHY

{Pei-Yun Tsai} (S'02-M'06) received her B.S., M.S., and Ph.D. in electrical engineering from the National Taiwan University, Taipei, Taiwan in 1994, 1996, and 2005, respectively. From 1996 to 2000, she worked at ASUStek in Taipei and participated in the team of optical storage systems. She is now an associate professor of Department of Electrical Engineering at National Central University, Taoyuan, Taiwan. She is the co-author of two books, OFDM Baseband Receiver Design for Wireless Communications (Wiley 2007) and Baseband Receiver Design for Wireless MIMO-OFDM Communications (Wiley 2012).

Prof. Tsai has received the Acer Longtern Award and 1st Asian Solid-State Circuit Conference Student Design Contest Outstanding Award in 2005. She has also received MXIC Golden Silicon Award in 2005 and 2010. Her research interests include baseband signal processing algorithms and VLSI design for digital communication systems.

Day 2 (October 25, 2015)

Panel Discussions - Big Data Analytics, Data Science and Machine Learning: Challenges and Opportunities

Moderator and Panelist

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BIOGRAPHY

Hsuan-Cheng Huang received his B.A., M.A., and Ph.D. degrees in physics from National Taiwan University in 1992, 1994 and 1998, respectively. He was engaged in experimental high-energy physics research at Taiwan and at High Energy Accelerator Research Organization, Japan, and awarded NSC Distinguished Postdoctoral Fellowship in 2003. Encouraged by the emerging of systems biology, Dr. Huang joined National Yang-Ming University in 2004 and is currently a Professor and the Director of the Institute of Biomedical Informatics, also affiliated with the Center for Systems and Synthetic Biology. In 2007, he received the NSC Wu Ta-You Memorial Award, an honor for excellent young investigators in Taiwan. Now he serves as an Editorial Board Member of Scientific Reports, an Associate Editor and Deputy Section Editor of BMC Systems Biology, and an Executive Board Member in Taiwan Society of Evolution and Computational Biology. His research interests include bioinformatics, computational and systems biology, and network biology. Currently, Dr. Huang endeavors his research efforts to computational analysis and modeling of biological networks, and applies them to unravel molecular mechanisms of cancer cell response, non-coding RNA regulation, as well as other biological processes..

Panel Discussions - Big Data Analytics, Data Science and Machine Learning: Challenges and Opportunities

Panelist

Yu Shyr

Harold L. Moses Chair in Cancer Research
Director, Vanderbilt Center for Quantitative Sciences
Director, Vanderbilt Technologies for Advanced Genomics Analysis and Research Design
Professor of Biostatistics, Biomedical Informatics, and Cancer Biology
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BIOGRAPHY

Yu Shyr received his bachelor's degree in statistics from Tamkang University in Taiwan in 1985 and received his master's degree in statistics from Michigan State University, East Lansing, Michigan, USA, in 1989. He then received his Ph.D. in biostatistics from the University of Michigan, Ann Arbor, Michigan, USA, in 1994. He subsequently joined the faculty at Vanderbilt University School of Medicine in Nashville, Tennessee, USA.

At Vanderbilt, he has collaborated on numerous research projects; assisted investigators in developing clinical research protocols; collaborated on multiple grants funded through external peer-reviewed mechanisms; and developed biostatistical and bioinformatic methodologies for clinical trial design, high-dimensional data preprocessing, estimating relative potency in a parallel line bioassay, and other statistical and bioinformatic approaches, published in journals such as Nature, NEJM, JAMA, Cell, Lancet, Nature Medicine, Nature Protocol, Statistics in Medicine, Bioinformatics, Clinical Trials, Computational Statistics and Data Analysis, and BMC Bioinformatics. He is currently the Harold L. Moses Chair in Cancer Research, Director of the Vanderbilt Center for Quantitative Sciences (CQS), and the Director of the Vanderbilt Technologies for Advanced Genomics Analysis and Research Design (VANGARD). He serves as a professor of biostatistics, biomedical informatics, cancer biology, and health policy. His current research interests focus on developing statistical bioinformatics methods for analyzing next-generation sequencing data, including a series of papers on estimating the sample size requirements for studies conducting RNA sequencing analysis.

Dr. Shyr is a Fellow of the American Statistical Association and the US Food and Drug Administration advisory committee voting member. He has served as a member of the US National Cancer Institute (NCI) Developmental Therapeutics Study Section and the Population and Patient-oriented Training subcommittee; he also has served on numerous NIH/NCI SPORE, P01, and CCSG review panels/committees, as well as the epidemiology section of the U.S. Army Medical Research and Materiel Command Breast Cancer Research Program (BCRP). Dr. Shyr has presented as an invited faculty member in the ASCO Educational Section on Advanced Concepts in Clinical Trial Design and Methodology and he is the co-course director for the AACR/ASCO Methods in Clinical Cancer Research Vail Workshop. In

addition to this, he has prepared statistical workshops worldwide and presented them in countries, such as, Belgium, The Netherlands, Germany, Austria, Taiwan, Japan, China, Saudi Arabia and Malaysia. He currently serves on 13 external advisory boards for university and medical center institutions and is a member of the editorial board for the Journal of Clinical Oncology, Clinical Cancer Research, Cancer and Cancer Prevention Research Journal, the ASCO's Cancer Research Committee, and he is the associate editor for JAMA Oncology. He directs the biostatistics and bioinformatics cores for the NCI-funded Vanderbilt University Breast Cancer SPORE, GI Cancer SPORE, and other program projects, and he is the principle investigator of the NCI U01 grant of Barrett's esophagus translational research network coordinating center (BETRNetCC). To date, he has delivered more than 200 abstracts at professional meetings and has published more than 375 peer-reviewed papers in a variety of high-impact journals.

Panel Discussions - Big Data Analytics, Data Science and Machine Learning: Challenges and Opportunities

Panelist

Hirotada Mori

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BIOGRAPHY

Name: Hirotada Mori
Birth: Kyoto, Japan 1956. Feb. 5

Education and degrees:

Dept. Agriculture, Kyoto Univ. Kyoto, Japan	BS	1980	ecology
Dept. Science, Kyoto Univ. Kyoto, Japan	MS	1985	biophysics
Dept. Science, Kyoto Univ. Kyoto, Japan	PhD	1989	biophysics

Job Career:
1. Assistant Researcher, 1985/4-1985/10, Shiga Medical University
2. Assistant Researcher, 1985/11-1989/9, Medical Department, Kumamoto University
3. Assistant Researcher, 1989/10 – 1993/4, Research Center for Virus, Kyoto University
4. Associate Professor, 1993/5 – 1996/3, Bioinformatics, Research and Education Center for Genetic Information, Nara Institute of Science and Technology
5. Professor, 1996/4- present, Systems Microbiology, Graduate School of Biological Sciences, Nara Institute of Science and Technology
6. Professor, 2001/4- 2011/3, Institute for Advanced Biosciences, Keio University

Research interest:

My major research interest is to elucidation of relationships between genes so-called "network biology" in the field of systems biology. Research direction is focusing more fundamental biology using *Escherichia coli K-12*. My research career in this field started in 1989, when the Japanese E. coli genome project launched, and since then I have always been focusing on the biology on global aspect. After completion of genome sequencing, we started to construct comprehensive experimental resources, such as ORF plasmid clone library and single gene deletion library for making systematic and comprehensive analyses possible for this well studied bacterium. Using such comprehensive resources, our first target was the construction of DNA microarray and transcriptome analysis using those. Our research activities were expanding variety of omics approaches, such as proteomics for comprehensive protein-protein interaction, metabolomics to measure and analyze central metabolic pathway quantitatively and currently focusing on genetic interaction by synthetic lethal/sickness analysis using double knockout strains.

Honors:
1. 2009 Jan. Fellow, American Academy for Microbiology, USA
2. 2010 Mar. Fellow, The Royal Society of Chemistry, UK

Memberships in professional societies:

1. The Molecular Biology Society of Japan
2. The Biophysical Society of Japan
3. Society of Genome Microbiology, Japan
4. American Society for Microbiology
5. Editor for BMC Microbiology

Publication (Major 10 papers):

1. Otsuka, Y., Muto, A., Takeuchi, R., Okada, C., Ishikawa, M., Nakamura, K., Yamamoto, N., Dose, H., Nakahigashi, K., Tanishima, S., Suharnan, S., Nomura, W., Nakayashiki, T., Aref, W.G., Bochner, B.R., Conway, T., Gribskov, M., Kihara, D., Rudd, K.E., Tohsato, Y., Wanner, B.L. & Mori, H. GenoBase: comprehensive resource database of Escherichia coli K-12. Nucleic Acids Res 43, D606-17 (2015).
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Panel Discussions - Big Data Analytics, Data Science and Machine Learning: Challenges and Opportunities

Panelist

Chien-Yu Chen

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BIOGRAPHY

Dr. Chien-Yu Chen (1974 ~) is currently a professor of department of Bio-Industrial Mechatronics Engineering, National Taiwan University. She holds a B.S. degree of Electrical Engineering from National Taiwan University (1996), a M.S. degree of Electrical Engineering from Stanford University (1998), and a Ph.D degree of Computer Science and Information Engineering from National Taiwan University (2003). During the Ph.D program, she initiated the research of Bioinformatics, and has mainly focused on developing algorithms for studying molecular biology. She has been an Assistant Professor of Graduate School of Biotechnology and Bioinformatics in Yuan Ze University from Feb. 2004 to July 2005, where she began her academic career.

As a computational biologist, her research centers on two problems: sequence analysis and expression data analysis. On sequence analysis, the research topics span several effective sequence-based methods for predicting protein functional sites associated with protein-DNA interactions, protein-ligand interactions, and protein-protein interactions. The basic idea behind those prediction methods is exploiting pattern mining technology in finding concurrent conserved regions among protein families. For another research topic, expression data analysis, she utilizes the state of the art clustering and classification techniques on microarray or RNA-seq datasets for patient outcome prediction, time-course data analysis, and association discovery. Moreover, she applies pattern mining skills to identifying transcription factor binding sites directly from ChIP-chip or ChIP-seq data and combines expression data for constructing regulatory networks.

Panel Discussions - Big Data Analytics, Data Science and Machine Learning: Challenges and Opportunities

Panelist

Aichi Chien

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BIOGRAPHY

Aichi Chien, Ph.D. is an Associate Professor in the Department of Radiological Sciences and the Biomedical Physics IDP Graduate Program in the UCLA Medical School since 2009; a faculty member of Medical School Short Term Training Program (SSTP) and Cross-disciplinary Scholars in Science and Technology (CSST) program since 2010, and faculty in the UCLA Center for Domain Specific Computing (CDSC) since 2011.

Dr. Chien received her Bachelor's Degree from National Taiwan University, Dept. of Agricultural Machinery Engineering in 1999, Taipei, Taiwan. She then completed her Master's Degree on the subject of Micro/Nano Resonators in the Dept. of Mechanical and Aerospace Engineering, Cornell University, Ithaca, NY; and her PhD Degree in Biomedical Engineering at the University of California, Los Angeles, CA on the topic of MEMS/NEMS implantable devices for cardiovascular disease. She went on to complete Postdoctoral Fellowship training in endovascular treatment in the Division of Interventional Neuroradiology in the UCLA David Geffen School of Medicine.

Dr. Chien's research interests include cerebral vascular disease and treatment effectiveness analysis, and encompass the integration of science and engineering for clinical decision-making and individualized medicine. Her research broadly impacts the medical community and medical device industry. Her research has been featured in various news, including Fierce Medical Devices, Interventional News, Endovascular Today, and Neuro News. She has published more than 70 peer-reviewed publications of original research in high impact factor medical journals such as Stroke, Journal of Vascular and Interventional Radiology, Neurosurgery, Journal of Neurosurgery, and American Journal of Neuroradiology, including 22 papers as first author. She has received many awards, including the Brain Aneurysm Foundation Research Grant Award, the SIR Ring Career Development Award, the Cerebrovascular Research Award from The Aneurysm and AVM Foundation, the Bee Foundation Medical Research Award, the American Heart Association Outreach Award, Heart Failure Society of America Award, and Young Investigator Award from the Cardiovascular System Dynamics Society. She is also the lead inventor on more than five US Patents and International Patents; Principle Investigator in a Philips Healthcare research grant and Radiology Exploratory grants. She is currently a Co-Investigator on two NIH R01 projects and one NSF (CCF) multi-disciplinary program. She regularly gives lectures in universities and medical centers in the US and internationally.

Technical Session D2-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Session Chair

Aichi Chien

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BIOGRAPHY

Aichi Chien, Ph.D. is an Associate Professor in the Department of Radiological Sciences and the Biomedical Physics IDP Graduate Program in the UCLA Medical School since 2009; a faculty member of Medical School Short Term Training Program (SSTP) and Cross-disciplinary Scholars in Science and Technology (CSST) program since 2010, and faculty in the UCLA Center for Domain Specific Computing (CDSC) since 2011.

Dr. Chien received her Bachelor's Degree from National Taiwan University, Dept. of Agricultural Machinery Engineering in 1999, Taipei, Taiwan. She then completed her Master's Degree on the subject of Micro/Nano Resonators in the Dept. of Mechanical and Aerospace Engineering, Cornell University, Ithaca, NY; and her PhD Degree in Biomedical Engineering at the University of California, Los Angeles, CA on the topic of MEMS/NEMS implantable devices for cardiovascular disease. She went on to complete Postdoctoral Fellowship training in endovascular treatment in the Division of Interventional Neuroradiology in the UCLA David Geffen School of Medicine.

Dr. Chien's research interests include cerebral vascular disease and treatment effectiveness analysis, and encompass the integration of science and engineering for clinical decision-making and individualized medicine. Her research broadly impacts the medical community and medical device industry. Her research has been featured in various news, including Fierce Medical Devices, Interventional News, Endovascular Today, and Neuro News. She has published more than 70 peer-reviewed publications of original research in high impact factor medical journals such as Stroke, Journal of Vascular and Interventional Radiology, Neurosurgery, Journal of Neurosurgery, and American Journal of Neuroradiology, including 22 papers as first author. She has received many awards, including the Brain Aneurysm Foundation Research Grant Award, the SIR Ring Career Development Award, the Cerebrovascular Research Award from The Aneurysm and AVM Foundation, the Bee Foundation Medical Research Award, the American Heart Association Outreach Award, Heart Failure Society of America Award, and Young Investigator Award from the Cardiovascular System Dynamics Society. She is also the lead inventor on more than five US Patents and International Patents; Principle Investigator in a Philips Healthcare research grant and Radiology Exploratory grants. She is currently a Co-Investigator on two NIH R01 projects and one NSF (CCF) multi-disciplinary program. She regularly gives lectures in universities and medical centers in the US and internationally.

Technical Session D2-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Identifying simple sequence repeats (SSRs) for personal genomes

Tun-Wen Pai

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ABSTRACT

Simple sequence repeats (SSRs) are abundant in human genomes. A large number of SSRs have been shown to be associated with genetic diseases and gene regulatory functions, and have been applied as genetic markers for strain identification and and forensic analyses. High-throughput next generation sequencers provide new cutting-edge computing techniques for genome-scale analyses, and cross-genome comparisons identify polymorphic SSRs for various individuals or groups. An automated and efficient system called ISP for detecting human polymorphic SSRs at the genome scale is designed, and it is freely available at http://isp.cs.ntou.edu.tw/. Assembled contigs from next generation sequencing data were aligned and calibrated according to selected reference sequences. To verify identified polymorphic SSRs, human genomes from the 1000 Genomes Project, highly conserved homologous genes, human-unique genes, and disease-related genes were collected and verified. For example, a set of 477 polymorphic SSRs could be identified from 492 human-unique genes, among which 26 SSRs were retrieved and clustered into three different groups for comparison. More statistical results will be illustrated and discussed in the speech.

BIOGRAPHY

Tun-Wen Pai received his Ph.D. degree in electrical and computer engineering from Duke University, Durham, NC, USA, in 1993. From 1993 to 1996, he joined the Telecommunication Laboratories governed by the Ministry of Transportation and Communications of Taiwan, where he served as an associate researcher and a project leader to develop kernel technologies for intelligent official document analysis and optical character recognition systems. After three year working experience in governmental research laboratories, he switched to academic fields as an associated professor. He works currently as a full professor at the Department of Computer Science and Engineering, National Taiwan Ocean University, Keelung, Taiwan, where he served as the Department Chairman from 2002 to 2004. His research interests are in biomedical image analysis, Structural bioinformatics, and genomic data analysis. Prof. Pai is a member of IEEE society and the International Society for Computational Biology (ISCB).

Technical Session D2-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Contribution of Sequence Motif, Chromatin State and DNA Structure Features to Predictive Models of Transcription Factor Binding in Yeast

Huai-Kuang Tsai

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(中央研究院資訊科學研究所蔡懷寬博士)

ABSTRACT

Transcription factor (TF) binding is determined by the presence of specific sequence motifs (SM) and chromatin accessibility, where the latter is influenced by both chromatin state (CS) and DNA structure (DS) properties. Although SM, CS, and DS have been used to predict TF binding sites, a predictive model that jointly considers CS and DS has not been developed to predict either TF-specific binding or general binding properties of TFs. Using budding yeast as model, we found that machine learning classifiers trained with either CS or DS features alone perform better in predicting TF-specific binding compared to SM based classifiers. In addition, simultaneously considering CS and DS further improves the accuracy of the TF binding predictions, indicating the highly complementary nature of these two properties. The contributions of SM, CS, and DS features to binding site predictions differ greatly between TFs, allowing TF-specific predictions and potentially reflecting different TF binding mechanisms. In addition, a "TF-agnostic" predictive model based on three DNA “intrinsic properties” (in silico predicted nucleosome occupancy, major groove geometry, and dinucleotide free energy) that can be calculated from genomic sequences alone has performance that rivals the model incorporating experiment-derived data. This intrinsic property model allows prediction of binding regions not only across TFs, but also across DNA-binding domain families with distinct structural folds. Furthermore, these predicted binding regions can help identify TF binding sites that have a significant impact on target gene expression. Because the intrinsic property model allows prediction of binding regions across DNA-binding domain families, it is TF agnostic and likely describes general binding potential of TFs. Thus, our findings suggest that it is feasible to establish a TF agnostic model for identifying functional regulatory regions in potentially any sequenced genome.

BIOGRAPHY

Huai-Kuang Tsai received the B.S., the M.S., and the Ph.D. degrees in Computer Science and Information Engineering from the National Taiwan University, Taipei, Taiwan, in 1996, 1998, and 2003, respectively. He was a postdoctoral fellow at the Academia Sinica between 2003 and 2006. Currently he is an Associate Research Fellow at Institute of Information Science, Academia Sinica. His research interests include computational biology, bioinformatics, metagenomics, evolutionary computation, and data mining.

Technical Session D2-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Combination of Genomic Technologies and Bioinformatics for Exploring New Toxicogenomics Biomarkers

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ABSTRACT

The epigenetic effects on DNA methylation, histone modification, and expression of non-coding RNAs (including microRNAs) of environmental chemicals have expanded our understanding of the etiology of human complex diseases such as cancers and diabetes.

Multiple lines of evidence from in vitro and in vivo models have established that epigenetic modifications caused by in utero exposure to environmental toxicants can induce alterations in gene expression that may persist throughout life. Epigenetics is an important mechanism in the ability of environmental chemicals to influence health and disease.

Aberrant epigenetic signaling is becoming to be known as a central component of human disease, and the reversible nature of the epigenetic modifications provides an exciting opportunity for the development of clinically relevant therapeutics.

In my talk, I will present few web servers developed in my lab for analyzing genomic data. Furthermore, I will provide a few studies how we integrates a number of computational and statistical methods, experiment results, genes, chemicals, diseases, pathway and GO with instant and visualization functionalities of toxicogenomics.

BIOGRAPHY

Sher Singh received his B.S. (1996) and Ph.D. (2001) degree in Bioenvironmental Systems Engineering from the National Taiwan University. He was a postdoctoral fellow at the NTU Center for Genomic Medicine, R.O.C. Bioinformatics and Biostatistics Core Facility between 2004 and 2006. Currently he is an Associate Professor of Department of Life Science, College of Science, National Taiwan Normal University. Dr. Singh's research integrates bioinformatics, genomics, and biotechnology to study the environment chemicals-induced responses and mechanisms related to genomics and epigenomics effect. Multiple microarray platforms, including gene expression, methylation, and microRNA arrays are performed to dissect how genomic variations and transcriptional modulations regulate cellular functions after environment chemicals exposure. His research program is to develop systems biology approaches to study toxicogenomics. Different mathematical models and statistical methods are utilized to integrate data from multiple platforms to provide a

comprehensive analysis on genomics.

Dr. Singh is the person in charge of Bioinformatics & Biotechnology Program for National Taiwan Normal University, which provide a learning platform for students and professionals exchange their research results and latest information.

Over the years, Dr. Singh had published a number of articles in the biomedical journals and research articles, such as Genomics, Gene, Journal of Biotechnology, Stem Cells and Development, New England Journal of Medicine, Applied and Environmental Microbiology, Journal of Cellular Biochemistry, Environmental Toxicology, Cancer Cell, etc.

Technical Session D2-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Identification of B-cell Epitopes Based on Immunoinformatics Approaches

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ABSTRACT

Development of computational tools that can accurately predict presence and location of B-cell epitopes on pathogenic proteins has a valuable application to the field of vaccinology. Because of the highly variable yet enigmatic nature of B-cell epitopes, their prediction presents a great challenge to computational immunologists. We propose a method, which adapts a linear averaging scheme on biological properties using a support vector machine model to predict both linear and conformational B-cell epitopes. These properties include position specific scoring matrix, an amino acid ratio scale, and a set of physicochemical scales obtained via a feature selection process. Finally, a three-way data split procedure is used during the validation process to prevent over-estimation of prediction performance and avoid bias in our experiment results. In our proposed method, first we use a non-redundant linear B-cell epitope benchmark dataset curated by Sollner et al. for feature selection and parameter optimization. Evaluated by a three-way data split procedure, our method achieves significant improvement for the Sollner dataset. In addition, the same parameters are used to evaluate performance on other independent linear B-cell epitope test datasets, our method attains the area under the receiver operating curve (AUC) which ranges from 0.9874 to 0.9950 and an accuracy which ranges from 93.73% to 97.31%. Compared with other current models, our method achieves a significant improvement with respect to several evaluation measures. Thus, we have shown that an appropriate combination of evolutionary information and propensity scales with a support vector machine model can significantly enhance the prediction performance of both linear and conformational B-cell epitopes.

BIOGRAPHY

Dr. Emily Chia-Yu Su holds a B.S. degree of Computer Science from National Taiwan Normal University (2001), a M.S. degree of Computer Science and Information Engineering from National Taiwan University (2003), and a Ph.D. degree of Bioinformatics from a joint program of Taiwan International Graduate Program from Academia Sinica and Institute of Bioinformatics from National Chiao Tung University (2009). She has been a postdoctoral fellow of Institute of Information Science, Academia Sinica in 2009. Currently, she is an assistant professor of Graduate Institute of Biomedical Informatics in Taipei Medical University. Her research interests include bioinformatics, proteomics, medical informatics, immunoinformatics, machine learning, and text mining.

Technical Session D2-W1-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Biomarker discovery—Issues in ranking, model selection, and p-value calculation

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ABSTRACT

The correct diagnosis of cancer patients conventionally depends on the pathologist's experience and ability to distinguish cancer tissue from normal tissue under a microscope. Advances in technology for measuring the abundance of, e.g., proteins and mRNAs in tissue samples make it interesting to search for an optimal subset of these for classification of samples as cancer or normal. This search for an optimal subset of molecules is in Statistics and Machine learning known as variable selection, features selection, and subset selection. It is still considered an unsolved problem and heuristic search procedures are used when an exhaustive search is computationally unfeasible.

In this talk, I give a brief introduction to biomarker discovery in cancer research. I discuss issues of identification of biomarkers that provide distinct signatures for prediction of tissues as cancer or normal, exemplified by a recent study of cancer signaling signatures in human colon cancer. More precisely, I discuss ranking of individual features versus combinations of features, model over-fitting, and confidence evaluation. I show that the optimal subset for separation of cancer tissues from normal tissues does not contain any of the proteins in the top quintile in terms of significant difference between the groups according to Mann-Whitney U-test or correlation to the diagnosis. I also demonstrate how Monte Carlo simulations of the separation with random class assignment can be used to calculate p-values for observing any specific separation by chance and selection of the optimal number of proteins in the subset based on these p-values. Both selection of the optimal number of biomarkers and calculation of p-values corrected for multiple hypothesis testing are essential to obtain a subset of biomarkers that yield robust predictions for clinical use.

BIOGRAPHY

Dr. Torbjörn Nordling obtained both his Ph.D. in Automatic Control (2013) and his M.Sc. in Engineering Physics (2005) from KTH Royal Institute of Technology in Stockholm, Sweden. He has specialised in mathematical modelling of biological systems and developed both new theory and methodology, in particular, for robust network inference and variable selection.

He is currently an Assistant Professor at the Dept. of Mechanical Engineering at National Cheng Kung University in Taiwan. He is also associated with Stockholm Bioinformatics Center at the Science for Life Laboratory in Sweden. Previously he has done a PostDoc at the Dept. of

Immunology, Genetics and Pathology at Uppsala University in Sweden. He has been a visiting researcher at Telethon Institute of Genetics and Medicine in Naples, Italy and ERATO Kitano Symbiotic Systems Project at Japan Science and Technology Agency in Tokyo, Japan. He is the founder of Nordron AB, a startup specialised in data analysis, and a co-founder of Jagah Systems AB, an award winning indoor geolocalisation startup. He has co-authored 8 peer-reviewed journal articles and 4 full-length conference articles. His research is currently focused on inference of causal influences among genes, e.g. based on qRT-PCR data, and biomarker discovery, e.g. based on protein measurements in Colon Cancer tissue biopsies.

Dr. Torbjörn Nordling is a member of IEEE Sweden Section since 8 years. He has received numerous scholarships, e.g. the Sweden-Japan foundation grant.

Technical Session D2-W2-T1: Medicine and Life Sciences, Biological and Biomedical Sciences

Workshop Co-chair and Session Chair

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BIOGRAPHY

Nei-Li Chan received a BSc degree in Chemistry in 1991 from National Taiwan University, Taiwan. After two years of compulsory military service as a Second Lieutenant in the Taiwanese Army, he enrolled in the Biochemistry doctoral program offered by the University of Iowa (USA) and completed his PhD degree in 1998. From 1999 to 2001, he conducted post-doctoral training with Prof. Chris Hill (University of Utah, USA). He then returned to Taiwan and joined the faculty of National Chung Hsing University. He moved to National Taiwan University in 2007, where he is currently appointed as a Professor of Biochemistry and Molecular Biology.

He uses various biochemical and biophysical techniques, including X-ray crystallography, to study the structure and function of proteins. In recent years, he has been actively engaged in the "structural-based design of type II topoisomerase isozyme-specific anticancer agents" and the elucidation of "structural basis of antizyme-mediated proteosomal degradation pathway".

Selected Publications

1) Wu, H.-Y., Chen, S.-F., Hsieh, J.-Y., Chou, F., Wang, Y.-H., Lin, W.-T., Lee, P.-Y., Yu, Y.-J., Lin, L.-Y., Lin, T.-S., Lin, C.-L., Liu, G.-Y., Tzeng, S.-R.*, Hung, H.-C.*, & **Chan, N.-L.*** (2015) Structural Basis of Antizyme-Mediated Regulation of Polyamine Homeostasis. Proc. Natl. Acad. Sci. U.S.A. (published ahead of print August 24, 2015, doi:10.1073/pnas.1508187112)

2) Chang, C.-C., Lin, L.-Y., Zou, X.-W., Huang, C.-C.*, & **Chan, N.-L.*** (2015) Structural Basis of the Mercury(II)-Mediated Conformational Switching of the Dual-Function Transcriptional Regulator MerR. Nucleic Acids Res (Epub ahead of print, PMID: 26150423)

3) Wu, C.-C., Li, Y.-C., Wang, Y.-R., Li, T.-K.*, & **Chan, N.-L.*** (2013) On the structural basis and design guidelines for type II topoisomerase-targeting anticancer drugs. Nucleic Acids Res, 41:10630-40.

4) Wu, C.-C., Li, T.-K., Farh, L., Lin, L.-Y., Lin, T.-S., Yu, Y.-J., Yen, T.-J., Chiang, C.-W., & **Chan, N.-L.*** (2011) Structural basis of type II topoisomerase inhibition by the anticancer drug etoposide. Science, 333:459-62

Technical Session D2-W2-T1: Medicine and Life Sciences, Biological and Biomedical Sciences

The interaction between metabolism to immunity

Chia-Lin Hsu

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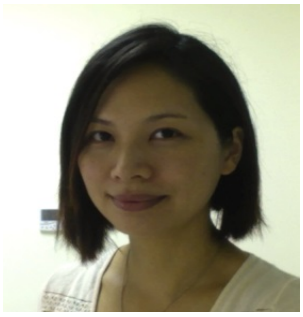
ABSTRACT

Metabolism and immunity have long been considered as two distinct cellular responses. However, in a grand view, both systems work to regain body's homeostasis. With recent advances in understanding the immunological aspects in metabolic diseases, it is becoming clear that there is a close interplay between metabolism and immunity. For example, lysosomal storage diseases (LSDs) are a group of heterogeneous disorders caused by defects in lysosomal enzymes or transporters, resulting in accumulation of un-degraded macromolecules or metabolites. This accumulation disrupts the cell's normal functioning and gives rise to the clinical manifestations of LSDs. In this talk, I would like to discuss how metabolism may affect the homeostasis of immune system.

BIOGRAPHY



2002-2007: Ph.D. in Immunology, Duke University, U.S.A.
1999-2002: M.S. in Microbiology & Immunology, National Yang-Ming University
1995-1999: B.S. in Zoology, National Taiwan University

Upon graduation from Duke University, she received her postdoctoral training at Genentech, a San Francisco-based biotechnology company. During this period, she discovered that the nucleoside equilibrium is crucial to the homeostasis of immune system, and when out-of-balance, can lead to lysosomal storage disease-like phenotypes. The findings were published in Science, 2012. Dr. Hsu then accepted the position as Senior Scientist at the Center of Innovative Therapeutics, Pfizer. She was the biology lead of a multi-centers project that aims to develop immune-modulatory therapeutics with the combined efforts from both pharmaceutical and academic laboratories. She returned to Taiwan in 2013, and now is an Assistant Professor at the Institute of Microbiology and Immunology, National Yang-Ming University.

Trained as an immunologist, Dr. Hsu have always been intrigued by how complicated and effective our immune system is. To successfully fight off the pathogen invasion, immune system has to go through recognition of foreign insult, initiation of inflammatory response, and resolution phase to regain homeostasis. Dysregulation of any of these steps can result in diseases. Activation of immune response is an energy-consuming event since active production of proteins and cell proliferation are crucial parts of the inflammatory response. To meet the metabolic demand and recycle metabolites, lysosomes possess a group of membrane proteins that are responsible for transporting substances in and out of the lysosome. Dr. Hsu's research

interest is to understand how these metabolite transporters respond and facilitate the inflammatory response.

Technical Session D2-W2-T1: Medicine and Life Sciences, Biological and Biomedical Sciences

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ABSTRACT

Retinoic-acid-inducible gene-I (RIG-I) and RIG-I-like helicases (RLRs) are key cytosolic sensors to recognize pathogen-associated molecular patterns (PAMP). Once bound to non-self RNA, RIG-I can engage host protective innate immunity against viral infection through MAVS, which is a mitochondria-associated transmembrane protein. The interaction between RIG-I and MAVS at mitochondria-associated membrane is the crucial onset of MAVS-mediated interferon production pathway during acute phase of viral infection, but it is unclear how RIG-I, a cytosolic protein, can interact with membrane-localized MAVS. Here we show that RIG-I activation is regulated by its reversible acetylation. Acetyl-mimetic mutants of RIG-I could not form virus-induced homodimers, suggesting that acetyl-lysine residues of the RIG-I repressor domain prevent RIG-I from homodimerization. During acute infection, deacetylation of RIG-I RD occurs and promotes RIG-I dimerization upon ligand binding. Our results define direct deacetylation of RIG-I by HDAC6 as a key step in the activation of RIG-I to promote innate antiviral immunity.

Furthermore, RIG-I, TRIM25, and 14-3-3ε trimerize to form a translocon during acute phase of viral infection. TRIM25 is known as an E3 ubiquitin ligase of RIG-I5. In previous reports, the chaperon 14-3-3ε expression is up-regulated during viral infection6, and it can serve as mitochondrial targeting protein7. Both TRIM25 and 14-3-3ε are required for RIG-I translocon formation through interacting with the CARD domains of RIG-I. RIG-I/TRIM25/14-3-3ε trimer formation during virus infection is regulated by the conformational change of RIG-I governed by its repressor domain, which is known as the off/on switch for immune signaling. Once translocon is formed, RIG-I is relocalized from diffuse throughout the cytoplasm to associate to the peri-nuclear region and in context with a membrane-associated compartment.

Our results demonstrate that RIG-I deacetylation and later association with an intracellular membrane compartment are important for downstream signaling, presenting a model of which the molecular mechanisms of RIG-I pathway signaling of innate immunity against RNA virus infection. We anticipate our findings to address the critical steps to initiate host defense as well as novel regulatory mechanisms for innate immune signaling. Future studies in the acetylation status and the localization of RLRs and other signaling molecules will be intriguing and relevant in the field of innate immunity.

BIOGRAPHY

Dr. Helene Minyi Liu was born in Taipei, Taiwan in 1979. She graduated from National Taiwan University majoring in Medical Technology in 2002, and soon after that, she went to the U.S. for her post-baccalaureate studies. Helene received her Master degree in 2004 and Ph.D. in 2008 both from the Department of Molecular Microbiology and Immunology at University of Southern California, in Los Angeles, USA. Her doctoral dissertation focused on the molecular

mechanisms of the RNA replication and translation of Hepatitis C Virus (HCV).

With her doctoral degree, Helene was then recruited by Dr. Michael Gale Jr. to the Department of Immunology in University of Washington, Seattle as a Post-doctoral Fellow in 2009. She continued her research in host-virus-interactions in the aspect of innate immunity against HCV. She focused on how the cytosolic RNA sensors could be targeted to mitochondria for downstream signaling and interferon induction. Her studies in the Gale Lab were concluded in 2 research papers: "Mitochondrial-associated endoplasmic reticulum membranes (MAM) form innate immune synapses and are targeted by hepatitis C virus." in PNAS, 2011 and "The Mitochondrial Targeting Chaperone 14-3-3ε Regulates a RIG-I Translocon that Mediates Membrane Association and Innate Antiviral Immunity" in Cell Host & Microbe, 2012. In 2013, she returned to Taiwan and joined the Department of Clinical Laboratory Sciences and Medical Biotechnology in National Taiwan University as an Assistant Professor. Her interests in the innate immunity against RNA virus infections are carried on in her own lab.

Dr. Liu is currently involving in Taiwan Society of Virology, American Society of Virology, and International Cytokine & Interferon Society.

Technical Session D2-W2-T1: Medicine and Life Sciences, Biological and Biomedical Sciences

Application of dendritic cell platform in medical research

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ABSTRACT

Dendritic cells (DCs) play a critical role in the initiation and regulation of immune responses. Increasing evidences have indicated that manipulation of DCs can serve as an effective strategy for immunotherapy. Thus, he decided to focus on DC research as his career. Reviewing his past works, he has established a mouse DC-based platform to study DC biology. There are two major topics for studying the function and regulation of DCs in immune responses. One is examining the endogenous factors of DCs. He studies the role of DCs in immune system by using various transgenic and knock-out mice, such as deficiency of Src or Syk kinase. In addition, the applications of DCs in some infectious diseases are also evaluated. Another topic is searching the exogenous factors of DCs. He studies the functions of DCs in immune responses by screening various materials from foods, herbs, chemicals, and nanoparticles. He collaborates with several research groups and has identified many compounds which may have potential to be applied in immunotherapy. In summary, his works are actually interested in both basic research and applied science, and he keeps leading a group of researchers in DC study.

BIOGRAPHY

Dr. Chu received his B.S. (1989) in Plant Pathology from the National Chung Hsin University. He received his M.S. (1991) from the National Tsing Hua University and Ph.D. (2000) from the National Defense Medical Center/Academia Sinica, and was a postdoctoral fellow at the University of California at San Francisco between 2000 and 2005. He was an Assistant Investigator of National Health Research Institutes between 2005 and 2010, and then became an Assistant Professor of Graduate Institute of Immunology, National Taiwan University in 2011. Currently he is an Associate Professor. Dr. Chu's research focuses on DC research. He has authored forty peer-reviewed papers, 5 patents, and serves as peer reviewer for twenty journals.

Technical Session D2-W2-T1: Medicine and Life Sciences, Biological and Biomedical Sciences

Recombinant lipoimmunogen-based therapeutic HPV vaccine

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ABSTRACT

Human papillomaviruses (HPVs) infection could account for the development of several cancers, in particular, the cervical cancer which is the second leading cause of cancer death in women worldwide. Currently, HPV prophylactic vaccination against HPV infection is expected to reduce cervical cancer incidence. However, 500,000 new cases of invasive cervical cancer are diagnosed worldwide every year. Although prophylactic HPV vaccines have been used in many countries, the vaccine coverage rate is still low and cost is high. Therefore, to control of cervical cancer mortality, therapeutic medicine is still an urgent need. It is known that the E7 oncoprotein of human papillomavirus (HPV) is an ideal target for developing immunotherapeutic strategies against HPV-associated tumors. Since protein-based immunogen alone is poorly eliciting the cytotoxic T-lymphocyte (CTL) responses and hardly to be exploited for therapeutic purpose. In our previous studies, we reported that the recombinant lipoprotein containing inactive E7 (E7m) biologically linking with bacterial lipid moiety was able to activate the maturation of mouse bone marrow-derived dendritic cells through toll-like receptor 2 (TLR2), skew the immune responses toward the Th1, and induce the E7-specific CTL responses. However, the anti-tumor effects of rlipo-E7m are limited in small tumor. To increase the anti-tumor effects on large tumor, the innate receptor agonists were used for combination therapy. We found that a TLR9 agonist (an unmethylated CpG oligodeoxynucleotide, CpG ODN) synergistically enhances CTL responses and eradicates large tumors (6-8 mm in diameter) when combined with rlipo-E7m. Furthermore, we observed that combined treatment with rlipo-E7m and CpG ODN effectively increases tumor infiltrating CTLs and reduces the numbers of immunosuppressive cells, myeloid-derived suppressor cells (MDSCs), macrophages and regulatory T cells (Tregs) in the tumor microenvironment. These findings suggest that the dramatic anti-tumor effects of the recombinant lipoprotein together with CpG ODN might reflect the amplification of CTL responses and repression of the immunosuppressive environment. This promising approach could be applied for the development of additional therapeutic cancer vaccines.

BIOGRAPHY

Shih-Jen Liu received his BS in pharmacy at 1989 from Kaohsiung Medical College, Taiwan. After 4 years, He got his Master degree in pharmacology from National Cheng-Kung University, Taiwan at 1993. He then finished his Ph.D. degree in life Science from National Defense Medical Center at 1998. He spent 5-years (1998-2003) in a biotechnological company to develop dendritic cells-based immunotherapy. He and his collaborators conducted the first private company-involved phase I clinical trial in Taiwan. He joined Vaccine Research and

Development Center of National Health Research Institutes (NHRI) in 2004. He is now an

Associate Investigator at National Institute of Infectious Diseases and Vaccinology in NHRI, and an Associate Professor in China Medical University, Taiwan. His research interests include discovery of human cytotoxic T lymphocyte (CTL) epitopes to develop therapeutic vaccines and studies of the molecular mechanism of novel adjuvants. He also found that the antigen presentation mechanisms of lipopetides are different according to the lipid moiety. The TLR2 agonist conjugated long peptide could regulate the process of antigen presentation. Currently, he collaborates with his colleagues to develop recombinant lipoprotein platform technologies and applied to the therapeutic HPV vaccine. This approach is promising for eliminating large tumor and reducing the tumor associated immunosuppressive cells number.

His works have received numerous honors. The “Therapeutic HPV Vaccine” was awarded The ninth “National Innovation Award” by the Institute for Biotechnology and Medicine Industry (2013). The recombinant lipoprotein technology was awarded the seventh “National Innovation Award” by the Institute for Biotechnology and Medicine Industry (2010), and “Silver Invention Award” by the Ministry of Economic Affair, Taiwan (2012). He has more than 50 publications and numerous patents. His work has had a tremendous impact on elucidating the vaccinology and immunology of development of therapeutic vaccines to HPV-associated cancers.

Technical Session D2-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Session Chair

Chihchen Chen

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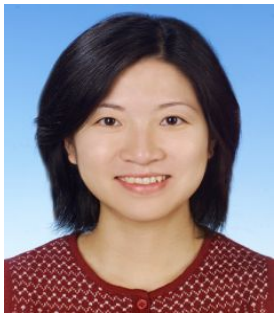
(清華大學奈米工程與微系統研究所陳致真教授)

BIOGRAPHY



Chihchen Chen was born in Taipei, Taiwan. She received her B.S. (1995) and M.S. (1997) in Electrical Engineering from the National Taiwan University. She was an R&D engineer at ASUS Computer Inc., Taiwan from 1997 to 1999. She received her Ph.D. (2006) from the University of Washington at Seattle, WA, with dual degrees in Bioengineering and Nanotechnology. She was a postdoctoral associate at the Massachusetts General Hospital between 2006 and 2009.

Currently she is an Associate Professor of the Institute of NanoEngineering and MicroSystems, Department of Power Mechanical Engineering at the National Tsing Hua University, Hsinchu, Taiwan, where she started her own research group in the summer of 2010. Her areas of expertise and research interests are micro- and nano-fluidic technologies for applications in biology and medicine, with a focus on the isolation and characterization of the cellular and sub-cellular components.

Dr. Chen is a member of the International Society for Extracellular Vesicles, and a member on the Product Advisory Board of Journal of Visualized Experiments (JoVE).

Technical Session D2-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Three-dimensional refractive-index microscopy for live-cell imaging

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ABSTRACT

Three-dimensional (3D) refractive-index (RI) microscopy, based on quantitative phase microscopy and diffraction tomography, is an emerging technique suitable for live-cell imaging due to its label-free and fast 3D imaging capabilities. We have developed a common-path system to acquire 3D RI microscopic images of transparent specimens with excellent speed and stability. The refractive index of biological specimens represents the local mass density of biomolecules. Preliminary results of imaging cancer cells of epithelial origin, erythrocytes, and white blood cells will be presented. In addition, RI images of thin slices of epithelial tissue from the esophagus in 14 patients were collected and analyzed to investigate the light scattering properties of both normal and precancerous epithelial tissues.

BIOGRAPHY

Dr. Kung-Bin Sung received a B.S. degree in Electrical Engineering from National Taiwan University, Taiwan. He received M.S. and Ph.D. degrees from The University of Texas at Austin in 1999 and 2003, respectively. He joined Intel Corporation as a research scientist in 2003 and collaborated with researchers at the Fred Hutchinson Cancer Research Center on research projects related to surface-enhanced Raman spectroscopy. Since July 2006 he has been with the Department of Electrical Engineering and the Graduate Institute of Biomedical Electronics and Bioinformatics in National Taiwan University, where he is currently an Associate Professor. His research focuses on optical spectroscopy and microscopy for the diagnostics of diseases, especially precancerous lesions and early cancers.

Technical Session D2-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Fiber-needle optical coherence tomography image-guided system to assist epidural anesthesia

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ABSTRACT

Epidural blockade is one type of neuraxial block. It is an effective way for analgesia associated with a spectrum of healthy people and seriously ill patients. However, epidural needle insertion is traditionally a blind technique whose success depends upon the experience of the operator. The technique of the loss of resistance (LOR) to air or hanging drops is the most common method used to identify the epidural space (ES). However, using the LOR technique, the epidural failure rate could be up to 10% owing to incorrect catheter placement. Even though there have been many approaches to assist the anesthesiologists in performing neuraxial anesthesia, none of the prior arts may be said as an unrestricted technique. The lack of a design that is with sufficient accuracy to the targets of interest and automatic indication of needle placement makes it difficult to all-round implementation of field usage of objectiveness. Clinicians are still looking for practical neuraxial techniques that allow "real time" observation of the epidural catheter introduction and drug deposition.

Optical coherence tomography (OCT) was originally demonstrated in 1991 as a unique biomedical imaging modality capable of cross-sectional imaging of the human eye at an axial resolution of approximately 10 to 15 μm. OCT provides a non-invasive, depth-resolved, non-destructive imaging, at a higher resolution than ultrasonography, and at a deeper skin imaging depth than confocal microscopy. This talk is an overview of the research in National Yang Ming University on OCT development and its biomedical applications, especially we introduced a novel method using a fiber-needle based OCT image guided system for anesthesia procedure. We anticipate that this technique will reduce the occurrence of failed epidural blocks and other complications such as dural punctures. In addition to provide a support system for image-guiding in epidural anesthesia, this innovative technology is also helpful for the monitoring of other surgical or treatment procedures, whose success may have high societal impact.

BIOGRAPHY

Wen-Chuan Kuo received her B.S. (1999) and M.S. (2001) in Radiological Science from the National Yang Ming University, graduated from the National Taiwan University in 2005 with a Ph.D. degree in Electric Engineering. She was an Assistant Professor between 2005 and 2009, an Associate Professor between 2009 and 2011 at the National Taiwan Normal University. She is currently a Professor at Institute of Biophotonics, and a faculty member of Biophotonics & Molecular Imaging Research Center (BMIRC) in National Yang-Ming University. Dr. Kuo's research interests include functional and surgical-guiding optical coherence tomography (OCT)

and the development of optical instrumentation for biomedical applications. She has authored more than forty peer-reviewed journals and book chapters on these topics, and is now collaborating with a number of clinical doctors in several medical research fields.

Technical Session D2-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Meng-Tsan Tsai

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ABSTRACT

BIOGRAPHY

Technical Session D2-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

High-Speed Direct Visualization of Dynamics at the Nanoscale in Biological Systems

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ABSTRACT

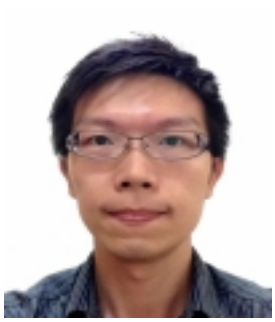
Optical microscopy has been an indispensable tool in the research of various fields including the life sciences. As the techniques of fluorescence optical microscope advance, ultrasensitive detection down to single-molecule level and superresolution imaging in biological cells have become routine. At first glance, such sensitivity and resolution show promise for direct visualization of biological events with molecular clarity. A closer look, however, reveals the limitations of the existing fluorescence approaches that are still struggling to provide spatiotemporal resolutions required for observing nanoscopic dynamics of single molecules in biological cells. Photobleaching and blinking of the fluorescent tags obviously complicate the measurements for dynamics. Saturation of the fluorescence signal as the result of inherent fluorescence lifetime limits the maximal amount of signal per unit time, which sets a stringent constrain in high-speed observation of rapid processes.

In this talk, I will present a novel scattering-based high-speed optical microscopy technique for the investigation of dynamics in biological cells at the nanometer scale. Scattering signal is stable and without saturation, and therefore ideal for high-speed detection. Importantly, scattering signal is also coherent, which allows for interferometric detection by which shot-noise limited sensitivity can be achieved at high speed. Using interferometric detection of scattering signal (iSCAT), we have recently demonstrated tracking of single 20 nm gold particles with 2 nm spatial precision up to 500,000 frames per second, setting a new standard of super localization of small nanoparticles. By labeling the nanoparticles to molecules in the biological membranes, motion of single lipid molecules in the membrane is directly observed at the molecular scale for the first time. We discovered nanostructures in lipid domains of liquid-ordered phase, which provides a new view of the regulation mechanism of lipid rafts in cell membranes. Using a similar imaging technique, we have succeeded in imaging and tracking of virus particles and cell organelles in living cells with unprecedented clarity.

BIOGRAPHY

Dr. Chia-Lung Hsieh was born in Taiwan in 1980. Dr. Hsieh received his Ph.D. degree from the department of electrical engineering of Caltech, Pasadena, U.S.A. in 2011.

He served the compulsory military service from 2004 to 2006. During his Ph.D. studies, he worked as a Research Assistant at the Swiss Federal Institute of Technology in Lausanne, Switzerland from 2007 to 2011. After graduation, he worked as a postdoctoral researcher at the Max Planck Institute for the Science of Light in Erlangen, Germany from 2011 to 2012. Since



December 2012, he has joined the Institute of Atomic and Molecular Sciences, Academia Sinica as an Assistant Research Fellow and the group leader of the Nano-Bio-Photonics Lab. He has been developing advanced techniques for the study of life sciences, combining the novel optical imaging systems and nanotechnology. His recent research focuses on high-speed direct visualization of dynamics in biological systems.

Dr. Hsieh is selected as an honorary member of the Phi Tau Phi Scholastic Honor Society in 2004, currently a member of the Optical Society of America and Biophysical Society. He received Taiwan Merit Scholarship from 2006 to 2009, Bor-Uei Chen Memorial Scholarship Award in 2006, and Acer Long Term Distinguished Paper Award in 2005.

Below are two selected publications related to the high-speed optical microscopy presented in this talk:

1. Lin YH, Chang WL, **Hsieh CL***, "Shot-noise limited localization of single 20 nm gold particles with nanometer spatial precision within microseconds," *Optics Express*, Vol. **22(8)**, pp. 9159-9170 (2014).

2. **Hsieh CL**, Spindler S, Ehrig J, Sandoghdar V*, "Tracking single particles on supported lipid membranes: multimobility diffusion and nanoscopic confinement," *J. Phys. Chem. B*, Vol. **118**(6), pp. 1545–1554 (2014).

Technical Session D2-W3-T1: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Bilirubin Molecular Imaging for the Diagnosis of Cancers

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ABSTRACT

Based on an infrared femtosecond Cr:forsterite laser, we developed a molecular imaging method of bilirubin dimers. At the wavelength of 1230nm, we selectively excited the two-photon red fluorescence of bilirubin dimers around 660 nm. Autofluorescences from other endogenous fluorophores were greatly suppressed. The molecular specificity of red fluorescence was further validated by a mass spectroscopy measurement. Using this distinct fluorescence measure, we found that poorly-differentiated hepatocellular carcinoma (HCC) tissues on-average showed 3.7-times lower concentration of bilirubins than the corresponding non-tumor parts. This feature can be used to define the boundary of HCC in the surgery. The fluorescence lifetime imaging microscopy measurements indicated that HCC tissues exhibited a longer lifetime (500 ps) than those of non-tumor parts (300 ps). Similarly, oral cancer cell lines had longer lifetimes (>330 ps) than those of non-tumor ones (250 ps). We anticipate the developed methods of bilirubin molecular imaging to be useful in diagnosing cancers or studying the dynamics of bilirubin metabolisms in live cells....

BIOGRAPHY

Tzu-Ming Liu was born in Keelung, Taiwan on August 31, 1977. He received the B.S. degree in Electrical Engineering from National Taiwan University in 1999 and the Ph.D. degrees in Photonics & Optoelectronics from National Taiwan University in 2004. When he was a Ph.D. student, he built high power femtosecond laser systems to study nonlinear optics. Throughout the postdoctoral research period between 2005 and 2009, he further applied femtosecond laser techniques in the studies of phonon physics, nanophotonics, and embryo development. He built miniaturized nonlinear optical microscopes based on scanning MEMS mirrors. He also studied microwave spectroscopy on nanomaterials and viruses.

Dr. Liu was an assistant professor since 2009 and is now an associate professor in the Institute of Biomedical Engineering, National Taiwan University. He developed an infrared femtosecond laser based nonlinear optical microscope to study nanophotonics, tumor stem cells, and pharmacokinetics of nanomedicines. Using this platform, he also aims to develop an in vivo flow cytometer of human to achieve in vivo complete blood counts. In 2012, he visited Wellman Center for Photomedicine, Massachusetts General Hospital in USA and built multicolor infrared femtosecond laser sources for multi-label multi-photon microscopy. From 2013, he developed a series of courses for medical device innovation and started to develop

medical devices for clinical diagnosis. Several clinical researches are conducting now with medical doctors in National Taiwan University Hospital.

He has received Excellent Young Faculty Grant from Ministry of Science & Technology, Taiwan in 2013. He led a student team to won the Outstanding Startup Award in 2014, which win the prizes with 2 million NT dollars.

Technical Session D2-W4-T1: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Session Chair

Ai-Chun Pang

Director and Professor, Graduate Institute of Networking and Multimedia
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BIOGRAPHY

Technical Session D2-W4-T1: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Interactive Technologies in Arts

Shih-Wei Sun

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ABSTRACT

In this talk, from the observation point of technologies, we will review the technologies from cave painting, building and sculpture, optical camera developing, to the modern interactive motion sensing technologies. From the artistic representation point of view, the applications from sensors and the feedback from audio-visual even 3D special effects bring different user experiences to the mental status. Furthermore, the extending possible challenges and opportunities in animation, film making, and future museum application directions will be addressed.

BIOGRAPHY

Dr. Shih-Wei Sun received the B.S. degree from Yuan-Ze University and Ph.D. degree from National Central University, Taiwan, in 2001 and 2007, respectively, both in Electrical Engineering. From 2007 to 2011, he was a post doctoral research fellow at the institute of information science, Academia Sinica. Since 2012, he is an assistant professor at the Department of New Media Art, Taipei National University of the Arts, Taiwan, where he currently leads the Ultra-Communication Vision Laboratory (ucVision Lab). His research interest includes: visual content analysis, computer vision and the application for interactive technologies, 3D signal processing for depth cameras, multi-camera scene analysis and synthesis, and the security for network and multimedia. He received a research award from the Prize Award of Multimedia Grand Challenge from the 2014 ACM Multimedia Conference. He published more than 40 international journal papers (SCI) and conference papers. He serves as the reviewers and technical program committee (TPC) members for many international SCI journals and academic conferences.

Technical Session D2-W4-T1: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Mental Disorder Detection and Measurement using Latent Dirichlet Allocation and SentiWordNet

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ABSTRACT

Nowadays, lifestyles are so busy that an increasing number of patients suffer from depression. Depression is a kind of mental illness that is hard to detect in early stage. Due to the lack of knowledge in depression, a lot of people suffer unconsciously and go through difficult life situations without timely support and understanding, which often makes avoiding tragedy too late. However, there are chances that whether or not a social media user is getting depressed can be predicted, as social media such as Twitter and Facebook has become a part of our lives and people tend to posting their diaries and feeling online. For this purpose, we build a MENS (MENtal Status) system for evaluating one's mental status regarding depression in this work. Based on SLDA, LDA and SentiWordNet, MENS is able to not only detect one's mental status but also describe the emotion intensity through the analysis of his/her online diaries. Experimental results on real datasets show that MENS performs well in detecting depressed patients, especially those with severe depression.

BIOGRAPHY

Chih-Hua Tai is currently an assistant professor in Department of Computer Science and Information Engineering, National Taipei University, New Taipei City, Taiwan. She received her B.S. degree in Computer Science from National Chengchi University (NCCU), Taipei, Taiwan, and Ph.D. degree from Department of Electrical Engineering, National Taiwan University (NTU), Taipei, Taiwan. She was a postdoctoral researcher at Research Center for IT innovation from August 2011 to July 2012, and a lecturer at Department of Computer Science and Information Engineering, National Taiwan University of Science and Technology (NTUST), Taipei, Taiwan from February 2012 to July 2012. Her research interests include privacy-preserving data mining, healthcare data mining, and social computing and marketing. She received the best paper award of the 2015 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining (ASONAM 2015).

Technical Session D2-W4-T1: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

A state-of-the art overview of computer-aided diagnosis in breast cancer

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ABSTRACT

Breast cancer is the most common cancer and the second leading cause of mortality for women nowadays. Breast ultrasound is used in distinguishing between benign and malignant tumors and tumor detection. With the quantification of the tumor characteristics in ultrasound, computer-aided diagnosis (CAD) systems were developed as a second reader in improving reader performance for tumor assessment.

This talk encapsulates the recent developments of ultrasound CAD in breast cancer. For tumor diagnosis, various image features from B-mode, color Doppler, and elastography were quantified and combined to provide malignancy evaluation. In screening, CAD was developed to detect potential abnormalities from automated breast ultrasound scanning system which can cover the whole breast but generate time-consuming image data for examination. In the role of precision medicine, radiogenomics analysis was proposed to associate quantitative image features with gene-expression patterns recently.

BIOGRAPHY

Chung-Ming Lo was born in Taipei, Taiwan (1979). He received his Ph.D. (2013) at the Department of Computer Science and Information Engineering from National Taiwan University at Taipei. He was an R&D engineer between 2003~2008 and was a postdoctoral fellow at National Taiwan University between 2013~2015. Currently, he is an Assistant Professor of Graduate Institute of Biomedical Informatics, Taipei Medical University and an Adjunct Assistant Professor of Department of Computer Science and Information Engineering, National Taipei University. His research interests includes medical image processing and computer-aided diagnosis\detection. He has authored invited book chapters, patents, and journal papers on these topics and served as the reviewer of numerous journals such as IEEE Transactions on Medical Imaging. He won Young Investigator Award from International Federation for Medical and Biological Engineering (2014) and Postdoc Academic Publication Award from Ministry of Science and Technology, Taiwan (2015).

Technical Session D2-W1-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Session Chair

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BIOGRAPHY

Tun-Wen Pai received his Ph.D. degree in electrical and computer engineering from Duke University, Durham, NC, USA, in 1993. From 1993 to 1996, he joined the Telecommunication Laboratories governed by the Ministry of Transportation and Communications of Taiwan, where he served as an associate researcher and a project leader to develop kernel technologies for intelligent official document analysis and optical character recognition systems. After three year working experience in governmental research laboratories, he switched to academic fields as an associated professor. He works currently as a full professor at the Department of Computer Science and Engineering, National Taiwan Ocean University, Keelung, Taiwan, where he served as the Department Chairman from 2002 to 2004. His research interests are in biomedical image analysis, Structural bioinformatics, and genomic data analysis. Prof. Pai is a member of IEEE society and the International Society for Computational Biology (ISCB).

Technical Session D2-W1-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Phylostratification of Human Cellular Networks

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ABSTRACT

Molecular networks, such as the protein-protein interaction (PPI) network, offer a conceptual framework for better understanding the functional organization of cells. However, the intricacy of network complexity complicates comprehensive analysis. Here, we adopted a phylogenic stratification method combined with force-directed graph simulation to decompose the human PPI network in a multi-dimensional manner. This network model enabled us to associate the network topological properties with evolutionary and biological implications. First, we found that ancient proteins occupy the core of the network, whereas young proteins tend to reside on the periphery. Second, the presence of age homophily suggests a possible selection pressure may have acted on the duplication and divergence process during the PPI network evolution. Lastly, functional analysis revealed that each age group possesses high specificity of enriched biological processes and pathway engagements, which could correspond to their evolutionary roles in eukaryotic cells. More interestingly, the network landscape closely coincides with the subcellular localization of proteins. Together, these findings suggest the potential of using conceptual frameworks to mimic the true functional organization in a living cell.

BIOGRAPHY

Hsuan-Cheng Huang received his B.A., M.A., and Ph.D. degrees in physics from National Taiwan University in 1992, 1994 and 1998, respectively. He was engaged in experimental high-energy physics research at Taiwan and at High Energy Accelerator Research Organization, Japan, and awarded NSC Distinguished Postdoctoral Fellowship in 2003. Encouraged by the emerging of systems biology, Dr. Huang joined National Yang-Ming University in 2004 and is currently a Professor and the Director of the Institute of Biomedical Informatics, also affiliated with the Center for Systems and Synthetic Biology. In 2007, he received the NSC Wu Ta-You Memorial Award, an honor for excellent young investigators in Taiwan. Now he serves as an Editorial Board Member of Scientific Reports, an Associate Editor and Deputy Section Editor of BMC Systems Biology, and an Executive Board Member in Taiwan Society of Evolution and Computational Biology. His research interests include bioinformatics, computational and systems biology, and network biology. Currently, Dr. Huang endeavors his research efforts to computational analysis and modeling of biological networks, and applies them to unravel molecular mechanisms of cancer cell response, non-coding RNA regulation, as well as other biological processes.

Technical Session D2-W1-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Extracting Functional Information from Dynamics of Biomolecular Systems in Extremely High Dimension

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ABSTRACT

The full description of a biomolecular system requires a 6N-dimensional phase space, where N is the number of atoms in the system. A typical biomolecular system that can be used to describe a self-sustained biochemical phenomenon usually consists of 10,000 to 10,000,000 atoms, if the solvent or other molecules that make up the environment of the biomolecules of interest are explicitly taken into account. This will make the dimensionality of the phase space intractably high. A common practice is to focus on the biomolecules of interest, and if proteins are such biomolecules, only the Cα atoms of the amino acids are considered. However, even with such enormous simplification adopted, the numbers of amino acids in a typical protein range from a few dozen to several thousands, which still makes the phase space a very high dimensional space, and any numerical analysis a non-trivial problem.

Normal mode analysis (NMA), i.e., the analysis of molecular vibrations that generates a series of vibrational modes independent to each other, is one popular way of further dimensionality reduction. By neglecting the vibrational modes whose amplitudes are significantly lower, dimensionality reduction usually can be achieved remarkably. By replacing the conformation of the potential energy minimum by the average conformation, and the Hessian matrix of the potential function at the minimum by the covariance matrix constructed from molecular dynamics simulations, one achieves the "quasi-harmonic analysis (QHA)", which is also known as the principal component analysis (PCA) or essential dynamics analysis (EDA). One of the most notable advantages of PCA is the preservation of the distance metric during the linear transformation. However, this essential feature of PCA, i.e., the use of linear transformation, also prevents PCA from discovering intrinsic non-linear degrees of freedom that underlies the complex natural phenomena. Non-linear dimensionality reduction approaches are currently intensively pursued to achieve more effective descriptions of biomolecular dynamics.

In this talk, I will discuss our recent molecular dynamics simulations of two proteins in two classes of well-known drug targets, i.e., topoisomerases and G protein coupled receptors. We found it beneficiary to employed Markov State Model (MSM) analysis to filter out noisy dynamics. To delineate geometric properties of the MSM macrostates, we then embedded them onto the low dimensional space with PCA to directly visualize the functional dynamics. Besides, correlated dynamics detected with mutual information (MI) analysis also help to characterize the prominent features about how proteins carry out their functions at the atomic level.

BIOGRAPHY

Dr. Jung-Hsin Lin was born in Taipei in 1968. He received his B. Sc. and M. Sc. in Physics at Department of Physics, National Taiwan University (NTU), and Ph.D. (Dr. rer. nat.) in Biophysics at Institut für Festkörperforschung (Institute of Condensed Matter Research), Forschungszentrum Jülich (Research Center Jülich), Germany, under the supervision of Dr. Artur Baumgaertner.

After his postdoctoral research at John von Neuman Institute for Computing (NIC) at Forschungszentrum Jülich, he worked as Bioinformatics Specialist at Howard Hughes Medical Institute at University of California San Diego (UCSD), U.S.A., under the supervision of Professor J. Andrew McCammon. During this period of time, he and his colleagues in UCSD proposed the relaxed complex scheme [J. Am. Chem. Soc. 124 5632-5633 (2002)] to accommodate the dynamics of biomolecules in molecular docking and structure-based computational drug design. This method was the first that successfully reproduced the "SAR by NMR" (a paradigm in fragment-based drug discovery) experimental results. After he returned to Taiwan, he and his colleagues in NTU proposed novel efficient global optimization algorithm for the molecular docking problem, and his lab has proposed generally-applicable robust scoring functions for protein-ligand interactions. He is a Research Fellow of Research Center for Applied Sciences (RCAS), Academia Sinica, and he has joint appointments with Institute of Biomedical Sciences (IBMS), Academia Sinica, and School of Pharmacy, NTU. His major research topics are on the developments and applications of computational methodologies for design and discovery of new drugs, and for unraveling the molecular mechanisms of biological systems based on fundamental physical chemical principles, with the help of molecular modeling and simulations.

Prof. Lin is a member of American Chemical Society, U.S. Biophysical Society, and Taiwan Biophysical Society. He frequently gave seminars and sometimes plenary lectures in international conferences. He serves as reviewers for more than 30 scientific journals, and he is currently serving in the Editorial Board of Advances in Physics X. He is the Chief Executive Officer of the Thematic Center for Biomedical Applications of RCAS since January, 2015.

Technical Session D2-W1-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Development of TOP-PCR (T Oligo-primed Polymerase Chain Reaction) for Efficient Amplification of Trace Amount of DNA in Body Fluids

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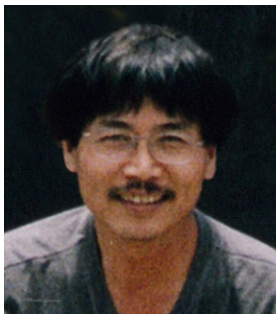
ABSTRACT

The paired-end ditag technology that we first developed in Singapore directly links the 5' terminal tag of ~18-20 bp of a genomic DNA fragment or cDNA to its corresponding 3' terminal tag for high throughput (HTP) sequencing. It has led to a number of important discoveries, but the procedure was tedious and not suitable for next-generation sequencing (NGS). To simplify the experimental procedure and increase the throughput, we recently invented a technology called barcoded Paired-End Ditag (bPED). In bPED procedure, a homogeneous half adaptor (HA) is first prepared by annealing T oligo (which carries an extra T at the 3' end) with P oligo (which has a phosphate group at the 5' end) at room temperature. In parallel, an extra A is enzymatically added to the 3' ends of the double-stranded target DNA fragments. HAs are then ligated to both ends of the target DNA fragments. A second ligation links the two HAs in the same fragment to form a full adaptor (within which a barcode is also created), and simultaneously circularize the target DNA molecule. A subsequent MmeI digestion releases the ditag sequences. By combining multiple bPED libraries, each labeled with a unique internal barcode, one can generate a multiplex barcoded Paired-End Ditag (mbPED) library for ultra high-throughput (UHTP) sequencing. The mbPED technology dramatically simplifies the experimental procedure because all bPED libraries can be manipulated as a single mbPED library during sequencing and for most part of the sequence data analysis. It is not only cost-effective, but also being able to save time and reduce cross-library bias, because all bPED libraries in the mbPED library are treated with the same procedure during most part of the experiment. To take the technology even further, by omitting the second ligation and allowing the HA-flanked target DNA constructs to be amplified by PCR using the T oligo alone as the primer, we developed T Oligo primed-Polymerase Chain Reaction (TOP-PCR) technology for efficiently amplification of trace amount of DNA fragments that may present in the body fluids for NGS-based analysis of genetic mutations. This technology is particularly useful if the sample volume or DNA concentration falls low the desired level, Also, it is able to rescue degraded DNA samples resulted from inappropriate or prolonged storage. The designs of all these technologies, including bPED, mbPED and TOP-PCR, are concordant with modern molecular cloning and NGS sequencing strategies which frequently add an extra 'A' to the 3' ends of the target DNA fragments, because the T oligo carries an extra 'T' at the 3' end for sticky-end ligation. Besides the simplicity in experimental procedure, these technologies conveys a number of advantages. For example, the half adaptor cannot self-ligate, so that its concentration can be well-maintained. Also, only one adaptor can be ligated to each terminus of the target DNA and only one full adaptor can be generated in each circularized construct during bPED and mbPED library construction. The bPED and mbPED approaches were

designed for the study of gene expression and regulation and identification of gene fusions, while TOP-PCR was designed for full-length amplification of potentially "all" low-abundance DNA fragments within a few Kb in size. We have empirically demonstrated its superior capability in amplifying low-abundance DNA fragments (< 0.01 pg) in cell-free plasma samples for NGS assays of cancer mutations. Results also suggested a strong potential of this approach for the diagnostics and study of genetic diseases and infectious agents.

BIOGRAPHY



Kuo-Ping Chiu was born in Changhwa County, Taiwan ROC. He got his PhD in microbiology from UC Davis, Davis, California in 1991 and did his postdoc at Harvard Medical School, Boston, Massachusetts on neurosciences during 1993-1996.

His research career is tightly associated with biotechnology development. His PhD research focused on intracellular amplification of mouse mammary tumor proviral DNA using in situ PCR to identify the infected cells, while his postdoctoral training was related to multiple colorimetric labeling of acetylcholine receptor subunit transcripts to study their coordinated expression pattern. These trainings have critical influence on his academic research career and industrial experience. His industrial experience started with a R&D Scientist position at Bio-Rad Laboratories, Hercules, California where he developed protocols and kits for antimicrobial susceptibility testing using flow cytometry (5/1996-4/1998). Later he switched from wetlab to Bioinformatics and worked for Genome Institute of Singapore on developing Paired-End diTag technology and methods for sequence data analysis (8/2002-8/2008). He moved back to Taiwan in 2008 working for Academia Sinica on developing DNA sequencing-related biotechnologies and studying gene expression and regulation/dysregulation in normal and cancer cells.

Professor Chiu is a member of The Chinese Society of Cell and Molecular Biology. He also teaches sequencing technologies, sequence data analysis and pathway analysis in a number of national universities including NTU, NCU, and National Yang-Ming University (NYMU). He has published about 30 research articles and a book entitled "Next-Generation Sequencing and Sequence Data Analysis" (Sharjah, United Arab Emirates, Bentham Science Publishers, 2015). He is holding 3 US patents related to paired-end ditag technologies. Another patent related to T Oligo-primed Polymerase Chain Reaction (TOP-PCR) is currently under processing.

Technical Session D2-W1-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Simple and efficient k-ordered FM-index construction for biological sequences

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ABSTRACT

Index structures, such as the Full-text index in Minute space (FM-index) derived from the Burrows–Wheeler transform and enhanced suffix arrays, have been widely used in NGS applications for mapping short reads to the references. Many efforts have been made to improve the efficacy of the construction of the index structure. One BWT variant, Schindler transform (a.k.a. sort transform, ST), uses only order-k contexts and is still invertible with some extra complexity and performance penalty. However, substantial advance in ST is still needed to put ST into practice for typical NGS applications. We herein propose an FM-index-like data structure, which requires no additional memory footprint than the conventional FM-index and can be constructed by novel, simple and highly parallelizable algorithms and still competent in string matching for general purposes. In our tests, the implementation proposed achieves significant speedups in indexing and searching compared to other BWT based tools. Two implementations of our algorithms are provided and were fully tested and compared with existing tools. We also applied our implementations to improve the most time consuming step in de novo assembly and thereby exemplified the broad utility of our work.

BIOGRAPHY

Jui-Hung Hung was born in Tainan City, Taiwan. He received his B.S. degree (2005) in Computer Science from National Central University, M.S. degree in Bioinformatics from National Chiao Tung University, and Ph.D. degree in Bioinformatics from Boston University. With post-doctoral experience with Dr. Zhiping Weng at University of Massachusetts Medical School, Hung conducted research in various topics of bioinformatics, especially the Next Generation Sequencing (NGS) analysis and bioinformatics algorithm design for parallel computing.

Technical Session D2-W2-T2: Medicine and Life Sciences, Biological and Biomedical Sciences

Session Chair

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BIOGRAPHY

Shih-Jen Liu received his BS in pharmacy at 1989 from Kaohsiung Medical College, Taiwan. After 4 years, He got his Master degree in pharmacology from National Cheng-Kung University, Taiwan at 1993. He then finished his Ph.D. degree in life Science from National Defense Medical Center at 1998. He spent 5-years (1998-2003) in a biotechnological company to develop dendritic cells-based immunotherapy. He and his collaborators conducted the first private company-involved phase I clinical trial in Taiwan. He joined Vaccine Research and Development Center of National Health Research Institutes (NHRI) in 2004. He is now an Associate Investigator at National Institute of Infectious Diseases and Vaccinology in NHRI, and an Associate Professor in China Medical University, Taiwan. His research interests include discovery of human cytotoxic T lymphocyte (CTL) epitopes to develop therapeutic vaccines and studies of the molecular mechanism of novel adjuvants. He also found that the antigen presentation mechanisms of lipopetides are different according to the lipid moiety. The TLR2 agonist conjugated long peptide could regulate the process of antigen presentation. Currently, he collaborates with his colleagues to develop recombinant lipoprotein platform technologies and applied to the therapeutic HPV vaccine. This approach is promising for eliminating large tumor and reducing the tumor associated immunosuppressive cells number.

His works have received numerous honors. The “Therapeutic HPV Vaccine” was awarded The ninth “National Innovation Award” by the Institute for Biotechnology and Medicine Industry (2013). The recombinant lipoprotein technology was awarded the seventh “National Innovation Award” by the Institute for Biotechnology and Medicine Industry (2010), and “Silver Invention Award” by the Ministry of Economic Affair, Taiwan (2012). He has more than 50 publications and numerous patents. His work has had a tremendous impact on elucidating the vaccinology and immunology of development of therapeutic vaccines to HPV-associated cancers.

Technical Session D2-W2-T2: Medicine and Life Sciences, Biological and Biomedical Sciences

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ABSTRACT

BIOGRAPHY

Technical Session D2-W2-T2: Medicine and Life Sciences, Biological and Biomedical Sciences

The effects of microRNAs in MAPK/ERK signaling pathway in Melanoma

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ABSTRACT

MicroRNAs (miRNAs) have revolutionized our comprehension of post-transcriptional regulation of gene expression and modulated a broad range of biological function including the pathogenesis of disease. Moreover, miRNAs act as oncomirs or as tumor suppressors applied in therapeutic targets.

The mitogen-activated protein kinase (MAPK) signaling pathway occupies an essential role in many cancer progressions. For instance, highly activated MAPK/ERK pathway is found in over 60 % of melanoma cells and related to proliferation, migration of tumor. However, there are many regulations of MAPK/ERK pathways still undefined and there is little identified miRNAs information linked to MAPK/ERK signaling pathway. It will be very important to study what miRNAs are associated with MAPK/ERK signaling pathway and how they mediate MAPK/ERK pathway.

We performed a miRNAs array screen by the MAPK/ERK signaling inhibitors to search miRNAs, which are involved in MAPK/ERK signaling pathway. We have successfully identified 22 miRNAs associated with MAPK/ERK pathway, and our initial study demonstrated that miR-524-5p plays an important function in regulating MAPK/ERK signaling. We showed that the expression of miR-524-5p is regulated by MAPK/ERK activity; and intriguingly, over-expression of miR-524-5p results in down regulation of MAPK/ERK signaling pathway. Furthermore, we demonstrated miR-524-5p mechanistically and directly represses two oncoproteins: BRAF and ERK2, and over-expression of miR-524-5p suppresses cell proliferation, migration, and transformation activity of activated MAPK/ERK in melanoma cells. Besides miR-524-5p, our recent results showed that the expression of another eight miRNAs have regulated by the activity of MAPK/ERK signaling. This research is to get the clear picture of molecular network of miRNAs in signaling pathways and functions of miRNAs. The knowledge can potentially be extended to discovery of new diagnosis or therapy targets for diseases and can be used in both basic and translational medicine research.

BIOGRAPHY

Nianhan Ma was born in Taiwan. She received her B.S. (1996) in Bontany from National Chung Hsing University and M.S. (1998) in Biochemistry from National Taiwan University. She attained her Ph.D. training in the field of genomic instability at Yale University in New Haven between 2003-2008. She was a research scholar at Memorial Sloan-Kettering Cancer Center in New York to expand her training in clinical cancer research from 2008-2010. She joined the

faculty of Institute of Systems Biology and Bioinformatics at National Central University in Taiwan in 2010. Dr. Ma's research has focused on investigating significant miRNAs as possible biomarkers or therapies for human diseases, and dissecting mechanism of herbs regarding to minimize side effects of chemotherapy. She has authored a peer-reviewed book chapter and journals on these topics. She was awarded as the excellent teacher award in 2013 and the outstanding research award in 2014 from National Central University.

Technical Session D2-W2-T2: Medicine and Life Sciences, Biological and Biomedical Sciences

Cellular Reprogramming Approaches for the Generation of Human Induced Neurons and Inner Ear Hair Cells

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ABSTRACT

Recent advances in somatic cell reprogramming have illustrated the malleability of the somatic epigenome, particularly through demonstrations of reprogramming of adult mouse and human fibroblasts and blood cells to induced pluripotent stem (iPS) cells. More recent studies showed direct lineage reprogramming of human fibroblasts to cardiomyocytes and induced neurons (iNs) under defined conditions. However, human cells appear to be less plastic and have a higher epigenetic hurdle for reprogramming to iNs. We have developed an efficient method to enhance neurite outgrowth of iNs reprogrammed from human fibroblasts as early as Day 14, when combined with miR124, BRN2 and MYT1L (IBM) under defined condition. Currently, we are applying this approach to generate human inner ear hair cells by combining different transcription factors.

BIOGRAPHY

Yi-Chao Hsu received his M.S. (2002) and Ph.D. (2005) from the National Yang-Ming University, Taipei, both in Pharmacology, and was a postdoctoral fellow at the Institute of Cellular and System Medicine, NHRI, Taiwan, between 2006 and 2012. Currently he is an Assistant Professor of Institute of Biomedical Sciences, Mackay Medical College, New Taipei City. Currently, Dr. Hsu's research focuses on cellular reprogramming and stem cell translation medicine, especially on neurological diseases and hearing loss.

Technical Session D2-W2-T2: Medicine and Life Sciences, Biological and Biomedical Sciences

Low-dose resveratrol ameliorates lupus nephritis by restoration of FcγRIIB expression on autoreactive B lymphocytes to induce apoptosis

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ABSTRACT

FcγRIIB is a dominant negative regulator of B cell activation and it is essential for protection against antibody-mediated autoimmune diseases. Recent evidence indicates that the surface expression of FcγRIIB is down-regulated specifically on B cells in patients with systemic lupus erythematosus (SLE), leading to uncontrolled expansion of B cells to produce massive amounts of autoantibodies. In contrast, overexpression of FcγRIIB in B cells reduces onset of lupus in MRL/lpr mice. We previously demonstrated that homo-aggregation of FcγRIIB by immune complexes (ICs) results in apoptosis in B cells when their expression level of FcγRIIB is sufficiently high. Here we show that upregulation of FcγRIIB's expression on B cells in full-blown MRL/lpr mice by a low-dose treatment of resveratrol renders autoreactive B cells susceptible to FcγRIIB-mediated apoptosis triggered by circulating excess ICs. Resveratrol inhibited NF-κB p65 to up-regulate transcription of FcγRIIB in B cells. While other immune cells were virtually unaffected the low-dose resveratrol significantly reduced the number of B cells in the spleen, blood and even bone marrow as a result of a concomitant increase of apoptosis through FcγRIIB. Consistently the serum level of autoantibodies significantly decreased, thereby leading to marked improvement of nephritis and extended survival in resveratrol treated mice. Taken together, our data demonstrate that restoration of the expression level of FcγRIIB on B cells by a low dose of resveratrol can allow excess ICs to trigger apoptosis and self-eliminate autoreactive B cells to alleviate lupus nephritis. Thus, our results underscore the potential of FcγRIIB for pharmacological modulation to treat autoimmune diseases by re-establishing a physiological checkpoint crucial for B cell homeostasis.

BIOGRAPHY

Shiang-Jong Tzeng is a principle investigator of the Graduate Institute of Pharmacology at National Taiwan University. He received his Ph.D. from the department of Biochemistry, Molecular Biology and Cell Biology of Northwestern University, Evanton, IL, USA. in 2000 and then went to National Institute of Allergy and Infectious Diseases (NIAID) for post-doctoral training. In addition, he is a medical doctor and specializes in obstetrics and gynecology. Dr. Tzeng's research interests include immune related disorders, immunotherapeutics and immunopharmacology. At present, his primary focus is on the inhibitory Fc receptor, FcγRIIB. Both in vitro and in vivo models are used to study FcγRIIB's functional role and its signal transduction. Since FcγRIIB is the dominant inhibitory receptor in B cells, Fc receptor biology and antibody-mediated immune dysfunction, e.g. systemic lupus erythematosus, are current research topics. In terms of the ligand of Fc

receptors, generation and characterization of human therapeutic antibodies, e.g. neutralizing antibodies for influenza, are current interests.

Technical Session D2-W3-T2: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Session Chair

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BIOGRAPHY

Dr. Kung-Bin Sung received a B.S. degree in Electrical Engineering from National Taiwan University, Taiwan. He received M.S. and Ph.D. degrees from The University of Texas at Austin in 1999 and 2003, respectively. He joined Intel Corporation as a research scientist in 2003 and collaborated with researchers at the Fred Hutchinson Cancer Research Center on research projects related to surface-enhanced Raman spectroscopy. Since July 2006 he has been with the Department of Electrical Engineering and the Graduate Institute of Biomedical Electronics and Bioinformatics in National Taiwan University, where he is currently an Associate Professor. His research focuses on optical spectroscopy and microscopy for the diagnostics of diseases, especially precancerous lesions and early cancers.

Technical Session D2-W3-T2: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Hybrid Nano-constructs for Cancer Therapy

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ABSTRACT

Two strategies using hybrid nano-constructs for cancer therapy were discussed herein. The first entails a design of photocaged folate nanoconjugates that selectively target cancer cells upon irradiation with UV light, where the folic acid (FA) was masked by a photocleavable o-nitrobenzyl (ONB) group through covalently binding to a- and g-carboxylate groups, that interact with folate receptors (FRs) on the cell surface. Subsequently the light-activated targeting and intracellular drug delivery were demonstrated using biodegradable PLGA@lipid hybrid nanoparticles [PLGA, poly(D,L-lactide-co-glycolide)] encapsulating the drug paclitaxel (Taxol). Light illumination triggered uncaging and activated FA for targeting. The FA-mediated cellular internalization allowed degradable PLGA@lipid nanoparticles to release Taxol, thereby causing a higher cytotoxicity to the target cells than the unactivated nanoparticles. The second involves the fabrication of a highly efficient, non-cytotoxic drug delivery platform designed for photodynamic therapy (PDT): phospholipid-capped, protoporphyrin IX-loaded and FITC-sensitized mesoporous silica nanocarriers (Lipo-FMSNs/PpIX). After derivatization with folate on the phospholipid-capped FMSNs (denoted fa-Lipo-FMSNs/PpIX, the so-called nanoPDT system), we confirmed the nanoPDT systems' selective targeting of and entry into the folic acid receptor-overexpressed HeLa cells by means of cell viability assessment and confocal microscopic analysis. The decrease in the unfavorable dark toxicity of fa-Lipo-FMSNs/PpIX enabled the delivery of high concentrations of PpIX into cells. Moreover, the cellular uptake of the nanoPDT systems was greater than that of free PpIX. Upon irradiation with visible light, the nanoPDT system generated singlet oxygen efficaciously in aqueous environments a decisive factor affecting its therapeutic applicability in PDT, demonstrating enhanced in vitro photocytotoxicity. Furthermore, an in vivo study of subcutaneous melanoma in nude mice inoculated with B16F10 cells revealed the capability for the nanoPDT system to mitigate nearly 65% of tumor growth.

BIOGRAPHY

Ja-an Annie Ho was born in Taipei, Taiwan at 1968. She received her PhD from College of Agriculture and Life Science, Cornell University (Ithaca, New York, USA) in 1998 with focuses in liposome technology and sensor development.

She is currently a Professor of Chemistry, who runs a Bioanalytical Chemistry and Nanobiomedicine Laboratory in the Department of Biochemical Science and Technology at the National Taiwan University (Taipei, Taiwan). Her group has focused on the development of various

immune- or genobiosensors for biomedical applications using nanomaterials. More recently her lab has become increasingly interested in the development of nano-drug delivery system to improve the efficacy of cancer therapies.

Professor Ho serves as Editorial Board Members for PLOS One (Open Access, 2013–present), Antibody Technology Journal (Dovepress, 2010–present), Journal of Food and Drug Analysis (Science Direct, Elsevier, 2014–present), and was Editorial Advisory Board Member for Talanta (Science Direct, Elsevier, 2005–2011). Professor Ho is a member of the American Chemical Society and Agricultural Chemical Society of Taiwan, who is the author of more than seventy publications on international journals.

Technical Session D2-W3-T2: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Polypeptide Multilayer-Coated Electrodes for Monitoring Differentiation of Human Mesenchymal Stem Cells into Cardiomyocytes

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ABSTRACT

Real-time label free techniques are desired when monitoring stem cell differentiation. Here, we applied electric cell-substrate impedance sensing (ECIS) to monitor cardiac differentiation of human mesenchymal stem cells (hMSCs) derived from umbilical cords. In this method, hMSCs were seeded on top of small gold film electrodes and allowed to form confluent cell layers, and the impedance time courses of the cell-covered electrodes throughout the induction towards cardiomyocytes were measured up to 10 days at 11 frequencies ranging from 62.5 Hz to 64 kHz. To enhance hMSC differentiation towards cardiomyocytes, we used cross-linked polypeptide multilayer films, a type of polyelectrolyte multilayer (PEM) films, to modify the microenvironment of the cells. The technique used to make these polypeptide multilayer films was the layer-by-layer deposition. Compared with the data of undifferentiated hMSCs, significantly lower impedance time courses of hMSCs treated with cardiac differentiation medium were observed. In addition, these two distinct time course profiles were detected as early as a few hours after induction and lasted for 10 days. To detect subtle changes in cell morphology in the early stage of cardiac differentiation, the frequency-dependent impedance data were analyzed with a theoretical cell-electrode model. The results showed that the decrease of measured impedance of differentiated cells was mainly due to a decrease of the junctional resistance between cells and an increase of the cell-substrate separation. We also analyzed the impedance changes between the differentiated groups with the cross-linked polypeptide multilayer film and without it. The results showed that hMSC differentiation towards cardiomyocytes is augmented when cross-linked polypeptide multilayer films were used.

BIOGRAPHY

Chun-Min Lo was born in Chia-Yi, Taiwan. He received his BS (1985) in physics from National Taiwan Normal University and MS (1987) in physics from National Tsing Hua University. He received his Ph.D. (1994) in physics from Rensselaer Polytechnic Institute, Troy, NY. He was a postdoctoral associate at the University of Toronto and the University of Massachusetts Medical School. He was an Assistant Professor at the Cleveland State University and at the University of South Florida. He is currently an Associate Professor in the Department of Biomedical Engineering at the National Yang-Ming University, Taipei, Taiwan. His research interests presently include electric cell-substrate impedance sensing, mechanobiology, and the application of polypeptide

multilayer films for stem cell differentiation. Dr. Lo is a member of American Physical Society, Biophysical Society, Biomedical Engineering Society, and the American Society for Cell Biology.

Technical Session D2-W3-T2: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Microfluidic chip-approach for dissociating neurosphere cell aggregates

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ABSTRACT

When cultured in-vitro, the self-renewal property of neural stem cells (NSC) results into spherical clusters of neural stem cells termed neurospheres. Neurospheres consist of multipotent NSCs, and thus they provide a useful model for studying the self-renewal and proliferation of neural stem cells. In neurosphere culture, dissociation of neurospheres into single neural stem cells is an indispensable step for the subculture and analysis of neural stem cells, and is usually achieved by enzymatic dissociation or manual pipetting. In this talk, the development of a microfluidic-chip-based method for neurosphere dissociation will be presented. The applicability of this device as demonstrated by using mouse neural stem cells models will also be demonstrated. This microfluidic-chip-based cell dissociation method may provide a useful tool for stem cell research and applications.

BIOGRAPHY

Chia-Hsien Hsu obtained his bachelor degree from National Chung Hsing University (1997) and master degree from National Chung Cheng University (1999) in Taiwan. He received his Ph.D. degree from University of Washington in USA (2006). From 2006 to 2009, Dr. Hsu worked as postdoctoral research fellow in Dr. Mehmet Toner's Labs at Harvard Medical School. After his Postdoctoral training, Dr. Hsu joined the Division of Medical Engineering Research at National Health Research Institutes in Taiwan, where he currently serves as an Assistant Investigator. Dr. Chia-Hsien Hsu's research interests include development and applications of Microfluidic technology in cancer, stem cell and regenerative medicine. Dr. Chia-Hsien Hsu has authored more than twenty peer-reviewed papers and two patents and severed as reviewer for several scientific journals.

Technical Session D2-W3-T2: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Development and Application of Functional Nanogenerators

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ABSTRACT

Self-powered nanosensors that can function without external power sources have recently been demonstrated as new approaches for pressure, pH, humidity, and temperature sensing. By harvesting energy directly from the environment to power biomedical devices, these self-powered sensors and systems are advantageous in minimizing the size, having long-term operation (little maintenance), and avoiding the use of environmentally unfriendly materials in battery.

Since the first invention of triboelectric nanogenerator (TENG) in 2012, it has been developed into a new energy technology. TENG has been applied to efficiently convert the mechanical vibration into electricity. The fundamental mechanism of the TENG is based on surface charge transfer, which is through the contact between two materials with different triboelectric polarity. The serial contact and separation of the material surfaces with opposite charges establishes a potential difference, which will drive the electrons flow through the external load. Because the capability of surface charge transfer depends on the physical and chemical properties of the surfaces, in this research we further functionalize the material surface for selective detection of light, mercury ion, and catechin molecule. The self-powered nanosensors developed here are future sensing system for unreachable and access-denied extreme environments.

BIOGRAPHY

Zong-Hong Lin received his B.S. (2003) and M.S. (2005) in Department of Chemistry from the National Chung Cheng University. He completed his Ph.D. (2009) from the National Taiwan University, also in Department of Chemistry. After one year in the army (2009-2010), he started his postdoctoral career at the National Taiwan University between 2010 and 2012. Then he joined Georgia Institute of Technology as a postdoctoral fellow between 2012 and 2014. Currently he is an Assistant Professor in Institute of Biomedical Engineering, National Tsing Hua University. Dr. Lin's research focuses on design of smart nanogenerators with high outputs, development of self-powered nanosensors and nanosystems, detection of biomolecules through surface-enhanced Raman spectroscopy, and preparation of functional nanomaterials for electrochemical and antibacterial applications. He has published over 70 papers (h-index 23) and served on the program and organizing committees of various international workshops and conferences.

Technical Session D2-W4-T2: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Session Chair

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BIOGRAPHY

Hung-Yu Wei is a Professor in Department of Electrical Engineering and Graduate Institute of Communications Engineering, National Taiwan University. He received the B.S. degree in electrical engineering from National Taiwan University in 1999. He received the M.S. and the Ph.D. degree in electrical engineering from Columbia University in 2001 and 2005 respectively. He was a summer intern at Telcordia Applied Research in 2000 and 2001. He was with NEC Labs America from 2003 to 2005. He joined Department of Electrical Engineering at the National Taiwan University in July 2005. His research interests include wireless mesh networks, mobility management in mobile Internet, sensor networks, cross-layer design and optimization in wireless multimedia communications, and game theoretical models for communications networks.

Dr. Wei received NTU Excellent Teaching Award in 2008. He also received "Recruiting Outstanding Young Scholar Award" from the Foundation for the Advancement of Outstanding Scholarship in 2006, K. T. Li Young Researcher Award from ACM Taipei/Taiwan Chapter and The Institute of Information and Computing Machinery in 2012, Ministry of Science and Technology Research Project for Excellent Young Scholars in 2014, Excellent Young Engineer Award from the Chinese Institute of Electrical Engineering in 2014, and Wu Ta You Memorial Award from MOST in 2015.He has been actively participating in NGMN, IEEE 802.16 and 3GPP standardization, and was a voting member of the IEEE 802.16 working group.

Technical Session D2-W4-T2: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

3D Liver Vessel Reconstruction from CT Images

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ABSTRACT

Liver segmentation from computed tomography (CT) images is important in clinical liver surgical planning. In this research, we focus on the liver vessel segmentation from CT images. Liver vessel segmentation is a challenging task due to the low quality of vessel information in the CT images, which leads to errors in vessel detection and vessel type classification due to the complex vessel structures, such as portal vein, and hepatic vein to the goal of this thesis is to improve the vessel segmentation result and classify the liver venous vessel into meaningful part.

In this talk, I will present an integrated framework for reconstructing 3D liver venous vessel model from 3D CT images. The proposed framework consists of vessel detection, vessel connectivity, vessel classification and vessel radius refinement. Experimental results will be shown to demonstrate the improved performance of the proposed algorithms on 20 CT datasets compared to the original tubular filter.

BIOGRAPHY

Shang-Hong Lai received the Ph.D. degree in electrical and computer engineering from University of Florida, Gainesville, in 1995. He joined Siemens Corporate Research in Princeton, New Jersey, USA, as a member of technical staff in 1995. Since 1999, he returned to Taiwan to be a faculty member in the Department of Computer Science, National Tsing Hua University, Taiwan. He is currently a professor and the chair in the same department. In 2004, he was a visiting scholar with Princeton University. Dr. Lai's research interests include computer vision, visual computing, pattern recognition, medical imaging, and multimedia signal processing. He has authored more than 200 papers published in the related international journals and conferences. Dr. Lai has been a member of program committee of several international conferences, including CVPR, ICCV, ECCV, ACCV, ACM MM, ICPR, PG, PSIVT and ICME. He has been an associate editor for Journal of Signal Processing Systems. Moreover, he also served as a guest editor for special issues in Journal of Visual Communication and Image Representation as well as Journal of Signal Processing Systems.

Technical Session D2-W4-T2: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Chii-Wann Lin

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ABSTRACT

BIOGRAPHY

Technical Session D2-W4-T2: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Neuromarkers for predicting the rehabilitation outcome after stroke

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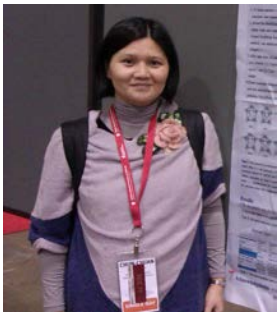
ABSTRACT

In this study, we aim to identify the key neuromakers that could allow for accurately predicting the rehabilitation outcome after stroke. Specifically, the pre-rehabilitation electroencephalogram (EEG) and machine learning technique will be used to extract the key patterns underlying the stroke recovery process. 37 stroke patients were recruited for this study. All patients underwent 24-hour occupational therapy and the rehabilitation outcome was measured with FM, TEMP and WMFT. We used supervised machine learning method and first divided the data into two groups -- good and general recovery, according to the following criterion : a level of 10% improvement of any above mentioned measures after rehabilitation was considered as good recovery, resulting in 20 good recovery patients. Before the rehabilitation, the EEG data were acquired during the shoulder flexion for eighty trials and were pre-processed offline for filtering and epoching. Dynamical Causal Modelling for induced responses (DCM_IR), an advanced signal processing method, was employed for extracting the EEG features. These extracted features entered Wrapper method to select the significant features , and the selected features went into the four different classifiers : SVM, Logistic Regression, NaiveBayes, J48) for two-class classification.

The classification result suggests that, the best accuracy rate was 0.92 when using DCM features of β+ frequencies of Type I data and Logistic Regression. Furthermore, the classification accuracy rate was up to 0.8319 when using only β frequency DCM features, indicating that beta rhythm within the motor network have a significant impact on recovery. We believe that our finding can help to facilitate the result of rehabilitation by developing a knowledge-based rehabilitation programme.

BIOGRAPHY



Chun-Chuan Chen was born in Taiwan in 1974. She received her BS and MS degrees from Department of Medical Radiation Technology, National Yang-Ming University, Taipei, Taiwan in 1997 and Institute of Biomedical Engineering, National Cheng-Kung University, Tainan, Taiwan in 1999, respectively. In 2009, Chun-Chuan Chen received her PhD from Wellcome Dept. Imaging Neuroscience, UCL, UK, She worked as a post-doc fellow at Institute of Biomedical Engineering, National Central University, Taiwan from 2009~2010. She was appointed as an assistant professor in 2010 and was promoted as an associate professor in 2015 at Institute of Biomedical Engineering, National Central

University, Taiwan. Her research interest is about exploring the intricate brain functions by means of network connections, spanning from methodology development toward scientific applications, in particular, in the field of motor networks in healthy and disease states, such as motor control, sensory-motor / visual-motor interactions/integrations, age-dependent motor network alternation, the mechanism underlying plastic changes in motor system after stroke.

Technical Session D2-W4-T2: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Shih-Ching Yeh

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ABSTRACT

BIOGRAPHY

Student Poster Competition

Session Chair

Hsueh-Fen Juan

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BIOGRAPHY

Hsueh-Fen Juan was born in 1969, Miao-Li, Taiwan. She received her BS and MS degree in Botany and PhD in Biochemical Sciences from National Taiwan University (NTU) in 1999. She worked as a research scientist in the Japan International Research Center for Agricultural Sciences (Tsukuba, Japan) during 2000-2001 and a postdoctoral research fellow in the Institute of Biological Chemistry, Academia Sinica (Taipei, Taiwan) during 2001-2002.

She started her academic career in the Department of Chemical Engineering, National Taipei University of Technology as an assistant professor and in the Department of Computer Science and Information Engineering at NTU as an adjunct assistant professor in 2002. She moved to NTU in 2004 as an assistant professor in the Department of Life Science and the Institute of Molecular and Cellular Biology. She was promoted to be an associate professor in 2006 and full professor in 2009. Dr. Juan is currently working on cancer systems biology, integrating transcriptomics, proteomics and bioinformatics for biomarker and drug discovery.

Prof. Juan has developed a number of novel methods to advance systems-biology research and applied such approach for drug discovery and elucidating molecular mechanism of drug responses in cancer cells. She has published more than 85 journal papers including prestigious journals such as Briefings in Bioinformatics, Proc. Natl. Acad. Sci. USA, Cancer Research, Nucleic Acids Research, Oncogene, Bioinformatics. She is now the editor of Scientific Reports (Nature Publishing Group), Computational and Mathematical Methods in Medicine (Hindawi Publishing Corporation), PeerJ, PeerJ Computer Science and Stem Cell Treatments (Publisher Frontiers, joining Nature Publishing Group). She also serves as a reviewer of various journals like Molecular and Cellular Proteomics (ASBMB), Proteomics (Wiley-VCH), BMC Bioinformatics, and has organized several international systems biology and bioinformatics symposiums. She is one of the founders of Center for Systems Biology (NTU), and currently the Board Member in The Taiwan Society for Biochemistry and Molecular Biology, Taiwan Proteomics Society, and Taiwan Bioinformatics and System Biology Society. Since Dr. Juan made significant contributions through systems biology approach to development of methodology and cancer therapy; she received the awards “Taiwan's Ten Outstanding Young Persons” (2008), FY2011 JSPS Invitation Fellowship Program for Research in Japan (2011), K. T. Li Breakthrough Award by Institute of Information and Computing Machinery (2012), and National Science Council (NSC) Award for Special Talents of the Colleges (2010-2015).

Student Poster Competition

Session Co-Chair

Chia-Lang Hsu

Postdoctoral Fellow, Institute of Molecular and Cellular Biology, and Department of Life Science
National Taiwan University
(台灣大學分子細胞生物學研究所許家郎博士)

BIOGRAPHY

Technical Session D2-W1-T3: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Session Chair

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BIOGRAPHY

Dr. Jung-Hsin Lin was born in Taipei in 1968. He received his B. Sc. and M. Sc. in Physics at Department of Physics, National Taiwan University (NTU), and Ph.D. (Dr. rer. nat.) in Biophysics at Institut für Festkörperforschung (Institute of Condensed Matter Research), Forschungszentrum Jülich (Research Center Jülich), Germany, under the supervision of Dr. Artur Baumgaertner.

After his postdoctoral research at John von Neuman Institute for Computing (NIC) at Forschungszentrum Jülich, he worked as Bioinformatics Specialist at Howard Hughes Medical Institute at University of California San Diego (UCSD), U.S.A., under the supervision of Professor J. Andrew McCammon. During this period of time, he and his colleagues in UCSD proposed the relaxed complex scheme [J. Am. Chem. Soc. 124 5632-5633 (2002)] to accommodate the dynamics of biomolecules in molecular docking and structure-based computational drug design. This method was the first that successfully reproduced the "SAR by NMR" (a paradigm in fragment-based drug discovery) experimental results. After he returned to Taiwan, he and his colleagues in NTU proposed novel efficient global optimization algorithm for the molecular docking problem, and his lab has proposed generally-applicable robust scoring functions for protein-ligand interactions. He is a Research Fellow of Research Center for Applied Sciences (RCAS), Academia Sinica, and he has joint appointments with Institute of Biomedical Sciences (IBMS), Academia Sinica, and School of Pharmacy, NTU. His major research topics are on the developments and applications of computational methodologies for design and discovery of new drugs, and for unraveling the molecular mechanisms of biological systems based on fundamental physical chemical principles, with the help of molecular modeling and simulations.

Prof. Lin is a member of American Chemical Society, U.S. Biophysical Society, and Taiwan Biophysical Society. He frequently gave seminars and sometimes plenary lectures in international conferences. He serves as reviewers for more than 30 scientific journals, and he is currently serving in the Editorial Board of Advances in Physics X. He is the Chief Executive Officer of the Thematic Center for Biomedical Applications of RCAS since January, 2015.

Technical Session D2-W1-T3: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

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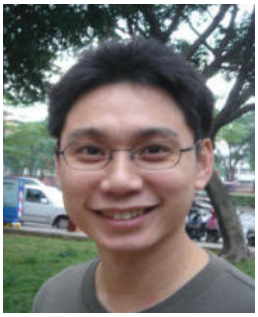
ABSTRACT

Mutation of a single amino acid residue can cause changes in a protein, which could then lead to a loss of protein function. Predicting the protein stability changes can provide several possible candidates for the novel protein designing. Although many prediction tools are available, the conflicting prediction results from different tools could cause confusion to users.

We proposed an integrated predictor, iStable, with grid computing architecture constructed by usingsequence information and prediction results from different element predictors. In the learning model, several machine learning methods were evaluated and adopted the support vector machine as an integrator, while not just choosing the majority answer given by element predictors. Furthermore, the role of the sequence information played was analyzed in our model, and an 11-window size was determined. On the other hand, iStable is available with two different input types: structural and sequential. After training and cross-validation, iStable has better performance than all of the element predictors on several datasets. Under different classifications and conditions for validation, this study has also shown better overall performance in different types of secondary structures, relative solvent accessibility circumstances, protein memberships in different superfamilies, and experimental conditions. The trained and validated version of iStable provides an accurate approach for prediction of protein stability changes. iStable is freely available online at: http://predictor.nchu.edu.tw/iStable.

BIOGRAPHY



I was born in Keelung, Taiwan on July 26th, 1969 and received my Ph.D. degree in Bioinformatics in 2006 from the Department of Computer Science, National Chiao Tung University, Hsinchu, Taiwan.

He is an Associate Professor of the Institute of Genomics and Bioinformatics at National Chung Hsing University, Taichung, Taiwan, where he has been since 2008. During 2003-2006, he was a Lecturer of Department of Information Management at China University of Technology and Yuanpei University of Medical Technology. During 2006-2008, he was an assistant of Department of Bioinformatics at Asia University. During 2008-2012, he was an assistant of Institute of Genomics and Bioinformatics at National Chung Hsing University. His lab had constructed OOGB database for Oncidium (Plant and Cell Physiology, 2011, cited: 28) and iStable web tool for protein stability changes problem (BMC Bioinformatics, 2013, cited: 15). His research interests center on developing new bioinformatics algorithms for improving the biological prediction systems.

Prof. Chu won the award for best paper at the 25th International Conference on Information Management. During 2010-2015, his publication list as the follows.

JOURNAL:

1. Chi-Wei Chen, Jerome Lin, and **Yen-Wei Chu*** (2013) iStable: Off-the-shelf Predictor Integration for Predicting Protein Stability Changes, BMC Bioinformatics, 14(suppl 2):S5, doi:10.1186/1471-2105-14-S2-S5

2. Wei-Jie Pan, Chi-Wei Chen, Heng-Hao Liang, **Yen-Wei Chu*** (2012) Selecting High Efficacy siRNAs by Computational Models, Advanced Science Letters, 18: 141-144.

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4. Po-Chang Chang, Wei-Jie Pan, Chi-Wei Chen,Yu-Ting Chen and **Yen-Wei Chu*** (2012) DEsi: an design engine of siRNA that integrates SVMs prediction and feature filters, Biocatalysis and Agricultural Biotechnology, doi: 10.1016/j.bcab.2012.01.005

5. Wei-Jie Pan, Chi-Wei Chen and **Yen-Wei Chu*** (2011) siPRED: Predicting siRNA efficacy using various characteristic methods, PLoS ONE, doi: 10.1371/journal.pone.0027602 (SCI: 4.092)

6. Yu-Yun Chang+, **Yen-Wei Chu+**, Chi-Wei Chen, Wei-Ming Leu, Hsing-Fun Hsu and Chang-Hsien Yang* (2011) Characterization of Oncidium 'Gower Ramsey' Transcriptomes using 454 GS-FLX Pyrosequencing and Their Application to the Identification of Genes Associated with Flowering Time, Plant and Cell Physiol., 52(9): 1532-1545.

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1. Ci-Jhou Liao, Liang-Jwu Chen, **Yen-Wei Chu*** (2014) Using machine learning approach to predict the flanking genes expression in T-DNA insertion activation-tagged rice lines, Summer Workshop on Plant Molecular Biology, Nantou County, Taiwan, July 4-6.

2. Chi-Wei Chen, Hui-Chih Hung, **Yen-Wei Chu*** (2014) Citrullination Sites Prediction by Machine Learning Approaches, Proceedings of the 19th Taiwan Academic Network Conference, pp. 1-13.

3. Chi-Wei Chen, Hui-Chih Hung, **Yen-Wei Chu*** (2013) Feature Model Integration by Evolutionary Computation for Predicting Protein Citrullination sites, Proceedings of the 19th Taiwan Academic Network Conference, pp. 1047-1052.

4. Hao-Chen Chang and **Yen-Wei Chu*** (2013) Gelatinase Substrate Cleavage Sites Prediction Using Machine Learning and Feature Selection, Proceedings of the 19th Taiwan Academic Network Conference, pp. 1053-1058.

5. Chi-Wei Chen, Jerome Lin, and **Yen-Wei Chu*** (2013) iStable: Off-the-shelf Predictor Integration for Predicting Protein Stability Changes, The Eleventh Asia Pacific Bioinformatics Conference, Vancouver, BC, Canada, January 21-23.

6. Wen-Pin Hu, Chi-Wei Chen, Jian-Shiun Chen, and **Yen-Wei Chu*** (2012) Evaluating various machine learning approaches for the sunspot number prediction. Symposium of university league in Changhua, Yunlin, and Chiayi, Taiwan, December 7.

7. Yu-Yun Chang, **Yen-Wei Chu**, Wei-Ming Leu and Chang-Hsien Yang* (2011).Characterization of Oncidium 'Gower Ramsey' transcriptome for using GS-FLX 454 pyrosequencing and its application for studies of flowering time associate genes. The International Conference Plant Gene Discovery Technologies. Venue. February 23- 26.

8. Yu-Yun Chang, **Yen-Wei Chu**, Hsing-Fun Hsu, Chi-Wei Chen, Wei-Ming Leu and Chang-Hsien Yang* (2011). Characterization of Oncidium 'Gower Ramsey' transcriptomes using 454 GS-FLX pyrosequencing and their application to theidentification of genes associated with flowering time. 2011 Canadian Plant Genomics Workshop, Niagara Falls, Ontario. Canada, August 22-25.

9. Wei-Jie Pan, Chi-Wei Chen and **Yen-Wei Chu*** (2011) High efficacy siRNA selection using machine learning approach, Proceedings of 2011 Joint Conference on 7th Taiwan Software Engineering (TCSE) and 22nd Object-Oriented Technology and Applications (OOTA), pp. 94-99

Technical Session D2-W1-T3: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Next-generation sequencing identifies novel, rare variants associated with human genetic diseases

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ABSTRACT

Noonan syndrome (NS) is one of several RASopathies, which are developmental disorders caused by mutations in genes encoding RAS-ERK pathway components. The cause of 20-30% of NS cases remains unknown, and distinguishing NS from other RASopathies and related disorders can be difficult. We used next-generation sequencing (NGS) to identify causative or candidate genes for 13 of 27 NS patients lacking known NS-associated mutations. Other patients harbor single variants in potential RAS-ERK pathway genes, suggesting rare private variants or other genetic mechanisms of NS pathogenesis. We also found mutations in causative genes for other developmental syndromes, which together with clinical reevaluation, prompted revision of the diagnosis. NGS can aid in the challenging diagnosis of young patients with developmental syndromes.

BIOGRAPHY

Peng-Chieh Chen was born in Kaohsiung, Taiwan in 1979. She completed her undergraduate degree, with major in chemistry and minor in life sciences, at National Tsing Hua University, Taiwan in 2001. She received her Ph.D. of biological sciences from University of California, Irvine in 2006.

She joined the lab of Dr. Raju Kucherlapati as a Post-doctoral Fellow at Harvard Medical School and Brigham and Women's Hospital in Boston during 2007-2012. Dr. Chen is now an Assistant Professor in the Institute of Clinical Medicine in the School of Medicine at National Cheng Kung University in Taiwan. Her research focuses on understanding the biology of human genetic disorders and cancers. She works on identifying the causative genetic events and the mechanisms of genetic factors lead to the pathogenesis of genetic disorders.

Dr. Chen is awarded with Post-doctoral Fellowship from American Heart Association. Her previous publication of a mouse model of Noonan syndrome in Journal of Clinical Research was highlighted by the editors and covered in the press. She also worked on the Cancer Genome Atlas projects on searching for structural variations in human colorectal cancers and was co-authors of several TCGA papers. Her recent study on identifying novel disease-causing genes for Noonan syndrome was published in PNAS and was also press reported.

Technical Session D2-W1-T3: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

The relationship between protein function and local structural conservation

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ABSTRACT

The protein-molecule interaction plays an important role in almost all cell function. Due to the progress of the structural genomics projects, there are more than 100,000 structures in Protein Data Bank (PDB). It is extremely important to identify the protein-molecule interaction sites. In practice, the protein-molecule interaction sites have highly constraints in structural and physical properties. For example, the Asp-His-Ser catalytic triads are easy to detect because of their conserved residues and stringently constrained geometry. The helix-turn-helix motif is a common recognition structural motif used by transcription regulators. The -metal binding motif plays an important role in non-specific DNA interactions and cleavage in host defense and apoptosis. The treble clef motif is a zinc-binding motif adaptable to diverse functions such as the binding of nucleic acid and hydrolysis of phosphodiester bonds. These structural motifs are involved in protein-molecule interaction and have the structural conservation of interaction sites. According to the properties, the computational methods can be developed to identify the protein-molecule interaction sites of protein.

Recently, we have developed a novel method to detect the structural motifs from protein structure (Lu et al. Proteins: Structure, Function, and Bioinformatics 2006). This method is called the fragment transformation method which is a local structural alignment algorithm combining both structural and sequence information to identify the local structure motifs. It should be noted that the short and discontinuous fragments of protein can also be processed by our approach. We already applied our method to detecting several structural motifs and ligand binding sites, such as the -metal motif, the treble clef finger motif, metal ion-binding sites and flavin- and nicotinamide adenine dinucleotide-binding sites. Our properties results were encouraging, indicating that we can effectively identify these local structural motifs in an automatic fashion. Our method provide a useful, effective means for automatic function annotation of structural genomics research through detecting structural motifs associated with particular functions.

BIOGRAPHY

Chih-Hao Lu was born in 1977, Taipei, Taiwan. He received his BS and PhD degree in department of Computer and Information Science, National Chiao Tung University, Taiwan in 2000 and Institute of Bioinformatics, National Chiao Tung University, Taiwan in 2007, respectively. He worked as a post-doc fellow at College of Biological Science and Technology, National Chiao Tung University, Taiwan from 2007 to 2008. He was an Assistant Professor at

Graduate Institute of Molecular Systems Biomedicine, China Medical University, Taiwan from 2008 to 2013 and Graduate Institute of Basic Medical Science, China Medical University, Taiwan from 2013 to 2014. He was promoted to be an Associate Professor at Graduate Institute of Basic Medical Science, China Medical University, Taiwan in Feb., 2015. Dr. Lu is currently working on structural bioinformatics, computational biology, systems biology and computer-aided drug design. His research interests include protein functional sites detection, protein-ligand binding sites identification and subcellular localization prediction. He is a member of Biophysical Society of Taiwan and Taiwan Bioimformatics and Systems Biology Society.

Technical Session D2-W1-T3: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Ensembl@YM: Tools for automating the build of virtualized genome annotation database, browser, and a light-weighted online editor of gene structures

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ABSTRACT

In recent years, technical advances in next-generation sequencing (NGS) have made whole-genome sequencing faster and cheaper, allowing even small groups to launch sequencing projects. Obtaining the complete genomic sequence of a new species is no longer a difficult task. However, one serious problem is about how to effectively mine the valuable information from these sequencing data and the experimental data. Obviously, we need a systematic approach, which can help us to integrate these data together and facilitate the results interpretation. Besides, new experimental findings might not be completely consistent with existing annotation generated by automatic gene finding algorithm and a tool for performing evidence-based annotation amendment would be needed.

1. Ensembl@YM: Virtual machine for Ensembl DB and web server

The Sanger Institute-EBI joint project – Ensembl provides a well organized genome browser which can integrate genomic annotation produced by the automatic pipeline with other available biological data and make all this publicly available via the web. This website is called Ensembl genome browser. Ensembl genome browser can integrate various types of data and is being used in worldwide. Besides, Ensembl is an open-source project, so any user can set up a local and private site for your genome. However, the procedure of building up a Ensembl genome browser is complicated. The main difficulties are two-fold: (1) there is a need to resolve the version dependency between different software, (2) there are quite a few configurations required to make the DB and web site functioning properly. Therefore, our goal is to establish a procedure to automate the process of establishing Ensembl genome browser in order to reduce time spent and errors occurred on manual operation.

2. Ensembl@YM: A light-weighted online editor of gene structures

NGS data usually contains more sequencing errors than those generated by Sanger sequencing method, which can lead to incorrect open-reading frame prediction as well as further similarity-based functional mapping. Usually additional bench work such as transcriptome analysis would be required to further improve the quality of the initially pure-computational based annotation. In brief, an initial genome annotation would be modified recurrently as more

experimental data becomes available. Our goal is to create a light-weighted online editor of gene structures, which can work seamlessly and cooperativly with the personalized virtual machine of Ensembl DB and web server. Once new pieces of evidence support a novel tissue-specific transcripts, this editor can allow users to easily build a new transcript for a gene by re-locating the exiting exon/intron junctions, or users may merge exons from two initially non-overlapping genes in order to create a new gene. In our experience, this functionality is very useful for manual curation of the annotation of NGS-based whole genome sequencing results, especially the ones assembled from the 3rd-generation PacBio platform that might contain a number of indels that could introduce errors in predicted open-reading frames.

BIOGRAPHY

Yen-Hua Huang was born in 1970, New Taipei City, Taiwan. He completed his undergraduate degree (medical doctor) in the medical school of National Yang-Ming University (NYMU), Taipei, Taiwan in 1995 and then received his master degree in the institute of biochemistry and molecular biology of NYMU in 1998. He received his Ph.D. degree (bioinformatics) in the joint Ph.D. program of University of Cambridge, UK and the Wellcome Trust Sanger Institute in 2009.

He joined the Center for Systems and Synthetic Biology of NYMU as a post-doc fellow during 2009 to 2014. Dr. Huang is now an Assistant Professor in the Institute of Biomedical Informatics of NYMU. His research interests include computational identification of functional elements in the genomes, NGS data analysis such as whole-genome annotation and disease gene finding, and finding regulatory mechanisms of cancer progression and drug resistence of cancer therapy.

Dr. Yen-Hua Huang received the Wellcome Trust PhD award. His publication about pathways integration was selected as one of the top 5% articles of Nucleic Acids Research in 2010. His work about finding the causative gene variant of spinocerebellar ataxia type 22 (SCA22) was reviewed by Nature Review Neurology in 2012. His work for finding the disease gene of Charcot-Marie-Tooth disease type 2 was chosen for press release of American Journal of Human Genetics in 2013.

Technical Session D2-W2-T3: Medicine and Life Sciences, Biological and Biomedical Sciences

Session Chair

Che Alex Ma

The Taiwan Bio-Development Foundation (TBF) Chair in Biotechnology
Associate Research Fellow, Genomics Research Center
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BIOGRAPHY

Technical Session D2-W2-T3: Medicine and Life Sciences, Biological and Biomedical Sciences

EZH2-mediated epigenetic regulation of cancer/stem cells

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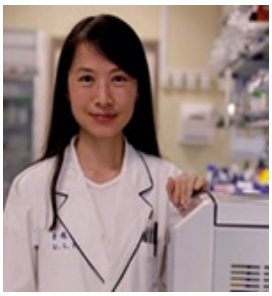
ABSTRACT

EZH2, a catalytic subunit of Polycomb repressive complex 2 (PRC2), is a histone lysine methyltransferase (HKMT) that methylates lysine 27 of histone H3, resulting in gene silencing. Mounting evidence shows that overexpression/amplification or mutations of EZH2 have been detected in a variety of cancers, and are associated with tumor development and progression. EZH2 also plays vital roles in stem cell maintenance and lineage differentiation. Thus, EZH2/EZH2-mediated signaling deregulation contributes to numerous human pathologies. Our work has demonstrated that CDK1-mediated phosphorylation of EZH2 at Thr487 disrupts EZH2 binding with other PRC2 components SUZ12 and EED, and thereby inhibits its methyltransferase activity, resulting in inhibition of cancer-cell invasion and promoting mesenchymal stem cell differentiation into osteoblasts. Here I will present our recent study on EZH2's multi-faceted function and role in cancer and stem cells that may provide important clinical implications.

BIOGRAPHY



Long-Yuan Li received her Ph.D. degree in microbiology from College of Medicine, National Taiwan University, Taipei, Taiwan in 2002, and conducted postdoctoral training in M.D. Anderson Cancer Center, Houston, Texas, USA. She joined the faculty of Graduate Institute of Cancer Biology, China Medical University, Taichung, Taiwan in 2006. Currently she is an Associate Professor of Graduate Institute of Cancer Biology, China Medical University.

Dr. Li's research interests include signaling regulation in cancers/stem cells and development of novel therapeutics and diagnostics for cancer and other human diseases. She is a member of American Association for Cancer Research, American Society for Cell Biology and The Chinese Society of Cell and Molecular Biology. She has published more than forty papers in journals including Cancer Research, Oncogene, Natural Cell Biology, Molecular Cell, etc. and received Ta-You Wu Memorial Award from Ministry of Science and Technology, Taiwan in 2012.

Technical Session D2-W2-T3: Medicine and Life Sciences, Biological and Biomedical Sciences

Immuno-Targeting ENO1 as A Novel Strategy for Cancer Therapy

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ABSTRACT

Alpha-Enolase (a-ENO; ENO1) is a catalytic enzyme participating in the penultimate step of glycolysis and also poses several non-metabolic functions, such as a heat shock protein in yeast, a structural protein in lens, and a plasminogen receptor in leukocytes. Previously, we showed that the ENO1 expression status is positively correlated with the disease progression of patients with non-small cell lung cancer (NSCLC), and development of the metastatic potential is also highly associated with the degree of its cell-surface distribution in tumor cells.

However, the immune response against ENO1 is reversely correlated with the clinical status of NSCLC patients. In this talk, we are going to demonstrate how to stimulate the immune responses to re-build antitumor immunities, and how this action may bestow a survival benefit in preclinical mouse models. Two therapeutic strategies will be discussed in this meeting. First, vaccination of the mice with mouse-homolog ENO1 (mENO1) recombinant protein with CpG adjuvant to generate high titer of anti-ENO1 cytotoxic T cell (CTL) activity and humoral ENO1 responses could result in a remarkable suppression on tumor growth.

Second, therapeutic effects of ENO1 monoclonal antibody specifically against the plasminogen-binding site of surface ENO1 will be intensively discussed. Both cell-based and animal studies consistently showed its profound inhibitory effect on cell migration, invasion and fibrinolysis, as well as on suppression of tumor growth and blockade of tumor metastasis. Collectively, ENO1 can be a potential good and safe target for MHC-I-dependent cancer immunotherapy, and its cell-surface form may also provide a great opportunity for an effective antibody therapy in the near future.

BIOGRAPHY

Neng-Yao Shih received his B.S. (1982) and M.S. (1984) in Biological Sciences from the Tunghai University in Taiwan, and received his Ph.D. (1996) in molecular immunology with his expertise on post-transcriptional regulation of immune genes from Arizona State University. After his doctorate study, he joined Dr. Andrey Shaw's lab in the Medical School of Washington University, St. Louis (1997), to study the role of a novel signaling molecule, CD2-associated protein, in T cell activation. He published this work on Science and American Journal of Pathology in 1999 and 2001. In 2001, he started to develop his scientific career in the National Institute of Cancer Research, National Health Research Institutes, where he is one of pioneers on identification of

immunogenic tumor-associated antigens (TAAs) from patients with

NSCLC and ovarian cancers in Taiwan. In the previous work, he demonstrated the expression status of those TAAs was highly associated with the clinical outcomes of the cancer patients, and showed that they could serve as therapeutic targets for cancers. More recent he found that re-stimulation of the immune responses against those TAAs can bestow a remarkable benefit on cancer prevention and therapy.

Technical Session D2-W2-T3: Medicine and Life Sciences, Biological and Biomedical Sciences

Oncogene MCT-1 promotes aneuploidy and tumor metastasis

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ABSTRACT

Aberrant activation of RNA-binding protein is implicated in tumorigenesis. Oncogene MCT-1 is an important RNA-binding protein involved in diverse biological functions including translation initiation, cell cycle regulation, mitotic checkpoint control, cell survival and DNA damage response. Our recent data have shown that MCT-1 gene is highly expressed in both invasive breast cancer and lung adenocarcinoma, suggesting that the enhanced MCT-1 activation is important for tumor development. Ectopic MCT-1 expression transformed normal breast epithelial cells and induced the proteasomal degradation of tumor suppressors, p53 and PTEN. Overexpressing MCT-1 in the PTEN-null cancer cells, Src signaling cascade was amplified that led to neoplastic multinucleation and chromosomal instability. Importantly, the activation of EMT and MMPs as well as the results of tumor cell migration, invasion and metastasis were promoted by gain-function of MCT-1 but repressed by loss-function of MCT-1. Moreover, tumor microenvironments increased with angiogenesis and M2 macrophage accumulation were promoted upon MCT-1 induction. Tumor suppressor miRNAs (miR-34a, miR-125b and miR-203) which have been identified to inhibit tumor metastasis and modulate microenvironment were upregulated in the MCT-1-deficient tumor. We speculate that the inhibition of MCT-1 oncogenicity combined with the induction of tumor suppressor miRNAs may improve the overall therapeutic effect of the invasive cancer treatment.

BIOGRAPHY

HSIN-LING HSU, Ph.D.

EXPERIENCE

2011/11-present **Associate Investigator**
National Health Research Institutes, Taiwan
Projects: Tumor metastasis, Signaling transduction, Mitotic regulation

2004-2011 **Assistant Investigator**
National Health Research Institutes, Taiwan
Projects: Tumorigenesis, DNA repair

2002-2004 **Research Assistant Professor**
Northwestern University Medical School, Chicago, IL
Projects: Tumorigenesis, DNA repair, Apoptosis

2001-2002 **Scientist/Biochemist**
Lawrence Berkeley National Laboratory, Berkeley, CA
Projects: Telomere maintenance, DNA repair

1999-2001 **Postdoctoral Fellow**
Lawrence Berkeley National Laboratory, Berkeley, CA
Projects: Telomere maintenance, DNA repair

1996-1999 **Postdoctoral Fellow**
Los Alamos National Laboratory, Los Alamos, NM
Projects: Telomere maintenance, DNA repair

1987-1989 **Instructor**
Tung-Hai University, Taichung, Taiwan
Lectures: Biology, Immunology, Microbiology, Genetics, and Physiology

EDUCATION

1999-2001 **Postdoctoral Fellow in Biochemistry**
Lawrence Berkeley National Laboratory, Berkeley, CA

1996-1999 **Postdoctoral Fellow in Biochemistry**
Los Alamos National Laboratory, Los Alamos, NM

1989-1996 **Ph.D. in Molecular Cellular Biology**
National Yang-Ming University, Taipei, Taiwan

1983-1987 **BS in Biology**
Tung-Hai University, Taichung, Taiwan

HONORS AND AWARD

2008-2011 NRPGM Grant Award, NSC

2007-2010 Young Investigator Career Development Award, NSC

2001 Telomere Award Given by the Telomere and Telomerase Meeting, Cold Spring Harbor

1996 1ST Prize of Dr. Chien-Tien Hsu's Science Award Given by the Chinese Society of Cell and Molecular Biology, Taiwan

1989-1996 Pre-doctoral Fellowship, National Yang-Ming University, Taipei, Taiwan

PUBLICATIONS

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Technical Session D2-W2-T3: Medicine and Life Sciences, Biological and Biomedical Sciences

Peering into Neural Stem Cells in Live Brain: Multidisciplinary Approaches to Investigating Neural Development and Disorder

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ABSTRACT

The vertebrate central nervous system (CNS) originates from a neuroepithelium composed of highly organized neuroepithelial and, subsequently, radial glial cells, which give rise to virtually all of the neurons and glia in the brain. During development, these neural stem cells and their progeny go through a series of motile events, which are tightly regulated by numerous genes. Any small perturbation in these processes can cause neural developmental disorders, such as lissencephaly, microcephaly, double cortex, focal cortical dysplasia, schizophrenia, and even autism. In order to study the etiology of these developmental disorders, we established animal models to elucidate the functions of their causal genes in vivo. For example, we knocked down the expression of the lissencephaly gene, LIS1, in the rat embryo using RNAi and in utero electroporation techniques and found that knockdown of LIS1 completely blocks the interkinetic nuclear migration (INM), as well as the subsequent radial migration of committed neuronal precursors (J Cell Biol, 176:935). We further developed a culture system to observe neural cells in brain slices using high resolution light microscopy. Live imaging of coexpressed histone, centrosome, and microtubule plus-end markers revealed that LIS1 is required for both nuclear and centrosome movement in the radially migrating cells (Nat Neurosci, 10:970). We have also applied these approaches to the behavior of neural stem cells and found that interkinetic nuclear migration involve a cell cycle-dependent switch between dynein- and nonconventional kinesin-driven nuclear transport (Nat Neurosci, 13:1463). We are currently using advanced two-photon microscopy to investigate the development neural connectivity in live animals of both normal and disease conditions. These approaches can be expanded to elucidate the mechanism of normal brain development and shed light on how various genes cause many other neural developmental disorders.

BIOGRAPHY

Dr. Jin-Wu Tsai received his Ph.D. from Columbia University, New York, USA. His lab uses stem cell and rodent animal models to investigate how embryonic neural stem and progenitor cells produce neurons. He also studies developmental brain disorders and explores the application of stem cell therapy to the treatment of these disorders. Dr. Tsai holds a dual B.S. degree in Physics and Zoology from National Taiwan University, Taipei, Taiwan. With a unique multidisciplinary background, he continued to pursue his M.S. degree in Microbiology and Immunology at National Yang-Ming University. Fascinated by stem cell biology and its broad potential in therapeutic applications, he embarked on stem cell research and conducted a series of studies on neural developmental

disorders. After his Ph.D., he continues his journey as Postdoctoral Fellow at New York University, and then University of California, San Francisco. Dr. Tsai then joined the Biomedical Imaging Depart of the Research and Development Division at Genentech Inc., one of the leaders in biotech industry. He was developing imaging technologies for drug discovery in treating neurodegenerative diseases. His research was published as cover stories of scientific journals, such as Nature, Nature Neuroscience, and the Journal of Cell Biology. In recognition of his contribution to these fields, Dr. Tsai received many honors, including the Brunie Prize in Neural Stem Cell Research, the Rover Award for Outstanding Achievement in Anatomy and Cell Biology, Wu Chien-Shiung Science Award, Genentech Recognition Award, etc. Dr. Tsai is also an inventor and holds a patent for an innovative optical cell observation method and a pending patent for targeting a gene for brain cancer treatment. He has been invited to give public speeches in scientific conferences worldwide, including in Australia, China, France, Japan, Taiwan, the United Kingdom, and the United States.

Technical Session D2-W3-T3: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Session Chair

Ja-An Annie Ho

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BIOGRAPHY

Ja-an Annie Ho was born in Taipei, Taiwan at 1968. She received her PhD from College of Agriculture and Life Science, Cornell University (Ithaca, New York, USA) in 1998 with focuses in liposome technology and sensor development.

She is currently a Professor of Chemistry, who runs a Bioanalytical Chemistry and Nanobiomedicine Laboratory in the Department of Biochemical Science and Technology at the National Taiwan University (Taipei, Taiwan). Her group has focused on the development of various immune- or genobiosensors for biomedical applications using nanomaterials. More recently her lab has become increasingly interested in the development of nano-drug delivery system to improve the efficacy of cancer therapies.

Professor Ho serves as Editorial Board Members for PLOS One (Open Access, 2013–present), Antibody Technology Journal (Dovepress, 2010–present), Journal of Food and Drug Analysis (Science Direct, Elsevier, 2014–present), and was Editorial Advisory Board Member for Talanta (Science Direct, Elsevier, 2005–2011). Professor Ho is a member of the American Chemical Society and Agricultural Chemical Society of Taiwan, who is the author of more than seventy publications on international journals.

Technical Session D2-W3-T3: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Her-Ming Chiueh

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National Chiao-Tung University
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ABSTRACT

BIOGRAPHY

Technical Session D2-W3-T3: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Novel Biodegradable Emulsions for Vaccine Adjuvant Development

Ming-Hsi Huang

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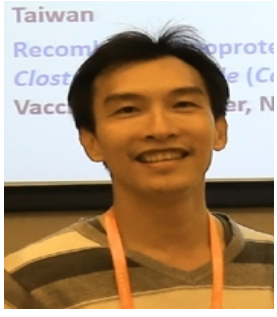
ABSTRACT

Vaccine adjuvants are conferred on the substance who helps to elicit a robust and effective antigen-specific immune response. They are added to many vaccines to increase their immunogenicity and efficacy: they can make existing vaccines more effective; they can help make previously impossible vaccines a reality; they can shrink vaccine dosage as antigen-sparing strategies; they can improve the efficacy of vaccines in specific human populations; they can overcome antigenic competition; or they can alternate immunization routes.

The objective of this talk is to examine the potential of novel vaccine formulations as adjuvants for prophylactic and therapeutic vaccine candidates. Our group studies on the engineering of amphiphilic bioresorbable polymers as a promising strategy for the delivery of vaccine antigens and/or immunostimulatory molecules. We optimized a novel emulsion-type delivery system comprised of a bioresorbable polymer, Span®85, and squalene to form a ready-to-use adjuvant, dubbed PELC. Immunogenicity studies in mice showed that single dose of PELC-formulated 0.5 μg HA of inactivated virus could induce better antigen-specific antibodies than those of 5 μg HA of non-adjuvanted virus. The use of PELC could be an antigen-sparing tool for a potential shortage of pandemic influenza vaccines. For therapeutic ends, we applied cancer immunotherapy of a HPV type 16 E7/TC-1 cells as tumor-associated antigen/tumor cells model to evaluate the adjuvanticity of PELC emulsion as well as the enhancement of anti-cancer immunity.

BIOGRAPHY



Ming-Hsi Huang obtained his PhD degree in 2004 in Chemistry-Biology Interface from University Montpellier I in France. From 2005-2009, he worked as a postdoctoral fellow in Vaccine Research and Development Center of National Health Research Institutes (NHRI). From 2009-2014, he worked as an Assistant Investigator in National Institute of Infectious Diseases and Vaccinology (NIIDV) of NHRI. Currently he is an Associate Investigator with NIIDV of NHRI.

Dr. Huang's major research interest at NIIDV has been focused on the development of novel delivery vehicles for generating vaccine-induced long-term immunity as well as immunoregulatory agents for manipulating effective/harmful immune responses. Currently he is working on the development of micro-encapsulation technology for a single-dose multivalent vaccine against

emerging infectious diseases, in particular influenza-associated illness and hand-foot-mouth disease. He also extends these aspects to optimize alternative immunization routes, such as subcutaneous, intramuscular or mucosal administration. These features are of great interest for further investigations of sustained delivery against pathogen-associated cancers and immune dysfunctions.

Dr. Huang has published at least 20 SCI journal articles, 1 book chapter, and filed 2 patents. The work accomplished by Dr Huang on cancer immunotherapy by formulating candidate HPV antigens with novel emulsion-type adjuvants which has been published in the leading journals in the field of biomaterials/nanomedicine.

Technical Session D2-W3-T3: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

An Innovative Bio-Sensing Scheme and Platform Embedded in a Dental Implant Fixture for Painless and Long-Term Bio-Medical Analysis

Chih-Cheng Lu

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ABSTRACT

A miniature intra-oral dental implant system including a built-in biosensor device is proposed in this presentation. The dental implant system, or platform, is replaced over maxilla and allows relatively non-invasive procedures for a novel bio-sensing scheme for human blood analysis. Due to placement of the implant fixture, periodontal ligaments and the pulp structure, which are regarded as the main origin of pain, are thus removed, and long-term, continuous blood analysis and management through maxillary bone marrow becomes achievable through the dental implant platform. The new pathway of biological sensing is for the first time presented to realize an accurate and painless approach without injections. The dental implant system mainly consists of an implant fixture and a prosthetic abutment, a biosensor module, a bluetooth 4.0 wireless module and a dc button cell battery. The electrochemical biosensor possesses three electrodes, including working, reference and counter ones, which are arranged to pass through the titanium implant fixture below the biosensor module. The electrodes are exposed to the blood pool inside the maxillary bone marrow and perform oxidation/reduction reactions with the coating of bio-sensing enzyme. To prove the proposed platform, the immobilization process of glucose oxidase (GOD) enzyme and in vitro detections of glucose levels are successfully carried out, and proven sensitivity, linearity and repeatability of the glucose biosensor system are obtained. In brief, the novel bio-sensing pathway and intra-oral biosensor platform may increasingly reveal their promising value and feasibilities in current bio-medical analysis, diagnosis, drug release and even healthcare technologies.

BIOGRAPHY

Dr. Chih-Cheng Lu received his bachelor and master degrees in mechanical engineering from National Sun Yat-Sen University and National Chung-Hsin University, Taiwan, in 1989 and 1994, respectively. He was a research staff working on precision engineering and MEMS at PIDC, Taiwan from 1994 to 1998. He completed his Ph.D. degree in electrical engineering at Engineering Department, Cambridge University, UK in 2003. He then served as an R&D manager in semiconductor industrial sectors from 2003 to 2005. He is currently an associate professor with Graduate Institute of Mechatronic Engineering, National Taipei University of Technology, Taiwan, and the supervisor of Advanced Microsystems and Devices

Laboratory. His research interests include MEMS, CMOS-MEMS smart sensors/actuators, bio-chemical and magnetic microsensors, gene/drug delivery and RFID applications for mechatronic and medical systems. He has authored and co-authored more than 60 international journal and conference papers in these areas since 2007 and has been a vigorous peer-reviewer for several internationally prominent journals.

Technical Session D2-W3-T3: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Fabrication and applications of proteome microarrays

Chien-Sheng Chen

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ABSTRACT

Our lab has a novel high-throughput protein purification technique to purify ~4000 E. coli proteins within 10 hours. These proteins were then spotted onto various glass surfaces to form high-density proteome chips. This novel high-throughput proteomic approach was successfully applied to many projects. First, a proteome chip assay was established to identify proteins involved in the recognition of potential base damages in DNA using a group of DNA probes each containing a mismatched base pair or an abasic site. A handful of proteins were found to recognize each type of probe with a high affinity and specificity. In addition to DNA repair study, we also set out to perform human serum profiling for the identification of biomarkers in inflammatory bowel diseases. Using a supervised learning algorithm (k-Top Scoring Pairs), we identified two sets of serum antibodies that were novel biomarkers for specifically distinguishing CD from healthy controls (accuracy: 86±4%), and CD from UC (accuracy: 80 ±2%), respectively. We also attempted to find the intracellular target of natural antimicrobial peptides by our E. coli proteome chips. Our study showed that Lfcin B inhibits the growth of bacteria by influencing the phosphorylation of two component system directly. In addition to E. coli proteome chip, we also fabricated yeast proteome chips for profiling lipid-protein interactions. We not only recovered many proteins that possessed known PI(3,5)P2-binding domains, but we also found two unknown Pfam domains (Pfam-B_8509 and Pfam-B_10446) that were enriched in our dataset. Among the 162 PI(3,5)P2-BPs, we found a novel motif, HRDIKP[ES]NJLL. A docking simulation showed that PI(3,5)P2 interacted primarily with lysine or arginine side chains of the newly identified PI(3,5)P2-binding kinases. Recently, we also used human proteome microarrays to identify HCV RNA 5'UTR-binding proteins. We found that hnRNP K interacts with virus RNA 5'-UTR and affect virus RNA replication.

BIOGRAPHY

Dr. Chien-Sheng Chen was born at Kaohsiung, Taiwan in 1974. He completed his doctoral training in the field of bioanalytical chemistry at Cornell University in 2005 and then joined Dr. Heng Zhu's lab at High Throughput Biology Center, Johns Hopkins University School of Medicine as a postdoctoral fellow. He joined the faculty of Systems Biology and Bioinformatics Institute at National Central University, Taiwan in 2008.

Dr. Chen' research interests focus on nano/micro-biosensing

technology. He developed unique assays for rapid detections and for proteomic research, such as protein function discovery, protein interaction, host-microbe interaction, and biomarker identification using a proteome chip approach.

Dr. Chen has been an associate editor in Journal of Integrated OMICS and an academic editor in PLoS One. He was awarded as the outstanding new faculty ,outstanding research as well as distinguished professor in National Central University and Academia Sinica Research Award for Junior Research Investigators.

The first paragraph may choose to contain a place and/or date of birth (list place, then date). Next, the author's educational background is listed. The degrees should be listed with type of degree in what field, which institution, city, state or country, and year degree was earned. The author's major field of study should be lowercased.

The second paragraph uses the pronoun of the person (he or she) and not the author's last name. It lists military and work experience, including summer and fellowship jobs. Job titles are capitalized. The current job must have a location; previous positions may be listed without one. Information concerning previous publications may be included. Try not to list more than three books or published articles. The format for listing publishers of a book within the biography is: title of book (city, state: publisher name, year) similar to a reference. Current and previous research interests end the paragraph.

The third paragraph begins with the author's title and last name (e.g., Dr. Smith, Prof. Jones, Mr. Kajor, Ms. Hunter). List any memberships in professional societies. Finally, list any awards, work, service, and publications. If a photograph is provided, the biography will be indented around it. The photograph is placed at the top left of the biography. Personal hobbies will be deleted from the biography.

Technical Session D2-W4-T3: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Session Chair

Sao-Jie Chen

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BIOGRAPHY

Technical Session D2-W4-T3: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Low Power Wireless ECG Acquisition Circuits and Systems for Body Sensor Networks

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ABSTRACT

The Low Power Wireless ECG Acquisition Circuits and Systems for Body Sensor Networks will be presented in this lecture. Heart diseases are always the ranked first cause of ten leading causes of death over ten years, and there are several medical devices are made to monitor their heart to avert the heart diseases. In recent years, body sensor networks (BSNs) based applications or devices have become more and more popular, and acceptable to the people for monitoring the real-time health information, such as the electrocardiogram (ECG). In order to enhance the portability and increase the popularization of BSNs, a low-power wireless ECG acquisition system on a chip (SOC) stuck on the body is required. In this lecture, a bio-signal acquisition system with the features of low power consumption, wireless transmission, and the on-time monitoring will be presented.

BIOGRAPHY

Shuenn-Yuh Lee was born in Taichung, Taiwan, in 1966. He received the B.S. degree from the National Taiwan Ocean University, Keelung, Taiwan, in 1988, and the M.S. and Ph.D. degrees from the National Cheng Kung University, Tainan, Taiwan, in 1994 and 1999, respectively.

He was an Associate Professor from 2006 and Professor from 2011, respectively, at the Department of Electrical Engineering, National Chung Cheng University, Chia-Yi, Taiwan. He is currently a Professor at the Department of Electrical Engineering, National Cheng Kung University, Tainan, Taiwan. He served as the Chairman of Heterogeneous Integration Consortium (HIC) under the VLSI Educational Program sponsored by Ministry of Education, Taiwan, from 2009 to 2011. He served as the Technical Program Chair (TPC) of the 2011/2014/2015 International Symposium on Bioelectronics & Bioinformatics (ISBB) and the 2013 IEEE International Conference on Orange Technologies (ICOT), and the Publication Chair for the 2012 IEEE Asia Pacific Conference on Circuits and Systems (APCCAS). His research interests include biomedical circuits and systems design, low-power signal acquisition systems, and wireless healthcare systems. He has published more than 20 papers on IEEE Transctions/Journals.

Dr. Lee is a senior member of IEEE Engineering in Medicine and Biology (EMB) Society, Circuits and Systems (CAS) Society, and Solid-State Circuits (SSC) Society. Moreover, he is a

member of IEICE and CIEE. From 2013, he serves as the Chairman of IEEE Solid-State Circuits Society Tainan Chapter.

Technical Session D2-W4-T3: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Microelectronic Contact Lens for Healthcare

Yu-Te Liao

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ABSTRACT

Unlike blood and body fluid, tears are directly accessible and provide a unique opportunity to develop a chemical interface between a sensor and the body. The eye provides a low scattering window for noninvasively monitoring as much health information as the blood since tears house a variety of physiological properties of analytes. Integrating a glucose sensor on a contact lens would provide a way to continuously and reliably sense metabolites in tear fluid without a separate sampling process and cause minimal disturbance to the eye. In this talk, we will present and discuss the design and implementation of fully-integrated microelectronic contact lens for intraocular pressure monitoring and tear glucose level detection.

BIOGRAPHY

Yu-Te Liao received the B.S. degree in electrical engineering from National Cheng-Kung University, Tainan, Taiwan, in 2003, the M.S. degree in electronics engineering from National Taiwan University, Taipei, Taiwan, in 2005, and the Ph.D. degree in electrical engineering from the University of Washington, Seattle, in 2011. In August 2011, he joined the Electrical Engineering Department, National Chung Cheng University, Chiayi, Taiwan, as an Assistant Professor. Currently, he is an Assistant Professor at the Department of Electrical and Computer Engineering, National Chiao Tung University, Hsinchu, Taiwan. His research interests are the design of low power RF integrated circuits, integrated sensors, and biomedical circuits and systems.

Technical Session D2-W4-T3: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Development of Wireless Sensing Devices for Diagnosis and Rehabilitation Application

Dr. Chao-Min Wu

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ABSTRACT

In recent years, our western style food consumption has led to the growth of stroke patient numbers. Therefore, the stroke rehabilitation has become one of the main important facilities in the hospital. The rehabilitation of a stroke patient can be presented by quantitative assessment index. Thus, it is desired to obtain the patient's rehabilitation condition by measuring the electromyography (EMG) of the patients. In the course of stroke patient rehabilitation, electromyography (EMG) provides not only an indicator of muscle strength and endurance but also an observation on co-ordination of muscles. In this talk, we present a wireless EMG sensing device we developed for diagnosis and rehabilitation application in an objective assessment system integrated with virtual reality training modules for the evaluation of rehabilitation performance. The ZigBee protocol was selected to develop this wireless rehabilitation device. Associated with the EEG to investigate the reformation of neural networks through analyzing the EEGs of prior-, during- and post-rehabilitation, this study investigated the correlation among these electrophysiological signals. In addition, a wireless automated auditory brainstem responses (AABR) measurement system developed with the embedded system and the smart phone and a PDA-based transient evoked otoacoustic emission (TEOAE) system for the newborn hearing screening will also be presented.

BIOGRAPHY

Chao-Min Wu received his B.S. (1982) in biomedical engineering from Chung-Yuan Christian University and M.S. (1987) in bioengineering from the University of Wyoming. He received his Ph.D. (1996) in biomedical engineering, from the Ohio State University at Columbus, OH, and was a postdoctoral fellow at the University of Wisconsin at Madison, WI between 1996 and 1998, and a Visiting Researcher at Human Information Processing Research Lab. at ATR, Kyoto, Japan (1998-2000). Before his PhD study, he was an engineer and assistant manager of the R&D department at SUNTEX Instrument Inc. He was an Assistant Professor of speech pathology and audiology, Chung-Shan Medical University (2000-2004). Currently, he is an Assistant Professor of Dept. of electrical engineering, National Central University. Dr. Wu is also a member of Engineering Society of Medicine and Biology, IEEE, and Acoustical Society of America, AIP. His research interest includes integration of bioinstrumentation, phonetics, and neural network model to study speech and hearing disorders, and combination of wireless,

multimedia, medical devices and sensor system to rehabilitation. He is the co-author of the book, Bioinstrumentation (Wiley 2004) and has received Special Award in 2012 Merry Electro-acoustic Thesis Award Contest.

Technical Session D2-W4-T3: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

EEG-based Functional Brain Network and its Clinical Applications

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ABSTRACT

Electroencephalography (EEG) is a brain-sensing technique to noninvasively measure electrical activity with higher temporal resolution than other brain-imaging techniques. The advantages of mobility, cost efficiency, and ease of access make EEG preferable to the study of brain diseases and cognitive processes under real-life stimulation. Along with conventional event-related potential (ERP) and time-frequency analysis of EEG signals, recent advances in functional connectivity and source imaging methods have largely progressed in exploration and understanding of underlying brain-network dynamics. This study was intended to investigate EEG oscillatory activity and phase synchronization in subjects with Asperger's syndrome (AS) during visual recognition of emotional faces. Emotional faces elicited comparable reaction times and evaluation scores between the two groups. The AS group had no visible N400 component and lower delta/theta synchronization in the temporal and occipital-parietal regions, and much weaker phase synchronization between distant scalp regions compared with the control group. We concluded the study by hypothesizing that AS subjects might have structural deficits in the amygdala and its related limbic structures, a site critical for recognition of emotional faces beyond conscious awareness, but they preserve the intact function in the cognitive pathway to keep up comparable behavioral performances as the healthy controls through voluntary control of attention. The results and paradigm in the experiment might benefit from developing further applications in psychosocial intervention and virtual reality mental training for Asperger's patients.

BIOGRAPHY

Yi-Li Tseng received her BS degree in the Department of Electrical Engineering from the National Cheng Kung University in 2006. She received her PhD degree in the Institute of Biomedical Engineering from the National Taiwan University in 2012, and completed her postdoctoral fellowship at the Institute of Statistical Science in Academic Sinica. Currently she is an assistant professor at the Department of Electrical Engineering in Fu-Jen Catholic University, New Taipei City, Taiwan. Her research work is on signal processing for real-life EEG and fMRI. She is conducting real life experiments on cognitive tasks involving memory of specific features of melody in classical music. Her research interests include physiological signal processing, cognitive neuroscience, and medical instru- mentation.

Technical Session D2-W1-T4: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Session Chair

Peng-Chieh Jessica Chen

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BIOGRAPHY

Peng-Chieh Chen was born in Kaohsiung, Taiwan in 1979. She completed her undergraduate degree, with major in chemistry and minor in life sciences, at National Tsing Hua University, Taiwan in 2001. She received her Ph.D. of biological sciences from University of California, Irvine in 2006.

She joined the lab of Dr. Raju Kucherlapati as a Post-doctoral Fellow at Harvard Medical School and Brigham and Women's Hospital in Boston during 2007-2012. Dr. Chen is now an Assistant Professor in the Institute of Clinical Medicine in the School of Medicine at National Cheng Kung University in Taiwan. Her research focuses on understanding the biology of human genetic disorders and cancers. She works on identifying the causative genetic events and the mechanisms of genetic factors lead to the pathogenesis of genetic disorders.

Dr. Chen is awarded with Post-doctoral Fellowship from American Heart Association. Her previous publication of a mouse model of Noonan syndrome in Journal of Clinical Research was highlighted by the editors and covered in the press. She also worked on the Cancer Genome Atlas projects on searching for structural variations in human colorectal cancers and was co-authors of several TCGA papers. Her recent study on identifying novel disease-causing genes for Noonan syndrome was published in PNAS and was also press reported.

Technical Session D2-W1-T4: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

A dynamics database housing ~ 11,000 PDB structures whereby mined data reveal dynamics prerequisites for protein functions and interactions

Lee-Wei Yang

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ABSTRACT

Proteins function through advantageously utilizing a repertoire of possible modes of intrinsic motions. Understanding such motions, of which the importance has been acknowledged in year 2013's Nobel Prize in Chemistry, is essential to accurately predict protein conformational changes, two body interactions, channel gating mechanisms and enzyme catalysis. With the advancement in forcefield optimization and appropriate physical approximations, protein dynamics are currently modeled at fine- and coarse-grained levels in great accuracy, evidenced by agreement between predicted quantity and experimental data from X-ray crystallography, NMR and folding kinetics. Here we present the only dynamics database that houses dynamics data (vibrational normal modes) of protein structures in a size commensurate with Protein Data Bank (PDB). The interface that presents such data are state of the art of its kind. Given the wealth of the data, we are able to find dynamics traits for enzyme active sites. Such traits are later used to predict the locations of enzyme active sites for protein structures of a resolution as low as 20 Angstrom. We further data-mined the database and develop the concept of intrinsic dynamics domains, including a domain plane (D-plane) and a domain axis (D-axis). It is found that a protein interacts with another at the interface where D-plane cuts through and forming a near-vertical angle between two intersecting D-axes from the two proteins over a set of 68 protein–protein complexes. The findings are then used to define quantitative criteria to filter out docking decoys unlikely to be native whereby the chance to find near-native hits is doubled. With the novel approach to partition a protein into "domains" of robust but disparate intrinsic dynamics, 90% of >720 catalytic residues in enzymes can be found within the first 50% of the residues closest to the interface of these dynamics domains. Our results also show that in 95% of the DNA-protein complexes, the DNA is cut through by protein's D-plane. The dynamics database, GNM 2.0, is made available at http://dyn.life.nthu.edu.tw/gnmdb/ and IDD website is provided at http://dyn.life.nthu.edu.tw/IDD/IDD.php

BIOGRAPHY

Lee-Wei Yang, currently an Associate Professor at National Tsing Hua University, received his B.S. in Chemical Engineering from National Taiwan University (1997), M.S. in Chemical Engineering from National Tsing Hua University (1999), and Ph.D. degree in Molecular Genetics and Biochemistry from School of Medicine, University of Pittsburgh (2005).

Dr Yang worked as a JSPS foreigner research fellow in University of Tokyo between 2006 and 2009. Then he did further postdoctoral trainings at La Jolla Bioengineering Institute and

Department of Chemistry, Harvard University till the year of 2011 when he took the offer of assistant professorship from Institute of Bioinformatics and Structural Biology, National Tsing Hua University in Taiwan.

Dr Yang's main research interests are protein dynamics/conformational changes and protein-protein/protein-peptide interactions. He and his lab members apply polymer physics, molecular mechanics, coarse-grained models and linear response theories to predict active sites, protein-protein binding sites, protein-DNA binding sites, NMR relaxation data and temperature factors of X-ray determined structures. The combined techniques also have helped structure refinements of DNA Polymerases, FGF2 dimers, FGF2-S100B complexes, LonC proteasome, CtPPase proton pump and frame-shifted structure of ribosome.

Dr. Yang has memberships of Biophysical Society of R.O.C. (since 2011), Biophysics Society (since 2004), ISMB (since 2006), Biophysical Society of Japan (since 2008) and Asia Pacific Bioinformatics Network (APBioNet) (since 2008). He was awarded with JSPS fellowship for foreign researchers (Dec, 2006 (~ 2009 Mar.)), Stephen L. Phillips Scientific Achievement Award (Oct, 2006), DCB Best Student Award + Annual Retreat Best Poster Award (May, 2006), Research fellowship (2003-Jun/2005), Scholarship for INTBP students of School of Medicine 2001-2003, The Phi Tau Phi honorary members (1999), China Technical Consultants, INC. Scholarship (1999), Mr. Liou Luo-Leou Scholarship (1998).

Technical Session D2-W1-T4: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Applications of Satellite Remote Sensing Technology for Disease Prediction

Ting-Wu Chuang

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ABSTRACT

Satellite remote sensing technologies produce an abundance of environmental data that are applicable to the study of human health. These data can in turn be used to map environmental conditions that influence the development and transmission of pathogens, habitats for vectors and hosts, and human exposure to disease. In particular, there has been strong interest in using earth observation data to develop early warning systems for forecasting epidemics of infectious diseases. Mosquito-borne diseases are appropriate targets for developing forecasting models due to its sensitivity to inter-annual fluctuations in temperature, rainfall, and other environmental conditions. This talk will give an overview of satellite remote sensing techniques and introduce how to develop different models to capture mosquito population dynamics and disease transmission by integrating multiple environmental parameters derived from satellite images. Two mosquito-borne diseases, West Nile virus in North America and Dengue Fever in Taiwan, will be discussed in the seminar to show how we can apply remote sensing technique to investigate environmental influences on disease transmission. Another example about snakebites in Costa Rica highlighted the integrated analysis of remote sensing and climate changes.

BIOGRAPHY

Dr. Ting-Wu Chuang received his B.S in Public Health from Taipei Medical University, M.S. in Epidemiology from National Taiwan University, and PhD in Epidemiology from the University of Michigan, Ann Arbor. Following a three-year post-doctoral training, he joined the faculty in the department of molecular parasitology and Tropical Diseases at Taipei Medical University in 2012. Dr. Chuang's research interests mainly focus on the influences of environmental changes on the transmission infectious diseases and the ecology of mosquito vectors.

Technical Session D2-W1-T4: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Identification of prognostic and predictive biomarkers for lung adenocarcinoma

Tzu-Pin Lu

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ABSTRACT

Lung cancer is the leading cause of cancer-related death worldwide. Two major subtypes of the lung cancer are adenocarcinoma and squamous cell carcinoma, and approximate 70-80% patients can be divided into these two subtypes. The overall five-year survival rate of lung cancer is below 20% even if numerous research efforts have been devoted to improving treatment. With the advancement in high-throughput technology, many studies have been performed to identify prognostic biomarkers for predicting survival in lung cancer. Challenges arise, however, when the number of overlapping genes across independent studies is very low. The inconsistency of identified prognostic biomarkers can be attributable to the individual differences and the different experimental protocols and analysis methods. To address this issue, a potential solution is to perform an analysis in simultaneously considering multiple datasets. In this talk, we will present a new approach to identify reproducible survival predictors for lung adenocarcinoma by incorporating the information from biological functions and signaling pathways. A total of 6 lung cancer microarray datasets and 24 cancer-related pathways from four online biological databases were analyzed. The Cox hazard regression model was used to develop a scoring scheme. The performances of the scoring model were evaluated by using a 2-fold cross-validation and a resampling test. A group of 16 genes involved in the apoptotic execution phase showed good predictability and can be applied in more than 700 patients with lung adenocarcinoma. Intriguingly, the risk scores were also associated with the efficacy of the drug ZD-6474 targeting EGFR. In conclusion, the results suggested that these 16 genes may serve as both prognostic and predictive biomarkers for lung adenocarcinoma in the future.

BIOGRAPHY

Tzu-Pin Lu received his Ph.D. (2011) from the Graduate Institute of Biomedical Electronics and Bioinformatics, National Taiwan University, Taipei, Taiwan. He has a double major in the department of Electrical Engineering and the department of Life Science for the bachelor's degree (2008) in National Taiwan University. His training was mainly at computer science, development of algorithms, and genetics.

After graduation, he became a postdoctoral fellow in the YongLin Biomedical Engineering Center, National Taiwan University (2011-2014) and the Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, Food and Drug Administration, Jefferson, Arkansas, United States (2012-2014). Currently, he is an Assistant Professor of Institute of Epidemiology and Preventive Medicine, Department of Public Health, College of Public Health, National Taiwan University, Taipei, Taiwan. His research interests include bioinformatics, high-throughput data analysis, and genetics of cancer and cardiovascular disease.

Prof. Lu has served as a reviewer for several international journals. He has published more than 20 peer-reviewed journal articles and conference papers. He is now the principal investigator (PI) and co-PI of three projects funded by the Ministry of Science and Technology, Taiwan.

Technical Session D2-W1-T4: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Stroke Risk Analysis for Early Detection and Aneurysm Assessment

Aichi Chien

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ABSTRACT

Cerebral angiography is commonly used for blood vessel examination and aneurysm detection. This process requires careful, visual inspection of angiography images. Automating detection and risk analysis of aneurysms and other malformations would assist diagnosis and allow the rapid processing of image from large numbers of patients, such as large clinical population studies. One of the important steps is to identify regions of arteries with risk of bleeding and risk of growth. In this talk, new technology assisting clinical stoke treatment and patient care will be discussed, as well as the latest findings based on this new analysis technology in stroke patients who have been followed to monitor their stroke risks.

BIOGRAPHY

Aichi Chien, Ph.D. is an Associate Professor in the Department of Radiological Sciences and the Biomedical Physics IDP Graduate Program in the UCLA Medical School since 2009; a faculty member of Medical School Short Term Training Program (SSTP) and Cross-disciplinary Scholars in Science and Technology (CSST) program since 2010, and faculty in the UCLA Center for Domain Specific Computing (CDSC) since 2011.

Dr. Chien received her Bachelor's Degree from National Taiwan University, Dept. of Agricultural Machinery Engineering in 1999, Taipei, Taiwan. She then completed her Master's Degree on the subject of Micro/Nano Resonators in the Dept. of Mechanical and Aerospace Engineering, Cornell University, Ithaca, NY; and her PhD Degree in Biomedical Engineering at the University of California, Los Angeles, CA on the topic of MEMS/NEMS implantable devices for cardiovascular disease. She went on to complete Postdoctoral Fellowship training in endovascular treatment in the Division of Interventional Neuroradiology in the UCLA David Geffen School of Medicine.

Dr. Chien's research interests include cerebral vascular disease and treatment effectiveness analysis, and encompass the integration of science and engineering for clinical decision-making and individualized medicine. Her research broadly impacts the medical community and medical device industry. Her research has been featured in various news, including Fierce Medical Devices, Interventional News, Endovascular Today, and Neuro News. She has published more than 70 peer-reviewed publications of original research in high impact factor medical journals such as Stroke, Journal of Vascular and Interventional Radiology,

Neurosurgery, Journal of Neurosurgery, and American Journal of Neuroradiology, including 22 papers as first author. She has received many awards, including the Brain Aneurysm Foundation Research Grant Award, the SIR Ring Career Development Award, the Cerebrovascular Research Award from The Aneurysm and AVM Foundation, the Bee Foundation Medical Research Award, the American Heart Association Outreach Award, Heart Failure Society of America Award, and Young Investigator Award from the Cardiovascular System Dynamics Society. She is also the lead inventor on more than five US Patents and International Patents; Principle Investigator in a Philips Healthcare research grant and Radiology Exploratory grants. She is currently a Co-Investigator on two NIH R01 projects and one NSF (CCF) multi-disciplinary program. She regularly gives lectures in universities and medical centers in the US and internationally.

Technical Session D2-W2-T4: Medicine and Life Sciences, Biological and Biomedical Sciences

Session Chair

Hsin-Ling Hsu

Associate Investigator, Institute of Molecular and Genomic Medicine
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BIOGRAPHY

HSIN-LING HSU, Ph.D.

EXPERIENCE

2011/11-present **Associate Investigator**
National Health Research Institutes, Taiwan
Projects: Tumor metastasis, Signaling transduction, Mitotic regulation

2004-2011 **Assistant Investigator**
National Health Research Institutes, Taiwan
Projects: Tumorigenesis, DNA repair

2002-2004 **Research Assistant Professor**
Northwestern University Medical School, Chicago, IL
Projects: Tumorigenesis, DNA repair, Apoptosis

2001-2002 **Scientist/Biochemist**
Lawrence Berkeley National Laboratory, Berkeley, CA
Projects: Telomere maintenance, DNA repair

1999-2001 **Postdoctoral Fellow**
Lawrence Berkeley National Laboratory, Berkeley, CA
Projects: Telomere maintenance, DNA repair

1996-1999 **Postdoctoral Fellow**
Los Alamos National Laboratory, Los Alamos, NM
Projects: Telomere maintenance, DNA repair

1987-1989 **Instructor**
Tung-Hai University, Taichung, Taiwan
Lectures: Biology, Immunology, Microbiology, Genetics, and Physiology

EDUCATION

1999-2001 **Postdoctoral Fellow in Biochemistry**
Lawrence Berkeley National Laboratory, Berkeley, CA

1996-1999 **Postdoctoral Fellow in Biochemistry**
Los Alamos National Laboratory, Los Alamos, NM

1989-1996 **Ph.D. in Molecular Cellular Biology**
National Yang-Ming University, Taipei, Taiwan

1983-1987 **BS in Biology**
Tung-Hai University, Taichung, Taiwan

HONORS AND AWARD

2008-2011 NRPGM Grant Award, NSC

2007-2010 Young Investigator Career Development Award, NSC

2001 Telomere Award Given by the Telomere and Telomerase Meeting, Cold Spring Harbor

1996 1ST Prize of Dr. Chien-Tien Hsu's Science Award Given by the Chinese Society of Cell and Molecular Biology, Taiwan

1989-1996 Pre-doctoral Fellowship, National Yang-Ming University, Taipei, Taiwan

PUBLICATIONS

1. **Hsu HL**, and Yeh NH. (1996) Dynamic changes of NuMA during the cell cycle and possible appearance of a truncated form of NuMA during apoptosis. **J. Cell Sci. 109:277-288**.
2. Yang CR, Yeh S, Leskovk K, Odegaard E, **Hsu HL**, Chang C, Kinsella TJ, Chen DJ, Boothman A. (1999) Isolation of Ku70-binding proteins (KUBs). **Nucleic Acids Res. 27:2165-2174**.
3. **Hsu HL**, Gilley D, Blackburn EH, Chen DJ. (1999) Ku is associated with the telomere in mammals. **Proc. Natl. Acad. Sci. U S A 96:12454-12458**.
4. **Hsu HL**, Gilley D, Galande SA, Hande MP, Allen B, Kim SH, Li GC, Campisi J, Kohwi-Shigematsu T, Chen DJ. (2000) Ku acts in a unique way at the mammalian telomere to prevent end joining. **Genes Dev 14:2807-2812**.
5. **Hsu HL**, Yannone S, Chen DJ. (2002) Defining interactions between DNA-PK and XRCC4/ligase IV. **DNA Repair 17: 1-11**.
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7. **Hsu HL**, Shi B, Gartenhaus RB. (2005) The MCT-1 oncogene product impairs cell cycle checkpoint control and transforms human mammary epithelial cells. **Oncogene. 24:4956-4964**
8. Lin HH, **Hsu HL**, Yeh, NH. (2007) Apoptotic cleavage of NuMA at the C-terminal end is related to nuclear disruption and death amplification. **J Biomed Sci. 14:681-694**.
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(2007) Phosphorylation of MCT-1 by p44/42 MAPKis required for its stabilization in

response to DNA damage. **Oncogene 26, 2283–2289. CORRIGENDUM Oncogene (2007) 26, 2674**.

11. Kasiappan R, Shih HJ, Chu KL, Chen WT, Liu HP, Huang SF, Choy CO, Shu CL, Din R, Chu JS, **Hsu HL.*(*corresponding author)**. (2009) Loss of p53 and MCT-1 overexpression synergistically promote chromosome instability and tumorigenicity. **Molecular Cancer Research**. 7:536-548.
12. Lu WC, Chen CJ, Hsu HC, **Hsu HL**, Chen L. (2010) The adaptor protein SH2B1β reduces hydrogen peroxide-induced cell death in PC12 cells and hippocampal neurons. **Journal of Molecular Signaling 5:17**.
13. Kasiappan R, Shih HJ, Wu MH, Choy CO, Lin TD, Chen L. **Hsu HL.* (*corresponding author)**. (2010) The antagonism between MCT-1 and p53 affects the tumorigenic outcomes. **Molecular Cancer 9:311.**
14. Wu CL, Chou Y.H, Chang YJ, Teng NY, **Hsu HL**, Chen L. (2012) Interplay between cell migration and neurite outgrowth determines SH2B1β-enhanced neurite regeneration of differentiated PC12 cells. PLoS One. 7:e34999.
15. Shih HJ, Chu KL, Wu MH, Wu PH, Chang WW, Chu JS, Wang LH, Takeuchi H, Ouchi T, **Hsu HL*(*corresponding author)**. (2012) The involvement of MCT-1 oncoprotein in inducing mitotic catastrophe and nuclear abnormalities. **Cell Cycle. 11: 934-952.**
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17. Wu MH, Chen YA, Chen HH, Chang KW, Chang IS, Wang LH, **Hsu HL* (*corresponding author)**. MCT-1 expression and PTEN deficiency synergistically promote neoplastic multinucleation through the Src/p190B signaling activation. **Oncogene. 2014. 33:5109-20.**

Technical Session D2-W2-T4: Medicine and Life Sciences, Biological and Biomedical Sciences

p53 negative regulators induce hepatic steatosis in zebrafish

Guor Mour Her

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ABSTRACT

p53 negative regulators (YY1,gankyrin,mdm2, Cop1 及 pirh2) had been confirmed to be overexpressed in hepatocellular carcinoma (HCC). Although relevant literature has reported on gankyrin functions in cellular proliferation and tumorigenesis, the steatohepatitic function of p53 negative regulators is poorly understood in animal model systems. The pathogenesis of fatty liver disease remains largely unknown. Here, we assessed the importance of hepatic fat accumulation on the progression of hepatitis in zebrafish by liver specific expression of p53 negative regulators. Transgenic zebrafish lines, P53Xs, which selectively express the P53X transgene (GFP-fused P53X gene) in liver, were established. P53X Liver phenotypes were evaluated by histopathology and molecular analysis of fatty acid (FA) metabolism-related genes expression. Most P53Xs (66~81%) displayed obvious emaciation starting at 4 months old. Over 99% of the emaciated P53Xs developed hepatic steatosis or steatohepatitis, which in turn led to liver hypoplasia. The liver histology of P53Xs displayed steatosis, lobular inflammation, and balloon degeneration, similar to non-alcoholic steatohepatitis (NASH). Oil red O stain detected the accumulation of fatty droplets in P53Xs. RT-PCR and Q-rt-PCR analysis revealed that P53X induced hepatic steatosis had significant increases in the expression of lipogenic genes, C/EBP-a, SREBP1, ChREBP and PPAR-g, which then activate key enzymes of the de novo FA synthesis, ACC1, FAS, SCD1, AGAPT, PAP and DGAT2. In addition, the steatohepatitic P53X liver progressed to liver degeneration and exhibited significant differential gene expression in apoptosis and stress. The P53X models exhibited both the genetic and functional factors involved in lipid accumulation and steatosis-associated liver injury. In addition, P53Xs with transmissible NASH-like phenotypes provide a promising model for studying liver disease.

BIOGRAPHY

I received my phD degree in Human Genetics at University of Edinburgh in 1998 ., I started post-Doc training at the University of Pennsylvania between 1998 and 2000 and at the institute of Zoology, Academia Sinica Between 2001 and 2004. I joined the Institute of Bioscience and Biotechnology Department of Life Science of National Taiwan Ocean University (NTOU) as a assistant professor in 2004 . In 2013, I joined the professor at the NTOU. I am interested in generating the “heritable metabolic disease models” and gain insight into the underlying the molecular pathogenesis of lipogenic signaling pathways, especially p53 and PPAR-damma signaling, leading to the steatohepatitis and tumor formation (early pre-neoplastic features). We

also use the “disease” transgenic zebrafish models in combination with the use of small molceules to screen for new anti-cancer drugs.

Present Appointment:

1. Professor, Institute of Bioscience and Biotechnology, National Taiwan Ocean University

Career Highlight: (in the past 5 years)

Aug. 2004-July 2008 Institute of Bioscience and Biotechnology Department of Life Science National Taiwan Ocean University (海大生技所)

Associate Professor
Aug. 2008-July 2013 Institute of Bioscience and Biotechnology Department of Life Science National Taiwan Ocean University (海大生技所)

Professor
Aug. 2013-present Institute of Bioscience and Biotechnology Department of Life Science National Taiwan Ocean University (海大生技所)

Award:

2002 Outstanding Poster Award of Institute of Zoology, Academia Sinica

2002 2002 Genomic Research Award for promising young scientist

2003 Distinguished Achievement in Poster Award of the 18th Joint Annual Conference of Biomedical Sciences in Taipei

2003 Outstanding Poster Award of the 3th Fall Camp for Era of Functional Genomics from Biomics, Virus Infection to protein Structure & Function, Taiwan Society for Biochemistry and Molecular Biology.

2012 Outstanding research Award of College of Life Science NTOU

2014 Excellent research Award of NTOU

Academic memberships:

The Chinese Society of Cell and Molecular Biology
Taiwan Marine Biotechnology Society)
Taiwan Developmental Biology Society)

Invited grants of reviewers for Taiwan national research council:
2000-present

Invited International Journals reviewers:

Editorial Board Member of Journal of Coastal Life Medicine (ELSEVIER Journal)
Guest Editor Invitation : Journal of Pharmacology & Clinical Toxicology
Journal of Fish Biology
Journal of Molecular Sciences
Cellular and Molecular Life Sciences (CMLS)

Disease Models & Mechanisms (DMM)
METHODS
PLOS ONE
Marine Biotechnology
Zebrafish
Gene
Journal of Marine Science and Technology
HISTOLOGY AND HISTOPATHOLOGY

Technical Session D2-W2-T4: Medicine and Life Sciences, Biological and Biomedical Sciences

"Translational bioinformatics: from information integration to in silico discovery"

Ueng-Cheng Yang

Associate Professor, Institute of Biomedical Informatics
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ABSTRACT

BIOGRAPHY

Technical Session D2-W2-T4: Medicine and Life Sciences, Biological and Biomedical Sciences

Roles of RBFOX3/NeuN in Epilepsy and Cognitive Impairments

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ABSTRACT

RBFOX3 deletions or mutations are associated with epilepsy and cognitive impairments, but the underlying mechanisms of these disorders is poorly understood. Here we show replication of human symptoms in Rbfox3 knockout mice. Rbfox3 knockout mice displayed increased seizure susceptibility, defective spatial acquisition and reversal learning, and decreased anxiety-related behaviors. Concentrating on hippocampal phenotypes, we found Rbfox3 knockout mice displayed increased expression of plasticity genes Arc and Egr4, and the synaptic transmission and plasticity were defective in the mutant perforant pathway. The mutant dentate granules cells exhibited an increased frequency, but normal amplitude, of excitatory synaptic events, and this change was associated with an increase in the neurotransmitter release probability and dendritic spine density. Taken together, our findings validate anatomical and functional abnormality in Rbfox3 knockout mice, and may offer mechanistic insights for human brain disorders with dysfunctional RBFOX3.

BIOGRAPHY

Born and raised in Taiwan, Dr. **Hsien-Sung Huang** received his B.S. degree in pharmacy in 1998 at Taipei Medical University and his M.S. degree in biochemistry and molecular biology in 2000 at National Taiwan University. Dr. Huang went to earn his Ph.D. degree in neuroscience at the University of Massachusetts Medical School in 2008 in the laboratory of Dr. Schahram Akbarian. His thesis work has provided important insight into how chromatin remodeling at GABAergic gene promoters could contribute to the etiology of schizophrenia. **Dr. Huang** finished his postdoctoral training in 2012 in the laboratory of Dr. Benjamin Philpot in the department of Cell Biology and Physiology, School of Medicine, University of North Carolina at Chapel Hill. He identified the first compound unsilencing the paternal allele of the ubiquitin protein ligase E3A (*Ube3a)*. Deletion or mutation of the maternal allele of *UBE3A* causes Angelman syndrome, which is a severe neurodevelopmental disorder. No effective treatment exists for Angelman syndrome. His work was thus the first to demonstrate a targeted small molecule approach for activating a disease-related imprinted gene. This finding is likely to transform the approaches that pharmaceutical industries are taking to ameliorate diseases associated with inappropriate gene silencing (e.g. imprinting disorders). His discovery was published on ***Nature*** and highlighted in reviews of ***Nature***, ***Science***, ***Nature Reviews Neurology***, ***Scientist***, NIMH's Top 10 Research Advances in 2011 and Faculty of 1000. Dr. Huang has been an assistant professor since 2013 in the Graduate Institute of Brain and Mind Sciences, College of Medicine, National Taiwan

University. He was the recipient of the NARSAD Young Investigator Award, FAOS Young Scholars' Creativity Award, NHRI Career Development Award, Essel Investigator, UNC Postdoctoral Award for Research Excellence, Keystone Symposia Scholarship, Julius Axelrod Lecture Travel Award, NC TraC$10K and $2K Award. His current research interest is to investigate the genomic flexibility and diversity in the brain and its implications in neurological and psychiatric disorders.

Birth place and date: Taiwan, Oct. 15, 1976

Education

INSTITUTION AND LOCATION	DEGREE	YEAR(s)	FIELD OF STUDY
Taipei Medical University, Taipei, Taiwan (3.7/4.0)	B.S.	1994-1998	Pharmacy
National Taiwan University, Taipei, Taiwan (3.7/4.0)	M.S.	1998-2000	Biochemistry
University of Massachusetts Medical School, Worcester, MA (3.6/4.0)	Ph.D.	2003-2008	Neuroscience
University of North Carolina, Chapel Hill, NC	Postdoc.	2008-2012	Neuroscience

Position

2000-2002 Military Instructor, Division of Health Service, Army Logistics School, Taipei, Taiwan

2002-2003 Research Assistant, Institute of Biomedical Sciences, Academia Sinica, Taipei, Taiwan

2008-2012 Postdoctoral Fellow, Department of Cell and Molecular Physiology, University of North Carolina School of Medicine, Chapel Hill, NC

2013- Assistant Professor, Graduate Institute of Brain and Mind Sciences, College of Medicine, National Taiwan University, Taipei, Taiwan

Honors and Awards

2009-2011 NARSAD Young Investigator Award
2009-2010 Essel Investigator
2009-2010 NCTraC$2K Award
2009-2010 NCTraC$10K Award
2010-2011 NCTraC$50K Award
2011 Keystone Symposia Scholarship
2012 UNC Postdoctoral Award for Research Excellence
2012 Julius Axelrod Lecture Travel Award
2013-2016 The Young Scholars' Creativity Award (FAOS)
2014-2017 Career Development Grant (NHRI)

Publications

Papers: 15 Citations: 1411 Years: 9 Cites/year: 157

1. Akbarian S, Huang HS (2006) Molecular and cellular mechanisms of altered GAD1/GAD67 expression in schizophrenia and related disorders. Brain Res Rev 52:293-304.

2. Huang HS, Matevossian A, Jiang Y, Akbarian S (2006) Chromatin immunoprecipitation in postmortem brain.
J Neurosci Methods 156:284-292.

3. Huang HS, Matevossian A, Whittle C, Kim SY, Schumacher A, Baker SP, Akbarian S (2007) Prefrontal dysfunction in schizophrenia involves mixed-lineage leukemia 1-regulated histone methylation at GABAergic gene promoters. J Neurosci 27:11254-11262.
(Highlighted in Nature Reviews Neuroscience, Nature Clinical Practice Neurology, Journal of Neuroscience, National Institute of Health (NIH) and National Institute of Mental Health (NIMH) websites)

4. Huang HS, Akbarian S (2007) GAD1 mRNA expression and DNA methylation in prefrontal cortex of subjects with schizophrenia. PLoS One 2:e809.

5. Jiang Y, Matevossian A, Huang HS, Straubhaar J, Akbarian S (2008) Isolation of neuronal chromatin from brain tissue. BMC Neurosci 9:42.

6. Mellios N, Huang HS, Grigorenko A, Rogaev E, Akbarian S (2008) A set of differentially expressed miRNAs, including miR-30a-5p, act as post-transcriptional inhibitors of BDNF in prefrontal cortex.
Hum Mol Genet 17:3030-3042.

7. Mellios N*, Huang HS*, Baker SP, Galdzicka M, Ginns E, Akbarian S (2009) Molecular determinants of dysregulated GABAergic gene expression in the prefrontal cortex of subjects with schizophrenia.
Biol Psychiatry 65:1006-1014.
(*Both authors contributed equally to this work)(the 3rd ranking paper of the nomination for the Ziskind Somerfeld Research Award)

8. Akbarian S, Huang HS (2009) Epigenetic regulation in human brain-focus on histone lysine methylation.
Biol Psychiatry 65:198-203.

9. McCoy PA, Huang HS, Philpot BD (2009) Advances in understanding visual cortex plasticity. Curr Opin Neurobiol 19:298-304.

10. Qin J, Van Buren D, Huang HS, Zou L, Mostoslavsky R, Akbarian S, Hock H (2010) Chromatin Protein L3mbtl1 is dispensable for development and tumor suppression in mice. J Biol Chem. 285:27767-75

11. Huang HS, Cheung I, Akbarian S (2010) RPP25 is developmentally regulated in prefrontal cortex and expressed at decreased levels in autism spectrum disorder. Autism Res. 3:153-61.

12. Huang HS, Allen JA, Mabb AM, King IF, Miriyala J, Taylor-Blake B, Sciaky N, Dutton JW, Lee HM, Chen X,
Jin J, Bridges AS, Zylka MJ, Roth BL, Philpot BD (2012) Topoisomerase inhibitors unsilence the dormant allele of Ube3a in neurons. Nature 481:185-189.
(Highlighted in Nature, Science, Nature Reviews Neurology, Action Potential (Nature), Faculty of 1000,
NIMH's Top 10 Research Advances in 2011, Most-viewed articles in 2011 (SFARI), Simons

Foundation Autism Research Initiative website, Autism Speaks website, Angelman Syndrome Foundation website, WRAL website and other media)

13. Huang HS, Burns AJ, Nonneman RJ, Baker LK, Riddick NV, Nikolova VD, Riday. TT, Yashiro K, Philpot BD, Moy SS (2013) Behavioral deficits in an Angelman syndrome model: Effects of genetic background and age. Behavioural Brain Research 243:79-90.

14. King IF, Yandava CN, Mabb AM, Hsiao JS, Huang HS, Pearson BL, Calabrese JM, Starmer J, Parker JS, Magnuson T, Chamberlain SJ, Philpot BD, Zylka MJ (2013) Topoisomerases facilitate transcription of long genes linked to autism. Nature 501:58-62
(Highlighted in Nature, Science Translational Medicine and Faculty of 1000)

15. Huang HS, Yoon BJ, Brooks S, Bakal R, Berrios J, Larsen RS, Wallace ML, Han JE, Chung EH, Zylka MJ, Philpot BD (2014) Snx14 regulates neuronal excitability, promotes synaptic transmission, and is imprinted in the brain of mice. PLoS One 9:e98383

Book chapter
Huang, HS., Philpot, B.D., Jiang, YH. (2013) Epigenetic Therapies in Neurological Diseases. In R.L. Jirtle and F.L. Tyson (Eds.), Environmental Epigenomics in Health and Disease (pp. 167-196). Heidelberg, Germany: Springer

Memberships in Professional Society

2005-present	Member	Society for Neuroscience
2011-present	Member	Society for Biological Psychiatry

Technical Session D2-W2-T4: Medicine and Life Sciences, Biological and Biomedical Sciences

Integrated systems and synthetic biology for cancer research

Hsueh-Fen Juan

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ABSTRACT

Systems biology is creating a new generation of biological research enabled by the genome revolution and provides a systems-level approach to understanding organisms and functional activities of their components by studying underneath complex interactions. The payoff for systems biology research is not only abstract theoretical understanding, but enable to design new biological function via 'synthetic biology'. Integrating systems and synthetic biology offers the opportunity to solve important challenges like eliminating disease. In this talk, I will present our recent work for cancer research via integrated systems and synthetic biology approach.

BIOGRAPHY

Hsueh-Fen Juan was born in 1969, Miao-Li, Taiwan. She received her BS and MS degree in Botany and PhD in Biochemical Sciences from National Taiwan University (NTU) in 1999. She worked as a research scientist in the Japan International Research Center for Agricultural Sciences (Tsukuba, Japan) during 2000-2001 and a postdoctoral research fellow in the Institute of Biological Chemistry, Academia Sinica (Taipei, Taiwan) during 2001-2002.

She started her academic career in the Department of Chemical Engineering, National Taipei University of Technology as an assistant professor and in the Department of Computer Science and Information Engineering at NTU as an adjunct assistant professor in 2002. She moved to NTU in 2004 as an assistant professor in the Department of Life Science and the Institute of Molecular and Cellular Biology. She was promoted to be an associate professor in 2006 and full professor in 2009. Dr. Juan is currently working on cancer systems biology, integrating transcriptomics, proteomics and bioinformatics for biomarker and drug discovery.

Prof. Juan has developed a number of novel methods to advance systems-biology research and applied such approach for drug discovery and elucidating molecular mechanism of drug responses in cancer cells. She has published more than 85 journal papers including prestigious journals such as Briefings in Bioinformatics, Proc. Natl. Acad. Sci. USA, Cancer Research, Nucleic Acids Research, Oncogene, Bioinformatics. She is now the editor of Scientific Reports (Nature Publishing Group), Computational and Mathematical Methods in Medicine (Hindawi Publishing Corporation), PeerJ, PeerJ Computer Science and Stem Cell Treatments

(Publisher Frontiers, joining Nature Publishing Group). She also serves as a reviewer of various journals like Molecular and Cellular Proteomics (ASBMB), Proteomics (Wiley-VCH), BMC Bioinformatics, and has organized several international systems biology and bioinformatics symposiums. She is one of the founders of Center for Systems Biology (NTU), and currently the Board Member in The Taiwan Society for Biochemistry and Molecular Biology, Taiwan Proteomics Society, and Taiwan Bioinformatics and System Biology Society. Since Dr. Juan made significant contributions through systems biology approach to development of methodology and cancer therapy; she received the awards “Taiwan's Ten Outstanding Young Persons” (2008), FY2011 JSPS Invitation Fellowship Program for Research in Japan (2011), K. T. Li Breakthrough Award by Institute of Information and Computing Machinery (2012), and National Science Council (NSC) Award for Special Talents of the Colleges (2010-2015).

Technical Session D2-W3-T4: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Session Chair

Her-Ming Chiueh

Associate Professor, Institute of Biomedical Engineering
National Chiao-Tung University
(交通大學生醫工程研究所闕河鳴教授)

BIOGRAPHY

Technical Session D2-W3-T4: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Wen-Yih Chen

Distinguished Professor, Department of Chemical and Materials Engineering
Institute of Systems Biology and Bioinformatics
National Central University
(中央大學化材系及生物與生物資訊研究所陳文逸特聘教授)

ABSTRACT

BIOGRAPHY

Technical Session D2-W3-T4: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Yen-Wen Lu

Associate Professor, Department of Bio-lndustrial Mechatronics Engineering
National Taiwan University
(臺灣大學生物產業機電工程系盧彥文教授)

ABSTRACT

BIOGRAPHY

Technical Session D2-W3-T4: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Impedimetric Monitoring of Cellular Activities in Microfluidic Systems

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ABSTRACT

Microfluidic system has been attracted attention in the past decade because of its capability of combining engineering and lift science. It is often interpreted to a miniaturized and automatic version of a conventional laboratory. One of the challenges is to implement appropriate sensing mechanism into such a miniaturized environment. Impedimetric sensing provides a real-time, non-invasive, and label-free measurement technique and the sensing output is represented by electrical signal which can easily interface with compact electronic circuit. In this talk, I shall introduce our recent developments in our laboratory, which are impedimetric monitoring of cellular activities including cell proliferation, chemosensitivity, and migration.

BIOGRAPHY

Kin Fong Lei received his B.Eng. in Power Mechanical Engineering from National Tsing-Hua University, Taiwan in 1998 and obtained his M.Phil. and Ph.D. from The Chinese University of Hong Kong in 2000 and 2005, respectively. In 2000, he was invited as a visiting research fellow at Budapest University of Technology and Economics, Hungary. In 2006, he was working at University of Western Ontario, Canada as a post-doctoral fellow. From 2007 to 2010, he was a Lecturer with The Hong Kong Polytechnic University. In 2010, he joined the Graduate Institute of Medical Mechatronics, Chang Gung University, Taiwan. His current research interests include microfluidics, impedimetric bio-sensing, rapid diagnostics, and cancer signaling pathway.

Technical Session D2-W3-T4: Biomaterials, Bio-SoC, Bio-Nanotech, Bio-NEMS/Bio-MEMS, and Biomedical Engineering and Systems

Chihchen Chen

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National Tsing Hua University
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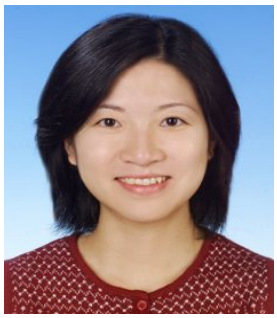
(清華大學奈米工程與微系統研究所陳致真教授)

BIOGRAPHY



Chihchen Chen was born in Taipei, Taiwan. She received her B.S. (1995) and M.S. (1997) in Electrical Engineering from the National Taiwan University. She was an R&D engineer at ASUS Computer Inc., Taiwan from 1997 to 1999. She received her Ph.D. (2006) from the University of Washington at Seattle, WA, with dual degrees in Bioengineering and Nanotechnology. She was a postdoctoral associate at the Massachusetts General Hospital between 2006 and 2009.

Currently she is an Associate Professor of the Institute of NanoEngineering and MicroSystems, Department of Power Mechanical Engineering at the National Tsing Hua University, Hsinchu, Taiwan, where she started her own research group in the summer of 2010. Her areas of expertise and research interests are micro- and nano-fluidic technologies for applications in biology and medicine, with a focus on the isolation and characterization of the cellular and sub-cellular components.

Dr. Chen is a member of the International Society for Extracellular Vesicles, and a member on the Product Advisory Board of Journal of Visualized Experiments (JoVE).

Technical Session D2-W4-T4: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Session Chair

Shuenn-Yuh Lee

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Email: ieesyl@mail.ncku.edu.tw
(成功大學電機工程學系李順裕教授)

BIOGRAPHY

Shuenn-Yuh Lee was born in Taichung, Taiwan, in 1966. He received the B.S. degree from the National Taiwan Ocean University, Keelung, Taiwan, in 1988, and the M.S. and Ph.D. degrees from the National Cheng Kung University, Tainan, Taiwan, in 1994 and 1999, respectively.

He was an Associate Professor from 2006 and Professor from 2011, respectively, at the Department of Electrical Engineering, National Chung Cheng University, Chia-Yi, Taiwan. He is currently a Professor at the Department of Electrical Engineering, National Cheng Kung University, Tainan, Taiwan. He served as the Chairman of Heterogeneous Integration Consortium (HIC) under the VLSI Educational Program sponsored by Ministry of Education, Taiwan, from 2009 to 2011. He served as the Technical Program Chair (TPC) of the 2011/2014/2015 International Symposium on Bioelectronics & Bioinformatics (ISBB) and the 2013 IEEE International Conference on Orange Technologies (ICOT), and the Publication Chair for the 2012 IEEE Asia Pacific Conference on Circuits and Systems (APCCAS). His research interests include biomedical circuits and systems design, low-power signal acquisition systems, and wireless healthcare systems. He has published more than 20 papers on IEEE Transctions/Journals.

Dr. Lee is a senior member of IEEE Engineering in Medicine and Biology (EMB) Society, Circuits and Systems (CAS) Society, and Solid-State Circuits (SSC) Society. Moreover, he is a member of IEICE and CIEE. From 2013, he serves as the Chairman of IEEE Solid-State Circuits Society Tainan Chapter.

Technical Session D2-W4-T4: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Intelligent Cloud Computing for Biotechnology via Deep Learning using Algorithm/Architecture Co-Design

Gwo Giun (Chris) Lee

Professor, Department of Electrical Engineering
National Cheng Kung University
(成功大學電機工程學系李國君教授)

ABSTRACT

NIKLAUS EMIL WIRTH introduced the innovative idea that Programming = Algorithm + Data Structure. Inspired by this paradigm, this talk advances this idea to the next level by stating that Design = Algorithm + Architecture. With concurrent exploration of algorithm and architecture entitled Algorithm/Architecture Co-exploration (AAC), a leading paradigm shift in advanced system design which will be incorporated into deep learning systems for big biomedical data analytics.

As computing such as in deep learning becomes exceedingly demanding and data becomes increasingly bigger, efficient parallel and flexible reconfigurable processing are crucial in the design of signal processing systems. Hence the analysis of algorithms for potential computing in parallel, efficient data storage and data transfer is crucial. AAC presents a technique which systematically lays out the full spectrum of potential parallel processing components eigen-decomposed into all possible data granularities. With data dependency minimization, this spectrum of independent graph components is resolved from a particular data granularity into lower and mixed granularities within the design space. This makes possible the study of potentials for homogeneous or heterogeneous parallelization at different granularities as opposed to conventional systolic array for homogeneous designs at single fixed granularity.

Because AAC was targeted for SoC systems with versatile platforms, the scope of system is extensible to be systems connected via signals in conveying information thus forming Internet of Things (IoT). This introduces a fundamental framework for general system design already with major impact to SoC systems and is readily broaden to cloud computing, automated systems such as sensor networks, IoT also including genomic/proteomic signal processing, medical image processing, and physiological signal processing systems via deep learning.

BIOGRAPHY

Gwo Giun (Chris) Lee (S'91-M'97-SM'07) received his B.S. degree in Electrical Engineering from National Taiwan University and both his M.S. and Ph.D. degrees in Electrical Engineering from University of Massachusetts. Dr. Lee has held several technical and managerial positions in the industry including System Architect in former Philips Semiconductors, USA, DSP Architect in Micrel Semiconductors, USA, and Director of Quanta Research Institute, Taiwan before joining the faculty team of the Department of Electrical Engineering in National Cheng Kung University (NCKU) in Tainan, Taiwan where he established the Media SoC Laboratory. He was also a visiting

Professor at "Swiss Federal Institute of Technology" (EPFL), Switzerland during 2007. Dr. Lee has authored more than 200 technical papers and is currently a member of the ISO/IEC MPEG standardization committee and was also the chief editor for the Reconfigurable Video Coding (RVC) Ad Hoc group. He was the Chair for the Complexity Analysis Ad HoC Group of ISO/IEC ITU JVT-3V in 3D Video Coding. Dr. Lee also serves as the Associate Editor for both IEEE Transactions on Circuits and Systems for Video Technology from 2009 till 2013 and Journal of Signal Processing Systems since 2010. He received the Best Associate Editor's Award for IEEE Transactions on Circuits and Systems for Video Technology in 2010 and the Best Paper Award for the BioCAS track in ISCAS 2012. Dr. Lee was also the Guest Editor for IEEE TCSVT's November, 2009 special issue on "Algorithm/ Architecture Co-Exploration for Visual Computing on Emergent Platforms". He is the Chair of the technical committee for "Visual Signal Processing & Communications" track and member of "Multimedia Systems Application" track for IEEE International Symposium on Circuits and Systems (ISCAS). Dr. Lee also serves as the technical committee member for both the Digital Implementation of Signal Processing Systems (DISPS) and the Industry Digital Signal Processing (IDSP) committees for IEEE Signal Processing Society and Circuits and Systems Society. Furthermore, he is currently the Chair of the Signal Processing Systems Track in Asia Pacific Signal and Information Processing Association (APSIPA). His research interests are focused on intelligent and biomedical algorithm, architecture, VLSI/SoC design, and Algorithm/Architecture Co-Exploration (AAC) for signal and information processing systems including cloud computing and Internet of Things.

Technical Session D2-W4-T4: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Facial Status Recognition for Baby Vomit and Drowsy Driver Detections

Chih-Peng Fan

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ABSTRACT

Recently, the birth rate has been reduced in both domestic and foreign societies, and the number of babies and young children is also decreased. Thus, the baby's safety becomes an important issue. Researching and developing an intelligent video-based baby watch and warning system can improve baby's security in indoor and in house environments. When a baby is in an emergency, such as vomits, the video-based watch and warning system can alert and notify parents or caregivers by facial status recognition.

For the past few years, accidents caused by the fatigue driving have occurred frequently. Some useful techniques for detecting driver drowsiness can be generally separated into the following categories: the eye and eyelid movements, the closed eyes period, the physiological state change (e.g. ECG, EEG), the vehicle's behavior (e.g. the driving speed), etc. For the issue of fatigue driver detections, the driver's drowsy status can be evaluated through the closed eyes period and the head gesture condition by facial status recognition.

This talk is an overview of the video-based facial status recognition for baby vomit and drowsy driver detections. For the proposed video-based baby vomit detection, the computational flow includes the eye features detection, the face extraction, the mouth region detection, and the vomit detection. The accuracy detection rate of vomits is up to 88%, and the false positive rate is less than 5%. For the proposed video-based drowsy driver detection, the system is split into two cascaded computational procedures: the driver eyes detection and the drowsy driver detection. The average open/closed eyes detection rates without/with glasses are 94% and 78%, respectively, and the accuracy of the drowsy status detection is up to 91%.

BIOGRAPHY

Chih-Peng Fan received the B.S., M.S., and, and Ph.D. degrees, all in electrical engineering, from the National Cheng Kung University, Taiwan, R.O.C., in 1991, 1993 and 1998, respectively. During October 1998 to January 2003, he was a design engineer with N100, Computer and Communications Research Laboratories (CCL), Industrial Technology Research Institute (ITRI), Hsinchu, Taiwan. In 2003, he joined the faculty of the Department of Electrical Engineering, National Chung Hsing University, Tai-chung, Taiwan, where he is currently a full Professor. He has published more than 80 technical journals and conference papers. His teaching and research interests include digital

video coding, digital image processing, VLSI signal processing, and baseband transceiver design and implementation.

Technical Session D2-W4-T4: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Opportunities and Challenges for Smartphone-based Audiometric Tests and Hearing Aids

Pei-Chun Li

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(馬偕醫學院聽力暨語言治療學系李沛群教授)

ABSTRACT

About one-third of people between the ages of 65 and 74 have hearing loss, and about half the people older than 85 have hearing problems. With the growing elderly population, the impact of having trouble hearing is increasing. The low aural rehabilitation adoption rates probably stem from following obstacles: the accessibility to screening services that can identify individuals with correctable hearing loss, the non-transparent pricing model, inadequate hearing aid features to accommodate communication behavioural changes and the need of integrating multimedia sound sources, and the unsatisfactory sound quality or understanding of speech in certain noisy environments. In addition, the fitting and fine tuning procedures of hearing aids may take several months, and the needs of hearing loss rehabilitation vary greatly and strongly depend on personal preference and corresponding auditory and cognitive capabilities. Thus the hearing impaired people are usually not motivated enough to go through these barriers and are not likely to benefit a lot from current hearing care products and services.

It is not difficult to imagine a new hearing care system of the future in which a smartphone plays a critical role. There are already many smartphone applications (apps) for otoscopic examination, hearing testing, auditory training, rehabilitation counseling, and personalized sound amplification. Other apps provide visual and tactile alerts. The internet and Bluetooth connectivity available on smartphones put the power of self fine-tuning and controlling audio input and output into the hands of users, and provide automated hearing profile and sound processing updates to sound amplification applications. However, whether a smartphone-based application can serve as an alternative treatment option to the traditional product is an issue requires comprehensive consideration. This talk summarizes the effort we have undertaken to answer following two questions:

1. Are these mobile medical applications reliable enough to perform screening tasks or assistive listening functions as medical devices?

2. Is it possible to design new hearing tests that can be conducted in noisy environment with standard earpods?

Our preliminary results indicate that the electro-acoustic performance is acceptable for users with moderately severe hearing loss, though calibration and maintenance procedures are required to provide long-term reliability. It is possible to use supra-threshold measurements such as most comfortable level in noisy environment to estimate the air conduction thresholds

in each ear, and the “anytime, anywhere” characteristics raised the accessibility of the hearing test.

BIOGRAPHY

Pei-Chun Li received his B.Sc. (1992) degree in Electrical Engineering from the National Taiwan University, Taiwan. He received his Ph.D. (2006) from the National Yang-Ming University in Biomedical Engineering. He co-founded Vital-Logic.com and eCareme.com around 1999, and participated in many new business ventures related to eHealth products and services. In 2009, he joined Aescu Technology, a startup with a mission of developing new hearing care service models and self-fitting hearing aids. He was responsible for managing product planning, both software and hardware research and development activities, production engineering, and quality assurance. Currently he is an Assistant Professor of Audiology and Speech-Language Pathology, a faculty member of Mackay Medical College. Dr. Li’s research interests are in the areas of signal processing for assistive listening, speech audiometry, and smartphone-based audiometric tests and aural rehabilitation tools.

Technical Session D2-W4-T4: Wireless, Multimedia and Virtual Reality Health, Biomedical Devices and Sensing Systems, Cyber Security, and the Internet of Things (IoT) for Health

Sao-Jie Chen

Professor, Graduate Institute of Electronics Engineering and
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(台灣大學電機工程學系陳少傑教授)

ABSTRACT

BIOGRAPHY